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P.W. Crous[1,2], M.J. Wingfield[3], T.I. Burgess[4], A.J. Carnegie[5], G.E.St.J. Hardy[4], D. Smith[6], B.A. Summerell[7], J.F. Cano-Lira[8], J. Guarro[8], J. Houbraken[1], L. Lombard[1], M.P. Martín[9], M. Sandoval-Denis[1,69], A.V. Alexandrova[10], C.W. Barnes[11], I.G. Baseia[12], J.D.P. Bezerra[13], V. Guarnaccia[1], T.W. May[14], M. Hernández-Restrepo[1], A.M. Stchigel[8], A.N. Miller[15], M.E. Ordoñez[16], V.P. Abreu[17], T. Accioly[18], C. Agnello[19], A. Agustin Colmán[17], C.C. Albuquerque[20], D.S. Alfredo[18], P. Alvarado[21], G.R. Araújo-Magalhães[22], S. Arauzo[23], T. Atkinson[24], A. Barili[16], R.W. Barreto[17], J.L. Bezerra[25], T.S. Cabral[26], F. Camello Rodríguez[27], R.H.S.F. Cruz[18], P.P. Daniëls[28], B.D.B. da Silva[29], D.A.C. de Almeida[30], A.A. de Carvalho Júnior[31], C.A. Decock[32], L. Delgat[33], S. Denman[34], R.A. Dimitrov[35], J. Edwards[36], A.G. Fedosova[37], R.J. Ferreira[38], A.L. Firmino[39], J.A. Flores[16], D. García[8], J. Gené[8], A. Giraldo[1], J.S. Góis[40], A.A.M. Gomes[17], C.M. Gonçalves[13], D.E. Gouliamova[41], M. Groenewald[1], B.V. Guéorguiev[42], M. Guevara-Suarez[8], L.F.P. Gusmão[30], K. Hosaka[43], V. Hubka[44], S.M. Huhndorf[45], M. Jadan[46], Ž. Jurjević[47], B. Kraak[1], V. Kučera[48], T.K.A. Kumar[49], I. Kušan[46], S.R. Lacerda[50], S. Lamlertthon[51], W.S. Lisboa[17], M. Loizides[52], J.J. Luangsa-ard[53], P. Lysková[54], W.P. Mac Cormack[55], D.M. Macedo[56], A.R. Machado[13], E.F. Malysheva[37], P. Marinho[57], N. Matočec[46], M. Meijer[1], A. Mešić[46], S. Mongkolsamrit[53], K.A. Moreira[22], O.V. Morozova[37], K.U. Nair[58], N. Nakamura[59], W. Noisripoom[53], I. Olariaga[60], R.J.V. Oliveira[13], L.M. Paiva[13], P. Pawar[58], O.L. Pereira[17], S.W. Peterson[61], M. Prieto[62], E. Rodríguez-Andrade[8], C. Rojo De Blas[63], M. Roy[64], E.S. Santos[65], R. Sharma[58], G.A. Silva[13], C.M. Souza-Motta[13], Y. Takeuchi-Kaneko[59], C. Tanaka[59], A. Thakur[58], M.Th. Smith[1], Z. Tkalčec[46], N. Valenzuela-Lopez[8,66], P. van der Kleij[67], A. Verbeken[33], M.G. Viana[65], X.W. Wang[68], J.Z. Groenewald[1]

Key words

ITS nrDNA barcodes
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Abstract Novel species of fungi described in this study include those from various countries as follows: **Antarctica**: *Cadophora antarctica* from soil. **Australia**: *Alfaria dandenongensis* on *Cyperaceae*, *Amphosoma persooniae* on *Persoonia* sp., *Anungitea nullicana* on *Eucalyptus* sp., *Bagadiella eucalypti* on *Eucalyptus globulus*, *Castanediella eucalyptigena* on *Eucalyptus* sp., *Cercospora dianellicola* on *Dianella* sp., *Cladoriella kinglakensis* on *Eucalyptus regnans*, *Cladoriella xanthorrhoeae* (incl. *Cladoriellaceae* fam. nov. and *Cladoriellales* ord. nov.) on *Xanthorrhoea* sp., *Cochlearomyces eucalypti* (incl. *Cochlearomyces* gen. nov. and *Cochlearomycetaceae* fam. nov.) on *Eucalyptus obliqua*, *Codinaea lambertiae* on *Lambertia formosa*, *Diaporthe obtusifoliae* on *Acacia obtusifolia*, *Didymella acaciae* on *Acacia melanoxylon*, *Dothidea eucalypti* on *Eucalyptus dalrympleana*, *Fitzroyomyces cyperi* (incl. *Fitzroyomyces* gen. nov.) on *Cyperaceae*, *Murramarangomyces corymbiae* (incl. *Murramarangomyces* gen. nov., *Murramarangomycetaceae* fam. nov. and *Murramarangomycetales* ord. nov.) on *Corymbia maculata*, *Neoanungitea eucalypti* (incl. *Neoanungitea* gen. nov.) on *Eucalyptus obliqua*, *Neoconiothyrium persooniae* (incl. *Neoconiothyrium* gen. nov.) on *Persoonia laurina* subsp. *laurina*, *Neocrinula lambertiae* (incl. *Neocrinulaceae* fam. nov.) on *Lambertia* sp., *Ochroconis podocarpi* on *Podocarpus grayae*, *Paraphysalospora eucalypti* (incl. *Paraphysalospora* gen. nov.) on *Eucalyptus sieberi*, *Pararamichloridium livistonae* (incl. *Pararamichloridium* gen. nov., *Pararamichloridiaceae* fam. nov. and *Pararamichloridiales* ord. nov.) on *Livistona* sp., *Pestalotiopsis dianellae* on *Dianella* sp., *Phaeosphaeria gahniae* on *Gahnia aspera*, *Phlogicylindrium tereticornis* on *Eucalyptus tereticornis*, *Pleopassalora acaciae* on *Acacia obliquinervia*, *Pseudodactylaria xanthorrhoeae* (incl. *Pseudodactylaria* gen. nov., *Pseudodactylariaceae* fam. nov. and *Pseudodactylariales* ord. nov.) on *Xanthorrhoea* sp., *Pseudosporidesmium lambertiae* (incl. *Pseudosporidesmiaceae* fam. nov.) on *Lambertia formosa*, *Saccharata acaciae* on *Acacia* sp., *Saccharata epacridis* on *Epacris* sp., *Saccharata hakeigena* on *Hakea sericea*, *Seiridium persooniae* on *Persoonia* sp., *Semifissispora tooloomensis* on *Eucalyptus dunnii*, *Stagonospora lomandrae* on *Lomandra longifolia*, *Stagonospora victoriana* on *Poaceae*, *Subramaniomyces podocarpi* on *Podocarpus elatus*, *Sympoventuria melaleucae* on *Melaleuca* sp., *Sympoventuria regnans* on *Eucalyptus regnans*, *Trichomerium eucalypti* on *Eucalyptus tereticornis*, *Vermiculariopsiella eucalypticola* on *Eucalyptus dalrympleana*, *Verrucoconiothyrium acaciae* on *Acacia falciformis*, *Xenopassalora petrophiles* (incl. *Xenopassalora* gen. nov.) on *Petrophile* sp., *Zasmidium dasypogonis* on *Dasypogon* sp., *Zasmidium gahniicola* on *Gahnia sieberiana*. **Brazil**: *Achaetomium lippiae* on *Lippia gracilis*, *Cyathus isometricus* on decaying wood, *Geastrum caririense* on soil, *Lycoperdon demoulinii* (incl. *Lycoperdon* subg. *Arenicola*) on soil, *Megatomentella cristata* (incl. *Megatomentella* gen. nov.) on unidentified plant, *Mutinus verrucosus* on soil, *Paraopeba schefflerae* (incl. *Paraopeba* gen. nov.) on *Schefflera morototoni*, *Phyllosticta catimbauensis* on *Mandevilla catimbauensis*, *Pseudocercospora angularis* on *Prunus persica*, *Pseudophialophora sorghi* on *Sorghum bicolor*, *Spumula piptadeniae* on *Piptadenia paniculata*. **Bulgaria**: *Yarrowia parophonii* from gut of *Parophonus hirsutulus*. **Croatia**: *Pyrenopeziza velebitica* on *Lonicera borbasiana*. **Cyprus**: *Peziza halophila* on coastal dunes.

Abstract (cont.)

Czech Republic: *Aspergillus contaminans* from human fingernail. **Ecuador**: *Cuphophyllus yacurensis* on forest soil, *Ganoderma podocarpense* on fallen tree trunk. **England**: *Pilidium anglicum* (incl. *Chaetomellales* ord. nov.) on *Eucalyptus* sp. **France**: *Planamyces parisiensis* (incl. *Planamyces* gen. nov.) on wood inside a house. **French Guiana**: *Lactifluus ceraceus* on soil. **Germany**: *Talaromyces musae* on *Musa* sp. **India**: *Hyalocladosporiella cannae* on *Canna indica*, *Nothophoma raii* from soil. **Italy**: *Setophaeosphaeria citri* on *Citrus reticulata*, *Yuccamyces citri* on *Citrus limon.* **Japan**: *Glutinomyces brunneus* (incl. *Glutinomyces* gen. nov.) from roots of *Quercus* sp. **Netherlands** (all from soil): *Collariella hilkhuijsenii*, *Fusarium petersiae*, *Gamsia kooimaniorum*, *Paracremonium binnewijzendii*, *Phaeoisaria annesophieae*, *Plectosphaerella niemeijerarum*, *Striaticonidium deklijnearum*, *Talaromyces annesophieae*, *Umbelopsis wiegerinckiae*, *Vandijckella johannae* (incl. *Vandijckella* gen. nov. and *Vandijckellaceae* fam. nov.), *Verhulstia trisororum* (incl. *Verhulstia* gen. nov.). **New Zealand**: *Lasiosphaeria similisorbina* on decorticated wood. **Papua New Guinea**: *Pseudosubramaniomyces* gen. nov. (based on *Pseudosubramaniomyces fusisaprophyticus* comb. nov.). **Slovakia**: *Hemileucoglossum pusillum* on soil. **South Africa**: *Tygervalleyomyces podocarpi* (incl. *Tygervalleyomyces* gen. nov.) on *Podocarpus falcatus.* **Spain**: *Coniella heterospora* from herbivorous dung, *Hymenochaete macrochloae* on *Macrochloa tenacissima*, *Ramaria cistophila* on shrubland of *Cistus ladanifer.* **Thailand**: *Polycephalomyces phaothaiensis* on *Coleoptera* larvae, buried in soil. **Uruguay**: *Penicillium uruguayense* from soil. **Vietnam**: *Entoloma nigrovelutinum* on forest soil, *Volvariella morozovae* on wood of unknown tree. Morphological and culture characteristics along with DNA barcodes are provided.

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[1] Westerdijk Fungal Biodiversity Institute, P.O. Box 85167, 3508 AD Utrecht, The Netherlands;
corresponding author e-mail: p.crous@westerdijkinstitute.nl.
[2] Department of Microbiology and Plant Pathology, Forestry and Agricultural Biotechnology Institute (FABI), University of Pretoria, P. Bag X20, Pretoria 0028, South Africa.
[3] Forestry and Agricultural Biotechnology Institute (FABI), University of Pretoria, Pretoria 0002, South Africa.
[4] Centre for Phytophthora Science and Management, Murdoch University, 90 South Street, Murdoch, WA 6150, Australia.
[5] Forest Health & Biosecurity, NSW Department of Primary Industries, Level 12, 10 Valentine Ave, Parramatta, NSW 2150, Locked Bag 5123, Parramatta, NSW 2124, Australia.
[6] Agriculture, Energy & Resources, Agriculture and Rural Division, Department of Economic Development, Jobs, Transport and Resources, Unit 3, 2 Codrington St, Cranbourne, Victoria 3977, Australia.
[7] Royal Botanic Gardens and Domain Trust, Mrs. Macquaries Road, Sydney, NSW 2000, Australia.
[8] Mycology Unit, Medical School and IISPV, Universitat Rovira i Virgili (URV), Sant Llorenç 21, 43201 Reus, Tarragona, Spain.
[9] Departamento de Micología, Real Jardín Botánico-CSIC, Plaza de Murillo 2, 28014 Madrid, Spain.
[10] Lomonosov Moscow State University, Leninskie Gory 1,12, 119234, Moscow, Russia / Joint Russian-Vietnamese Tropical Research and Technological Center, South Branch, Ho Chi Minh City, Vietnam.
[11] Instituto Nacional de Investigaciones Agropecuarias, Estación Experimental Santa Catalina, Panamericana Sur Km 1, Sector Cutuglahua, Pichincha, Ecuador.
[12] Departamento de Botânica e Zoologia, Universidade Federal do Rio Grande do Norte, Natal, Rio Grande do Norte, Brazil.
[13] Departamento de Micologia Prof. Chaves Batista, Universidade Federal de Pernambuco, Recife, Brazil.
[14] Royal Botanic Gardens Victoria, Birdwood Avenue, Melbourne, VIC 3004, Australia.
[15] University of Illinois Urbana-Champaign, Illinois Natural History Survey, 1816 South Oak Street, Champaign, Illinois, 61820, USA.
[16] Escuela de Ciencias Biológicas, Pontificia Universidad Católica del Ecuador, Av. 12 de octubre 1076 y Roca, Quito, Ecuador.
[17] Departamento de Fitopatologia, Universidade Federal de Viçosa, 36570-900, Viçosa, Minas Gerais, Brazil.
[18] Programa de Pós-graduação em Sistemática e Evolução, Universidade Federal do Rio Grande do Norte, Natal, Rio Grande do Norte, Brazil.
[19] Via A. Gramsci 11, 72023 Mesagne (BR), Italy.
[20] Departamento de Ciências Biológicas, Campus Universitário Central, Universidade do Estado do Rio Grande do Norte, Mossoró, Brazil.
[21] Av. Bruselas 2 3B, 33011 Oviedo, Spain.
[22] Programa de Pós-Graduação em Biociência Animal, Universidade Federal Rural de Pernambuco, Recife, Brazil.
[23] Errotari Mycological Society, Laubideta 6, 48200 Durango, Bizkaia, Spain.
[24] P.O. Box 20, Warrington, Otago 9471, New Zealand.
[25] Centro de Ciências Agrárias e Ambientais, Universidade Federal do Recôncavo da Bahia, Rua Rui Barbosa, 710, 44.380-000, Centro, Cruz das Almas, Bahia, Brazil.
[26] Instituto Nacional de Pesquisas da Amazônia, Manaus, Amazonas, Brazil.
[27] Avda. Pozo del Paraguas 14, 06500 San Vicente de Alcántara, Badajoz, Spain.
[28] Departamento de Botánica, Ecología y Fisiologia Vegetal, Universidad de Córdoba, 14071 Córdoba, Spain.
[29] Universidade Federal da Bahia, Salvador, Bahia, Brazil.
[30] Universidade Estadual de Feira de Santana, Av. Transnordestina, S/N – Novo Horizonte, 44036-900, Feira de Santana, Bahia, Brazil.
[31] Instituto de Pesquisas Jardim Botânico do Rio de Janeiro, Pacheco Leão 915, 22460-030, Rio de Janeiro, RJ, Brazil.
[32] Mycothèque de l'Université catholique de Louvain (MUCL, BCCMTM), Earth and Life Institute – ELIM – Mycology, Université catholique de Louvain, Croix du Sud 2 bte L7.05.06, B-1348 Louvain-la-Neuve, Belgium.
[33] Department of Biology, Ghent University, Karel Lodewijk Ledeganckstraat 35, Ghent, Belgium.
[34] Forest Research, Alice Holt Lodge, Farnham, GU10 4LH, Surrey, UK.
[35] Sofia University 'St. Kliment Ohridski', 5 James Bourchier Blvd., Sofia 1164, Bulgaria.
[36] Agriculture Victoria, Department of Economic Development, Jobs, Transport and Resources, AgriBio Centre for AgriBiosciences, 5 Ring Road, La Trobe University, Bundoora, Victoria 3083, Australia.
[37] Laboratory of Systematics and Geography of Fungi, Komarov Botanical Institute of the Russian Academy of Sciences, 197376, 2 Prof Popov Str., St Petersburg, Russia.
[38] Pós-graduação em Biologia de Fungos, Universidade Federal de Pernambuco, Recife, Pernambuco, Brazil.
[39] Instituto de Ciências Agrárias, Universidade Federal de Uberlândia, Minas Gerais, Brazil.
[40] Curso de Graduação em Ciências Biológicas, Centro de Biociências, Universidade Federal do Rio Grande do Norte, Natal, 59078-970, Brazil.
[41] The Stephan Angeloff Institute of Microbiology, Bulgarian Academy of Sciences, G. Bonchev 26, Sofia 1113, Bulgaria.
[42] National Museum of Natural History, 1 Tsar Osvoboditel Blvd., Sofia 1000, Bulgaria.
[43] National Museum of Nature and Science, Tsukuba, Ibaraki, Japan.
[44] Department of Botany, Faculty of Science, Charles University, Benátská 2, 128 01 Prague 2, Czech Republic.
[45] The Field Museum, Department of Botany, 1400 South Lake Shore Drive, Chicago, Illinois, 60605-2496, USA.
[46] Ruđer Bošković Institute, Bijenička cesta 54, HR-10000 Zagreb, Croatia.
[47] EMSL Analytical, Inc., 200 Route 130 North, Cinnaminson, NJ 08077, USA.
[48] Plant Biology and Biodiversity Center, Institute of Botany, Slovak Academy of Sciences, Dúbravská cesta 9, SK-845 23, Bratislava, Slovakia.
[49] The Zamorin's Guruvayurappan College, Kozhikode, Kerala 673014, India.
[50] Departamento de Ciências Biológicas, Universidade Regional do Cariri, Crato, Ceará, Brazil.
[51] Centre of Excellence in Fungal Research, Faculty of Medical Science Naresuan University, Phitsanulok, 65000, Thailand.
[52] P.O. Box 58499, 3734 Limassol, Cyprus.
[53] Microbe Interaction and Ecology Laboratory, BIOTEC, 113 Thailand Science Park, Pathum Thani 12120, Thailand.
[54] Laboratory of Medical Mycology, Department of Parasitology, Mycology and Mycobacteriology Prague, Public Health Institute in Usti nad Labem, Sokolovská 60, 186 00 Prague 8, Czech Republic.
[55] Departamento de Microbiología Ambiental y Ecofisiología, Instituto Antártico Argentino, Buenos Aires, Argentina.
[56] Departamento de Engenharia Florestal, Fundação da Universidade Regional de Blumenau, Blumenau, Santa Catarina, Brazil.

[57] Departamento de Biologia Celular e Genética, Universidade Federal do Rio Grande do Norte, Natal, Rio Grande do Norte, Brazil.
[58] National Centre for Microbial Resource (NCMR), National Centre for Cell Science, S.P. Pune University, Ganeshkhind, Pune, 411 007, Maharashtra, India.
[59] Laboratory of Terrestrial Microbial Ecology, Graduate School of Agriculture, Kyoto University, Kitashirakawa Oiwake-cho, Sakyo-ku, Kyoto 606-8502, Japan.
[60] Aranzadi Society of Sciences, Mycology section, Zorroagagaina 11, P.C. 200014, Donostia-San Sebastián, Basque Country, Spain.
[61] Mycotoxin Prevention and Applied Microbiology Research Unit, Agricultural Research Service, U.S. Department of Agriculture, 1815 North University Street, Peoria, IL 61604, USA.
[62] Área de Biodiversidad y Conservación, Universidad Rey Juan Carlos, c/ Tulipán, P.C. 28933, Móstoles, Madrid, Spain.
[63] IdForest. C/ Curtidores 17, 34004 Palencia, Spain.
[64] Laboratoire Evolution et Diversité Biologique, Université Paul, 118 route de Narbonne, 31062 Toulouse cedex, France.
[65] Departamento de Engenharia Química, Campus Universitário Lagoa Nova, Universidade Federal do Rio Grande do Norte, Natal, Brazil.
[66] Microbiology Unit, Medical Technology Department, Faculty of Health Science, University of Antofagasta, Av. Universidad de Antofagasta s/n, 02800 Antofagasta, Chile.
[67] Dupont Industrial Biosciences, Archimedesweg 30, 2333 CN Leiden, The Netherlands.
[68] State Key Laboratory of Mycology, Institute of Microbiology, Chinese Academy of Sciences, No. 3, 1st Beichen West Road, Chaoyang District, Beijing 100101, China.
[69] Faculty of Natural and Agricultural Sciences, Department of Plant Sciences, University of the Free State, P.O. Box 339, Bloemfontein 9300, South Africa.

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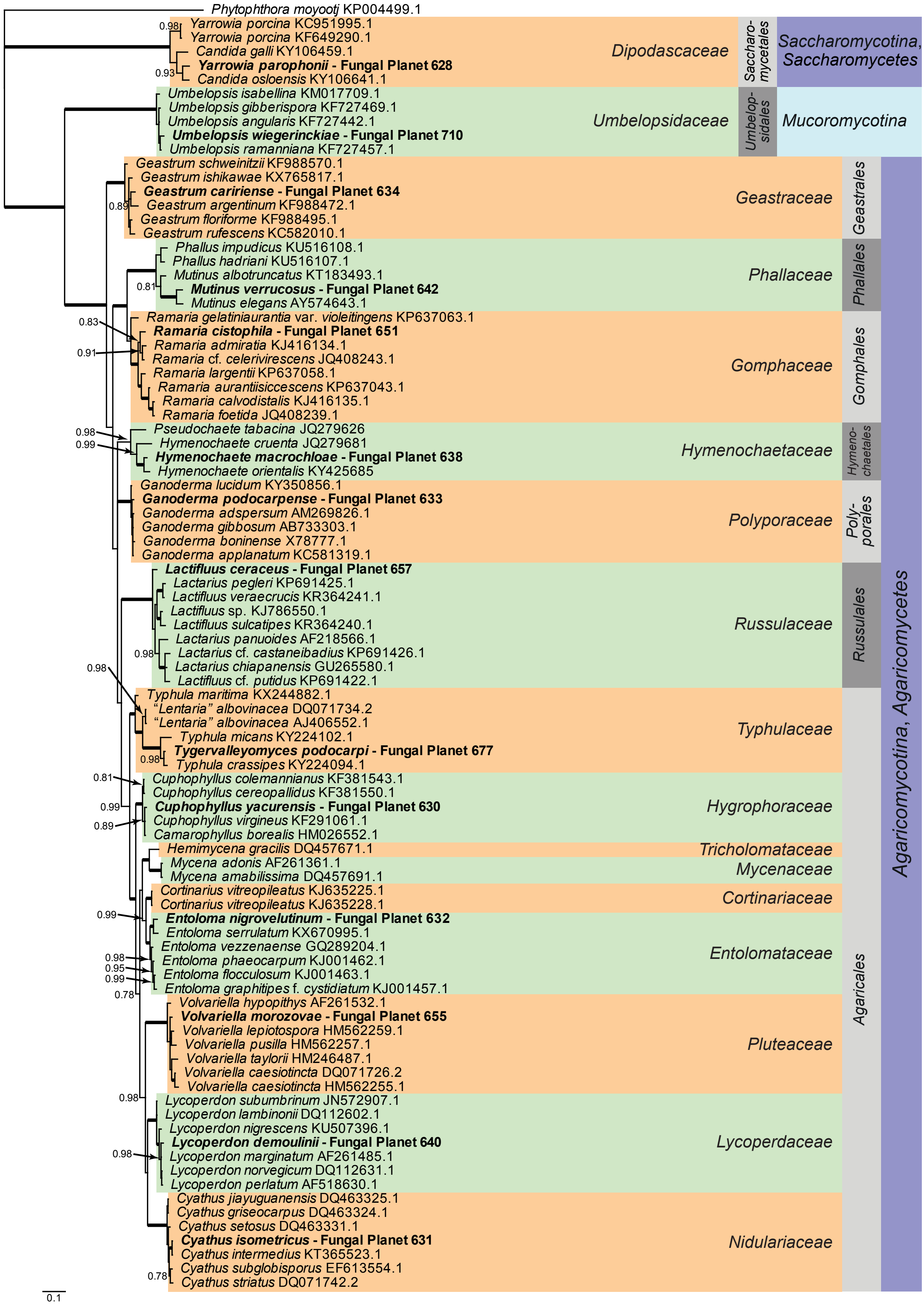
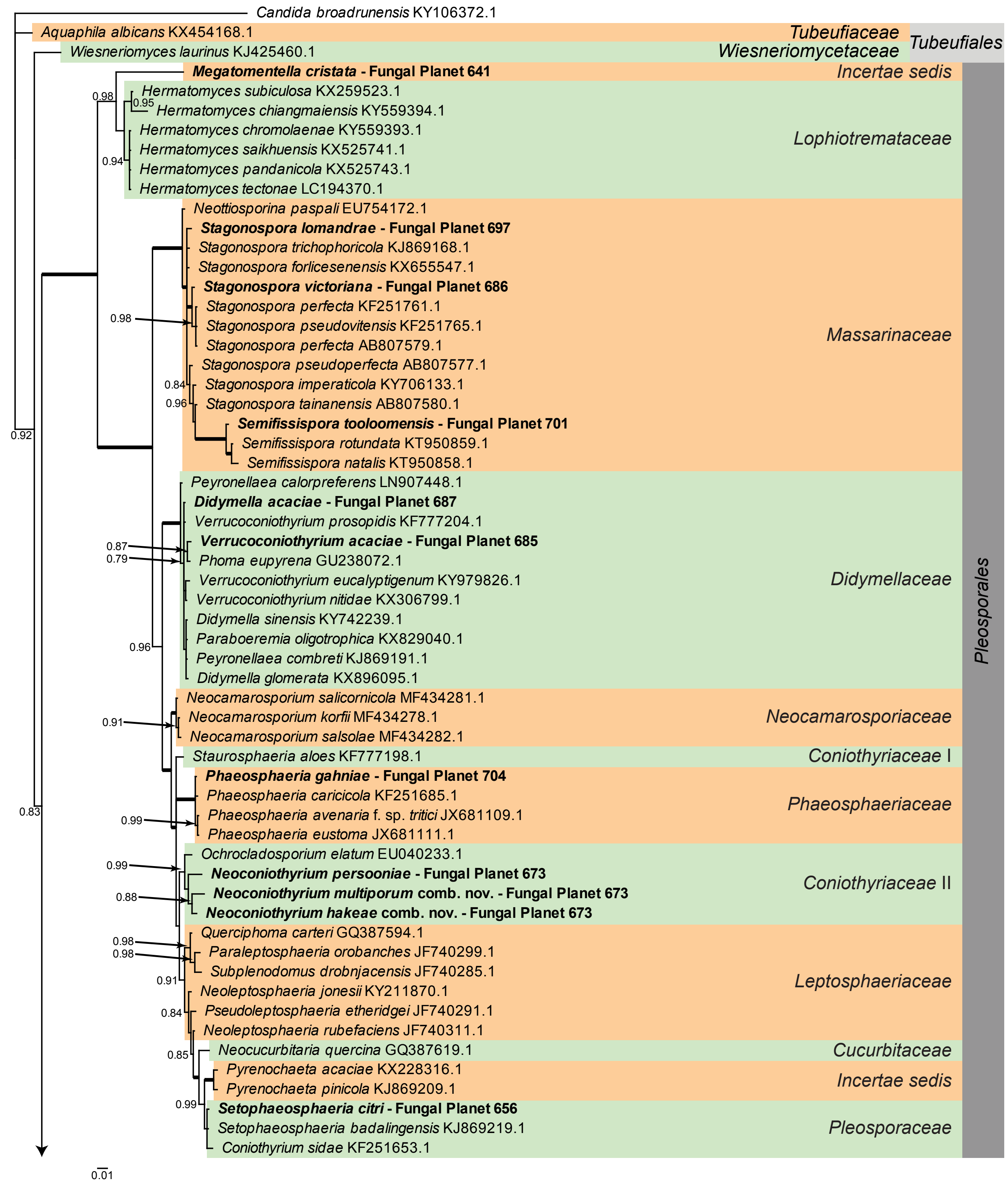


Overview *Saccharomycotina*, *Mucoromycotina* and *Agaricomycotina* phylogeny

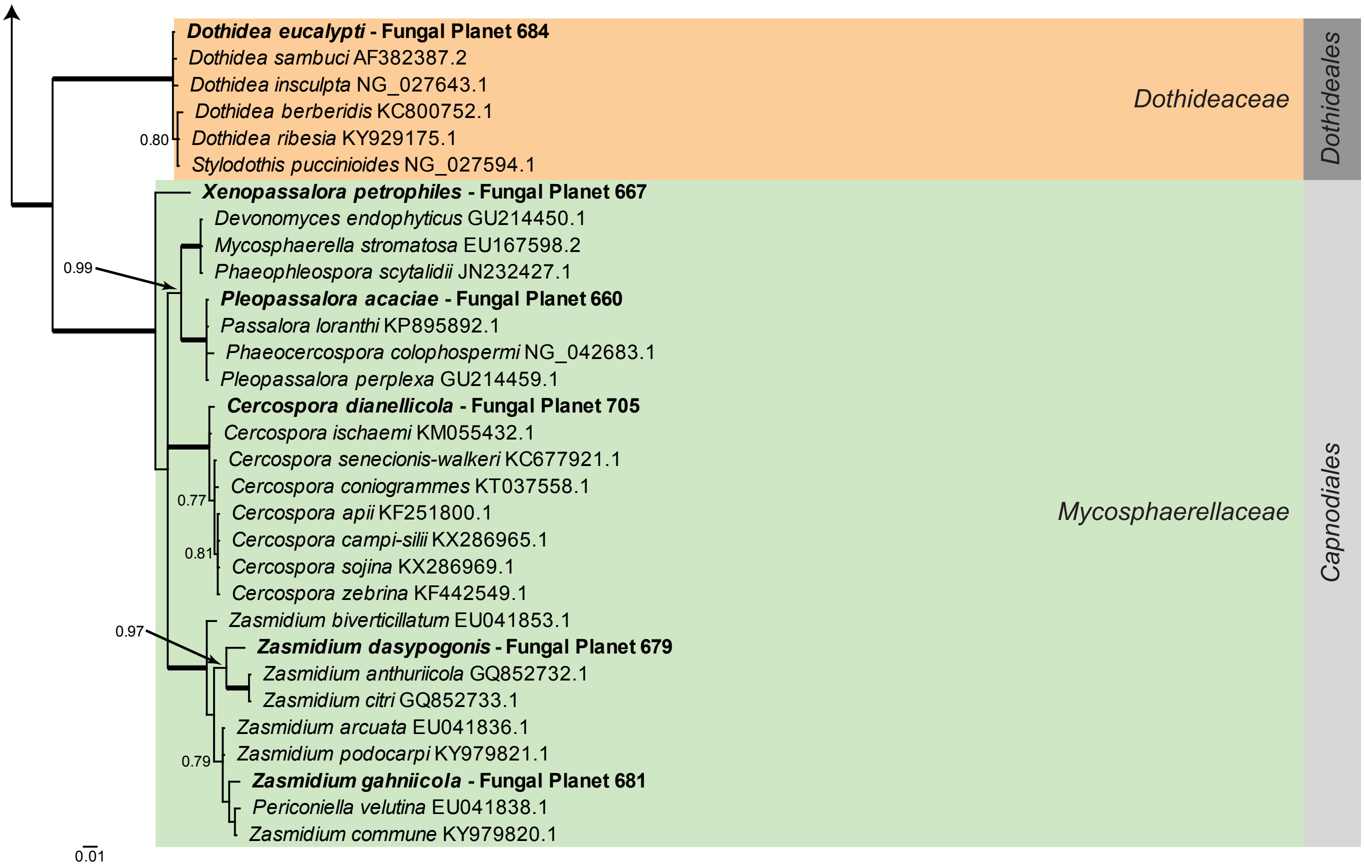
Consensus phylogram (50 % majority rule) of 18 452 trees resulting from a Bayesian analysis of the LSU sequence alignment (92 taxa including outgroup; 616 aligned positions; 426 unique site patterns) using MrBayes v. 3.2.6 (Ronquist et al. 2012). Bayesian posterior probabilities (PP) >0.74 are shown at the nodes and thickened lines represent nodes with PP = 1.00. The scale bar represents the expected changes per site. Families, orders, classes and subdivisions 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 *Phytophthora moyootj* (GenBank KP004499.1) 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 S21807).



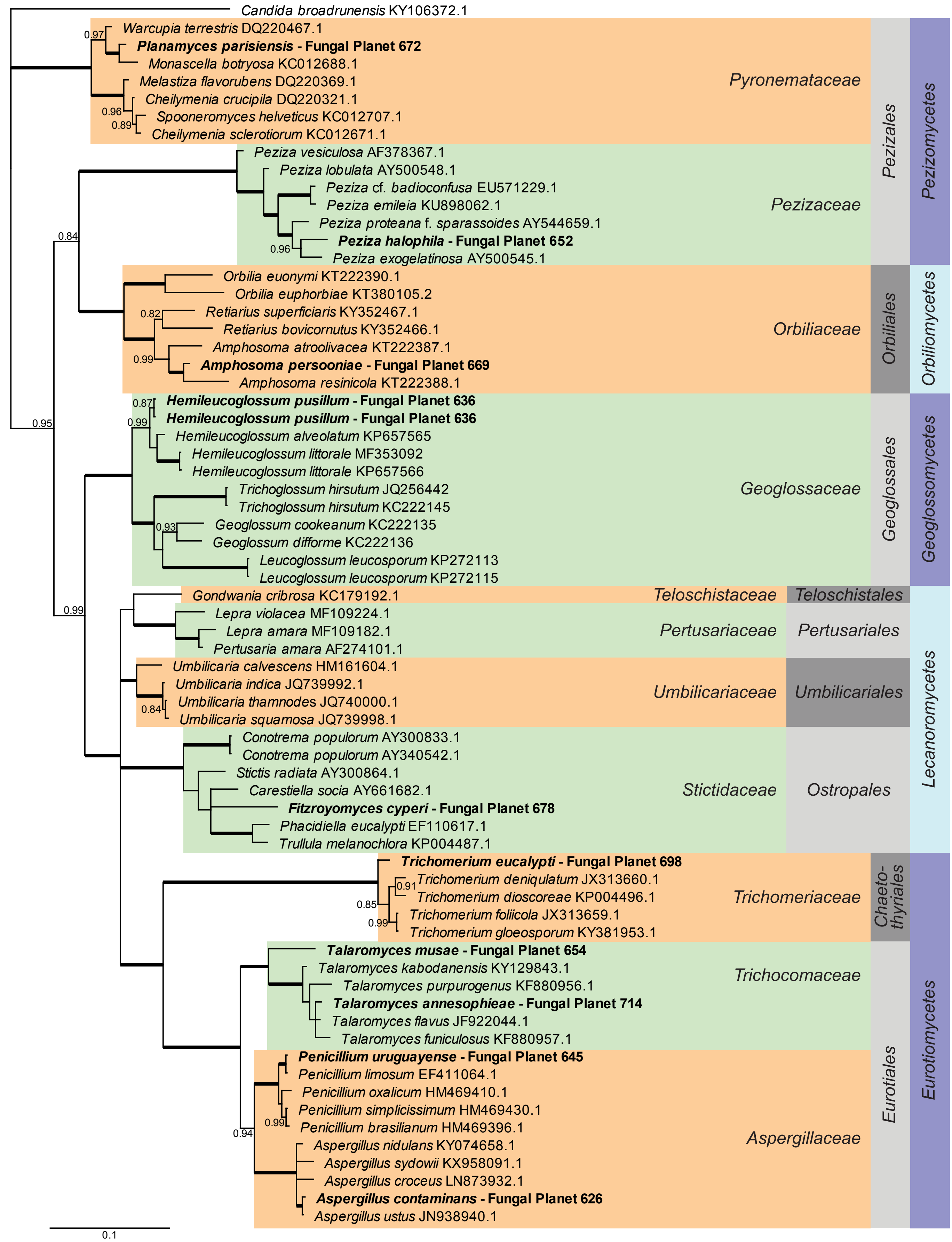
Overview *Dothideomycetes* phylogeny

Consensus phylogram (50 % majority rule) of 80 552 trees resulting from a Bayesian analysis of the LSU sequence alignment (153 taxa including outgroup; 779 aligned positions; 402 unique site patterns) using MrBayes v. 3.2.6 (Ronquist et al. 2012). Bayesian posterior probabilities (PP) >0.74 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 *Candida broadrunensis* (GenBank KY106372.1) 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 S21807).

Overview *Dothideomycetes* phylogeny (cont.)

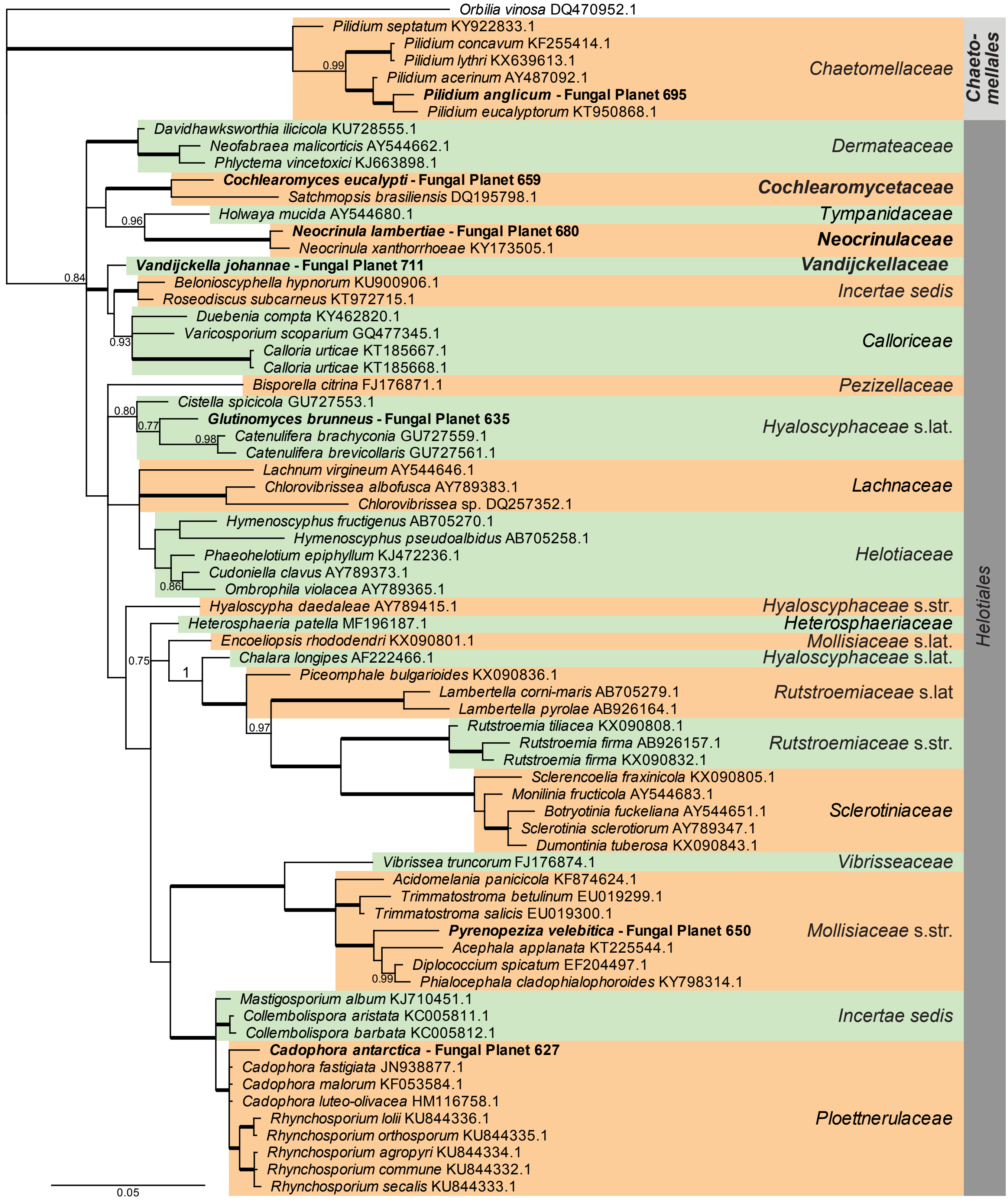


Overview *Dothideomycetes* phylogeny (cont.)



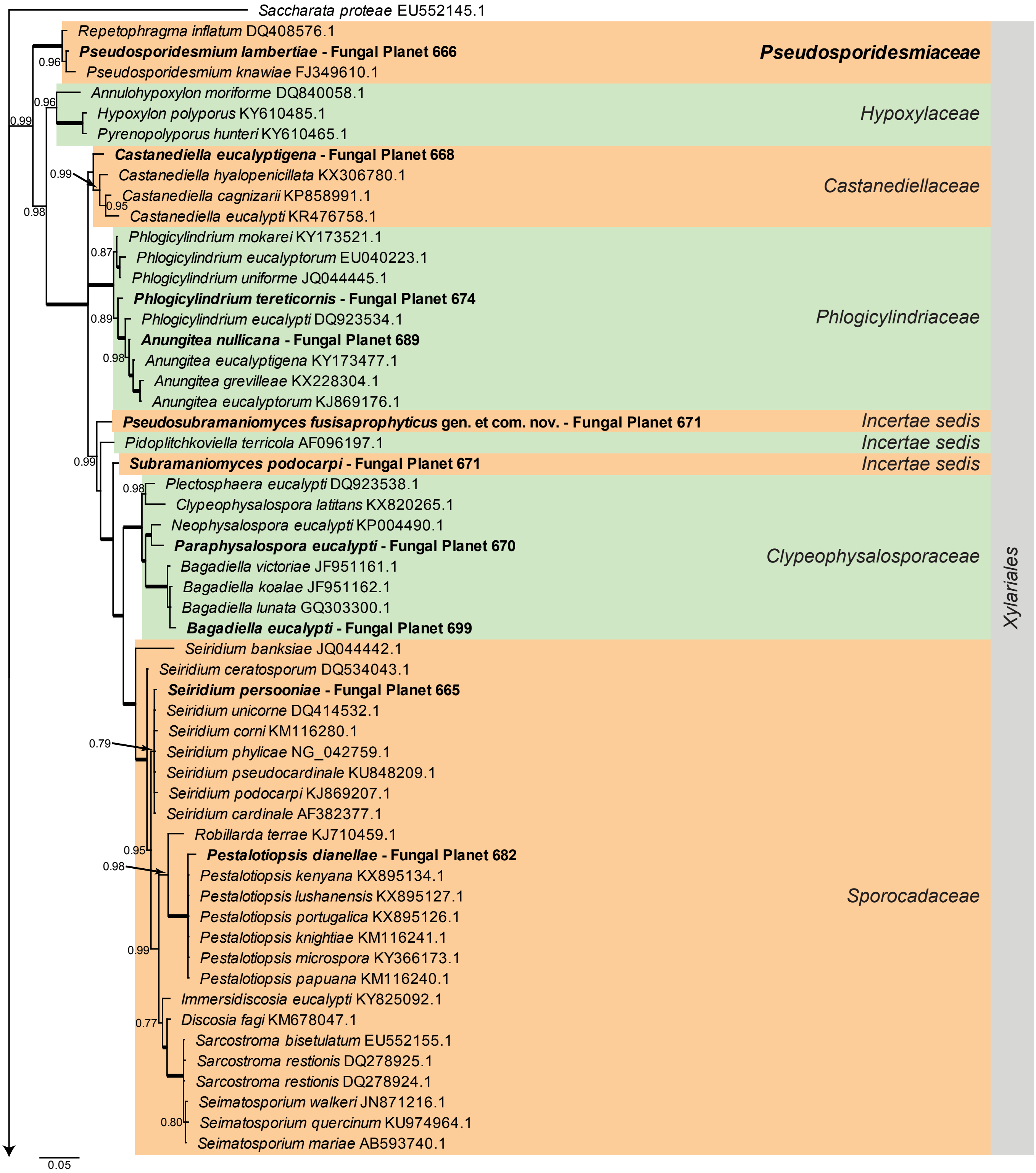
Overview *Pezizomycetes*, *Orbiliomycetes*, *Geoglossomycetes*, *Lecanoromycetes* and *Eurotiomycetes* phylogeny

Consensus phylogram (50 % majority rule) of 5 852 trees resulting from a Bayesian analysis of the LSU sequence alignment (69 taxa including outgroup; 831 aligned positions; 433 unique site patterns) using MrBayes v. 3.2.6 (Ronquist et al. 2012). Bayesian posterior probabilities (PP) >0.74 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 *Candida broadrunensis* (GenBank KY106372.1) 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 S21807).



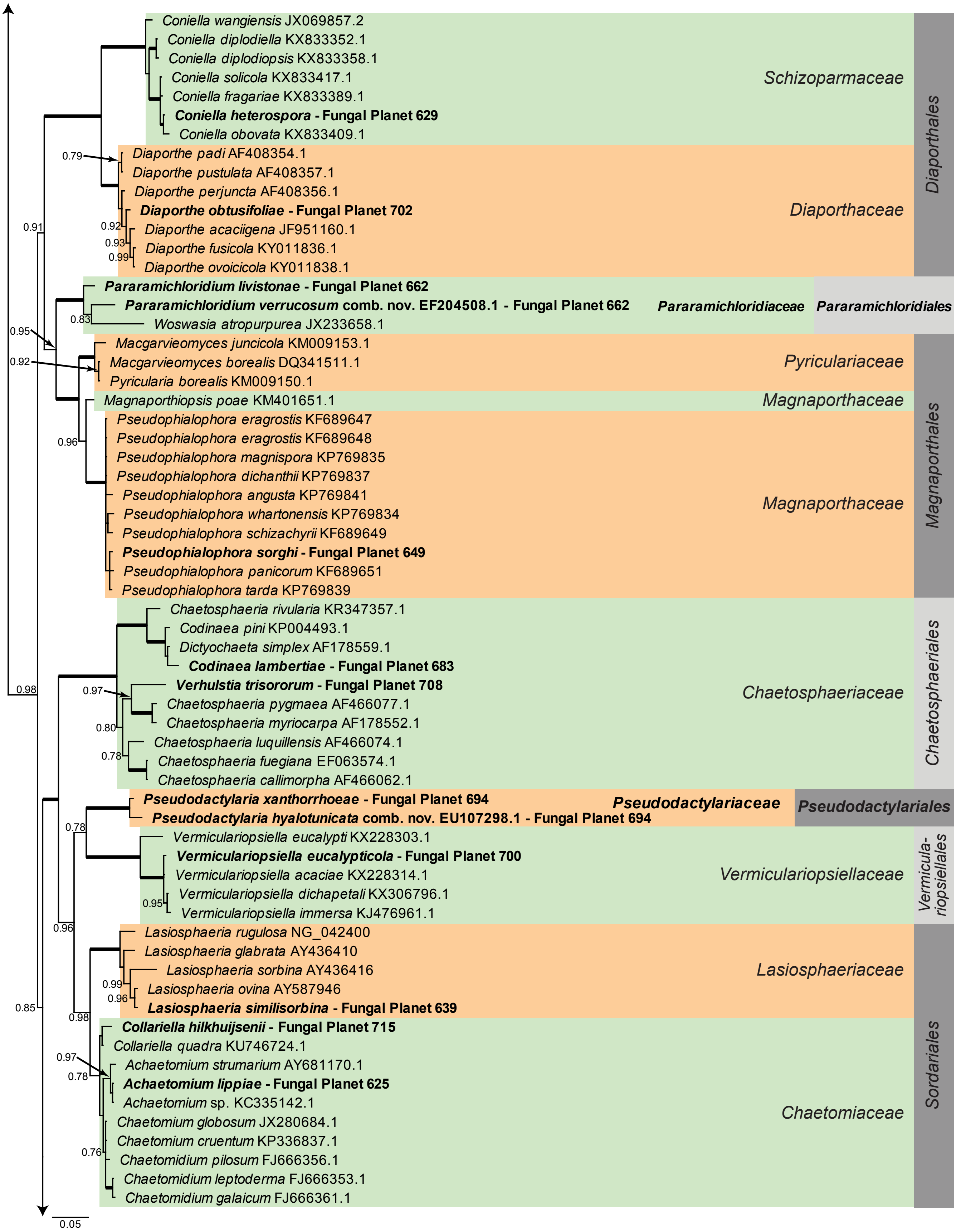
Overview *Leotiomycetes* phylogeny

Consensus phylogram (50 % majority rule) of 140 328 trees resulting from a Bayesian analysis of the LSU sequence alignment (70 taxa including outgroup; 816 aligned positions; 288 unique site patterns) using MrBayes v. 3.2.6 (Ronquist et al. 2012). Bayesian posterior probabilities (PP) >0.74 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 *Orbilia vinosa* (GenBank DQ470952.1) 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 S21807).

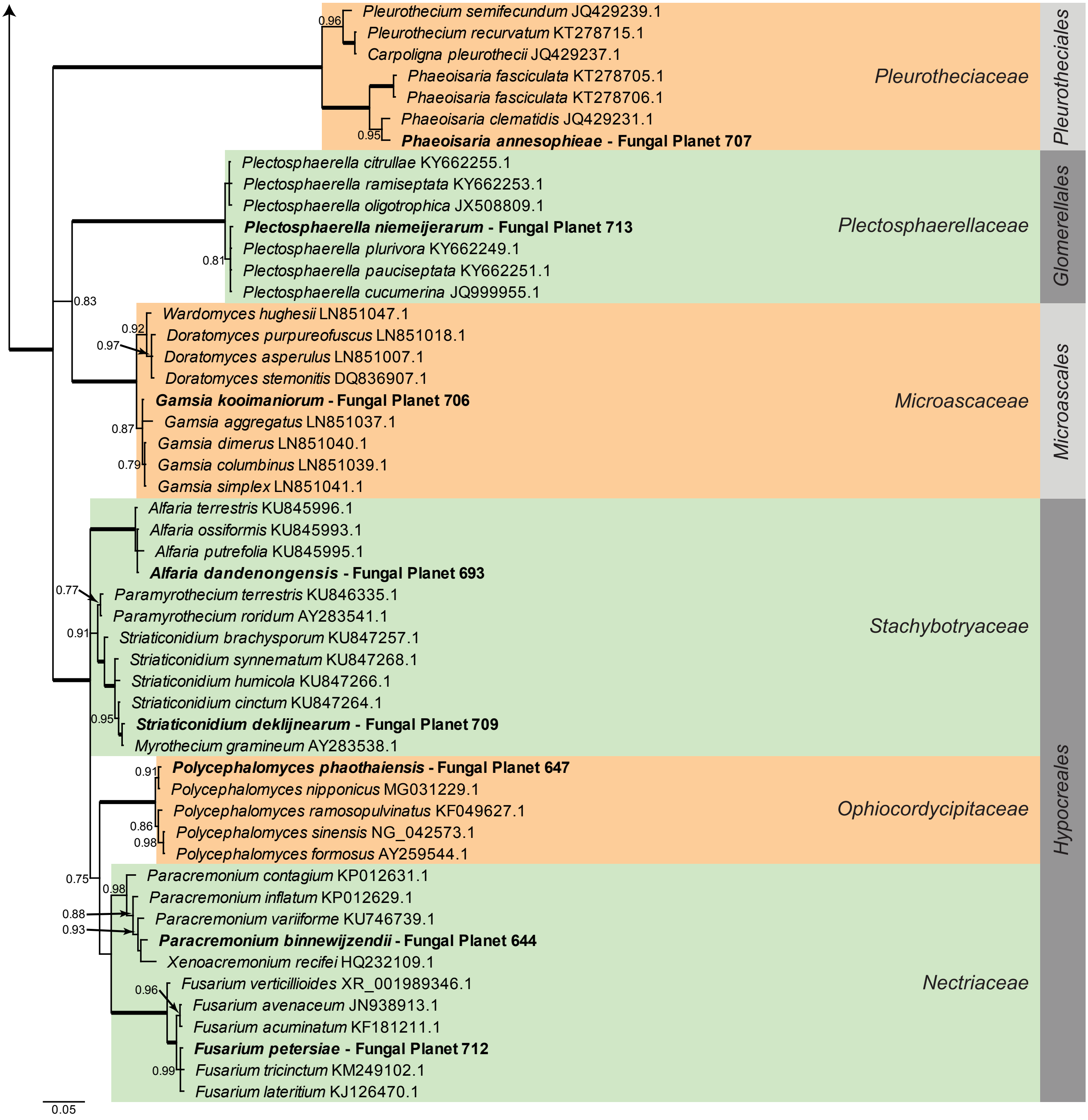


Overview *Sordariomycetes* phylogeny

Consensus phylogram (50 % majority rule) of 30 002 trees resulting from a Bayesian analysis of the LSU sequence alignment (170 taxa including outgroup; 771 aligned positions; 379 unique site patterns) using MrBayes v. 3.2.6 (Ronquist et al. 2012). Bayesian posterior probabilities (PP) >0.74 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 *Saccharata proteae* (GenBank EU552145.1) 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 S21807).



Overview *Sordariomycetes* phylogeny (cont.)



Overview *Sordariomycetes* phylogeny (cont.)


Achaetomium lippiae

Fungal Planet 625 – 20 December 2017

Achaetomium lippiae M.G. Viana, C.C. Albuq., E.S. Santos, J.D.P. Bezerra & L.M. Paiva, *sp. nov.*

Etymology. Name refers to the host plant, *Lippia*, from which this fungus was isolated as endophyte.

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

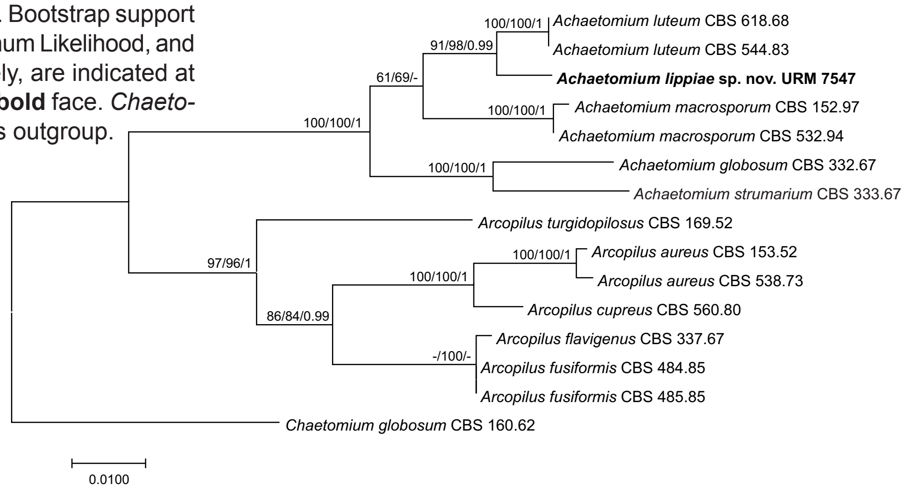
Mycelium subhyaline, septate, 2–3 µm wide hyphae. *Ascomata* superficial and immersed, solitary or gregarious, ostiolate, brown to dark brown, globose to subglobose, 122–160(–256) × 101.5–143(–212) µm. *Ascomatal wall* brown, *textura intricata* or *epidermoidea* in surface view. *Terminal* or *lateral hairs* not observed. *Asci* fasciculate, cylindrical to subcylindrical, 8-spored, soon evanescent, 35–60 × 8–9.5 µm, short-stipitate, without apical structures. *Paraphyses* and *periphyses* not observed. *Ascospores* 1-celled, brown to dark brown, limoniform, 10–16 × 5.5–6.5(–8) µm. *Chlamydospores* brown, globose to subglobose, terminal and intercalary, 10.5–14.5 × 8 µm. *Asexual morph* not observed.

Culture characteristics — Colonies covering Petri dishes after 2 wk at 25 °C. On PDA, colonies with cream to yellowish floccose aerial mycelium, reverse yellowish with centre pale brown. On MEA, colonies are similar to PDA with reverse yellowish to amber. On WA, colonies with sparse growth and whitish mycelium, reverse uncoloured.

Typus. Brazil, Rio Grande do Norte state, Mossoró municipality, Universidade do Estado do Rio Grande do Norte (S5°22'43.85" W37°30'12.25"), as endophyte from *Lippia gracilis* (*Verbenaceae*), Mar. 2015, *M.G. Viana* (holotype URM 90067, culture ex-type URM 7547, ITS, LSU and *BenA* sequences GenBank KY855413, KY855414 and KY855412, MycoBank MB820711).

Notes — According to morphological features and phylogenetic inferences, Wang et al. (2016a, b) demonstrated that *Achaetomium* is a monophyletic lineage in the family *Chaetomiaceae*. Based on our phylogenetic analyses using concatenated ITS, *BenA* and LSU sequences, *A. lippiae* is closely related to *A. luteum*. Based on a megablast search in GenBank, the ITS sequence of *A. lippiae* has 98 % (525/535) similarity to *A. luteum* (CBS 618.68; GenBank KX976571.1), 96 % (519/541) similarity to *A. macrosporum* (CBS 152.97; GenBank KX976573.1), and 95 % (519/541) similarity to *A. strumarium* (CBS 333.67; GenBank NR_144811.1), amongst others. On its LSU sequence, *A. lippiae* is 99 % (792/797) similar to *A. strumarium* (CBS 333.67; GenBank AY681170.1), amongst others. The *BenA* sequence has 95 % (400/423) similarity to *A. luteum* (CBS 618.68; GenBank KX976912.1), 89 % (377/423) similarity to *A. macrosporum* (CBS 152.97; GenBank KX976914.1) and 86 % (420/487) similarity to *A. strumarium* (CBS 333.67; GenBank AY681238.1). Morphologically, *A. lippiae* is different from *A. strumarium* in size of the ascomata ((120–)160–300 µm diam vs 122–159(–256) µm diam in *A. lippiae*), number of ascomatal hairs (3 µm vs absent in *A. lippiae*), size of asci (48–78 × 7–11 µm vs 35–60 × 8–9.5 µm in *A. lippiae*) and ascospores ((10–)11–13(–13.5) × 6–7.5 µm vs 10–16 × 5.5–6.5(–8) µm in *A. lippiae*), and presence of chlamydospores (absent vs present in *A. lippiae*) (Cannon 1986). *Achaetomium lippiae* also differ from *A. luteum* in ascomata size (116.2–182.6 × 99.6–157.7 µm), asci (37–40.7 µm) and ascospores (8.8–10.3 × 3.7–6.6 µm) (Rai et al. 1964); and from *A. macrosporum* in ascomata size (140–290 × 110–210 µm), asci (55–80 × 12–19 µm) and ascospores (16.5–21.5 × 10–13.5 µm) (Cannon 1986).

Maximum likelihood tree obtained by phylogenetic analyses of the combined ITS and LSU rDNA and *BenA* sequences was conducted in MEGA v. 7 (Kumar et al. 2016). Bootstrap support values from Maximum Parsimony and Maximum Likelihood, and Bayesian posterior probabilities, respectively, are indicated at the nodes. The new species is indicated in **bold** face. *Chaetomium globosum* (CBS 160.62) was used as outgroup.



Colour illustrations. *Lippia gracilis* in the Universidade do Estado do Rio Grande do Norte. Ascomata, ascomatal wall, ascus, ascospores, and chlamydospore. Scale bars = 25 µm and 10 µm, respectively.

Marcelino G. Viana & Everaldo S. Santos, Departamento de Engenharia Química, Campus Universitário Lagoa Nova,
Universidade Federal do Rio Grande do Norte, Natal, Brazil; e-mail: bergvianna@hotmail.com & everaldo@eq.ufrn.br
Cynthia C. Albuquerque, Departamento de Ciências Biológicas, Campus Universitário Central,
Universidade do Estado do Rio Grande do Norte, Mossoró, Brazil; e-mail: cycavalcanti@gmail.com
Jadson D.P. Bezerra & Laura M. Paiva, Departamento de Micologia Prof. Chaves Batista,
Universidade Federal de Pernambuco, Recife, Brazil; e-mail: jadsondpb@gmail.com & mesquitapaiva@terra.com.br


Aspergillus contaminans

Fungal Planet 626 – 20 December 2017

Aspergillus contaminans Hubka, Jurjević, S.W. Peterson & Lysková, *sp. nov.*

Etymology. *contaminans* (*con.ta'mi.nans*. L. adj.); contaminating, polluting, referring to the origin of the ex-type strain, which represented a clinical sample contaminant.

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

On MEA: *Stipes* pale brown with age becoming brown, smooth, occasionally finely roughened, (100–)250–600(–800) × 4–7(–8) µm; *conidial heads* radiate to columnar, pale brown to brown; biseriate; *vesicle* nearly globose or pyriform, (12–)15–24(–28) µm diam; *metulae* cylindrical, covering 1/2 to 2/3 (rarely all) of the vesicle, (3–)4–7(–8) × (2.5–)3–4(–5) µm; *phialides* ampulliform, (6–)7–9 × (2–)2.5–3(–3.5) µm; *conidia* globose to subglobose, occasionally ellipsoidal, rough-walled to spinose, green-brown in mass, 3–4(–4.5) µm diam including ornamentation (3.7 ± 0.2), spore body 2.3–3.5 µm diam (2.9 ± 0.2); *Hülle cells* subglobose, ovoid, elongated or irregularly shaped, frequently curved, 15–40(–52) × 8–18(–20) µm, L/W 1.1–3.8 (2.2 ± 0.7).

Culture characteristics — (in the dark, 25 °C after 7 d): Colonies on MEA 32–33 mm diam, sporulating area pale brown to olive-brown, good sporulation, mycelium white to pale yellow, floccose, centrally abundant aggregations of pale yellow Hülle cells, lightly overgrown with hyphae, exudate clear, no soluble pigments, reverse buff. Colonies on CYA 35–36 mm diam, sporulating area greyish brown, poor sporulation, inconspicuous, covered with white to very pale yellow mycelium, lightly floccose to nearly velutinous, radially and concentrically moderately deeply sulcate, pale yellow Hülle cell aggregations at the centre of the colony, exudate clear to pale yellow only at the centre of the colony, no soluble pigments, reverse buff yellow. Colonies on OA 31–32 mm diam, pale brown to brown, sporulation moderately good, mycelium white to pale, floccose, abundant aggregations of pale yellow Hülle cells covered with hyphae, exudate clear to pale brown, no soluble pigments, reverse pale brown. Colonies on PDA 30–31 mm diam, sporulation area pale buff to pale brown, very good sporulation at the centre of the colony, mycelium white to pale yellow, floccose, occasionally radially lightly sulcate, Hülle cells abundant, covered with a mat of hyphae, exudate clear to pale brown, no soluble pigments, reverse buff to pale yellow. Colonies on CY20S 30–31 mm diam, sporulating area brown, poor to good sporulation, mycelium white, floccose, no exudate, no soluble pigments, reverse pale to pale buff. Colonies on CREA growing more slowly compared with other media, 19–20 mm diam, poor sporulation, mycelium white, Hülle cells sparse, no production of acid compounds. No growth on MEA and CYA at 37 °C.

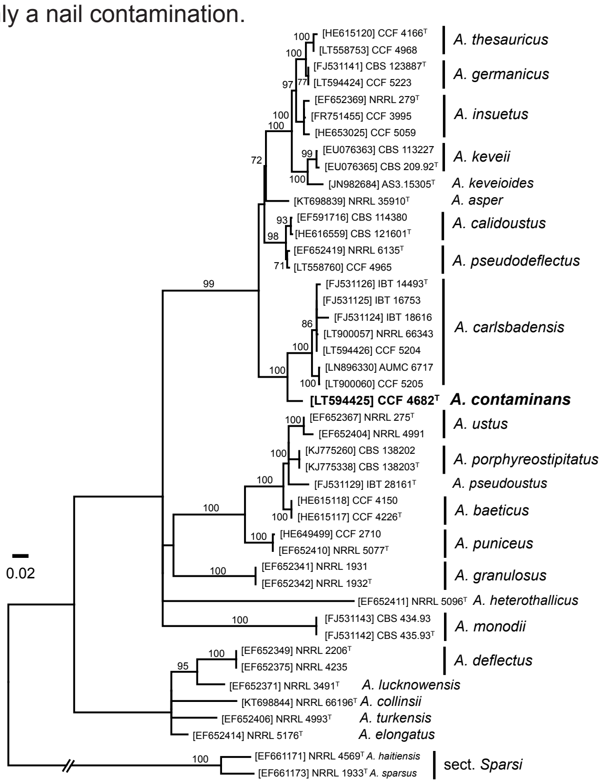
Typus. Czech Republic, Prague, fingernail of 18-yr-old woman (contamination), 2012, isol. *P. Lysková* (holotype PRM 944503, isotype PRM 935097, culture ex-type CCF 4682 = CBS 142451 = NRRL 66666; ITS, LSU, β-tubulin, calmodulin and *rpb2* sequences GenBank LT594451, LT855552, LT594443, LT594425 and LT594434, MycoBank MB821684).

Colour illustrations. Laboratory of Medical Mycology, Prague, Czech Republic where *A. contaminans* was isolated; 7-d-old colonies of *A. contaminans* on MEA; conidia; conidiophores; Hülle cells. Scale bars = 10 µm.

Notes — BLAST analysis with the ITS, β-tubulin, calmodulin and *rpb2* sequences of *A. contaminans* with the reference sequences published by Samson et al. (2014) showed highest hits with *A. carlsbadensis*: ITS 99 %; β-tubulin 97 %; calmodulin 94 %; *rpb2* 97 %.

Aspergillus contaminans belongs to *Aspergillus* sect. *Usti* and is morphologically similar to *A. carlsbadensis*. The two species can be distinguished by growth at 30 °C where *A. contaminans*, after 7 d, attains 2–4 mm on MEA and 4–5 mm on CYA, while *A. carlsbadensis* attains 28–32 mm on MEA and 19–24 mm on CYA.

Aspergillus contaminans was isolated from a fingernail of a Czech patient with mycologically proven onychomycosis caused by the zoophilic dermatophyte *Trichophyton benhamiae*. It was apparently not a cause of onychomycosis but represented only a nail contamination.



A 50 % majority rule consensus maximum likelihood tree calculated from calmodulin sequences showing the relationships of taxa within *Aspergillus* sect. *Usti*. The partitioning scheme and substitution models for analysis were selected using PartitionFinder v. 1.1.1 (Lanfear et al. 2012). The HKY+I model was used for introns, TrN model for the 1st, F81 for the 2nd and HKY+I for the 3rd codon positions. The tree was constructed with IQ-TREE v. 1.4.0 (Nguyen et al. 2015). The dataset contained 45 taxa and a total of 805 characters of which 419 were variable and 360 parsimony-informative. Bootstrap support values at branches were obtained by generating 1000 bootstrap replicates. Only bootstrap support values ≥ 70 % are shown; ex-type strains are indicated by a superscript ^{T}. The tree is rooted with *A. sparsus* NRRL 1933^{T} and *A. haitiensis* NRRL 4569^{T}.

Vit Hubka, Department of Botany, Faculty of Science, Charles University, Benátská 2, 128 01 Prague 2, Czech Republic; e-mail: hubka@biomed.cas.cz
Željko Jurjević, EMSL Analytical, Inc., 200 Route 130 North, Cinnaminson, NJ 08077, USA; e-mail: zjurjevic@emsl.com
Stephen W. Peterson, Mycotoxin Prevention and Applied Microbiology Research Unit, Agricultural Research Service,
U.S. Department of Agriculture, 1815 North University Street, Peoria, IL 61604, USA; e-mail: stephen.peterson@ars.usda.gov
Pavlína Lysková, Laboratory of Medical Mycology, Department of Parasitology, Mycology and Mycobacteriology Prague,
Public Health Institute in Usti nad Labem, Sokolovská 60, 186 00 Prague 8, Czech Republic; e-mail: Pavlina.Lyskova@zuusti.cz

Cadophora antarctica

Fungal Planet 627 – 20 December 2017

Cadophora antarctica Rodr.-Andrade, Stchigel, Mac Cormack & Cano, *sp. nov.*

Etymology. Named after the locality where it was collected, Antarctica.

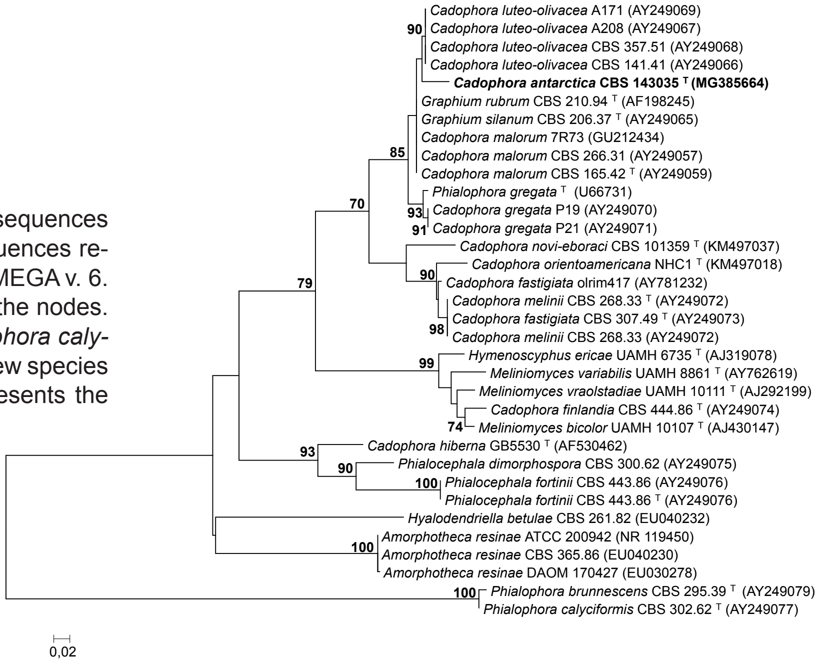
Classification — *Incertae sedis*, *Helotiales*, *Leotiomycetes*, *Pezizomycotina.*

Mycelium composed of hyaline to olivaceous brown, smooth to verrucous, thin- to thick-walled, septate, anastomosing hyphae, 2–4 µm wide. *Conidiophores* mostly reduced to a short chain of ramoconidia on a scar, laterally or terminally disposed on a recurved or compressed coiled hyphae, rarely well-developed, simple, stalked, erect or decumbent, up to 200 µm long, up to 4 µm broad. *Ramoconidia* holoblastic, 0(–1)-septate, brown to dark brown, sometimes inequilaterally coloured, with one side darker than the opposite, in longitudinal chains of up to six, smooth- and thick-walled, lemon-shaped, flask-shaped, clavate or nearly cylindrical, 5–13 × 2–4 µm, with one basal and up to four apical scars. *Conidia* holoblastic, aseptate, brown to dark brown, inequilaterally coloured, with one side darker than the other, disposed in long, simple or ramified chains, with up to four small-sized scars, smooth- and thick-walled, mostly broadly lens-shaped but inequilateral due to one side being more flattened than the other, 4–5 × 3–4 µm.

Culture characteristics — Colonies on MEA after 3 wk at 15 °C reaching 52–54 mm diam, velvety, zonate, successively pale grey (1D1), dark brown (6F4), medium grey (1E1), dark grey (1F1), pale grey (1B1) and greyish brown (5E3) from the centre towards the edge; exudates absent; diffusible pigment absent; sporulation abundant; reverse successively greyish orange (5B3), greyish brown (5E2), grey (7E1) and orange white (5A2) from the centre towards the edge. *Colonies* on OA after 3 wk of incubation at 15 °C 44–45 mm diam, flat, floccose at the centre, greyish brown (6D3) at the centre and brownish orange (5C4) at the edge; exudates absent; diffusible pigment absent; sporulation sparse; reverse greyish brown (6D3) at the centre and pale grey (1D1) at the edge. Minimum temperature of growth, 5 °C; optimum temperature of growth, 15 °C; maximum temperature of growth, 25 °C.

Typus. Antarctica, South Shetland archipelago, King George Island, near to Carlini's Argentinean scientific base, from a diesel-contaminated soil sample, 11 Jan. 2011, *A.M. Stchigel* (holotype CBS H-23211, cultures ex-type CBS 143035 = FMR 16056; ITS and LSU sequences GenBank MG385664 and MG385663, MycoBank MB822232).

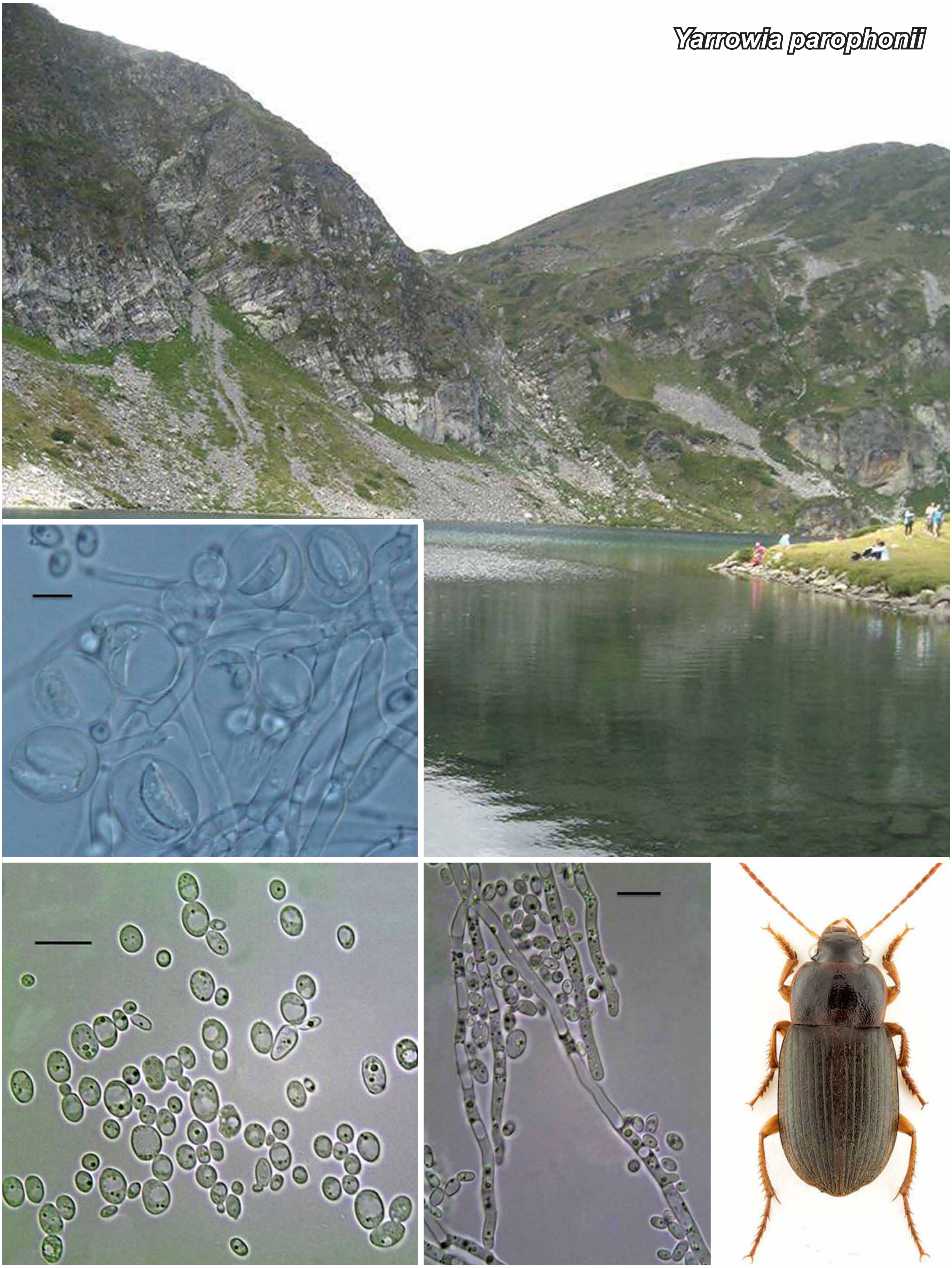
Notes — *Cadophora antarctica*, recovered from a soil sample contaminated with diesel in King George Island (Antarctica), displays the typical features of a psychrotrophic organism: it has an optimal temperature of growth at 15 °C and is not able to grow above 25 °C. *Cadophora antarctica* differs from all previously known species of the genus (Gramaje et al. 2011, Travadon et al. 2014), displaying holoblastic conidiogenesis, forming conidiophores morphologically similar to cladosporium-like taxa. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hit using the ITS sequence is with the ex-type strain of *Cadophora luteo-olivacea* (CBS 141.41, GenBank AY249066; Identities = 493/513 (97 %), Gaps 2/513 (0 %)); and using the LSU sequence it is with the same strain of *Cadophora luteo-olivacea* (GenBank AY249081; Identities = 533/541 (98 %), no gaps). Our ITS phylogenetic tree corroborated the placement of our isolate as a new species of the genus *Cadophora*, phylogenetically closely related to *Cadophora luteo-olivacea*.



Maximum likelihood tree obtained from the DNA sequences dataset from the ITS region of our isolate and sequences retrieved from GenBank. The tree was built by using MEGA v. 6. Bootstrap support values ≥ 70 % are presented at the nodes. *Phialophora brunnescens* CBS 295.39 and *Phialophora calyciformis* CBS 302.62 were used as outgroup. The new species proposed in this study is indicated in **bold**. ^{T} represents the ex-type strains.

Colour illustrations. Typical landscape of King George Island (South Shetland archipelago, Antarctica); colonies growing on different culture media (OA, PDA and MEA at 15 °C, and MEA at 5 °C; top picture); conidiophores and conidia. Scale bars = 10 µm.

Ernesto Rodríguez-Andrade, Alberto M. Stchigel, José F. Cano-Lira & Josep Guarro, Mycology Unit, Medical School and IISPV,
Universitat Rovira i Virgili (URV), Sant Llorenç 21, 43201 Reus, Tarragona, Spain;
e-mail: dc.ernesto.roan@outlook.com, albertomiguel.stchigel@urv.cat, jose.cano@urv.cat & josep.guarro@urv.cat
Walter P. Mac Cormack, Departamento de Microbiología Ambiental y Ecofisiología, Instituto Antártico Argentino, Buenos Aires, Argentina;
e-mail: wmac@ffyb.uba.ar


Yarrowia parophonii

Fungal Planet 628 – 20 December 2017

Yarrowia parophonii Gouliamova, R.A. Dimitrov, Guéorguiev, M.T. Sm., & M. Groenew., *sp. nov.*

Etymology. Named after the insect host *Parophonus hirsutulus* from which the ex-type strain was isolated.

Classification — *Dipodascaceae*, *Saccharomycetales*, *Saccharomycetes.*

After 5 d at 25 °C in yeast malt extract (YM) broth, cells are ovoid to globose, 2–6 × 3–9 µm in size. Vegetative reproduction is by multilateral budding. On glucose peptone yeast extract agar (GPYA) and 5 % malt agar (MA) after 7 d at 25 °C streak colonies are cream, butyrous, smooth, convex and with an entire margin. True hyphae are formed. After 1–2 wk of incubation at 25 °C 1–2 hat-shaped ascospores were observed on YM agar medium (Yarrow 1998). For full physiological test results see MycoBank MB819716.

Typus. Bulgaria, from the gut of *Parophonus hirsutulus* (*Carabidae*), 9 Aug. 2009, *D. Gouliamova* (holotype D189, ex-type cultures NBIMCC 8889 = CBS 12427 preserved in metabolically inactive state, D1/D2 domains of LSU rDNA and ITS (ITS1+2) sequences in GenBank JQ026370.2, JQ026371.2, MycoBank MB819716).

Additional materials examined. Bulgaria, from the gut of *Parophonus hirsutulus* (*Carabidae*), 9 Aug. 2009, *D. Gouliamova*, 83Y (NBIMCC 8888 = CBS 12462), 25L (NBIMCC 8900 = CBS 12468), 30L (NBIMCC 8902 = CBS 12466), BH1 (NBIMCC 9804 = CBS 12471), KL1 (NBIMCC 8903 = CBS 12465) and 29L (NBIMCC 8901 = CBS 12441), LSU sequences GenBank KC810944, KY457253–KY457257; ITS sequences GenBank KC810951, KY457248–KY457252, respectively.

Notes — The phylogenetic analysis of the combined ITS and LSU rDNA sequence alignment showed that the ex-type strain clusters with *C. oslonensis* (96 % identity; 679 conserved nt., 1 subst., 1 gap in ITS region; 16 subst. in LSU rDNA). The additional strains examined show 100 % sequence similarity to one another, with exception of strains 25L and BH1 which showed 99 % similarity in ITS (3 nt. subst.). The new strains, D189, 83Y, 25l, 30L and KL1 can be distinguished from *C. oslonensis* (CBS 10146T) based on assimilation profiles of twelve compounds (details in MycoBank MB819716). The strains are able to assimilate D-ribose (+/w/-), D-mannitol (+/w/-), gentobiose (+/w/-), Tween 40 (w), creatine (w) and can grow without vitamins (w), biotine and thiamine, pyridoxine and thiamine. The strains cannot assimilate L-sorbose, salicin and D-glucono 1.5 lactone. Hydrolysis of arbutin is negative. The strains were provisionally labelled mating type + (29L, 30L, KL1, 83Y, D189) and mating type – (25L, BH1) (Wickerham et al. 1970, Knutsen et al. 2007, Groenewald & Smith 2013). Based on our results we propose new combinations in the genus *Yarrowia* for the following *Candida* species.

Yarrowia galli (G. Péter et al.) Gouliamova, R.A. Dimitrov, M.T. Sm. & M. Groenew., *comb. nov.* — MycoBank MB819717

Basionym. Candida galli G. Péter et al., Antonie Van Leeuwenhoek 86: 107. 2004.

Colour illustrations. The Kidney Lake in Rila mountains, Bulgaria; *Parophonus hirsutulus* (photo credit Aleš Sedláček, http://www.hmyzfoto.cz); morphology of cells; true hyphae of *Y. paraphonii* D189ᵀ in YM broth (scale bars = 10 µm); cluster of asci, some with hat-shaped ascospores formed in crosses between strains D189T and 25L (scale bar = 5 µm).

Yarrowia oslonensis (Knutsen et al.) Gouliamova, R.A. Dimitrov, M.T. Sm., & M. Groenew., *comb. nov.* — MycoBank MB819718

Basionym. Candida osloniensis Knutsen et al., Int. J. Syst. Evol. Microbiol. 57: 2426. 2007.

Yarrowia alimentaria (Knutsen et al.) Gouliamova, R.A. Dimitrov, M.T. Sm., & M. Groenew., *comb. nov.* — MycoBank MB819719

Basionym. Candida alimentaria Knutsen et al., Int. J. Syst. Evol. Microbiol. 57: 2426. 2007.

Yarrowia hollandica (Knutsen et al.) Gouliamova, R.A. Dimitrov, M.T. Sm., & M. Groenew., *comb. nov.* — MycoBank MB819720

Basionym. Candida hollandica Knutsen et al., Int. J. Syst. Evol. Microbiol. 57: 2426. 2007.

Yarrowia phangngaensis (Limtong et al.) Gouliamova, R.A. Dimitrov, M.T. Sm., & M. Groenew., *comb. nov.* — MycoBank MB819721

Basionym. Candida phangngensis Limtong et al., Int. J. Syst. Evol. Microbiol. 58: 515. 2008.

Phylogenetic analysis of the combined ITS and LSU rDNA sequences of *Yarrowia paraphonii* D189^{T} and related species using a neighbour-joining analysis (Kimura two-parameter model; MEGA v. 6).

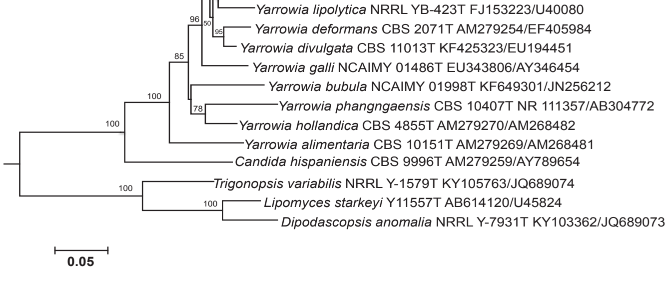
The following combinations were invalidly published, citing the MycoBank number of the basionym for the new combination (Crous et al. 2016b), and are herewith validated:

Priceomyces fermenticarens (Van der Walt & Baker) Gouliamova, R.A. Dimitrov, M.T. Sm., M.M. Stoilova-Disheva & M. Groenew., *comb. nov*. — MycoBank MB818692

Basionym. Candida fermenticarens Van der Walt & Baker, Bothalia 12: 561. 1978.

Priceomyces northwykensis (R.S. Rao et al.) Gouliamova, R.A. Dimitrov, M.T. Sm., M.M. Stoilova-Disheva & M. Groenew., *comb. nov*. — MycoBank MB818693

Basionym. Candida northwykensis R.S. Rao et al., Curr. Microbiol. 63: 115. 2011.



Dilnora E. Gouliamova, The Stephan Angeloff Institute of Microbiology, Bulgarian Academy of Sciences,
G. Bonchev 26, Sofia 1113, Bulgaria; e-mail: dilnorag@gmail.com
Roumen A. Dimitrov, Sofia University 'St. Kliment Ohridski', 5 James Bourchier Blvd., Sofia 1164, Bulgaria; e-mail: dimitrov@phys.uni-sofia.bg
Borislav V. Guéorguiev, National Museum of Natural History, 1 Tsar Osvoboditel Blvd., Sofia 1000, Bulgaria; e-mail: bobivg@yahoo.com
Maudy Th. Smith & Marizeth Groenewald, Westerdijk Fungal Biodiversity Institute, P.O. Box 85167,
3508 AD Utrecht, The Netherlands; e-mail: m.smith@westerdijkinstitute.nl & m.groenewald@westerdijkinstitute.nl


Coniella heterospora

Fungal Planet 629 – 20 December 2017

Coniella heterospora Valenzuela-Lopez, Cano, Guarro & Stchigel, *sp. nov.*

Etymology. Named after the variable shape of the conidia.

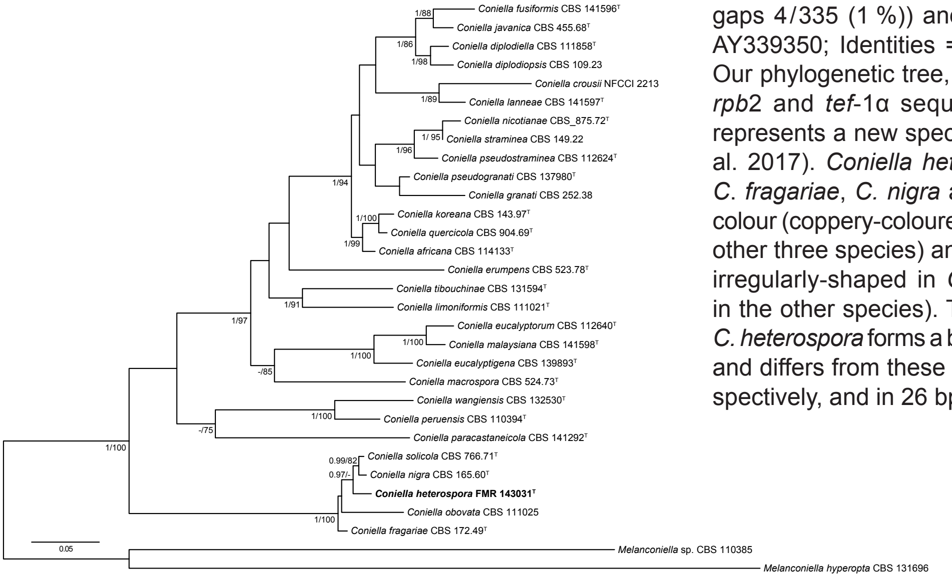
Classification — *Schizoparmaceae*, *Diaporthales*, *Sordariomycetes.*

Hyphae hyaline to pale brown, smooth- and thin- to thick-walled, septate, 2–5 µm wide. *Pycnidia* initially hyaline, becoming dark brown with age due to the production of conidia, glabrous, semi-immersed or superficial (OA), solitary, confluent with age, globose, (320–)370–500(–800) µm diam, without neck, ostiolate, pycnidial wall of *textura angularis*, 50–65 µm thick, 5–6-layered, composed of hyaline to pale brown or brown, flattened polygonal cells of 5–15 µm diam, on the inside of the pycnidium there is a basal central cushion-like structure composed of hyaline cells from which the conidiophores arise. *Conidiophores* densely aggregated, hyaline, branched at the base and with 2–3 supporting cells, or reduced to a single conidiogenous cell. *Conidiogenous cells* hyaline, determinate, smooth- and thin-walled, lageniform, 6.5–12(–16) × 1.5–2(–2.5) µm, 1–1.5 µm wide at apex. *Conidia* hyaline at first, becoming coppery-coloured when mature, aseptate, smooth- and thin- to thick-walled, mostly with a large guttula, sometimes biguttulate, variable in shape, mostly ellipsoidal, sometimes naviculate, limoniform, subsphaerical or irregularly-shaped, mostly laterally compressed, apex acute to nearly rounded, truncate at the base, with a longitudinal germ slit in older conidia, with a minute basal appendage formed by rests of the conidiogenous cell, (4.5–)5.5–8(–9.5) × (3–)4.5–6(–6.5) × 4–4.5(–5.5) µm.

Culture characteristics — Colonies on OA reaching 79 mm diam after 7 d at 25 ± 1 °C, flattened, white (M. 4A1); reverse white (M. 4A1). Colonies on MEA reaching 86 mm diam after 7 d at 25 ± 1 °C, floccose, brownish grey (M. 4D2) to dark grey (M. 4F1); reverse dark grey (M. 4F1). NaOH spot test negative. Crystals absent. Optimal temperature of sporulation and growth, 25 °C; minimum temperature of growth, 15 °C; maximum temperature of growth, 30 °C.

Typus. Spain, Huelva, Almonte, road HF6245 from Los Cabezudos village to Los Bodegones village, from herbivorous dung, Mar. 2016, coll. *C. González-García* and *G. Sisó*, isol. *N. Valenzuela-Lopez* (holotype CBS H-23198, cultures ex-type FMR 15231 = CBS 143031, ITS, LSU, *tef*-1α and *rpb*2 sequences GenBank LT800501, LT800500, LT800503 and LT800502, MycoBank MB820451).

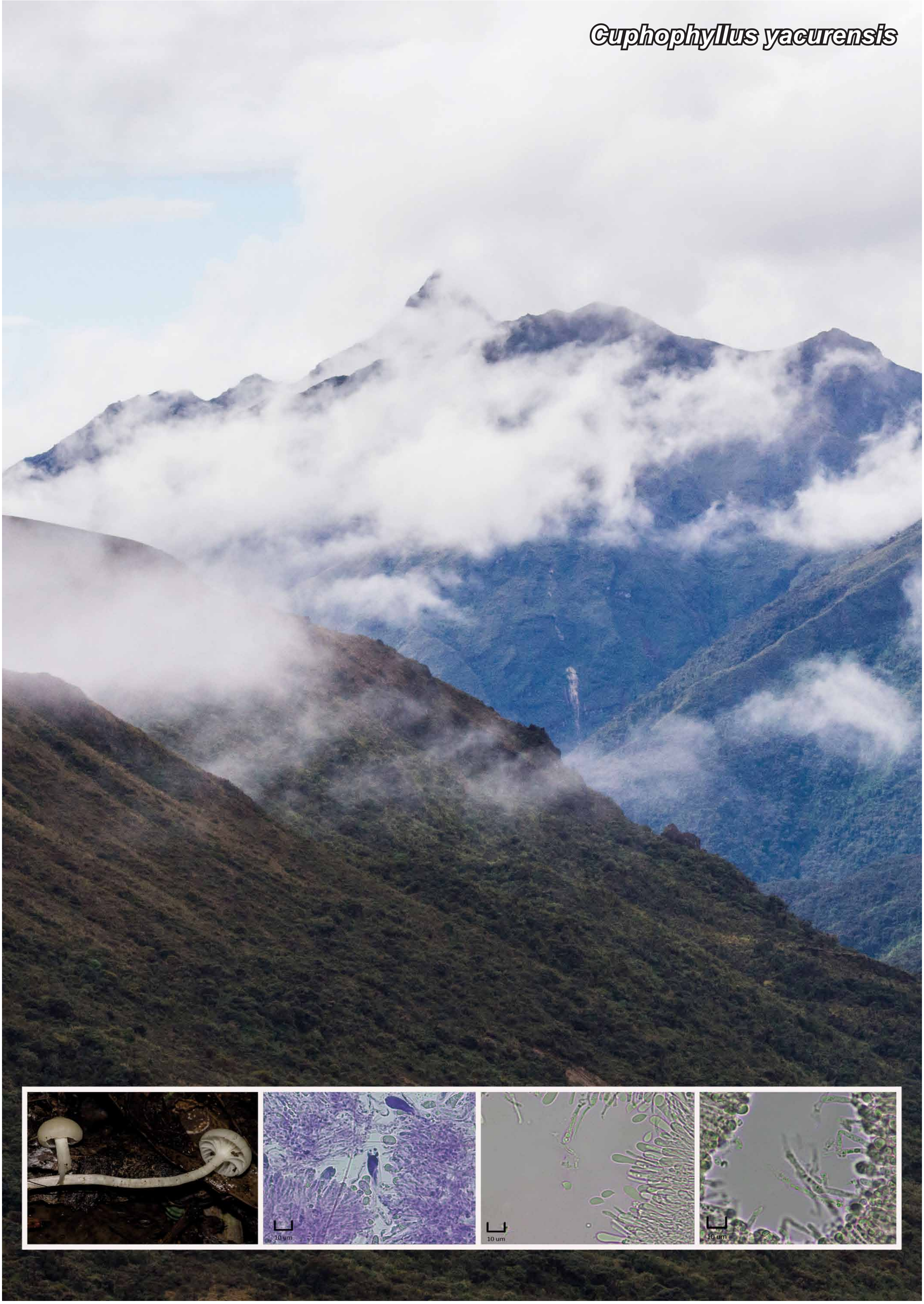
Notes — *Coniella heterospora* is characterised by the production of coppery-coloured conidia that are variable in shape. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hit using the LSU sequence is *C. fragariae* CBS 183.52 (GenBank KJ710442; Identities = 835/838 (99 %), no gaps). Closest hits using the ITS sequence are *C. fragariae* CBS 198.82 (GenBank KJ710465; Identities = 600/601 (99 %), no gaps) and *C. solicola* CPC 17308 (GenBank KX833598; Identities = 589/591 (99 %), no gaps). The closest hits using the *rpb*2 sequence are *C. solicola* CBS 114007 (GenBank KX833504; Identities = 756/767 (99 %), no gaps) and *C. fragariae* CBS 454.68 (GenBank KX833477; Identities = 751/767 (98 %), no gaps). The closest hits using the *tef*-1α sequence are *C. solicola* CPC 17308 (GenBank KX833702; Identities = 311/335 (93 %), gaps 4/335 (1 %)) and *C. fragariae* STE-U 3713 (GenBank AY339350; Identities = 327/359 (91 %), gaps 9/359 (2 %)). Our phylogenetic tree, built by using concatenated LSU, ITS, *rpb*2 and *tef*-1α sequences, corroborated that our isolate represents a new species (Alvarez et al. 2016, Marin-Felix et al. 2017). *Coniella heterospora* is morphologically similar to *C. fragariae*, *C. nigra* and *C. solicola*, but differs in conidium colour (coppery-coloured in *C. heterospora* vs dark brown in the other three species) and shape (very variable and sometimes irregularly-shaped in *C. heterospora*, and scarcely variable in the other species). The phylogenetic analysis showed that *C. heterospora* forms a basal branch with *C. solicola* and *C. nigra*, and differs from these species in 8 bp and 10 bp for *rpb*2, respectively, and in 26 bp for both *tef*-1α nucleotide sequences.



Maximum likelihood tree obtained from the combined DNA sequences dataset from four loci (LSU, ITS, *rpb2* and *tef*-1α) of our isolate and sequences retrieved from the GenBank database. Ex-type strains of the different species are indicated with ^{T}. The new species proposed in this study is indicated in **bold**. The Bayesian posterior probabilities (≥ 0.95) and RAxML bootstrap support values (≥ 70 %) are provided at the nodes. *Melanconiella hyperopta* CBS 131696 and *Melanconiella* sp. CBS 110385 were used as outgroup.

Colour illustrations. Los Cabezudos-Los Bodegones, Huelva, Spain; colony on MEA and OA after 14 d at 25 ± 1 °C; pycnidia under the stereomicroscope; conidiophores, conidiogenous cells and conidia; conidia, some of them showing minute basal cellular appendage (indicated by arrows). Scale bars: conidiophores = 20 µm, conidiogenous cells and conidia = 10 µm..

Nicomedes Valenzuela-Lopez, Mycology Unit, Medical School and IISPV, Universitat Rovira i Virgili (URV),
Sant Llorenç 21, 43201 Reus, Tarragona, Spain; Microbiology Unit, Medical Technology Department, Faculty of Health Science,
University of Antofagasta, Av. Universidad de Antofagasta s/n, 02800 Antofagasta, Chile; e-mail: nicomedes.vl@gmail.com
Alberto M. Stchigel, Josep Guarro & José F. Cano-Lira, Mycology Unit, Medical School and IISPV, Universitat Rovira i Virgili (URV),
Sant Llorenç 21, 43201 Reus, Tarragona, Spain; e-mail: alberto.stchigel@urv.cat, josep.guarro@urv.cat & jose.cano@urv.cat


Cuphophyllus yacurensis
10 um
10 um
10 um

Fungal Planet 630 – 20 December 2017

Cuphophyllus yacurensis A. Barili, C.W. Barnes & Ordoñez, *sp. nov.*

Etymology. Name reflects the locality where the species was collected.

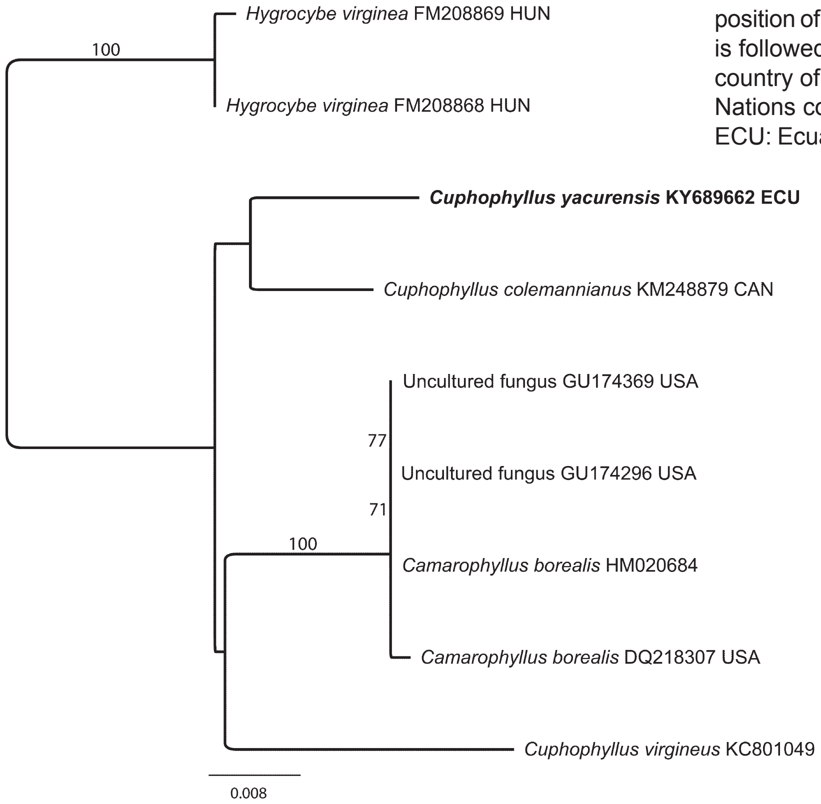
Classification — *Hygrophoraceae*, *Agaricales*, *Agaricomycetidae*, *Agaricomycetes*, *Basidiomycota.*

Basidiomata stipitate, pileus convex, 6 mm diam, white, surface smooth, dry, smooth margin. Texture slightly elastic, white, immutable. *Lamellae* white, thick, separate, decurrent, with lamellulae present, smooth margin. *Stipe* central, white, 40 × 1.5 mm, cylindrical, smooth, white cottony mycelia at the base. *Spore print* white. *Basidia* 32–37.5 × 7–7.5 µm, elongate, clavate, 2- and 4-spored, hyaline. *Clamp connections* present in the hymenium, lamellar trama irregular. *Pileipellis* as cutis. *Basidiospores* 8–9 × 5–5.5 µm, ellipsoid, amygdaloid, ovoid, smooth, non-amyloid, acyanophilic, non-dextrinoid, not metachromatic.

Habitat — Gregarious, on the ground, high montane forest.

Typus. ECUADOR, Zamora Chinchipe province, Yacuri National Park, alt. 3234 m, May 2015, *A. Barilli* (holotype QCAM 5891, Fungarium QCAM, ITS and LSU sequences GenBank KY689662 and KY780119, MycoBank MB820655, TreeBASE Submission ID 20679).

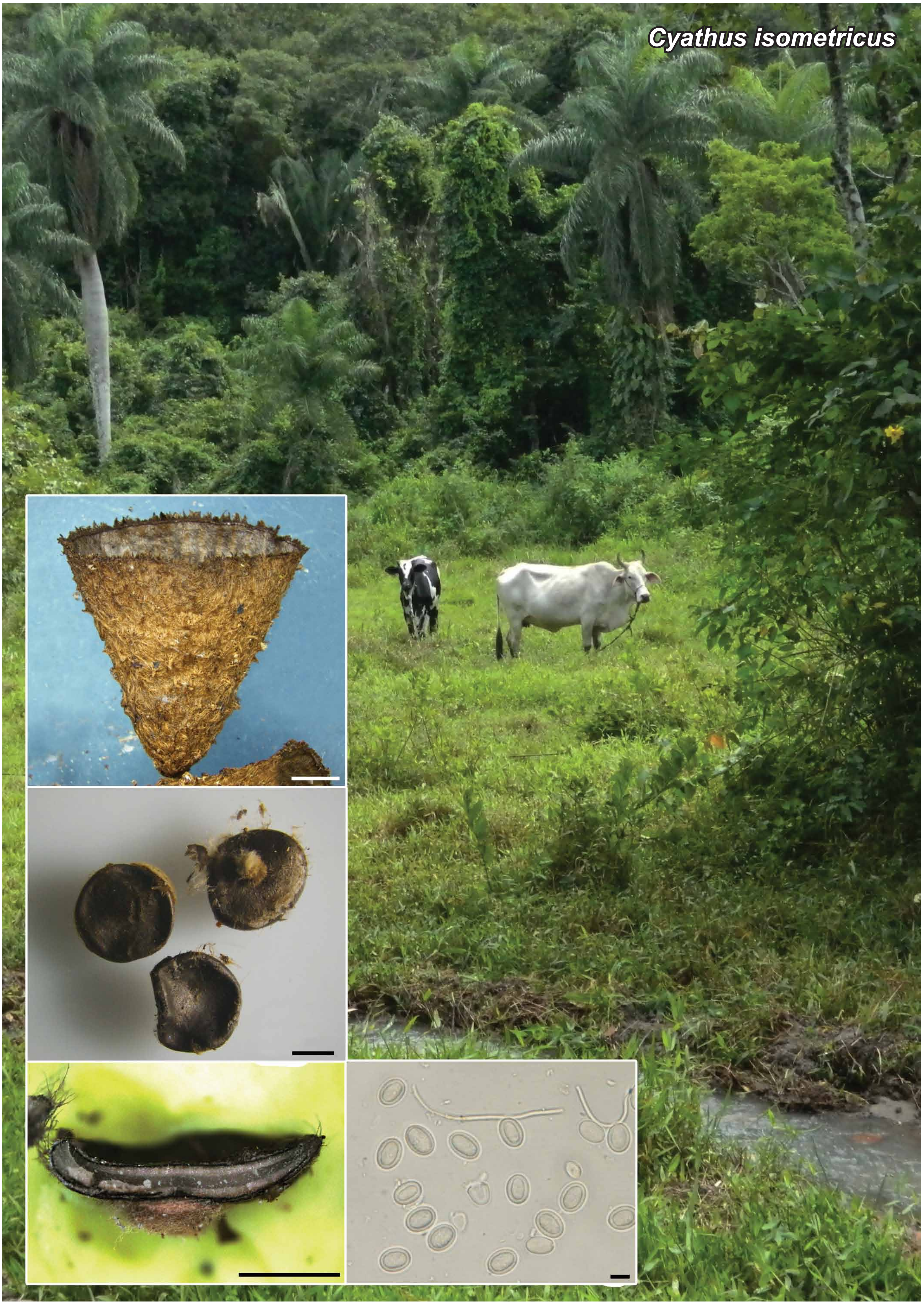
Notes — Phylogenetic analyses show *Cuphophyllus colemannianus* as the closest species to *C. yacurensis*, but several morphological differences were found. The pileus of *C. colemannianus* is larger (10–50 mm), pale brown, slimy surface, and striate margin, with intervenous lamellae, and larger basidia between 37–51 mm (Trudell & Ammirati 2009). A Blastn search was done with the complete ITS sequence of 634 bases of the *C. yacurensis* holotype (GenBank KY689662). The results showed the closest match to *C. colemannianus* from Canada (GenBank KM248879) with 97 % similarity from 21 base differences and 5 gaps. Following *C. colemannianus* in the Blastn search results were several uncultured fungi, *Camarophyllus borealis*, *Cuphophyllus virginea*, and two *Hygrocybe virginea* sequences. The phylogenetic analysis was done with the above-mentioned sequences and *Hygrocybe virginea* as the outgroup. The final alignment was trimmed to include ITS1 through ITS2 only and edited by hand for alignment errors.



The phylogenetic tree was constructed using the Maximum Likelihood plugin PHYML in Geneious R9 (http://www.geneious.com; Kearse et al. 2012), and the substitution model determined by jModelTest (Posada 2008) according to the Corrected Akaike Information Criterion (AICc). *Hygrocybe virginea* (GenBank FM208869 and FM208868) is the outgroup. Bootstrap support values ≥ 70 % are given above the branches. The phylogenetic position of *C. yacurensis* is indicated in **bold.** The species name is followed by the GenBank accession number, and when the country of origin was indicated, also by the three letter United Nations country code, in order of appearance HUN: Hungary, ECU: Ecuador, CAN: Canada, USA: United States of America.

Colour illustrations. Ecuador, Yacuri National Park; basidia; basidiospores and clamp connection.

Maria E. Ordoñez & Alessio Barili, Escuela de Ciencias Biológicas, Pontificia Universidad Católica del Ecuador,
Av. 12 de octubre 1076 y Roca, Quito, Ecuador;
e-mail: meordonez@puce.edu.ec & alessiobarili@hotmail.com
Charles W. Barnes, Instituto Nacional Autónomo de Investigaciones Agropecuarias, Estación Experimental Santa Catalina,
Panamericana Sur Km 1, Sector Cutuglahua, Pichincha, Ecuador;
e-mail: cbarnes333b@gmail.com


Cyathus isometricus

Fungal Planet 631 – 20 December 2017

Cyathus isometricus R. Cruz, J.S. Góis, P. Marinho & Baseia, *sp. nov.*

Etymology. Named in reference to the isometrical dimensions of the basidiomata.

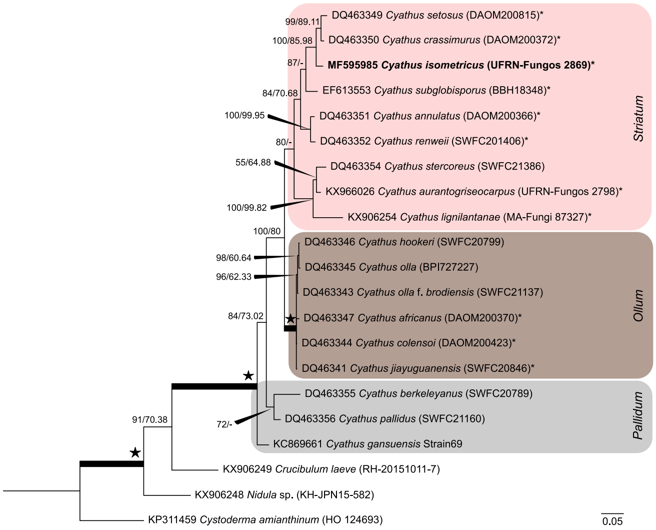
Classification — *Nidulariaceae*, *Agaricales*, *Agaricomycetes*.

Basidiomata infundibuliform to slightly campanulate, 7–11 mm in height, 7–11 mm in width at the upper part, isometrical with straight sides, not expanded in the mouth or forming a pedicel at the base. *Emplacement* 4 mm in width, conspicuous to inconspicuous, brown (7F6 Kornerup & Wanscher 1978). *Exoperidium* woolly (not hirsute), dark reddish brown to brown (6F6–7F6), provided with 0.4–0.75 mm tomentum, arranged in small, irregular and flexible tufts. External wall inconspicuously plicated, with 0.55–0.8 mm between the striae. *Mouth* finely fimbriated to finely setose, in a continuous pattern, 0.1–0.4 mm in height, dark greyish brown to dark brown (6F3–7F5). *Endoperidium* greyish brown (7E3–7F3), inconspicuously plicated, with 0.55–0.8 mm between the striae. Weak but perceptibly bright, slightly contrasting with the exoperidium. *Stipe* and *epiphragm* not observed in the sample. *Peridioles* greyish brown (8F2–8F3), 2.35–2.7 × 2.1–2.5 mm, circular in shape, sometimes angular to irregular, smooth surface, tunic indistinct and provided with double layered cortex: internal cortex black, external cortex greyish brown (8F3) and separated by a thin and compacted hyphal layer, greyish in colour. *Basidiospores* smooth, hyaline, 14–18 × 10–13 µm (L = 16.02; W = 11.42), slightly elliptical to elongated (Q = 1.29–1.62), elliptical in average (Qm = 1.41), apicule absent and spore wall 1.5–3 µm thick.

Typus. Brazil, Paraíba, Areia, Ecological Reserve Mata do Pau-Ferro, on decaying wood, 23 July 2014, *J.O. Souza*, *D.S. Alfredo* & *E.S. Sousa* (holotype UFRN-Fungos 2869, paratype UFRN-Fungos 2870, ITS and LSU sequences GenBank MF595985 and MF595986, MycoBank MB822200).

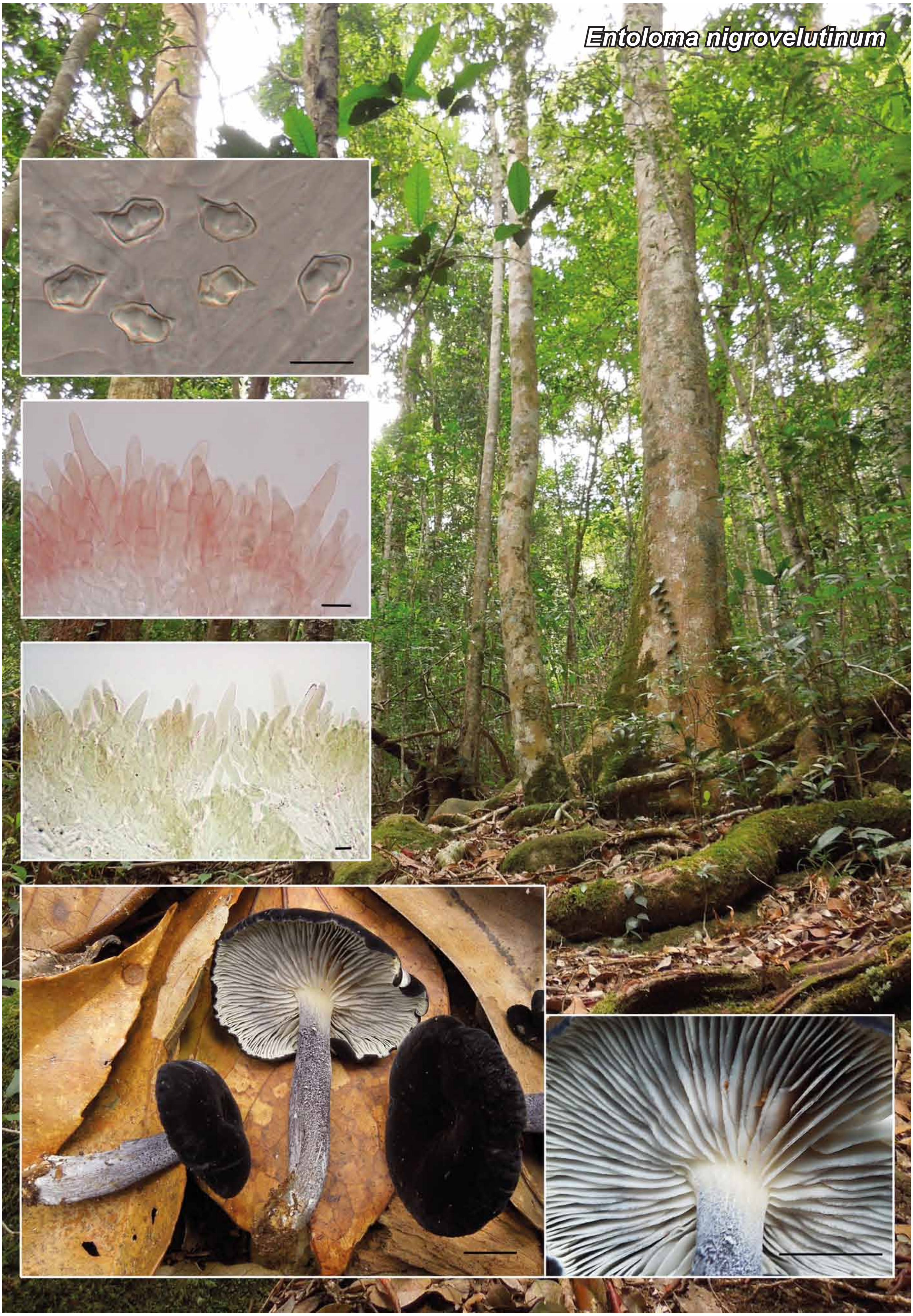
Notes — Following Brodie's (1975) classification, *Cyathus isometricus* has characteristics that would group it both in group I (*olla*) or in group III (*triplex*); in the classification based on phylogenetic data by Zhao et al. (2007), it can be grouped in the clade *striatum*. From Brodie's (1975, 1984) group I (*olla*), *C. isometricus* presents similarities with *C. earlei*, such as the basidiomata measurements, spore size and apicule absent; however, the holotype of *C. earlei* (BPI 703410) shows emplacement with prominent hyphae (cotonous), exoperidium hirsute and endoperidium with platinum bright, both paler in colour (exoperidium 5D7–5D8 and endoperidium 6C2–5C3), small peridioles (1.6–1.97 × 1.45–1.87 mm) brown in colour (5F5), with rugose surface and subhomogeneous double layered cortex. From Brodie's (1975) group III (*triplex*), the new species can be compared with *C. setosus*, a species that groups with *C. isometricus* and *C. crassimurus* in the phylogenetic analyses (comments below). From the same collection site, *C. isometricus* has morphological similarities with *C. calvescens*, however, the latter can be distinguished by the presence of a pedicel in the basidiomata, tomentum finely woolly (almost glabrous), and the subhomogeneous double layered cortex (Cruz & Baseia 2014). Phylogenetically, *C. isometricus* grouped (PP = 100; MPbs = 85.98) in the clade formed by *C. crassimurus* and *C. setosus*. *Cyathus setosus* presents similar macroscopic measures and woolly exoperidium with short tomentum, and both *C. crassimurus* and *C. setosus* have spores with the same measurements and shape of *C. isometricus.* However, *C. setosus* (holotype DAOM 200815) presents exo- and endoperidium with paler colour than in *C. isometricus* (exoperidium 5E8, endoperidium 5D4–5F6), external wall smooth, smaller peridioles in its width (1.5–2 mm), setose mouth, and double layered cortex with black intermedial layer. For *C. crassimurus* (holotype DAOM 200372), this species has macroscopic small sizes (4–5 × 4–6.5 mm, height by width), peridium with thick and rigid wall, exoperidium smooth, hirsute, endoperidium with platinum bright and paler colour (5C2), and smaller peridioles (1–1.5 × 1–1.5 mm), bronze (5E5).

Colour illustrations. Brazil, Paraiba, Areia, environment near the locality where the type species was collected in the Ecological Reserve Mata do Pau-Ferro; peridium (scale bar = 2 mm); upper view of peridioles (scale bar = 1 mm); cross section showing the double-layered cortex, with internal black cortex, external greyish brown (8F3) cortex, and separated by a thin and compacted greyish hyphal layer (scale bar = 1 mm); basidiospores (scale bar = 10 µm). All images from the holotype, UFRN-Fungos 2869.



The 50 % majority rule Bayesian tree was inferred from ITS sequences with the model T92 + G using MrBayes v. 3.2.6 (Ronquist et al. 2012). A maximum parsimony analysis was done (PAUP v. 4.0a156), and similar topology was obtained (not shown). Bayesian posterior probabilities (PP) from 10 M generations, and maximum parsimony bootstrap (MPbs) support values from 10 000 replications and random addition sequences repeated 10 times, are indicated on the branches. The star (★) represents nodes with maximum PP and MPbs. Type species are marked with asterisks (*) and the new species is in **bold**. The scale bar indicates the estimated number of nucleotide substitutions per site. Sequence alignment is available in TreeBASE (http://purl.org/phylo/treebase/phylows/study/TB2:S21396).

Rhudson H.S.F. Cruz, Programa de Pós-graduação em Sistemática e Evolução, Centro de Biociências,
Universidade Federal do Rio Grande do Norte, Natal, 59078-970, Brazil; e-mail: rhudsoncruz@yahoo.com.br
Jefferson S. Góis, Curso de Graduação em Ciências Biológicas, Centro de Biociências,
Universidade Federal do Rio Grande do Norte, Natal, 59078-970, Brazil; e-mail: jeff.gois@outlook.com
Paulo Marinho, Departamento de Biologia Celular e Genética, Universidade Federal do Rio Grande do Norte, Natal,
Rio Grande do Norte, Brazil; e-mail: paulomarinho@hotmail.com
Iuri G. Baseia, Departamento de Botânica e Zoologia, Universidade Federal do Rio Grande do Norte, Natal,
Rio Grande do Norte, Brazil; e-mail: iuribaseia@gmail.com


Entoloma nigrovelutinum

Fungal Planet 632 – 20 December 2017

Entoloma nigrovelutinum O.V. Morozova & A.V. Alexandrova, *sp. nov.*

Etymology. The epithet refers to bluish black and velvety pileus surface – from Latin *nigrus* (black) and *velutinus* (velvety).

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

Basidiomata medium-sized, collybioid to tricholomatoid. *Pileus* 15–40 mm diam, initially hemispherical to convex, becoming applanate with or without central depression, with involute margin, not hygrophanous, not translucently striate, blackish blue to dark violet (18F6–8, 19F6–8; Kornerup & Wanscher 1978), entirely uniformly velvety. *Lamellae* moderately distant, adnexed, adnate-emarginate or adnate with small decurrent tooth, bluish grey (19B2–3), becoming greyish pink, with dark blackish blue serrulate edge. *Stipe* 30–70 × 4–6 mm, cylindrical, broadened or tapering towards the base, longitudinally striate, covered with blackish blue (19F6–8) squamules on a whitish background, with white apex, white tomentose at base. *Context* white, bluish under the pileus surface. *Smell* faint, taste not reported. *Spores* (8.5–)9.5(–10.5) × (6–)6.5(–7) µm, Q = (1.4–)1.5(–1.6), heterodiametrical, with 5–6 angles in side-view. *Basidia* 36–40.5 × 9.7–10.5 µm, 1–4-spored, narrowly clavate to clavate, clampless. *Cheilocystidia* 35–65 × 5.5–10.5 µm, forming a sterile edge, cylindrical, lageniform or fusiform, sometimes septate with dark intracellular pigment. *Pileipellis* a well-differentiated trichoderm of cylindrical to slightly inflated or fusiform hyphae 10–20 µm wide with swollen terminal elements and bluish violaceous intracellular pigment, brownish in KOH. *Caulocystidia* as cylindrical hairs, 40–120 × 6–10 µm. *Clamp-connections* absent.

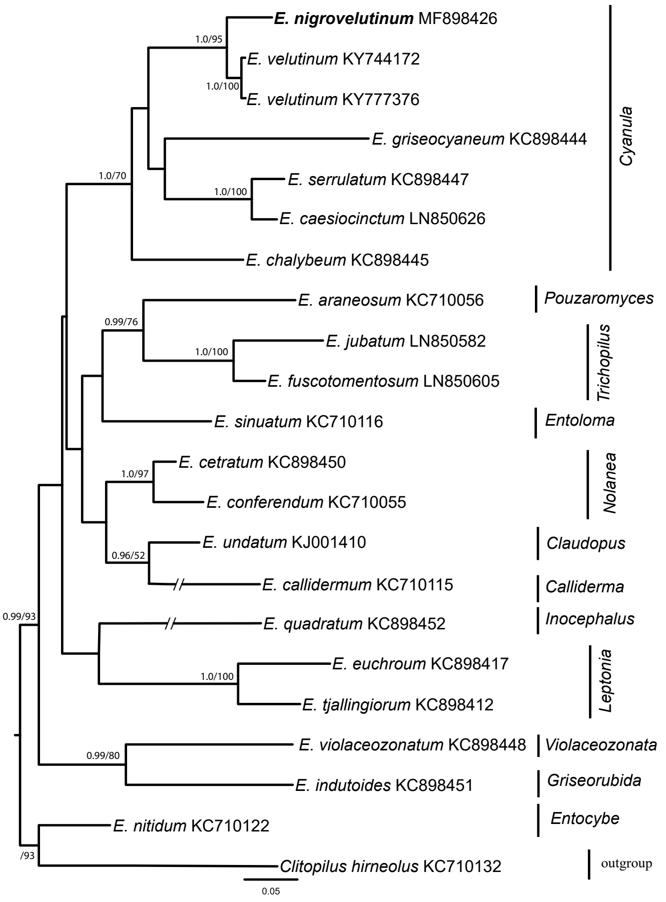
Habit, Habitat and Distribution — In small groups on soil in tropical montane evergreen mixed forests. Known from Vietnam.

Typus. Vietnam, Đắk Lắk Province, Krông Bông District, Bông Krang communes, Krông Kmar, Chư Yang Sin National Park, 1.5 km W of Chu Pan Phan Mt, 12.375567°N 108.354404°E, alt. 1700 m, tropical montane evergreen mixed forest (*Fagaceae*, *Magnoliaceae*, *Theaceae*, *Podocarpaceae*), 9 Apr. 2012, *A. Alexandrova* (holotype LE295077, ITS and LSU sequences GenBank MF898426 and MF898427, MycoBank MB822676).

Notes — *Entoloma nigrovelutinum* is a remarkable species with bluish black basidiomata characterised by a trichoderm structure of the pileipellis and absence of clamp-connections. The structure of pileipellis makes it superficially similar to species of the subgenus *Trichopilus* (Aime et al. 2010) or *Calliderma* (Morgado et al. 2013). Due to the stipitipellis structure it also has a resemblance to some *Leptonia* species (Morozova et al. 2014), or members of the newly proposed section *Violaceozonata* with *serrulatum*-type lamellae edge. However, the absence of clamp-connections combined with the form of the cheilocystidia suggests that this species belongs to the subgenus *Cyanula*. The position of the species within the *Cyanula*-clade has been confirmed based on the molecular analysis.

The closest species *Entoloma velutinum* from USA (Tennessee) differs by the more slender habit, deeply depressed pileus, and p-distance = 4 %.

Colour illustrations. Vietnam, Chu Yang Sin National Park, tropical montane evergreen mixed forest, type locality; spores; cheilocystidia; pileipellis; basidiomata (all from holotype). Scale bars = 1 cm (basidiomata), 10 µm (spores, cheilocystidia and pileipellis).



Phylogenetic tree derived from Bayesian analysis based on nrITS1-5.8S-ITS2 data. Analysis was performed under GTR model, for 5 M generations, using MrBayes v. 3.2.1 (Ronquist et al. 2012). The ML analysis was run in the RAxML server (https://embnet.vital-it.ch/raxml-bb/ (Stamatakis et al. 2008)). Posterior probability (PP > 0.95) values from the Bayesian analysis followed by bootstrap support values from the Maximum Likelihood (BS > 50 %) analysis are added to the left of a node (PP/BS).

Olga V. Morozova, Komarov Botanical Institute of the Russian Academy of Sciences,
197376, 2 Prof. Popov Str., Saint Petersburg, Russia;
e-mail: OMorozova@binran.ru
Alina V. Alexandrova, Lomonosov Moscow State University (MSU), Faculty of Biology,
119234, 1, 12 Leninskie Gory Str., Moscow, Russia;
e-mail: alina-alex2011@yandex.ru


Ganoderma podocarpense

Fungal Planet 633 – 20 December 2017

Ganoderma podocarpense J.A. Flores, C.W. Barnes & Ordoñez, *sp. nov.*

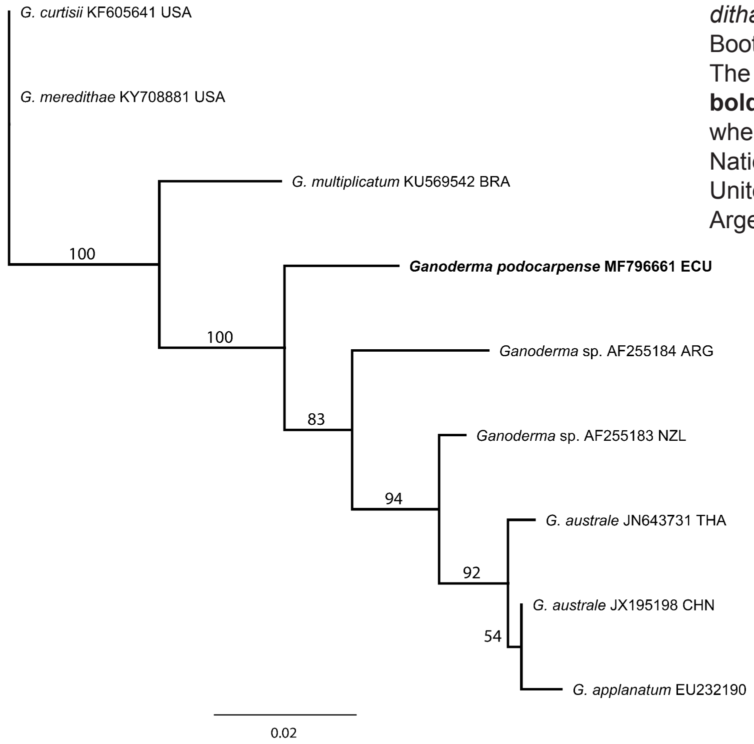
Etymology. Name reflects the locality where the species was collected.

Classification — *Polyporaceae*, *Polyporales*, *Agaricomycetes*.

Basidiomata perennial, flattened, flabelliform, 3.2 × 2.5 cm, woody, hard consistency when dry, pileus glabrous, zonate, opaque, dark brown, covered with cinnamon coloured basidiospores, margin slightly lighter in colour. Black cuticle of uniform width throughout the basidiomata. Context woody, 0.4 cm in width, no resin bands. Hymenial surface pale brown when fresh or dry, turns darker upon contact, pores round, smooth, 5 per mm, thick wall; tubes brown, hymenium 7 mm in width, not stratified. Cutis trichoderm. *Hyphal system* trimitic, generative hyphae yellow, 3.5 μm wide, thin-walled, skeletal hyphae brown, predominant, 8 μm wide, thick-walled to solid, connective hyphae hyaline, thin, 2.5 μm wide. *Basidia* not observed. *Basidiospores* ellipsoid, double-walled, truncate, brown, 8–10 × 5–6 μm, Q = 1.6.

Habit — Solitary, on fallen tree trunk.

Typus. Ecuador, Zamora Chinchipe province, Podocarpus National Park, Ecuador, alt. 1 002 m, June 2016, *J. Flores* (holotype QCAM6422, Fungarium QCAM, ITS and LSU sequences GenBank MF796661 and MF796660, MycoBank MB822575, TreeBASE Submission ID 21473).



Colour illustrations. Ecuador, Podocarpus National Park; basidiomata; hymenium; basidiospores (scale bar = 5 μm) and pileipellis (scale bar = 10 μm).

Notes — Based on morphology the sample belongs to the *G. applanatum* complex (Gottlieb & Wright 1999). According to the Neotropical Polypores key (Ryvarden 2004) *G. citriporum* is the closest species, given the presence of a lateral stipe and brown context colour. However, *G. podocarpense* differs in most morphological characteristics. Amongst the most contrasting are the smaller size of the stipe, absence of resin bands in the context, different colour of the hymenium and the trimitic hyphal system. The complete ITS sequence of 554 bases of the *G. podocarpense* holotype was used for the Blastn search; the ITS length followed Moncalvo & Buchanan (2008). The Blastn results gave the two highest scores to *Ganoderma* sp. from Argentina (GenBank AF255184) and *Ganoderma* sp. from New Zealand (GenBank AF255183) reported by Moncalvo & Buchanan (2008) as part of the *G. australe*-*applanatum* species complex. *Ganoderma podocarpense* had 23 single base differences with 4 gaps, and 24 single base differences with 5 gaps from the two highest Blastn scores respectively. The six highest Blastn scores, plus *G. curtisii* and *G. meredithae*, Blastn scores eight and nine, were used in the phylogenetic analysis. The final alignment was edited by hand for alignment errors.

The phylogenetic tree was constructed using the Maximum Likelihood plugin PHYML in Geneious R9 (http://www.geneious.com; Kearse et al. 2012), and the substitution model determined by jModelTest (Posada 2008) according to the Corrected Akaike Information Criterion (AICc). *Ganoderma curtisii* and *G. meredithae* (GenBank KF605641 and KY708881) is the outgroup. Bootstrap support values ≥ 50 % are given above the branches. The phylogenetic position of *G. podocarpense* is indicated in **bold**. The species name is followed by the GenBank ID, and when the country of origin was indicated, the three letter United Nations country code is used, in order of appearance: USA: United States of America, BRA: Brazil, ECU: Ecuador, ARG: Argentina, NZL: New Zealand, THA: Thailand, CHN: China.

Maria E. Ordoñez & Jorge A. Flores, Escuela de Ciencias Biológicas, Pontificia Universidad Católica del Ecuador,
Av. 12 de octubre 1076 y Roca, Quito, Ecuador; e-mail: meordonez@puce.edu.ec & jafa_90@hotmail.com
Charles W. Barnes, Instituto Nacional de Investigaciones Agropecuarias, Estación Experimental Santa Catalina,
Panamericana Sur Km 1, Sector Cutuglahua, Pichincha, Ecuador; e-mail: cbarnes333b@gmail.com


Geastrum caririense

Fungal Planet 634 – 20 December 2017

Geastrum caririense R.J. Ferreira, Accioly, S.R. Lacerda, M.P. Martín & Baseia, *sp. nov.*

Etymology. In reference to the type locality, Cariri region.

Classification — *Geastraceae*, *Geastrales*, *Agaricomycetes*.

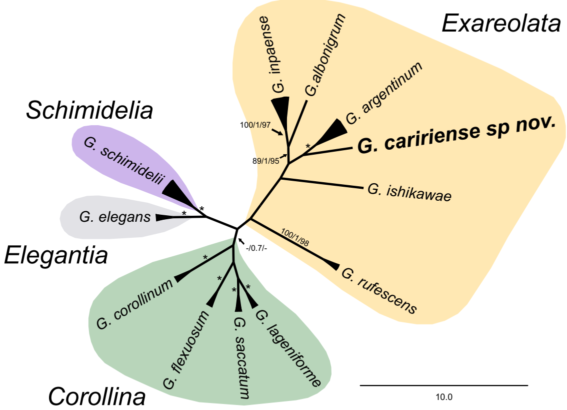
Unexpanded *basidiomata* epigeous, globose to subglobose, just prior to slightly open, umbonate, 14–23 mm high × 15–28 mm wide, surface rugose with irregular cracks, brown to pale brown (5E5 to 6D4, Kornerup & Wanscher 1978), with a few soil incrustations. Expanded basidiomata saccate, 12–29 mm in height (including peristome) × 24–58 mm wide. *Exoperidium* splitting into 4–10 revolute, triangular and irregular rays, non-hygroscopic. *Mycelial layer* slightly encrusted with soil at the base, persistent, orange to pale brown (KW6A4 to KW6D4) or brownish orange (KW6C3), formed by hyaline to greenish hyphae in 5 % KOH, branched, 1.6–3(–4) µm wide, lumen evident, sinuous walls, 0.6 ± 0.1 µm thick. *Fibrous layer* papery, pastel red to brownish orange (KW7A4 to KW6C3), 1–2.5 mm thick when fresh, formed by hyaline hyphae in 5 % KOH, 2–4.5 µm wide, lumen evident, branched, straight walls, 0.7 ± 0.1 µm thick. *Pseudoparenchymatous layer* persistent, glabrous, brownish grey to reddish grey (KW8D2 to KW8B4), cracking at the ray bends and tending to form a pseudoparenchymatous collar around the endoperidium in some specimens, formed by pyriform to oval cells, 19.5–48(–54.5) µm high × 27–58 µm wide, pale yellow in 5 % KOH, straight walls, 0.6 ± 0.2 µm thick. *Endoperidial body* globose to subglobose, 8–19 mm high × 10–21 wide, sessile, glabrous, grey to greyish brown (KW5D1 to KW5E3), apophysis absent. Peristome fibrillose to lacerate in age, mammiform, with the same colour as the endoperidium, up to 1–3 mm high, slightly delimited by a greyish white (KW1B1) annulum. Mature gleba powdery, brownish grey to dark brown (KW7E2 to KW8F4). *Eucapillitium* (2–)2.5–5 µm wide, branched, encrusted, verrucose, lumen evident, pale brown in 5 % KOH, straight walls, 0.6 ± 0.1 µm thick. *Basidiospores* globose to subglobose, 4.5–6.5 µm high × 5–7 µm diam (($\dot{x}$) = 5.7 ± 0.5 × 5.5 ± 0.5, Q_m = 1.05, n = 30), brown in 5 % KOH, densely covered by columnar warts with truncate apex, 0.4–0.6 µm, confluent around the apiculum.

Habitat, Habit and Distribution — Growing on leaf-litter on the shaded ground of the forest; solitary to gregarious. The distribution of *G. caririense* is restricted to the municipality of Crato, Ceará State, Brazil. The specimens were found in the Caatinga domain in a permanent protection area in Araripe National Forest, Cariri region.

Typus. Brazil, Ceará, Crato, Floresta Nacional do Araripe, alt. 972 m, S 07°14'51.0" W39°28'43.8", on soil covered by leaf litter, 1 May 2014, *R.J. Ferreira* 71 (holotype UFRN-Fungos 2266, ITS and LSU sequence GenBank MF158626 and MF158627, MycoBank MB822275; isotype HCDAL 17).

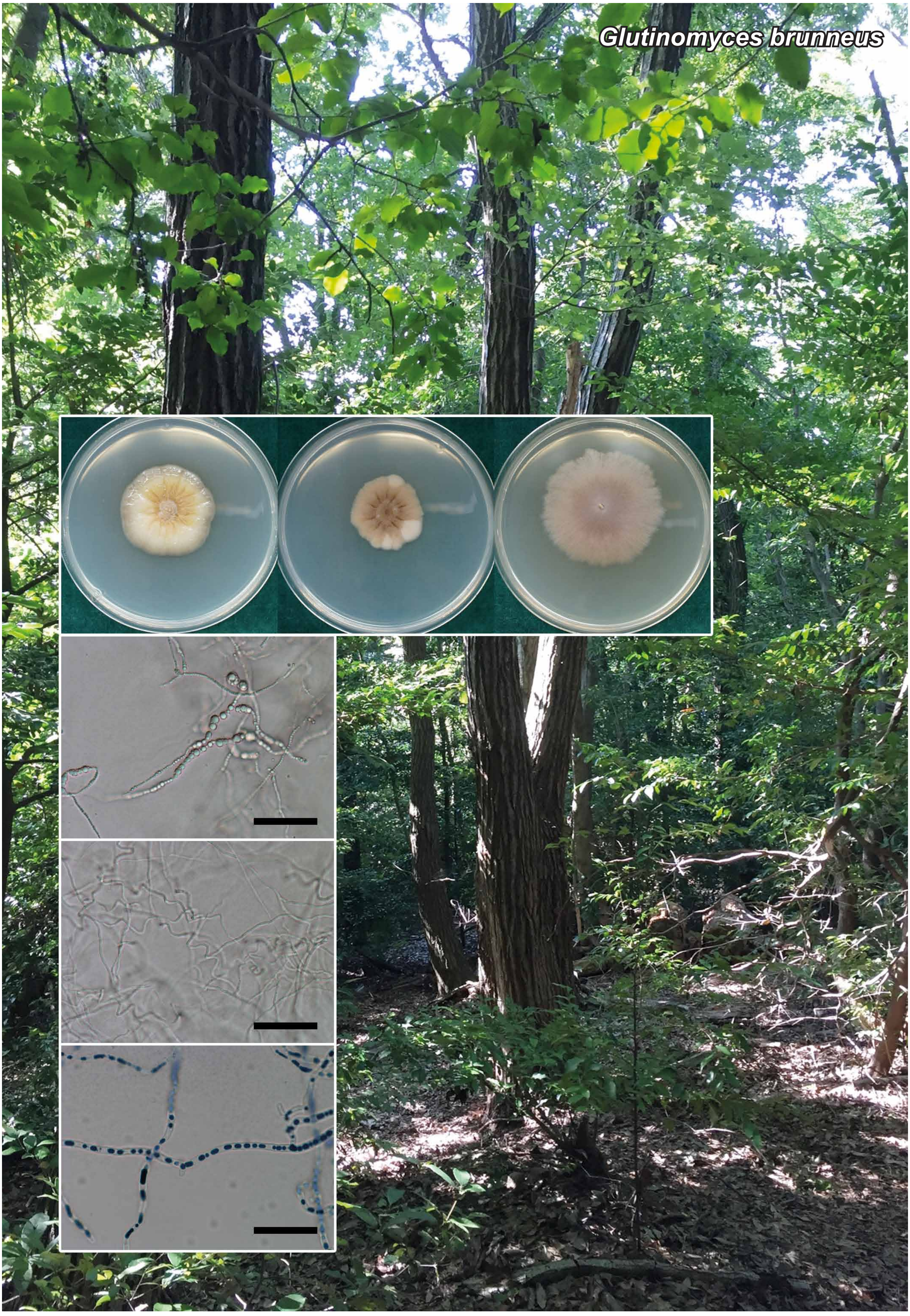
Colour illustrations. Brazil, Pernambuco, Floresta Nacional do Araripe, where the specimens were collected; immature basidiome *in situ* (HCDAL 17); mature basidiome *in situ* (UFRN-Fungi 2266); basidiospores under SEM (UFRN-Fungi 2266); verrucose capillitium under SEM (UFRN-Fungi 2266). Scale bars: basidiomata = 10 mm, basidiospores and capillitium = 2 µm.

Notes — *Geastrum caririense* is mainly characterised by its brownish and cracked mycelial layer, peristome, fibrillose to lacerate, poorly delimited, basidiospores with columnar warts confluent around the apiculum. *Geastrum inpaense* is morphologically close to *G. caririense*; however, it is easily distinguished by the non-cracked mycelial layer with presence of mycelial tufts, and smaller spores of 2.5–4 µm in width including ornamentation (Cabral et al. 2014). Another related species is *G. albonigrum*, but it clearly differs by its hairy and detached mycelial layer and smaller basidiospores of 4–5 µm in width including ornamentation (Sousa et al. 2014). *Geastrum argentinum* also resembles *G. caririense*, but has a peeling-off coriaceous mycelial layer, non-delimited peristome, and develops on a subiculum (Zamora et al. 2013). On the other hand, *Geastrum ishikawae* can be distinguished from *G. caririense* by its cottony to woolly mycelial layer, pruinose endoperidium, non-delimited with coarsely folded peristome, and basidiospore size and ornamentation, 4.5–7 µm diam including ornamentation (Crous et al. 2016a). *Geastrum rufescens* differs from this new species by the cracked and evanescent pseudoparenchymatous layer in age, non-delimited peristome and mycelial layer strongly encrusted with debris and sand (Sunhede 1989). *Geastrum aculeatum*, *G. echinulatum* and *G. litchiforme* are morphologically similar to *G. caririense*, but they have an aculeate, equinulated and pilose mycelial layer, respectively (Silva et al. 2013, Hemmes & Desjardin 2011). Moreover, molecular data from ITS and LSU show with high support that *G. caririense* is different from the other species in sect. *Exareolata*.



One of the 189 equally most parsimonious trees of ITS nrDNA sequences was obtained after a Branch and Bound parsimony search using PAUP v. 4 (Swofford 2003). The new *Geastrum* species, *G. caririense*, is shown in **bold**. The accession numbers from EMBL/GenBank databases are indicated. Bootstrap support values greater than 50 % are indicated on the branches, as well as posterior probabilities obtained after a Bayesian analyses in MrBayes (Ronquist 2012). *Geastrum elegans* was included as outgroup. CorelDRAW® X8 software was used to edit the final tree.

Renato J. Ferreira, Pós-graduação em Biologia de Fungos, Universidade Federal de Pernambuco,
Recife, Pernambuco Brazil; e-mail: renatojuciano@hotmail.com
Thiago Accioly, Programa de Pós-graduação em Sistemática e Evolução, Universidade Federal do Rio Grande do Norte,
Natal, Rio Grande do Norte, Brazil; e-mail: thiagoaccioly@hotmail.com
Sirleis R. Lacerda, Departamento de Ciências Biológicas, Universidade Regional do Cariri,
Crato, Ceará, Brazil; e-mail: sirleisrl@gmail.com
María P. Martín, Departamento de Micología, Real Jardín Botánico-CSIC,
Plaza de Murillo 2, 28014 Madrid, Spain; e-mail: maripaz@rjb.csic.es
Iuri G. Baseia, Departamento de Botânica e Zoologia, Universidade Federal do Rio Grande do Norte,
Natal, Rio Grande do Norte, Brazil; e-mail: iuri.baseia@gmail.com


Glutinomyces brunneus

Fungal Planet 635 – 20 December 2017

Glutinomyces Nor. Nakam., *gen. nov.*

Etymology. Glutino- (L), after the mucoid colony exudates on PDA plates; -myces (G), after fungus.

Classification — *Hyaloscyphaceae*, *Helotiales*, *Leotiomycetes*.

Mycelia colonise living roots of plants. Colonies are sometimes overlaid with sticky exudates, especially during the early period of cultivation. Septate hyphae are present that vary in diameter, even within a single colony. These are often swollen to form chlamydospore-like structures.

Type species. *Glutinomyces brunneus* Nor. Nakam.
MycoBank MB822387.

Glutinomyces brunneus Nor. Nakam., *sp. nov.*

Etymology. *brunneus* (L), refers to the brown colony colour.

Colonies grown for 28 d on potato dextrose agar (PDA) (Nissui, Tokyo, Japan) at 25 °C are 36 mm diam, pale greyish brown to dark greyish brown, flat and sulcate. Colonies are tough and sometimes overlaid with sticky exudates, and are glabrous or at times forming ridges. The colony margin is erose to undulate. A yellow to red pigment is uniformly diffused around the colony. Hyphae on PDA are septate, hyaline, 1.5–4.5 µm wide, and are often swollen. Colonies grown for 28 d on modified Norkran's C (MNC) (Yamada & Katsuya 1995) at 25 °C are 32 mm diam, light greyish brown (1317) to greyish brown (1919), flat and sulcate. Colonies are tough and exudates are lacking, and are glabrous. The colony margin is erose to undulate. A yellow to red pigment is uniformly diffused around the colony. Hyphae on MNC are septate, hyaline, 1.5–4.5 µm wide, and are often swollen and form a spiral pattern. Colonies grown for 28 d on 2 % malt extract agar (MEA) at 25 °C are 45 mm diam, greyish yellow (2212) to greyish brown (1919), flat and glabrous. The colony margin is filamentous to undulate. Hyphae on MEA are septate, hyaline, 1.5–4 µm wide, and are often swollen and produce chlamydospore-like structures. Colonies remain sterile.

Colour illustrations. *Quercus serrata* trees in Japanese secondary forest; colony morphology of *Glutinomyces brunneus* on PDA (left), MNC (centre) and MEA (right) (after 28 d at 25 °C); chlamydospore-like swellings, spiral hyphae and oil droplets in the hyphae stained using sudan black. Scale bars = 50 µm.

Typus. JAPAN, Kyoto prefecture, Kyoto city, Takaragaike park, isolated from surface-sterilised roots of *Quercus* sp., July 2015, *N. Nakamura* (holotype preserved metabolically inactive JCM 32230, ITS and LSU sequences GenBank LC218306 and LC315171, MycoBank MB822896).

Additional material examined. JAPAN, Kyoto prefecture, Kyoto city, Mt Kinugasa, isolated from surface-sterilised roots of *Quercus serrata*, Mar. 2016, *N. Nakamura*, JCM 32231, ITS sequence GenBank LC218301; Mt Kodaiji, isolated from surface-sterilised roots of *Castanopsis cuspidata*, Feb. 2016, *N. Nakamura*, JCM 32232, ITS sequence GenBank LC218296.

Notes — BLAST searches of the ITS sequence did not retrieve any close sequences other than unidentified fungal root endophytes. The ITS and LSU sequences placed *G. brunneus* in the *Hyaloscyphaceae* (order *Helotiales*).

Noritaka Nakamura, Chihiro Tanaka & Yuko Takeuchi-Kaneko, Laboratory of Terrestrial Microbial Ecology,
Graduate School of Agriculture, Kyoto University, Kitashirakawa Oiwake-cho, Sakyo-ku, Kyoto 606-8502, Japan;
e-mail: nakamura.noritaka.54r@st.kyoto-u.ac.jp, chihiro@kais.kyoto-u.ac.jp & yuuko@kais.kyoto-u.ac.jp


Hemileucoglossum pusillum

Fungal Planet 636 – 20 December 2017

Hemileucoglossum pusillum V. Kučera, Fedosova & Arauzo, *sp. nov.*

Etymology. Name reflects the small size of ascocarps, resulting in the fungus being inconspicuous and hard to detect.

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

Ascocarps scattered to gregarious, clavate, stipitate, 0.8–3.5 cm tall, 0.1–0.5 cm wide, black throughout. *Ascigenous part* clavate, broadly clavate or compressed, c. 1/4–1/2 of the total ascocarp length, 0.2–1.1 cm long, black, concolorous with the stipe, compressed or oval in cross section, sharply delimited from the stipe, smooth both in fresh and dry conditions. *Stipe* terete, cylindrical, oval in cross section, slender to robust, conspicuously hairy with dark brown setose hairs in tufts in upper part of the stipe when fresh, rough to squamulose when dry. *Asci* clavate to broadly clavate, (135–)141.5–181.5(–187) × (14–)15.5–23.5(–25) µm (measured in water), Q = (6.3–)6.8–8.7(–9.5), 8-spored, with euamyloid apical ring and inamyloid wall in MLZ and IKI. *Ascospores* elongate-clavate, subfusiform to fusiform, narrowed to the base, sometimes slightly curved, (41–)50–76.5(–82) × (5–)5.5–7.5(–8) µm (in water), Q = (8.5–)12.6(–15.2), hyaline, finally in some asci becoming brown, predominantly 3–4-septate, rarely with 0–5(–6) septa. *Ascoconidia* not observed. *Paraphyses* cylindrical, sparsely septate, 2–3 µm diam, straight to slightly curved and inflated at the apex, hyaline at basal part to pale brown at the apex, embedded in a dense brown amorphous matter, extending beyond the asci. *Apical cells* usually inflated and constricted or pyriform, sometimes proliferating (12.5–)18.5–46(–54) × (4.5–)6–8.5(–11) µm. *Stipe surface* squamulose of protruding paraphysal elements forming scales and with tufts of dark brown setose septate hairs (85–)90–120(–144) µm long, straight, moderately septate, basal cell usually inflated, (7–)10–13(–17.5) µm, medial part (4.5–)5.5–7(–9.5) µm and apical part (2–)3 µm with rounded apex. For supplementary description and iconography see *H. littorale* in Arauzo & Iglesias (2014).

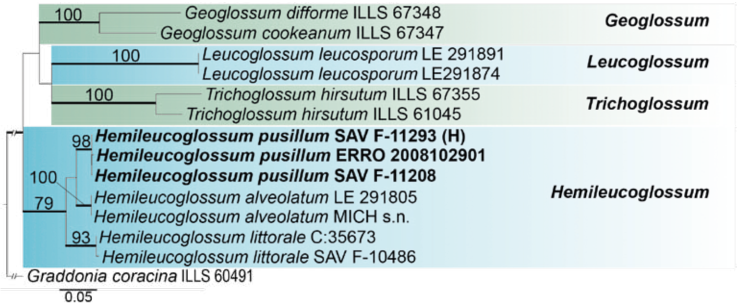
Colour illustrations. Veľká Fatra Mts, Stankovany, calcareous fen Močiar with mineral spring; spores; paraphyses and asci; asci and amyloid reaction of the ascal apical ring; setose hairs of the stipe surface; ascocarps (all from holotype); type locality. Scale bars = 1 cm (ascocarps), 20 µm (microscopic structures).

Habit, Habitat & Distribution — In small groups on soil in the vicinity of a mineral spring of the fen, in peat-bog and sandy bank of the river. The species is known only from five localities, two in Slovakia and three in Spain (Arauzo & Iglesias 2014).

Typus. Slovakia, Veľká Fatra Mts, calcareous fen Močiar, Stankovany, c. 1.7 km NW from the village centre, N49°09'14.53" E19°09'6.39", alt. 440 m, fen with mineral spring, in association of *Triglochin palustre*, *Trichophorum pumilum*, *Centaurium littorale* subsp. *uliginosum*, on gravel soil, 11 Nov. 2016, *V. Kučera* (holotype SAV F-11293, ITS and LSU sequences GenBank MF353090 and MF353093, MycoBank MB821845).

Additional specimens examined. Slovakia, Veľká Fatra Mts, Rojkov, c. 500 m NWW from the centre, Rojkovské rašelinisko National Reserve, N49°08'54.7" E19°09'17.4", alt. 438 m, peat bog, on soil, 8 Oct. 2014, *V. Kučera*, SAV F-11208, ITS and LSU sequences GenBank MF353088 and MF353091. – Spain, Bizkaia, Iurreta, N43°11'18.7" W02°37'57.9", alt. 135 m, sandy shore of the river Zaldai with *Carex pendula*, *Chamaecyparis lawsoniana*, *Fraxinus excelsior*, *Alnus glutinosa*, 29 Oct. 2008, *S. Arauzo*, ERRO-2008102901, ITS sequence GenBank KP144108 (as *H. littorale* in Arauzo & Iglesias 2014).

Notes — Arauzo & Iglesias (2014) introduced a new genus *Hemileucoglossum* for four species of *Geoglossum* with setose hairs on the stipe, predominantly hyaline mature ascospores and paraphyses agglutinated by a dense brown amorphous material. The type species of the genus *H. littorale* occur in localities with *Littorela uniflora* plants (Kers & Carlsson 1996) and differs from *H. pusillum* in shorter and narrower asci (120–145 × 18–20 µm) and spores (50–60 × 4–6 µm) and presence of long brown branched hyphae (30–80 × 2–5 µm) on the stipe surface. *Hemileucoglossum alveolatum* has more septate (up to 15) and longer (60–95 × 4–5 µm) ascospores (Durand 1908), *H. elongatum* differs in curved shape of apical cells of paraphyses (Nannfeldt 1942), and *H. intermedium* has spores with 7–11 septa (Durand 1908).



Maximum likelihood tree (RAxML web server) was obtained from the ITS-LSU dataset sequences of *Hemileucoglossum pusillum* (H: holotype) and other *Geoglossaceae* species (TreeBASE submission ID 21213). The Bayesian analysis (MrBayes v. 3.2.5) was performed for 1 M generations under SYM+G model for ITS and GTR+G model for LSU. Numbers above branches indicate Maximum likelihood bootstrap values > 75 %, thickened branches indicate Bayesian posterior probabilities > 0.95. The scale bar represents the number of nucleotide changes per site.

Viktor Kučera, Plant Biology and Biodiversity Center, Institute of Botany, Slovak Academy of Sciences,
Dúbravská cesta 9, SK-845 23, Bratislava, Slovakia; e-mail: viktor.kucera@savba.sk
Anna G. Fedosova, Laboratory of Systematics and Geography of Fungi, Komarov Botanical Institute of the Russian Academy of Sciences,
197376, 2 Prof Popov Str., Saint Petersburg, Russia; e-mail: anna.fedosova@gmail.com
Sabino Arauzo, Errotari Mycological Society, Laubideta 6, 48200 Durango, Bizkaia, Spain;
e-mail: sabino@errotari.com


Hyalocladosporiella cannae

Fungal Planet 637 – 20 December 2017

Hyalocladosporiella cannae T.K.A. Kumar, *sp. nov.*

Etymology. Named after the host genus *Canna*, from which the fungus was isolated.

Classification — *Incertae sedis*, *Chaetothyriales*, *Eurotiomycetes*.

Mycelium consisting of hyaline to olivaceous grey, branched, septate, 1–3 µm diam hyphae. *Conidiophores* dimorphic, solitary and in loose fascicles. *Microconidiophores* erect, cylindrical, almost straight, geniculate, 1–2-septate, pale brown to olivaceous brown, smooth, thick-walled (1 µm), 15–40 × 3–4 µm. *Macroconidiophores* erect, cylindrical, flexuous, geniculate, 4–8-septate, pale brown to olivaceous brown, smooth, thick-walled (1 µm), 50–130 × 4–5 µm. *Conidiogenous cells* integrated, terminal, subcylindrical, smooth, pale brown to brown, slightly thick-walled, 10–15 × 3–4 µm; loci sympodially arranged, slightly thickened and darkened. *Primary ramoconidia* ellipsoid to cylindrical, hyaline to pale olivaceous grey, smooth, 0–3-septate, slightly thick-walled, 30–40 × 5–6 µm; hila thickened and darkened. *Secondary ramoconidia* ellipsoid to cylindrical, hyaline, smooth, guttulate, 0–3-septate, slightly thick-walled, 16–23 × 4–6 µm; hila thickened. *Intercalary conidia* fusoid-ellipsoid, hyaline, guttulate, smooth, 0–2 septate, slightly constricted around the septum in some, thin-walled, 6–15 × 2–3 µm; loci thickened and darker. *Terminal conidia* lemoniform to pyriform to guttuliform, ellipsoid or fusoid, hyaline, guttulate, smooth, aseptate, thin-walled, 3–6 × 1–3 µm; loci thickened and darker.

Culture characteristics — Colonies reaching 30 mm diam after 1 wk at 28 °C on Sabouraud's agar (SA), then growth suddenly slowing down and cultures becoming non-viable and dead, erumpent, folded with smooth margins, aerial mycelium moderate. Surface on SA olivaceous grey, smoke-grey at the centre, reverse olivaceous grey.

Typus. India, Kerala, Kozhikode, on leaves of *Canna indica* (*Cannaceae*), 20 Aug. 2014, *T.K.A. Kumar* (holotype CAL 1342, ITS sequence GenBank MF072396, MycoBank MB821283).

Colour illustrations. *Canna indica* in Kerala; portion of leaf with mycelial growth; conidiophores and conidia. Scale bars = 10 µm.

Notes — *Hyalocladosporiella cannae* is morphologically and genetically distinct from the only other described species in the genus, *H. tectonae* (Crous et al. 2014a). Morphologically, *H. cannae* can be distinguished from *H. tectonae* by the former's shorter macroconidiophores, wider ramoconidia, shorter intercalary conidia that are 0–2-septate, and much shorter lemoniform to pyriform to guttuliform, or ellipsoid to fusoid terminal conidia that lack septa.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the ITS sequences are several unidentified environmental samples, GenBank KT328894 (Identities = 579/579 (100 %), no gaps), GenBank GU054168 (Identities = 579/579 (100 %), no gaps), GenBank KM265975 (Identities = 549/549 (100 %), no gaps), GenBank KF435240 (Identities = 543/543 (100 %), no gaps), GenBank KF436120 (Identities = 526/526 (100 %), no gaps), GenBank KM265610 (Identities = 494/494 (100 %), no gaps) and *H. tectonae* (GenBank KJ869142; Identities = 550/581 (95 %), Gaps = 7/581 (1 %)). Interestingly, uredospores of *Puccinia thaliae* were observed among the hyphae of *H. cannae* growing on *Canna indica* leaves. However, evidence to prove hyperparasitism by *H. cannae* was not obtained.

T.K. Arun Kumar, The Zamorin's Guruvayurappan College, Kozhikode, Kerala 673014, India;
e-mail: tkakumar@gmail.com


Hymenochaete macrochloae

Fungal Planet 638 – 20 December 2017

Hymenochaete macrochloae Olariaga & M. Prieto, *sp. nov.*

Etymology. The epithet refers to its host, *Macrochloa tenacissima*.

Classification — *Hymenochaetaceae*, *Hymenochaetales*, *Agaricomycetes*.

Basidioma annual, effuse, with appressed margin, loosely adnate, sometimes raised at the margin when old, brittle when dry, initially orbicular, confluent afterwards, up to 5 cm diam. *Hymenophore* smooth, initially even, minutely cracked in aged basidiomata, cinnamon brown (6C8, 6D8) (Kornerup & Wanscher 1978). *Margin* appressed, slightly fimbriate and yellowish brown (5B7) in young basidiomata, smooth and concolorous with the hymenophore in older basidiomata. *Basidioma section* 60–130 µm thick, not stratified, composed of the hymenium and the context. *Basidia* claviform, 4-spored, clampless, the lower 2/3 embedded in a resinous brown matter, 18–25 × 4–5.5 µm. *Basidiospores* ellipsoid in side view, thin-walled, smooth, hyaline, sometimes brown, multiguttulate, non-amyloid, 5.5–7 × 3–4 µm (L_m = 6.1–6.5; W_m = 3.5–3.8; Q_m = 1.7–1.8). *Setae* abundant, arising from the subhymenium or the upper part of the context, projecting up to 50 µm over the hymenium, subulate, dark brown, thick-walled (up to 3 µm thick), smooth, rarely with a few hyphae forming a sheath, sometimes gibbose at the base, often with a bi- or trifurcate base, (30–)69–87(–100) × 6.5–9(–10) µm. Context formed by interwoven generative hyphae, cylindrical, moderately thick-walled, often branched at a right angle, golden brown, clampless, 2.5–4 µm diam. Basal layer of vaguely parallel-arranged hyphae observed in aged basidiomata. *Crystals* sometimes present on the subhymenial and context hyphae, bipyramidal to sphaeroid, 2–3 µm diam.

Distribution — Currently known from several localities in the central area of the Iberian Peninsula.

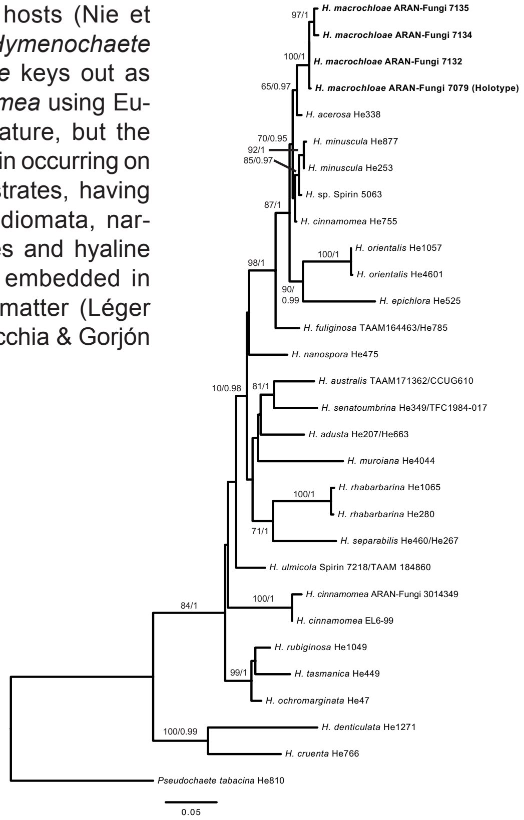
Phylogeny — ITS-LSU analyses reveal that specimens of *H. macrochloae* form a clade with maximum support in both analyses and are included in a major clade together with *H. acerosa*, *H. epichlora*, *H. minuscula*, *H. orientalis*, and an Asian specimen assigned to *H. cinnamomea* (support values 87/1). Sequences from European material of *H. cinnamomea* fall outside this clade. Based on a megablast search of the NCBIs GenBank nucleotide sequence database closest hits to the ITS sequence of the holotype of *H. macrochloae* are *H. fuliginosa* (GenBank JQ279545; Identities = 649/667 (97 %), Gaps = 3/667 (0 %)), *H. acerosa* (GenBank NR120042; Identities = 647/667 (97 %), Gaps = 2/667 (0 %)) and *Hymenochaete* sp. (GenBank KM017419; Identities = 644/665 (97 %), Gaps = 3/665 (0 %)).

Typus. Spain, Toledo, Villarubia de Santiago, Valdelaparrilla, 654 m a.s.l., on dead stems in the core of cushions of *Macrochloa tenacissima*, 19 Dec. 2016, *M. Prieto & I. Olariaga* (holotype ARAN-Fungi 7079, ITS and LSU sequences GenBank MF990738 and MF990745, MycoBank MB822948). Isotypes at AH and UPS.

Colour illustrations. *Macrochloa tenacissima* community where the holotype of *Hymenochaete macrochloae* was encountered; basidiomata growing on dead stems of *M. tenacissima*, setae, basidia, multiguttulate basidiospores in H_2O (left) and basidiospores with homogeneous content in KOH 5 % (right). Scale bars = 10 µm.

Additional material examined: Spain, Madrid, Aranjuez, El Regajal, 562 m a.s.l., on dead stems of *Macrochloa tenacissima*, 14 Feb. 2016, *M. Prieto* & *I. Olariaga*, ARAN-Fungi 7132, ITS and LSU sequences GenBank MF990739 and MF990744; Madrid, Arganda del Rey, El Dragón, 620 m a.s.l., on dead stems of *M. tenacissima*, 21 Apr. 2017, *I. Olariaga*, ARAN-Fungi 7133; Madrid, Arganda del Rey, Dehesa de Carrascal, 630 m a.s.l., on dead stems of *M. tenacissima*, 21 Apr. 2017, *I. Olariaga*, ARAN-Fungi 7134, ITS and LSU sequences GenBank MF990740 and MF990745; Madrid, San Martín de la Vega, El Rincón Verde, 585 m a.s.l., on dead stems of *M. tenacissima*, 23 Apr. 2017, *I. Olariaga*, ARAN-Fungi 7135, ITS and LSU sequences GenBank MF990741 and MF990746). ***Hymenochaete cinnamomea***: Spain, Basque Country, Irun, Elurretxe, on dead wood of *Fagus sylvatica*, 14 Mar. 2014, *J.M. Lekuona*, ARAN-Fungi 3014349, ITS and LSU sequence GenBank MF990742 and MF990747).

Notes — *Hymenochaete macrochloae* is characterised by producing thin basidiomata, short setae with a furcate to multifurcate base, basidia embedded in a resinous brown matter and being apparently restricted to *Macrochloa tenacissima* – an endemic *Poaceae* from arid areas of the Western Mediterranean countries. *Hymenochaete acerosa* differs from *H. macrochloae* in its considerably longer setae, basidia not embedded in a resinous matter and occurring on angiosperm wood (He & Li 2011). *Hymenochaete orientalis* shares with *H. macrochloae* setae that sometimes have a furcate base, but it has longer setae and inhabits bambusoid hosts (Nie et al. 2017). *Hymenochaete macrochloae* keys out as *H. cinnamomea* using European literature, but the latter differs in occurring on woody substrates, having thicker basidiomata, narrower spores and hyaline basidia not embedded in a resinous matter (Léger 1998, Bernicchia & Gorjón 2010).



Maximum likelihood (ML) tree inferred from ITS-LSU sequences. The Bayesian analysis (MrBayes v. 3.3) was performed using mixed models of evolution for 20 M generations. Supported values of maximum likelihood bootstrap (BP-ML) and posterior probabilities (PP) are depicted at the nodes (BP-ML: > 70 % / PP: > 0.95 are shown).

Ibai Olariaga, Aranzadi Society of Sciences, Mycology section, Zorroagagaina 11, P.C. 200014,
Donostia-San Sebastián, Basque Country, Spain; e-mail: ibai.olariaga@ehu.eus
María Prieto, Área de Biodiversidad y Conservación, Universidad Rey Juan Carlos, c/Tulipán, P.C. 28933,
Móstoles, Madrid, Spain; e-mail: maria.prieto@urjc.es


Lasiosphaeria similisorbina

Fungal Planet 639 – 20 December 2017

Lasiosphaeria similisorbina A.N. Mill., T.J. Atk. & Huhndorf, *sp. nov.*

Etymology. The specific epithet refers to the resemblance of this taxon to *L. sorbina*.

Classification — *Lasiosphaeriaceae*, *Sordariales*, *Sordariomycetes*.

Ascomata ampulliform to ovoid, papillate, 400–500 µm diam, 500–600 µm high, numerous, scattered to gregarious, superficial; young ascomata tomentose, white, tomentum becoming tightly appressed, crust-like and cream to waxy and brownish grey with age, occasionally areolate, finally tomentum wearing away and ascomata becoming black and glabrous; neck conical, glabrous, black. *Ascomatal wall* of *textura angularis* in surface view, in longitudinal section 3-layered, 36–90 µm thick, inner layer pseudoparenchymatous, 7–24 µm thick, composed of 4–6 layers of elongate, flattened, hyaline to pale brown cells, middle layer pseudoparenchymatous, 12–34 µm thick, composed of 5–8 layers of polygonal to angular, pale brown cells, outer layer prosenchymatous, 17–32 µm thick, composed of several to few layers of hyphae depending on age of ascomata, hyphae 1–3 µm wide, hyaline to pale brown, septate, thin-walled. *Ascomatal apex* with periphyses. *Centrum* with yellow pigments that quickly diffuse in water. *Paraphyses* filiform, 2–5 µm wide, longer than asci, hyaline, numerous, septate, unbranched, persistent. *Asci* cylindrical, 160–230 × 14–20 µm, stipitate, stipe 27–80(–120) × 4–5.5 µm, numerous, unitunicate, thin-walled, apex truncate; ring narrow, shallow, refractive; subapical globule typically absent, with 8, bi- to triseriate ascospores. *Ascospores* short cylindrical, ends rounded, 32–45(–50) × 5–7.5(–10) µm (39.5 ± 4 × 6 ± 0.5), allantoid to occasionally geniculate, usually aseptate, becoming up to 7-septate with age, hyaline to yellowish, occasionally containing globose, refractive oil droplets, appendages absent, occasionally producing phialides directly from the ascospores.

Culture characteristics — Colonies (of holotype and paratypes) moderately slow-growing on all media, covering the WA, CMA and PDA plates in 28 d, silky and hyaline on WA and CMA, felty and white (5A1–5A2) on PDA; margin even, appressed, hyaline on all media; reverse same as the mat. *Asexual morph*: Hyphae largely undifferentiated, 1–4 µm wide, thin-walled, hyaline. *Conidiogenous cells* phialides, abundantly produced from hyphae as single terminal phialides on WA and CMA, not seen on PDA, delimited by a basal septum, monophialidic, cylindrical to lageniform, 8–15 × 1.5–5 µm at widest part, hyaline; collarette absent. *Conidia* pyriform to obclavate, truncate at base, 2.5–5.5 × 2–3 µm, hyaline.

Habitat & Distribution — Decorticated, well-decayed wood of *Freycinetia*, *Fuchsia*, *Nothofagus* and *Podocarpus* in mixed native forest. Known only from the North and South Islands of New Zealand.

Colour illustrations. Background photo of typical subtropical forest in the North Island of New Zealand; ascomata; longitudinal section through ascoma, longitudinal section through ascomal wall; ascus; ascus apex; ascospore, and phialides. Photos: Andrew Miller. Scale bars: 500 µm (ascomata), 100 µm (ascomal sections), 10 µm (all others).

Typus. New Zealand, North Island, Gisborne, Urewera National Park, Lake Waikaremoana, vic. of motor camp, Ngamoko Track, on decorticated wood, 30 May 1983, *G.J. Samuels*, *P.R. Johnston*, *T. Matsushime & A.Y. Rossman*, AR 1884 (holotype at BPI, isotype at ILLS, culture ex-type AR 1884-1 (isolate died before deposition), ITS-LSU GenBank sequence MF806376, MycoBank MB822647).

Additional material examined. New Zealand, North Island, Gisborne, Urewera National Park, Lake Waikaremoana, vic. of motor camp, Ngamoko Track, on decorticated wood, 30 May 1983, *G.J. Samuels*, *P.R. Johnston*, *T. Matsushime & A.Y. Rossman*, AR 1885 (BPI); Tongariro National Park, Erua Scarp, on 5 cm branch of decorticated, well-decayed wood in mixed podocarp-broadleaf forest, 6 Apr. 2005, *A. Bell*, TJA786; Rangitikei, Rangiwahia Reserve, Ruahine Forest Park, -39.8095, 176.1289, 21 May 2015, *A. Bell*, Herb. no. 1245 = PDD 110487 = ILLS 81090, isolates ANM Acc#874-1, -2, -3, -4, -5 (all isolates died in culture before deposition), ITS-LSU GenBank sequence MF806374; near Wellington, Rimutaka Forest Park, on log of *Freycinetia banksii*, -41.3518S, 174.9228E, 20 Jan. 2013, *A.N. Miller*, *J.A. Miller*, *A. Bell & D.P. Mahoney*, Herb. no. 1200 = PDD 103345 = ILLS 81088, isolates ANM Acc#617-1, -2, -3, -4, -5, -6, -7 (all isolates died in culture before deposition), ITS-LSU GenBank sequence MF806375 (as *L. sorbina* in Bell & Mahoney 2016); South Island, South Canterbury, Peel Forest, Kaihikatea Walk, on decorticated, well-decayed wood in *Podocarpus dacrydioides* forest with mixed other natives and some pasture, 26 May 2002, *T.J. Atkinson*, TJA144; Southland, Hokanui State Forest, on undetermined wood, 22 Apr. 1985, *G.J. Samuels*, *P.K. Buchanan & L.M. Kohn*, PDD 47762, cultures GJS 85-105 = CBS 124344 (as *L. ovina*; neither specimen nor CBS culture examined in this study), ITS sequence GenBank MF806377 kindly provided by P. Crous for use in this study; near Dunedin, Woodside Glen, on decorticated wood of 5 cm branch of *Fuchsia excorticata*, late 2005, *N. Hesom-Williams*, TJA212; Woodside Glen, near Outram, Otago, on wood of unidentified tree, -45.8501S, 170.1648E, 15 May 2008, *A. Bell*, *D.P. Mahoney*, Herb. no. 1044 = PDD 94223 = ILLS 81089, ITS-LSU GenBank sequence MF806373; North Canterbury, Oxford, Oxford Forest, near Eyre Stream, on bark of 4 cm branch of *Nothofagus*?, 24 Oct. 2005, *Jerry Cooper*, TJA907. See Appendices 2 and 3 in Atkinson (2006) for additional specimens examined.

Notes — *Lasiosphaeria similisorbina* possesses the typical characters known for the genus: tomentose ascomata containing yellow centrum pigments (Miller & Huhndorf 2004a, b). This species can be distinguished by its whitish ascomata, lack of a distinct ascal subapical globule, and short cylindrical ascospores that lack appendages. It has ascomata resembling *L. ovina*, but asci and ascospores similar to *L. sorbina*. *Lasiosphaeria ovina* has a distinct ascal subapical globule and ascospores with appendages, whereas *L. sorbina* has ascomata with greyish, pinkish or orange tomentum. Small (~2 µm diam) subapical globules are occasionally observed in water mounts of fresh material (e.g., TJA786), but these disappear in Shear's Mounting Media (Atkinson 2006). However, two collections from Leith Saddle, Dunedin (TJA927, TJA931) and one from Nelson (PDD 36624), have subapical globules that remain visible in Shear's Mounting Media. As none of these three collections have been sequenced, it is possible they represent a different taxon. *Lasiosphaeria similisorbina* is only known from New Zealand, whereas *L. ovina* and *L. sorbina* are widespread throughout north temperate regions. Whether *L. ovina* and *L. sorbina* truly exist in New Zealand awaits confirmation via molecular sequencing. See MycoBank for supplementary information.

Andrew N. Miller, University of Illinois Urbana-Champaign, Illinois Natural History Survey, 1816 South Oak Street,
Champaign, Illinois, 61820, USA; e-mail: amiller7@illinois.edu
Toni Atkinson, P.O. Box 20, Warrington, Otago 9471, New Zealand; e-mail: tonijatkinson@gmail.com
Sabine M. Huhndorf, The Field Museum, Department of Botany, 1400 South Lake Shore Drive, Chicago,
Illinois, 60605-2496, USA; e-mail: shuhndorf@fieldmuseum.org


Lycoperdon demoulinii
e
d
c
b
a

Fungal Planet 640 – 20 December 2017

Lycoperdon subg. ***Arenicola*** Alfredo, M.P. Martín & Baseia, *subg. nov.*

Etymology. Name refers to the basidiomata growing in sandy soil and the exoperidium encrusted with sand grains.

Classification — *Lycoperdaceae*, *Agaricales*, *Agaricomycetes*.

Basidiomata mature pyriform to turbinate, *exoperidium* incrusted with grains of sand, ornamentation of two types: verrucae in specimens of *L. arenicola* or spines in specimens of *L. demoulinii*; the apical ornamentation falling off with age, leaving a smooth to areolate surface of the endoperidium; *gleba* powdery with age. *Basal exoperidium* composed of chains of globose to subglobose sphaerocysts at the spine base, and arranged in regular chains of cells in the spine apices (like in *L. perlatum*). *Apical endoperidium* composed of mycosclerids with irregular form, apical dehiscence composed of interwoven hyphae with inflated terminations. *Capillitium* aseptate and branched. *Paracapillitium* absent or septate and incrusted with amorphous hyaline glebal membrane (in specimens of *L. arenicola*). *Basidiospores* globose, punctate to slightly verrucose (A–B) (sensu Demoulin (1972), where A–D indicates smooth/punctate basidiospores ‘A’ to strongly verrucose ‘D’) under light microscope, and minute verrucae under Scanning Electron Microscope.

Ecology & Distribution — The specimens of *Lycoperdon* subg. *Arenicola* have single to gregarious habitats, growing in Atlantic rainforest on sand dune or in amazon rainforest (*L. arenicola* species). Until now, the distribution of *L.* subg. *Arenicola* is restricted to Brazil.

Type species. *Lycoperdon arenicola* (Alfredo & Baseia) Baseia, Alfredo & M.P. Martín.

MycoBank MB818186.

Lycoperdon demoulinii Baseia, Alfredo & M.P. Martín, *sp. nov.*

Etymology. In honour to Prof. Vincent Demoulin, for his contribution to the study of the genus *Lycoperdon*.

Basidiomata mature epigeous, pyriform to turbinate, 16–20 × 11–21 mm. *Exoperidium* incrusted with grains of sand, ornamentation of black spines (14F4) 0.6–1 mm long at the apical portion, and black verrucae (14F3) at the basal portion; the apical spines falling off with age. *Endoperidium* yellowish white (3A2) to yellowish grey (3A3), surface marked by areoles. *Gleba* powdery brown. *Basal exoperidium* composed of globose to subglobose sphaerocysts, 20–39 × 19–27 µm, disposed in non-regular chain at the base of the spines, which remains on endoperidium surface after the spines have fallen off, walls 1–2.2 µm thick, while the spines are formed by regular chains of sphaerocysts (like in *L. perlatum*), globose to pyriform, 21–28 × 14–18 µm, walls < 1.5 µm thick. *Apical endoperidium* composed of interwoven hyphae with inflated terminations, 8–17 µm diam, walls 1.3–2.2 µm thick, mixed with mycosclerids, irregular shape, 40–75 × 10–34 µm, walls 2–3.7 µm thick, weakly dextrinoid. *Capillitium* 3–5 µm diam, without pores and septa, walls 1–1.8 µm thick. *Paracapillitium* absent or rare. *Basidiospores* globose, 4–4.5 µm diam, punctate (A–B) often A in LM.

Ecology & Distribution — The specimens have a gregarious habitat, growing in the Atlantic rainforest on sand dunes. Until now the distribution of *L. demoulinii* is restricted to Brazil.

Colour illustrations. Brazil, Rio Grande do Norte, Natal, Parque Estadual Dunas de Natal, field track of locality type where the specimens were collected; a. dry specimen; b. detail of exoperidium ornamentation; c. detail of endoperidium surface areolate; d. mycosclerids from apical endoperidium; e. capillitium and basidiospores punctate in LM. All images from holotype UFRN-Fungos 655. Scale bars: a = 10 mm; b–c = 2 mm; d = 20 µm; e = 5 µm.

Typus. Brazil, Rio Grande do Norte, Natal, Parque Estadual Dunas de Natal, S35°21'40" W06°18'18", in dunes growing on sandy soil, 24 June 2006, leg. *M.M.B. Barbosa & I.G. Baseia* (holotype UFRN-Fungos 655, ITS and LSU sequences GenBank KU958307 and KU958308; isotype S35°21'40" W06°18'18", 11 May 2011, leg. *B.D.B. Silva et al.* UFRN-Fungos 2554, ITS and LSU sequences GenBank KU958309 and KU958310, MycoBank MB816279).

Notes — The molecular analyses, based on ITS and LSU nrDNA sequences, obtained by Alfredo et al. (2017) revealed *Lycoperdon* subg. *Arenicola* proposed here as the sister clade of *L.* subg. *Morganella.* Moreover, the two specimens of *L. demoulinii* grouped in a well-supported clade (bootstrap, bs = 100 %; posterior probability, pp = 1.0) and separate from *L. arenicola* (bs = 84 %, pp = 1.0).

Lycoperdon demoulinii can be clearly distinguished from *L. arenicola* since in *L. demoulinii* the exoperidium ornamentation is formed by big spines (0.6–1 mm long) that fall off leaving an endoperidium surface marked by areoles; while in *L. arenicola* these features are not present (Alfredo et al. 2014, 2017). *Lycoperdon americanum* and *L. echinatum* are species morphologically similar to *L. demoulinii* in that they have the exoperidium ornamentation formed by spines, and the endoperidium surface is areolate; in *L. demoulinii* the spines are smaller than in *L. americanum* (3 mm long) (Demoulin 1972) and *L. echinatum* (3–6 mm long) (Demoulin 1983, Calonge 1998). Also, the basidiospore ornamentation is different among these species: in *L. demoulinii* are mostly punctate (A) (although B can be found), whereas in *L. americanum* and *L. echinatum* they are verrucose (C).

Donis S. Alfredo, Programa de Pós-graduação em Sistemática e Evolução, Universidade Federal do Rio Grande do Norte, Natal,
Rio Grande do Norte, Brazil; e-mail: donis.s.a@hotmail.com
María P. Martín, Departamento de Micología, Real Jardín Botánico-CSIC, Plaza de Murillo 2,
28014 Madrid, Spain; e-mail: maripaz@rjb.csic.es
Iuri G. Baseia, Departamento de Botânica e Zoologia, Universidade Federal do Rio Grande do Norte, Natal,
Rio Grande do Norte, Brazil; e-mail: iuri.baseia@gmail.com


Megatomentella cristata
5 mm
200 µm
200 µm
200 µm
200 µm
20 µm
20 µm
20 µm
20 µm
20 µm
10 µm

Fungal Planet 641 – 20 December 2017

Megatomentella D.A.C. Almeida, Gusmão & A.N. Mill., *gen. nov.*

Etymology. Referring to the well-developed tomentum.

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

Ascomata superficial, globose, tomentose, subiculum present, ostiolate. *Beak* ridge-like, laterally compressed, opening by an elongate, slit-like ostiole. *Pseudoparaphyses* trabeculate, with gelatinous coating. *Asci* clavate, long-stipitate, thin-walled, bitunicate, fissitunicate, apex rounded, octosporous. *Ascospores* biseriate, fusiform, curved, septate, hyaline, without sheath, guttulate.

Type species. *Megatomentella cristata* D.A.C. Almeida, Gusmão & A.N. Mill.
MycoBank MB822811.

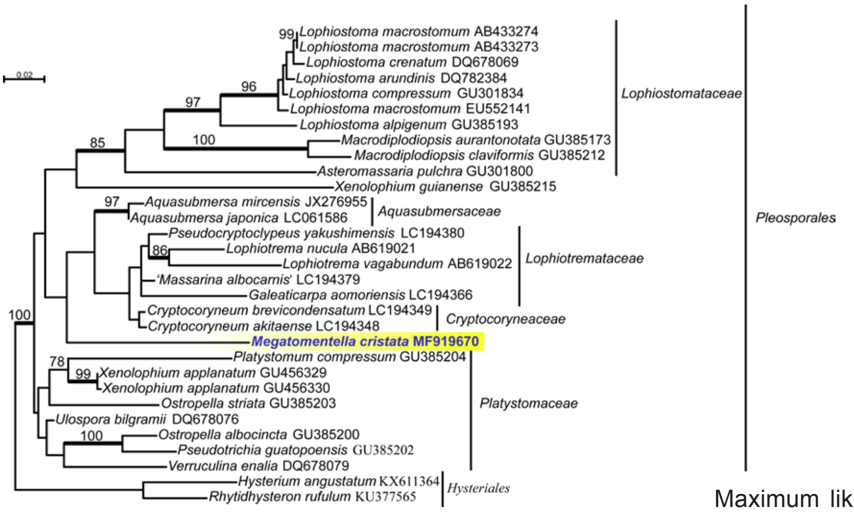
Megatomentella cristata D.A.C. Almeida, Gusmão & A.N. Mill., *sp. nov.*

Etymology. From Latin *cristatus*. Referring to the laterally compressed ascomal neck, resembling a crest.

Ascomata 340–480 × 300–480 µm, superficial, numerous, densely aggregated, globose, ostiolate, surface roughened, tomentose, sometimes forming subgroups with continuous tomentum giving an areolate aspect. *Beak* 145–220 µm long, 90–130 µm high, apical, laterally compressed, opening by an elongate, slit-like ostiole of same length; subiculum abundant, formed by brown, branched hyphae appressed to substrate. *Ascomatal wall* in longitudinal section 2-layered, 26–53 µm thick, inner layer pseudoparenchymatous, 15–28 µm thick, of *textura angularis* alternating with *textura prismatica*, composed of 8–10 layers of polygonal to elongate, pale brown, thick-walled, pseudoparenchymatic cells, outer layer heavily-melanised, 21–33 µm thick, not showing individual cell structure. *Pseudoparaphyses* 1–1.5 µm wide, trabeculate, with gelatinous coating. *Asci* 109–225 × 8–12 µm, spore-bearing part 48–73 µm, stipe 49–170 µm, clavate, long-stipitate, thin-walled, bitunicate, fissitunicate, apex rounded, octosporous. *Ascospores* 17–27 × 3.5–6 µm, biseriate, fusiform, straight or curved, 1-septate, upper cell swollen near the septum, hyaline, without sheath, guttulate, guttules spherical.

Typus. Brazil, Ceará, Ubajara, Ubajara National Park, on branches of unidentified plant, 4 May 2012, *D.A.C. Almeida* (holotype HUEFS 155135, ITS and LSU sequences GenBank MF919671 and MF919670, MycoBank MB822842).

Notes — *Megatomentella* is similar to *Ostropella* and *Xenolophium* in the morphological characteristics of the ascomata, which are superficial, globose with a slit-like ostiole, and the long-stipitate asci enclosing eight, fusiform ascospores. However, the ascomata of these two genera differ from *Megatomentella* by having papillae instead of a distinct laterally compressed beak and the ascospores are usually pigmented and constricted at the septa. *Lophiostoma* can also be compared to our material in the ascomata opening by a slit-like ostiole, but it is distinct in having immersed to erumpent ascomata lacking tomentum and by short-stipitate asci. Additionally, our specimen grouped in an independent clade within *Pleosporales*, but separate from the type species of these three genera: *L. macrostomum*, *O. albocincta* and *X. applanatum*. *Megatomentella* may represent a member of a distinct family in *Pleosporales*, but a multi-gene phylogeny is necessary to add support to this clade before a new family is warranted.



Maximum likelihood (ML) phylogenetic tree obtained using RAxML in CIPRES based on LSU nrDNA. Numbers above branches refer to bootstrap support values ≥ 70 % and thickened branches indicate significant Bayesian posterior probabilities ≥ 95 %. The new genus is highlighted in yellow. GenBank accession numbers for the LSU sequences are given after taxon names.

Colour illustrations. Brazil, Ubajara National Park, field track inside an enclave of Atlantic Forest located on a mountaintop where the species was collected; ascomata; longitudinal section through ascomal wall; ascus; ascus apex showing fissitunicate dehiscence; centrum with several asci and pseudoparaphyses; ascospores. Scale bars (as indicated).

Davi A.C. de Almeida & Luís F.P. Gusmão, Universidade Estadual de Feira de Santana, Av. Transnordestina, S/N – Novo Horizonte,
44036-900, Feira de Santana, Bahia, Brazil; e-mail: daviaugusto@gmail.com
Andrew N. Miller, University of Illinois Urbana-Champaign, Illinois Natural History Survey, 1816 South Oak Street,
Champaign, Illinois, 61820, USA; e-mail: amiller7@illinois.edu


Mutinus verrucosus

Fungal Planet 642 – 20 December 2017

Mutinus verrucosus T.S. Cabral, B.D.B. Silva, K. Hosaka, M.P. Martín & Baseia, *sp. nov.*

Etymology. In reference to the verrucose surface of the fertile portion of the pseudostipe.

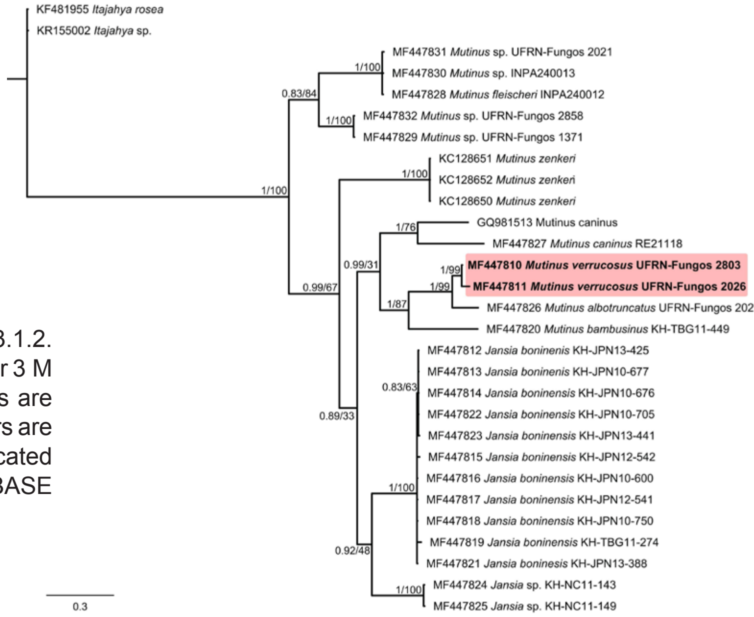
Classification — *Phallaceae*, *Phallales*, *Agaricomycetes.*

Unexpanded *basidiome* (egg) ovoid to pyriform, 11–18 mm high × 6–8 mm diam, epigeous. *Exoperidium* membranaceus, smooth, white to yellowish white (4A2), with white rhizomorphs at the base attached to the soil. *Endoperidium* with gelatinous content, hyaline. Expanded basidiome composed of a pseudostipe and volva. *Pseudostipe* cylindrical, 80 mm high × 6 mm diam, acuminated at the apex, hollow, spongy, apically perforated; sterile portion white at the bottom, becoming yellowish white (4A2) close to the fertile portion, chambered; fertile portion (receptacle) 22 mm high, reaching 1/3 of the total length of the pseudostipe, brownish red (9D6, 9E6), thick, obclavate but slightly truncate at the tip, with a pore at the apex, surface strongly verrucose. *Gleba* on the terminal portion of receptacle, mucilaginous, olive brown (4F3). *Pseudostipe* composed of pseudoparenchymatous cells, hyaline, irregular shaped, 20–57.5 × 18–47 µm. *Volva* formed by filamentous hyphae, septate, branched, hyaline, 2.6–4.5 µm diam. *Rhizomorphs* composed of filamentous hyphae, septate, hyaline, 1–5 µm diam, with crystals disposed in globose cells (14.5–50.5 × 17–50 µm). *Basidiospores* cylindrical, 4–5 × 2–2.5 µm [x = 4.3 ± 0.1 × 2.4 ± 0.6 µm, Q_m = 1.7, n = 20], smooth, hyaline.

Typus. Brazil, Rio Grande do Norte, Baía Formosa, Reserva Particular do Patrimônio Natural Mata da Estrela, growing on soil, 2012, *B.D.B. da Silva* (holotype UFRN-Fungos 2026, ITS and LSU sequences GenBank MF447811 and MF447809, MycoBank MB822002).

Additional material examined. Brazil, Pará, Belterra, Floresta Nacional do Tapajós, 2014, *T.S. Cabral*, UFRN-Fungos 2803, ITS and LSU sequences GenBank MF447810 and MF447808.

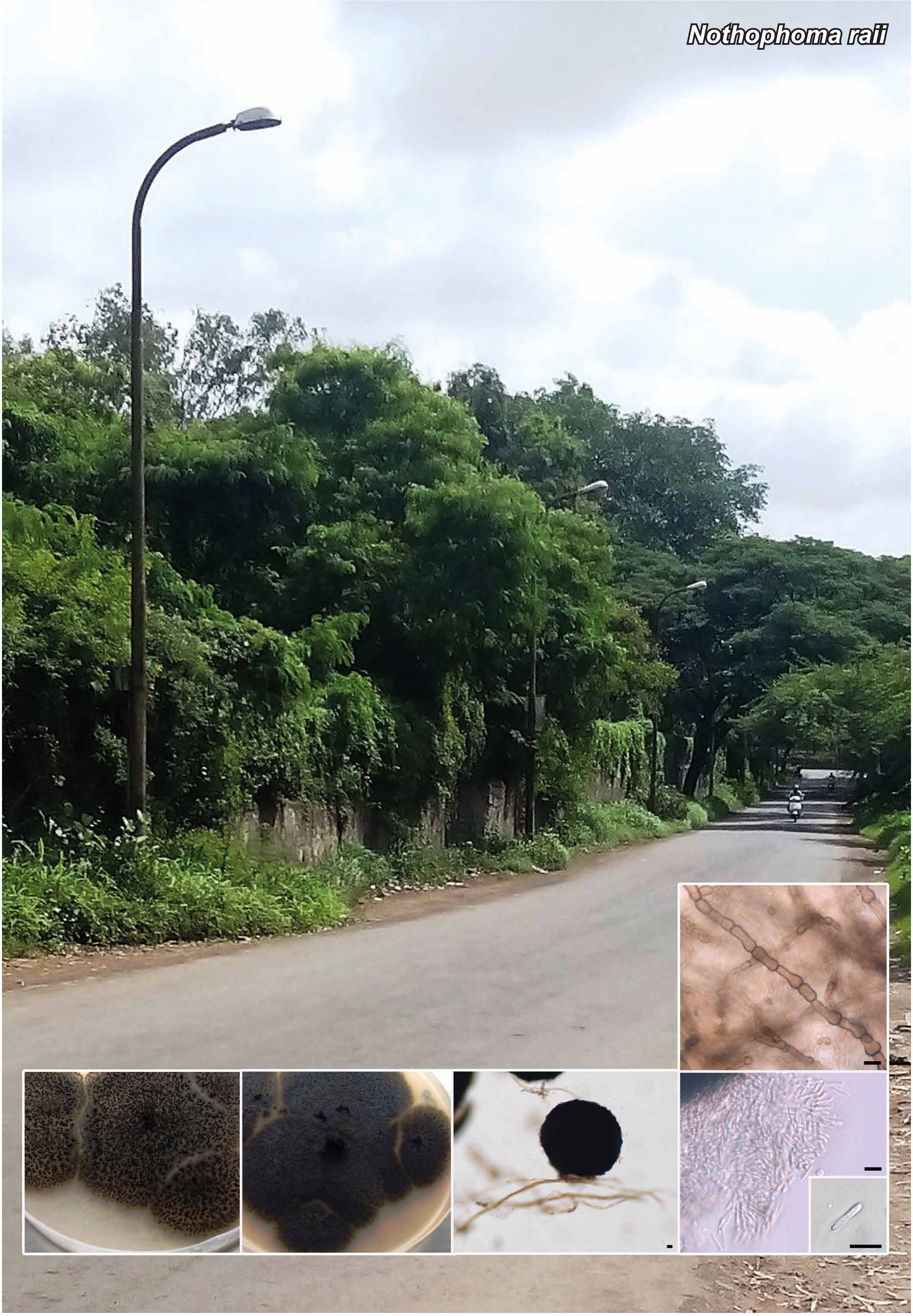
Notes — *Mutinus verrucosus* is morphologically close to *M. proximus* and *M. penzigii*, due to the nature of the surface of the apical portion. There is little information on *M. proximus*, especially about the surface of the receptacle; however, it is different from *M. verrucosus* by having smaller basidiomata (up to 5 mm high), and the imperforate orange-red receptacle (Massee 1891). *Mutinus penzigii* was initially described based on a specimen registered as *Jansia elegans* from Java (Penzig 1899); this species is characterised by the peg-shaped processes on the surface of the receptacle (Lloyd 1909, Fischer 1910), which is different from the verrucose receptacle found in *M. verrucosus*. These species also differ in habitat: *M. penzigii* was found on rotten bamboo stems, while *M. verrucosus* is found on soil. Another morphologically similar species to *M. verrucosus* is *M. boninensis*, due to its white pseudostipe and brownish red receptacle perforated at the apex, but *M. boninensis* has an annulated surface of the apical portion (Lloyd 1909, Kobayasi 1937). On the other hand, *M. borneensis* resembles *M. verrucosus* with the white pseudostipe (Penzig 1899, Kibby 2015), but the apical portion surface is an irregular fragile network of variable meshes, and with brownish colour. Based on ITS nrDNA phylogenetic analyses, *M. verrucosus* is close to *M. albotruncatus* with high support values (posterior probability = 1; bootstrap = 99 %); however, *M. albotruncatus* has a pale brown receptacle with slightly verrucose surface and doliiform to cylindrical shape (Da Silva et al. 2015).



ITS nrDNA phylogenetic tree obtained with MrBayes v. 3.1.2. (Huelsenbeck & Ronquist 2001) under GTR+I+G model for 3 M generations. Both type and paratype of the new species are marked with a rectangle. The GenBank accession numbers are indicated before species names. Support values are indicated on the branches (posterior probabilities/bootstrap). TreeBASE submission ID 21112.

Colour illustrations. Brazil, Rio Grande do Norte, Baía Formosa, Reserva Particular do Patrimônio Natural Mata da Estrela (Photo: Rhudson H.S.F. Cruz). On top, apically perforated fertile portion and fresh basidiome of *Mutinus verrucosus* (UFRN-Fungos 2026 and UFRN-Fungos 2803); scale bars = 10 mm. On bottom, crystals disposed in globose cells (red arrow) found on rhizomorphs; hyphae of rhizomorphs; and spores; scale bars = 40, 20 and 10 µm, respectively.

Tiara S. Cabral, Instituto Nacional de Pesquisas da Amazônia, Manaus, Amazonas, Brazil; e-mail: ttiara@gmail.com
Bianca D.B. da Silva, Universidade Federal da Bahia, Salvador, Bahia, Brazil; e-mail: biancadeni@yahoo.com.br
Kentaro Hosaka, National Museum of Nature and Science, Tsukuba, Ibaraki, Japan; e-mail: khosaka@kahaku.go.jp
María P. Martín, Departamento de Micología, Real Jardín Botánico-CSIC, Plaza de Murillo 2, 28014 Madrid, Spain; e-mail: maripaz@rjb.csic.es
Iuri G. Baseia, Universidade Federal do Rio Grande do Norte, Natal, Rio Grande do Norte, Brazil; e-mail: iuri.baseia@gmail.com


Nothophoma raii

Fungal Planet 643 – 20 December 2017

Nothophoma raii Rohit Sharma, *sp. nov.*

Etymology. The species is named in the honour of Prof. Mahendra K. Rai, SGB Amaravati University, India, for his contribution to the systematics of the genus *Phoma*.

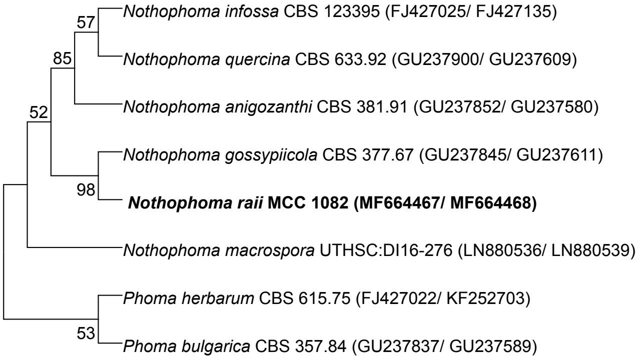
Classification — *Didymellaceae*, *Pleosporales*, *Pleosporomycetidae*, *Dothideomycetes.*

Conidiomata pycnidial, 194.3–315.5 × 195.6–411.3 µm, globose to subglobose, solitary or confluent, scattered across the Petri dish, glabrous, with or without non-papillate ostiole, sometimes projections around the ostiolum, initially brown, later brownish black; peridium 3–5-layered, 15–25 µm thick, cells of pycnidial wall composed of angular dark brown cells, 9.7–14.4 µm diam, thick-walled, *Conidiogenous cells* hyaline, thin-walled, bottle-shaped. *Conidia* aseptate, 11–14.5 × 1.5–2.5 µm, ellipsoidal, with several small, scattered guttules. *Chlamydospores* present, elongated barrel-shaped, in chains, olivaceous brown, 11–21.5 µm × 4.5–8.5 µm diam. *Hyphae* pale to dark brown, thin- to thick-walled, smooth, septate, anastomosing. *Sexual morph* not observed.

Culture characteristics — The fungus was isolated from soil on customized HK Medium 30A (sucrose 1 g, casein enzymic hydrolysate 0.75 g, yeast extract 0.25 g, pancreatic digest of casein 0.154 g, papaic digest of soybean meal 0.027 g, sodium chloride 0.045 g, dipotassium hydrogen phosphate 0.022 g, agar 15.0 g) (Hi-Media, India) reaching 60 mm diam in 7 d at 28 °C; moist, flattened, irregular margin, indefinite shape, did not produce pycnidia, front and reverse are black coloured. Colonies on CA attaining 50 mm in 7 d at 25 °C, brownish black, flattened or effused, compact, reverse concolorous, and margins regular with mycelia embedded in the medium. Colonies on OA attaining 60 mm in 7 d at 25 °C, brown olivaceous, flattened or effused, compact, reverse concolorous, and margins thread like with mycelia embedded in the medium. Black dot-like pycnidia formed in OA and CA after 1 mo of incubation that are darker than the mycelia. Pycnidia are larger and more abundant on OA.

Habitat — Soil.

Distribution — India (Pimpri, Pune, Maharashtra).



Colour illustrations. India, Maharashtra, Pune, Pimpri industrial area near antibiotic producing industry; colony on OA and CA after 30 d at 25 °C, conidiomata under microscope, hyaline conidia, thick-walled elongated and barrel-shaped chlamydospores. Scale bars = 10 µm.

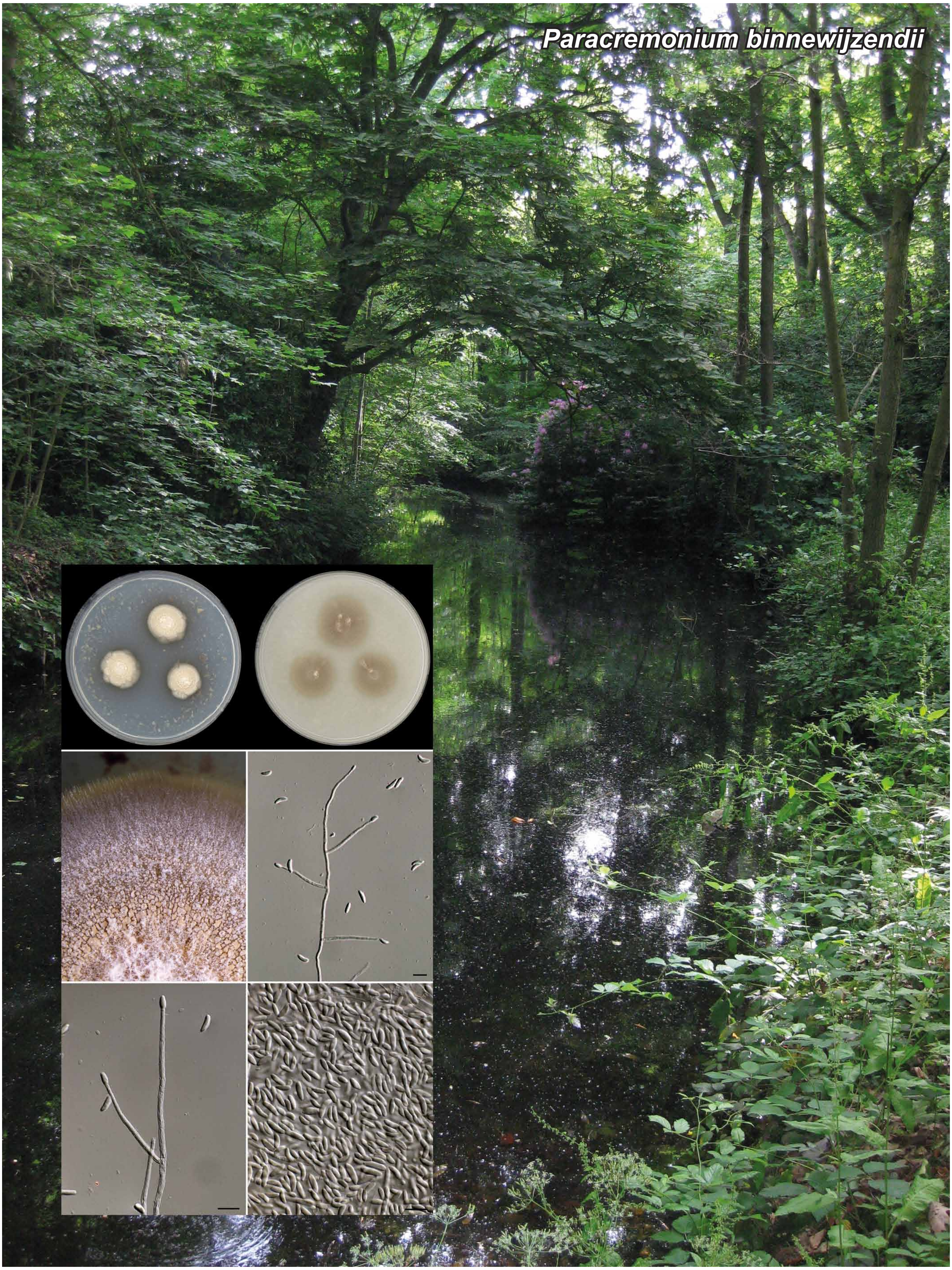
Typus. India, Pune (Pimpri), Maharashtra, soil from industrial area, 1 Aug. 2012, *R. Sharma* (holotype preserved in metabolically inactive state MCC 1082, ITS and *β-tub* sequences GenBank MF664467 and MF664468, MycoBank MB822354).

Notes — The genus *Nothophoma* (*Didymellaceae*, *Pleosporales*) was established by transferring five species of *Phoma* section macrospora with *Nothophoma infossa* as type species (Chen et al. 2015). *Nothophoma* is a close relative of *Phoma* characterized by aseptate, ovoid, oblong to ellipsoidal conidia, and its distinct phylogenetic position (Chen et al. 2015). It now comprises six species viz., *N. anigozanthi*, *N. arachidis-hypogaeae*, *N. gossypiicola*, *N. infossa* and *N. quercina.* The MP phylogenetic tree constructed by using the ITS and *β-tub* sequences showed that MCC 1082 represents a new species of the genus *Nothophoma* clustering together with *N. gossypiicola* with a bootstrap value of 98 %. *Nothophoma raii* differs from *N. gossypiicola* by its higher growth rate on OA, larger pycnidia (194.3–315.5 × 195.6–411.3 µm vs 100–250 µm) and slightly longer but narrower conidia (11–14.5 × 1.7–2.5 µm vs 10–12.5 × 2.5–3.5 µm). The chlamydospores of *N. raii* are also larger than *N. gossypiicola* (11–21.5 × 4.5–8.5 vs 8–12 µm).

Phylogenetic Analysis — Two phylogenetic trees of ITS and *β-tub* regions were prepared using sequences of *N. raii* and other *Nothophoma* species from GenBank and Crous et al. (2016b) showing the phylogenetic position of the new species. The BLASTn results of ITS sequence of *N. raii* (GenBank MF664467) with fungal ex-type sequences showed closest similarity with *N. anigozanthi* CBS 381.91 (GenBank NR_135992.1; Identities = 426/434 (98 %), Gaps = 2/434 (0 %)) and *N. infossa* CBS 123395 (GenBank NR_135968; Identities = 423/434 (97 %), Gaps = 2/434 (0 %)). A phylogenetic tree showed that it clustered with *N. gossypiicola* CBS 377.67. The BLASTn results of *β-tub* sequence of *N. raii* MCC 1082 (GenBank MF664468) with ex-type sequences showed maximum similarity with *Dothiora bupleuricola* strain CBS 112.75 (GenBank KU728618; Identities = 489/497 (98 %), Gaps = 0/497(0 %)), *Verrucoconiothyrium eucalyptigenum* CBS 142535 (GenBank KY979935; Identities= 456/497 (92 %), Gaps = 1/497 (0 %)) and *N. anigozanthi* strain CBS 381.91 (GenBank GU237580; Identities = 313/335 (93 %), Gaps = 1/335 (0 %)). A phylogenetic tree of *β-tub* sequences including *N. raii* MCC 1082 shows that it clusters with *N. gossypiicola* CBS 377.67.

Maximum parsimony phylogram of ITS and *β-tub* sequence analysis; species of *Phoma* are used as outgroup. The phylogenetic position of *N. raii* is indicated in **bold**. Branches with bootstrap support (BS) ≥ 50 % (based on 1 000 replicates) are shown.

Rohit Sharma, Amey Thakur, Prafull Pawar & Karthika U. Nair, National Centre for Microbial Resource (NCMR), National Centre for Cell Science,
S.P. Pune University, Ganeshkhind, Pune, 411 007, Maharashtra, India; e-mail: rohit@nccs.res.in



Paracremonium binnewijzendii

Fungal Planet 644 – 20 December 2017

Paracremonium binnewijzendii Houbraken, van der Kleij & L. Lombard, *sp. nov.*

Etymology. Named after Daan Binnewijzend, who collected this species.

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

No sexual morph or chlamydospores observed. *Mycelium* consisting of hyaline, septate, branched, 2–4 µm diam hyphae. *Conidiogenous cells* subcylindrical, hyaline, smooth, unbranched, erect, slightly tapering towards apex with an inconspicuous collarette, (17.5–)30–55(–65) × 1.5–3 µm, 0(–1)-septate. *Conidia* formed in slimy heads at apices of conidiogenous cells, aseptate, ellipsoidal to fusoid, occasionally curved, smooth, (6–)7–11(–13) × (1.5–)2.5–3.5(–4.5) µm, mean ± standard deviation 8.5 ± 1.6 × 3.0 ± 0.5.

Culture characteristics — Colony diam, 7 d, in mm: PDA (25 °C) 16–23; PDA (30 °C) 18–25; PDA (37 °C) 8–13; MEA (25 °C) 16–22; SNA (25 °C) 20–25.

PDA, 25 °C: Colonies low convex; sporulation profuse; aerial mycelium present in centre, white; soluble pigments in agar orange-brown; margin slightly irregular; conidia *en masse* orange-pink; reverse orange-brown in centre, margin pale orange-brown. MEA, 25 °C: Colonies centrally elevated, slightly radially and concentric sulcate; sporulation poor; mycelium white to pale brown, synnematously bundled; soluble pigments absent; margin slightly irregular; conidial colour inconspicuous; reverse reddish brown. OA, 25 °C: Colonies effuse; sporulation moderate; mycelium white; aerial mycelium absent; conidia *en masse* pink-orange, in centre; reverse red-brown.

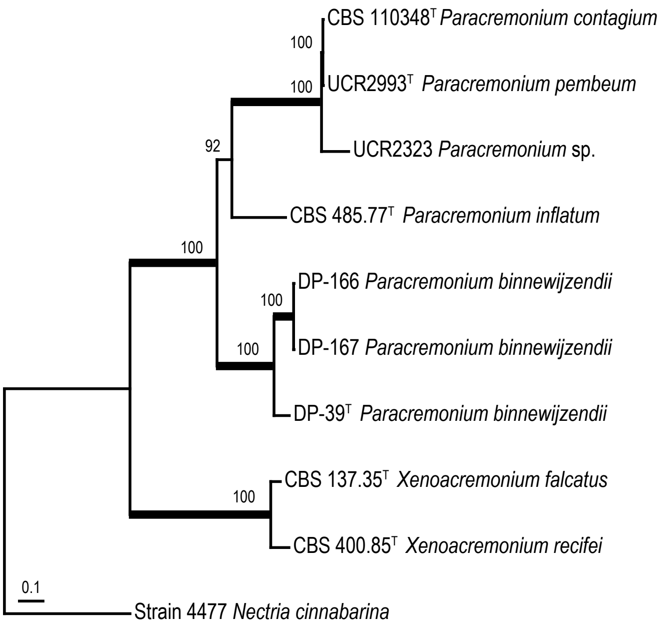
Typus. Netherlands, Leiden, ex soil from stream embankment, 2015, *D. Binnewijzend* (holotype CBS H-23246, culture ex-type DP-39 = CBS 143277; ITS, LSU and *BenA* sequences GenBank MG250173, MG250174 and MG254816, MycoBank MB823317).

Additional material examined. Netherlands, Leiden, isol. soil from stream embankment, 2015, *D. Binnewijzend* (DP-166; DP-167 = CBS 143278).

Notes — The genus *Paracremonium* was recently established for different strains from a group of fungi previously treated as *Acremonium recifei* (Lombard et al. 2015). Four species are currently accepted in *Paracremonium*, *P. binnewijzendii* (described here), *P. contagium*, *P. inflatum* and *P. pembeum*. *Paracremonium binnewijzendii* was isolated from stream embankments (The Netherlands), while *P. contagium* (Canada) and *P. inflatum* (India, Colombia) are associated with human infections, and *P. pembeum* with trees (*Acer negundo*, *Persea americana*, *Platanus racemosa*, *Ricinus communis*) and heads of *Euwallacea* sp. (California, USA) (Lombard et al. 2015, Lynch et al. 2016).

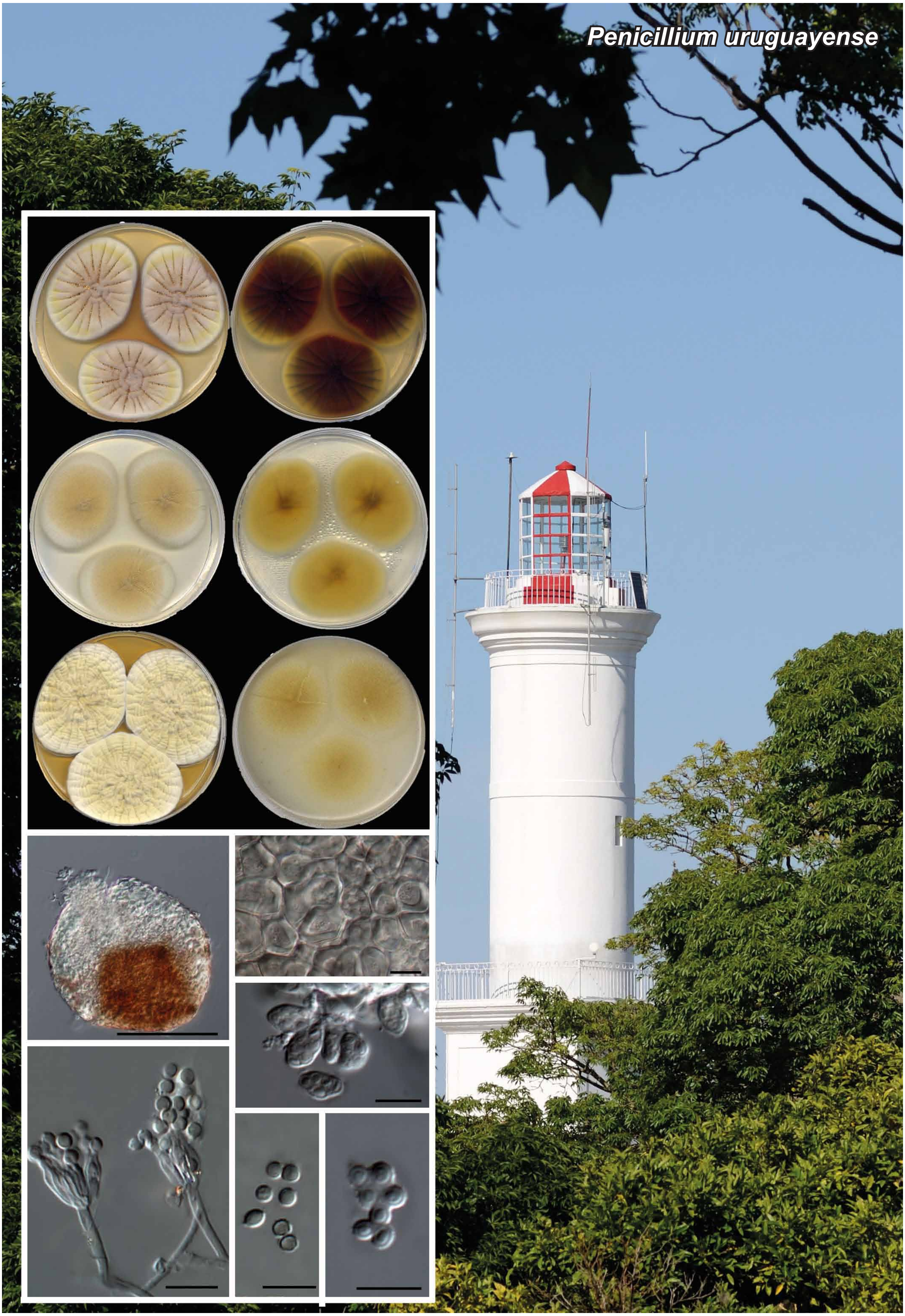
Paracremonium binnewijzendii can be distinguished from the other species in the genus by its conidial size: the conidia of *P. binnewijzendii* are generally more than 7 µm in length, and the conidia of the other species in the genus are usually less than 7 µm long. *Paracremonium inflatum* can be distinguished from the other species by the production of sterile coils from which conidiophores radiate, and *P. pembeum* is the sole species in the genus that produces globose to ellipsoidal, hyaline, thick-walled chlamydospores. No chlamydospores or coiled hyphae were observed in *P. contagium* (Lombard et al. 2015, Lynch et al. 2016).

The phylogenetic tree (*BenA*+ITS+LSU) was inferred using the Maximum Likelihood method using the RAxML-HPC v. 8.2.8 BlackBox. Bootstrap support values are indicated at the nodes (1 000 bootstraps). The scale bar indicates the expected number of changes per site. *Paracremonium binnewijzendii* is phylogenetically unique and is basal to other species in the genus.



Colour illustrations. Stream embankment in Leiden, The Netherlands; PDA (left), OA (right) (7-d-old colonies); detail of colony on PDA; conidiophores; conidia. Scale bars = 10 µm.

Jos Houbraken & Lorenzo Lombard, Westerdijk Fungal Biodiversity Institute, P.O. Box 85167, 3508 AD Utrecht, The Netherlands;
e-mail: j.houbraken@westerdijkinstitute.nl & l.lombard@westerdijkinstitute.nl
Pim van der Kleij, Dupont Industrial Biosciences, Archimedesweg 30, 2333 CN Leiden, The Netherlands;
e-mail: Pim.van.der.Kley@dupont.com


Penicillium uruguayense

Fungal Planet 645 – 20 December 2017

Penicillium uruguayense Guevara-Suarez, Dania García, Cano & Gené, *sp. nov.*

Etymology. Name refers to Uruguay, where the fungus was isolated.

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

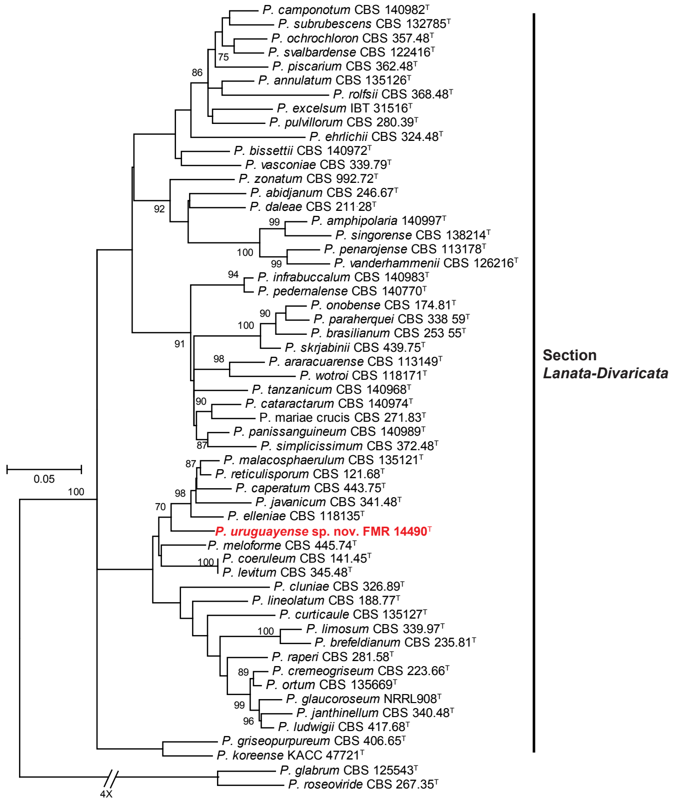
Colony diam in 7 d (mm) — On CYA: 25 °C 48–50, 30 °C 54–56, 37 °C 39–50; on MEA: 25 °C 44–47, 30 °C 50–52, 37 °C 42–45; on YES: 25 °C 53–55, 30 °C 54–56; 37 °C 50–53; on OA: 25 °C 40–45, 30 °C 50–60, 37 °C 40–45; on DG18: 25 °C 10–12; on CREA: 25 °C 10–12, weak acid production.

Colony characters at 25 °C in 7 d — On CYA, colonies velvety, slightly raised at the centre, radially sulcate, mycelium brownish grey (7C2) to yellow (3A7), margin entire; reverse reddish brown (9F8) to greyish yellow (3B5); conidial sporulation absent; abundant production of cleistothecia; exudate present, consisting of small hyaline to yellow droplets along the sulcus; soluble pigment golden yellow (5B7). On MEA, colonies granular, flat, mycelium white, margin entire; reverse greyish yellow (4B5); abundant cleistothecia; conidial sporulation absent; exudate and soluble pigment absent. On YES, colonies somewhat cerebriform at the centre, radially sulcate towards the periphery, mycelium white; reverse brown (6E8); sporulation absent; exudate and soluble pigment absent. On OA, colonies granular, flat, mycelium white, margin entire; reverse light yellow (2A5); abundant production of cleistothecia; conidial sporulation scarce, with conidial masses dull green; exudate and soluble pigment absent.

Micromorphology — *Conidiophores* only observed on OA, monoverticillate; stipes 20–50 × 2–2.5 µm, smooth-walled, hyaline. *Phialides* in verticils of 3–4 per verticil, ampulliform, 8–10 × 2–2.5 µm. *Conidia* globose to subglobose, 2.5–3 × 2–3 µm, smooth-walled. *Cleistothecia* ripen after 1–2 wk on CYA, MEA and OA at 25 °C, superficial, globose, 90–210 µm diam, greyish yellow. *Asci* clavate to ovoid, 7–9 × 5–7 µm. *Ascospores* mostly subglobose, 3–4 × 3–3.5 µm, finely spiny, with conspicuously pleated subequatorial crests.

Typus. Uruguay, Colonia Del Sacramento, from soil, 2007, collector unknown (holotype FMR H-14490, cultures ex-type CBS 143247 = FMR 14490; LSU, ITS, *BenA* and *CaM* sequences GenBank LT904730, LT904729, LT904699 and LT904698, MycoBank MB822920).

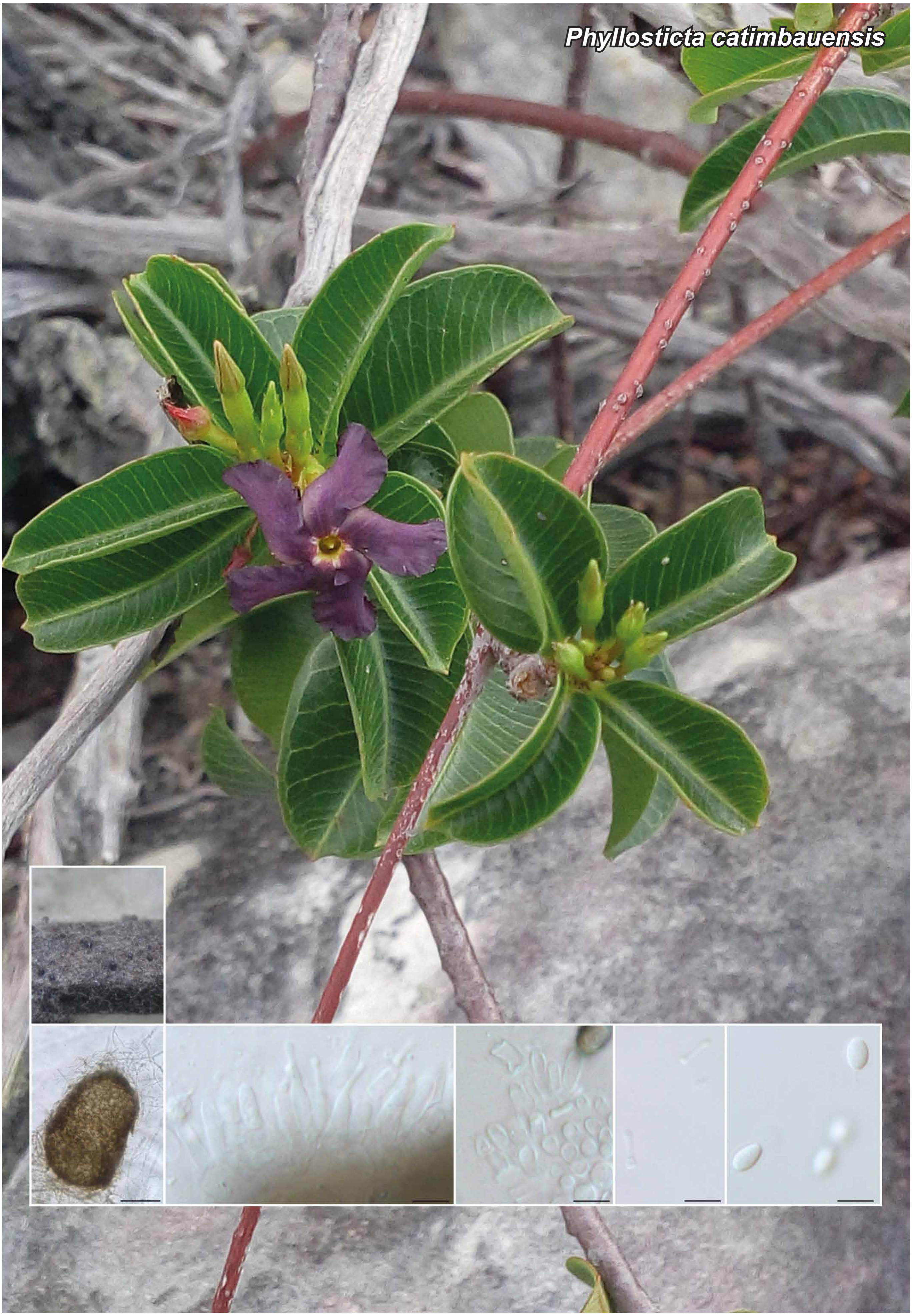
Notes — *Penicillium uruguayense* belongs to sect. *Lanata-Divaricata.* Phylogenetically, it is located in a basal branch in the *P. javanicum* clade (Visagie et al. 2015). This clade includes other sexually reproducing species, i.e., *P. caperatum*, *P. elleniae*, *P. javanicum*, *P. malacosphaerulum* and *P. reticulisporum. Penicillium uruguayense* is characterised by having good growth at 37 °C on all media tested, by the production of acid on CREA and by its restrictive growth on DG18. Within the *P. javanicum* clade, only *P. elleniae* and *P. caperatum* produce acid on CREA. However, the latter two species have ascospores with two longitudinal flanges or equatorial ridges (Visagie et al. 2015), which are inconspicuous and subequatorial in *P. uruguayense*. In addition, *P. caperatum* has smooth ascospores, whereas in *P. elleniae* and *P. uruguayense* they are spinose. The latter two can be differentiated by their conidial ornamentation, i.e., spinose in *P. elleniae* and smooth in *P. uruguayense*. *Penicillium malacosphaerulum* and *P. reticulisporum* also have smooth conidia, but their ascospores are finely rough-walled with two longitudinal flanges. *Penicillium javanicum* and *P. uruguayense* are the only species in the clade showing ascospores with an inconspicuous longitudinal furrow, but unlike the other related species, *P. javanicum* produces roughened stipes.



Maximum likelihood (ML) tree obtained from the analysis of ITS, *Ben*A and *CaM* sequence data. Bootstrap support values above 70 % are shown at the nodes. The alignment included 1 387 bp (ITS 490 bp, *Ben*A 444 bp, *CaM* 453 pb) and was performed with ClustalW and MUSCLE. Kimura-2-parameter (K2P) with Gamma distribution and invariant sites (G+I) was used as the best nucleotide substitution model. Both the alignment and tree were constructed with MEGA v. 6.06 (Tamura et al. 2013). The name in red is the new species described. ^{T} = type strain.

Colour illustrations. Lighthouse at Colonia Del Sacramento, Uruguay (image credit: Rosa Cabecinhas and Alcino Cunha); colonies growing on CYA observe, CYA reverse, MEA observe, MEA reverse, YES observe and OA observe, after 15 d at 25 °C; ascoma, peridial wall; asci; conidiophores; conidia; ascospores. Scale bars: 100 µm (ascoma), 10 µm (all others).

Marcela Guevara-Suarez, Dania García, Josep F. Cano-Lira, Josep Guarro & Josepa Gené, Mycology Unit, Medical School and IISPV,
Universitat Rovira i Virgili (URV), Sant Llorenç 21, 43201 Reus, Tarragona, Spain;
e-mail: marcelita726@gmail.com, dania.garcias@urv.cat, jose.cano@urv.cat, josep.guarro@urv.cat & josepa.gene@urv.cat


Phyllosticta catimbauensis

Fungal Planet 646 – 20 December 2017

Phyllosticta catimbauensis G.R. Araújo-Magalhães, J.D.P. Bezerra, A.R. Machado, Souza-Motta & K.A. Moreira, *sp. nov.*

Etymology. Name refers to the Catimbau National Park, a protected area of the Brazilian tropical dry forest where this fungus was isolated as endophyte from *Mandevilla catimbauensis*.

Classification — *Phyllostictaceae*, *Botryosphaeriales*, *Dothideomycetes.*

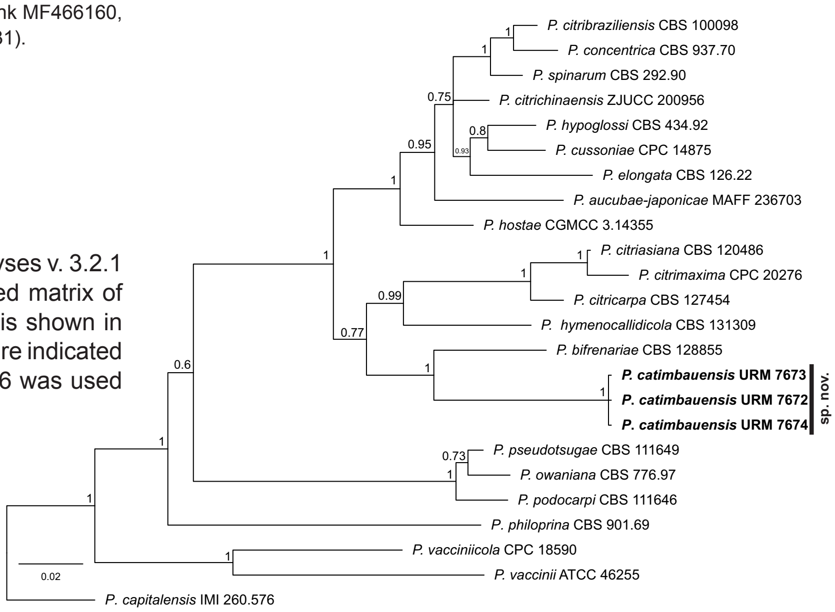
Conidiomata pycnidial, solitary or aggregated, dark brown to black, erumpent, globose to subglobose, 160–280 µm diam, exuding hyaline to crystalline conidia masses; wall of medium brown thick-walled cells of *textura angularis*. *Conidiophores* hyaline, smooth, 0–1-septate, densely aggregated, cylindrical, reduced to conidiogenous cells, or with one supporting cell, that can be branched at the base. *Conidiogenous cells* terminal, subcylindrical to ampulliform, hyaline, smooth, 9.5–10.5 × 3–3.5 µm; proliferating several times percurrently at apex. *Conidia* (8.5–)9.5(–10.5) × 5.5–6 µm, solitary, hyaline, aseptate, thin- and smooth-walled, granular, ellipsoid, globose, subglobose, broadly ellipsoidal or obovoid, tapering towards a narrow truncate base, 2.5–3.5 µm diam, enclosed in a persistent mucoid sheath, 1.5–2.5 µm thick, and bearing a hyaline, apical mucoid appendage, 3–6.5 × 1–1.5 µm, flexible, unbranched, tapering towards an acutely rounded tip. *Spermatia* aseptate, dumbbell-shaped, 5.5–9.5 × 1.5–2 µm.

Culture characteristics — Colonies covering Petri dishes after 2 mo at 25 °C. On PDA, colonies with irregular margins, and sparse aerial mycelium, surface grey to dark grey and reverse olivaceous-grey to dark grey. On MEA, surface yellowish to dark brown and reverse amber to buff. On OA surface and reverse grey to dark grey.

Typus. Brazil, Pernambuco state, Buíque municipality, Catimbau National Park (S8°36'35" W37°14'40"), as endophyte from *Mandevilla catimbauensis* (*Apocynaceae*), May 2015, *G.R. Araújo* (holotype URM 90488, culture ex-type URM 7672; ITS, LSU, *actA* and *tef1* sequences GenBank MF466160, MF466163, MF466157 and MF466155, MycoBank MB822131).

Additional material examined. Brazil, Pernambuco state, Buíque municipality, Catimbau National Park (S8°36'35" W37°14'40"), as endophyte from *M. catimbauensis*, May 2015, *G.R. Araújo*, URM 7673, URM 7674, (ITS, LSU, *actA* and *tef1* sequences GenBank MF466159, MF466162, MF466156, MF466154, and MF466161, MF466164, MF466158, MF466153, respectively.

Notes — Species of *Phyllosticta* are reported around the world as plant pathogenic, endophytic and saprobic (Van der Aa & Vanev 2002). Although the majority of these species are known as pathogens of specific plant hosts, several *Phyllosticta* spp. have been isolated as endophytes (Guarnaccia et al. 2017). Based on megablast searches in GenBank, LSU sequences of *P. catimbauensis* have high identity (99 %) to *Phyllosticta* species (e.g., *P. podocarpi*; CBS 111646; GenBank KF206323.1). On ITS sequences, *P. catimbauensis* is 99 % (540/547) similar to *Phyllosticta* sp. (LGMF1196; GenBank JX559614.1), amongst others. Using *actA* sequences, *P. catimbauensis* has low similarity of 91 % (198/217) to *P. bifrenariae* (VIC 30556 = CBS 128855; GenBank JF343649.1). On *tef1* sequences *P. catimbauensis* has 96 % (323/337) similarity to *Phyllosticta* sp. (GZAAS6.1404; GenBank KR025445.1), amongst others. Morphologically, *P. catimbauensis* is different from *P. bifrenariae* in size of the pycnidia (up to 250 µm vs 160–280 µm diam in *P. catimbauensis*), conidiogenous cells (7–10 × 4–5 µm vs 9.5–10.5 × 3–3.5 µm in *P. catimbauensis*), conidia ((10–)11–13(–16) × (7–)8–9 µm vs (8.5–)9.5(–10.5) × 5.5–6 µm in *P. catimbauensis*), appendages (6–20 × 1–1.5 µm vs 3–6.5 × 1–1.5 µm), spermatia (5–10 × 1.5–2 µm vs 5.5–9.5 × 1.5–2) (Glienke et al. 2011). In the phylogenetic analyses, *P. catimbauensis* is closely related to *P. bifrenariae*.



Bayesian inference analysis conducted with MrBayses v. 3.2.1 at CIPRES science gateway using a concatenated matrix of *actA*, *tef1* and ITS sequences. The new species is shown in **bold**. Bayesian posterior probabilities above 0.60 are indicated at the nodes. *Phyllosticta capitalensis* IMI 260.576 was used as outgroup.

Colour illustrations. *Mandevilla catimbauensis* in the Catimbau National Park; conidiomata; conidiogenous cells; spermatia, and conidia. Scale bars = 10 µm.

Gianne R. Araújo-Magalhães & Keila A. Moreira, Programa de Pós-Graduação em Biociência Animal,
Universidade Federal Rural de Pernambuco, Recife, Brazil; e-mail: gianne.rizzuto@gmail.com & moreirakeila@hotmail.com
Jadson D.P. Bezerra, Alexandre R. Machado & Cristina M. Souza-Motta, Departamento de Micologia Prof. Chaves Batista,
Universidade Federal de Pernambuco, Recife, Brazil; e-mail: jadsondpb@gmail.com, alexandrerm.agro@yahoo.com.br & cristina.motta@ufpe.br


Polycephalomyces phaothaiensis

Fungal Planet 647 – 20 December 2017

Polycephalomyces phaothaiensis Mongkols., Noisripoom, Lamlertthon & Luangsa-ard, *sp. nov.*

Etymology. Named after the place where the species was found – Ban Phaothai community forest, Phitsanulok Province, Thailand.

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

Stromata numerous, 0.5–2.5 mm in length and 1–1.5 mm in breadth, cylindrical, reddish brown. *Rhizoids* flexuous, arising from the head of *Coleoptera* larva, c. 1–3.5 cm long under the ground. Fertile part hemispherical perithecial plates, some terminal, many subterminal, pale yellowish brown, 0.5–4 mm diam, 1–2 mm high. *Perithecia* ovoid with protruding apices, (900–)-950–1 067(–1 100) × (350–)352–429(–450) µm. *Asci* cylindrical, (300–)432–581(–700) × 3–4(–5) µm. *Ascospores* hyaline, filiform, cylindrical, breaking into small truncate part-spores, (3–)3.5–5.5(–6) × 1–1.5 µm.

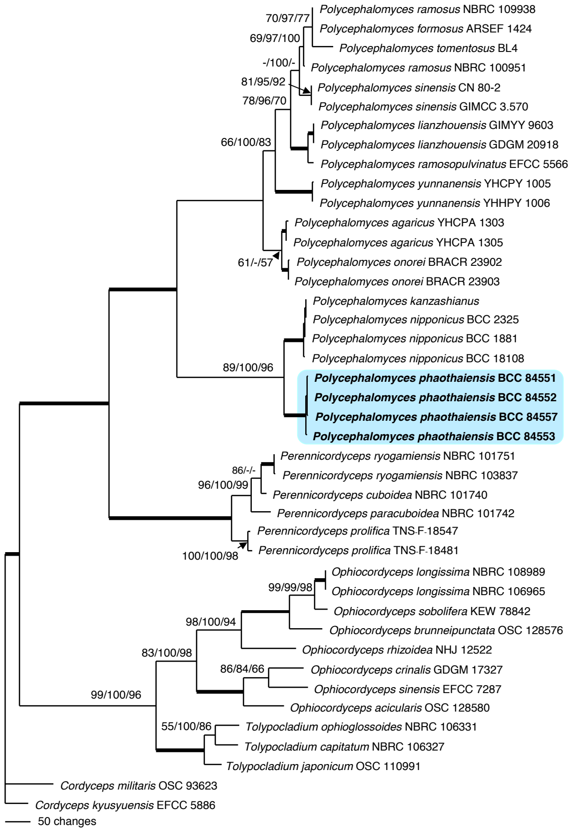
Culture characteristics — Colonies developed from germinating ascospores. The ascospores germinated within 12 h on PDA. Colonies on PDA moderately growing, c. 1 cm diam in 7 d at 25 °C. Colonies white, cottony and with abundant mycelial density. Synnemata forming after 21 d, solitary, unbranched, up to 2 mm long. Conidial mass produced on subterminal part of synnemata or covering the surface of colony. Two types of phialides present: α-phialides consisting of verticillate branches with phialides in whorls of 2–5. Entire phialides (7–)9–16(–22) × 1–2 µm, with cylindrical basal portion; α-conidia fusoid to globose, 2–3 × 1.5–2 µm, in conidial masses on PDA. β-phialides consisting of erect conidiophores either arising from aerial or vegetative hyphae. Phialides solitary along the hyphae. Entire phialides (12–)15–23(–25) × 2–2.5 µm, awl-shaped; β-conidia fusiform, in chains, (3–)4–6.5(–8) × (1–)1.5–2(–2.5) µm.

Typus. THAILAND, Phitsanulok Prov., Noen Maprang district, 16.734'N 100.658'E, alt. 520 m, on *Coleoptera* larva, buried in soil, 27 June 2017, *S. Lamlertthon (SL)*, *S. Mongkolsamrit (SM)*, *K. Tasanathai (KT) & W. Noisripoom (WN)* (holotype BBH42883, culture ex-type BCC84553, ITS, LSU, *tef* and *rpb1* sequences GenBank MF959733, MF959737, MF959742 and MF959745, MycoBank MB822770).

Additional materials examined. THAILAND, Phitsanulok Prov., Noen Maprang district, 16.734'N 100.658'E, alt. 520 m, on *Coleoptera* larvae, buried in soil, 27 June 2017, *SL*, *SM*, *KT*, *WN*, BBH42881, BBC84551, ITS, LSU, *tef* and *rpb1* sequences GenBank MF959731, MF959735, MF959739 and MF959743, BBH42882, BCC84552, ITS, LSU, *tef* and *rpb1* sequences GenBank MF959732, MF959736, MF959740 and MF959744; 28 June 2017, *SL*, *SM*, *KT*, *WN*, BBH42884, BCC84557, ITS, LSU, *tef* and *rpb1* sequences GenBank MF959734, MF959738, MF959741 and MF959746.

Notes — Until recently 10 species of *Polycephalomyces* infecting insects have been reported and only five species are reported as hyperparasites. *Polycephalomyces* species are reported from China, Japan, Ecuador and Thailand. The natural samples can be found buried in soil, on fallen leaves and plant stems. Our phylogenetic analyses and morphological assessment support the placement of *P. phaothaiensis* in *Polycephalomyces* s.lat. as amended by Kepler et al. (2013). In Thailand, *P. phaothaiensis* was originally identified as a species complex of *P. nipponicus* based on the macroscopic feature of producing multiple stromata with several terminal and subterminal perithecial plates. Although the gross morphology of *P. phaothaiensis* resembles *P. nipponicus*, it differs significantly in the sizes of the perithecia and asci. In *P. phaothaiensis*, perithecia and asci are longer and wider than those reported for *P. nipponicus* (800–950 × 300–370 µm; 530–600 × 3.1–3.5 µm) by Kobayasi (1941). Additionally, the results of our phylogenetic study using ITS rDNA, LSU, *tef* and *rpb1* sequences clearly places *P. phaothaiensis* distinctly from *P. nipponicus*.

Colour illustrations. Type locality – a trail in Ban Phaothai community forest (photo by W. Sangsawang); stromata; fertile part with perithecial plates; perithecia; asci; ascus tip; part-spores; culture on PDA; α-phialides; α-conidia; β-phialides and β-conidia. Scale bars: stromata, culture on PDA = 10 mm, fertile part with perithecial plates = 1 mm, perithecia = 500 µm, asci = 50 µm, ascus, part-spores = 5 µm, phialides, conidia = 10 µm.



The phylogenetic tree with *P. phaothaiensis* was constructed on the combined dataset comprising ITS, LSU, *tef* and *rpb1*. The phylogenetic tree was analysed using maximum parsimony (MP), maximum likelihood (ML) and Bayesian inference. ML analysis was run with RAxML-VI-HPC2 v. 8.2.10 (Stamatakis 2014) under a GTR model, with 1 000 bootstrap replicates. Bayesian phylogenetic inference was calculated with MrBayes v. 3.0b4 (Ronquist & Huelsenbeck 2003), with 3 M generations and under the same model. Numbers at the significant nodes represent MP bootstrap support values / Bayesian posterior probabilities (multiplied by 100) / ML bootstrap support values. Bold lines in the tree represent branches with values of 99–100 % for all three statistics.

Suchada Mongkolsamrit, Wasana Noisripoom & Janet Jennifer Luangsa-ard, Microbe Interaction and Ecology Laboratory, BIOTEC,
113 Thailand Science Park, Pathum Thani 12120, Thailand;
e-mail: suchada@biotec.or.th, wasana.noi@biotec.or.th, jajen@biotec.or.th
Supaporn Lamlertthon, Centre of Excellence in Fungal Research, Faculty of Medical Science Naresuan University,
Phitsanulok, 65000, Thailand; e-mail: supapornl@nu.ac.th


Pseudocercospora angularis

Fungal Planet 648 – 20 December 2017

Pseudocercospora angularis W.S. Lisboa, D.M. Macedo & R.W. Barreto, *sp. nov.*

Etymology. Named after angular leaf spots.

Classification — *Mycosphaerellaceae*, *Capnodiales*, *Dothideomycetes*.

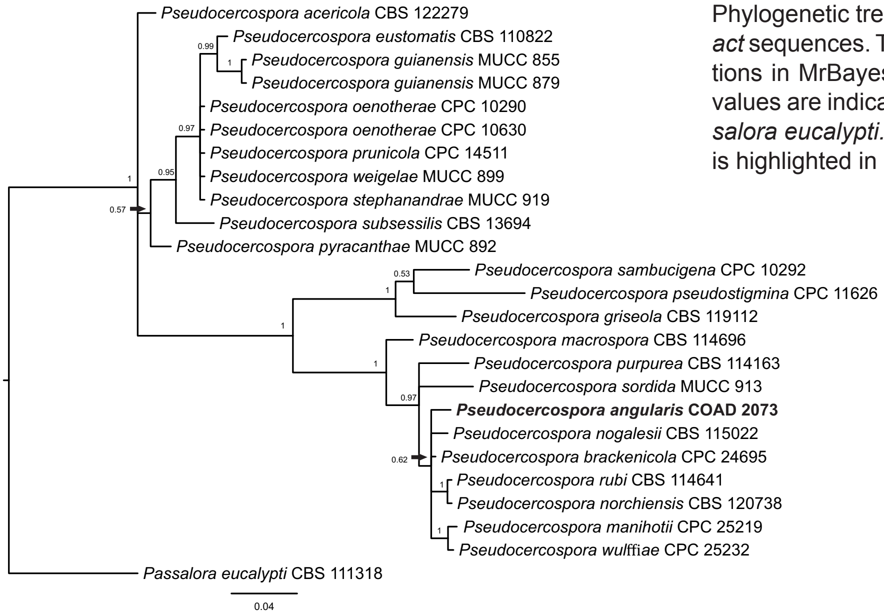
Lesions on the leaves diamond to variously angular-shaped, 4–8 × 3–11 mm, coalescing and leading to leaf necrosis. *Internal mycelium* 1–5 µm diam, branched, septate, hyaline to subhyaline. *Stromata* erumpent, pulvinate to subsphaerical, 20–40 × 25–63 µm, composed of pale to dark brown *textura angularis*. *Conidiophores* sporodochial, reduced to conidiogenous cells, epigenous, subcylindrical, 11–40 × 1.5–4 µm, aseptate, unbranched, pale to dark brown, smooth. *Conidiogenous loci* 1–2 µm diam, unthickened, not darkened. *Conidia* cylindrical to subcylindrical, mostly slightly curved, occasionally straight, 20–60 × 1.5–3 µm, apex rounded, base obconically truncate to truncate, 2–7-septate, hilum neither thickened, nor darkened, 1.5–3 µm diam, eguttulate, subhyaline, smooth.

Culture characteristics — Colonies on PDA and MEA circular, up to 32 mm diam after 17 d at 25 °C; flat with a raised centre of dense velvety aerial mycelium, evenly pale olivaceous grey; reverse olivaceous grey at the edges and dark grey; colonies sterile.

Typus. Brazil, Minas Gerais, Viçosa, Infectarium of the Departamento de Fitopatologia – Universidade Federal de Viçosa, on leaves of *Prunus persica* (*Rosaceae*), 30 May 2015, *W.S. Lisboa* INF 68 (holotype VIC 44083, culture ex-type COAD 2073, ITS and *act* sequences GenBank KX793125 and KX793124, MycoBank MB821107).

Notes — *Pseudocercospora* is the second largest genus of cercosporoid fungi containing fungi which were originally placed in *Cercospora* but have conidia which are generally pigmented and have hila which are unthickened and not darkened. They are often found causing leaf spots on a wide range of plant hosts, including several crop species of economic importance (Crous et al. 2013, Bakhshi et al. 2014, Silva et al. 2016). There are two species of *Pseudocercospora* described on *Prunus persicae*, namely *Pseudocercospora pruni-persicicola* and *P. prunicola.* The former has wider and longer conidia, 20–90 × 3–4 µm, than *P. angularis* (Hsieh & Goh 1990), and the latter has larger stromata (15–50 × 75 µm) and smaller conidiogenous cells, 5–15 × 3–4 µm (Braun & Mel'nik 1997). DNA information (*act*) is available only for *P. prunicola*, but *P. angularis* is phylogenetically clearly distinct.

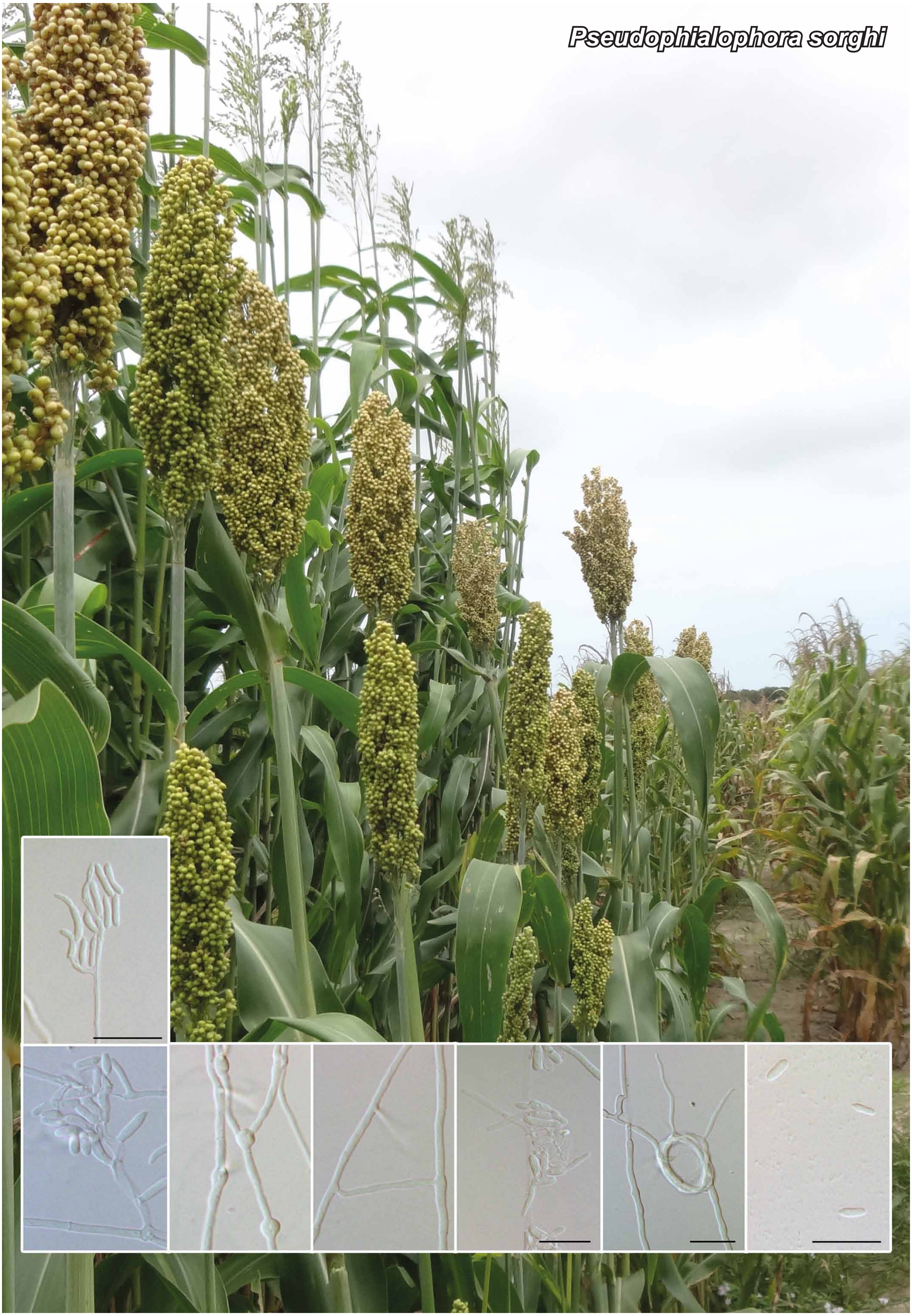
A megablast search of NCBIs GenBank nucleotide database of the closest ITS sequences yielded *Pseudocercospora norchiensis* as the closest option (GenBank EF394859; Identities = 545/546 (99 %); Gaps = 1/546 (0 %)). For *act* the highest similarity was found for *P. brackenicola* (GenBank KT037606; Identities = 209/214 (98 %); no gaps). A phylogenetic tree was constructed with the actin region (known to better explain molecular affinities in this group of fungi) and, together with morphological data justified the proposition of a new species to accommodate the fungus found on *Prunus persica.*



Phylogenetic tree inferred from a Bayesian analysis based on *act* sequences. The analysis was performed with 10 M generations in MrBayes v. 3.2.1. The Bayesian posterior probability values are indicated at the nodes. The tree was rooted to *Passalora eucalypti.* The specimen representing the new species is highlighted in **bold** face.

Colour illustrations. *Prunus persica* plant at the Infectarium of the Universidade Federal de Viçosa (Viçosa, state of Minas Gerais, Brazil) showing leaf spot symptoms to which *Pseudocercospora angularis* was associated; close-up of the angular, diamond-shaped yellow spots leading to tissue necrosis; sporodochia bearing tufts of conidia; stromata bearing conidiogenous cells and conidia. Scale bars = 20 µm.

Willyane S. Lisboa & Robert W. Barreto, Departamento de Fitopatologia, Universidade Federal de Viçosa,
Viçosa, Minas Gerais, Brazil; e-mail: willyane.lisboa@ufv.br & rbarreto@ufv.br
Davi M. Macedo, Departamento de Engenharia Florestal, Fundação da Universidade Regional de Blumenau,
Blumenau, Santa Catarina, Brazil; e-mail: dmmesk@yahoo.com.br


Pseudophialophora sorghi

Fungal Planet 649 – 20 December 2017

Pseudophialophora sorghi R.J.V. Oliveira, C.M. Gonç., G.A. Silva & J.L. Bezerra, *sp. nov.*

Etymology. Name refers to the host plant, *Sorghum bicolor*, from which this fungus was isolated as endophyte.

Classification — *Magnaporthaceae*, *Magnaporthales*, *Sordariomycetes*.

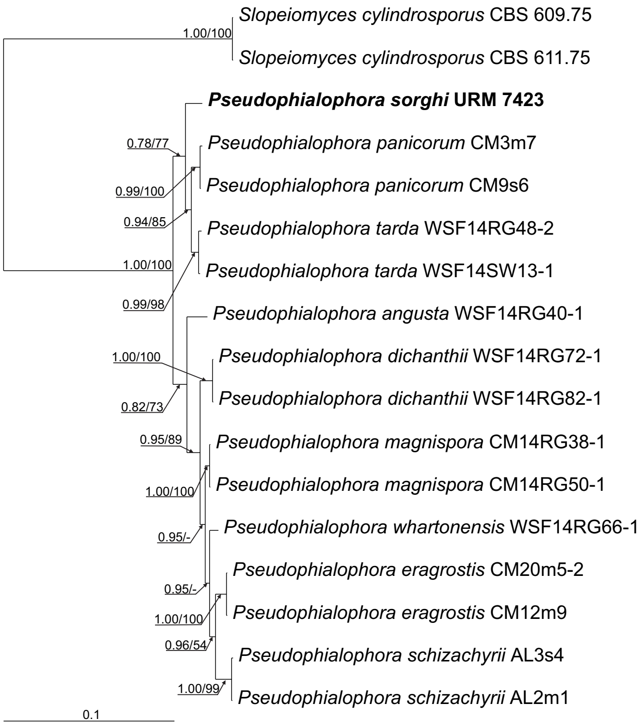
Hyphae hyaline, septate, branched, sometimes forming sterile coils. *Conidiophores* micronematous, simple or branched, hyaline, septate, non-constricted, cylindrical, straight to flexuous, apex attenuated, base not inflated. *Conidiogenous cells* polyphialidic, hyaline, simple or branched, attenuated, 4–22 × 3.5 µm. *Chlamydospores* intercalary, globose to subglobose. *Anastomosis* sometimes observed between conidiogenous cells and between conidia. *Conidia* aggregated in slimy heads, oblong ellipsoidal to ellipsoidal, aseptate, hyaline, smooth, 5–8.5 × 2–3 µm.

Culture characteristics — Colonies on PDA growing up to 1.2 cm diam after 7 d in the dark at 25 °C, dark grey, surface pale grey, aerial mycelia whitish to pale grey, reverse dark grey.

Typus. Brazil, Pernambuco, Serra Talhada (S07°59'00" W38°19'16"), as endophyte in roots of *Sorghum bicolor* (*Poaceae*), Dec. 2014, *R.J.V. Oliveira* (holotype as metabolically inactive culture, URM 7423, ITS, LSU, *rpb1* and *tef1* sequences GenBank KY421938, KY421941, KY421944 and KY421942, MycoBank MB819580).

Notes — The phylogenetic analyses of the four-gene dataset (*tef1*, *rpb1*, ITS and LSU rDNA) showed that *Pseudophialophora sorghi* formed a distinct clade with other species of *Pseudophialophora* with high support values. On ITS *P. sorghi* is 96 % (456/474) similar to *P. panicorum* (strain CM3m7, GenBank KF689652) and 96 % (443/463) to *P. tarda* (strain WSF14RG48-2, GenBank KP769840). The LSU sequence is 99 % (564/568) similar to *P. panicorum* (strain CM3m7, GenBank KF689642) and 99 % (566/568) to *P. tarda* (strain WSF14RG48-2, GenBank KP769832). The *rpb1* sequence is 99 % (602/608) similar to *P. panicorum* (strain CM9s6, GenBank KF689621) and 99 % (603/608) to *P. tarda* (strain WSF14RG48-2, GenBank KP784823). The *tef1* sequence is 99 % (884/893) similar to *P. panicorum* (strain CM3m7, GenBank KF689632) and 99 % (883/893) to *P. tarda* (strain WSF14SW13-1, GenBank KP784830). In the phylogenetic analysis *P. sorghi* is nearest to *P. panicorum* and *P. tarda*. However, colonies of *P. sorghi* are dark grey while *P. tarda* presents colonies yellowish and *P. panicorum* presents colonies yellow-green. Furthermore, conidia of *P. sorghi* (5–8.5 × 2–3 µm) are slightly smaller than conidia of *P. tarda* (7.5–9.5 × 2.5–3.5 µm) and conidia of *P. panicorum* (7.5–11.5 × 3.5–5 µm) (Luo et al. 2014, 2015). Anastomosis between conidiogenous cells and between conidia of *P. sorghi* were sometimes observed. This has never been reported in any species of *Pseudophialophora*.

Colour illustrations. *Sorghum bicolor* in the Instituto Agronômico de Pernambuco, Serra Talhada, Brazil; conidiophores; conidia, chlamydospores, sterile coils, anastomosis between conidiogenous cells, conidia and between hyphae. Scale bars = 20 µm.



Phylogenetic tree of the *Pseudophialophora* constructed using concatenated *tef1*, *rpb1*, ITS and LSU sequences. *Slopeiomyces cylindrosporus* (CBS 609.75 and CBS 611.75) was used as outgroup. Support values are from Bayesian inference and Maximum Likelihood (ML) analyses, respectively. The new species is in **bold** face. Support values of at least 50 % are shown at nodes.

Rafael J.V. Oliveira, Camila M. Gonçalves & Gladstone A. Silva, Departamento de Micologia Prof. Chaves Batista,
Universidade Federal de Pernambuco, Recife, Brazil;
e-mail: rafaelvilela87@gmail.com, mila24melo@gmail.com & gladstonesilva@yahoo.com
José L. Bezerra, Centro de Ciências Agrárias e Ambientais, Universidade Federal do Recôncavo da Bahia,
Rua Rui Barbosa, 710, 44.380-000, Centro, Cruz das Almas, Bahia, Brazil; e-mail: jlulabezerra@hotmail.com


Pyrenopeziza velebitica

Fungal Planet 650 – 20 December 2017

Pyrenopeziza velebitica Matočec, I. Kušan, Jadan, Tkalčec & Mešić, *sp. nov.*

Etymology. Named after the mountain, Velebit, on which it was collected.

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

Ascomata apothecial, collectively or solitary erumpent in early stage of development, emerging from longitudinal crack of the twig periderm, when fully expanded speciously superficial, at first globular, then hemispherically expanding, deep cupulate when mature, ± circular from the top view, *0.4–1.3 mm and †0.3–0.7 mm diam, solitary or crowded. Hymenium steel grey, not wrinkled; margin sharp, whitish pubescent, entire, not lobed, permanently inrolled; excipular surface hazel brown, somewhat mealy rugulose. *Hymenium* *65–75 µm thick. *Asci* cylindrical-ventricose with subconical apex, *68–79 × 8.5–10.5 µm, †55–61 × 5–6.5 µm, *pars sporifera* *28.5–34.5 µm, 8- (rarely 4-)spored, base cylindrical-truncate, arising from narrow repetitive croziers, apical apparatus moderately refractive in water, in Lugol's solution apical ring strongly amyloid (3bb) of *Calycina*-type. *Ascospores* subscutuliform, bilaterally symmetrical, aseptate, *(10–)10.5–*12.5*–14(–14.5) × 2.5–*2.9*–3(–3.5) µm, †9.5–11.5 × 2–2.5 µm, *Q = (3–)3.5–*4.3*–5, †Q = 3.5–4.5, hyaline, smooth, sporoplasm containing several small to medium sized lipid bodies, bi- to triseriate when inside living asci, with abundant sheath enveloping whole spores when freshly ejected. *Paraphyses* cylindrical-lanceolate, more rarely clavate, apical cell *30–66.5 × 3–5(–5.5) µm, †20–53.5 × 3–4 µm, *containing several subhyaline, strongly refractive globose vacuolar bodies which readily coalesce in still living cells, wall thin and hyaline, sometimes covered with strongly refractive golden yellow patches. *Subhymenium* slightly differentiated from medullary excipulum, *5–7 µm thick at the upper flank, of hyaline *densely packed small ± cylindrical cells *2.5–4(–7) µm wide. *Medullary excipulum* moderately gelatinised, very reduced at the upper flank, of hyaline *textura porrecta*, *8–12 µm thick; considerably thicker at the middle flank, of *textura intricata-porrecta* *14–23 µm thick; cells *2.5–4.5 µm wide. *Ectal excipulum* *52–68 µm thick at the middle flank, differentiated into two layers: inner layer *27–36 µm thick at the middle flank, of hyaline *textura angularis* with cells *4.5–17 × 4–11 µm; outer layer *24–30 µm thick at the middle flank, of brown *textura globulosa-angularis* with cells *5–11 × 4.5–10 µm. Outermost cells on the upper flank giving rise 1–4-celled hairs, *(12.5–)20–60 µm long, running at high angle to the excipular surface, with ± moniliform cells *6–13.3 µm wide, wall tobacco-brownish; terminal cells broadest, clavate-rhomboid to shortly lanceolate, *12.5–28.5 × 8.5–13 µm, wall brown to rusty brown, covered with dark brown thick patchy warts. Hairs on marginal rim flexuous, undulate, smooth, hyaline and thin-walled, cylindrical to subclavate, rapidly collapsing, *20–65 × 4–8 µm. *Subiculum* abundant, hyphae arising from lower and basal flank, wavy, almost not branched, evenly septate, with occasional short knotty lateral protuberations, walls thickened, smooth, but darker brown hyphae adpressed to the excipular surface and some distant lighter coloured hyphae finely warted, hyphae mostly greyish yellow to hazel brown, †2.5–4 µm wide. Ascus amyloidity corresponds to the system given in Baral (1987). For full description see MycoBank, under MB818668.

Distribution & Habitat — The species is known so far only from Mt Velebit, Croatia. All three existing collections are bound to the living branches of *Lonicera borbasiana* (*Dipsacales*), in the alpine karstic habitat.

Typus. Croatia, Lika-Senj County, Sjeverni Velebit National Park, northern part of Mt Velebit, Hajdučki kukovi area, 850 m E-NE from Vratarski kuk peak (1 676 m), 1 530 m a.s.l., N44°46'05" E15°00'46"; on wounds and bark of semidecorticated twigs of still living *Lonicera borbasiana* (*Caprifoliaceae*), 28 May 2017, *N. Matočec* (holotype CNF 2/10097, ITS and LSU sequences GenBank MF593628 and MF593629, MycoBank MB818668).

Additional material examined. Croatia, Lika-Senj County, Sjeverni Velebit National Park, northern part of Mt Velebit - 2 collections: Premužić trail, 1 300 m SE from Veliki Zavižan peak (1 676 m), 1 520 m a.s.l., N44°47'36" E14°59'03", 24 June 2009, *I. Kušan* & *N. Matočec*, CNF 2/8237, and Hajdučki kukovi area, 900 m E-NE from Vratarski kuk peak (1 676 m), 1 570 m a.s.l., N44°46'02" E15°00'53", 28 May 2017, *N. Matočec*, CNF 2/10099; both collections on semi-decorticated twigs of still living *Lonicera borbasiana*.

Notes — The genus *Pyrenopeziza* s.str. was erected by Fuckel (1870) for blackish, cupulate and hairy apothecial fungi with vertically striate structures on the excipular surface, inhabiting various kinds of dead herbaceous stems, leaves and petioles, canes, more rarely on wood and bark remnants. Approximately at the same time, in the middle of the 20th century, several authors dealt with the boundaries and the concept of the genus (viz. Hütter 1958, Gremmen 1958, Schüepp 1959). Today, more than 300 names are assigned to the genus but the modern comprehensive taxonomic analysis of the whole genus and its allies is still lacking. The generic name *Pyrenopeziza* is conserved against *Cylindrosporium* and *Cylindrodochium* (see May 2017). Although the genus is comprised of numerous species, the new species along with the most similar *Pyrenopeziza lonicerae* (Nannfeldt 1932) is easily recognizable by its robust apothecia with permanently inrolled sharp margin and thick excipulum consisting of continuous and thick cortex composed of several thick-walled cell-layers, marginal hairs exceeding 50 µm in length, lacking periphyses, amyloid asci, and occurring on woody plants (*Lonicera* spp.). *Pyrenopeziza velebitica* can be differentiated from *P. lonicerae* by: 1) larger spores (†9.4–11.4 × 2–2.4 µm vs †8–10 × 2 µm); 2) differently shaped paraphyses (cylindrical-lanceolate to clavate, †3–4 µm diam vs filiform, to 2 µm diam); 3) longer asci (†55–61 µm vs †50–55 µm); and 4) ± moniliform hair-like processes. *Pyrenopeziza symphoricarpi* occurs on a similar substrate (*Symphoricarpos* sp., *Caprifoliaceae*), but differs from *P. velebitica* and *P. lonicerae* in having inamyloid asci that are 50–60 µm long (Dennis 1963). The ITS sequence of *P. velebitica* was compared to DNA sequences of diverse generic representatives from mollisioid fungi downloaded from GenBank (see phylogenetic tree in MycoBank, under MB818668).

Colour illustrations. Croatia, Mt Velebit, alpine habitat in the Hajdučki kukovi area, type locality; living ascospores and a dead ascospore; living asci, crozier cell, and dead asci in IKI; living and dead paraphyses; upper flank hairs; living ascomata; vertical median section of the excipulum. Scale bars = 1 mm (apothecia), 10 µm (microscopic structures).

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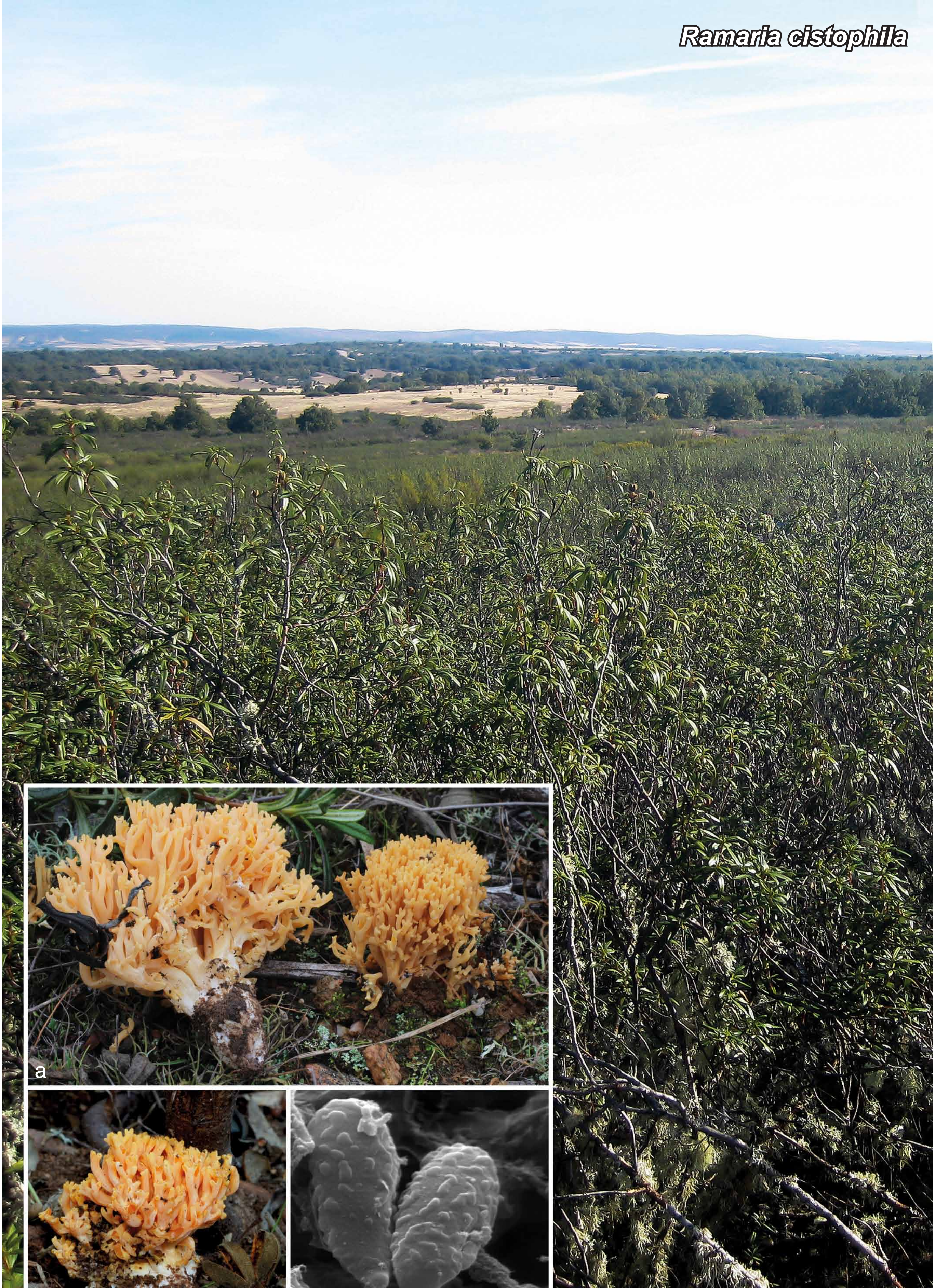
* denotes living material.

† indicates a dried specimen.

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


Ramaria cistophila
a
b
c

Fungal Planet 651 – 20 December 2017

Ramaria cistophila P.P. Daniëls, M.P. Martín, C. Rojo & Camello, *sp. nov.*

Etymology. From Greek kistos (χιστός) and philos (φίλος), referring to its host plants affinity, which are mainly *Cistus* species.

Classification — *Gomphaceae*, *Gomphales*, *Phallomycetidae*, *Agaricomycetes*.

Macroscopic characteristics — *Basidiomata* branched, initially obconical or obovoid, then campanulate or widely obovoid, 4–6 × 3–5.5 cm. *Base* glabrous, with basal branches 5–16 mm thick, white; mycelium inconspicuous, white. *Ramification* polychotomous in the basal zone, otherwise, usually trichotomous, U- and V-shaped, ramification range 3–6; branches cylindrical, initially densely grouped, then divergent; orange yellow to orange with orange yellow spore print. *Apices* obtuse, short, initially yellow, then concolorous with the branches. *Context* fibrous, compact, brittle in the branches, homogeneous, concolorous with external surface; *taste* sour in branches, softer through the base; *flavour* which reminds one of a rubber eraser. Chemical reactions: FSW (+) bluish green in hymenophore.

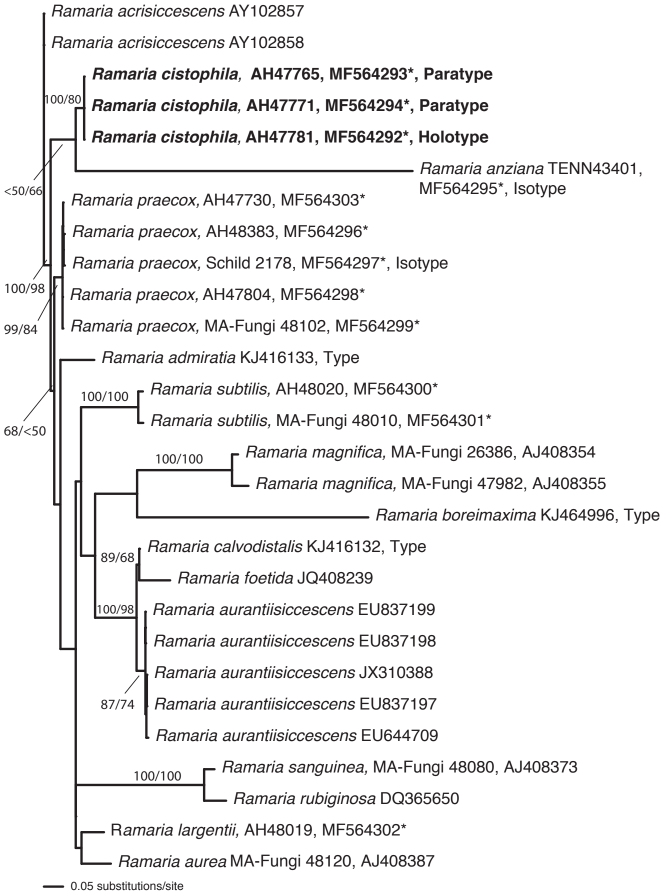
Microscopic characteristics — *Generative hyphae* without clamps, partially with ampulliform septa up to 15 µm diam, with conspicuous granular ornamentation; hyphae of 4–9 µm wide in the trama, with thin to moderately thick walls; hyphae of the mycelium 2–4(–5) µm wide, with thin to moderately thick walls; those of the external part sometimes with amorphous crystalline or granular incrustations. *Secretory hyphae* in the trama and in the mycelium, the former linear and 2–4 µm wide, the latter acanthodendroid 1.5–3 µm wide. *Hyphidia* filiform, 2–4 µm wide. *Basidia* claviform, without basal clamp, (46–)50–73(–80) × (8.5–)9–11 µm, with 4 sterigmata. *Spores* oblong-elliptical, (8.5–)9.5–11.5(–13) × 4–5(–5.5) µm (Lm = 10.9 µm; Wm = 4.7 µm; Em = 2.3); spore wall thin, yellowish with verrucose ornamentation.

Typus. Spain, Zamora, Mellanes, La Sierra, alt. 840 m, shrubland of *Cistus ladanifer*, 19 Nov. 2015, *C. Rojo*, AH 47781 (holotype, Herbarium of Alcalá de Henares University; isotype, MA-Fungi 90716, Herbarium of the Real Jardín Botánico-CSIC, Madrid; ITS sequence GenBank MF564292, MycoBank MB822118).

Additional materials examined. Spain, Cáceres, Aliseda, alt. 450 m, shrubland of *Cistus ladanifer*, 24 Jan. 2015, *F. Camello*, AH 47771, ITS and LSU sequences GenBank MF564294 and MF564304; Cádiz, Jimena de la Frontera, Las Casillas, under *Quercus suber*, 29 Nov. 2014, *A. Lobo*, AH 47764; Cádiz, Jimena de la Frontera, Los Gavilanes, under *Quercus suber* and *Cistus*, 29 Nov. 2014, *L. Estrada*, AH 47765, ITS sequence GenBank MF564293; Zamora, Mellanes, La Sierra, alt. 840 m, shrubland of *Cistus ladanifer*, 2 Nov. 2015, *C. Rojo*, AH 47782.

Notes — Although the appearance and micromorphology looks like a small-sized basidiome of *Ramaria aurea*, *R. cistophila* has a dark green positive reaction with FSW, it grows in a Mediterranean climate with *Cistus* shrubs and *Quercus suber* trees, and it has a different ITS sequence. Other quite similar unclamped species of *Ramaria* are *R. neoformosa* and *R. fagetorum*, but they have larger basidiomata and grow in the eurosiberian region. *Ramaria magnifica* (= *R. sardiniensis*) differs by bearing a violet to purple hue on the base context and has a different ITS sequence; *R. dolomitica* also has a violet hue when bruised. The molecular analyses (parsimony and maximum likelihood), based on three collections of *Ramaria cistophila*, and a number of previously unpublished sequences from our team, clearly grouped the new sequences with *R. anziana* (isotype) from Australia, collected under *Nothofagus.* However, *R. anziana* has shorter spores (7–10.5 µm long according to Young 2014), and has a pinkish colour on branches. Other closely related species is *R. praecox* from Europe but it is a vernal fruiting species with a different colour pattern, being completely yellow.

Colour illustrations. Spain, Zamora, Mellanes, shrubland of *Cistus ladanifer*; a. basidiome (AH 47781); b. basidiome (AH 47771); c. spores (AH 47765). Scale bar = 2 µm.



The single maximum likelihood tree obtained through heuristic search with the model GTR + I + G selected in PAUP v. 4.0b10. Sequences of *Ramaria acrisiccescens* were included as outgroup. Number at nodes represent percentage of bootstrap support from parsimony (first number) and maximum likelihood (second number) analyses; only bootstrap support > 50 % are indicated. The *R. cistophila* sequences are marked in **bold**. The accession numbers from GenBank sequences are indicated at all the terminals (* after GenBank Accession Number: new sequences obtained in this study).

Pablo P. Daniëls, Departamento de Botánica, Ecología y Fisiologia Vegetal, Universidad de Córdoba,
14071 Córdoba, Spain; e-mail: ppdaniels@hotmail.com
María P. Martín, Departamento de Micología, Real Jardín Botánico-CSIC, Plaza de Murillo 2, 28014 Madrid, Spain; e-mail: maripaz@rjb.csic.es
Carlos Rojo De Blas, IdForest. C/ Curtidores 17, 34004 Palencia, Spain; e-mail: carlosrojo84@gmail.com
Francisco Camello Rodríguez, Avda. Pozo del Paraguas 14, 06500 San Vicente de Alcántara, Badajoz, Spain; e-mail: frankamello@hotmail.com


Peziza halophila

Fungal Planet 652 – 20 December 2017

Peziza halophila Loizides, Agnello & P. Alvarado, *sp. nov.*

Etymology. *Halophila* = ἁλόφιλη (salt-loving); from the Greek noun ἅλας = salt, ultimately from ἅλς = sea, and the female adjective φίλη = friend, loving.

Classification — *Pezizaceae*, *Pezizales*, *Pezizomycetes*.

Ascomata 2–6(–8) mm diam, sessile, broadly attached to the substrate, discoid to saucer-shaped at first, soon pulvinate and usually undulating; margin poorly delineated, usually undifferentiated. *Hymenium* glabrous to somewhat furrowed at maturity, dark violet-purple, sepia-brown or purple-brown, drying black. *Outer surface* concolorous or slightly paler than the hymenium. *Context* thin and brittle, purple-brown to sepia-brown, with a strong spermatic odour. *Ascospores* (15–)16–17.5(–18) × (9.5–)10–11.5(–12) µm (Me = 16.6 × 11.1; Q = 1.3–1.6; Qm = 1.49), broadly ellipsoid, biguttulate, thick-walled, hyaline and smooth when immature, developing fine, isolated low warts at full maturity. *Asci* 250–350 × 12–15 µm, cylindrical, 8-spored, uniseriate, thick-walled, with a tapering aporhynchous base. *Amyloidity* intense on the apical arc and linearly fading 10–30 µm downwards. *Paraphyses* subcylindrical, 4–5 µm wide, occasionally bifurcate, fasciculate, with dissolved ochraceous to pale brown or golden-brown pigment, indistinctly septate and frequently exceeding the length of the asci; apices capitate, subcapitate, or clavate, usually bent and enlarged to 7–10 µm wide, filled with dark brown to purple-brown refractive granulose or vacuolar content, becoming red-brown to purple-red in Melzer's reagent. *Subhymenium* gelatinised, composed of chains of subangular to shortly elongated cells (*textura angularis*/*prismatica*). *Medullar excipulum* poorly differentiated, gelatinised; upper layer mostly composed of elongated cells < 50 µm across, lower layer mostly composed of spherical cells 15–45 µm across. *Ectal excipulum* a *textura intricata* of interwoven, occasionally branching, septate, thick-walled hyphae < 8 µm wide, with scattered or locally fasciculate hair-like terminal elements, projecting 100–200(–400) µm.

Habit, Habitat & Distribution — Halophytic, fruiting in large troops between January and February on flooded coastal sands and salt marshes, often in close proximity to the shore. So far only known from the island of Cyprus.

Typus. Cyprus, Akrotiri Lemesou, on embryonic coastal dunes, 21 Jan. 2017, *M. Loizides* (holotype in Venice Herbarium: MCVE 29341, LSU sequence GenBank MG262327, MycoBank MB823270).

Additional material examined. Cyprus, Lady's Mile, on embryonic coastal dunes, 18 Jan. 2012, *M. Loizides*, ML21181P1; *ibid.*, 26 Jan. 2017, *M. Loizides*, ML71162P1 (ITS and LSU sequences GenBank MG262328 and MG262325); Akrotiri Lemesou, on salt marshes, 21 Jan. 2017, *M. Loizides*, ML71162P2 (LSU sequence GenBank MG262326).

Colour illustrations. Holotype collection area at Akrotiri coast, Cyprus. Inserts: Top: ascocarps in situ, scale bar = 10 mm; bottom (left to right): asci and paraphyses in water, scale bar = 20 µm; asci and paraphyses in Melzer's reagent, scale bar = 20 µm; spores in water (top) and in Cotton Blue (bottom), scale bars = 10 µm; ascus in Congo Red, scale bar = 50 µm; ectal excipulum and hyphoid terminal elements in Congo Red, scale bar = 200 µm (from holotype collection).

Notes — Phylogenetic studies, based on LSU, ITS, *rpb2* and β-tubulin rDNA regions, have shown the genus *Peziza* to be polyphyletic (Norman & Egger 1996, 1999, Hansen et al. 2001, 2002, 2005, Tedersoo et al. 2006, Hansen & Pfister 2006). Pfister et al. (2016), recently adopted a narrow taxonomical concept, placing several taxa previously included in *Peziza* s.lat. in the genera *Adelphella*, *Galactinia*, *Lepidotia* and *Pachyella*. Our collections from Cyprus nest within the core clade of *Peziza*, related to the type species *P. vesiculosa*, and are especially close to *P. proteana* and *P. exogelatinosa*.

Interestingly, *P. halophila* exhibits transitional morphological features between *Peziza* and *Pachyella*. Species within *Peziza* s.str. share an intense amyloid reaction of the ascus apex (Hansen et al. 2001, 2002, Vizzini et al. 2016) and this feature is prominent in *P. halophila*. The broadly attached, pulvinate apothecia on the other hand, along with the presence of gelatinous tissue and absence of croziers, have been traditionally viewed as pachyelloid characters and have been used in the past to discriminate between the two genera (Le Gal 1963, Pfister 1973). The presence of a filamentous outer layer terminating in long hyphoid hairs has also been associated with *Pachyella*, but in the latter it is typically embedded in a gelatinous matrix, whereas in *P. halophila* gelatinous tissue is mostly confined to the middle layers. The dextrinoid content of the paraphyses is an unusual feature, which, together with the minute apothecia and halophytic ecology, make *P. halophila* unique within the genus.

Based on publicly available sequences, *P. proteana* is the closest relative of *P. halophila* (97 % LSU sequence similarity), but differs dramatically in its typical form, producing much larger, pale brown ascomata with lilac tinges and has much smaller, coarsely warted spores. *Peziza exogelatinosa*, described from calcareous woodlands in Denmark, is also genetically similar (96 % LSU sequence similarity) and shares with *P. halophila* a violet-brown to violet-black hymenium as well as similarly-sized, minutely warted biguttulate spores measuring 16.3–18.8 × 8.8–10 µm (Hansen et al. 1998). This species, however, produces considerably larger and often cupulate ascomata < 35 mm across, has asci with a pleurorhynchous base and a gelatinised ectal excipulum of globose cells (*textura globulosa*). *Peziza lobulata* and *P. subviolacea* (96 % and 94 % LSU sequence similarity, respectively) also have violet-purple hymenia, but are predominantly carbonicolous and produce larger cupulate ascomata 20–30 mm across, with smaller spores measuring 11–15 × 6–8 µm (Svrček 1976, 1977). The recently described *Peziza simplex* (Dougoud & Moyne 2012, no sequence available) could also be compared with *P. halophila*, since it produces small pulvinate ascomata 2–5(–6) mm across with occasional violet tinges and has asci lacking croziers. It differs in its smooth, non-verrucose spores, an ectal excipulum of globose/angular cells (*textura globulosa*/*angularis*) and a non-halophytic ecology.

Michael Loizides, P.O. Box 58499, 3734 Limassol, Cyprus; e-mail: michael.loizides@yahoo.com
Carlo Agnello, Via A. Gramsci 11, 72023 Mesagne (BR), Italy; e-mail: agnellocarlo@libero.it
Pablo Alvarado, Av. Bruselas 2 3B, 33011 Oviedo, Spain; e-mail: pablo.alvarado@gmail.com

Spumula piptadeniae

Fungal Planet 653 – 20 December 2017

Spumula piptadeniae A.A. Carvalho, Colmán & R.W. Barreto, *sp. nov*.

Etymology. Named after the host, *Piptadenia*.

Classification — *Raveneliaceae*, *Pucciniales*, *Pucciniomycetes*.

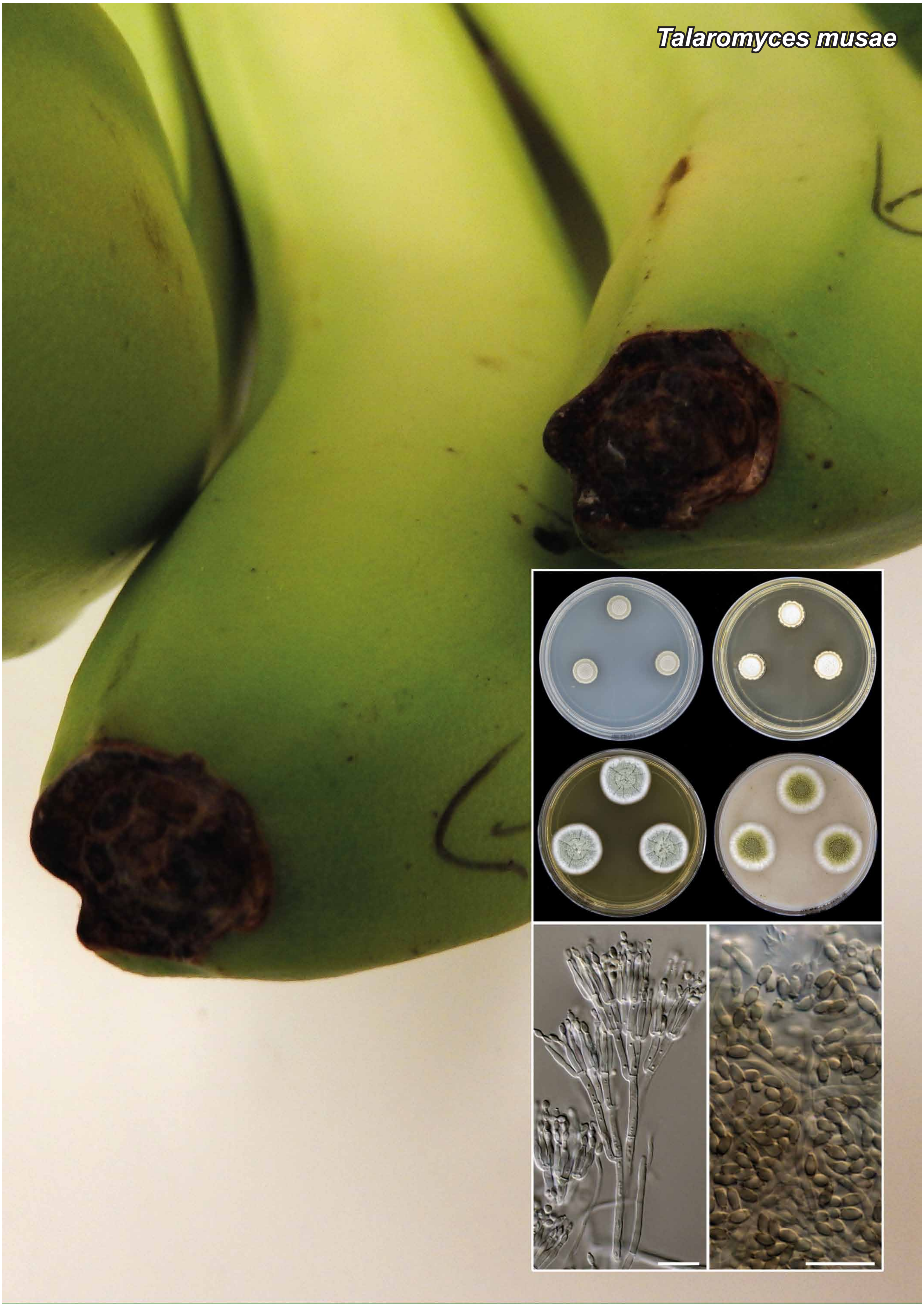
Spermogonia and *aecia* unknown. *Uredinia* hypophylous, subepidermal, pale cinnamon brown, scattered, c. 1 mm diam. *Urediniospores* 21–25 × 16–19 µm, mostly obovoid to ellipsoid, wall cinnamon-brown, 0.80–1.30 µm thick laterally and apically, echinulate, pores 3–4(–5), bizonate or equatorial. *Telia* hypophylous, subepidermal in origin, becoming erumpent; paraphyses mostly peripheral, numerous, approximately 8–12 µm wide and up to 70 µm long, 1–2-septate, cylindrical incurved, wall often unilaterally or bilaterally thickened, 2–5 µm, hyaline; teliospores globoid when viewed from above or below (61–)65–75(–84) µm diam, very widely ovoid when viewed laterally, chestnut-brown, 12–18 probasidial cells across, each cell 15–31 µm, cells in one or rarely two layers, 6–8 central cells, 15–23 µm diam; tubercles conical, 6–10 µm long, 3–5.5 µm wide at base, (1–)2–6 per cell, cysts pendent, globoid, 2–5 but mostly 5, hyaline, pedicel unihyphal, hyaline.

Typus. Brazil, state of Rio de Janeiro, Guapimirim, roadside of BR 116, on *Piptadenia paniculata*, Aug. 2014, *R.W. Barreto 1929* (holotype VIC 42673, isotype RB, MycoBank MB822390).

Colour illustrations. *Piptadenia panicuata* growing at Guapimirim, Rio de Janeiro State, Brazil; symptoms and signs caused by *Spumula piptadeniae* on the leaves of *Piptadenia paniculata*; urediniospores obovoid to ellipsoid; urediniospores echinulate and with germ pores (whitish spots); teliospores with conical tubercles and globoid cysts; teliospores with one-stalked pedicels; paraphyses; teliospores in Scanning Electron Microscopy. Scale bars = 20 µm, 20 µm, 20 µm, 10 µm, 10 µm, 40 µm.

Notes — All members of *Ravenelia* have two or multiple-stalked teliospore pedicels, whereas members of *Spumula*, including *Spumula piptadeniae*, have teliospores supported by single-stalked pedicels. *Spumula piptadeniae* differs from other species with conical ornamentations (such as *S. debile*, *Ravenelia theiseniana* and *R. minuta*) by the following characteristics: *S. debile* and *R. palenquensis* are microcyclic and do not produce urediniospores as in *S. piptadeniae*. Teliospore heads are smaller (33–45 µm) in *R. minuta* and bear conical ornaments that are smaller (3 µm) than those observed on *S. piptadeniae. Ravenelia minuta* also has smaller numbers of probasidial cells (3–5) and its paraphyses are 3–4-septate. Other *Ravenelia* species reported on *Piptadenia* are markedly different from *S. piptadeniae*, *R. henningsiana*, *R. simplex* and *R. theisseniana*, as besides having teliospores with two to multiple-stalked teliospores, they have teliospores bearing other kinds of ornamentations. *Ravenelia henningsiana* has smooth teliospores, *R. simplex* has narrowly rounded cones or papillae, and *R. theisseniana* has teliospores with tuberculate and bifurcate or knobbed ornaments.

Anibal A. de Carvalho Júnior, Instituto de Pesquisas Jardim Botânico do Rio de Janeiro,
Pacheco Leão 915, 22460-030, Rio de Janeiro, RJ, Brazil; e-mail: anibal@jbrj.gov.br
Adans Agustin Colmán & Robert W. Barreto, Departamento de Fitopatologia, Universidade Federal de Viçosa,
36570-900, Viçosa, MG, Brazil; e-mail: adan-colman@hotmail.com & rbarreto@ufv.br


Talaromyces musae

Fungal Planet 654 – 20 December 2017

Talaromyces musae Houbraken, Kraak & M. Meijer, *sp. nov.*

Etymology. Name refers to *Musa* (banana), the original substrate of the ex-type strain.

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

Conidiophores 50–150 µm long, predominantly terverticillate, occasionally biverticillate, branches adpressed, 12–30 µm long, stipes 2–2.5 µm wide, smooth-walled, non-vesiculate. *Metulae* cylindrical, 2–5, (8–)9–12(–14) × 1.5–2.5 µm. *Phialides* acerose, 3–6(–8) per metula, 9–11 × 2–2.5 µm. *Conidia* in long, distorted chains, smooth-walled, ellipsoid or barrel-shaped, often with connectives on both sides, 3–3.5 × 1.5–2 µm. *Ascomata* not observed.

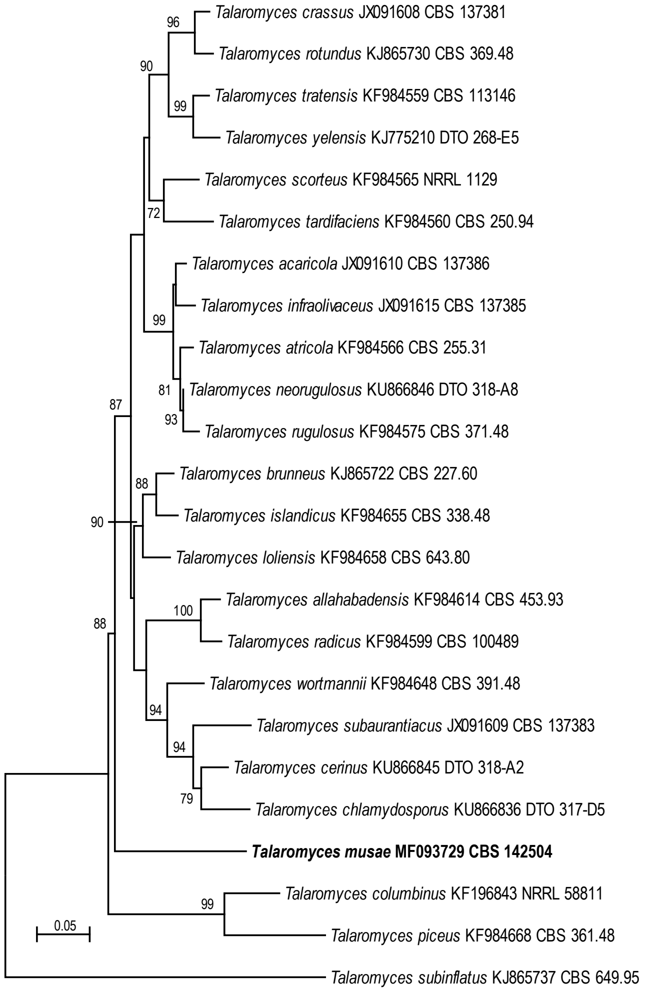
Culture characteristics — Colony diam, 7 d, in mm: CYA 12–16; CYA 30 °C 9–14; CYA 37 °C no growth; CYAS 2–5; MEA 25–30; MEA 30 °C 27–31; OA 25–30; DG18 19–24; YES 12–16; creatine agar 4–8, poor growth, acid production absent.

CYA, 25 °C: Colonies slightly flat, non-sulcate; colony texture granular in centre, velvety towards edges; sporulation moderate to good; conidia grey in centre, greyish green towards edges; mycelium white; exudate absent; soluble pigment absent after 7 d, present after 14 d, brown; margin entire; reverse pale brown. YES, 25 °C: Colonies slightly raised in centre, non-sulcate; colony texture velvety; sporulation poor; mycelium white in centre, pale brown at the margin; exudate present, small pale brown; soluble pigments absent after 7 d, present after 14 d, terracotta; margin undulate; reverse brown. MEA, 25 °C: Colonies flat, concentrically and radially sulcate; colony *texture granular*; sporulation good; conidia yellow-green; mycelium white; exudate absent; soluble pigments absent; margin entire; reverse dark brown in centre, brown at margin.

Typus. Germany, Hamburg (imported), from tip of banana, 2017, coll. *A. Hesselink*, isol. *M. Meijer* & *B. Kraak* (holotype CBS H-23138, culture ex-type CBS 142504 = DTO 366-C5, ITS, *BenA*, *CaM* and *rpb2* sequences GenBank MF072316, MF093729, MF093728 and MF093727, MycoBank MB821051).

Notes — Maximum Likelihood analysis based on partial β-tubulin (*BenA*) sequences revealed that *Talaromyces musae* belongs to section *Islandici*. The species is phylogenetically unique and has a basal position to the majority of species belonging to this section. *Talaromyces musae* grows, like the other members of this section, restrictedly on agar media such as CYA (12–16 mm). However, most species of this section produce yellow mycelium and this feature is not observed in this species. *Talaromyces musae* is unique in predominantly producing terverticillate conidiophores and smooth-walled, ellipsoid or barrel-shaped conidia that often have connectives on both sides (Yilmaz et al. 2014, 2016).

Colour illustrations. Bananas; from top-left to bottom-right (7-d-old colonies), CYA, obverse; YES, obverse; MEA, obverse; OA, obverse; conidiophores; conidia. Scale bars = 10 µm.



The *BenA* phylogenetic tree was inferred using the Maximum Likelihood method based on the Kimura 2-parameter model in MEGA v. 6.06. Bootstrap support values are indicated at the nodes (1 000 bootstraps); all values below 70 % are deleted. The scale bar indicates the expected number of changes per site.

Jos Houbraken, Bart Kraak, Martin Meijer, Westerdijk Fungal Biodiversity Institute,
Department of Applied and Industrial Mycology,
P.O. Box 85167, 3508 AD Utrecht, The Netherlands;
e-mail: j.houbraken@westerdijkinstitute.nl, b.kraak@westerdijkinstitute.nl & m.meijer@westerdijkinstitute.nl


Volvariella morozovae

Fungal Planet 655 – 20 December 2017

Volvariella morozovae E.F. Malysheva & A.V. Alexandrova, *sp. nov.*

Etymology. Named after the Russian mycologist, Dr Olga Morozova, known as an exceptional specialist in *Entolomataceae* taxonomy, and an experienced researcher of the mycobiota of Vietnam.

Classification — *Pluteaceae*, *Agaricales*, *Agaricomycetes*.

Basidiocarps medium-sized. *Pileus* 30–40 mm, broadly campanulate, later expanded, without umbo; non-hygrophanous; not viscid; sandy brown, cinereous, pale brownish grey, darker at centre – grey-brown or dirty brown, towards margin paler to beige or whitish; radially silky fibrillose to hairy with some short hairs ascending, with slightly serrulated margin fringed with fluffy fibrils. *Lamellae* crowded to fairly distant, free, hardly ventricose, initially whitish then pink to brownish pink, with concolorous entire edge. *Stipe* 35–50 × 3–4 mm, cylindrical, not or somewhat broadening towards base, up to 6–7 mm, white or with light ochraceous or buff shades; entirely minutely pubescent. *Volva* thin, membranous, saccate, sordid grey-brown to olivaceous brown with rusty brown spots, irregularly lobed, with felted to woolly outer surface. *Context* white. *Smell* and *taste* indistinct. *Basidiospores* 5–6.2 × 3.3–4.3 µm, Q = 1.30–1.65, Q* = 1.46, elongate-ellipsoid to lacrymoid, some rather ovoid, hyaline in KOH, thick-walled. *Basidia* 13.5–20 × 7–8.5 µm, 4-spored, broadly clavate with a medial constriction at maturity. *Cheilocystidia* 40–55 × 13–18 µm, variable in shape, mainly ventricose-lageniform, broadly fusiform, sometimes with apical excrescences or subglobose apex, some proportion utriform, thin- or slightly thick-walled. *Pleurocystidia* rare, 45–50 × 18–30 µm, utriform or broadly clavate, slightly thick-walled. *Pileipellis* a cutis, made up of short-celled, slightly thick-walled hyphae, 20–35 µm wide, with intracellular grey-brown pigment; transforming into a trichoderm at centre of pileus, with cylindrical, fusiform or sublageniform terminal elements more than 100 µm long. *Stipitipellis* a cutis, made up of long, cylindrical, hyaline hyphae, 10–12 µm wide; hairs of stipe cylindrical, up to 150–200 µm long. *Clamp connections* absent in all parts examined.

Habitat & Distribution — Solitary, on wood in tropical low-mountainous, polydominant, constantly moist forests. So far only known from the type locality.

Typus. Vietnam, Gia Lai Province, Mang Yang districts, A Yun commune, A Yun village, Kon Ka Kinh National Park, path along the river, on wood of unknown tree, 14 May 2016, *O. Morozova* (holotype LE 313229, ITS and LSU sequences GenBank MF377507 and MF377508, MycoBank MB821859).

Colour illustrations. Vietnam, Kon Ka Kinh National Park; basidiocarp; cheilocystidia; pleurocystidia; basidiospores (all from holotype). Scale bars = 1 cm (basidiocarp), 10 µm (microscopic structures).

Notes — *Volvariella morozovae* is characterised by its medium-sized and slender basidiocarps with pale brownish grey and hairy pilei, olivaceous brown or rusty brown felted volva, small (5–6.2 × 3.3–4.3 µm) elongate-ellipsoid to lacrymoid basidiospores.

There are several fairly well-known species with small or medium-sized basidiocarps, grey or brown pilei and coloured volva, among them *Volvariella cinerascens*, *V. fuscidula*, *V. murinella*, *V. nigrodisca* and *V. taylorii*. The studied Vietnamese collection does not agree in all aspects with the description of any of these species (MycoBank supplementary data).

The result of megablast search of GenBank database using the ITS (625 bp) sequence of *V. morozovae* showed *Volvariella* sp. from India (GenBank KR349630), *V. taylorii* from Italy (GenBank LN877891) and *V. nullicystidiata* from Brazil (GenBank EU920671) as the closest hits, but with extremely low indexes of similarity: 87 %, 85 % and 84 %, respectively.

Ekaterina F. Malysheva, Komarov Botanical Institute of the Russian Academy of Sciences,
Prof. Popov Str. 2, RUS-197376, St. Petersburg, Russia; e-mail: e_malysheva@binran.ru
Alina V. Alexandrova, Lomonosov Moscow State University, Leninskie Gory 1, 12, 119234, Moscow, Russia /
Joint Russian-Vietnamese Tropical Research and Technological Center, South Branch, Ho Chi Minh City, Vietnam;
e-mail: alina-alex2011@yandex.ru


Setophaeosphaeria citri

Fungal Planet 656 – 20 December 2017

Setophaeosphaeria citri Guarnaccia & Crous, *sp. nov.*

Etymology. Name refers to *Citrus*, the plant genus from which this fungus was collected.

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

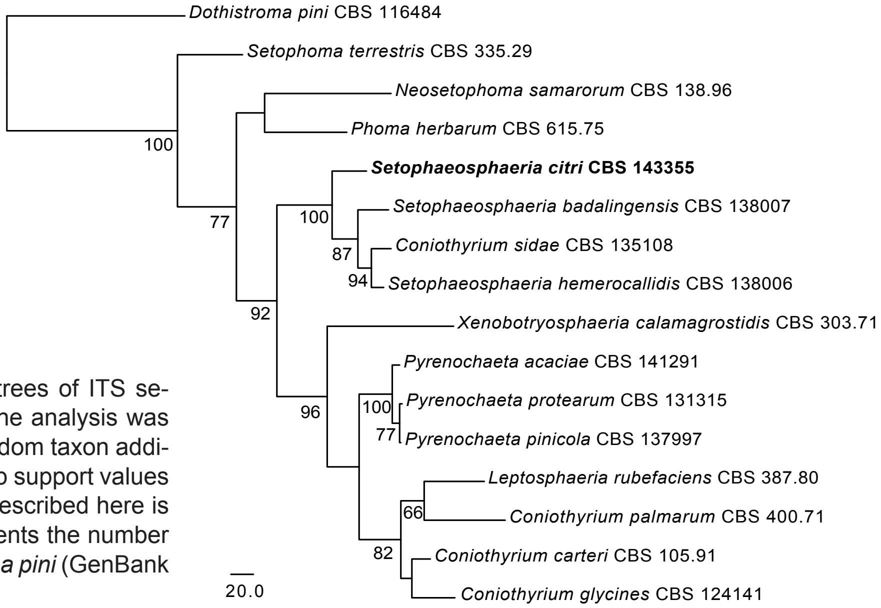
Ascomata not observed. *Conidiomata* immersed (on PDA and OA) to erumpent (on PNA), pycnidial, brown, globose, erumpent, with central, round to ellipsoid ostiole, to 250 µm diam; wall of 6–8 layers of pale brown *textura angularis*. *Setae* brown, unbranched, flexuous, septate, covering conidiomata, smooth, with obtuse to rounded ends, to 150 µm long, 2–2.5 µm wide. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* lining the inner cavity, hyaline, smooth, ampulliform, 3–7 × 3–4 µm. *Conidia* solitary, aseptate, hyaline, smooth, guttulate, subcylindrical with obtuse ends, straight or gently curved, 3.5–5 × 2–3 µm.

Culture characteristics — Colonies covering the entire plate after 4 wk at 22 °C. On MEA, PDA and OA spreading, with sparse aerial mycelium and embedded conidiomata, surface folded, lobed, surface smoke-grey to dark grey. Reverse olivaceous grey on MEA and PDA, dark grey to black on OA.

Typus. Italy, Massafra, Taranto, Apulia, on twigs of *Citrus reticulata* (*Rutaceae*), 9 June 2015, *V. Guarnaccia* (holotype CBS H-23240, culture ex-type CPC 27148 = CBS 143355; ITS and LSU sequences GenBank MG263524 and MG263525, MycoBank MB823316).

Notes — The genus *Setophaeosphaeria* was recently described including two species, *S. hemerocallidis* and *S. badalingensis*. Another species previously known as *Phaeosphaeria setosa* was also included (Crous et al. 2014a). When present, ascomata are pseudothecial, immersed on leaves and stems, producing ellipsoid, bitunicate, 8-spored asci. The ascospores are pale brown, fusoid to ellipsoid, with mucoid caps at each end, guttulate and septate. Conidiomata develop readily in culture and are pycnidial, brown, globose, producing hyaline, subcylindrical, guttulate, aseptate conidia. *Setophaeosphaeria citri* is phylogenetically distinct from *S. badalingensis*, *S. hemerocallidis* and *S. setosa*, and also has smaller conidia than those observed in *S. badalingensis*, (5–)6(–7) × (2.5–)3 µm. Moreover, *S. citri* forms only conidiomata whilst *S. hemerocallidis* produces ascomata with ascospores and also presents larger conidia, (11–)13–16(–19) × (3–)3.5(–4) µm (Crous et al. 2014a). No *Setophaeosphaeria* species are known from *Citrus*.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the ITS sequence are *S. hemerocallidis* (GenBank KJ869161; Identities = 387/407 (95 %), Gaps = 1/407 (0 %)), *S. badalingensis* (GenBank KJ869162; Identities = 443/489 (91 %), Gaps = 13/489 (2 %)) and *Coniothyrium sidae* (GenBank KF251149; Identities = 439/483 (91 %), Gaps = 18/483 (3 %)). Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the LSU sequence are *S. badalingensis* (GenBank KJ869219; Identities = 783/786 (99 %), Gaps = 0/786 (0 %)), *Coniothyrium sidae* (GenBank KF251653; Identities = 782/786 (99 %), Gaps = 0/786 (0 %)) and *Pyrenochaeta acaciae* (GenBank KX228316; Identities = 776/786 (99 %), Gaps = 0/786 (0 %)).



The first of two equally most parsimonious trees of ITS sequences obtained from a heuristic search. The analysis was conducted with PAUP* v. 4.0b10 with 100 random taxon additions and 1 000 bootstrap replicates. Bootstrap support values are shown at the nodes. The novel species described here is shown in **bold** face and the scale bar represents the number of changes. The tree was rooted to *Dothistroma pini* (GenBank JX901736).

Colour illustrations. Young plantation of *Citrus reticulata*; colony on PDA, conidiomata sporulating on PNA, setae, conidiogenous cells and conidia. Scale bars = 10 µm.

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


Lactifluus ceraceus

Fungal Planet 657 – 20 December 2017

Lactifluus ceraceus Delgat & M. Roy, *sp. nov.*

Etymology. Refers to the waxy surface of the cap.

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

Pileus 64–98 mm diam, infundibuliform to deeply infundibuliform; margin straight to slightly inflexed, slightly sulcate; surface smooth, glabrous, waxy but not viscose, orange (+/- 4B7 to 5B7). *Stipe* 83–112 × 18–26 mm, cylindrical; surface smooth, yellow-orange, with a slight greenish tinge (4A5 to 4C5), slightly paler at the top. *Lamellae* decurrent, very broad, thick, brittle, transvenose and slightly intervenose, distant, paler than pileus and stipe, cream yellow (2A3); edge concolorous and entire. *Context* yellowish white, unchanging when cut, very slowly changing to very light blue-green with gaiac, changing to orange-red with $FeSO_4$. *Smell* weak, pleasant. *Taste* fruity. *Latex* absent. *Basidiospores* broadly ellipsoid, 5.4–*6.4–6.9*–8.1 × 4.4–*5.2–5.5*–6.2 µm (Q = 1.12–*1.23–1.25*–1.35); ornamentation amyloid, composed of broad irregular warts and ridges, forming an incomplete reticulum, with some isolated warts; plage distinct and inamyloid. *Basidia* 43–68 × 7.5–10 µm, subclavate, 4-spored. *Pleurocystidia* abundant, 49–92 × 5–9 µm, cylindrical to subclavate, with an obtuse, mucronate, slightly rostrate or moniliform apex, slightly thick-walled. *Pseudocystidia* absent. *Lamellar edge* fertile. *Hymenophoral trama* cellular, with large sphaerocytes and very few lactifers. *Pileipellis* a lampropalisade; elements of the suprapellis 8–42 × 3.5–6 µm, cylindrical to utriform, thick-walled, some septate; subpellis composed of slightly thick-walled globose/isodiametric cells.

Distribution — So far only known from French Guiana. Occurring in primary terra-firme forests.

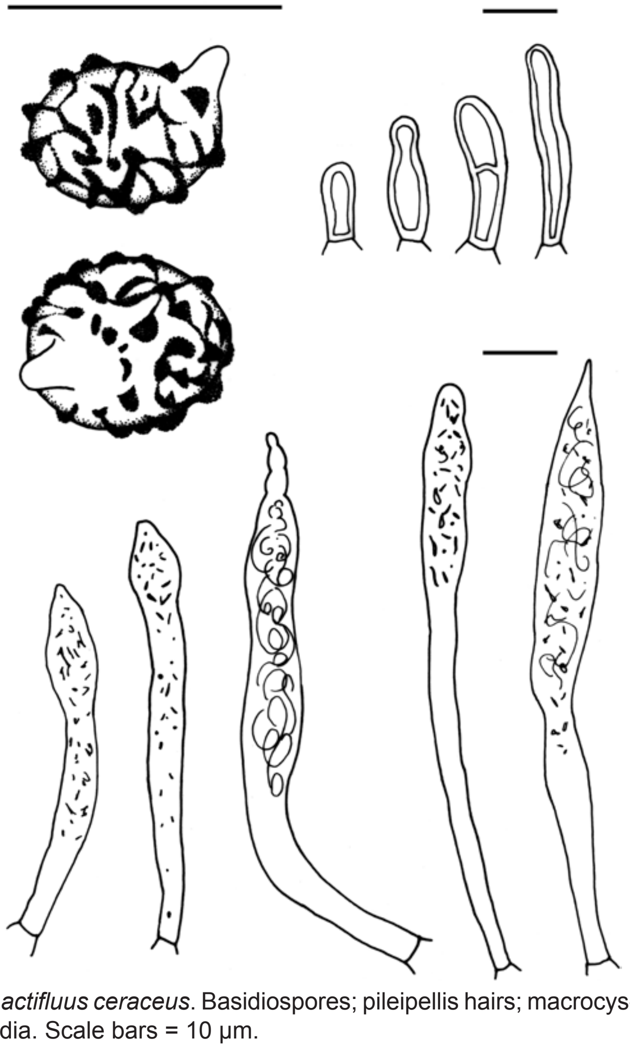
Typus. French Guiana, Reserve Naturelle La Trinité, terra-firme forest, slope, on the trail from Camp Aya to the inselberg de la Roche Bénitier, N4°37'09" W53°24'33", 15 Apr. 2016, *L. Delgat* (holotype LD16-005 (GENT), ITS and LSU sequences GenBank KY884995 and MG253925, MycoBank MB820812).

Additional material examined. French Guiana, Regina, Nouragues station, terra-firme forest, plateau, 6 July 2013, *M. Roy*, PC0713390 (PC), ITS and LSU sequences GenBank KY884996 and KJ786583.

Colour illustrations. Tropical rainforest in Reserve Naturelle La Trinité near Camp Aya; basidiocarps, cystidia, basidia and pileipellis. Scale bars = 10 µm.

Notes — *Lactifluus ceraceus* belongs to *L.* subg. *Pseudogymnocarpi*, which is supported by molecular data (ITS phylogeny: MycoBank supplementary data), as well as by morphological characters, such as the lampropalisade structure of the pileipellis and the yellow/orange cap colour. *Lactifluus ceraceus* is part of *L.* sect. *Polysphaerophori*, a section which contains exclusively Neotropical species. This placement is based on molecular data, since this section has not yet been clearly characterized morphologically.

Lactifluus ceraceus morphologically closely resembles *Lactarius amazonensis**. However, *Lactarius amazonensis* has larger spores (8.5–11 × 7–8.5 µm) and its macrocystidia have a more fusoid shape compared to the cylindrical or subclavate shape of the macrocystidia of *L. ceraceus*. *Lactifluus ceraceus* is also morphologically similar to *Lactarius brasiliensis**. But the spores of *Lactarius brasiliensis* are larger (7.5–11 × 7–8 µm) and subglobose. Furthermore, *Lactarius brasiliensis* differs by having numerous and conspicuous laticiferous hyphae.



Lactifluus ceraceus. Basidiospores; pileipellis hairs; macrocystidia. Scale bars = 10 µm.

Lynn Delgat & Annemieke Verbeken, Department of Biology, Ghent University,
Karel Lodewijk Ledeganckstraat 35, Ghent, Belgium; e-mail: lynn.delgat@ugent.be
Mélanie Roy, Laboratoire Evolution et Diversité Biologique, Université Paul, 118 route de Narbonne, 31062 Toulouse cedex, France

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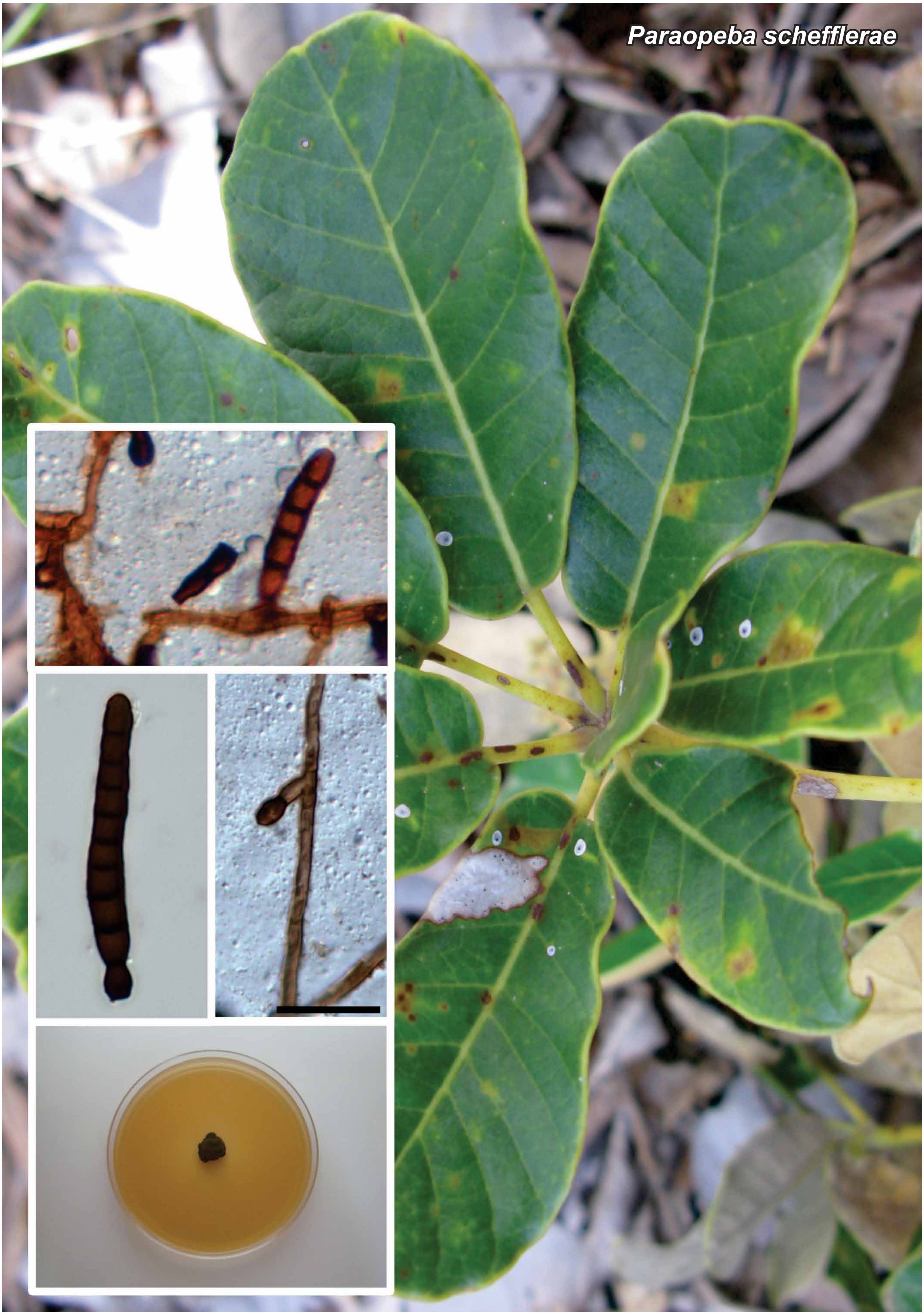
* these two species are yet to be recombined in *Lactifluus*.


Paraopeba schefflerae

Fungal Planet 658 – 20 December 2017

Paraopeba V.P. Abreu, A.A.M. Gomes, Firmino & O.L. Pereira, *gen. nov.*

Etymology. Name refers to the city of Paraopeba, state of Minas Gerais, Brazil, where the fungus was first found.

Classification — *Asterinaceae*, *Asterinales*, *Dothideomycetes*.

Leaf spots epiphyllous, circular to irregular, single to confluent, brown. *Hyphae* straight to slightly flexuous, brown, septate, smooth. *Appressoria* numerous, entire, globose to cylindrical, alternate to unilateral, unicellular, brown, penetration peg central on the appressorial cell. *Conidiogenous cells* schizolytic, cylindrical to elliptical, light brown to brown, smooth. *Conidia* cylindrical, multicellular, brown, smooth, rounded ends, septate. *Sexual morph* unknown.

Type species. *Paraopeba schefflerae* V.P. Abreu, A.A.M. Gomes, Firmino & O.L. Pereira.
MycoBank MB821209.

Paraopeba schefflerae V.P. Abreu, A.A.M. Gomes, Firmino & O.L. Pereira, *sp. nov.*

Etymology. Named after its host genus, *Schefflera*.

Leaf spots epiphyllous, circular to irregular, single to confluent, brown, 2–8 mm diam. *Hyphae* straight to slightly flexuous, brown, septate, 1.5–3.5 µm diam, smooth. *Appressoria* numerous, entire, globose to cylindrical, alternate to unilateral, unicellular, 3–6 × 4.5–6.5 µm, brown, penetration peg central on the appressorial cell. *Conidiogenous cells* schizolytic, cylindrical to elliptical, 4.5–10 × 3.5–6.5 µm, pale brown to brown, smooth. *Conidia* cylindrical, multicellular (3–14 cells), brown, smooth, rounded ends, 18–85 × 4.5–7 µm, 2–13-septate. *Sexual morph* unknown.

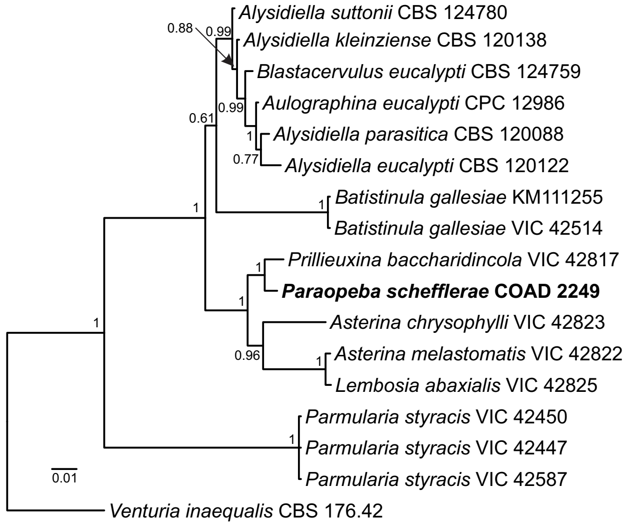
Culture characteristics — The colony grows slowly on malt extract agar, reaching 7 mm diam after 40 d at 25 °C with a photoperiod of 12 h; margins irregular, with aerial mycelium sparse, black, colonies fertile.

Typus. Brazil, Minas Gerais, Paraopeba, Floresta Nacional de Paraopeba (FLONA-Paraopeba), on leaves of *Schefflera morototoni* (*Araliaceae*), 30 Jan. 2016, *V.P. Abreu & O.L. Pereira* (holotype VIC 44232, culture ex-type COAD 2249; ITS and LSU sequences GenBank KY952164 and KY952165, MycoBank MB821409).

Notes — The order *Asterinales* is characterised by epiphytic fungi, biotrophic parasites, with superficial non-ostiolate ascomata, opening irregularly at maturity; surface mycelium and haustoria are present in several genera (Bezerra 2004). The *Asterinales* is composed by two families, *Asterinaceae* and *Parmulariaceae* (Guatimosim et al. 2015, Giraldo et al. 2017). Members of *Asterinaceae* are characterised by producing black colonies consisting of a brown mycelium on the leaf surface (Guatimosim et al. 2015). Asexual morphs (hyphomycetous and coelomycetous) have been observed in some *Asterinaceae* (Summerell et al. 2006, Hongsanan et al. 2016). The conidia of *Paraopeba schefflerae* are formed in schizolytic conidiogenous cells while conidia of *Alysidiella*, *Blastacervulus* and *Asterostomula* are formed in sporodochial, acervular and pycnothyrial conidiomata, respectively (Summerell et al. 2006, Giraldo et al. 2017). Additionally, the appressorial cells are present in *Paraopeba*, but have not been observed in *Alysidiella*, *Blastacervulus* and *Asterostomula* (Summerell et al. 2006, Giraldo et al. 2017). Bayesian inference analysis (alignment and tree were deposited into TreeBASE under accession number S21280) suggests that *Paraopeba schefflerae* is related to members of *Asterinaceae*, and represents a different genus in this family. *Paraopeba schefflerae* is phylogenetically close but clearly distinct from *Prillieuxina baccharidincola*. Phylogenetic analysis and morphological comparisons support the introduction of *Paraopeba* as a new genus of *Asterinaceae* and *Paraopeba schefflerae* as the type species of this genus. To our knowledge this is the first *Asterinaceae* member described colonising *Schefflera morototoni* leaves. In addition, *Paraopeba schefflerae* is a rare case of *Asterinaceae* known from culture (ex-type COAD 2249).

ITS. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the ITS sequence are *Alysidiella parasitica* (GenBank NR_132811; Identities = 457/513 (89 %), Gaps = 9/513 (1 %)), *Alysidiella suttonii* (GenBank HM628774; Identities = 460/517 (89 %), Gaps = 11/517 (2 %)) and *Blastacervulus eucalypti* (GenBank GQ303271; Identities = 460/517 (89 %), Gaps = 11/517 (2 %)).

LSU. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the LSU sequence are *Prillieuxina baccharidincola* (GenBank KP143735; Identities = 742/755 (98 %), Gaps = 2/755 (0 %)), *Asterina melastomatis* (GenBank KP143739; Identities = 722/757 (95 %), Gaps = 4/757 (0 %)) and *Asterina chrysophylli* (GenBank KP143738; Identities = 717/755 (95 %), Gaps = 2/755 (0 %)).



Phylogenetic tree inferred from Bayesian analysis based on LSU sequences. The analysis was performed with 10 M generations in MrBayes v. 3.2.6. The Bayesian posterior probability values are indicated at the nodes. The tree was rooted to *Venturia inaequalis* CBS 176.42. The new species is highlighted in **bold**.

Colour illustrations. Leaves of *Schefflera morototoni* in Floresta Nacional de Paraopeba, state of Minas Gerais, Brazil; conidia formed on superficial mycelium; thick-walled pigmented conidium; conidium being formed in the conidiogenous cell; colony on MEA after 40 d at 25 °C. Scale bar = 20 µm.

Vanessa P. Abreu, André A.M. Gomes & Olinto L. Pereira, Departamento de Fitopatologia, Universidade Federal de Viçosa,
36570-900, Viçosa, Minas Gerais, Brazil; e-mail: vanessa.abreu@ufv.br, andreangelomg@gmail.com & oliparini@ufv.br
André L. Firmino, Instituto de Ciências Agrárias, Universidade Federal de Uberlândia, Minas Gerais, Brazil; e-mail: andrefirmino@ufu.br


Cochlearomyces eucalypti

Fungal Planet 659 – 20 December 2017

Cochlearomycetaceae Crous, *fam. nov.*

Classification — *Cochlearomycetaceae*, *Helotiales*, *Leotiomycetes.*

Mycelium immersed, dark brown, branched, septate. *Coelomycetous conidiomata* infundibuliform to nidulariaceous, superficial, separate, dark brown to black, sessile; basal wall several cells thick, of dark brown *textura angularis*, periclinal wall one cell thick, of vertically elongated thick-walled, brown *textura prismatica*. *Conidiophores* 1–2-septate, hyaline, sparingly branched, restricted to the base of the conidioma. *Hyphomycetous conidiomata* solitary, erect, dark brown, appearing as upside-down teaspoons; synnemata dark brown, smooth, base lobate, with rhizoids; basal cells dark brown, verruculose, subglobose; synnematal stalk with ellipsoid conidiogenous region; hyphal elements continuing above conidiogenous region, mostly aggregated, but at times separating into two stalks, ends subobtuse. *Conidiophores* aggregated in ellipsoid brown conidiogenous zone, hyaline, smooth, subcylindrical, branched, septate. *Conidiogenous cells* terminal and intercalary, doliiform to subcylindrical to lageniform, phialidic. *Conidia* solitary, aseptate, hyaline, smooth, cylindrical, straight with obtuse ends.

Type genus. *Cochlearomyces* Crous.
MycoBank MB823461.

Notes — *Cochlearomycetaceae* includes *Cochlearomyces* and the genus *Satchmopsis*, which is based on *S. brasiliensis* (holotype Brazil Minas Gerais, Viçosa, on leaf litter of *Eucalyptus paniculata*, 18 Dec. 1973, *C.S. Hodges*, holotype IMI 181534c. Epitype designated here, Colombia, on *Eucalyptus* leaf litter, Feb. 2004, *M.J. Wingfield*, CBS H-18048, MBT379399; cultures ex-epitype CPC 10972–10974; see Crous et al. 2006).

Cochlearomyces Crous, *gen. nov.*

Etymology. Name refers to the conidiophores that appear as inverted spoons.

Synnemata solitary, at times in small clusters, erect, dark brown, somewhat flexuous, appearing as inverted spoons under the dissecting microscope; synnemata dark brown, smooth, base lobate, with rhizoids; basal cells dark brown, verruculose, subglobose; synnematal stalk consisting of 6–20 hyphal elements, with ellipsoid conidiogenous region; hyphal elements continuing above conidiogenous region, mostly aggregated, but at times separating into two stalks, ends subobtuse. *Conidiophores* aggregated in ellipsoid brown conidiogenous zone, arising from roughened inner cells, becoming hyaline, smooth, subcylindrical, branched, septate. *Conidiogenous cells* terminal and intercalary, doliiform to subcylindrical, phialidic. *Conidia* solitary, aseptate, hyaline, smooth, cylindrical, straight with obtuse ends.

Type species. *Cochlearomyces eucalypti* Crous.
MycoBank MB823365.

Cochlearomyces eucalypti Crous, *sp. nov.*

Etymology. Name refers to *Eucalyptus*, the host genus from which this fungus was collected.

Synnemata solitary, at times in small clusters, erect, dark brown, somewhat flexuous, appearing as inverted spoons under the dissecting microscope; synnemata dark brown, smooth, base lobate, 20–40 µm diam, with rhizoids; basal cells dark brown, verruculose, subglobose, 5–7 µm diam, giving rise to dark brown hyphae, 4–5 µm diam, verruculose, septate; in culture these hyphae become hyaline, but encased in a mucoid sheath; synnematal stalk consisting of 6–20 hyphal elements, stalk 10–15 µm diam at base, 200–300 µm long, with ellipsoid conidiogenous region 120–150 µm from base, 50–80 µm diam, with roughened brown, thick-walled obtuse cells (3–5 µm diam) forming a lobate margin; hyphal elements continuing above conidiogenous region, 50–100 µm long, mostly aggregated, but at times separating into two stalks, ends subobtuse, 2 µm diam. *Conidiophores* aggregated in ellipsoid brown conidiogenous zone, arising from roughened inner cells, becoming hyaline, smooth, subcylindrical, branched, 1–3-septate, 12–20 × 2.5–3.5 µm. *Conidiogenous cells* terminal and intercalary, doliiform to subcylindrical, tapering to phialidic apex with periclinal thickening, 5–7 × 2–3 µm. *Conidia* solitary, aseptate, hyaline, smooth, cylindrical, straight with obtuse ends, (10–)12–13(–15) × 1.5(–2) µm *in vivo*, 8–10 × 2 µm *in vitro*, with 1–2 small guttules.

Colour illustrations. Silvan Reservoir Park; conidiophores (scale bars = 80 µm), conidiogenous cells and conidia (scale bars = 10 µm).

Culture characteristics — Colonies white on SNA, creamy on OA, with sienna inner region due to sporulation, reaching 30 mm diam after 1 mo at 25 °C; aerial mycelium absent, margins smooth, even.

Typus. Australia, Victoria, Melbourne, Dandenong Ranges, Silvan Reservoir Park, leaf litter of *Eucalyptus obliqua* (*Myrtaceae*), 1 Dec. 2016, *P.W. Crous* (CBS H-23076, cultures ex-type CPC 33051 = CBS 142622, ITS and LSU sequences GenBank MG386025 and MG386081, MycoBank MB823366).

Notes — Among the genera of hyphomycetes presently known (Seifert et al. 2011), *Cochlearomyces* is unique in having erect, brown synnemata that form a shield, bearing phialides that give rise to aseptate, cylindrical conidia. *Cochlearomyces* clusters close to, but is morphologically quite distinct from, *Claussenomyces* and *Satchmopsis*, two genera with turbinate sporocarps (Crous et al. 2006, Medardi 2007).

Based on a megablast search using the ITS sequence, the closest matches in NCBIs GenBank nucleotide database were *Holwaya mucida* (GenBank DQ257357; Identities = 504/545 (92 %), 7 gaps (1 %)), *Patinella hyalophaea* (GenBank KT876978; Identities 503/548 (92 %), 12 gaps (2 %)) and *Flagellospora curvula* (GenBank KC834045; Identities 500/548 (91 %), 8 gaps (1 %)). The highest similarities using the LSU sequence were *Claussenomyces prasinulus* (GenBank KX090815; Identities 821/849 (97 %), 4 gaps (0 %)), *Satchmopsis brasiliensis* (GenBank DQ195798; Identities 833/868 (96 %), 4 gaps (0 %)) and *Crinula caliciiformis* (GenBank AY544680; Identities 855/895 (96 %), 8 gaps (0 %)).

Pedro W. Crous & Johannes Z. Groenewald, Westerdijk Fungal Biodiversity Institute, P.O. Box 85167,
3508 AD Utrecht, The Netherlands; e-mail: p.crous@westerdijkinstitute.nl & e.groenewald@westerdijkinstitute.nl
Michael J. Wingfield, Forestry and Agricultural Biotechnology Institute (FABI), University of Pretoria,Pretoria 0002, South Africa;
e-mail: mike.wingfield@fabi.up.ac.za
David Smith, Agriculture, Energy & Resources, Agriculture and Rural Division, Department of Economic Development, Jobs, Transport and Resources,
Unit 3, 2 Codrington St, Cranbourne, Victoria 3977, Australia; e-mail: david.smith@ecodev.vic.gov.au


Pleopassalora acaciae

Fungal Planet 660 – 20 December 2017

Pleopassalora acaciae Crous & J. Edwards, *sp. nov.*

Etymology. Name refers to *Acacia*, the host genus from which this fungus was collected.

Classification — *Mycosphaerellaceae*, *Capnodiales*, *Dothideomycetes.*

Leaf spots mostly epiphyllous, rarely amphigenous, irregular, dark brown, 1–2 mm diam, turning pale grey in centre with age. *Conidiomata* pycnidial, solitary, immersed, breaking through the epidermis by irregular rupture, 100–200 μm diam; wall of 3–6 layers of medium brown *textura angularis*, exuding a slimy conidial cirrhus. In culture sporulating via large dark brown to black sporodochia, producing a dark brown conidial mass. On OA: *Stroma* consisting of brown, verruculose cells that give rise to aggregated conidiophores. *Conidiophores* medium brown, verruculose, subcylindrical, 0–1-septate, 15–20 × 4–7 μm. *Conidiogenous cells* terminal, verruculose, medium brown, subcylindrical, proliferating sympodially and percurrently, 7–15 × 4–7 μm. *Conidia* solitary, medium brown, verruculose, subcylindrical, apex obtuse, base truncate, 4–5 μm diam with marginal frill; hilum unthickened not darkened, 5–8-septate, (30–)40–52(–55) × (5–)6(–7) μm.

Culture characteristics — Colonies flat, spreading, surface folded, with moderate aerial mycelium and feathery, lobate margins, reaching 8 mm diam after 2 wk at 25 °C. On MEA surface olivaceous grey, reverse iron-grey. On PDA surface pale olivaceous grey, reverse olivaceous grey. On OA surface olivaceous grey.

Typus. Australia, Victoria, Narbethong, on leaves of *Acacia obliquinervia* (*Fabaceae*), 6 May 2007, *S. Morley* (holotype CBS H-23096, cultures ex-type VPRI 40697 = CPC 28354 = CBS 142533, ITS, LSU and *actA* sequences GenBank MG386026, MG386082 and MG386134, MycoBank MB823367).

Additional material examined. Australia, New South Wales, Nullica State Forest, on leaves of *Acacia falciformis*, 29 Nov. 2016, *P.W. Crous*, specimen CBS H-23316, culture CPC 32718 = CBS 143451, ITS sequence GenBank MG386027.

Colour illustrations. Leaves of *Acacia* sp.; conidiomata sporulating on OA, conidiophores and conidia. Scale bars = 10 μm.

Notes — Beilharz et al. (2004) introduced *Passalora perplexa* to accommodate a pleomorphic cercosporoid fungus causing a prominent leaf spot disease of *Acacia crassicarpa* in Australia and Indonesia. *Passalora perplexa* has subsequently been relegated to *Pleopassalora*, which is phylogenetically distinct from *Passalora* s.str. (Videira et al. 2017). *Pleopassalora acaciae* (occurring on *Acacia obliquinervia* in Australia) is morphologically distinct from *P. perplexa* (Type 1 conidia in sporodochia; 20–35 × 3–6 μm, (1–)3(–4)-septate; Beilharz et al. 2004), by producing medium brown conidia in slimy masses, 5–8-septate, 35–55 × 5–7 μm.

Based on a megablast search using the ITS sequence, the best matches were '*Passalora' loranthi* (GenBank EU514280; Identities = 493/505 (98 %), 7 gaps (1 %)), followed by *Exutisphaerella laricina* (GenBank EU167595; Identities = 526/542 (97 %), 5 gaps (0 %)), *Phaeocercospora juniperina* (GenBank KC870045; Identities 507/522 (97 %), 3 gaps (0 %)) and *Passalora sequoiae* (as *Mycosphaerella laricina*; GenBank GU214667; Identities = 524/540 (97 %), 2 gaps (0 %)). Based on the LSU sequence, the best matches were with *Pleopassalora perplexa* (GenBank GU214459; Identities 833/833 (100 %), no gaps), '*Passalora' loranthi* (GenBank KP895892; Identities 832/832 (100 %), no gaps) and *Phaeocercospora colophospermi* (GenBank NG_042683; Identities 830/833 (99 %), no gaps). The megablast search using the *actA* sequence only yielded most similar results with less than 91 % similarity and belonging to *Pseudocercospora* and *Ramularia*, for example. The highest similarities using the *actA* sequence were with species of *Mycosphaerellaceae*, for example *Pseudocercospora cruenta* (GenBank JQ325012; Identities 516/583 (89 %), 15 gaps (2 %)), *Zasmidium commune* (GenBank KY979857; Identities 509/583 (87 %), 12 gaps (2 %)) and *Ramularia glennii* (GenBank KJ504433; Identities 454/504 (90 %), 9 gaps (1 %)).

Pedro W. Crous & Johannes Z. Groenewald, Westerdijk Fungal Biodiversity Institute, P.O. Box 85167,
3508 AD Utrecht, The Netherlands; e-mail: p.crous@westerdijkinstitute.nl & e.groenewald@westerdijkinstitute.nl
Jacqueline Edwards, Agriculture Victoria, Department of Economic Development, Jobs, Transport and Resources,
AgriBio Centre for AgriBiosciences, 5 Ring Road, La Trobe University, Bundoora, Victoria 3083, Australia;
e-mail: jacky.edwards@ecodev.vic.gov.au


Saccharata acaciae

Fungal Planet 661 – 20 December 2017

Saccharata acaciae Crous, *sp. nov.*

Etymology. Name refers to *Acacia*, the host genus from which this fungus was collected.

Classification — *Saccharataceae*, *Botryosphaeriales*, *Dothideomycetes.*

Conidiomata solitary or aggregated, brown, globose, 100–200 µm diam, pycnidial with central ostiole; wall of 6–10 layers of pale brown *textura angularis*. *Paraphyses* intermingled among conidiophores, septate, hyaline, smooth, hyphae-like with obtuse ends, 2.5–3.5 µm diam. *Conidiophores* lining the inner cavity, hyaline, smooth, reduced to conidiogenous cells, or with a supporting cell. *Conidiogenous cells* hyaline, smooth, doliiform, 5–15 × 4–7 µm, proliferating percurrently at apex. *Conidia* solitary, aseptate, hyaline, smooth, prominently guttulate to granular, thin-walled, subcylindrical to fusoid-ellipsoid, apex obtuse, tapering in lower third to truncate base, 3–6 µm diam, with minute marginal frill, (25–)27–33(–42) × (6.5–)7–8(–9) µm.

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

Typus. Australia, New South Wales, Fitzroy Falls, Morton National Park, on leaves of *Acacia* sp. (*Fabaceae*), 26 Nov. 2016, *P.W. Crous* (holotype CBS H-23264, culture ex-type CPC 32181 = CBS 143167, ITS and LSU sequences GenBank MG386028 and MG386083, MycoBank MB823368).

Colour illustrations. Symptomatic leaves of *Acacia* sp. at Fitzroy Falls; conidiomata sporulating on OA, conidiogenous cells and conidia. Scale bars = 10 µm.

Notes — The genus *Saccharata* clusters in the *Saccharataceae* in the *Botryosphaeriales* (Slippers et al. 2013), and is commonly associated with members of *Myrtaceae* and *Proteaceae*. *Saccharata acaciae* is phylogenetically closely related to *S. hakeae*, which is known from *Hakea baxteri* in the Stirling Range National Park in Western Australia. Morphologically, the conidia of *S. hakeae* are similar in range, (24–)28–31(–33) × (6.5–)7–8 µm to those of *S. acaciae*. However, conidiomata of *S. acaciae* (100–200 µm diam) are smaller though than those of *S. hakeae* (200–300 µm diam), which lack paraphyses, and have larger conidiophores, being 0–1-septate, 10–25 × 2.5–3.5 µm (Crous et al. 2016a).

Based on a megablast search using the ITS sequence, the closest matches in NCBIs GenBank nucleotide database were *S. hakeae* (GenBank KY173454; Identities 546/548 (99 %), 1 gap (0 %)), *S. banksiae* (GenBank KY173449; Identities 518/556 (93 %), 9 gaps (1 %)) and *S. petrophiles* (GenBank KY173463; Identities 513/554 (93 %), 9 gaps (1 %)). The highest similarities using the LSU sequence were *S. hakeae* (GenBank KY173542; Identities 827/830 (99 %), no gaps), *S. proteae* (GenBank EU552145; Identities 837/860 (97 %), 2 gaps (0 %)) and *S. intermedia* (GenBank GU229889; Identities 832/855 (97 %), 2 gaps (0 %)).

Pedro W. Crous & Johannes Z. Groenewald, Westerdijk Fungal Biodiversity Institute, P.O. Box 85167,
3508 AD Utrecht, The Netherlands; e-mail: p.crous@westerdijkinstitute.nl & e.groenewald@westerdijkinstitute.nl
Michael J. Wingfield, Forestry and Agricultural Biotechnology Institute (FABI), University of Pretoria, Pretoria 0002, South Africa;
e-mail: mike.wingfield@fabi.up.ac.za
Treena I. Burgess & Giles E.St.J. Hardy, Centre for Phytophthora Science and Management, Murdoch University,
90 South Street, Murdoch, WA 6150, Australia;
e-mail: tburgess@murdoch.edu.au & g-hardy@murdoch.edu.au


Pararamichloridium livistonae

Fungal Planet 662 – 20 December 2017

Pararamichloridiales Crous, *ord. nov*.

MycoBank MB823462.

Pararamichloridiaceae Crous, *fam. nov.*

Mycelium consisting of hyaline, smooth, septate, branched, hyphae. *Conidiophores* erect, solitary, straight to flexuous, branched at apex or not, subcylindrical, subhyaline to medium brown, smooth, septate. *Conidiogenous cells* terminal and intercalary, subcylindrical, subhyaline to medium brown, smooth, polyblastic. *Conidia* solitary, hyaline, smooth, aseptate, thin-walled, clavate to ellipsoid. *Stromata* purple to brown, containing globose perithecia with cylindrical necks, extending above stroma. *Paraphyses* numerous, hyaline, septate. *Asci* cylindrical, 8-spored, with inamyloid annulus. *Ascospores* globose, hyaline, with verruculose epispore.

Type genus. *Pararamichloridium* Crous.
MycoBank MB823463.

Notes — The order *Pararamichloridiales* presently contains two genera, namely *Pararamichloridium* and *Woswasia* (see Jaklitsch et al. 2013).

Pararamichloridium Crous, *gen. nov.*

Etymology. Named refers to its morphological similarity to *Ramichloridium*.

Mycelium consisting of hyaline, smooth, septate, branched, hyphae. *Conidiophores* erect, solitary, straight to flexuous, branched at apex or not, subcylindrical, medium brown, smooth, septate. *Conidiogenous cells* terminal and intercalary, subcylindrical, medium brown, smooth, with swollen apex and at times swollen intercalary conidiogenous zone with clustered denticles (at times in a short rachis); denticles with slightly thickened scars. *Conidia* solitary, hyaline, smooth, granular, aseptate, thin-walled, clavate, apex obtuse, tapering in lower third to truncate, slightly thickened hilum.

Type species. *Pararamichloridium livistonae* Crous.
MycoBank MB823369.

Pararamichloridium livistonae Crous, *sp. nov.*

Etymology. Name refers to *Livistona*, the host genus from which this fungus was collected.

Mycelium consisting of hyaline, smooth, septate, branched, 1.5–2.5 µm diam hyphae. *Conidiophores* erect, solitary, straight to flexuous, branched at apex or not, subcylindrical, medium brown, smooth, 1–4-septate, 30–80 × 2.5–3 µm. *Conidiogenous cells* terminal and intercalary, subcylindrical, medium brown, smooth, 10–25 × 2.5–5 µm, with swollen apex and at times swollen intercalary conidiogenous zone with clustered denticles (at times in a short rachis); denticles 1 × 1 µm, with slightly thickened scars. *Conidia* solitary, hyaline, smooth, granular, aseptate, thin-walled, clavate, apex obtuse, tapering in lower third to truncate hilum, 0.5 µm diam, slightly thickened, (7–)8–9 × 2 µm.

Culture characteristics — Colonies flat, spreading, surface folded, with sparse aerial mycelium and feathery margins. On MEA surface cinnamon, reverse sepia with dark brick diffuse pigment. On PDA surface vinaceous buff, reverse isabelline, with diffuse brick pigment. On OA surface hazel with diffuse brick pigment.

Typus. Australia, New South Wales, Murramarang National Park, on leaves of *Livistona australis* (*Arecaceae*), 27 Nov. 2016, *P.W. Crous* (holotype CBS H-23265, culture ex-type CPC 32156 = CBS 143166, ITS and LSU sequences GenBank MG386029 and MG386084, MycoBank MB823370).

Notes — *Pararamichloridium* is a typical ramichloridium-like genus sensu Arzanlou et al. (2007). However, it clusters distant from *Ramichloridium apiculatum* (Videira et al. 2017), and is closely related to *Spadicoides verrucosa* (Rao & De Hoog 1986). The latter fungus was originally placed in *Spadicoides* due to its determinate, tretic conidiophores, although it has aseptate conidia, and sporulates well in culture (in contrast to *Spadicoides* s.str.). *Spadicoides verrucosa* differs from *Pararamichloridium* by having pale brown, verruculose conidia, but its clearly not a member of *Spadicoides*. Based on its close phylogenetic affinity, it is therefore allocated to *Pararamichloridium.*

Based on a megablast search using the ITS sequence, the closest matches in NCBIs GenBank nucleotide database were only distant matches with species in *Sordariomycetes*, such as *Spadicoides* sp. (GenBank KU747624; Identities 399/464 (86 %), 41 gaps (8 %)) and *Phomatospora striatigera* (GenBank NR_145386; Identities 521/650 (80 %), 59 gaps (9 %)). Our ITS sequence is only 85 % similar to the ITS sequence of *Spadicoides verrucosa* CBS 128.86 (GenBank MG386030; Identities 380/447 (85 %), 22 gaps (4 %)). The highest similarities using the LSU sequence were *Spadicoides verrucosa* (GenBank EF204508; Identities 801/833 (96 %), 3 gaps (0 %)), *Magnaporthiopsis poae* (GenBank KM401651; Identities 791/835 (95 %), 2 gaps (0 %)) and *Woswasia atropurpurea* (GenBank JX233658; Identities 788/835 (94 %), 2 gaps (0 %)).

Pararamichloridium verrucosum (V. Rao & de Hoog) Crous, *comb. nov.* — MycoBank MB823371

Basionym. *Spadicoides verrucosa* V. Rao & de Hoog, Stud. Mycol. 28: 42. 1986.

Typus. India, Andhra Pradesh, Adilabad, on various fungi on old *Bambusa* leaves, Jan. 1983, *V. Rao* (holotype CBS H-3891, ex-type culture CBS 128.86).

Colour illustrations. *Livistona australis* at Murramarang National Park; leaf spots, conidiophores and conidia. Scale bars = 10 µm.

Pedro W. Crous & Johannes Z. Groenewald, Westerdijk Fungal Biodiversity Institute, P.O. Box 85167,
3508 AD Utrecht, The Netherlands; e-mail: p.crous@westerdijkinstitute.nl & e.groenewald@westerdijkinstitute.nl
Michael J. Wingfield, Forestry and Agricultural Biotechnology Institute (FABI), University of Pretoria, Pretoria 0002, South Africa;
e-mail: mike.wingfield@fabi.up.ac.za
Brett A. Summerell, Royal Botanic Gardens and Domain Trust, Mrs. Macquaries Road, Sydney, NSW 2000, Australia;
e-mail: brett.summerell@rbgsyd.nsw.gov.au
Angus J. Carnegie, Forest Health & Biosecurity, NSW Department of Primary Industries, Level 12, 10 Valentine Ave,
Parramatta, NSW 2150, Locked Bag 5123, Parramatta, NSW 2124, Australia; e-mail: angus.carnegie@dpi.nsw.gov.au


Neoanungitea eucalypti

Fungal Planet 663 – 20 December 2017

Neoanungitea Crous, *gen nov.*

Etymology. Named refers to its morphological similarity to *Anungitea*.

Mycelium consisting of hyaline to pale brown, smooth to verruculose, branched, septate hyphae. *Conidiophores* erect, solitary, frequently arising from a brown stroma or from superficial hyphae, subcylindrical, flexuous, medium brown, roughened, multiseptate, thick-walled. *Conidiogenous cells* terminal, subcylindrical, medium brown, finely roughened, forming a terminal rachis with several sympodial loci, flat-tipped, unthickened. *Conidia* in short, branched chains, fusoid-ellipsoid, septate, pale brown, roughened, ends obtuse, hila slightly thickened.

Type species. *Neoanungitea eucalypti* Crous.
MycoBank MB823489.

Neoanungitea eucalypti Crous, *sp. nov.*

Etymology. Name refers to *Eucalyptus*, the host genus from which this fungus was collected.

Classification — *Microthyriaceae*, *Microthyriales*, *Dothideomycetes.*

Mycelium consisting of hyaline to pale brown, smooth to verruculose, branched, septate, 2.5–3.5 µm diam hyphae. *Conidiophores* erect, solitary, frequently arising from a brown stroma or from superficial hyphae, subcylindrical, flexuous, medium brown, roughened, multiseptate, thick-walled, 30–160 × 4–6 µm. *Conidiogenous cells* terminal, subcylindrical, medium brown, finely roughened, 20–60 × 4–7 µm, forming a terminal rachis with several sympodial loci, flat-tipped, unthickened, 2.5–3.5 µm diam. *Conidia* in short, branched chains, fusoid-ellipsoid, (0–)3-septate, pale brown, roughened, ends obtuse, hila slightly thickened, 1–1.5 µm diam, (13–)15–17(–22) × (3.5–)4–5 µm.

Culture characteristics — Colonies erumpent, spreading, with moderate aerial mycelium and feathery margins, reaching 8 mm diam after 2 wk at 25 °C. On MEA, PDA and OA surface amber, reverse chestnut.

Typus. Australia, Victoria, Silvan Reservoir Park, on leaves of *Eucalyptus obliqua* (*Myrtaceae*), 1 Dec. 2016, *P.W. Crous* (holotype CBS H-23266, culture ex-type CPC 32667 = CBS 143173, ITS-LSU sequence GenBank MG386031, MycoBank MB823372).

Notes — *Anungitea* is characterised by having an apical conidiogenous cell with conspicuous denticles, while *Anungitopsis* has indistinguishable scars arranged in a rachis (Seifert et al. 2011). *Neoanungitea* has a rachis much like *Anungitopsis*, but has conspicuous flat-tipped sympodial loci, somewhat resembling *Anungitea*. *Neoanungitea* is therefore introduced as a genus sharing features of both *Anungitea* and *Anungitopsis.*

Based on a megablast search using the ITS sequence, the closest match in NCBIs GenBank nucleotide database was with *Anungitopsis speciosa* (GenBank EU035401; Identities 491/608 (81 %), 42 gaps (6 %)); all other results were only based on similarity to the 5.8S nrRNA gene sequences. The highest similarities using the LSU sequence were *Anungitopsis speciosa* (GenBank EU035401; Identities 719/813 (97 %), no gaps), *Spirosphaera beverwijkiana* (GenBank HQ696657; Identities 764/827 (92 %), 8 gaps (0 %)), *Microthyrium propagulensis* (GenBank KU948989; Identities 764/833 (92 %), 12 gaps (1 %)) and *Microthyrium microscopicum* (GenBank GU301846; Identities 746/817 (91 %), 27 gaps (3 %)).

Colour illustrations. Silvan Reservoir Park; conidiophores and conidia. Scale bars = 10 µm.

Pedro W. Crous & Johannes Z. Groenewald, Westerdijk Fungal Biodiversity Institute, P.O. Box 85167,
3508 AD Utrecht, The Netherlands; e-mail: p.crous@westerdijkinstitute.nl & e.groenewald@westerdijkinstitute.nl
Michael J. Wingfield, Forestry and Agricultural Biotechnology Institute (FABI), University of Pretoria, Pretoria 0002, South Africa;
e-mail: mike.wingfield@fabi.up.ac.za
David Smith, Agriculture, Energy & Resources, Agriculture and Rural Division, Department of Economic Development, Jobs, Transport and Resources,
Unit 3, 2 Codrington St, Cranbourne, Victoria 3977, Australia; e-mail: david.smith@ecodev.vic.gov.au


Ochroconis podocarpi

Fungal Planet 664 – 20 December 2017

Ochroconis podocarpi Crous, *sp. nov.*

Etymology. Name refers to *Podocarpus*, the host genus from which this fungus was collected.

Classification — *Sympoventuriaceae*, *Venturiales*, *Dothideomycetes.*

Mycelium consisting of smooth, pale brown to medium brown, septate, branched, 1.5–2 µm diam hyphae, giving rise to hyphal strands and hyphal coils. *Conidiophores* erect, 1-septate, unbranched, medium brown, smooth, subcylindrical, 5–16 × 2 µm. *Conidiogenous cells* terminal, medium brown, smooth, subcylindrical, 5–12 × 2 µm, with 1–4 terminal cylindrical denticles, 1–1.5 × 1 µm. *Conidia* solitary, medianly 1-septate, fusoid-ellipsoid to subcylindrical, apex obtuse, base with truncate scar, 0.5 µm diam, medium brown, verruculose, (6–)7–9(–10) × 2(–2.5) µm.

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

Typus. AUSTRALIA, New South Wales, Australian Botanic Garden, Mount Annan, on leaves of *Podocarpus grayae* (*Podocarpaceae*), 25 Nov. 2016, *P.W. Crous* (holotype CBS H-23267, culture ex-type CPC 32829 = CBS 143174, ITS, LSU and *tub2* sequences GenBank MG386032, MG386085 and MG386162, MycoBank MB823373).

Notes — The genus *Ochroconis* is characterised by olivaceous to brown colonies, pigmented conidiophores, and sympodial conidiogenesis with denticles that give rise to septate, pigmented, verruculose conidia. *Ochroconis podocarpi* is phylogenetically closely related to, but distinct from *O. humicola* (CBS 116655 ex-type from peat soil, Canada), which is a species characterised by rapid growth, and conidiophores up to 300 µm in length (Giraldo et al. 2014).

Based on a megablast search using the ITS sequence, the closest matches in NCBIs GenBank nucleotide database were *Ochroconis bacilliformis* (GenBank KP798632; Identities 360/414 (87 %), 23 gaps (5 %)), *Ochroconis robusta* (GenBank KP798633; Identities 363/418 (87 %), 30 gaps (7 %)) and *Ochroconis constricta* (GenBank KX610329; Identities 335/383 (87 %), 13 gaps (3 %)). The highest similarities using the LSU sequence were *Ochroconis humicola* (GenBank KF156124; Identities 775/799 (97 %), 7 gaps (0 %)), *Ochroconis musae* (GenBank KT272088; Identities 816/852 (96 %), 4 gaps (0 %)) and *Ochroconis mirabilis* (GenBank KF282661; Identities 812/849 (96 %), 5 gaps (0 %)). The highest similarities using the *tub2* sequence were *Ochroconis longiphorum* (GenBank KF156182; Identities 374/461 (81 %), 8 gaps (1 %)), *Ochroconis macrozamiae* (GenBank KF156191; Identities 375/467 (80 %), 19 gaps (4 %)) and *Ochroconis gamsii* (GenBank HQ877664; Identities 371/463 (80 %), 19 gaps (4 %)).

Colour illustrations. *Podocarpus grayae*; conidiophores and conidia. Scale bars = 10 µm.

Pedro W. Crous & Johannes Z. Groenewald, Westerdijk Fungal Biodiversity Institute, P.O. Box 85167,
3508 AD Utrecht, The Netherlands; e-mail: p.crous@westerdijkinstitute.nl & e.groenewald@westerdijkinstitute.nl
Michael J. Wingfield, Forestry and Agricultural Biotechnology Institute (FABI), University of Pretoria, Pretoria 0002, South Africa;
e-mail: mike.wingfield@fabi.up.ac.za
Treena I. Burgess & Giles E.St.J. Hardy, Centre for Phytophthora Science and Management, Murdoch University,
90 South Street, Murdoch, WA 6150, Australia;
e-mail: tburgess@murdoch.edu.au & g-hardy@murdoch.edu.au


Seiridium persooniae

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Seiridium persooniae Crous, *sp. nov.*

Etymology. Name refers to *Persoonia*, the host genus from which this fungus was collected.

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

Conidiomata stromatic, separate, globose, erumpent, black, up to 300 µm diam, unilocular; walls of 4–8 layers of brown *textura angularis. Conidiophores* lining the inner cavity, subcylindrical, branched below, hyaline, smooth, 2–3-septate, up to 50 µm long. *Conidiogenous cells* integrated, terminal and lateral, subcylindrical, 10–20 × 2.5–3 µm, proliferating percurrently at apex. *Conidia* fusoid, wall smooth, not constricted at septa, 5-septate with central pore, guttulate, (20–)25–35(–38) × (9–)10(–12) µm, wall 1 µm thick; basal cell obconic, subhyaline with single unbranched central appendage, 1 µm long (rarely present); apical cell bluntly rounded, subhyaline with central unbranched appendage, 1–2 µm long.

Culture characteristics — Colonies flat, spreading, with moderate aerial mycelium and feathery margins, reaching 45 mm diam after 2 wk at 25 °C. On MEA surface dirty white with patches of olivaceous grey, reverse iron-grey in centre, luteous in outer region. On PDA surface dirty white, reverse olivaceous grey. On OA surface dirty white.

Typus. Australia, New South Wales, Nunnock Swamp, on leaves of *Persoonia* sp. (*Proteaceae*), 28 Nov. 2016, *P.W. Crous* (holotype CBS H-23268, culture ex-type CPC 32301 = CBS 143445, ITS, LSU and *tub2* sequences GenBank MG386033, MG386086 and MG386163, MycoBank MB823374).

Notes — The genus *Seiridium* includes several plant pathogenic species causing cankers on *Cupressaceae*. Of the species presently known, none have been described from *Persoonia*. Phylogenetically, *S. persooniae* is closely related to *S. unicorne* (on *Cupressus*, *Juniperus*, *Thuja*; conidia fusiform, 5–6-septate, (23–)24–30 × (7–)7.5–9.5(–10) µm, apical appendage 3–10 µm, basal appendage 3–6 µm; Nag Raj 1993), but distinct in that it has larger conidia and shorter appendages.

Based on a megablast search using the ITS sequence, the closest matches in NCBIs GenBank nucleotide database were *Seiridium cardinale* (GenBank AF405305; Identities 536/556 (96 %), 17 gaps (3 %)), *Seiridium cupressi* (GenBank FJ430600; Identities 543/564 (96 %), 17 gaps (3 %)) and *Seiridium phylicae* (GenBank KC005788; Identities 559/581 (96 %), 17 gaps (2 %)). The highest similarities using the LSU sequence were *Seiridium unicorne* (GenBank DQ414532; Identities 833/834 (99 %), no gaps), *Seiridium pseudocardinale* (GenBank KU848209; Identities 832/833 (99 %), no gaps) and *Seiridium phylicae* (GenBank NG_042759; Identities 842/844 (99 %), 1 gap (0 %)). The highest similarities using the *tub2* sequence were *Seiridium phylicae* (GenBank KC005819; Identities 437/451 (97 %), 2 gaps (0 %)), *Seiridium cardinale* (GenBank DQ926973; Identities 356/368 (97 %), 1 gap (0 %)) and *Seiridium cupressi* (GenBank DQ926979; Identities 354/367 (96 %), 1 gap (0 %)).

Colour illustrations. *Lomatia myricoides* growing intermixed with *Persoonia* sp. in Nunnock Swamp; conidiomata sporulating on OA, conidiophores and conidia. Scale bars = 10 µm.

Pedro W. Crous & Johannes Z. Groenewald, Westerdijk Fungal Biodiversity Institute, P.O. Box 85167,
3508 AD Utrecht, The Netherlands; e-mail: p.crous@westerdijkinstitute.nl & e.groenewald@westerdijkinstitute.nl
Michael J. Wingfield, Forestry and Agricultural Biotechnology Institute (FABI), University of Pretoria, Pretoria 0002, South Africa;
e-mail: mike.wingfield@fabi.up.ac.za
Brett A. Summerell, Royal Botanic Gardens and Domain Trust, Mrs. Macquaries Road, Sydney, NSW 2000, Australia;
e-mail: brett.summerell@rbgsyd.nsw.gov.au
Angus J. Carnegie, Forest Health & Biosecurity, NSW Department of Primary Industries, Level 12, 10 Valentine Ave,
Parramatta, NSW 2150, Locked Bag 5123, Parramatta, NSW 2124, Australia; e-mail: angus.carnegie@dpi.nsw.gov.au


Pseudosporidesmium lambertiae

Fungal Planet 666 – 20 December 2017

Pseudosporidesmiaceae Crous, *fam. nov.*

Classification — *Pseudosporidesmiaceae*, *Xylariales*, *Sordariomycetes.*

Mycelium consisting of branched, septate, pale brown, hyphae. *Conidiophores* solitary or in clusters, flexuous or erect, somewhat repent, arising from superficial hyphae, rejuvenating percurrently; stipe cylindrical, brown, smooth, thick-walled, mostly unbranched. *Conidiogenous cells* terminal, cylindrical, brown; scars truncate, unthickened. *Conidia* solitary, obclavate, apex subobtuse, base truncate, euseptate, smooth-walled, brown. Conidia frequently remain attached to the sides of the percurrently rejuvenating conidiophore (delayed secession), creating the impression of sympodial proliferation.

Type genus. *Pseudosporidesmium* K.D. Hyde & McKenzie.
MycoBank MB823464.

Notes — *Pseudosporidesmiaceae* includes species of *Pseudosporidesmium* and a taxon tentatively identified as *Repetophragma inflatum* (GenBank DQ408576.1), of which the identification could not be confirmed, suggesting it may well be a species of *Pseudosporidesmium*.

Pseudosporidesmium lambertiae Crous, *sp. nov.*

Etymology. Name refers to *Lambertia*, the host genus from which this fungus was collected.

Mycelium consisting of branched, septate, pale brown, 2–3 µm diam hyphae. *Conidiophores* solitary or in clusters of up to three, flexuous or erect, somewhat repent, arising from superficial hyphae, rejuvenating percurrently, base mostly not swollen, and lacking rhizoids; stipe cylindrical, brown, smooth, thick-walled, mostly unbranched, 100–300 × 5–7 µm. *Conidiogenous cells* terminal, cylindrical, brown, 10–20 × 6–7 µm; scars truncate, unthickened, 6–7 µm diam. *Conidia* solitary, obclavate, apex subobtuse, base truncate, 6–7 µm diam, (2–)4-euseptate, smooth-walled, guttulate, (37–)45–55(–60) × (11–)14–15 µm, basal cell pale brown, conidium body medium brown, apical cell pale brown, forming a long beak with subobtuse apex. *Conidia* frequently remain attached to the sides of the percurrently rejuvenating conidiophore (delayed secession), creating the impression of sympodial proliferation.

Culture characteristics — Colonies erumpent, spreading, with abundant aerial mycelium and feathery margins, reaching 30 mm diam after 2 wk at 25 °C. On MEA, PDA and OA surface olivaceous grey, reverse iron-grey.

Typus. Australia, New South Wales, Fitzroy Falls, Morton National Park, on leaves of *Lambertia formosa* (*Proteaceae*), 26 Nov. 2016, *P.W. Crous* (holotype CBS H-23269, culture ex-type CPC 32206 = CBS 143169, ITS and LSU sequences GenBank MG386034 and MG386087, MycoBank MB823375).

Colour illustrations. *Lambertia formosa* at Fitzroy Falls; conidiophores and conidia. Scale bars = 10 µm.

Notes — *Pseudosporidesmium lambertiae* is closely related to the ex-type strain of *Sporidesmium knawiae* and a specimen identified as *Repetophragma inflatum* (voucher NN42958; GenBank DQ408576.1). Su et al. (2016) established the genus *Pseudosporidesmium* based on the fact that conidiophores of *Sporidesmium knawiae* show percurrent rejuvenation, and those of *Sporidesmium* s.str. do not, and tend to have percurrent proliferation at the apex. Because the genus *Sporidesmium* is polyphyletic, we follow this decision, although it should be noted that the type species of *Sporidesmium* has not yet been collected, and thus the phylogeny of the genus remains unsettled. *Pseudosporidesmium lambertiae* differs from *P. knawiae* by having 4-euseptate conidia that are longer and narrower, (60–)65–70(–80) × (10–)11–12(–13) µm, than those of *P. knawiae* (Crous et al. 2008).

Based on a megablast search using the ITS sequence, the closest matches in NCBIs GenBank nucleotide database were *Pseudosporidesmium knawiae* (GenBank FJ349609; Identities 343/381 (90 %), 20 gaps (5 %)), *Nigrospora oryzae* (GenBank KX355191; Identities 306/359 (85 %), 26 gaps (7 %)) and *Anungitea grevilleae* (GenBank KX228252; Identities 299/351 (85 %), 18 gaps (5 %)). The highest similarities using the LSU sequence were *Repetophragma inflatum* (GenBank DQ408576; Identities 787/792 (99 %), 1 gap (0 %)), *Pseudosporidesmium knawiae* (GenBank FJ349610; Identities 785/792 (99 %), no gaps) and *Annulohypoxylon moriforme* (GenBank DQ840058; Identities 753/798 (94 %), 10 gaps (1 %)).

Pedro W. Crous & Johannes Z. Groenewald, Westerdijk Fungal Biodiversity Institute, P.O. Box 85167,
3508 AD Utrecht, The Netherlands; e-mail: p.crous@westerdijkinstitute.nl & e.groenewald@westerdijkinstitute.nl
Michael J. Wingfield, Forestry and Agricultural Biotechnology Institute (FABI), University of Pretoria, Pretoria 0002, South Africa;
e-mail: mike.wingfield@fabi.up.ac.za
Treena I. Burgess & Giles E.St.J. Hardy, Centre for Phytophthora Science and Management, Murdoch University,
90 South Street, Murdoch, WA 6150, Australia;
e-mail: tburgess@murdoch.edu.au & g-hardy@murdoch.edu.au


Xenopassalora petrophiles

Fungal Planet 667 – 20 December 2017

Xenopassalora Crous, *gen. nov*.

Etymology. Named refers to its morphological similarity to the genus *Passalora*.

Classification — *Mycosphaerellaceae*, *Capnodiales*, *Dothideomycetes.*

Phytopathogenic, associated with small red-brown leaf spots. *Mycelium* consisting of brown, verruculose to warty, septate, branched, thick-walled hyphae, at time encased in mucoid layer and forming a brown stroma of pseudoparenchymatal cells; hyphae becoming prominently constricted at septa, cells swelling, becoming muriformly septate. *Conidiophores* solitary, erect on hyphae, geniculous-flexuous, septate, dark brown, thick-walled, roughened. *Conidiogenous cells* terminal, integrated, medium brown, smooth, consisting of a rachis of sympodial loci; scars round, thickened, darkened. *Conidia* solitary, aseptate, medium brown, guttulate, verruculose, ellipsoid, apex obtuse, tapering in lower third to truncate hilum, thickened, darkened.

Type species. *Xenopassalora petrophiles* Crous.
MycoBank MB823376.

Xenopassalora petrophiles Crous, *sp. nov*.

Etymology. Name refers to *Petrophile*, the host genus from which this fungus was collected.

Phytopathogenic, associated with small red-brown leaf spots. *Mycelium* consisting of brown, verruculose to warty, septate, branched, thick-walled, 4–5 µm diam hyphae, at time encased in mucoid layer and forming a brown stroma of pseudoparenchymatal cells; hyphae becoming prominently constricted at septa, cells swelling, becoming muriformly septate, up to 20 µm diam. *Conidiophores* solitary, erect on hyphae, geniculous-flexuous, 2–8-septate, dark brown, thick-walled, roughened, 15–90 × 3–5 µm. *Conidiogenous cells* terminal, integrated, medium brown, smooth, consisting of a rachis of sympodial loci, 15–30 × 4–5 µm; scars round, thickened, darkened, 1–1.5 µm diam. *Conidia* solitary, aseptate, medium brown, guttulate, verruculose, ellipsoid, apex obtuse, tapering in lower third to truncate hilum, 1–1.5 µm diam, thickened, darkened, (5–)6–7(–9) × (4–)5(–5.5) µm.

Culture characteristics — Colonies erumpent, spreading, surface folded, with moderate aerial mycelium and even, lobate margins, reaching 10 mm diam after 2 wk at 25 °C. On MEA, PDA and OA surface olivaceous grey, reverse iron-grey.

Typus. Australia, New South Wales, Fitzroy Falls, on leaves of *Petrophile pedunculata* (*Proteaceae*), 26 Nov. 2016, *P.W. Crous* (holotype CBS H-23270, culture ex-type CPC 32085 = CBS 143180, ITS, LSU and *rpb2* sequences GenBank MG386035, MG386088 and MG386140, MycoBank MB823377).

Notes — No passalora-like fungal records are known from *Petrophile*, and it can be assumed that *X. petrophiles*, which also has no matches with fungal taxa presently known from DNA sequence, represents a new species. Because of its pigmented aseptate conidia, it is reminiscent of the *Ramichloridium* complex, but is distinct in that it does not form a rachis, and denticles are absent. Conidial hila and scars are thickened and darkened, as found in the *Passalora* complex. However, the aseptate conidia, and solitary conidiophores, are rather distinct features. Phylogenetically, it also does not cluster in any genus of *Mycosphaerellaceae* (Videira et al. 2017), and thus we introduce a new genus, *Xenopassalora*, to accommodate it.

Based on a megablast search using the ITS sequence, the closest matches in NCBIs GenBank nucleotide database were *Paracercosporidium microsorum* (as *Mycosphaerella microsora*; GenBank EU167599; Identities 496/534 (93 %), 14 gaps (2 %)), *Passalora arctostaphyli* (GenBank KJ152782; Identities 494/532 (93 %), 11 gaps (2 %)) and *Pantospora guazumae* (GenBank NR_119971; Identities 494/534 (93 %), 14 gaps (2 %)). The highest similarities using the LSU sequence were *Phaeophleospora scytalidii* (GenBank JN232427; Identities 808/836 (97 %), 3 gaps (0 %)), *Devonomyces endophyticus* (as *Mycosphaerella* sp.; GenBank GU214450; Identities 808/836 (97 %), 3 gaps (0 %)) and *Mycosphaerella stromatosa* (GenBank EU167598.2; Identities 808/836 (97 %), 3 gaps (0 %)). The highest similarities using the *rpb2* sequence were distant hits with *Fusoidiella depressa* (GenBank KX348055; Identities 600/785 (76 %), 10 gaps (1 %)), *Zasmidium anthuriicola* (GenBank KT216547; Identities 632/835 (76 %), 34 gaps (4 %)) and *Ramularia vizellae* (GenBank KP894758; Identities 620/822 (75 %), 30 gaps (3 %)).

Colour illustrations. *Petrophile pedunculata* at Fitzroy Falls; conidiophores and conidia. Scale bars = 10 µm.

Pedro W. Crous & Johannes Z. Groenewald, Westerdijk Fungal Biodiversity Institute, P.O. Box 85167,
3508 AD Utrecht, The Netherlands; e-mail: p.crous@westerdijkinstitute.nl & e.groenewald@westerdijkinstitute.nl
Michael J. Wingfield, Forestry and Agricultural Biotechnology Institute (FABI), University of Pretoria, Pretoria 0002, South Africa;
e-mail: mike.wingfield@fabi.up.ac.za
Treena I. Burgess & Giles E.St.J. Hardy, Centre for Phytophthora Science and Management, Murdoch University,
90 South Street, Murdoch, WA 6150, Australia;
e-mail: tburgess@murdoch.edu.au & g-hardy@murdoch.edu.au


Castanediella eucalyptigena

Fungal Planet 668 – 20 December 2017

Castanediella eucalyptigena Crous, *sp. nov.*

Etymology. Name refers to *Eucalyptus*, the host genus from which this fungus was collected.

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

Mycelium consisting of hyaline, smooth, branched, septate, 2–4 µm diam hyphae. *Conidiophores* erect on hyphae, subcylindrical, smooth, hyaline, 0–2-septate, frequently reduced to conidiogenous loci on hyphae, up to 15 µm tall, 3–5 µm diam. *Conidiogenous cells* hyaline, smooth, solitary, terminal and intercalary, ampulliform or subcylindrical, polyblastic, with inconspicuous scars at apex, 2–10 × 2–5 µm. In older cultures (4 wk) conidiophores and conidiogenous cells become pale brown. *Conidia* solitary but aggregated in mucoid clusters, hyaline, smooth, aseptate, falcate, tapering to acute ends that are subobtusely rounded, biguttulate, (13–)18–24(–30) × 2(–2.5) µm.

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

Typus. Australia, New South Wales, Barren Grounds Nature Reserve, on leaves of *Eucalyptus* sp. (*Myrtaceae*), 26 Nov. 2016, *P.W. Crous* (holotype CBS H-23272, culture ex-type CPC 32055 = CBS 143178, ITS and LSU sequences GenBank MG386036 and MG386089, MycoBank MB823378).

Colour illustrations. Barren Grounds Nature Reserve; conidiophores and conidia. Scale bars = 10 µm.

Notes — The genus *Castanediella* is morphologically similar to *Microdochium*, but differs in having brown, branched conidiophores (Crous et al. 2015b, Hernández-Restrepo et al. 2016, 2017). Several species of *Castanediella* are known from *Eucalyptus* (Crous et al. 2016a), but *C. eucalyptigena* is phylogenetically distinct from all taxa presently known.

Based on a megablast search using the ITS sequence, the closest matches in NCBIs GenBank nucleotide database were *Xyladictyochaeta lusitanica* (GenBank KY853479; Identities 531/576 (92 %), 12 gaps (2 %)), *C. cagnizarii* (GenBank KP859054; Identities 517/575 (90 %), 30 gaps (5 %)) and *C. malaysiana* (GenBank KX306752; Identities 520/580 (90 %), 24 gaps (4 %)). The highest similarities using the LSU sequence were *C. cagnizarii* (GenBank KP858991; Identities 793/814 (97 %), 3 gaps (0 %)), *Pidoplitchkoviella terricola* (GenBank AF096197; Identities 799/822 (97 %), 5 gaps (0 %)) and *C. eucalypti* (GenBank KR476758; Identities 794/819 (97 %), 1 gap (0 %)).

Pedro W. Crous & Johannes Z. Groenewald, Westerdijk Fungal Biodiversity Institute, P.O. Box 85167,
3508 AD Utrecht, The Netherlands; e-mail: p.crous@westerdijkinstitute.nl & e.groenewald@westerdijkinstitute.nl
Michael J. Wingfield, Forestry and Agricultural Biotechnology Institute (FABI), University of Pretoria, Pretoria 0002, South Africa;
e-mail: mike.wingfield@fabi.up.ac.za
Treena I. Burgess & Giles E.St.J. Hardy, Centre for Phytophthora Science and Management, Murdoch University,
90 South Street, Murdoch, WA 6150, Australia;
e-mail: tburgess@murdoch.edu.au & g-hardy@murdoch.edu.au


Amphosoma persooniae

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Amphosoma persooniae Crous, *sp. nov.*

Etymology. Name refers to *Persoonia*, the host genus from which this fungus was collected.

Classification — *Orbiliaceae*, *Orbiliales*, *Orbiliomycetes*.

Associated with prominent stem cankers on *Persoonia*; cankers were covered by prominent back conidiomata. *Conidiomata* pycnidial, globose, 90–180 µm diam, dark brown, with central ostiole, 20–30 µm diam, exuding a crystalline conidial mass; outer conidiomatal wall covered with brown, verruculose, septate hyphae, 2–2.5 µm diam; wall of 3–5 layers of brown *textura angularis. Conidiophores* lining the inner cavity, hyaline, smooth, branched, 1–4-septate, 10–40 × 2–2.5 µm. *Conidiogenous cells* terminal and intercalary, hyaline, smooth, subcylindrical, phialidic with prominent periclinal thickening, 5–17 × 2–2.5 µm. A few conidiogenous cells also appear to proliferate percurrently. *Conidia* hyaline, smooth-walled, guttulate, aseptate, subcylindrical, straight, apex obtuse, base truncate, 1–1.5 µm diam, (4.5–)5–6(–7) × (2–)2.5(–3) µm.

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

Typus. Australia, New South Wales, Tullarwalla Creek, on stems of *Persoonia* sp. (*Proteaceae*), 27 Sept. 2016, *P.W. Crous* (holotype CBS H-23273, culture ex-type CPC 32235 = CBS 143171, ITS and LSU sequences GenBank MG386037 and MG386090, MycoBank MB823379).

Colour illustrations. Stem canker on *Persoonia* sp.; conidiomata sporulating on PDA, conidiomatal ostiole, conidiophores and conidia. Scale bars = 10 µm.

Notes — *Amphosoma persooniae* is phylogenetically related to species of *Amphosoma* (Baral et al. 2017). Although *Amphosoma* is supposed to have trinacrium-like asexual morphs, *A. persooniae* appears phoma-like in morphology (see Chen et al. 2015). Upon initial incubation, several white apothecia resembling *Amphosoma* were observed, although the cultures were derived from the phoma-like morph that also developed on the twigs. Although no inoculations were performed, conidiomata were associated with prominent stem cankers on *Persoonia*, suggesting that this could be a plant pathogen, but further collections are required to resolve its ecology.

Based on a megablast search using the ITS sequence, the closest matches in NCBIs GenBank nucleotide database were *Amphosoma resinicola* (GenBank KT222388; Identities 482/565 (85 %), 23 gaps (4 %)) and *Amphosoma atroolivacea* (GenBank KT222387; Identities 468/570 (82 %), 42 gaps (7 %)). The highest similarities using the LSU sequence were *Amphosoma atroolivacea* (GenBank KT222387; Identities 827/854 (97 %), 4 gaps (0 %)), *Amphosoma resinicola* (GenBank KT222388; Identities 822/852 (96 %), no gaps) and *Retiarius superficiaris* (GenBank KY352467; Identities 747/785 (95 %), 3 gaps (0 %)).

Pedro W. Crous & Johannes Z. Groenewald, Westerdijk Fungal Biodiversity Institute, P.O. Box 85167,
3508 AD Utrecht, The Netherlands; e-mail: p.crous@westerdijkinstitute.nl & e.groenewald@westerdijkinstitute.nl
Michael J. Wingfield, Forestry and Agricultural Biotechnology Institute (FABI), University of Pretoria, Pretoria 0002, South Africa;
e-mail: mike.wingfield@fabi.up.ac.za
Brett A. Summerell, Royal Botanic Gardens and Domain Trust, Mrs. Macquaries Road, Sydney, NSW 2000, Australia;
e-mail: brett.summerell@rbgsyd.nsw.gov.au
Angus J. Carnegie, Forest Health & Biosecurity, NSW Department of Primary Industries, Level 12, 10 Valentine Ave,
Parramatta, NSW 2150, Locked Bag 5123, Parramatta, NSW 2124, Australia; e-mail: angus.carnegie@dpi.nsw.gov.au


Paraphysalospora eucalypti

Fungal Planet 670 – 20 December 2017

Paraphysalospora Crous, *gen nov.*

Etymology. Named refers to *Physalospora*, a morphologically similar genus.

Classification — *Clypeophysalosporaceae*, *Xylariales*, *Sordariomycetes.*

Ascospores hyaline, smooth, limoniform with cylindrical appendage at each end. *Conidiomata* sporodochial, with buff, slimy conidial mass. *Conidiophores* subcylindrical, pale brown, smooth, branched, septate. *Conidiogenous cells* terminal and intercalary, subcylindrical, pale brown, smooth, phialidic with prominent periclinal thickening. *Conidia* solitary, hyaline, smooth, aseptate, sickle-shaped, apex subobtuse, base truncate.

Type species. *Paraphysalospora eucalypti* Crous.
MycoBank MB823380.

Paraphysalospora eucalypti Crous, *sp. nov.*

Etymology. Name refers to *Eucalyptus*, the host genus from which this fungus was collected.

Single ascospores shot onto MEA, but ascomata not traced on leaf tissue. *Ascospores* hyaline, smooth, limoniform with cylindrical appendage at each end, 45–50 × 15–20 µm. *Conidiomata* sporodochial on OA and SNA, up to 400 µm diam, with buff, slimy conidial mass. *Conidiophores* subcylindrical, pale brown, smooth, branched, septate, up to 80 µm tall. *Conidiogenous cells* terminal and intercalary, subcylindrical, pale brown, smooth, 10–20 × 2.5 µm, phialidic with prominent periclinal thickening. *Conidia* solitary, hyaline, smooth, aseptate, sickle-shaped, apex subobtuse, base truncate, (13–)15–17(–20) × 1.5 µm.

Culture characteristics — Colonies erumpent, spreading, surface folded, with sparse aerial mycelium and smooth, lobate margins, reaching 10 mm diam after 2 wk at 25 °C. On MEA, PDA and OA surface dirty white, reverse luteous.

Typus. Australia, New South Wales, Barren Grounds Nature Reserve, on leaves of *Eucalyptus sieberi* (*Myrtaceae*), 26 Nov. 2016, *P.W. Crous* (holotype CBS H-23274, culture ex-type CPC 32053 = CBS 143177, ITS and LSU sequences GenBank MG386038 and MG386091, MycoBank MB823381).

Notes — The genus *Paraphysalospora* is related to *Clypeophysalospora* and *Neophysalospora* (*Xylariales*), both occurring on *Eucalyptus* (Crous et al. 2014b, Giraldo et al. 2017). Based on the ascospore shape, mucoid appendages and sporodochial asexual morph, *Paraphysalospora* clearly represents yet another genus in this complex. There were only a few ascomata on the leaf tissue, and hence the ascomatal anatomy remains to be elucidated pending further collections.

Based on a megablast search using the ITS sequence, the closest matches in NCBIs GenBank nucleotide database were *Castanediella hyalopenicillata* (GenBank KX306751; Identities 397/427 (93 %), 3 gaps (0 %)), *Bagadiella lunata* (GenBank NR_132832; Identities 567/610 (93 %), 20 gaps (3 %)) and *B. koalae* (GenBank JF951142; Identities 565/611 (92 %), 21 gaps (3 %)). The highest similarities using the LSU sequence were *Neophysalospora eucalypti* (GenBank KP004490; Identities 821/839 (98 %), 2 gaps (0 %)), *Clypeophysalospora latitans* (GenBank KX820265; Identities 772/792 (97 %), 1 gap (0 %)) and *Plectosphaera eucalypti* (GenBank DQ923538; Identities 828/853 (97 %), 4 gaps (0 %)).

Colour illustrations. Barren Grounds Nature Reserve; conidiomata sporulating on OA, conidiophores, conidia and germinating ascospores. 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@westerdijkinstitute.nl & e.groenewald@westerdijkinstitute.nl
Michael J. Wingfield, Forestry and Agricultural Biotechnology Institute (FABI), University of Pretoria, Pretoria 0002, South Africa;
e-mail: mike.wingfield@fabi.up.ac.za
Treena I. Burgess & Giles E.St.J. Hardy, Centre for Phytophthora Science and Management, Murdoch University,
90 South Street, Murdoch, WA 6150, Australia;
e-mail: tburgess@murdoch.edu.au & g-hardy@murdoch.edu.au


Subramaniomyces podocarpi

Fungal Planet 671 – 20 December 2017

Subramaniomyces podocarpi Crous, *sp. nov.*

Etymology. Name refers to *Podocarpus*, the host genus from which this fungus was collected.

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

Mycelium consisting of hyaline, smooth, septate, branched, 1.5–2.5 µm diam hyphae. *Setae* solitary or in fascicles, erect, flexuous, medium brown, thick-walled, smooth, multi-septate, subcylindrical, apex obtuse, base lacking rhizoids, constricted and narrowing to where it arises from hyphae, up to 300 µm tall, 4–6 µm wide. *Conidiophores* pale brown, smooth, arranged along setae, positioned at septa, consisting of a globose basal cell, 5–7 µm diam, giving rise to 2–3 lateral branches that are 1–2-septate, with a terminal conidiogenous cell. *Conidiogenous cells* pale brown, smooth, terminal, subcylindrical, ends obtuse, with one to several pimple-like denticles, 0.5–1 µm long, inconspicuous, 6–8 × 3.5–4.5 µm. *Conidia* aseptate, pale brown, verruculose, fusoid-ellipsoid, apex acutely rounded or truncate, base truncate, 1 µm diam, in branched chains, 15–17(–19) × (3–)4 µm.

Culture characteristics — Colonies erumpent, spreading, with moderate aerial mycelium and smooth, lobate margins, covering the dish after 2 wk at 25 °C. On MEA surface dirty white, reverse sienna. On PDA surface and reverse amber. On OA surface chestnut.

Typus. Australia, New South Wales, Australian Botanic Garden, Mount Annan, on leaves of *Podocarpus elatus* (*Podocarpaceae*), 25 Nov. 2016, *P.W. Crous* (holotype CBS H-23275, culture ex-type CPC 32031 = CBS 143176, ITS and LSU sequences GenBank MG386039 and MG386092, MycoBank MB823382).

Notes — *Subramaniomyces* is reminiscent of the genus *Zanclospora* (Hernández-Restrepo et al. 2017), although the conidiogenous cells are arranged differently, and its mode of conidiogenesis is distinct, having several small denticles. *Subramaniomyces podocarpi* resembles the type species, *S. indicus* (on leaf litter in India, conidia 15–26.5 × 3–3.5 µm; Varghese & Rao 1979), although conidia of *S. podocarpi* differ in being shorter and wider. The genus *Subramaniomyces* is polyphyletic, and *S. fusisaprophyticus* clearly represents a distinct genus (see below). Based on a megablast search using the ITS sequence, the closest matches in NCBIs GenBank nucleotide database were *Parapleurotheciopsis inaequiseptata* (GenBank EU040235; Identities 511/568 (90 %), 10 gaps (1 %)), *Wardomyces moseri* (GenBank LN850995; Identities 515/570 (90 %), 25 gaps (4 %)) and *Sarcostroma bisetulatum* (GenBank EU552155; Identities 506/566 (89 %), 18 gaps (3 %)). The highest similarities using the LSU sequence were *Pidoplitchkoviella terricola* (GenBank AF096197; Identities 821/846 (97 %), 2 gaps (0 %)), *Immersidiscosia eucalypti* (GenBank KY825092; Identities 821/848 (97 %), 5 gaps (0 %)), *Discosia fagi* (GenBank KM678047; Identities 820/848 (97 %), 5 gaps (0 %)) and *Subramaniomyces fusisaprophyticus* (GenBank EU040241; Identities 817/846 (97 %), 1 gap (0 %)).

Pseudosubramaniomyces Crous, *gen. nov.*

Etymology. Name refers to *Subramaniomyces*, a morphologically similar genus.

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

Mycelium consisting of pale brown, smooth, branched, septate hyphae, immersed and superficial. *Conidiophores* solitary, erect, pale brown at base, hyaline at apex, smooth, subcylindrical, 0–multi-septate, flexuous. *Conidiogenous cells* subcylindrical, hyaline, smooth, terminal, polyblastic, with cylindrical denticles. *Conidia* aseptate, in dry acropetal chains, ellipsoid to fusoid, pale brown to subhyaline; hila unthickened, not darkened.

Type species. *Pseudosubramaniomyces fusisaprophyticus* (Matsush.) Crous.

MycoBank MB823465.

Pseudosubramaniomyces fusisaprophyticus (Matsush.) Crous, *comb. nov.*

MycoBank MB823466.

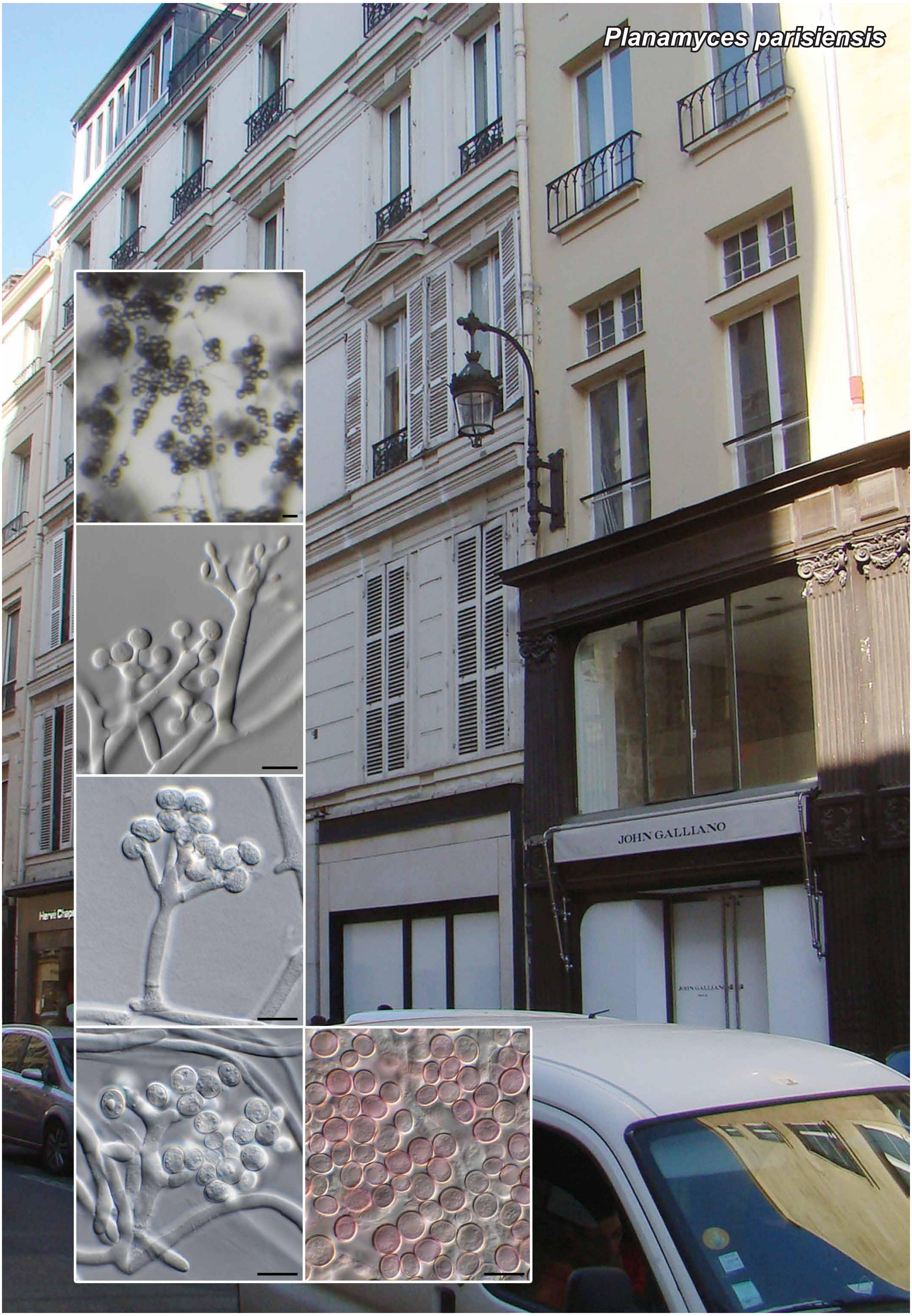
Basionym. *Ramularia fusisaprophytica* Matsush., Microfungi of the Solomon Islands and Papua New Guinea (Osaka): 48. 1971.

Synonym. *Subramaniomyces fusisaprophyticus* (Matsush.) P.M. Kirk, Trans. Brit. Mycol. Soc. 78: 71. 1982.

Notes — *Pseudosubramaniomyces* is distinct from *Subramaniomyces* in the arrangement of its conidiogenous cells (see Kirk 1982). *Pseudosubramaniomyces* lacks lateral conidiogenous cells along the length of the conidiophore stipe, and tends to have pale brown conidiophores, in contrast to the dark brown stipes of *Subramaniomyces.*

Colour illustrations. *Podocarpus elatus*; conidiophores, conidiogenous cells and conidia. Scale bars = 10 µm.

Pedro W. Crous & Johannes Z. Groenewald, Westerdijk Fungal Biodiversity Institute, P.O. Box 85167,
3508 AD Utrecht, The Netherlands; e-mail: p.crous@westerdijkinstitute.nl & e.groenewald@westerdijkinstitute.nl
Michael J. Wingfield, Forestry and Agricultural Biotechnology Institute (FABI), University of Pretoria, Pretoria 0002, South Africa;
e-mail: mike.wingfield@fabi.up.ac.za
Treena I. Burgess & Giles E.St.J. Hardy, Centre for Phytophthora Science and Management, Murdoch University,
90 South Street, Murdoch, WA 6150, Australia;
e-mail: tburgess@murdoch.edu.au & g-hardy@murdoch.edu.au


Planamyces parisiensis
JOHN GALLIANO

Fungal Planet 672 – 20 December 2017

Planamyces Crous & Decock, *gen. nov.*

Etymology. Named after its characteristic conidia, which are flattened in side view.

Classification — *Pyronemataceae*, *Pezizales*, *Pezizomycetes*.

Mycelium consisting of hyaline, smooth, branched, septate hyphae. *Conidiophores* solitary, erect, arising from superficial hyphae, hyaline, smooth, subcylindrical, multiseptate, flexuous, developing terminal and intercalary branches that give rise to clusters of conidiophores; lateral branches hyaline, smooth, subcylindrical, giving rise to conidiogenous cells, frequently two, with bifurcate positioning. *Conidiogenous cells* subcylindrical, hyaline, smooth, clavate at apex; apex with several denticles, with apical and lateral holoblastic loci. *Conidia* solitary, globose but flattened in side view, hyaline, smooth, aseptate, becoming saffron with age, and developing small warts.

Type species. *Planamyces parisiensis* Crous & Decock.
MycoBank MB823383.

Planamyces parisiensis Crous & Decock, *sp. nov.*

Etymology. Named refers to Paris, the city where this species was collected.

Mycelium consisting of hyaline, smooth, branched, septate, 3–5 µm diam hyphae. *Conidiophores* solitary, erect, arising from superficial hyphae, hyaline, smooth, subcylindrical, multiseptate, flexuous, developing terminal and intercalary branches that give rise to clusters of conidiophores; lateral branches hyaline, smooth, subcylindrical, 15–35 × 5–7 µm, giving rise to conidiogenous cells, frequently two, with bifurcate positioning. *Conidiogenous cells* subcylindrical, hyaline, smooth, clavate at apex, 15–35 × 5–10 µm; apex with several denticles, 3–6 × 2–3 µm, with apical and lateral holoblastic loci. *Conidia* solitary, globose but flattened in side view, hyaline, smooth, aseptate, becoming saffron with age, and developing small warts, (6–)7–8(–9) µm in surface view, 5–6 µm diam in side view.

Culture characteristics — Colonies spreading, abundant aerial mycelium, covering dish after 2 wk at 25 °C. On MEA, PDA and OA surface and reverse dirty white with patches of peach.

Typus. France, Paris, from wood inside a house, 2017, *C. Decock* (holotype CBS H-23276, culture ex-type CPC 31694 = CBS 143165, ITS, LSU and *rpb2* sequences GenBank MG386040, MG386093 and MG386141, MycoBank MB823384).

Colour illustrations. Apartment block in Paris, close to where the fungus was collected; conidiophores sporulating on SNA, conidiophores and conidia. Scale bars = 10 µm.

Notes — Based on morphology, *Planamyces* appears quite distinct from the genera of hyphomycetes presently known (Seifert et al. 2011). Its hyaline conidiophores give rise to a cluster of conidiogenous cells, that in turn produce several denticles, forming globose conidia (flattened in side view) that turn saffron and finely warty with age. *Planamyces* is related to the sexual genera *Monascella* and *Warcupia*, but these genera lack asexual morphs, complicating a direct morphological comparison.

Based on a megablast search using the ITS sequence, the closest matches in NCBIs GenBank nucleotide database were *Monascella botryosa* (GenBank NR_145208; Identities 534/624 (86 %), 41 gaps (6 %)), *Sporendonema purpurascens* (GenBank GQ272632; Identities 514/601 (86 %), 25 gaps (4 %)) and *Scutellinia cejpii* (GenBank KJ619951; Identities 519/639 (81 %), 46 gaps (7 %)). The highest similarities using the LSU sequence were *Monascella botryosa* (GenBank KC012688; Identities 842/856 (98 %), no gaps), *Warcupia terrestris* (GenBank DQ220467; Identities 842/856 (98 %), no gaps) and *Melastiza flavorubens* (GenBank DQ220369; Identities 822/856 (96 %), no gaps). The highest similarities using the *rpb2* sequence were distant hits with *Otidea mirabilis* (GenBank JN993547; Identities 653/821 (80 %), 6 gaps (0 %)), *Otidea concinna* (GenBank JN993545; Identities 654/822 (80 %), 8 gaps (0 %)) and *Otidea onotica* (GenBank JN993551; Identities 650/819 (79 %), 6 gaps (0 %)).

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


Neoconiothyrium persooniae

Fungal Planet 673 – 20 December 2017

Neoconiothyrium Crous, *gen. nov.*

Etymology. Name refers to *Coniothyrium*, a morphologically similar genus.

Classification — *Coniothyriaceae*, *Pleosporales*, *Dothideomycetes.*

Conidiomata superficial, ellipsoid to obpyriform, solitary, with 1–2 papillate ostioles; conidiomata hyaline on agar, becoming pigmented during sporulation; wall of 3–6 layers of thick-walled cells; surface with or without setae*. Conidiophores* reduced to conidiogenous cells lining the inner cavity, hyaline, smooth, doliiform to ampulliform, phialidic, with periclinal thickening or percurrent proliferation. *Conidia* solitary, hyaline to medium brown, smooth to finely verruculose, ellipsoid to subclavate or subcylindrical, 0–1-septate.

Type species. *Neoconiothyrium persooniae* Crous.
MycoBank MB823385.

Neoconiothyrium persooniae Crous, *sp. nov.*

Etymology. Name refers to *Persoonia*, the host genus from which this fungus was collected.

Sporulating on OA. *Conidiomata* superficial, ellipsoid to obpyriform, 100–200 µm diam, solitary, with 1–2 papillate ostioles, 10–15 µm diam; conidiomata hyaline on agar, becoming pigmented during sporulation, but wall of 3–6 layers of thick-walled cells, hyaline *textura angularis. Conidiophores* reduced to conidiogenous cells lining the inner cavity, hyaline, smooth, doliiform to ampulliform, phialidic, with periclinal thickening or percurrent proliferation, 5–8 × 4–5 µm. *Conidia* solitary, medium brown, finely verruculose, ellipsoid to subclavate, aseptate, becoming cylindrical and at times 1-septate, apex subobtuse, base bluntly rounded, (5–)6–7(–8) × 3(–4) µm.

Culture characteristics — Colonies erumpent, spreading, with moderate aerial mycelium and smooth, lobate margins, covering the dish after 1 mo at 25 °C. On MEA surface pale mouse grey, reverse dark mouse grey. On PDA surface and reverse mouse grey. On OA surface mouse grey.

Typus. Australia, New South Wales, Australian Botanic Garden, Mount Annan, on leaves of *Persoonia laurina* subsp. *laurina* (*Proteaceae*), 25 Nov. 2016, *P.W. Crous* (holotype CBS H-23277, culture ex-type CPC 32021 = CBS 143175, ITS and LSU sequences GenBank MG386041 and MG386094, MycoBank MB823386).

Notes — *Neoconiothyrium persooniae* is phylogenetically related to *C. multipora* (De Gruyter et al. 2013) and *C. hakeae* (Crous et al. 2016a), which in turn cluster apart from *Coniothyrium* s.str., and clearly represent a distinct genus. Morphologically, however, this clade appears to be quite variable, as in *C. hakeae* the conidiomata are covered in setae (absent in *C. persooniae*), and the conidia are globose to broadly ellipsoid and aseptate. In contrast, conidia are initially ellipsoid and aseptate, becoming cylindrical and 1-septate in *C. persooniae*. Phylogenetically, they cluster together as sister genus to *Ochrocladosporium*.

Based on a megablast search using the ITS sequence, the closest matches in NCBIs GenBank nucleotide database were *Leptosphaeria proteicola* (GenBank JQ044439; Identities 455/482 (94 %), 7 gaps (1 %)), *Querciphoma carteri* (GenBank KF251209; Identities 524/572 (92 %), 16 gaps (2 %)), *Hazslinszkyomyces aloes* (GenBank NR_137821; Identities 536/591 (91 %), 16 gaps (2 %)) and *Ochrocladosporium elatum* (GenBank EU040233; Identities 536/588 (3 %), 30 gaps (5 %)). The highest similarities using the LSU sequence were *Coniothyrium hakeae* (GenBank KY173490; Identities 821/833 (99 %), no gaps), *Ochrocladosporium elatum* (GenBank EU040233; Identities 836/850 (98 %), 1 gap (0 %)) and *Coniothyrium telephii* (GenBank LN907332; Identities 839/855 (98 %), no gaps).

Neoconiothyrium hakeae (Crous & Barber) Crous, *comb. nov.* — MycoBank MB823387

Basionym. *Coniothyrium hakeae* Crous & Barber, Persoonia 37: 347. 2016.

Neoconiothyrium multiporum (V.H. Pawar et al.) Crous, *comb. nov.* — MycoBank MB823388

Basionym. *Phoma multipora* V.H. Pawar et al., Trans. Brit. Mycol. Soc. 50: 260. 1967.

Synonym. *Coniothyrium multiporum* (V.H. Pawar et al.) Verkley & Gruyter, Stud. Mycol. 75: 24. 2012.

Colour illustrations. *Persoonia laurina* subsp. *laurina*; conidioma sporulating on SNA, conidiogenous cells and conidia. Scale bars = 10 µm.

Pedro W. Crous & Johannes Z. Groenewald, Westerdijk Fungal Biodiversity Institute, P.O. Box 85167,
3508 AD Utrecht, The Netherlands; e-mail: p.crous@westerdijkinstitute.nl & e.groenewald@westerdijkinstitute.nl
Michael J. Wingfield, Forestry and Agricultural Biotechnology Institute (FABI), University of Pretoria, Pretoria 0002, South Africa;
e-mail: mike.wingfield@fabi.up.ac.za
Treena I. Burgess & Giles E.St.J. Hardy, Centre for Phytophthora Science and Management, Murdoch University,
90 South Street, Murdoch, WA 6150, Australia;
e-mail: tburgess@murdoch.edu.au & g-hardy@murdoch.edu.au


Phlogicylindrium tereticornis

Fungal Planet 674 – 20 December 2017

Phlogicylindrium tereticornis Crous, *sp. nov.*

Etymology. Name refers to *Eucalyptus tereticornis*, the host species from which this fungus was collected.

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

Associated with amphigenous, circular to angular, brown leaf spots (3–7 mm diam), with red-purple margins. On SNA. *Conidiomata* sporodochial, with *conidiophores* subcylindrical, hyaline, smooth, giving rise to terminal *conidiogenous cells*, 3–8 × 2–3 µm, proliferating sympodially. *Conidia* solitary, hyaline, smooth, medianly septate, straight to curved subcylindrical, guttulate, tapering to subobtuse apex and truncate hilum, (20–) 25–35(–40) × (2–)3 µm.

Culture characteristics — Colonies erumpent, spreading, with sparse aerial mycelium and feathery margins, reaching 30 mm diam after 2 wk at 25 °C. On MEA surface saffron, reverse amber. On PDA surface chestnut, reverse amber. On OA surface hazel.

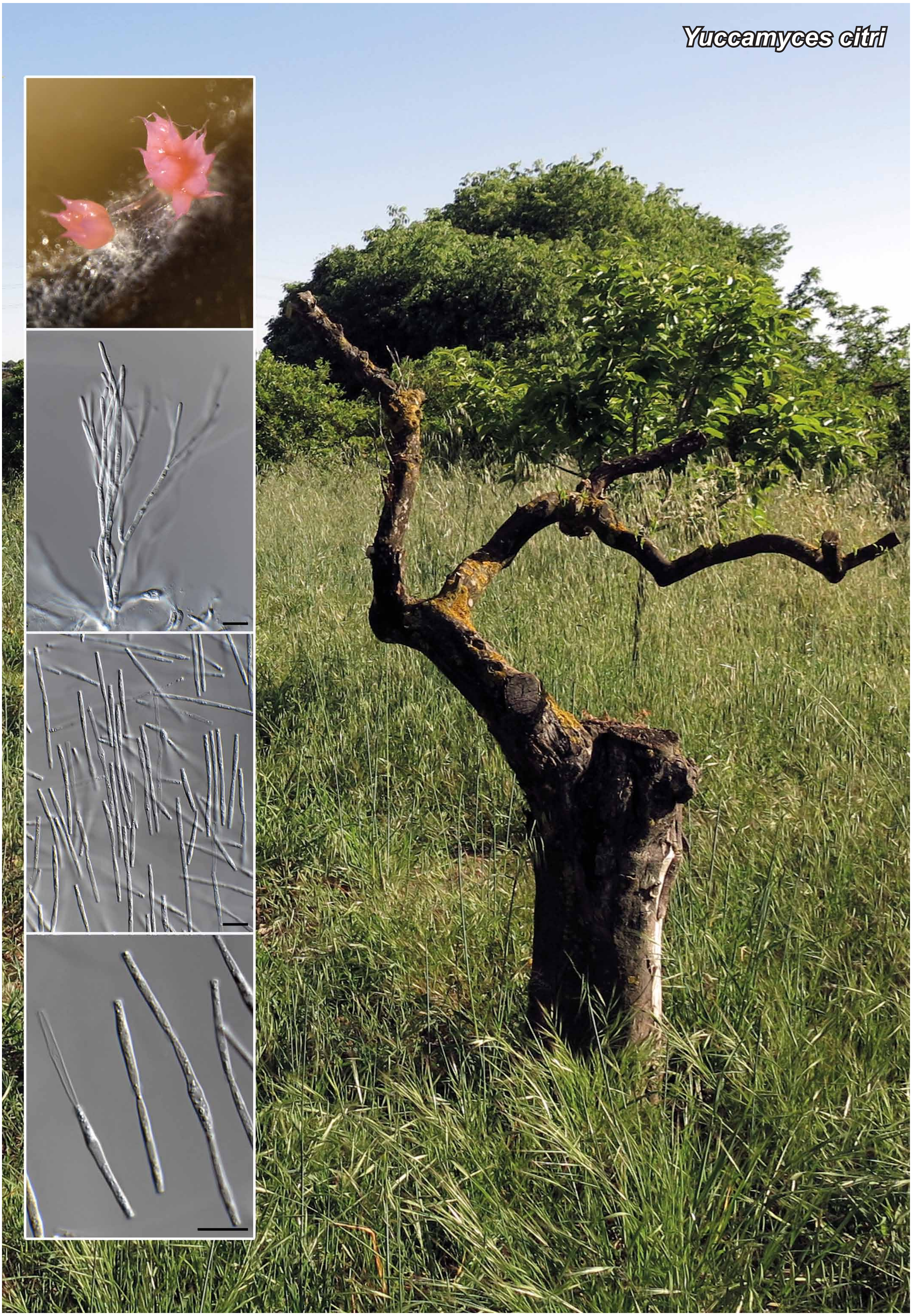
Typus. Australia, New South Wales, Australian Botanic Garden, Mount Annan, on leaves of *Eucalyptus tereticornis* (*Myrtaceae*), 25 Nov. 2016, *P.W. Crous* (holotype CBS H-23279, culture ex-type CPC 32197 = CBS 143168, ITS, LSU, *rpb2* and *tef1* sequences GenBank MG386042, MG386095, MG386142 and MG386151, MycoBank MB823389).

Colour illustrations. Symptomatic *Eucalyptus* leaves; conidiogenous cells on PNA, and conidia. Scale bars = 10 µm.

Notes — *Phlogicylindrium* is characterised by forming sporodochia, and having sympodially proliferating conidiogenous cells that give rise to hyaline, subcylindrical, septate conidia (Summerell et al. 2006). The present collection appears to be phylogenetically closely allied to *Phlogicylindrium*, and as it is also morphologically similar, we describe it here as *P. tereticornis*. The foliar symptoms associated with the fungus were quite dramatic, but the occurrence of *Phlogicylindrium* on these lesions may be secondary.

Based on a megablast search using the ITS sequence, the closest matches in NCBIs GenBank nucleotide database were *Phlogicylindrium eucalyptorum* (GenBank EU040223; Identities 417/436 (96 %), 1 gap (0 %)), *P. eucalypti* (GenBank NR_132813; Identities 425/449 (95 %), 1 gap (0 %)) and *P. uniforme* (GenBank JQ044426; Identities 425/449 (95 %), 2 gaps (0 %)). The highest similarities using the LSU sequence were *P. mokarei* (GenBank KY173521; Identities 810/818 (99 %), no gaps), *P. uniforme* (GenBank JQ044445; Identities 830/840 (99 %), no gaps) and *P. eucalyptorum* (GenBank EU040223; Identities 830/840 (99 %), no gaps). The highest similarities using the *rpb2* sequence were distant hits with *Creosphaeria sassafras* (GenBank KU684308; Identities 647/820 (79 %), 12 gaps (1 %)), *Lopadostoma linospermum* (GenBank KC774544; Identities 658/848 (78 %), 15 gaps (1 %)) and *Daldinia concentrica* (GenBank DQ368651; Identities 638/828 (77 %), 15 gaps (1 %)). No significant hits were found when the *tef1* sequence was used in a blast search.

Pedro W. Crous & Johannes Z. Groenewald, Westerdijk Fungal Biodiversity Institute, P.O. Box 85167,
3508 AD Utrecht, The Netherlands; e-mail: p.crous@westerdijkinstitute.nl & e.groenewald@westerdijkinstitute.nl
Michael J. Wingfield, Forestry and Agricultural Biotechnology Institute (FABI), University of Pretoria, Pretoria 0002, South Africa;
e-mail: mike.wingfield@fabi.up.ac.za
Treena I. Burgess & Giles E.St.J. Hardy, Centre for Phytophthora Science and Management, Murdoch University,
90 South Street, Murdoch, WA 6150, Australia;
e-mail: tburgess@murdoch.edu.au & g-hardy@murdoch.edu.au


Yuccamyces citri

Fungal Planet 675 – 20 December 2017

Yuccamyces citri Crous, *sp. nov.*

Etymology. Name refers to *Citrus*, the host genus from which this fungus was collected.

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

Conidiophores erect, aggregated in penicillate tufts, forming upright sporodochia, hyaline, smooth, individually hyaline, but sporodochia distinctly pink in colour; conidiophores subcylindrical, septate, branched, up to 150 µm tall, 3–6-septate, 3–4 µm diam. *Conidiogenous cells* terminal and intercalary, subcylindrical, smooth, 15–25 × 2.5–3 µm, proliferating sympodially at apex. *Conidia* in slimy, branched chains, hyaline, smooth, guttulate, subcylindrical but widest in middle of each cell, and with characteristic taper toward septum, 1–2-septate, individual cells 15–20 × 2–3 µm, 1-septate, conidia 32–45 µm long, 2-septate conidia 55–65 µm long; conidia anastomosing with age.

Culture characteristics — Colonies flat, spreading, with sparse aerial mycelium and feathery margins, reaching 50 mm diam after 1 mo at 25 °C. On MEA, PDA and OA surface chestnut, reverse fuscous black.

Typus. Italy, Catania, Mascali, on leaf litter of *Citrus limon* (*Rutaceae*), 30 Jan. 2016, *V. Guarnaccia* (holotype CBS H-23280, culture ex-type CPC 30046 = CBS 143161, ITS and LSU sequences GenBank MG386043 and MG386096, MycoBank MB823390).

Notes — *Yuccamyces citri* is very similar to the type of the genus, *Y. purpureus* (on *Flacourtia indica*, India; colonies become pinkish purple due to the accumulation of conidia; Dyko & Sutton 1979). In *Y. citri*, sporodochia also turn pink at maturity (similar to that of the type), but conidia are shorter and wider (55–65 × 2–3 µm) than those of *Y. purpureus* (46–72 × 1.5–2 µm). Dyko & Sutton (1979) speculated that the genus is a basidiomycete, but *Yuccamyces* is related to *Hysteropatella* (*Patellariaceae*).

Based on a megablast search using the ITS sequence, the closest matches in NCBIs GenBank nucleotide database were *Yuccamyces pilosus* (GenBank MG386044; Identities 685/789 (87 %), 51 gaps (6 %)), *Neodactylaria obpyriformis* (GenBank LT839090; Identities 334/386 (87 %), 13 gaps (3 %)), *Neoscytalidium dimidiatum* (GenBank FM211429; Identities 478/595 (80 %), 45 gaps (7 %)) and *Neofusicoccum mediterraneum* (GenBank GU799463; Identities 401/483 (83 %), 32 gaps (6 %)). The highest similarities using the LSU sequence were *Yuccamyces pilosus* (GenBank MG386097; Identities 813/853 (95 %), 3 gaps (0 %)), *Hysteropatella elliptica* (GenBank KM220948; Identities 805/853 (94 %), 3 gaps (0 %)), *Hysteropatella prostii* (GenBank KT876980; Identities 805/853 (94 %), 3 gaps (0 %)) and *Hysteropatella clavispora* (GenBank AY541493; Identities 805/853 (94 %), 3 gaps (0 %)).

Colour illustrations. Citrus limon tree growing in Italy; conidiomata sporulating on PDA, conidiophores and conidia. Scale bars = 10 µm.

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


Murramarangomyces corymbiae

Fungal Planet 676 – 20 December 2017

Murramarangomycetales Crous, *ord. nov*.

MycoBank MB823433.

Murramarangomycetaceae Crous, *fam. nov*.

MycoBank MB823434.

Classification — *Murramarangomycetaceae*, *Murramarangomycetales*, *Dothideomycetes.*

The diagnosis of the order *Murramarangomycetales* and family *Murramarangomycetaceae* is based on the type genus, *Murramarangomyces.*

Murramarangomyces Crous, *gen. nov*.

Etymology. Name refers to the location where it was collected, Murramarang, Australia.

Mycelium consisting of hyaline, smooth hyphae, irregular, constricted at septa, forming brown, thick-walled cells that become fertile *conidiogenous cells*, aggregated in cauliflower-like clusters of brown, doliiform to globose, brown conidiogenous cells, phialidic, giving rise to solitary conidia. *Conidia* in slimy mass, aseptate, hyaline, smooth, bacilliform.

Type species. *Murramarangomyces corymbiae* Crous.
MycoBank MB823391.

Murramarangomyces corymbiae Crous, *sp. nov*.

Etymology. Name refers to *Corymbia*, the host genus from which this fungus was collected.

Leaf spots circular, hypophyllous, dark brown, circular, 3–5 mm diam, but several fungi are associated with these spots, so the occurrence could be secondary. *Mycelium* consisting of hyaline, smooth, 2–5 µm diam hyphae, irregular, constricted at septa, forming brown, thick-walled cells that become fertile *conidiogenous cells*, aggregated in cauliflower-like clusters of doliiform to globose, brown conidiogenous cells, 3–5 µm diam, phialidic, giving rise to solitary conidia. *Conidia* in slimy mass, aseptate, hyaline, smooth, bacilliform, 3–5 × 1.5–2 µm.

Culture characteristics — Colonies erumpent, spreading, with sparse aerial mycelium and feathery, lobate margins, reaching 4 mm diam after 1 mo at 25 °C. On MEA, PDA and OA surface and reverse chestnut.

Typus. AUSTRALIA, New South Wales, close to Murramarang, on leaves of *Corymbia maculata* (*Myrtaceae*), 27 Nov. 2016, *P.W. Crous* (holotype CBS H-23281, culture ex-type CPC 33000 = CBS 143434, ITS and LSU sequences GenBank MG386045 and MG386098, MycoBank MB823392).

Colour illustrations. *Corymbia* tree in Murramarang; conidiomata sporulating on OA, conidiogenous cells and conidia. Scale bars = 10 µm.

Notes — *Murramarangomyces* is related to the hyphomycete genus *Gonatophragmium* (*Dothideomycetes*), but is somewhat reminiscent of *Paramycoleptodiscus* (Crous et al. 2016b). Morphologically it is quite distinct however, in having creeping hyphae that give rise to aggregated brown clusters of phialidic conidiogenous cells (as in *Paramycoleptodiscus*), that form hyaline, smooth, aseptate conidia. When it was first isolated, several black, round hysterothecia was also present on the leaf spots, although the sexual-asexual link could not be confirmed, and further collections would be required to fully resolve its life cycle.

Based on a megablast search using the ITS sequence, only some similarities to the 5.8S nrRNA gene were found and these results were inconclusive. The highest similarities using the LSU sequence were *Lepra violacea* (GenBank MF109224; Identities 582/668 (87 %), 16 gaps (2 %)), *Lepra amara* (GenBank MF109182; Identities 581/669 (87 %), 18 gaps (2 %)) and *Gonatophragmium triuniae* (GenBank KP004479; Identities 626/728 (86 %), 15 gaps (2 %)).

Pedro W. Crous & Johannes Z. Groenewald, Westerdijk Fungal Biodiversity Institute, P.O. Box 85167,
3508 AD Utrecht, The Netherlands; e-mail: p.crous@westerdijkinstitute.nl & e.groenewald@westerdijkinstitute.nl
Michael J. Wingfield, Forestry and Agricultural Biotechnology Institute (FABI), University of Pretoria, Pretoria 0002, South Africa;
e-mail: mike.wingfield@fabi.up.ac.za
Brett A. Summerell, Royal Botanic Gardens and Domain Trust, Mrs. Macquaries Road,
Sydney, NSW 2000, Australia; e-mail: brett.summerell@rbgsyd.nsw.gov.au
Angus J. Carnegie, Forest Health & Biosecurity, NSW Department of Primary Industries, Level 12, 10 Valentine Ave,
Parramatta, NSW 2150, Locked Bag 5123, Parramatta, NSW 2124, Australia; e-mail: angus.carnegie@dpi.nsw.gov.au


Tygervalleyomyces podocarpi

Fungal Planet 677 – 20 December 2017

Tygervalleyomyces Crous, *gen. nov.*

Etymology. Name refers to the location where it was collected, Tyger Valley, South Africa.

Classification — *Typhulaceae*, *Agaricales*, *Agaricomycetes*.

Conidiomata cupulate, brown, up to 200 µm diam; walls of 3–5 layers of brown *textura angularis*. In culture forming sporodochia with mucoid conidial mass. *Conidiophores* cylindrical, hyaline, smooth, flexuous, septate. *Conidiogenous cells* terminal, cylindrical, hyaline, smooth, proliferating percurrently with proliferations widely dispersed over the length of the conidiogenous cell. *Paraphyses* similar to conidiophores but sterile, dispersed among conidiophores, frequently extending above them in length. *Conidia* solitary, cylindrical, with apex obtuse, base truncate with minute marginal frill, straight, aseptate, granular to guttulate.

Type species. *Tygervalleyomyces podocarpi* Crous.
MycoBank MB823393.

Tygervalleyomyces podocarpi Crous, *sp. nov.*

Etymology. Name refers to *Podocarpus*, the host genus from which this fungus was collected.

Conidiomata cupulate, brown, up to 200 µm diam, forming on *Podocarpus* leaf litter; walls of 3–5 layers of brown *textura angularis*. On MEA forming sporodochia with mucoid conidial mass. *Conidiophores* cylindrical, hyaline, smooth, flexuous, 1–3-septate, 50–100 × 3–4 µm. *Conidiogenous cells* terminal, cylindrical, hyaline, smooth, 20–50 × 2–3 µm, proliferating percurrently with proliferations widely dispersed over the length of the conidiogenous cell. *Paraphyses* similar to conidiophores but sterile, dispersed among conidiophores, frequently extending above them in length. *Conidia* solitary, cylindrical, with apex obtuse, base truncate with minute marginal frill, straight, aseptate, granular to guttulate, (18–)20–26(–35) × 3(–4) µm.

Culture characteristics — Colonies flat, spreading, with sparse aerial mycelium and smooth, lobate margins, covering the dish after 1 mo at 25 °C. On MEA, PDA and OA surface and reverse pale luteous.

Typus. South Africa, Western Cape Province, Tyger Valley, on leaf litter of *Podocarpus falcatus*, 1 Jan. 2016, *P.W. Crous* (holotype CBS H-23282, culture ex-type CPC 29979 = CBS 143487, ITS and LSU sequences GenBank MG386046 and MG386099, MycoBank MB823394).

Notes — *Tygervalleyomyces* is a genus of coelomycetes with cupulate conidiomata with affinities to *Typhulaceae*. Based on a megablast search using the ITS sequence, the closest matches in NCBIs GenBank nucleotide database were only distant hits with members of *Agaricales*.

The highest similarities using the LSU sequence were *Typhula crassipes* (GenBank KY224094; Identities 845/858 (98 %), 1 gap (0 %)), *Typhula micans* (GenBank KY224102; Identities 824/858 (96 %), 1 gap (0 %)) and *Lentaria albovinacea* (GenBank DQ071734; Identities 827/888 (93 %), 5 gaps (0 %)).

Colour illustrations. *Podocarpus falcatus*; conidiophores and conidia. Scale bars = 10 µm.

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


Fitzroyomyces cyperi

Fungal Planet 678 – 20 December 2017

Fitzroyomyces Crous, *gen. nov*.

Etymology. Name refers to the location where it was collected, Fitzroy Falls, Australia.

Classification — *Stictidaceae*, *Ostropales*, *Lecanoromycetes.*

Conidiomata pycnidial, immersed, globose, with central ostiole exuding creamy conidial mass; wall of 2–3 layers of pale brown *textura angularis. Conidiophores* lining the inner cavity, hyaline, smooth, subcylindrical, septate, irregularly branched. *Conidiogenous cells* terminal and intercalary, subcylindrical to ampulliform, hyaline, smooth, proliferating percurrently at apex. *Conidia* hyaline, smooth, cylindrical, apex obtuse, base truncate with or without minute marginal frill, granular, multiseptate, flexuous.

Type species. Fitzroyomyces cyperi Crous.
MycoBank MB823395.

Fitzroyomyces cyperi Crous, *sp. nov.*

Etymology. Name refers to *Cyperaceae*, the substrate from which this fungus was collected.

Conidiomata pycnidial, immersed, globose, up to 200 µm diam, with central ostiole exuding creamy conidial mass; wall of 2–3 layers of pale brown *textura angularis. Conidiophores* lining the inner cavity, hyaline, smooth, subcylindrical, 1–2-septate, irregularly branched, 7–20 × 2–3 µm. *Conidiogenous cells* terminal and intercalary, subcylindrical to ampulliform, hyaline, smooth, proliferating percurrently at apex, 5–7 × 1.5–2 µm. *Conidia* hyaline, smooth, cylindrical, apex obtuse, base truncate with or without minute marginal frill, granular, multiseptate, flexuous, (35–)45–75(–90) × 2(–2.5) µm.

Culture characteristics — Colonies erumpent, spreading, surface folded, with sparse to moderate aerial mycelium and smooth, lobate margins, reaching 25 mm diam after 1 mo at 25 °C. On MEA surface dirty white, reverse apricot. On PDA surface dirty white, reverse saffron. On OA surface pale luteous.

Typus. Australia, New South Wales, Fitzroy Falls, Morton National Park, on leaves of *Cyperaceae*, 26 Nov. 2016, *P.W. Crous* (holotype CBS H-23283, culture ex-type CPC 32209 = CBS 143170, ITS and LSU sequences GenBank MG386047 and MG386100, MycoBank MB823396).

Colour illustrations. Fitzroy Falls; conidioma sporulating on SNA, conidiophores and conidia. Scale bars = 10 µm.

Notes — *Fitzroyomyces* is a new genus of coelomycetes that is septoria-like in morphology, but phylogenetically distinct from the genera presently known in this complex (see Quaedvlieg et al. 2013, Verkley et al. 2013).

Based on a megablast search using the ITS sequence, the closest matches in NCBIs GenBank nucleotide database were *Phacidiella podocarpi* (GenBank NR_137934; Identities 554/648 (85 %), 26 gaps (4 %)), *Trullula melanochlora* (GenBank KP004459; Identities 568/692 (82 %), 41 gaps (5 %)) and *Phacidiella eucalypti* (GenBank EF110620; Identities 507/602 (84 %), 41 gaps (6 %)). The highest similarities using the LSU sequence were *Carestiella socia* (GenBank AY661682; Identities 808/862 (94 %), 6 gaps (0 %)), *Stictis radiata* (GenBank AY300864; Identities 728/783 (93 %), 3 gaps (0 %)) and *Conotrema populorum* (GenBank AY300833; Identities 800/862 (93 %), 11 gaps (1 %)).

Pedro W. Crous & Johannes Z. Groenewald, Westerdijk Fungal Biodiversity Institute, P.O. Box 85167,
3508 AD Utrecht, The Netherlands; e-mail: p.crous@westerdijkinstitute.nl & e.groenewald@westerdijkinstitute.nl
Michael J. Wingfield, Forestry and Agricultural Biotechnology Institute (FABI), University of Pretoria, Pretoria 0002, South Africa;
e-mail: mike.wingfield@fabi.up.ac.za
Treena I. Burgess & Giles E.St.J. Hardy, Centre for Phytophthora Science and Management, Murdoch University,
90 South Street, Murdoch, WA 6150, Australia;
e-mail: tburgess@murdoch.edu.au & g-hardy@murdoch.edu.au


Zasmidium dasypogonis

Fungal Planet 679 – 20 December 2017

Zasmidium dasypogonis Crous, *sp. nov.*

Etymology. Name refers to *Dasypogon*, the host genus from which this fungus was collected.

Classification — *Mycosphaerellaceae*, *Capnodiales*, *Dothideomycetes.*

Mycelium consisting of pale brown, smooth to verruculose, branched, septate, 2–3 µm hyphae. *Conidiophores* solitary, erect, medium brown, smooth, subcylindrical, straight to geniculous-sinuous, 1–6-septate, 15–100 × 5–8 µm, mostly unbranched. *Conidiogenous cells* terminal and intercalary, subcylindrical, medium brown, smooth, 7–30 × 5–7 µm; scars sympodial, darkened, thickened, refractive, 2–3 µm diam. *Conidia* solitary, medium brown, verruculose, subcylindrical, apex subobtuse, base truncate, hilum thickened, darkened, refractive, 2–3 µm diam, 1–6-septate, (30–)35–45(–55) × (3.5–)5–6 µm.

Culture characteristics — Colonies erumpent, spreading, with moderate aerial mycelium and feathery, lobate margins, reaching 20 mm diam after 2 wk at 25 °C. On MEA surface and reverse pale olivaceous grey, reverse olivaceous grey with diffuse red pigment. On PDA surface and reverse iron-grey, with diffuse red pigment. On OA surface olivaceous grey with diffuse red pigment.

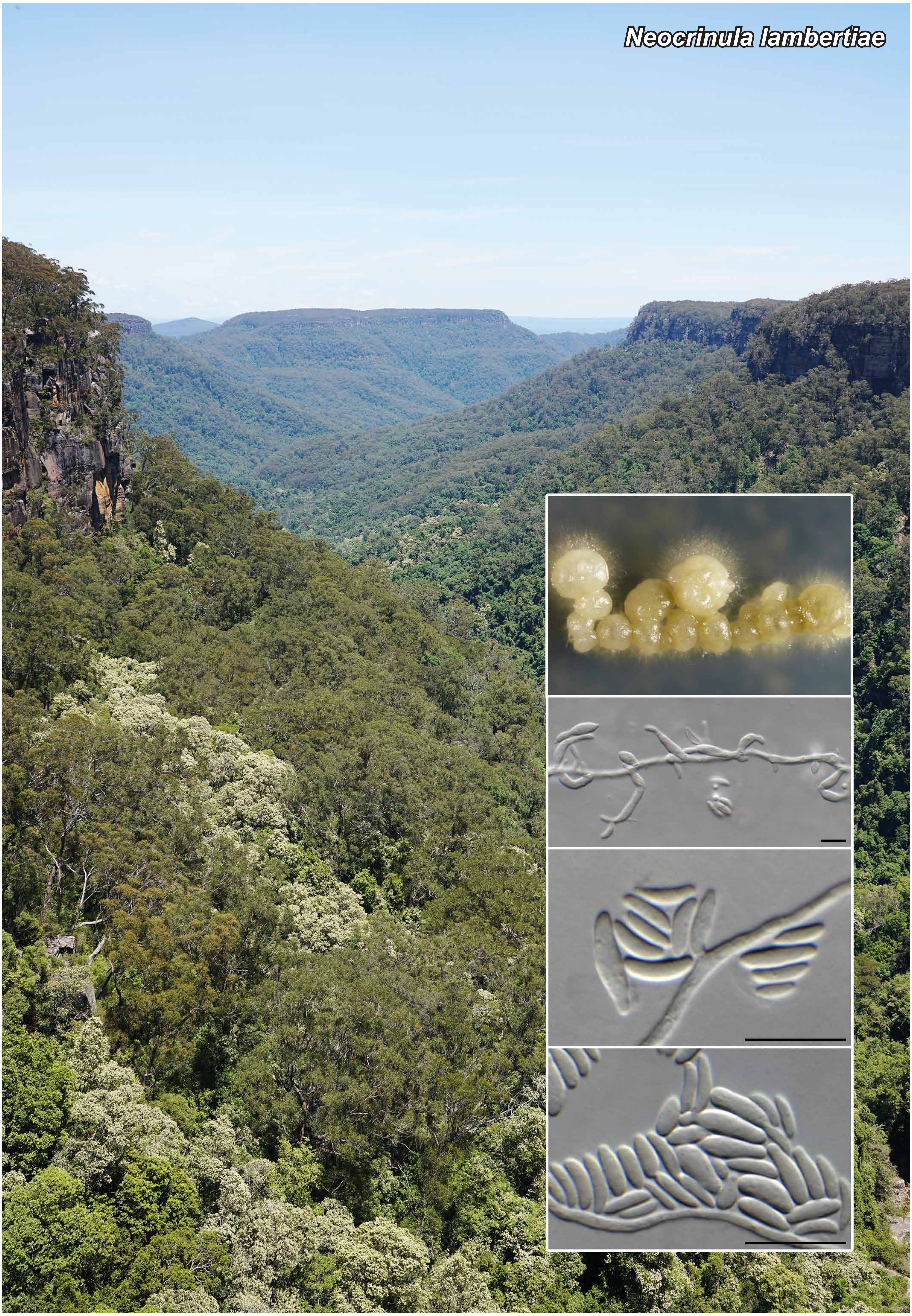
Typus. Australia, Western Australia, Denmark, Lights Beach, on *Dasypogon* sp. (*Dasypogonaceae*), 19 Sept. 2015, *P.W. Crous* (holotype CBS H-23284, culture ex-type CPC 29308 = CBS 143397, ITS and LSU sequences GenBank MG386048 and MG386101, MycoBank MB823397).

Notes — There are no cercosporoid fungi known from *Dasypogon*. *Zasmidium dasypogonis* is phylogenetically related to species that were formerly treated as *Ramichloridium*. However, the genus *Ramichloridium* based on the type species (*Ramichloridium apiculatum*) is a member of *Dissoconiaceae* (Arzanlou et al. 2007), and other ramichloridium-like taxa in this clade were subsequently placed in the genus *Zasmidium* (Videira et al. 2017).

Based on a megablast search using the ITS sequence, the closest matches in NCBIs GenBank nucleotide database were *Zasmidium podocarpi* (GenBank KY979766; Identities 584/618 (94 %), 9 gaps (1 %)), *Z. commune* (GenBank KY979762; Identities 599/634 (94 %), 11 gaps (1 %)) and *Z. velutinum* (as *Periconiella velutina*; GenBank EU041781; Identities 519/554 (94 %), 10 gaps (1 %)). The highest similarities using the LSU sequence were *Z. biverticillatum* (as *Ramichloridium biverticillatum*; GenBank EU041853; Identities 825/840 (98 %), 2 gaps (0 %)), *Z. arcuata* (as *Periconiella arcuata*; GenBank EU041836; Identities 824/840 (98 %), 2 gaps (0 %)) and *Z. podocarpi* GenBank KY979821; Identities 787/803 (98 %), 2 gaps (0 %)).

Colour illustrations. *Dasypogon* sp.; conidiophores sporulating on PNA, conidiophores and conidia. Scale bars = 10 µm.

Pedro W. Crous & Johannes Z. Groenewald, Westerdijk Fungal Biodiversity Institute, P.O. Box 85167,
3508 AD Utrecht, The Netherlands; e-mail: p.crous@westerdijkinstitute.nl & e.groenewald@westerdijkinstitute.nl
Michael J. Wingfield, Forestry and Agricultural Biotechnology Institute (FABI), University of Pretoria, Pretoria 0002, South Africa;
e-mail: mike.wingfield@fabi.up.ac.za
Treena I. Burgess & Giles E.St.J. Hardy, Centre for Phytophthora Science and Management, Murdoch University,
90 South Street, Murdoch, WA 6150, Australia;
e-mail: tburgess@murdoch.edu.au & g-hardy@murdoch.edu.au


Neocrinula lambertiae

Fungal Planet 680 – 20 December 2017

Neocrinulaceae Crous, *fam. nov.*

Classification — *Neocrinulaceae*, *Helotiales*, *Leotiomycetes*.

Mycelium consisting of branched, septate, hyaline to brown, smooth to verruculose hyphae. *Conidiomata* sporodochial or synnematous, hyaline to brown, consisting of densely aggregated conidiophores. *Conidiophores* hyaline to brown, smooth to verruculose, subcylindrical, branched, septate. *Conidiogenous cells* phialidic, with periclinal thickening, cymbiform to ampulliform or subcylindrical, hyaline, smooth. *Conidia* solitary, hyaline, smooth, granular, aggregating in slimy mass, aseptate, fusoid-ellipsoid, prominently curved, apex subobtuse, base bluntly rounded to truncate.

Type genus. *Neocrinula* Crous.
MycoBank MB823467.

Neocrinula lambertiae Crous, *sp. nov.*

Etymology. Name refers to *Lambertia*, the host genus from which this fungus was collected.

Mycelium consisting of branched, septate, hyaline, smooth, 2–2.5 µm diam hyphae. *Conidiomata* erumpent sporodochia, up to 350 µm diam, consisting of densely aggregated conidiophores. *Conidiophores* hyaline, smooth, subcylindrical, branched, multiseptate, up to 70 µm tall, 2–3 µm diam, frequently reduced to conidiogenous cells. *Conidiogenous cells* phialidic, with periclinal thickening, cymbiform to ampulliform or subcylindrical, hyaline, smooth, 7–15 × 2–3 µm. *Conidia* solitary, hyaline, smooth, granular, aggregating in slimy mass, aseptate, fusoid-ellipsoid, prominently curved, apex subobtuse, base bluntly rounded, (4–)7–8(–10) × 2(–3) µm.

Culture characteristics — Colonies erumpent, spreading, with sparse aerial mycelium and feathery, lobate margins, reaching 5 mm diam after 2 wk at 25 °C. On MEA and PDA surface and reverse pale luteous. On OA surface dirty white.

Typus. AUSTRALIA, New South Wales, Fitzroy Falls, Morton National Park, on leaves of *Lambertia formosa* (*Proteaceae*), 26 Nov. 2016, *P.W. Crous* (holotype CBS H-23285, culture ex-type CPC 32211 = CBS 143423, ITS and LSU sequences GenBank MG386049 and MG386102, MycoBank MB823398).

Colour illustrations. Fitzroy Falls; conidiomata sporulating on SNA, conidiophores and conidia. Scale bars = 10 µm.

Notes — *Neocrinula* was recently introduced for a synnematal fungus occurring on *Xanthorrhoea* in Australia (Crous et al. 2017a). *Neocrinula lambertiae* differs from *N. xanthorrhoeae* in the sense that it does not form synnemata, but rather forms sporodochia in culture (although solitary conidiophores when observed on the host *in vivo*). The fact that synnemata and solitary conidiophores could occur in the same genus as has been noted by Videira et al. (2016) in the *Ramularia* generic complex. The phialidic mode of conidiogenesis, and hyaline, aseptate, fusoid-ellipsoid conidia are the same, suggesting that *N. lambertiae* represents the second species of the genus.

Based on a megablast search using the ITS sequence, the closest matches in NCBIs GenBank nucleotide database were *Neocrinula xanthorrhoeae* (GenBank KY173414; Identities 489/517 (95 %), 2 gaps (0 %)), *Claussenomyces kirschsteinianus* (GenBank KY689628; Identities 470/532 (88 %), 12 gaps (2 %)) and *Davidhawksworthia ilicicola* (GenBank KU728517; Identities 461/520 (89 %), 16 gaps (3 %)). The highest similarities using the LSU sequence were *Neocrinula xanthorrhoeae* (GenBank KY173505; Identities 874/887 (99 %), no gaps), *Encoeliopsis rhododendri* (GenBank KX090801; Identities 798/840 (95 %), 13 gaps (1 %)) and *Davidhawksworthia ilicicola* (GenBank KU728555; Identities 820/864 (95 %), 13 gaps (1 %)).

Pedro W. Crous & Johannes Z. Groenewald, Westerdijk Fungal Biodiversity Institute, P.O. Box 85167,
3508 AD Utrecht, The Netherlands; e-mail: p.crous@westerdijkinstitute.nl & e.groenewald@westerdijkinstitute.nl
Michael J. Wingfield, Forestry and Agricultural Biotechnology Institute (FABI), University of Pretoria, Pretoria 0002, South Africa;
e-mail: mike.wingfield@fabi.up.ac.za
Treena I. Burgess & Giles E.St.J. Hardy, Centre for Phytophthora Science and Management, Murdoch University,
90 South Street, Murdoch, WA 6150, Australia;
e-mail: tburgess@murdoch.edu.au & g-hardy@murdoch.edu.au


Zasmidium gahniicola

Fungal Planet 681 – 20 December 2017

Zasmidium gahniicola Crous, *sp. nov.*

Etymology. Name refers to *Gahnia*, the host genus from which this fungus was collected.

Classification — *Mycosphaerellaceae*, *Capnodiales*, *Dothideomycetes.*

Mycelium consisting of medium brown, verruculose, branched, septate, 2–2.5 µm diam hyphae. *Conidiophores* solitary, erect, straight to flexuous, 70–120 × 2–3.5 µm, thick-walled, dark brown, finely verruculose, 4–6-septate. *Conidiogenous cells* integrated, terminal, subcylindrical, medium brown, finely roughened, 15–40 × 3 µm; scars thickened, darkened, somewhat refractive, 1 µm diam, arranged in a rachis. *Conidia* solitary, verruculose, medium brown, subcylindrical, 1(–3)-septate, straight, apex obtuse, tapering in basal cell to truncate hilum, 1 µm diam, thickened, darkened, slightly refractive, (9–)13–18(–20) × (3.5–)4(–5) µm.

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

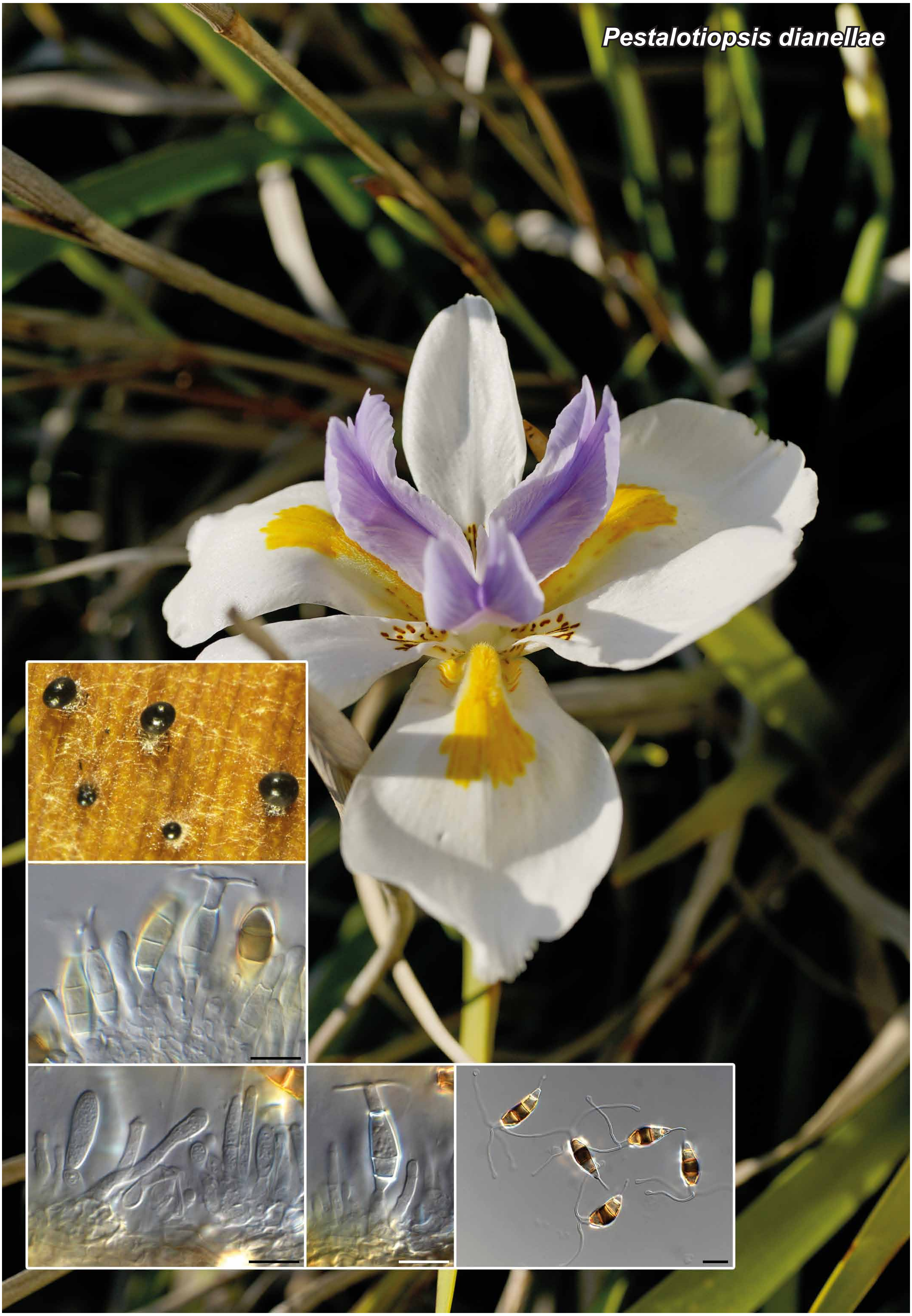
Typus. AUSTRALIA, New South Wales, Barren Grounds Nature Reserve, on leaves of *Gahnia sieberiana* (*Cyperaceae*), 26 Nov. 2016, *P.W. Crous* (holotype CBS H-23286, culture ex-type CPC 32219 = CBS 143422, ITS and LSU sequences GenBank MG386050 and MG386103, MycoBank MB823399).

Colour illustrations. *Gahnia sieberiana*; conidiophores sporulating on SNA, conidiogenous cells and conidia. Scale bars = 10 µm.

Notes — The only cercosporoid fungus known from *Gahnia* is *Zasmidium gahniae*, occurring on *G. lacera* and *G. setifolia* in New Zealand. It is characterised by having solitary, straight, cylindrical to narrowly obclavate, pluriseptate conidia (20–300 × 3–5 µm; Braun et al. 2014), and is thus quite distinct from those of *Z. gahniicola*.

Based on a megablast search using the ITS sequence, the closest matches in NCBIs GenBank nucleotide database were *Zasmidium podocarpi* (GenBank KY979766; Identities 507/531 (95 %), 2 gaps (0 %)), *Z. commune* (GenBank KY979762; Identities 504/533 (95 %), 6 gaps (1 %)) and *Z. strelitziae* (as *Ramichloridium strelitziae*; GenBank EU041803; Identities 499/532 (94 %), 5 gaps (0 %)). The highest similarities using the LSU sequence were *Z. velutinum* (as *Periconiella velutina*; GenBank EU041838; Identities 811/817 (99 %), no gaps), *Z. commune* (GenBank KY979820; Identities 804/810 (99 %), no gaps) and *Z. arcuata* (as *Periconiella arcuata*; GenBank EU041836; Identities 830/837 (99 %), no gaps).

Pedro W. Crous & Johannes Z. Groenewald, Westerdijk Fungal Biodiversity Institute, P.O. Box 85167,
3508 AD Utrecht, The Netherlands; e-mail: p.crous@westerdijkinstitute.nl & e.groenewald@westerdijkinstitute.nl
Michael J. Wingfield, Forestry and Agricultural Biotechnology Institute (FABI), University of Pretoria, Pretoria 0002, South Africa;
e-mail: mike.wingfield@fabi.up.ac.za
Treena I. Burgess & Giles E.St.J. Hardy, Centre for Phytophthora Science and Management, Murdoch University,
90 South Street, Murdoch, WA 6150, Australia;
e-mail: tburgess@murdoch.edu.au & g-hardy@murdoch.edu.au


Pestalotiopsis dianellae

Fungal Planet 682 – 20 December 2017

Pestalotiopsis dianellae Crous, *sp. nov.*

Etymology. Name refers to *Dianella*, the host genus from which this fungus was collected.

Classification — *Pestalotiopsidaceae*, *Xylariales*, *Sordariomycetes.*

Conidiomata pycnidial, globose, separate, immersed to erumpent on banana leaf agar, dark brown to black, 100–350 µm diam, exuding a globose, dark brown conidial mass. *Conidiophores* 0–1-septate, branched at the base, subcylindrical, mostly reduced to conidiogenous cells, hyaline, smooth, up to 30 µm tall. *Conidiogenous cells* integrated, ampulliform to subcylindrical, proliferating percurrently at apex, 6–20 × 3–4 µm. *Conidia* fusoid, straight, 4-septate, (22–)24–25(–27) × 7(–8) µm, somewhat constricted at septa, basal cell conic to obconic with truncate hilum, 3–5 µm long; three median cells 15–19 µm long, doliiform, verruculose, dark brown, versicoloured, (second cell from basal cell honey brown, third cell dark brown, fourth cell honey brown, each cell 5–6 µm long); apical cell cylindrical, hyaline, thin and smooth-walled, 3–6 µm long, with 2–4 tubular apical appendages, each arising from different locus, swollen at tip, filiform, flexuous, unbranched, 18–45 µm long; basal appendage single, tubular, unbranched, centric, 5–10 µm long, frequently swollen at tip.

Culture characteristics — Colonies erumpent, spreading, with moderate aerial mycelium and smooth, lobate margins, covering dish after 2 wk at 25 °C. On MEA surface luteous, reverse sienna. On PDA surface dirty white, reverse ochreous. On OA surface dirty white.

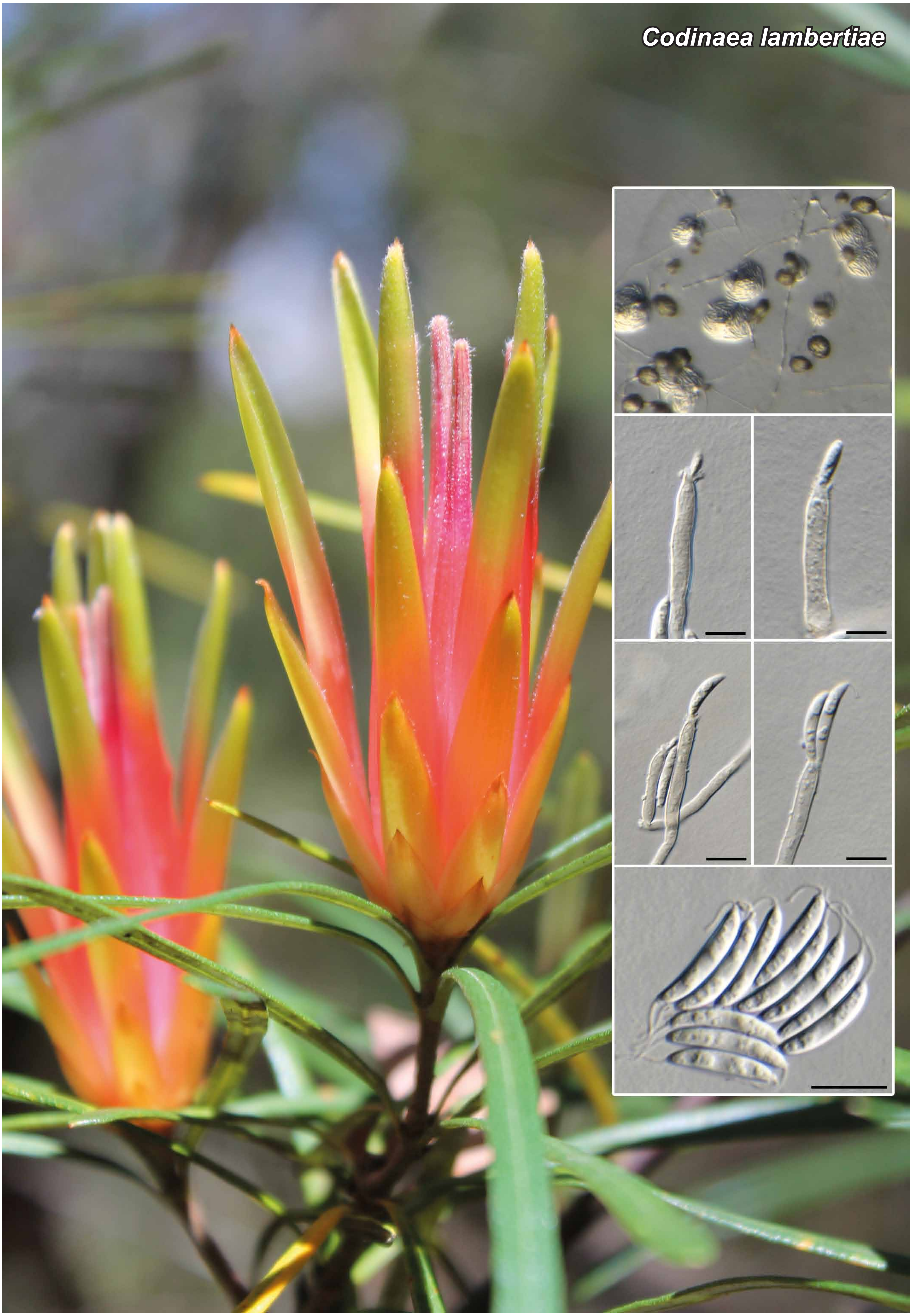
Typus. Australia, Victoria, Mount Best Tin Mine Road, on *Dianella* sp. (*Liliaceae*), 28 Nov. 2016, *P.W. Crous* (holotype CBS H-23287, culture ex-type CPC 32261 = CBS 143421, ITS, LSU and *tub2* sequences GenBank MG386051, MG386104 and MG386164, MycoBank MB823400).

Notes — Of the species of *Pestalotiopsis* presently known from their DNA, *P. dianellae* is most closely related to *P. arceuthobii*, *P. microspora* and *P. portugalica*, from which it is morphologically quite distinct. In general, it is more similar to species with knobbed apical appendages like *P. spathulata* and *P. theae* (Maharachchikumbura et al. 2014), but the latter are again phylogenetically distinct from *P. dianellae*, and hence it is described here as new.

Based on a megablast search using the ITS sequence, the closest matches in NCBIs GenBank nucleotide database were *P. arceuthobii* (GenBank NR_147561; Identities 571/579 (99 %), no gaps), *P. microspora* (GenBank AF377291; Identities 571/579 (99 %), no gaps) and *P. portugalica* (GenBank NR_147556; Identities 570/581 (98 %), 2 gaps (0 %)). The highest similarities using the LSU sequence were *P. microspora* (GenBank KY366173; Identities 838/844 (99 %), no gaps), *P. knightiae* (GenBank KM116241; Identities 838/844 (99 %), no gaps) and *P. papuana* (GenBank KM116240; Identities 838/844 (99 %), no gaps). The highest similarities using the *tub2* sequence were *P. distincta* (GenBank KX895293; Identities 416/440 (95 %), no gaps), *P. portugalica* (GenBank KX895338; Identities 412/441 (93 %), no gaps) and *P. monochaeta* (GenBank KX642435; Identities 426/456 (93 %), 4 gaps (0 %)).

Colour illustrations. *Dianella* sp.; conidiomata sporulating on banana leaf agar, conidiophores and conidia. Scale bars = 10 µm.

Pedro W. Crous & Johannes Z. Groenewald, Westerdijk Fungal Biodiversity Institute, P.O. Box 85167,
3508 AD Utrecht, The Netherlands; e-mail: p.crous@westerdijkinstitute.nl & e.groenewald@westerdijkinstitute.nl
Michael J. Wingfield, Forestry and Agricultural Biotechnology Institute (FABI), University of Pretoria, Pretoria 0002, South Africa;
e-mail: mike.wingfield@fabi.up.ac.za
Brett A. Summerell, Royal Botanic Gardens and Domain Trust, Mrs. Macquaries Road, Sydney, NSW 2000, Australia;
e-mail: brett.summerell@rbgsyd.nsw.gov.au
Angus J. Carnegie, Forest Health & Biosecurity, NSW Department of Primary Industries, Level 12, 10 Valentine Ave,
Parramatta, NSW 2150, Locked Bag 5123, Parramatta, NSW 2124, Australia; e-mail: angus.carnegie@dpi.nsw.gov.au


Codinaea lambertiae

Fungal Planet 683 – 20 December 2017

Codinaea lambertiae Crous, *sp. nov.*

Etymology. Name refers to *Lambertia*, the host genus from which this fungus was collected.

Classification — *Chaetosphaeriaceae*, *Chaetosphaeriales*, *Sordariomycetes.*

Mycelium consisting of hyaline, smooth, septate, branched, 2–3 µm diam hyphae. *Conidiophores* solitary, arising from creeping hyphae, flexuous, 100–200 × 3 µm, multiseptate, becoming pale to medium brown in fertile region, mostly unbranched, rarely branched close to apex. *Conidiogenous cells* integrated, apical, rarely intercalary, subcylindrical, medium brown, smooth, 15–35 × 2.3–5 µm, phialidic with flared apical collarette, 3.5–4.5 µm diam. *Conidia* solitary, aggregating in slimy mass, hyaline, smooth, aseptate, curved, fusoid-ellipsoid, guttulate, apex subacutely rounded, base truncate, 1 µm diam, (13–)14–15(–18) × (2.5–)3 µm, with single appendage at each end, flexuous, unbranched, 5–8 µm long.

Culture characteristics — Colonies flat, spreading, with sparse aerial mycelium and feathery, lobate margins, reaching 30 mm diam after 2 wk at 25 °C. On MEA surface pale olivaceous grey, reverse smoke grey. On PDA surface and reverse smoke grey. On OA surface iron-grey.

Typus. AUSTRALIA, New South Wales, Fitzroy Falls, Morton National Park, on leaves of *Lambertia formosa* (*Proteaceae*), 26 Nov. 2016, *P.W. Crous* (holotype CBS H-23288, culture ex-type CPC 32289 = CBS 143419, ITS and LSU sequences GenBank MG386052 and MG386105, MycoBank MB823401).

Notes — *Codinaea* (setulate conidia) is distinguished from *Dictyochaeta* (asetulate conidia) (Réblová & Winka 2000), and thus the present collection is described as a new species of *Codinaea*. Phylogenetically, *C. lambertiae* is part of the *C. simplex* species complex (Hughes & Kendrick 1968, Crous et al. 2014b), but appears to be distinct based on DNA sequence.

Based on a megablast search using the ITS sequence, the closest matches in NCBIs GenBank nucleotide database were *Dictyochaeta simplex* (GenBank EF029193; Identities 506/514 (98 %), 1 gap (0 %)), *Dictyochaeta fertilis* (GenBank AF178540; Identities 491/501 (98 %), 3 gaps (0 %)) and *Codinaea pini* (GenBank NR_137943; Identities 490/530 (92 %), 20 gaps (3 %)). The highest similarities using the LSU sequence were *Dictyochaeta simplex* (GenBank AF178559; Identities 822/831 (99 %), no gaps), *Codinaea pini* (GenBank KP004493; Identities 826/838 (99 %), 1 gap (0 %)) and *Chaetosphaeria rivularia* (GenBank KR347357; Identities 810/838 (97 %), 1 gap (0 %)).

Colour illustrations. Lambertia formosa; conidiophores sporulating on PNA, conidiogenous cells and conidia. Scale bars = 10 µm.

Pedro W. Crous & Johannes Z. Groenewald, Westerdijk Fungal Biodiversity Institute, P.O. Box 85167,
3508 AD Utrecht, The Netherlands; e-mail: p.crous@westerdijkinstitute.nl & e.groenewald@westerdijkinstitute.nl
Michael J. Wingfield, Forestry and Agricultural Biotechnology Institute (FABI), University of Pretoria, Pretoria 0002, South Africa;
e-mail: mike.wingfield@fabi.up.ac.za
Treena I. Burgess & Giles E.St.J. Hardy, Centre for Phytophthora Science and Management, Murdoch University,
90 South Street, Murdoch, WA 6150, Australia;
e-mail: tburgess@murdoch.edu.au & g-hardy@murdoch.edu.au


Dothidea eucalypti

Fungal Planet 684 – 20 December 2017

Dothidea eucalypti Crous, *sp. nov.*

Etymology. Name refers to *Eucalyptus*, the host genus from which this fungus was collected.

Classification — *Dothideaceae*, *Dothideales*, *Dothideomycetes*.

Conidiomata separate, erumpent, pycnidial, brown, 50–250 µm diam with central ostiole, exuding a crystalline conidial mass; wall of 3–6 layers of brown *textura angularis*. *Conidiophores* reduced to conidiogenous cells, lining the inner cavity, pale brown, smooth, doliiform, 6–10 × 4–5 µm, with central phialidic locus. *Conidia* hyaline, smooth, guttulate, aseptate, subcylindrical, apex obtuse, base truncate, (7–)8–10(–12) × (2.5–)3 µm. *Hyphae* 3–5 µm diam, brown, thick-walled, verruculose, constricted at septa, giving rise to hormonema-like synasexual morph.

Culture characteristics — Colonies flat, spreading, with sparse to moderate aerial mycelium and feathery, lobate margins, reaching 60 mm diam after 2 wk at 25 °C. On MEA, PDA and OA surface and reverse greenish black.

Typus. Australia, New South Wales, South East Forests National Park, on leaves of *Eucalyptus dalrympleana* (*Myrtaceae*), 28 Nov. 2016, *P.W. Crous* (holotype CBS H-23290, culture ex-type CPC 32313 = CBS 143417, ITS, LSU and *tef1* sequences GenBank MG386053, MG386106 and MG386152, MycoBank MB823402).

Notes — Genera in the *Dothideaceae* commonly form *Dothichiza* and hormonema-like morphs in culture (Crous & Groenewald 2017), which were also seen in cultures of *Dothidea eucalypti* in this study.

Based on a megablast search using the ITS sequence, the closest matches in NCBIs GenBank nucleotide database were *Dothidea berberidis* (GenBank EU167601; Identities 497/515 (97 %), 3 gaps (0 %)), *Dothidea ribesia* (GenBank KY929142; Identities 501/515 (97 %), 3 gaps (0 %)) and *Dothidea hippophaeos* (GenBank KF147924; Identities 497/515 (97 %), 2 gaps (0 %)). The highest similarities using the LSU sequence were *Dothidea sambuci* (GenBank AF382387; Identities 856/857 (99 %), no gaps), *Dothidea ribesia* (GenBank KY929175; Identities 855/857 (99 %), no gaps) and *Dothidea insculpta* (GenBank NG_027643; Identities 854/856 (99 %), no gaps). The highest similarities using the *tef1* sequence were *Dothidea ribesia* (GenBank KY929192; Identities 153/207 (74 %), 26 gaps (12 %)), *Dothiora phillyreae* (GenBank KU728590; Identities 134/179 (75 %), 19 gaps (10 %)) and *Dothiora agapanthi* (GenBank KU728578; Identities 160/225 (71 %), 19 gaps (8 %)).

Colour illustrations. South East Forests National Park; conidiomata sporulating on banana leaf agar, conidioma (scale bar = 200 µm), conidiogenous cells, hormonema-like synasexual morph and conidia (scale bars = 10 µm).

Pedro W. Crous & Johannes Z. Groenewald, Westerdijk Fungal Biodiversity Institute, P.O. Box 85167,
3508 AD Utrecht, The Netherlands; e-mail: p.crous@westerdijkinstitute.nl & e.groenewald@westerdijkinstitute.nl
Michael J. Wingfield, Forestry and Agricultural Biotechnology Institute (FABI), University of Pretoria, Pretoria 0002, South Africa;
e-mail: mike.wingfield@fabi.up.ac.za
Brett A. Summerell, Royal Botanic Gardens and Domain Trust, Mrs. Macquaries Road, Sydney, NSW 2000, Australia;
e-mail: brett.summerell@rbgsyd.nsw.gov.au
Angus J. Carnegie, Forest Health & Biosecurity, NSW Department of Primary Industries, Level 12, 10 Valentine Ave,
Parramatta, NSW 2150, Locked Bag 5123, Parramatta, NSW 2124, Australia; e-mail: angus.carnegie@dpi.nsw.gov.au


Verrucoconiothyrium acaciae

Fungal Planet 685 – 20 December 2017

Verrucoconiothyrium acaciae Crous, *sp. nov.*

Etymology. Name refers to *Acacia*, the host genus from which this fungus was collected.

Classification — *Didymellaceae*, *Pleosporales*, *Dothideomycetes.*

Conidiomata solitary, globose, 100–250 µm diam, brown with central ostiole, 10–15 µm diam; wall of 3–4 layers of brown *textura angularis*. *Conidiophores* reduced to conidiogenous cells, ampulliform, hyaline, smooth, 5–8 × 5–6 µm, phialidic with minute percurrent proliferations at apex. *Conidia* solitary, aseptate, fusoid-ellipsoid, medium brown, verruculose, apex obtuse to subobtuse, base truncate, 1.5 µm diam, (6.5–)8–9(–10) × (3–)3.5(–4) µm.

Culture characteristics — Colonies flat, spreading, with moderate aerial mycelium and feathery, lobate margins, reaching 50 mm diam after 2 wk at 25 °C. On MEA surface and reverse saffron with black conidiomata. On PDA surface grey olivaceous, reverse mouse grey. On OA surface pale luteous with black conidiomata.

Typus. Australia, New South Wales, Nullica State Forest, on leaves of *Acacia falciformis* (*Fabaceae*), 29 Nov. 2016, *P.W. Crous* (holotype CBS H-23292, culture ex-type CPC 32330 = CBS 143448, ITS, LSU, *rpb2* and *tub2* sequences GenBank MG386054, MG386107, MG386143 and MG386165, MycoBank MB823403).

Notes — *Verrucoconiothyrium* (Crous et al. 2015a) accommodates coniothyrium-like species with verruculose conidia.

Based on a megablast search using the ITS sequence, the closest matches in NCBIs GenBank nucleotide database were *V. nitidae* (GenBank JN712452; Identities 521/530 (98 %), 4 gaps (0 %)), *V. eucalyptigenum* (GenBank KY979771; Identities 515/531 (97 %), 5 gaps (0 %)) and *V. prosopidis* (GenBank NR_137604; Identities 514/531 (97 %), 5 gaps (0 %)). The highest similarities using the LSU sequence were 99 % to species from numerous genera in *Didymellaceae*, e.g., *Phoma eupyrena* (GenBank GU238072; Identities 851/854 (99 %), no gaps), *Didymella glomerata* (GenBank KX896095; Identities 850/854 (99 %), no gaps) and *Peyronellaea calorpreferens* (GenBank LN907448; Identities 850/854 (99 %), no gaps). The highest similarities using the *rpb2* sequence were *V. eucalyptigenum* (GenBank KY979852; Identities 790/841 (94 %), no gaps), *Nothophoma gossypiicola* (GenBank KT389658; Identities 552/595 (93 %), no gaps) and *N. infossa* (GenBank KT389659; Identities 532/580 (92 %), no gaps). The highest similarities using the *tub2* sequence were *V. eucalyptigenum* (GenBank KY979935; Identities 311/326 (95 %), no gaps), *V. nitidae* (as *Coniothyrium nitidae*; GenBank JN712647; Identities 305/321 (95 %), 3 gaps (0 %)) and *Nothophoma quercina* (GenBank KU973704; Identities 307/328 (94 %), no gaps).

Colour illustrations. *Acacia* sp.; conidiomata sporulating on PDA, conidiogenous cells and conidia. Scale bars = 10 µm.

Pedro W. Crous & Johannes Z. Groenewald, Westerdijk Fungal Biodiversity Institute, P.O. Box 85167,
3508 AD Utrecht, The Netherlands; e-mail: p.crous@westerdijkinstitute.nl & e.groenewald@westerdijkinstitute.nl
Michael J. Wingfield, Forestry and Agricultural Biotechnology Institute (FABI), University of Pretoria, Pretoria 0002, South Africa;
e-mail: mike.wingfield@fabi.up.ac.za
Brett A. Summerell, Royal Botanic Gardens and Domain Trust, Mrs. Macquaries Road, Sydney, NSW 2000, Australia;
e-mail: brett.summerell@rbgsyd.nsw.gov.au
Angus J. Carnegie, Forest Health & Biosecurity, NSW Department of Primary Industries, Level 12, 10 Valentine Ave,
Parramatta, NSW 2150, Locked Bag 5123, Parramatta, NSW 2124, Australia; e-mail: angus.carnegie@dpi.nsw.gov.au


Stagonospora victoriana

Fungal Planet 686 – 20 December 2017

Stagonospora victoriana Crous, *sp. nov.*

Etymology. Name refers to the state of Victoria, Australia, where this fungus was collected.

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

Conidiomata separate, erumpent, globose, pale brown, 150–200 µm diam, with central ostiole. *Conidiophores* reduced to conidiogenous cells lining inner cavity, hyaline, smooth, doliiform to ellipsoid, 8–17 × 7–10 µm, proliferating percurrently near apex. *Conidia* solitary, fusoid-ellipsoid, hyaline, smooth, granular, multiseptate, (1–)3-euseptate, apex obtuse, base bluntly rounded, 4–5 µm diam, (28–)33–38(–45) × (9–)11–12(–13) µm.

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

Typus. Australia, Victoria, Mount Best Tin Mine Road, on *Poaceae* at pond, 28 Nov. 2016, *P.W. Crous* (holotype CBS H-23294, culture ex-type CPC 32498 = CBS 143403, ITS, LSU, *tef1* and *tub2* sequences GenBank MG386055, MG386108, MG386153 and MG386166, MycoBank MB823404).

Notes — Quaedvlieg et al. (2013) circumscribed *Stagonospora* to include species with conidiogenous cells that proliferate percurrently, or via phialides with periclinal thickening, and conidia that are subcylindrical to fusoid-ellipsoidal. The present collection is related to species of *Stagonospora*, clustering adjacent to *S. pseudovitensis* (conidia 3-septate, 25–36 × 6–8 µm), from which it is morphologically distinct (Quaedvlieg et al. 2013).

Based on a megablast search using the ITS sequence, the closest matches in NCBIs GenBank nucleotide database were *S. perfecta* (GenBank NR_138388; Identities 513/531 (97 %), 3 gaps (0 %)), *S. bicolor* (as *Saccharicola bicolor*; GenBank KP276515; Identities 459/476 (96 %), 2 gaps (0 %)) and *S. pseudovitensis* (GenBank KF251262; Identities 512/532 (96 %), 4 gaps (0 %)). The highest similarities using the LSU sequence were *S. pseudovitensis* (GenBank KF251765; Identities 834/837 (99 %), no gaps), *S. perfecta* (GenBank AB807579; Identities 844/848 (99 %), no gaps) and *S. trichophoricola* (GenBank KJ869168; Identities 835/840 (99 %), no gaps). The highest similarities using the *tef1* sequence were distant hits with *Helminthosporium tiliae* (GenBank KY984457; Identities 248/308 (81 %), 21 gaps (6 %)), *H. oligosporum* (GenBank KY984451; Identities 218/266 (82 %), 17 gaps (6 %)) and *H. microsorum* (GenBank KY984448; Identities 214/262 (82 %), 14 gaps (5 %)). The highest similarities using the *tub2* sequence were distant hits with *S. pseudovitensis* (GenBank KF252744; Identities 271/305 (89 %), 2 gaps (0 %)), *S. chrysopyla* (GenBank KM033943; Identities 385/446 (86 %), 11 gaps (2 %)) and *Corynespora cassiicola* (GenBank KU605322; Identities 310/384 (81 %), 16 gaps (4 %)).

Colour illustrations. Pond at Mount Best Tin Mine Road; conidiomata sporulating on OA, conidiogenous cells and conidia. Scale bars = 10 µm.

Pedro W. Crous & Johannes Z. Groenewald, Westerdijk Fungal Biodiversity Institute, P.O. Box 85167,
3508 AD Utrecht, The Netherlands; e-mail: p.crous@westerdijkinstitute.nl & e.groenewald@westerdijkinstitute.nl
Michael J. Wingfield, Forestry and Agricultural Biotechnology Institute (FABI), University of Pretoria, Pretoria 0002, South Africa;
e-mail: mike.wingfield@fabi.up.ac.za
Brett A. Summerell, Royal Botanic Gardens and Domain Trust, Mrs. Macquaries Road, Sydney, NSW 2000, Australia;
e-mail: brett.summerell@rbgsyd.nsw.gov.au
Angus J. Carnegie, Forest Health & Biosecurity, NSW Department of Primary Industries, Level 12, 10 Valentine Ave,
Parramatta, NSW 2150, Locked Bag 5123, Parramatta, NSW 2124, Australia; e-mail: angus.carnegie@dpi.nsw.gov.au


Didymella acaciae

Fungal Planet 687 – 20 December 2017

Didymella acaciae Crous, *sp. nov.*

Etymology. Name refers to *Acacia*, the host genus from which this fungus was collected.

Classification — *Didymellaceae*, *Pleosporales*, *Dothideomycetes.*

Conidiomata pycnidial, solitary, globose, 80–150 µm diam on SNA, up to 350 µm diam on OA with 1–2 ostioles, ostiole papillate, 40–50 µm diam; wall of 3–4 layers of pale to medium brown *textura angularis. Conidiophores* reduced to conidiogenous cells lining the inner cavity, hyaline, smooth, ampulliform to globose, 4–6 × 4–6 µm, proliferating percurrently at apex. *Conidia* solitary, hyaline, smooth, guttulate to granular, straight, medianly 1-septate, cylindrical, apex obtuse, base truncate, 1.5–3 µm diam, (16–)18–21(–25) × (3–)3.5(–4) µm.

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

Typus. Australia, New South Wales, Merimbula, on leaves of *Acacia melanoxylon* (*Fabaceae*), 28 Nov. 2016, *P.W. Crous* (holotype CBS H-23295, culture ex-type CPC 32504 = CBS 143404, ITS, LSU, *rpb2*, *tef1* and *tub2* sequences GenBank MG386056, MG386109, MG386144, MG386154 and MG386167, MycoBank MB823425).

Notes — *Didymella acaciae* is closely related to several genera, including *Verrucoconiothyrium*, *Didymella*, *Paraboeremia* and *Peyronellaea* (Chen et al. 2015). *Didymella acaciae* is phoma-like in morphology, suggesting that it would be better suited in *Didymella* for the present. However, additional taxa, and more informative genes are required to fully resolve its placement within this generic complex.

Based on a megablast search using the ITS sequence, the closest matches in NCBIs GenBank nucleotide database were *Verrucoconiothyrium nitidae* (GenBank KX306774; Identities 523/535 (98 %), 2 gaps (0 %)), *V. prosopidis* (GenBank NR_137604; Identities 523/536 (98 %), 3 gaps (0 %)) and *V. eucalyptigenum* (GenBank KY979771; Identities 520/536 (97 %), 3 gaps (0 %)). The highest similarities using the LSU sequence were 99 % to species from numerous genera in *Didymellaceae*, e.g., *Didymella sinensis* (GenBank KY742239; Identities 853/854 (99 %), no gaps), *Paraboeremia oligotrophica* (GenBank KX829040; Identities 853/854 (99 %), no gaps) and *Peyronellaea combreti* (GenBank KJ869191; Identities 853/854 (99 %), no gaps). The highest similarities using the *rpb2* sequence were *V. eucalyptigenum* (GenBank KY979852; Identities 685/729 (94 %), no gaps), *Nothophoma infossa* (GenBank KT389659; Identities 545/592 (92 %), no gaps) and *N. arachidis-hypogaeae* (GenBank KT389656; Identities 547/595 (92 %), no gaps). The highest similarities using the *tef1* sequence were *V. eucalyptigenum* (GenBank KY979904; Identities 202/221 (91 %), 8 gaps (3 %)), *N. quercina* (as *Phoma fungicola*; GenBank KC357259; Identities 199/222 (90 %), 10 gaps (4 %)) and *Ascochyta pisi* (GenBank DQ386494; Identities 189/211 (90 %), 5 gaps (2 %)). The highest similarities using the *tub2* sequence were *V. eucalyptigenum* (GenBank KY979935; Identities 176/187 (94 %), no gaps), *N. quercina* (GenBank KU973706; Identities 173/184 (94 %), no gaps) and *Allophoma zantedeschiae* (GenBank KX033401; Identities 175/187 (94 %), no gaps).

Colour illustrations. Symptomatic leaves of *Acacia melanoxylon*; conidiomata sporulating on PNA, conidiogenous cells and conidia. Scale bars = 10 µm.

Pedro W. Crous & Johannes Z. Groenewald, Westerdijk Fungal Biodiversity Institute, P.O. Box 85167,
3508 AD Utrecht, The Netherlands; e-mail: p.crous@westerdijkinstitute.nl & e.groenewald@westerdijkinstitute.nl
Michael J. Wingfield, Forestry and Agricultural Biotechnology Institute (FABI), University of Pretoria, Pretoria 0002, South Africa;
e-mail: mike.wingfield@fabi.up.ac.za
Brett A. Summerell, Royal Botanic Gardens and Domain Trust, Mrs. Macquaries Road, Sydney, NSW 2000, Australia;
e-mail: brett.summerell@rbgsyd.nsw.gov.au
Angus J. Carnegie, Forest Health & Biosecurity, NSW Department of Primary Industries, Level 12, 10 Valentine Ave,
Parramatta, NSW 2150, Locked Bag 5123, Parramatta, NSW 2124, Australia; e-mail: angus.carnegie@dpi.nsw.gov.au


Saccharata hakeigena

Fungal Planet 688 – 20 December 2017

Saccharata hakeigena Crous, *sp. nov.*

Etymology. Name refers to *Hakea*, the host genus from which this fungus was collected.

Classification — *Saccharataceae*, *Botryosphaeriales*, *Dothideomycetes.*

Conidiomata separate, pycnidial, globose, dark brown, 150–250 µm diam, with central ostiole; wall of 3–8 layers of brown *textura angularis. Conidiophores* 0–2-septate, subcylindrical, hyaline, smooth, branched or not, 20–30 × 5–6 µm. *Conidiogenous cells* mostly terminal, subcylindrical, hyaline, smooth, 15–20 × 3–4 µm, proliferating percurrently at apex. *Paraphyses* intermingled among conidiophores, subcylindrical, branched, up to 40 µm long, 3–5 µm diam. *Conidia* solitary, hyaline, smooth, guttulate, granular, aseptate, fusoid-ellipsoid, apex obtuse, base truncate, 4 µm diam, (25–)27–33(–35) × (6–)7–8 µm.

Culture characteristics — Colonies flat, spreading, with moderate aerial mycelium and feathery margins, reaching 30 mm diam after 2 wk at 25 °C. On MEA, PDA and OA surface smoke grey, reverse olivaceous grey.

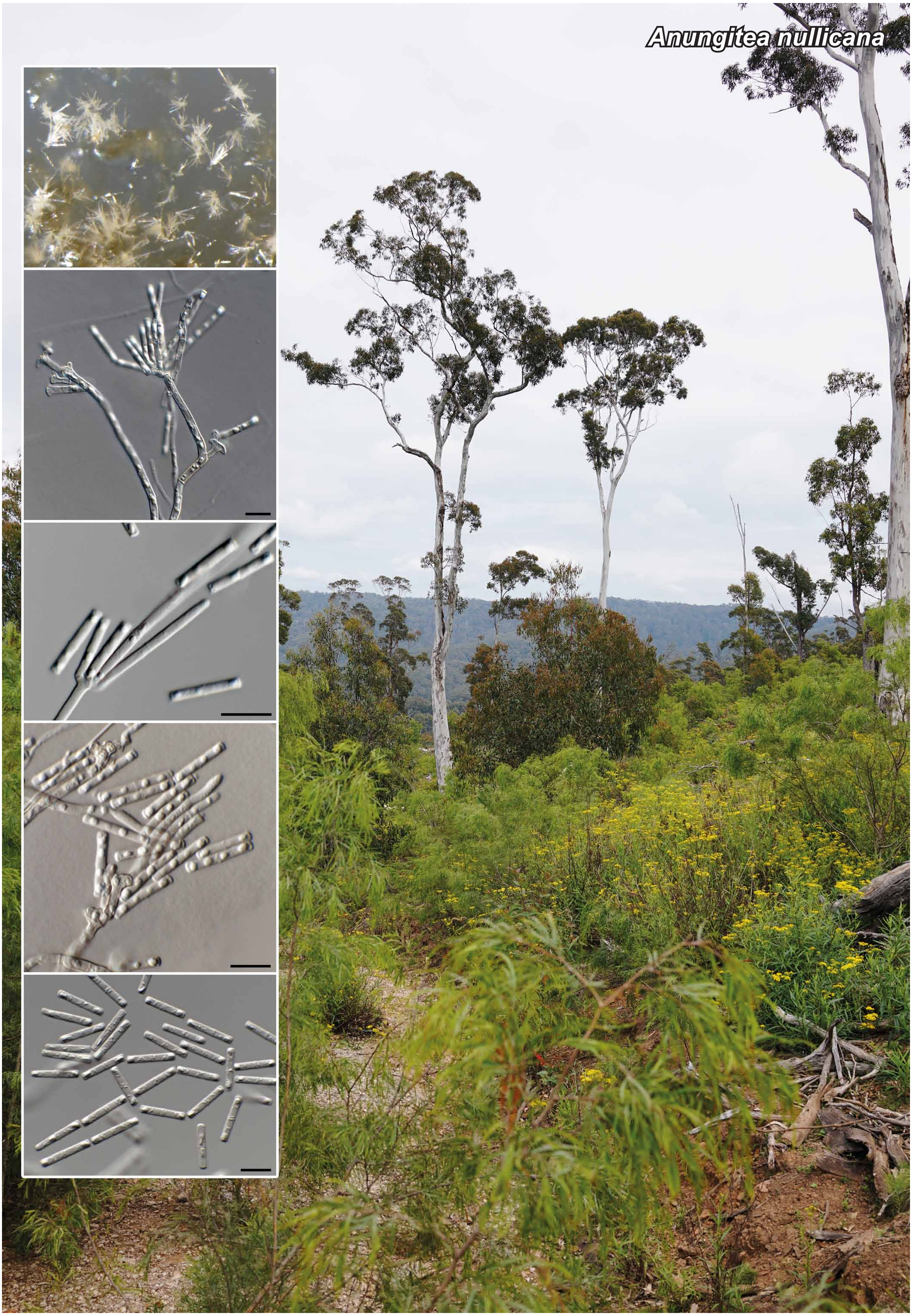
Typus. AUSTRALIA, New South Wales, Nullica State Forest, on *Hakea sericea* (*Proteaceae*), 29 Nov. 2016, *P.W. Crous* (holotype CBS H-23296, culture ex-type CPC 32520 = CBS 143405, ITS, LSU, *rpb2* and *tef1* sequences GenBank MG386057, MG386110, MG386145 and MG386155, MycoBank MB823405).

Notes — Species of the genus *Saccharata* are commonly known to occur on species of *Proteaceae* and *Myrtaceae* in the southern hemisphere (Marincowitz et al. 2008). Two species are known from *Hakea*, namely *S. hakeicola* (conidia aseptate, (23–)27–29(–32) × (5–)5.5(–6) µm), and *S. hakeae* (conidia aseptate, (24–)28–31(–33) × (6.5–)7–8 µm). *Saccharata hakeigena* is morphologically similar to *S. hakeae*, but can be distinguished based on the presence of paraphyses (absent in *S. hakeae*), and its DNA phylogeny.

Based on a megablast search using the ITS sequence, the closest matches in NCBIs GenBank nucleotide database were *S. hakeae* (GenBank KY173452; Identities 538/558 (96 %), 3 gaps (0 %)), *Septorioides strobi* (GenBank KT884694; Identities 400/436 (92 %), 4 gaps (0 %)) and *S. eucalyptorum* (GenBank KY173451; Identities 514/561 (92 %), 20 gaps (3 %)). The highest similarities using the LSU sequence were *S. capensis* (GenBank KF766390; Identities 834/856 (97 %), 2 gaps (0 %)), *S. intermedia* (GenBank GU229889; Identities 830/854 (97 %), 2 gaps (0 %)) and *S. kirstenboschensis* (GenBank FJ372409; Identities 827/851 (97 %), 2 gaps (0 %)). The highest similarities using the *rpb2* sequence were *S. daviesiae* (GenBank KY173589; Identities 678/849 (80 %), 33 gaps (3 %)) and *Septorioides pini-thunbergii* (GenBank KX464075; Identities 385/496 (78 %), 15 gaps (3 %)). The highest similarities using the *tef1* sequence were *S. banksiae* (GenBank KY173596; Identities 173/217 (80 %), 14 gaps (6 %)) and *Septorioides proteae* (GenBank KF531789; Identities 148/181 (82 %), 9 gaps (4 %)).

Colour illustrations. Bankia sp. growing intermixed with *Hakea sericea*; conidiogenous cells and conidia. Scale bars = 10 µm.

Pedro W. Crous & Johannes Z. Groenewald, Westerdijk Fungal Biodiversity Institute, P.O. Box 85167,
3508 AD Utrecht, The Netherlands; e-mail: p.crous@westerdijkinstitute.nl & e.groenewald@westerdijkinstitute.nl
Michael J. Wingfield, Forestry and Agricultural Biotechnology Institute (FABI), University of Pretoria, Pretoria 0002, South Africa;
e-mail: mike.wingfield@fabi.up.ac.za
Brett A. Summerell, Royal Botanic Gardens and Domain Trust, Mrs. Macquaries Road, Sydney, NSW 2000, Australia;
e-mail: brett.summerell@rbgsyd.nsw.gov.au
Angus J. Carnegie, Forest Health & Biosecurity, NSW Department of Primary Industries, Level 12, 10 Valentine Ave,
Parramatta, NSW 2150, Locked Bag 5123, Parramatta, NSW 2124, Australia; e-mail: angus.carnegie@dpi.nsw.gov.au


Anungitea nullicana

Fungal Planet 689 – 20 December 2017

Anungitea nullicana Crous, *sp. nov.*

Etymology. Name refers to Nullica State Forest, Australia, where this fungus was collected.

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

Mycelium consisting of hyaline, smooth, branched, septate, 3–3.5 µm diam hyphae. *Conidiophores* solitary, erect, subcylindrical, mostly unbranched, medium brown, smooth, 50–100 × 3–4 µm, 4–8-septate. *Conidiogenous cells* terminal and intercalary, pale brown, subcylindrical with terminal clusters of denticulate-like sympodial loci, 2 µm diam, not thickened nor darkened, 10–15 × 2 µm, conidiogenous head up to 10 µm diam. *Ramoconidia* uncommon, pale brown with terminal head of sympodial loci, 12–22 × 2 µm, head up to 10 µm diam. *Conidia* in long unbranched chains, hyaline, smooth, cylindrical with truncate ends, medianly 1-septate, with 2 large guttules per cell, (12–)14–17(–20) × 2.5(–3) µm.

Culture characteristics — Colonies flat, spreading, with sparse to moderate aerial mycelium and smooth, lobate margins, reaching 30 mm diam after 2 wk at 25 °C. On MEA surface amber, reverse chestnut. On PDA surface and reverse chestnut. On OA surface buff in centre, isabelline in outer zone.

Typus. Australia, New South Wales, Nullica State Forest, on leaf litter of *Eucalyptus* sp. (*Myrtaceae*), 29 Nov. 2016, *P.W. Crous* (holotype CBS H-23297, culture ex-type CPC 32528 = CBS 143406, ITS and LSU sequences GenBank MG386058 and MG386111, MycoBank MB823406).

Notes — *Anungitea* is characterised by species with pigmented, solitary conidiophores, bearing a head with denticles with flattened conidiogenous scars that are neither unthickened nor darkened, and chains of cylindrical, 1-septate subhyaline conidia (Sutton 1973). *Anungitea nullicana* (conidia 1-septate, (12–)14–17(–20) × 2.5(–3) µm) is morphologically similar to *A. eucalyptigena* (conidia 0–1-septate, (11–)14–16(–18) × (2–)2.5(–3) µm) and *A. eucalyptorum* (conidia 0–1-septate, (13–)14–15(–17) × 2.5(–3) µm) (Crous et al. 2014a), and these species are best distinguished based on their DNA data.

Based on a megablast search using the ITS sequence, the closest matches in NCBIs GenBank nucleotide database were *A. eucalyptigena* (GenBank KY173383; Identities 561/570 (98 %), no gaps), *A. grevilleae* (GenBank KX228252; Identities 543/571 (95 %), 11 gaps (1 %)) and *A. eucalyptorum* (GenBank NR_132904; Identities 540/570 (95 %), 12 gaps (2 %)). The highest similarities using the LSU sequence were *A. eucalyptigena* (GenBank KY173477; Identities 818/821 (99 %), no gaps), *Phlogicylindrium eucalypti* (GenBank DQ923534; Identities 836/842 (99 %), 1 gap (0 %)) and *A. eucalyptorum* (GenBank KJ869176; Identities 833/841 (99 %), no gaps).

Colour illustrations. Nullica State Forest; conidiophores sporulating on PNA, conidiophores and conidia. Scale bars = 10 µm.

Pedro W. Crous & Johannes Z. Groenewald, Westerdijk Fungal Biodiversity Institute, P.O. Box 85167,
3508 AD Utrecht, The Netherlands; e-mail: p.crous@westerdijkinstitute.nl & e.groenewald@westerdijkinstitute.nl
Michael J. Wingfield, Forestry and Agricultural Biotechnology Institute (FABI), University of Pretoria, Pretoria 0002, South Africa;
e-mail: mike.wingfield@fabi.up.ac.za
Brett A. Summerell, Royal Botanic Gardens and Domain Trust, Mrs. Macquaries Road, Sydney, NSW 2000, Australia;
e-mail: brett.summerell@rbgsyd.nsw.gov.au
Angus J. Carnegie, Forest Health & Biosecurity, NSW Department of Primary Industries, Level 12, 10 Valentine Ave,
Parramatta, NSW 2150, Locked Bag 5123, Parramatta, NSW 2124, Australia; e-mail: angus.carnegie@dpi.nsw.gov.au


Sympoventuria melaleucae

Fungal Planet 690 – 20 December 2017

Sympoventuria melaleucae Crous, *sp. nov.*

Etymology. Name refers to *Melaleuca*, the host genus from which this fungus was collected.

Classification — *Sympoventuriaceae*, *Venturiales*, *Dothideomycetes.*

Mycelium consisting of smooth, pale brown, septate, branched, 2–3 µm diam hyphae. *Conidiophores* reduced to conidiogenous loci on hyphae, 3–7 × 2–3 µm; scars truncate, unthickened, not darkened, 1–1.5 µm diam. *Conidia* in long, branched chains, pale brown, smooth, fusoid-ellipsoid, 0–1-septate, prominently guttulate, (8–)11–17(–25) × 2–3 µm; hila truncate, unthickened, 1–2 µm diam.

Culture characteristics — Colonies erumpent, spreading, with moderate aerial mycelium and smooth, lobate margins, reaching 20 mm diam after 2 wk at 25 °C. On MEA, PDA and OA surface amber, reverse chestnut.

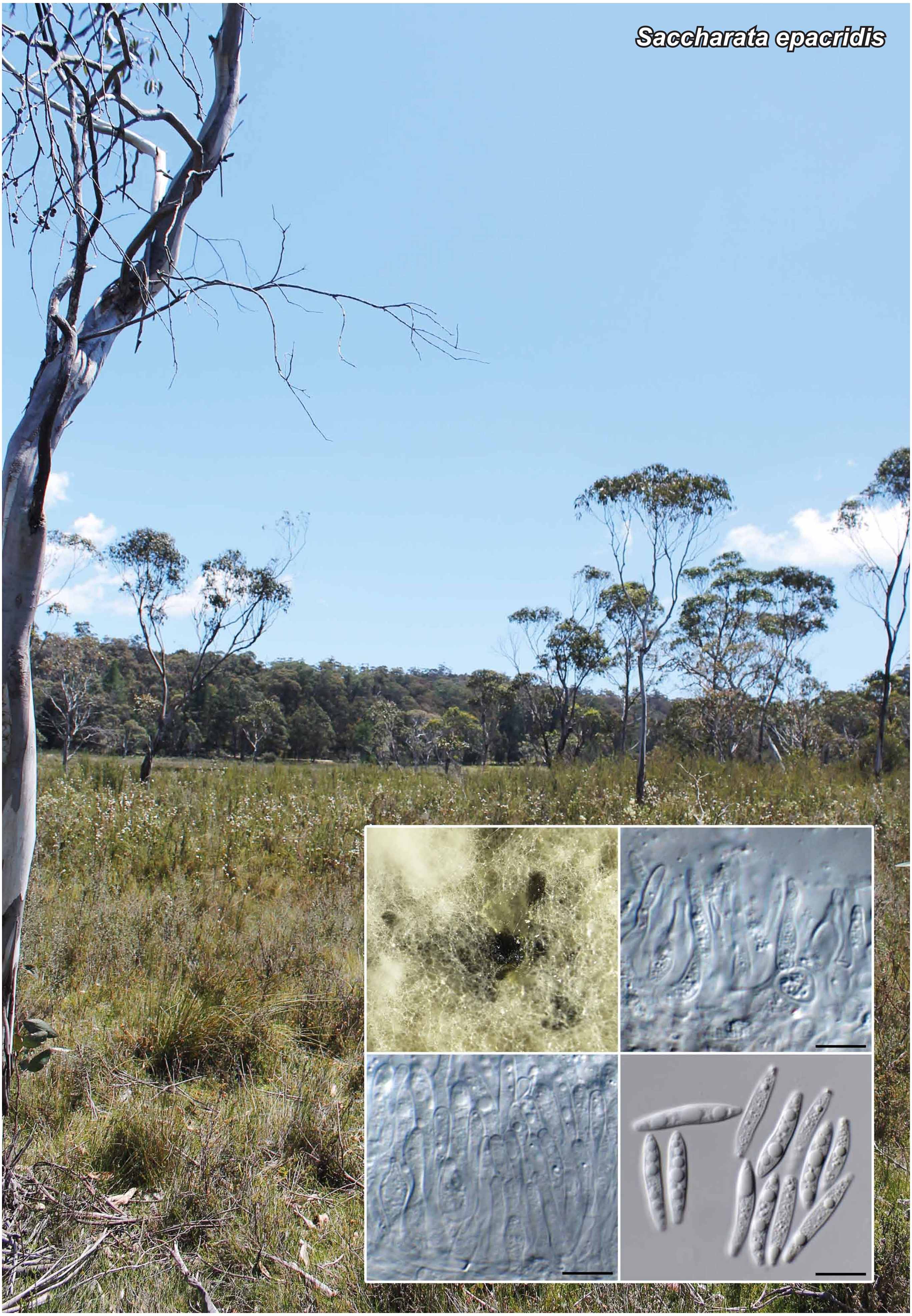
Typus. Australia, Victoria, Royal Botanic Gardens Victoria, Melbourne Gardens, on leaves of *Melaleuca* sp. (*Proteaceae*), 2 Dec. 2016, *P.W. Crous* (holotype CBS H-23298, culture ex-type CPC 32576 = CBS 143407, ITS, LSU and *tub2* sequences GenBank MG386059, MG386112 and MG386168, MycoBank MB823407).

Colour illustrations. *Melaleuca* sp.; conidiophores sporulating on PNA, conidiophores, conidiogenous cells and conidia. Scale bars = 10 µm.

Notes — *Sympoventuria* was introduced for a venturia-like ascomycete with a distinct hyphomycete asexual morph occurring on *Eucalyptus* leaf litter in South Africa (Crous et al. 2007). *Sympoventuria melaleucae* adds one additional taxon to the genus, this time occurring on *Proteaceae*, but again collected in the southern hemisphere. *Sympoventuria melaleucae* (conidia 0–1-septate, (8–)11–17(–25) × 2–3 µm) can be distinguished from *S. capensis* (conidia (1–)3(–5)-septate, 10–65 × 2.5–5 µm; Crous et al. 2007), in that it has smaller, 0–1-septate conidia.

Based on a megablast search using the ITS sequence, the closest matches in NCBIs GenBank nucleotide database were *S. capensis* (GenBank NR_121323; Identities 521/563 (93 %), 8 gaps (1 %)) and *Fusicladium africanum* (GenBank EU035424; Identities 514/565 (91 %), 8 gaps (1 %)). The highest similarities using the LSU sequence were *S. capensis* (GenBank KF156104; Identities 785/790 (99 %), no gaps), *Scolecobasidium excentricum* (GenBank KF156105; Identities 782/790 (99 %), 1 gap (0 %)) and *Fusicladium africanum* (GenBank EU035424; Identities 838/850 (99 %), no gaps). No significant hits were found when the *tub2* sequence was used in a blast search.

Pedro W. Crous & Johannes Z. Groenewald, Westerdijk Fungal Biodiversity Institute, P.O. Box 85167,
3508 AD Utrecht, The Netherlands; e-mail: p.crous@westerdijkinstitute.nl & e.groenewald@westerdijkinstitute.nl
Michael J. Wingfield, Forestry and Agricultural Biotechnology Institute (FABI), University of Pretoria, Pretoria 0002, South Africa;
e-mail: mike.wingfield@fabi.up.ac.za
Tom W. May, Royal Botanic Gardens Victoria, Birdwood Avenue, Melbourne, VIC 3004, Australia;
e-mail: tom.may@rbg.vic.gov.au


Saccharata epacridis

Fungal Planet 691 – 20 December 2017

Saccharata epacridis Crous, *sp. nov.*

Etymology. Name refers to *Epacris*, the host genus from which this fungus was collected.

Classification — *Saccharataceae*, *Botryosphaeriales*, *Dothideomycetes.*

Conidiomata pycnidial, globose, erumpent, dark brown, 200–250 µm diam, with central ostiole; wall of 3–8 layers of brown *textura angularis. Conidiophores* lining the inner cavity, hyaline, smooth, 0–2-septate, subcylindrical, branched, 15–30 × 3–4 µm. *Conidiogenous cells* terminal and intercalary, subcylindrical, hyaline, smooth, 10–15 × 3–4 µm, proliferating percurrently at apex. *Conidia* solitary, hyaline, smooth, aseptate, fusoid-ellipsoid, guttulate, apex subacutely rounded, base truncate, 1–2 µm diam, (17–)20–22(–25) × (3–)3.5(–4) µm.

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

Typus. Australia, Victoria, Mount Best Tin Mine Road, on *Epacris* sp. (*Ericaceae*), 28 Nov. 2016, *P.W. Crous* (holotype CBS H-23299, culture ex-type CPC 32594 = CBS 143408, ITS and LSU sequences GenBank MG386060 and MG386113, MycoBank MB823408).

Colour illustrations. Mount Best Tin Mine Road; conidiomata sporulating on OA, conidiogenous cells and conidia. Scale bars = 10 µm.

Notes — *Saccharata epacridis* (conidia aseptate, (17–)20–22(–25) × (3–)3.5(–4) µm) is phylogenetically related to *S. lambertiae* (conidia (0–)1(–2)-septate, (9–)20–23(–25) × (4–)5–6(–7) µm) and *S. petrophiles* (conidia aseptate, (15–)28–33(–35) × (4.5–)5(–5.5) µm; Crous et al. 2016a), but can be distinguished based on conidium morphology and DNA phylogeny.

Based on a megablast search using the ITS sequence, the closest matches in NCBIs GenBank nucleotide database were *Saccharata* ‘sp. 1’ (GenBank JN225922; Identities 499/502 (99 %), no gaps), *S. kirstenboschensis* (GenBank NR_137021; Identities 488/504 (97 %), 2 gaps (0 %)) and *S. lambertiae* (GenBank KY173459; Identities 465/482 (96 %), no gaps). The highest similarities using the LSU sequence were *S. lambertiae* (GenBank KY173549; Identities 826/827 (99 %), no gaps), *S. petrophiles* (GenBank KY173553; Identities 804/805 (99 %), no gaps) and *S. proteae* (GenBank KX464546; Identities 845/849 (99 %), no gaps).

Pedro W. Crous & Johannes Z. Groenewald, Westerdijk Fungal Biodiversity Institute, P.O. Box 85167,
3508 AD Utrecht, The Netherlands; e-mail: p.crous@westerdijkinstitute.nl & e.groenewald@westerdijkinstitute.nl
Michael J. Wingfield, Forestry and Agricultural Biotechnology Institute (FABI), University of Pretoria, Pretoria 0002, South Africa;
e-mail: mike.wingfield@fabi.up.ac.za
Brett A. Summerell, Royal Botanic Gardens and Domain Trust, Mrs. Macquaries Road, Sydney, NSW 2000, Australia;
e-mail: brett.summerell@rbgsyd.nsw.gov.au
Angus J. Carnegie, Forest Health & Biosecurity, NSW Department of Primary Industries, Level 12, 10 Valentine Ave,
Parramatta, NSW 2150, Locked Bag 5123, Parramatta, NSW 2124, Australia; e-mail: angus.carnegie@dpi.nsw.gov.au


Cladoriella xanthorrhoeae

Fungal Planet 692 – 20 December 2017

Cladoriellales Crous, *ord. nov.*

MycoBank MB823435.

Cladoriellaceae Crous, *fam. nov.*

MycoBank MB823436.

Classification — *Cladoriellaceae*, *Cladoriellales*, *Dothideomycetes.*

The diagnosis of the order *Cladoriellales* and family *Cladoriellaceae* is based on the type genus, *Cladoriella.*

Type genus. *Cladoriella* Crous.

External *hyphae* coiling on the leaf surface, medium to dark brown, thick-walled, smooth to finely verruculose, branched, septate, with swollen cells giving rise to conidiophores; hyphodium-like structures present, simple, intercalary. *Conidiophores* separate, erect, medium to dark brown, smooth to finely verruculose, thick-walled, subcylindrical, straight, septate. *Conidiogenous cells* terminal or intercalary, mono- or polytretic, sympodial, with 1–2 conspicuous loci, thickened, darkened, refractive, with a minute central pore. *Conidia* frequently remaining attached in long acropetal chains, simple or branched, narrowly ellipsoidal to cylindrical or fusoid, septate, medium brown, thick-walled, finely verruculose, apical conidium with rounded apex, additional conidia with truncate, conspicuous hila; thickened, darkened, refractive, with a minute central pore. *Chlamydospores* absent. *Sexual morph* unknown.

Cladoriella xanthorrhoeae Crous, *sp. nov.*

Etymology. Name refers to *Xanthorrhoea*, the host genus from which this fungus was collected.

Mycelium consisting of medium brown, smooth, septate, branched, 2–3 µm diam hyphae. *Conidiophores* integrated, arising as terminal ends of hyphae, with *conidiogenous cells* integrated, subcylindrical, medium brown, smooth, 5–10 × 2–2.5 µm. *Conidia* arranged in branched, erect chains. *Ramoconidia* fusoid-ellipsoid or subcylindrical, 0–1-septate, medium brown, finely verruculose, 11–20 × 3–5 µm. *Conidia* fusoid-ellipsoid, medium brown, finely verruculose, medianly (0–)1(–2)-septate, (10–)12–15(–20) × (2.5–)3–4 µm; hila thickened, darkened, and refractive, 1.5–2 µm diam.

Culture characteristics — Colonies erumpent, spreading, with moderate aerial mycelium and smooth, lobate margins, reaching 8 mm diam after 2 wk at 25 °C. On MEA, PDA and OA surface brown vinaceous, reverse chestnut, with diffuse vinaceous pigment in agar.

Typus. Australia, New South Wales, Nullica State Forest, on *Xanthorrhoea* sp. (*Asphodelaceae*), 29 Nov. 2016, *P.W. Crous* (holotype CBS H-23300, culture ex-type CPC 32432 = CBS 143398, ITS and LSU sequences GenBank MG386061 and MG386114, MycoBank MB823409); additional culture CPC 32714, ITS and LSU sequences GenBank MG386062 and MG386115.

Colour illustrations. Dead leaves of *Xanthorrhoea* sp.; conidiophores sporulating on PNA, conidiophores and conidia. Scale bars = 10 µm.

Notes — *Cladoriella* was established to accommodate a cladosporium-like genus occurring on *Eucalyptus* leaf litter in South Africa (Crous et al. 2006). Of the species presently known, *C. xanthorrhoeae* (conidia fusoid-ellipsoid, (0–)1(–2)-septate, (10–)12–15(–20) × (2.5–)3–4 µm) is related to, but distinct from *C. rubrigena* (conidia 0–1-septate, (11–)14–17(–20) × 3.5–4.2 µm) and *C. eucalypti* (conidia 1–3-septate, (8–)15–20(–25) × 2–2.5(–3) µm; Cheewangkoon et al. 2009). This is the first record of a species of *Cladoriella* occurring on a host other than *Eucalyptus*.

Based on a megablast search using the ITS sequence, the closest matches in NCBIs GenBank nucleotide database were *C. rubrigena* (GenBank GQ303273; Identities 498/552 (90 %), 15 gaps (2 %)), *C. eucalypti* (GenBank EU040224; Identities 485/537 (90 %), 15 gaps (2 %)) and *C. paleospora* (GenBank NR_132833; Identities 309/360 (86 %), 12 gaps (3 %)). The highest similarities using the LSU sequence were *C. rubrigena* (GenBank GQ303304; Identities 837/851 (98 %), 2 gaps (0 %)), *C. eucalypti* (GenBank EU040224; Identities 831/846 (98 %), 2 gaps (0 %)) and *Kellermania micranthae* (GenBank NG_042706; Identities 792/853 (93 %), 16 gaps (1 %)).

Pedro W. Crous & Johannes Z. Groenewald, Westerdijk Fungal Biodiversity Institute, P.O. Box 85167,
3508 AD Utrecht, The Netherlands; e-mail: p.crous@westerdijkinstitute.nl & e.groenewald@westerdijkinstitute.nl
Michael J. Wingfield, Forestry and Agricultural Biotechnology Institute (FABI), University of Pretoria, Pretoria 0002, South Africa;
e-mail: mike.wingfield@fabi.up.ac.za
Brett A. Summerell, Royal Botanic Gardens and Domain Trust, Mrs. Macquaries Road, Sydney, NSW 2000, Australia;
e-mail: brett.summerell@rbgsyd.nsw.gov.au
Angus J. Carnegie, Forest Health & Biosecurity, NSW Department of Primary Industries, Level 12, 10 Valentine Ave,
Parramatta, NSW 2150, Locked Bag 5123, Parramatta, NSW 2124, Australia; e-mail: angus.carnegie@dpi.nsw.gov.au


Alfaria dandenongensis

Fungal Planet 693 – 20 December 2017

Alfaria dandenongensis Crous, *sp. nov.*

Etymology. Name refers to the Dandenong Ranges, Australia, where this fungus was collected.

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

Conidiomata sporodochial, black with slimy conidial masses, surrounded by dark brown setae; conidiomata up to 300 µm diam, basal stroma of hyaline *textura epidermoidea*, giving rise to a dense complex of conidiophores and setae. *Setae* flexuous, surrounding sporodochium, unbranched, thick-walled, apex obtuse, dark brown, verruculose to warty, multiseptate, 100–200 × 6–9 µm. *Conidiophores* densely aggregated, arising from hyaline basal stroma, becoming pigmented and verruculose towards conidiogenous region, subcylindrical, 2–5-septate, branched, 25–60 × 3–4 µm. *Conidiogenous cells* integrated, terminal and lateral, subcylindrical, becoming pigmented and verruculose at upper region, proliferating percurrently, 10–17 × 3–4 µm. *Conidia* solitary, cylindrical, straight, apex subobtuse, base truncate, 1–1.5 µm diam, aseptate, guttulate, granular, verruculose, olivaceous brown, (8–)9–11(–12) × (2–)2.5–3 µm.

Culture characteristics — Colonies erumpent, spreading, with moderate aerial mycelium and smooth, lobate margins, reaching 40 mm diam after 2 wk at 25 °C. On MEA surface dirty white, reverse amber. On PDA surface and reverse pale luteous. On OA surface pale luteous.

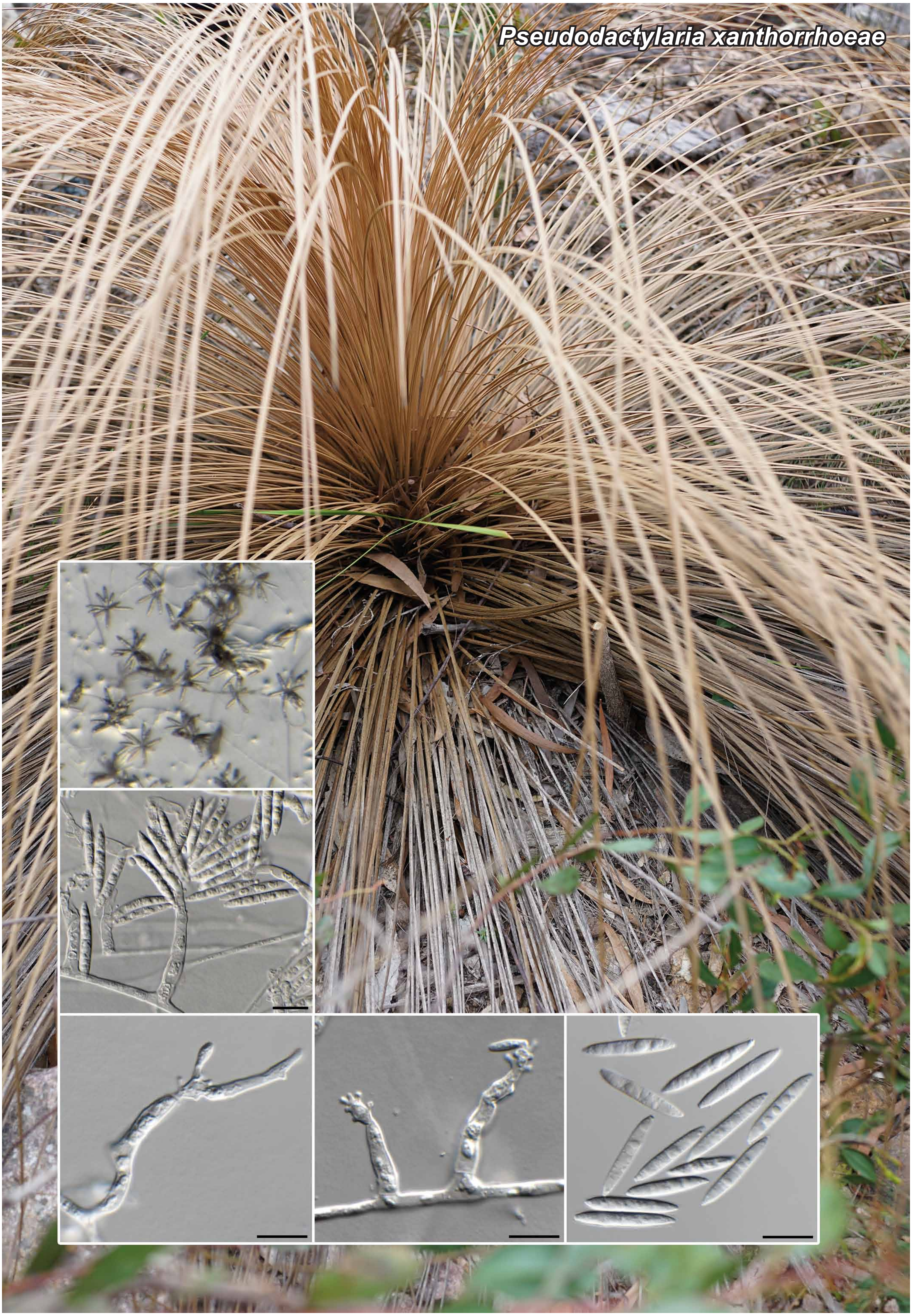
Typus. Australia, Victoria, Melbourne, Dandenong Ranges, Silvan Reservoir Park, leaf litter of *Cyperaceae*, 1 Dec. 2016, *P.W. Crous* (holotype CBS H-23301, culture ex-type CPC 32450 = CBS 143399, ITS, LSU, *cmdA* and *rpb2* sequences GenBank MG386063, MG386116, MG386135 and MG386146, MycoBank MB823410).

Notes — *Alfaria* was originally established for a genus of ascomycetes causing a disease on *Cyperus esculentus* in Spain (Crous et al. 2014a). In a subsequent study, Lombard et al. (2016) added several species which are phylogenetically related to *A. dandenongensis* (conidia (8–)9–11(–12) × (2–)2.5–3 µm), namely *A. ossiformis* (conidia 5–7 × 2–3 µm) and *A. putrefolia* (cultures sterile; Lombard et al. 2016). Phylogenetically, however, *A. dandenongensis* is also distinct from other taxa in the genus.

Based on a megablast search using the ITS sequence, the closest matches in NCBIs GenBank nucleotide database were *A. putrefolia* (GenBank KU845985; Identities 562/568 (99 %), 1 gap (0 %)), *Xepiculopsis graminea* (as *Myrothecium gramineum*; GenBank JX406554; Identities 496/504 (98 %), 2 gaps (0 %)) and *A. ossiformis* (GenBank NR_145068; Identities 561/572 (98 %), 4 gaps (0 %)). The highest similarities using the LSU sequence were *A. ossiformis* (GenBank KU845993; Identities 822/822 (100 %), no gaps), *A. terrestris* (GenBank KU845996; Identities 821/822 (99 %), no gaps) and *A. putrefolia* (GenBank KU845995; Identities 817/822 (99 %), 1 gap (0 %)). The highest similarities using the *cmdA* sequence were with *A. ossiformis* (GenBank KU845977; Identities 443/503 (88 %), 9 gaps (1 %)), *A. terrestris* (GenBank KU845978; Identities 401/443 (91 %), 6 gaps (1 %)) and *A. thymi* (GenBank KU845981; Identities 386/430 (90 %), 8 gaps (1 %)). The highest similarities using the *rpb2* sequence were *A. putrefolia* (GenBank KU846003; Identities 688/724 (95 %), no gaps), *A. ossiformis* (GenBank KU846002; Identities 667/724 (92 %), no gaps) and *A. terrestris* (GenBank KU846005; Identities 643/720 (89 %), 2 gaps (0 %)).

Colour illustrations. Silvan Reservoir Park; conidiomata sporulating on OA, setae, conidiophores, conidiogenous cells and conidia. Scale bars = 10 µm.

Pedro W. Crous & Johannes Z. Groenewald, Westerdijk Fungal Biodiversity Institute, P.O. Box 85167,
3508 AD Utrecht, The Netherlands; e-mail: p.crous@westerdijkinstitute.nl & e.groenewald@westerdijkinstitute.nl
Michael J. Wingfield, Forestry and Agricultural Biotechnology Institute (FABI), University of Pretoria, Pretoria 0002, South Africa;
e-mail: mike.wingfield@fabi.up.ac.za
David Smith, Agriculture, Energy & Resources, Agriculture and Rural Division, Department of Economic Development, Jobs, Transport and Resources,
Unit 3, 2 Codrington St, Cranbourne Victoria 3977, Australia; e-mail: david.smith@ecodev.vic.gov.au


Pseudodactylaria xanthorrhoeae

Fungal Planet 694 – 20 December 2017

Pseudodactylariales Crous, *ord. nov*.

MycoBank MB823468.

Pseudodactylariaceae Crous, *fam. nov.*

MycoBank MB823469.

Classification — *Pseudodactylariaceae*, *Pseudodactylariales*, *Sordariomycetes.*

The diagnosis of the order *Pseudodactylariales* and family *Pseudodactylariaceae* is based on the type genus, *Pseudodactylaria.*

Type genus. *Pseudodactylaria* Crous.

Pseudodactylaria Crous, *gen. nov.*

Etymology. Name refers to its morphological similarity to the genus *Dactylaria*.

Mycelium consisting of hyaline, smooth, branched, septate hyphae. *Conidiophores* erect, hyaline, smooth, subcylindrical, straight to flexuous, unbranched, thick-walled, septate. *Conidiogenous cells* terminal, integrated, subcylindrical with apical taper; apical part forming a rachis with numerous aggregated cylindrical denticles; scars cicatrized, not thickened nor darkened, refractive if viewed from above. *Conidia* solitary, aggregating in slimy mass, fusoid-ellipsoid, hyaline, smooth, surrounded by a thin mucilaginous sheath, prominently guttulate, medianly 1-septate, apex subobtuse, base truncate, somewhat refractive.

Type species. *Pseudodactylaria xanthorrhoeae* Crous.
MycoBank MB823411.

Pseudodactylaria xanthorrhoeae Crous, *sp. nov.*

Etymology. Name refers to *Xanthorrhoea*, the host genus from which this fungus was collected.

Mycelium consisting of hyaline, smooth, branched, septate, 2–3 µm diam hyphae. *Conidiophores* erect, hyaline, smooth, subcylindrical, straight to flexuous, unbranched, thick-walled, 1–3-septate, 20–50 × 4–5 µm. *Conidiogenous cells* terminal, integrated, subcylindrical with apical taper, 15–30 × 3–4 µm; apical part forming a rachis with numerous aggregated cylindrical denticles, 1–3 × 1 µm; scars cicatrized, not thickened nor darkened, refractive if viewed from above. *Conidia* solitary, aggregating in slimy mass, fusoid-ellipsoid, hyaline, smooth, surrounded by a thin mucilaginous sheath, prominently guttulate, medianly 1-septate, apex subobtuse, base truncate, 1–1.5 µm diam, somewhat refractive, (20–)22–27(–33) × (3–)3.5(–4) µm.

Culture characteristics — Colonies erumpent, spreading, surface folded, with moderate aerial mycelium and smooth, lobate margins, reaching 20 mm diam after 2 wk at 25 °C. On MEA and PDA surface amber to isabelline, reverse isabelline. On OA surface amber to isabelline, reverse hazel.

Typus. Australia, New South Wales, Nullica State Forest, on *Xanthorrhoea* sp. (*Asphodelaceae*), 29 Nov. 2016, *P.W. Crous* (holotype CBS H-23302, culture ex-type CPC 32430 = CBS 143414, ITS and LSU sequences GenBank MG386064 and MG386117, MycoBank MB823412); additional culture CPC 32714.

Colour illustrations. Dead leaves of *Xanthorrhoea* sp.; conidiophores sporulating on PNA, conidiophores and conidia. Scale bars = 10 µm.

Notes — *Pseudodactylaria* resembles species of *Dactylaria* (hyaline conidiophores and septate, hyaline conidia formed on denticles; De Hoog 1985), but can be distinguished by having 1-septate conidia encased in a mucoid sheath, which is absent in species of *Dactylaria* s.str. Furthermore, *Pseudodactylaria* represents an undescribed family and order, which are also introduced here as *Pseudodactylariaceae* and *Pseudodactylariales*, respectively.

Based on a megablast search using the ITS sequence, the closest matches in NCBIs GenBank nucleotide database were distant hits with unidentified *Sordariomycetes* and *Pseudobotrytis terrestris* (GenBank KF733463; Identities 496/562 (88 %), 18 gaps (3 %)), *Cercophora solaris* (GenBank KX171948; Identities 498/566 (88 %), 25 gaps (4 %)) and *Cercophora sulphurella* (GenBank AY587913; Identities 497/568 (88 %), 25 gaps (4 %)). The highest similarities using the LSU sequence were *Dactylaria hyalotunicata* (GenBank EU107298; Identities 826/835 (99 %), 2 gaps (0 %)), *Melanocarpus albomyces* (GenBank JQ067902; Identities 790/835 (95 %), 2 gaps (0 %)) and *Achaetomium strumarium* (GenBank AY681170; Identities 786/833 (94 %), 3 gaps (0 %)).

Pseudodactylaria hyalotunicata (K.M. Tsuí et al.) Crous, *comb. nov*. — MycoBank MB823413

Basionym. *Dactylaria hyalotunicata* K.M. Tsuí et al., Sydowia 49: 182. 1997.

Pedro W. Crous & Johannes Z. Groenewald, Westerdijk Fungal Biodiversity Institute, P.O. Box 85167,
3508 AD Utrecht, The Netherlands; e-mail: p.crous@westerdijkinstitute.nl & e.groenewald@westerdijkinstitute.nl
Michael J. Wingfield, Forestry and Agricultural Biotechnology Institute (FABI), University of Pretoria, Pretoria 0002, South Africa;
e-mail: mike.wingfield@fabi.up.ac.za
Brett A. Summerell, Royal Botanic Gardens and Domain Trust, Mrs. Macquaries Road, Sydney, NSW 2000, Australia;
e-mail: brett.summerell@rbgsyd.nsw.gov.au
Angus J. Carnegie, Forest Health & Biosecurity, NSW Department of Primary Industries, Level 12, 10 Valentine Ave,
Parramatta, NSW 2150, Locked Bag 5123, Parramatta, NSW 2124, Australia; e-mail: angus.carnegie@dpi.nsw.gov.au


Pilidium anglicum

Fungal Planet 695 – 20 December 2017

Chaetomellales Crous & Denman, *ord. nov.*

MycoBank MB823491.

Classification – *Chaetomellaceae*, *Chaetomellales*, *Leotiomycetes.*

Ascomata apothecial, immersed to erumpent, sessile to substipitate; hymenium plane to convex, whitish, exterior ochraceous to red-brown, hairless or with scattered, long brown setae. *Setae* absent (*Pilidium*) or present (*Chaetomella*), dark brown, thick-walled, septate, smooth, apically subclavate, straight or curled at apex. *Paraphyses* simple, apically branched. *Asci* 8-spored, cylindrical-clavate, with rounded, thick-walled, inamyloid apex. *Ascospores* hyaline, ellipsoid-fusoid, aseptate. Asexual morph dimorphic. *Pycnidial morph* sessile, dark brown to black, usually opening by fissures. *Sporodochial morph* sessile to long-stalked; conidiomata with or without brown setae. *Conidiogenous cells* phialidic. *Conidia* straight to falcate with pointed ends, 0–1-septate. Parasitic or saprobic on leaves, herbaceous stems and fruits of dicots.

Chaetomellaceae Baral, P.R. Johnst. & Rossman, Index Fungorum 225: 1. 2015

Type genus. *Chaetomella* Fuckel.

Notes — Although formerly seen as a family of *Helotiales*, the *Chaetomellaceae* represent a phylogenetically distinct order in the *Leotiomycetes*, presently including the genera *Chaetomella* and *Pilidium*.

Pilidium anglicum Crous & Denman, *sp. nov.*

Etymology. Name refers to the country where this species was collected, England.

Conidiomata pycnidial, globose, medium brown, superficial, solitary, smooth, 200–400 µm diam; wall of 3–4 layers of medium brown *textura angularis. Conidiophores* hyaline, smooth, subcylindrical, branched, 1–2-septate, 15–22 × 2.5–4 µm. *Conidiogenous cells* terminal, hyaline, smooth, subcylindrical, phialidic with periclinal thickening, 10–15 × 1.5–2 µm. *Conidia* hyaline, smooth, aseptate, guttulate, fusiform, falcate, apex acutely rounded, base truncate, 1 µm diam, (12–)13–14(–15) × 1.5(–2) µm.

Culture characteristics — Colonies flat, spreading, surface folded, with moderate aerial mycelium and smooth, lobate margins, reaching 50 mm diam after 2 wk at 25 °C. On MEA surface ochreous in centre, amber in outer zone, with diffuse amber pigment, and reverse chestnut. On PDA surface buff, reverse chestnut. On OA surface buff.

Typus. UK, England, Upton Grey, on leaves of *Eucalyptus* sp. (*Myrtaceae*), 30 Dec. 2016, *P.W. Crous* (holotype CBS H-23303, culture ex-type CPC 32486 = CBS 143402, ITS and LSU sequences GenBank MG386065 and MG386118, MycoBank MB823414).

Colour illustrations. Upton Grey; conidiomata sporulating on banana leaf agar, conidiogenous cells and conidia. Scale bars = 10 µm.

Notes — *Pilidium* (*Hainesia* synasexual morphs, and *Discohainesia* sexual morphs) was recently treated by Rossman et al. (2004) and Marin-Felix et al. (2017). *Pilidium anglicum* is phylogenetically closely related to *P. acerinum* (conidia 8.5–14.5 × 1.5–2.5 µm; Rossman et al. 2004) and *P. eucalyptorum* (conidia 5–8 × 1.5–2.5 µm; Crous et al. 2015c), though these species have smaller conidia than those of *P. anglicum* (conidia 12–15 × 1.5–2 µm).

Based on a megablast search using the ITS sequence, the closest matches in NCBIs GenBank nucleotide database were *P. acerinum* (GenBank NR_119500; Identities 461/471 (98 %), 2 gaps (0 %)), *P. concavum* (GenBank AY487094; Identities 452/470 (96 %), 3 gaps (0 %)) and *P. eucalyptorum* (GenBank KT950854; Identities 448/465 (96 %), 1 gaps (0 %)). The highest similarities using the LSU sequence were *P. acerinum* (GenBank AY487092; Identities 833/841 (99 %), no gaps), *P. eucalyptorum* (GenBank KT950868; Identities 789/798 (99 %), no gaps) and *P. concavum* (GenBank KF255414; Identities 824/847 (99 %), no gaps).

Pedro W. Crous & Johannes Z. Groenewald, Westerdijk Fungal Biodiversity Institute, P.O. Box 85167,
3508 AD Utrecht, The Netherlands; e-mail: p.crous@westerdijkinstitute.nl & e.groenewald@westerdijkinstitute.nl
Sandra Denman, Forest Research, Alice Holt Lodge, Farnham, GU10 4LH, Surrey, UK; e-mail: Sandra.Denman@forestry.gsi.gov.uk


Sympoventuria regnans

Fungal Planet 696 – 20 December 2017

Sympoventuria regnans Crous, *sp. nov.*

Etymology. Name refers to *Eucalyptus regnans*, the host species from which this fungus was collected.

Classification — *Sympoventuriaceae*, *Venturiales*, *Dothideomycetes.*

Mycelium consisting of smooth, pale brown, septate, branched, 2–3 µm diam hyphae. *Conidiophores* erect, subcylindrical, medium brown, smooth, mostly unbranched, 0–2-septate, 7–25 × 3–4 µm. *Conidiogenous cells* terminal, subcylindrical, medium brown, smooth, 10–17 × 3–4 µm; apex with one to several sympodial loci, thickened, darkened, somewhat refractive, 1 µm diam. *Conidia* occurring in long chains, rarely branched. *Ramoconidia* uncommon, medium brown, smooth, fusoid-ellipsoid to subcylindrical, 0–1-septate, 10–20 × 3–4 µm. *Conidia* medium brown, smooth, guttulate, fusoid-ellipsoid, 0–1-septate, (8–)10–15(–20) × (2.5–)3 µm.

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

Typus. AUSTRALIA, Victoria, La Trobe State Forest, on leaves of *Eucalyptus regnans* (*Myrtaceae*), 30 Nov. 2016, *P.W. Crous* (holotype CBS H-23304, culture ex-type CPC 32720 = CBS 143411, ITS, LSU and *tub2* sequences GenBank MG386066, MG386119 and MG386169, MycoBank MB823415).

Notes — *Sympoventuria regnans* is phylogenetically closely related to *Fusicladium eucalypticola* (on *Eucalyptus robusta*, La Réunion, conidia fusoid-ellipsoid, (5–)7–10(–12) × (2.5–)3(–4) µm; Crous et al. 2016b) and *F. eucalypti* (on *Eucalyptus* sp., Queensland, Australia, conidia (7–)8–9(–10) × (2–)2.5(–3) µm; Crous et al. 2010), but can be distinguished based on its larger conidia (8–20 × 2.5–3 µm). Further studies are presently underway to address the taxonomy of the genus *Sympoventuria*.

Based on a megablast search using the ITS sequence, the closest matches in NCBIs GenBank nucleotide database were *Fusicladium eucalypti* (GenBank HQ599600; Identities 560/584 (96 %), 5 gaps (0 %)), *Fusicladium eucalypticola* (GenBank NR_145402; Identities 517/538 (96 %), 4 gaps (0 %)) and *Fusicladium africanum* (GenBank EU035424; Identities 483/597 (81 %), 31 gaps (5 %)). The highest similarities using the LSU sequence were *Fusicladium eucalypticola* (GenBank KX228329; Identities 841/852 (99 %), 1 gap (0 %)), *Fusicladium eucalypti* (GenBank HQ599601; Identities 840/852 (99 %), 1 gap (0 %)) and *Fusicladium africanum* (GenBank EU035424; Identities 797/853 (93 %), 2 gaps (0 %)). No significant hits were found when the *tub2* sequence was used in a blast search.

Colour illustrations. *Eucalyptus regnans* at La Trobe State Forest; conidiophores sporulating on PNA, and conidia. Scale bars = 10 µm.

Pedro W. Crous & Johannes Z. Groenewald, Westerdijk Fungal Biodiversity Institute, P.O. Box 85167,
3508 AD Utrecht, The Netherlands; e-mail: p.crous@westerdijkinstitute.nl & e.groenewald@westerdijkinstitute.nl
Michael J. Wingfield, Forestry and Agricultural Biotechnology Institute (FABI), University of Pretoria, Pretoria 0002, South Africa;
e-mail: mike.wingfield@fabi.up.ac.za
Brett A. Summerell, Royal Botanic Gardens and Domain Trust, Mrs. Macquaries Road, Sydney, NSW 2000, Australia;
e-mail: brett.summerell@rbgsyd.nsw.gov.au
Angus J. Carnegie, Forest Health & Biosecurity, NSW Department of Primary Industries, Level 12, 10 Valentine Ave,
Parramatta, NSW 2150, Locked Bag 5123, Parramatta, NSW 2124, Australia; e-mail: angus.carnegie@dpi.nsw.gov.au


Stagonospora lomandrae

Fungal Planet 697 – 20 December 2017

Stagonospora lomandrae Crous, *sp. nov.*

Etymology. Name refers to *Lomandra*, the host genus from which this fungus was collected.

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

Conidiomata immersed, pycnidial, 200–300 µm diam, globose, brown, with central ostiole, 30–40 µm diam, substomatal; wall of 3–4 layers of brown *textura angularis. Conidiophores* reduced to conidiogenous cells lining the inner cavity, hyaline, smooth, ampulliform, phialidic with percurrent proliferation at apex, 8–12 × 4–6 µm. *Conidia* (18–)19–21(–22) × (5–)6 µm, solitary, hyaline, smooth, prominently guttulate, subcylindrical, straight, apex obtuse, base truncate, 2 µm diam, 2-septate, with a septum a third in from each end. *Microconidia* in same conidioma, hyaline, smooth, guttulate, ellipsoid, apex obtuse, base truncate. *Ascomata* similar to conidiomata in anatomy. *Pseudoparaphyses* intermingled among asci, hyaline, smooth, septate, branched, hyphae-like, 2–3 µm diam, constricted at septa. *Asci* 8-spored, bitunicate, fissitunicate, narrowly ellipsoid to slightly clavate, 60–80 × 15–17 µm. *Ascospores* triseriate, fusoid-ellipsoid, hyaline to pale brown with thin mucoid sheath, constricted at median septum, developing two additional septa in apical cell (which is swollen and wider than basal cell), and one septum in basal cell, (18–)20–25(–27) × (5–)7(–8) µm.

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

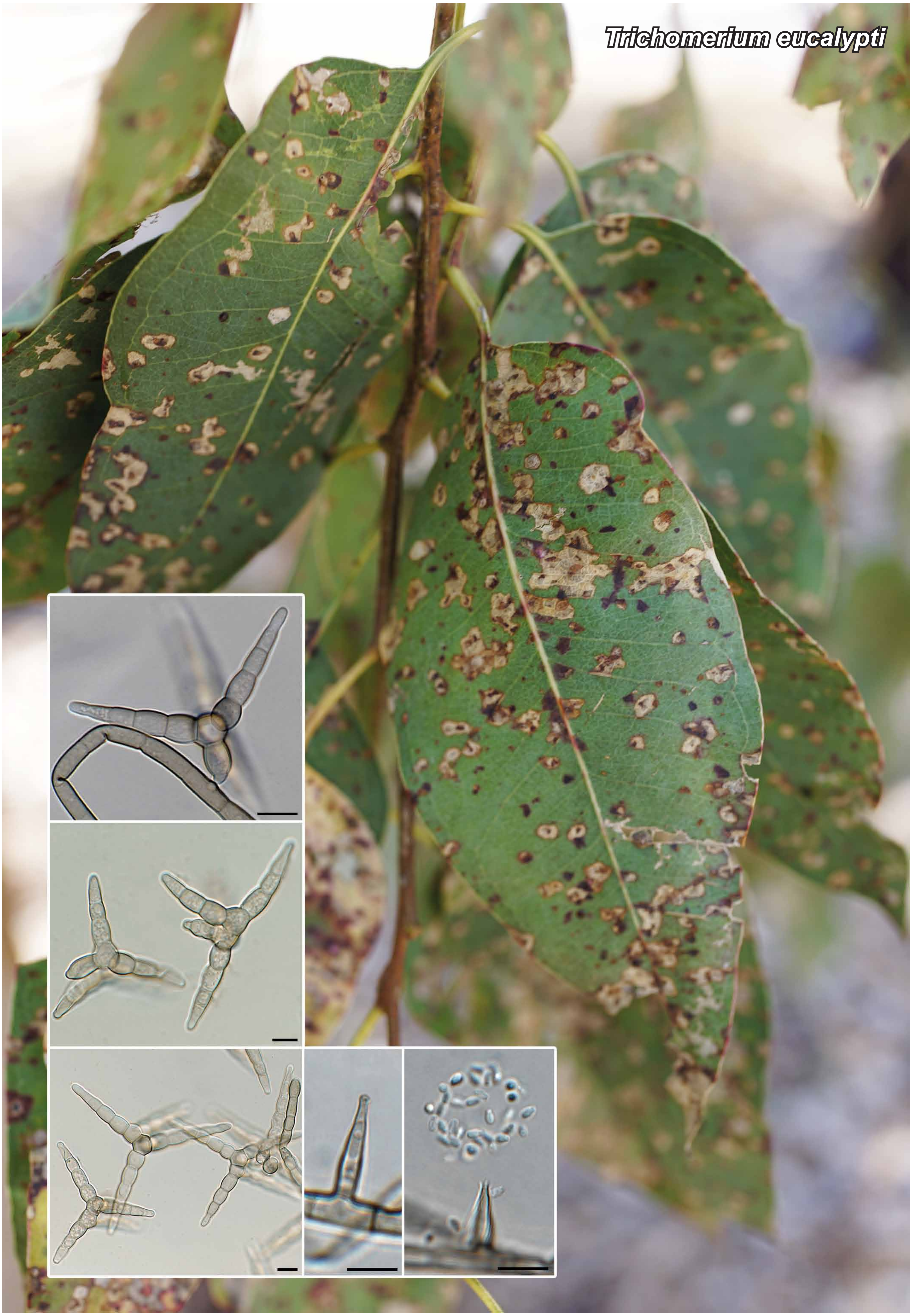
Typus. Australia, New South Wales, Sussex Inlet, on leaves of *Lomandra longifolia* (*Asparagaceae*), 27 Nov. 2016, *P.W. Crous* (holotype CBS H-23307, culture ex-type CPC 32073 = CBS 143447, ITS, LSU, *rpb2* and *tef1* sequences GenBank MG386067, MG386120, MG386147 and MG386156, MycoBank MB823416).

Colour illustrations. *Lomandra longifolia* at Sussex Inlet; ascomata sporulating on OA, asci and pseudoparaphyses, conidiogenous cells and conidia. Scale bars = 10 µm.

Notes — *Stagonospora* was revised by Quaedvlieg et al. (2013). *Stagonospora lomandrae* is phylogenetically related to *S. pseudoperfecta* (ascospores 21–30.5 × 5–7 µm, 1-septate, with mucoid sheath, conidia aseptate, 21.5–26 × 4–5.5 µm; Tanaka et al. 2015) and *S. trichophoricola* (conidia 1–3(–4)-septate, (12–)18–22(–25) × 4(–5) µm; Crous et al. 2014a), but is morphologically and phylogenetically distinct.

Based on a megablast search using the ITS sequence, the closest matches in NCBIs GenBank nucleotide database were *Stagonospora bicolor* (as *Saccharicola bicolor*; GenBank KP117300; Identities 485/497 (98 %), 4 gaps (0 %)), *S. trichophoricola* (GenBank KJ869110; Identities 518/531 (98 %), 4 gaps (0 %)) and *S. pseudoperfecta* (GenBank AB809641; Identities 485/499 (97 %), 3 gaps (0 %)). The highest similarities using the LSU sequence *S. forlicesenensis* (GenBank KX655547; Identities 854/857 (99 %), no gaps), *S. pseudoperfecta* (GenBank AB807577; Identities 845/849 (99 %), no gaps) and *S. trichophoricola* (GenBank KJ869168; Identities 836/840 (99 %), no gaps). The highest similarities using the *rpb2* sequence were distant hits with *Neottiosporina paspali* (GenBank GU371779; Identities 749/848 (88 %), 1 gap (0 %)), *Helminthosporium microsorum* (GenBank KY984390; Identities 718/848 (85 %), no gaps) and *H. quercinum* (GenBank KY984398; Identities 712/848 (84 %), no gaps). The highest similarities using the *tef1* sequence were distant hits with *H. oligosporum* (GenBank KY984451; Identities 226/269 (84 %), 12 gaps (4 %)), *H. tiliae* (GenBank KY984457; Identities 224/269 (83 %), 12 gaps (4 %)) and *H. quercinum* (GenBank KY984454; Identities 219/267 (82 %), 13 gaps (4 %)).

Pedro W. Crous & Johannes Z. Groenewald, Westerdijk Fungal Biodiversity Institute, P.O. Box 85167,
3508 AD Utrecht, The Netherlands; e-mail: p.crous@westerdijkinstitute.nl & e.groenewald@westerdijkinstitute.nl
Michael J. Wingfield, Forestry and Agricultural Biotechnology Institute (FABI), University of Pretoria, Pretoria 0002, South Africa;
e-mail: mike.wingfield@fabi.up.ac.za
Brett A. Summerell, Royal Botanic Gardens and Domain Trust, Mrs. Macquaries Road, Sydney, NSW 2000, Australia;
e-mail: brett.summerell@rbgsyd.nsw.gov.au
Angus J. Carnegie, Forest Health & Biosecurity, NSW Department of Primary Industries, Level 12, 10 Valentine Ave,
Parramatta, NSW 2150, Locked Bag 5123, Parramatta, NSW 2124, Australia; e-mail: angus.carnegie@dpi.nsw.gov.au


Trichomerium eucalypti

Fungal Planet 698 – 20 December 2017

Trichomerium eucalypti Crous, *sp. nov.*

Etymology. Name refers to *Eucalyptus*, the host genus from which this fungus was collected.

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

Mycelium consisting of smooth, branched, septate, 4–5 µm diam, brown hyphae. *Conidiophores* reduced to conidiogenous loci on hyphae, inconspicuous, 1–5 × 2 µm, not thickened nor darkened. *Conidia* solitary, medium brown, smooth, guttulate, star-shaped, with two globose central cells giving rise to four irregular radiating arms of 4–5(–7) cells, tapering from point of attachment to subobtuse apices, constricted at septa, 30–80 × 8–10 µm; conidia also have a fifth branch of 1–2 cells tapering to a subobtuse apex, 15–30 × 7–8 µm, which is the branch that attaches to the conidiogenous locus on hyphae. *Microconidiogenous cells* on hyphae solitary, ampulliform, medium brown, smooth, phialidic, 10–17 × 3–4 µm. *Microconidia* bacilliform, hyaline, smooth, aseptate, ends rounded, 2–3 × 2 µm.

Culture characteristics — Colonies erumpent, spreading, with moderate aerial mycelium and even, lobate margins, reaching 10–20 mm diam after 2 wk at 25 °C. On MEA, PDA and OA surface olivaceous grey, reverse iron-grey.

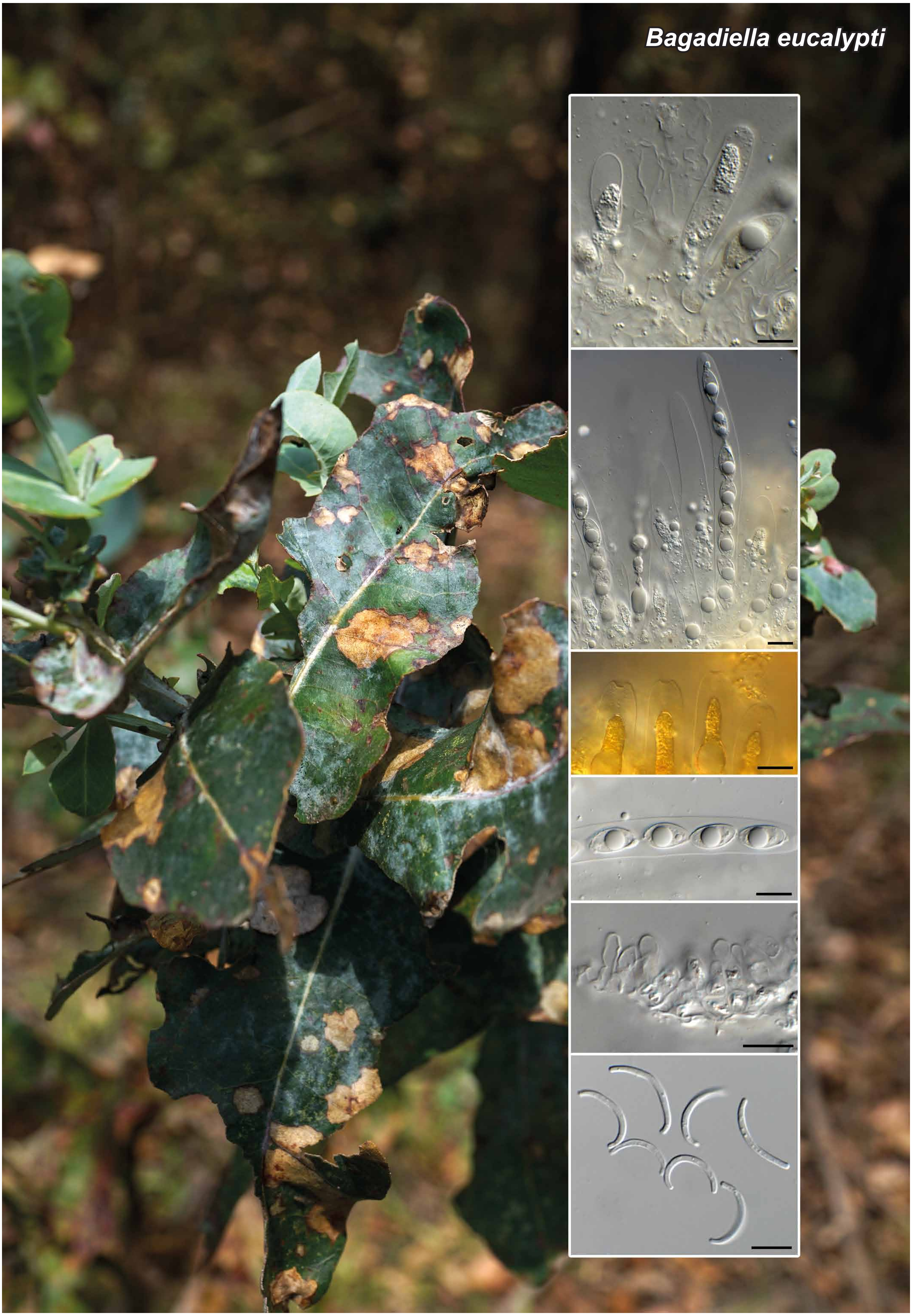
Typus. Australia, New South Wales, Australian Botanical Garden, Mount Annan, on leaves of *Eucalyptus tereticornis* (*Myrtaceae*), 25 Nov. 2016, *P.W. Crous* (holotype CBS H-23309, culture ex-type CPC 32199 = CBS 143443, ITS and LSU sequences GenBank MG386068 and MG386121, MycoBank MB823417).

Notes — Species of *Trichomerium* are usually encountered as sooty molds that grow on honey dew excrements from insects on living plant leaves and stems. The genus *Trichomerium* has *Tripospermum* asexual morphs (Crous et al. 2014b).

Based on a megablast search using the ITS sequence, the closest matches in NCBIs GenBank nucleotide database were '*Trimmatostroma*' *cordae* (GenBank AJ244263; Identities 591/607 (97 %), 9 gaps (1 %)), *Trichomerium foliicola* (GenBank JX313653; Identities 611/659 (93 %), 13 gaps (1 %)) and *T. gleosporum* (GenBank JX313656; Identities 610/659 (93 %), 13 gaps (1 %)). The highest similarities using the LSU sequence were *T. foliicola* (GenBank JX313659; Identities 830/846 (98 %), no gaps), *T. gloeosporum* (GenBank KY381953; Identities 823/839 (98 %), no gaps) and *T. dioscoreae* (GenBank KP004496; Identities 834/851 (98 %), no gaps).

Colour illustrations. Symptomatic leaves of *Eucalyptus tereticornis*; *Trichomerium* conidia, microconidiogenous cells and microconidia. 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@westerdijkinstitute.nl & e.groenewald@westerdijkinstitute.nl
Michael J. Wingfield, Forestry and Agricultural Biotechnology Institute (FABI), University of Pretoria, Pretoria 0002, South Africa;
e-mail: mike.wingfield@fabi.up.ac.za
Treena I. Burgess & Giles E.St.J. Hardy, Centre for Phytophthora Science and Management, Murdoch University,
90 South Street, Murdoch, WA 6150, Australia;
e-mail: tburgess@murdoch.edu.au & g-hardy@murdoch.edu.au


Bagadiella eucalypti

Fungal Planet 699 – 20 December 2017

Bagadiella eucalypti Crous, *sp. nov.*

Etymology. Name refers to *Eucalyptus*, the host genus from which this fungus was collected.

Classification — *Clypeophysalospora*, *Xylariales*, *Sordariomycetes.*

Associated with amphigenous, pale brown leaf spots, co-occurring with *Teratosphaeria*. *Mycelium* consisting of pale brown, smooth, septate, branched, 2–3 µm diam hyphae. *Conidiogenous cells* integrated, as terminal ends on hyphae, pale brown, smooth, subcylindrical, 10–17 × 2 µm, monophialidic with flared collarette. *Conidia* solitary, hyaline, smooth, subcylindrical, apex obtuse, base truncate, strongly curved, (12–)14–17(–21) × (1.5–)2 µm. *Ascomata* immersed, globose, not visible on the surface, 150–250 µm diam, with periphysate ostiolar channel; wall of 3–4 layers of medium brown *textura angularis. Asci* 8-spored, cylindrical, unitunicate, apical apparatus reacting in Melzer's reagent, 110–130 × 10–13 µm. *Paraphyses* hyaline, smooth, cellular, intermingled between asci, 4–6 µm diam, constricted at septa, unbranched. *Ascospores* uniseriate, aseptate, guttulate, ellipsoid, ends acutely rounded, smooth, hyaline, (13–)15–16(–18) × (6.5–)7 µm.

Culture characteristics — Colonies flat, spreading, with moderate aerial mycelium and feathery, lobate margins, reaching 30 mm diam after 2 wk at 25 °C. On MEA surface honey to buff, reverse cinnamon. On PDA surface and reverse buff. On OA surface buff.

Typus. Australia, Victoria, Nowa Nowa, on leaves of *Eucalyptus globulus* (*Myrtaceae*), 30 Nov. 2016, *P.W. Crous* (holotype CBS H-23310, culture ex-type CPC 32619 = CBS 143439, ITS and LSU sequences GenBank MG386069 and MG386122, MycoBank MB823418).

Notes — *Bagadiella* was established for a group of endophytic hyphomycetes occurring on leaves of *Eucalyptus* (Cheewangkoon et al. 2009). These fungi are usually observed to start sporulating once leaves are incubated in damp chambers, with conidiophores being associated with pale yellow leaf blotches, although it should be noted that no pathogenicity experiments have as yet been conducted with members of the genus.

Bagadiella eucalypti is related to other species of the genus, but is phylogenetically distinct. The present taxon also represents the first report of a sexual morph for *Bagadiella*, showing it to be related to genera such as *Neophysalospora*, *Clypeophysalospora* and *Paraphysalospora* (Crous et al. 2014b, Giraldo et al. 2017).

Based on a megablast search using the ITS sequence, the closest matches in NCBIs GenBank nucleotide database were *Bagadiella lunata* (GenBank NR_132832; Identities 588/600 (98 %), 2 gaps (0 %)), *B. koalae* (GenBank JF951142; Identities 586/601 (98 %), 3 gaps (0 %)) and *B. victoriae* (GenBank JF951141; Identities 584/604 (97 %), 5 gaps (0 %)). The highest similarities using the LSU sequence were *B. lunata* (GenBank GQ303300; Identities 844/848 (99 %), no gaps), *B. koalae* (GenBank JF951162; Identities 842/847 (99 %), no gaps) and *B. victoriae* (GenBank JF951161; Identities 842/848 (99 %), no gaps).

Colour illustrations. Symptomatic leaves of *Eucalyptus globulus*; asci and ascospores, conidiogenous cells and conidia. Scale bars = 10 µm.

Pedro W. Crous & Johannes Z. Groenewald, Westerdijk Fungal Biodiversity Institute, P.O. Box 85167,
3508 AD Utrecht, The Netherlands; e-mail: p.crous@westerdijkinstitute.nl & e.groenewald@westerdijkinstitute.nl
Michael J. Wingfield, Forestry and Agricultural Biotechnology Institute (FABI), University of Pretoria, Pretoria 0002, South Africa;
e-mail: mike.wingfield@fabi.up.ac.za
Brett A. Summerell, Royal Botanic Gardens and Domain Trust, Mrs. Macquaries Road, Sydney, NSW 2000, Australia;
e-mail: brett.summerell@rbgsyd.nsw.gov.au
Angus J. Carnegie, Forest Health & Biosecurity, NSW Department of Primary Industries, Level 12, 10 Valentine Ave,
Parramatta, NSW 2150, Locked Bag 5123, Parramatta, NSW 2124, Australia; e-mail: angus.carnegie@dpi.nsw.gov.au


Vermiculariopsiella eucalypticola

Fungal Planet 700 – 20 December 2017

Vermiculariopsiella eucalypticola Crous, *sp. nov.*

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

Classification — *Vermiculariopsiellaceae*, *Vermiculariopsiellales*, *Sordariomycetes.*

Conidiomata sporodochial, 200–500 µm diam, with slimy creamy conidial mass, base of pale brown pseudoparenchymatal cells, giving rise to densely aggregated conidiophores. *Setae* dispersed throughout sporodochia, thick-walled, brown, verruculose, branched at apex, initially dichotomously branched, appearing heart-shaped, with additional branches developing with age, 150–400 × 6–11 µm. *Conidiophores* subcylindrical, pale brown, verruculose, 0–1-septate, branched at first septum, 14–20 × 4–5 µm. *Conidiogenous cells* terminal and intercalary, ampulliform, pale brown, verruculose, phialidic, apex twisted to the side, periclinal thickening and collarette present, 10–15 × 3–3.5 µm. *Conidia* solitary, aseptate, hyaline, smooth, guttulate, subcylindrical to fusoid, inequilateral, inner plane straight, outer plane convex, apex subobtuse, but constricted towards inner plane, base truncate, hilum excentric, 0.5–1 µm diam, (9–)12–14(–16) × (2–)2.5 µm.

Culture characteristics — Colonies flat, spreading, with sparse aerial mycelium and feathery, lobate margins, reaching 40–50 mm diam after 2 wk at 25 °C. On MEA surface hazel, reverse amber. On PDA surface and reverse rosy buff. On OA surface hazel.

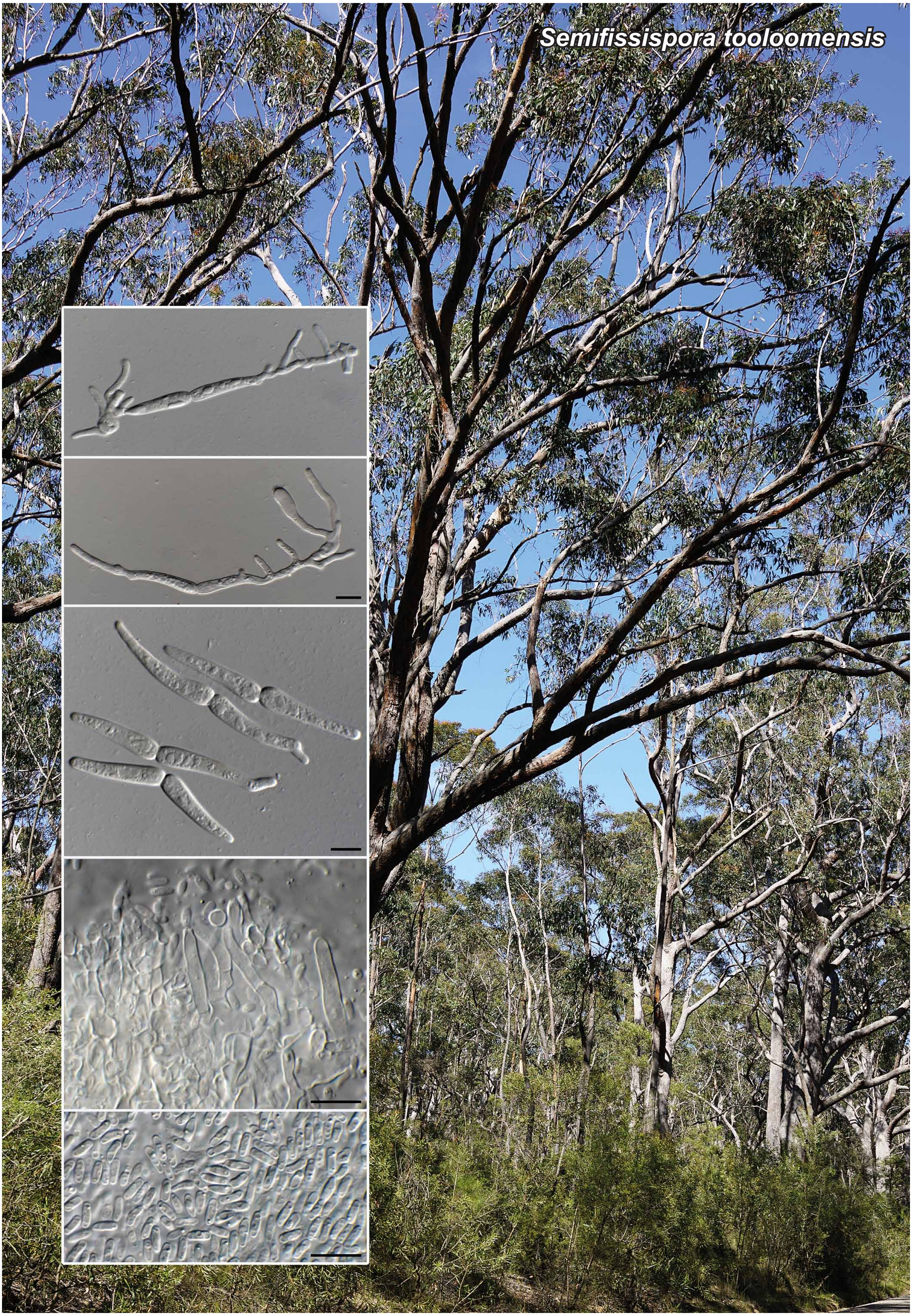
Typus. AUSTRALIA, New South Wales, South East Forests National Park, on leaves of *Eucalyptus dalrympleana* (*Myrtaceae*), 28 Nov. 2016, *P.W. Crous* (holotype CBS H-23313, culture ex-type CPC 32506 = CBS 143442, ITS and LSU sequences GenBank MG386070 and MG386123, MycoBank MB823419).

Colour illustrations. South East Forests National Park; conidioma sporulating on PNA, setae, conidiogenous cells and conidia. Scale bars = 10 µm.

Notes — *Vermiculariopsiella* has sporodochia with brown, erect setae dispersed throughout, and subhyaline conidiophores that give rise to phialidic conidiogenous cells with prominently curved apices, and hyaline, aseptate conidia. *Vermiculariopsiella eucalypticola* is phylogenetically related to *V. dichapetali* (conidia (10–)17–22(–24) × 2.5(–3) µm, setae erect, straight to flexuous; Crous et al. 2014a), but is morphologically clearly distinct. A unique feature of *V. eucalypticola* are its setae, being dichotomously branched, and therefore more reminiscent of the genus *Gyrothrix* (although the conidiogenesis and conidia are typical of *Vermiculariopsiella*, suggesting that setae are not that informative at the generic level).

Based on a megablast search using the ITS sequence, the closest matches in NCBIs GenBank nucleotide database were *V. dichapetali* (GenBank KX306771; Identities 520/538 (97 %), 5 gaps (0 %)), *V. immersa* (GenBank KY853476; Identities 511/534 (96 %), 1 gaps (0 %)) and *V. acaciae* (GenBank NR_145253; Identities 513/540 (95 %), 12 gaps (2 %)). The highest similarities using the LSU sequence were *V. acaciae* (GenBank KX228314; Identities 840/842 (99 %), no gaps), *V. dichapetali* (GenBank KX306796; Identities 714/716 (99 %), no gaps) and *V. immersa* (GenBank KJ476961; Identities 817/823 (99 %), 3 gaps (0 %)).

Pedro W. Crous & Johannes Z. Groenewald, Westerdijk Fungal Biodiversity Institute, P.O. Box 85167,
3508 AD Utrecht, The Netherlands; e-mail: p.crous@westerdijkinstitute.nl & e.groenewald@westerdijkinstitute.nl
Michael J. Wingfield, Forestry and Agricultural Biotechnology Institute (FABI), University of Pretoria, Pretoria 0002, South Africa;
e-mail: mike.wingfield@fabi.up.ac.za
Brett A. Summerell, Royal Botanic Gardens and Domain Trust, Mrs. Macquaries Road, Sydney, NSW 2000, Australia;
e-mail: brett.summerell@rbgsyd.nsw.gov.au
Angus J. Carnegie, Forest Health & Biosecurity, NSW Department of Primary Industries, Level 12, 10 Valentine Ave,
Parramatta, NSW 2150, Locked Bag 5123, Parramatta, NSW 2124, Australia; e-mail: angus.carnegie@dpi.nsw.gov.au


Semifissispora tooloomensis

Fungal Planet 701 – 20 December 2017

Semifissispora tooloomensis Crous, *sp. nov.*

Etymology. Named after the area where it was collected, close to Tooloom National Park, Australia.

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

Ascospores shot onto MEA. *Ascospores* fusoid-ellipsoid, hyaline, smooth, guttulate, medianly 1-septate, prominently constricted at septum, tapering towards subobtuse apices, apical cell (22–)25–27(–30) × 6(–7) µm, basal cell (22–)27–32(–33) × 6 µm. No mature ascomata could be located in the leaf tissue. On OA forming pale brown sporodochial *conidiomata*, with slimy conidial masses of hyaline conidia. *Conidiophores* hyaline, smooth, subcylindrical, branched, up to 50 µm tall, 3–4 µm diam. *Conidiogenous cells* terminal and intercalary, hyaline, smooth, subcylindrical, phialidic, 10–20 × 2.5–3 µm. *Conidia* solitary, aseptate, hyaline, smooth, subcylindrical, guttulate, apex obtuse, base truncate, 3–6 × 2 µm.

Culture characteristics — Colonies flat, spreading, with sparse aerial mycelium and feathery, lobate margins, reaching 60 mm diam after 2 wk at 25 °C. On MEA surface dirty white, reverse sienna. On PDA surface dirty white, reverse pale luteous. On OA surface dirty white.

Typus. Australia, New South Wales, close to Tooloom National Park, on leaves of *Eucalyptus dunnii*, 20 Jan. 2016, *A.J. Carnegie* (holotype CBS H-23314, culture ex-type CPC 31680 = CBS 143431, ITS, LSU and *gapdh* sequences GenBank MG386071, MG386124 and MG386136, MycoBank MB823420).

Colour illustrations. Tooloom National Park; germinating ascospores, ascospores, conidiophores and conidia. Scale bars = 10 µm.

Notes — *Semifissispora* was established by Swart (1982) for a group of ascomycetes occurring on leaf litter of *Eucalyptus* in Australia, and was recently shown to belong to *Massarinaceae*, *Dothideomycetes* (Crous et al. 2015c). Although assumed to be saprobic, ascomata have also been observed on bleached leaf areas, suggesting taxa could be weakly pathogenic, though no inoculation experiments have been conducted to confirm this. The genus is presently known from four species, namely *S. fusiformis* (apical cells 10–18 × 5–6 µm, basal cells 14–19 × 4–6 µm), *S. rotundata* (apical cells 15–20 × 7–9 µm, basal cells 15–10 × 5.5–7 µm), *S. elongata* (apical cells 18–25 × 4–6 µm, basal cells 22–26 × 3.5–5 µm), *S. natalis* (apical cells 22–28 × 7–10 µm, basal cells 23–31 × 6.5–7.5 µm) (Swart 1982, Crous et al. 2015c). *Semifissispora tooloomensis* can be distinguished from these species based on its ascospore dimensions (apical cells 22–30 × 6–7 µm, basal cell 22–33 × 6 µm).

Based on a megablast search using the ITS sequence, the closest matches in NCBIs GenBank nucleotide database were *S. rotundata* (GenBank KT950847; Identities 517/544 (95 %), 10 gaps (1 %)), *S. natalis* (GenBank NR_145195; Identities 513/548 (94 %), 14 gaps (2 %)) and *Stagonospora pseudopaludosa* (GenBank NR_137840; Identities 488/558 (87 %), 23 gaps (4 %)). The highest similarities using the LSU sequence were *S. rotundata* (GenBank KT950859; Identities 853/858 (99 %), no gaps), *S. natalis* (GenBank KT950858; Identities 837/846 (99 %), no gaps) and *Stagonospora tainanensis* (GenBank AB807580; Identities 824/850 (97 %), 2 gaps (0 %)). The highest similarities using the *gapdh* sequence were with *S. natalis* (GenBank KT950875; Identities 486/526 (92 %), 10 gaps (1 %)), *Curvularia spicifera* (GenBank KT351793; Identities 386/462 (84 %), 6 gaps (1 %)) and *Curvularia trifolii* (GenBank KP645345; Identities 383/461 (83 %), 7 gaps (1 %)).

Pedro W. Crous & Johannes Z. Groenewald, Westerdijk Fungal Biodiversity Institute, P.O. Box 85167,
3508 AD Utrecht, The Netherlands; e-mail: p.crous@westerdijkinstitute.nl & e.groenewald@westerdijkinstitute.nl
Michael J. Wingfield, Forestry and Agricultural Biotechnology Institute (FABI), University of Pretoria, Pretoria 0002, South Africa;
e-mail: mike.wingfield@fabi.up.ac.za
Angus J. Carnegie, Forest Health & Biosecurity, NSW Department of Primary Industries, Level 12, 10 Valentine Ave,
Parramatta, NSW 2150, Locked Bag 5123, Parramatta, NSW 2124, Australia; e-mail: angus.carnegie@dpi.nsw.gov.au


Diaporthe obtusifoliae

Fungal Planet 702 – 20 December 2017

Diaporthe obtusifoliae Crous, *sp. nov.*

Etymology. Named after the host species from which it was isolated, *Acacia obtusifolia*.

Classification — *Diaporthaceae*, *Diaporthales*, *Sordariomycetes*.

Leaf spots amphigenous, medium brown, circular with a raised margin, 1–4 mm diam, coalescing with age to form larger blotches. *Conidiomata* pycnidial, immersed, globose, 180–250 µm diam, medium brown, with central ostiole; wall of 4–6 layers of medium brown *textura angularis. Conidiophores* lining the inner cavity, hyaline, smooth, subcylindrical, branched, 1–2-septate, 25–40 × 4–6 µm. *Conidiogenous cells* terminal and intercalary, subcylindrical with slight apical taper, 10–25 × 3–5 µm; proliferating percurrently near apex. *Conidia* solitary, aseptate, ellipsoid, apex subobtuse, base with truncate hilum, 2 µm diam, slightly thickened and refractive; conidia hyaline, smooth, guttulate, becoming pale brown with age, (12–)14–16(–18) × (6–)6.5–7 µm.

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

Typus. Australia, New South Wales, Gnupa State Forest, on leaves of *Acacia obtusifolia* (*Fabaceae*), 29 Nov. 2016, *P.W. Crous* (holotype CBS H-23318, culture ex-type CPC 32336 = CBS 143449, ITS, LSU and *his3* sequences GenBank MG386072, MG386125 and MG386137, MycoBank MB823421).

Notes — Although *D. obtusifoliae* is morphologically distinct from the typical *Diaporthe* spp. by forming broadly ellipsoid conidia, it clusters within the genus. Based on morphology it is distinct from *D. acaciarum* (on *A. tortilis*, Tanzania, alpha conidia (6–)6.5–7(–7.5) × (2–)2.5(–3) µm; Crous et al. 2014b) and *D. acaciigena* (on *A. retinodes*, Australia, alpha conidia ellipsoid to subclavate, (9–)10–11(–12) × (4–)6–6.5(–7) µm; Crous et al. 2011). It is also distinct from *D. scobina*, to which it is most closely related (Gomes et al. 2013).

Based on a megablast search using the ITS sequence, the closest matches in NCBIs GenBank nucleotide database were *D. acaciigena* (GenBank NR_137113; Identities 538/568 (95 %), 7 gaps (1 %)), *D. scobina* (GenBank KC343195; Identities 534/572 (93 %), 20 gaps (3 %)) and *D. padi* var. *padi* (GenBank KC343170; Identities 531/569 (93 %), 18 gaps (3 %)). The highest similarities using the LSU sequence were *D. perjuncta* (GenBank AF408356; Identities 829/835 (99 %), no gaps), *D. fusicola* (GenBank KY011836; Identities 825/832 (99 %), no gaps) and *D. ovoicicola* (GenBank KY011838; Identities 818/825 (99 %), no gaps). The highest similarities using the *his3* sequence were with *D. acaciigena* (GenBank KC343489; Identities 356/385 (92 %), 13 gaps (3 %)), *D. pustulata* (GenBank KC343671; Identities 349/382 (91 %), 10 gaps (2 %)) and *D. amygdali* (GenBank KP293563; Identities 349/384 (91 %), 10 gaps (2 %)).

Colour illustrations. Symptomatic leaves of *Acacia obtusifolia*; leaf spots, conidiomata sporulating on PDA, conidiophores and conidia. Scale bars = 10 µm.

Pedro W. Crous & Johannes Z. Groenewald, Westerdijk Fungal Biodiversity Institute, P.O. Box 85167,
3508 AD Utrecht, The Netherlands; e-mail: p.crous@westerdijkinstitute.nl & e.groenewald@westerdijkinstitute.nl
Michael J. Wingfield, Forestry and Agricultural Biotechnology Institute (FABI), University of Pretoria, Pretoria 0002, South Africa;
e-mail: mike.wingfield@fabi.up.ac.za
Brett A. Summerell, Royal Botanic Gardens and Domain Trust, Mrs. Macquaries Road, Sydney, NSW 2000, Australia;
e-mail: brett.summerell@rbgsyd.nsw.gov.au
Angus J. Carnegie, Forest Health & Biosecurity, NSW Department of Primary Industries, Level 12, 10 Valentine Ave,
Parramatta, NSW 2150, Locked Bag 5123, Parramatta, NSW 2124, Australia; e-mail: angus.carnegie@dpi.nsw.gov.au


Cladoriella kinglakensis

Fungal Planet 703 – 20 December 2017

Cladoriella kinglakensis Crous, *sp. nov.*

Etymology. Named after Kinglake National Park, Australia.

Classification — *Cladoriellaceae*, *Cladoriellales*, *Dothideomycetes.*

Conidiophores erect, solitary or in fascicles of 3–4, dark brown, smooth, straight to flexuous, mostly unbranched, 2–19-septate, 60–200 × 4–5 µm. *Conidiogenous cells* integrated, terminal and intercalary, subcylindrical, medium brown, smooth, 15–20 × 3–4 µm; scars thickened and darkened, 2 µm diam, proliferating sympodially. *Ramoconidia* medium brown, smooth, guttulate, subcylindrical, 0–1-septate, 15–30 × 3–4 µm. *Conidia* aseptate, in branched chains, medium brown, smooth, guttulate, fusoid-ellipsoid with truncate ends, aseptate, hila thickened and darkened, 2 µm diam, (10–)13–15(–18) × (3–)3.5(–4) µm.

Culture characteristics — Colonies erumpent, spreading, surface folded with moderate aerial mycelium and smooth, lobate margins, reaching 10 mm diam after 2 wk at 25 °C. On MEA and PDA surface olivaceous grey, reverse iron-grey. On OA surface olivaceous grey with diffuse red pigment.

Typus. Australia, Victoria, near Kinglake National Park, on leaves of *Eucalyptus regnans* (*Myrtaceae*), 1 Dec. 2016, *P.W. Crous* (holotype CBS H-23319, culture ex-type CPC 32730 = CBS 143452, ITS and LSU sequences GenBank MG386073 and MG386126, MycoBank MB823422).

Colour illustrations. Symptomatic *Eucalyptus* leaves; conidiophores sporulating on PNA, conidiophores and conidia. Scale bars = 10 µm.

Notes — Several species of *Cladoriella* are known from *Eucalyptus*. Of these, *C. kinglakensis* is related to *C. paleospora* (conidia 0–1-septate, 6–10 × 3.5–4 µm; Cheewangkoon et al. 2009), but is distinct phylogenetically, and also has larger conidia.

Based on a megablast search using the ITS sequence, the closest matches in NCBIs GenBank nucleotide database were *C. paleospora* (GenBank NR_132833; Identities 499/513 (97 %), 4 gaps (0 %)) and *C. eucalypti* (GenBank EU040224; Identities 475/580 (82 %), 56 gaps (9 %)). The highest similarities using the LSU sequence were *C. paleospora* (GenBank GQ303303; Identities 593/603 (98 %), no gaps), *C. rubrigena* (GenBank GQ303304; Identities 791/851 (93 %), 5 gaps (0 %)) and *C. eucalypti* (GenBank EU040224; Identities 784/847 (93 %), 5 gaps (0 %)).

Pedro W. Crous & Johannes Z. Groenewald, Westerdijk Fungal Biodiversity Institute, P.O. Box 85167,
3508 AD Utrecht, The Netherlands; e-mail: p.crous@westerdijkinstitute.nl & e.groenewald@westerdijkinstitute.nl
Michael J. Wingfield, Forestry and Agricultural Biotechnology Institute (FABI), University of Pretoria, Pretoria 0002, South Africa;
e-mail: mike.wingfield@fabi.up.ac.za
David Smith, Agriculture, Energy & Resources, Agriculture and Rural Division, Department of Economic Development, Jobs, Transport and Resources,
Unit 3, 2 Codrington St, Cranbourne Victoria 3977, Australia; e-mail: david.smith@ecodev.vic.gov.au


Phaeosphaeria gahniae

Fungal Planet 704 – 20 December 2017

Phaeosphaeria gahniae Crous, *sp. nov.*

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

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

Ascomata solitary, globose, brown, 180–220 µm diam, with 1–2 papillate ostioles; wall of 6–8 layers of brown *textura angularis*. *Pseudoparaphyses* intermingled among asci, hyaline, septate, branched, cellular, 3–5 µm diam. *Asci* fasciculate, stipitate, subcylindrical, bitunicate with ocular chamber, 1–1.5 µm diam, 60–90 × 9–10 µm. *Ascospores* bi- to triseriate, medium brown, smooth, fusoid-ellipsoid with obtuse ends, guttulate, 3(–4)-septate, second cell from apex slightly swollen, (18–)20–22(–25) × (4.5–)5 µm.

Culture characteristics — Colonies erumpent, spreading, with moderate aerial mycelium and feathery, lobate margins, reaching 40 mm diam after 2 wk at 25 °C. On MEA surface olivaceous grey, reverse grey olivaceous with patches of saffron. On PDA surface dirty white, reverse pale luteous. On OA surface saffron.

Typus. Australia, Victoria, Royal Botanic Gardens Victoria, Melbourne Gardens, on leaves of *Gahnia aspera* (*Cyperaceae*), 2 Dec. 2016, *P.W. Crous* (holotype CBS H-23320, culture ex-type CPC 32454 = CBS 143450, ITS, LSU, *rpb2*, *tef1* and *tub2* sequences GenBank MG386074, MG386127, MG386148, MG386157 and MG386170, MycoBank MB823423).

Colour illustrations. *Gahnia aspera*; ascomata sporulating on OA, asci, pseudoparaphyses and ascospores. Scale bars = 10 µm.

Notes — *Phaeosphaeria* was epitypified by Quaedvlieg et al. (2013), fixing the generic application of the name. We were unable to locate any *Phaeosphaeria* spp. known from *Gahnia*, and this species is consequently described as new.

Based on a megablast search using the ITS sequence, the closest matches in NCBIs GenBank nucleotide database were *Pringsheimia euphorbiae* (GenBank NR_145344; Identities 506/552 (92 %), 7 gaps (1 %)), *Phaeosphaeria caricicola* (GenBank KF251182; Identities 517/566 (91 %), 9 gaps (1 %)) and *P. caricicola* (GenBank AF439474; Identities 473/522 (91 %), 9 gaps (1 %)). The highest similarities using the LSU sequence were *P. eustoma* (GenBank JX681111; Identities 851/853 (99 %), no gaps), *P. avenaria* f. sp. *tritici* (GenBank JX681109; Identities 851/853 (99 %), no gaps) and *P. caricicola* (GenBank KF251685; Identities 851/853 (99 %), no gaps). The highest similarities using the *rpb2* sequence were *Loratospora aestuarii* (GenBank GU371760; Identities 627/757 (83 %), 8 gaps (1 %)), *Parastagonospora nodorum* (as *Phaeosphaeria nodorum*; GenBank DQ499803; Identities 613/7667 (80 %), 12 gaps (1 %)) and *Banksiophoma australiensis* (GenBank KY979846; Identities 611/768 (80 %), 14 gaps (1 %)). No significant hits were found when the *tef1* sequence was used in a blast search. The highest similarities using the *tub2* sequence were from diverse genera such as *Alternaria conjuncta* (GenBank JQ671992; Identities 309/352 (88 %), 13 gaps (3 %)), *Didymocyrtis banksiae* (GenBank KY979923; Identities 302/343 (88 %), 4 gaps (1 %)), *Pleospora incompta* (GenBank KU973708; Identities 306/346 (88 %), 7 gaps (2 %)) and *Phaeosphaeria avenaria* f. sp. *triticae* (GenBank AY786329; Identities 302/346 (87 %), 5 gaps (1 %)).

Pedro W. Crous & Johannes Z. Groenewald, Westerdijk Fungal Biodiversity Institute, P.O. Box 85167,
3508 AD Utrecht, The Netherlands; e-mail: p.crous@westerdijkinstitute.nl & e.groenewald@westerdijkinstitute.nl
Michael J. Wingfield, Forestry and Agricultural Biotechnology Institute (FABI), University of Pretoria, Pretoria 0002, South Africa;
e-mail: mike.wingfield@fabi.up.ac.za
Tom W. May, Royal Botanic Gardens Victoria, Birdwood Avenue, Melbourne, VIC 3004, Australia;
e-mail: tom.may@rbg.vic.gov.au


Cercospora dianellicola

Fungal Planet 705 – 20 December 2017

Cercospora dianellicola Crous, *sp. nov.*

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

Classification — *Mycosphaerellaceae*, *Capnodiales*, *Dothideomycetes.*

On potato dextrose agar. *Conidiophores* solitary to fasciculate, arising from superficial hyphae but most frequently from a well-developed erumpent stroma up to 200 µm diam (ascomatal initials), erect, flexuous-geniculate, subcylindrical, 1–5-septate, branched below or unbranched, 70–150 × 4–6 µm, medium brown, thick-walled, basal region roughened. *Conidiogenous cells* terminal and intercalary, proliferating sympodially, medium brown, smooth, subcylindrical with slight apical taper, scars thickened, darkened, 1–2 µm diam, 25–60 × 4–5 µm. *Conidia* solitary, undergoing microcyclic conidiation in culture, hyaline, smooth, granular, obclavate but subcylindrical when small, 3–6-septate, curved, apex subobtuse, base obconically truncate, hilum slightly thickened and darkened, 2 µm diam, (13–)26–33(–40) × (3–)4 µm.

Culture characteristics — Colonies erumpent, spreading, with moderate aerial mycelium and feathery, lobate margins, reaching 40 mm diam after 1 mo at 25 °C. On MEA, PDA and OA surface grey olivaceous, reverse iron-grey.

Typus. Australia, Victoria, Mount Best Tin Mine Road, on *Dianella* sp. (*Iridaceae*), 28 Nov. 2016, *P.W. Crous* (holotype CBS H-23321, culture ex-type CPC 32597 = CBS 143453, ITS, LSU, *actA* and *cmdA* sequences GenBank MG386075, MG386128, MG674152 and MG674153, MycoBank MB823424).

Notes — Several species of *Mycosphaerellaceae* have been described from *Dianella*, namely *Mycosphaerella queenslandica*, *M. dianellae* and *Cercospora dianellae*, the latter which has since been shown to be a member of *Zasmidium* (Bensch et al. 2012). Because its not possible to determine to which asexual genus the two *Mycosphaerella* spp. belong (Videira et al. 2017), *C. dianellicola* is accepted as the only confirmed *Cercospora* sp. occurring on this host.

Based on a megablast search using the ITS sequence, the closest matches in NCBIs GenBank nucleotide database were *C. asparagi* (GenBank KY549098; Identities 533/536 (99 %), 2 gaps (0 %)), *C. malayensis* (GenBank MF435168; Identities 533/536 (99 %), 2 gaps (0 %)) and *C. glycinicola* (GenBank NR_147293; Identities 533/536 (99 %), 2 gaps (0 %)). The highest similarities using the LSU sequence were *C. ischaemi* (GenBank KM055432; Identities 828/830 (99 %), no gaps), *C. senecionis-walkeri* (GenBank KC677921; Identities 832/836 (99 %), no gaps) and *C. sojina* (GenBank KX286969; Identities 831/836 (99 %), no gaps). The highest similarities using the *actA* sequence were *C. beticola* (GenBank AF443281; Identities 552/618 (89 %), 25 gaps (4 %)), *C. sojina* (GenBank JQ325008; Identities 540/610 (89 %), 15 gaps (2 %)) and *C. malayensis* (GenBank KY082664; Identities 540/612 (88 %), 19 gaps (3 %)). The highest similarities using the *cmdA* sequence were *C. coniogrammes* (GenBank KT037466; Identities 374/445 (84 %), 13 gaps (2 %)), *C.* cf. *malloti* (GenBank KT193753; Identities 375/446 (84 %), 13 gaps (2 %)) and *C. cypericola* (GenBank KT193727; Identities 376/447 (84 %), 15 gaps (3 %)).

Colour illustrations. *Dianella* sp. at Mount Best Tin Mine Road; conidiophores sporulating on PNA and conidia. Scale bars = 10 µm.

Pedro W. Crous & Johannes Z. Groenewald, Westerdijk Fungal Biodiversity Institute, P.O. Box 85167,
3508 AD Utrecht, The Netherlands; e-mail: p.crous@westerdijkinstitute.nl & e.groenewald@westerdijkinstitute.nl
Michael J. Wingfield, Forestry and Agricultural Biotechnology Institute (FABI), University of Pretoria, Pretoria 0002, South Africa;
e-mail: mike.wingfield@fabi.up.ac.za
Brett A. Summerell, Royal Botanic Gardens and Domain Trust, Mrs. Macquaries Road, Sydney, NSW 2000, Australia;
e-mail: brett.summerell@rbgsyd.nsw.gov.au
Angus J. Carnegie, Forest Health & Biosecurity, NSW Department of Primary Industries, Level 12, 10 Valentine Ave,
Parramatta, NSW 2150, Locked Bag 5123, Parramatta, NSW 2124, Australia; e-mail: angus.carnegie@dpi.nsw.gov.au


Gamsia kooimaniorum

Fungal Planet 706 – 20 December 2017

Gamsia kooimaniorum Sandoval-Denis, *sp. nov.*

Etymology. Named for Noud and Robin Kooiman, collectors of the sample from which this fungus was isolated. This species was discovered during a Citizen Science project in the Netherlands, 'Wereldfaam, een schimmel met je eigen naam', describing novel fungal species isolated from Dutch soils.

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

Hyphae hyaline, septate, 1.5–2.5 µm wide, smooth- and thin-walled. *Conidiophores* of two types: i) mostly undifferentiated, unbranched or rarely laterally branched once, produced abundantly, borne laterally and singly on the aerial hyphae, 0–1(–2)-septate, (12–)15–24.5(–28) × (1.5–)2–4(–7) µm, hyaline to subhyaline, smooth- and thin-walled, producing conidia on terminal polyblastic conidiogenous cells. *Conidiogenous cells* polyblastic, subcylindrical to cylindrical with a swollen apical part, (1.5–)4.5–10.5(–14) × (1.5–)2–3.5(–5.5) µm, hyaline to somewhat darkening at the apex, smooth- and thin-walled, with 1–8 apical conidiogenous loci. *Conidia* aseptate, ovoid to broadly ellipsoidal, with a rounded to pointed apex, flat at the base, pale to dark brown, (5.5–)7–9(–10.5) × (4–)5–6.5(–7) µm smooth- and thick-walled, often with a conspicuous longitudinal germ slit, borne solitary in lateral succession and forming large apical clusters; ii) unbranched, rarely branched one or two times from a short, cylindrical and swollen basal cell, mostly grouped in dense sporodochia, rarely borne solitary on the aerial hyphae, 0–1-septate, 17–22(–23) × (3–)4–4.5(–5.5) µm, hyaline to subhyaline, smooth- and thin-walled, producing conidia on terminal annellidic conidiogenous cells. *Conidiogenous cells* annellides, subcylindrical to cylindrical, tapering gently toward the apex, (7.5–)9.5–16(–18) × (3–)4–4.5 µm, hyaline, smooth- and thin-walled, annellations inconspicuous. *Conidia* catenate, aseptate, oval, ellipsoidal to bullet-shaped, apex rounded, truncate at the base, 7.5–8.5(–10) × 4.5–5.5 µm, hyaline, smooth- and thick-walled.

Culture characteristics — Colonies on MEA reaching 30–40 mm diam in 7 d at 25 °C. Colony surface iron-grey to greenish black with white to pale olivaceous grey patches and a thin white external margin, umbonate to crateriform, radially folded, velvety to dusty; margins regular entire to undulate. Reverse olivaceous grey to iron-grey with greenish black centre, without diffusible pigments. On PDA reaching 17–20 mm diam in 7 d at 25 °C. Colony surface ochreous, umber to olivaceous, flat, felty to velvety, with white to vinaceous buff floccose patches toward the periphery; aerial mycelium abundant and short; colony margins irregular, undulate to lobate. Reverse pale vinaceous buff, without diffusible pigments. On OA reaching 21–26 mm diam in 7 d. Colony colour greenish black to leaden black and velvety at the centre becoming white and membranous toward the margins, flat to slightly raised, radiated at the margins; aerial mycelium abundant, short and dense; margins regular, entire to somewhat undulate. Reverse iron-grey without diffusible pigments.

Colour illustrations. Background, Noud and Robin Kooiman at the collection site; conidiophores bearing annellidic conidiogenous cells and chains of conidia; conidiophores bearing polyblastic conidiogenous cells and conidia in apical clusters. Scale bars = 10 µm.

Typus. The Netherlands, Vleuten, from garden soil, Feb. 2017, *N. Kooiman & R. Kooiman* (holotype CBS H-23222, culture ex-type CBS 143185; ITS, LSU and *tub2* sequences GenBank LT904719, LT904720 and LT904701, MycoBank MB822628).

Notes — *Gamsia* includes three species: *G. aggregata*, *G. columbina* (Sandoval-Denis et al. 2016) and *G. kooimaniorum*, described here, characterised by mostly simple, unbranched conidiophores which distinguishes *Gamsia* from their closest relative *Wardomyces* (Morelet 1969, Ellis 1976). Using rDNA and *tub2* sequences *G. kooimaniorum* is phylogenetically more closely related to *G. aggregata*. However, both species exhibit marked differences, particularly in their polyblastic conidiogenous cells, which are steadily hyaline with the multiple conidiogenous loci distributed along the apex and lateral portions of the cell in *G. aggregata*, whereas those in *G. kooimaniorum* tend to darken in the apex, while the conidiogenous loci are clustered in the apical part of the cell; producing also solitary conidia of different shapes (broadly ellipsoidal to obovoidal and rounded in *G. aggregata* vs ovoid to broadly ellipsoidal and sometimes pointed in *G. kooimaniorum*). Morphologically, however, *G. kooimaniorum* most closely resembles *G. columbina*, from which it can be differentiated by its somewhat larger solitary conidia ((5.5–)7–9(–10.5) × (4–)5–6.5(–7) µm vs 6–13 × 3.5–6.5 µm in *G. columbina*) and its aseptate annellidic conidia (vs consistently 1-septate annelloconidia in *G. columbina*).

Marcelo Sandoval-Denis, Westerdijk Fungal Biodiversity Institute, P.O. Box 85167,
3508 AD Utrecht, The Netherlands; e-mail: m.sandoval@westerdijkinstitute.nl


Phaeoisaria annesophieae

Fungal Planet 707 – 20 December 2017

Phaeoisaria annesophieae Hern.-Restr., *sp. nov.*

Etymology. *annesophieae*, refers to the name of the collector of the ex-type strain, Anne-Sophie den Boer. This species was discovered during a Citizen Science project in the Netherlands, 'Wereldfaam, een schimmel met je eigen naam', describing novel fungal species isolated from Dutch soils.

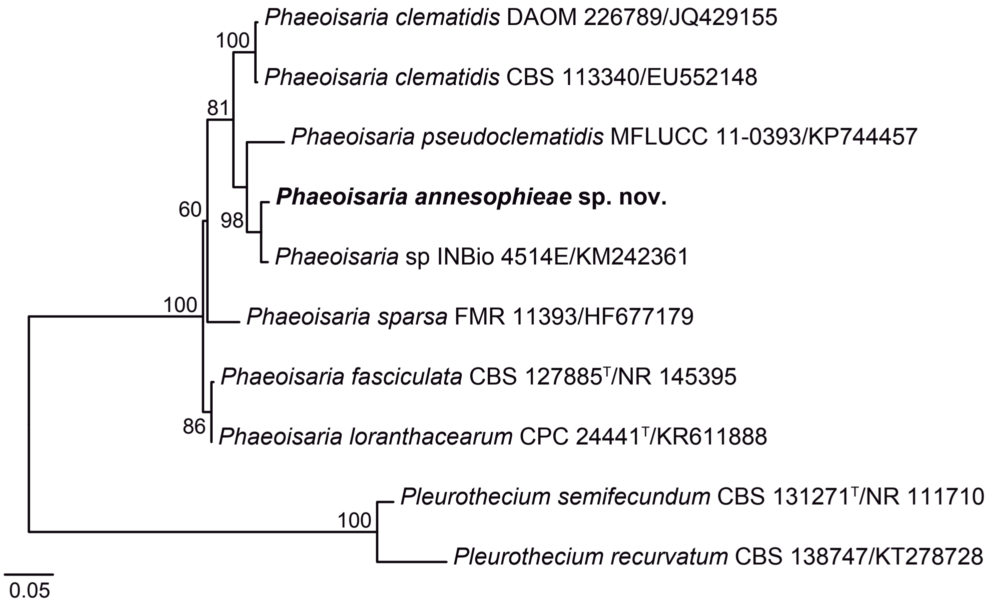
Classification — *Pleurotheciaceae*, *Pleurotheciales*, *Sordariomycetes*.

Description on OA. *Mycelium* hyaline to pale brown, composed of smooth-walled, septate, 1.5–3 µm wide hyphae. *Synnemata* absent. *Conidiophores* indeterminate, sometimes grouping in strands of 2–4 hyphae, semi-macronematous reduced to a single conidiogenous cell, arising from aerial hyphae, cylindrical, hyaline to pale brown. *Conidiogenous cells* polyblastic, integrated, terminal or intercalary, cylindrical, hyaline, smooth-walled, 12–39 × 1–3.5 µm, forming conidia sympodially on conspicuous denticles, 1–1.5 µm long, 0.5–1 µm wide, scattered or clustered in the apical region. *Conidia* ellipsoidal to obovoid, straight or slightly curved, rounded at the ends or sometimes tapering toward the base, hyaline, aseptate, guttulate, smooth-walled, 4.5–9 × 2–3.5 µm. *Chlamydospores* terminal, globose, pyriform, first hyaline becoming brown to dark brown, 9–18 × 7–9.5 µm. *Sexual morph* not observed.

Culture characteristics — Colonies reaching 50 mm diam on OA after 4 wk at 25 °C. Aerial mycelium beige to pale brown, at first smooth, later cottony; reverse brown. Sporulation appears first in the centre of the colony, later present over the whole colony; sporulating colony with submerged mycelium brown and aerial mycelium beige with a powdery appearance.

Typus. The Netherlands, Geldermalsen, isolated from soil, Mar. 2017, *A.-S. den Boer* (holotype CBS H-23231, cultures ex-type CBS 143235; ITS and LSU sequences GenBank MG022180 and MG022159, MycoBank MB823031).

Notes — *Phaeoisaria annesophieae* is phylogenetically related to *Phaeoisaria* sp. INBio4514E (KM242361), the *Ph. clematidis* species complex and *Ph. pseudoclematidis*. *Phaeoisaria* originally comprised species with conidiophores grouped in synnemata, with polyblastic and denticulate conidiogenous cells (Höhnel 1909, Ellis 1971, Castañeda-Ruiz et al. 2002, Seifert et al. 2011, Mel'nik 2012). Nonetheless, some species has been added to the genus that lack synnemata, i.e., *Ph. fasciculata* (Réblová et al. 2016) and *Ph. loranthacearum* (Crous et al. 2015a), as well as the new species, *P. annesophieae*. *Phaeoisaria annesophieae* is easily distinguished from the other species of the genus by producing chlamydospores in culture.



The phylogenetic tree based on ITS sequences was inferred using a maximum likelihood analysis in the RAxML black box v. 8 (Stamatakis 2014). Bootstrap support values are indicated at the nodes and values below 50 % are not shown. The scale bar indicates the expected number of changes per site.

Colour illustrations. Garden where the soil sample was collected; colony overview on OA, conidiogenous cells, conidia and chlamydospores. Scale bars = 10 µm.

Margarita Hernández-Restrepo, Westerdijk Fungal Biodiversity Institute, P.O. Box 85167,
3508 AD Utrecht, The Netherlands; e-mail: m.hernandez@westerdijkinstitute.nl


Verhulstia trisororum

Fungal Planet 708 – 20 December 2017

Verhulstia Hern.-Rest., *gen. nov.*

Etymology. Named for the family name Verhulst, whose members collected the soil sample from which the fungus was isolated. This species was discovered during a Citizen Science project in the Netherlands, 'Wereldfaam, een schimmel met je eigen naam', describing novel fungal species isolated from Dutch soils.

Classification — *Chaetosphaeriaceae*, *Chaetosphaeriales*, *Sordariomycetes.*

Description on OA. *Conidiomata* sporodochial, scattered to gregarious, superficial, hyaline becoming brown with age, globose, setose with a central white conidial mass, basal stroma of *textura angularis*. *Setae* arising from outer elements of the stroma, abundant, subulate to subcylindrical, basal cell pale brown, other cells brown to dark brown, apex paler, rounded, verrucose to warty, straight to flexuous, multiseptate. *Conidiophores* arising from the stroma in dense layers, unbranched, cylindrical, septate, hyaline to pale brown toward the apex. *Conidiogenous cells* integrated, terminal, lageniform to subcylindrical, phialidic with a collarette, hyaline to pale brown. *Conidia* cylindrical to ellipsoidal, or obovoid, curved at the apex, aseptate, hyaline, smooth.

Type species. Verhulstia trisororum Hern.-Rest.
MycoBank MB823032.

Verhulstia trisororum Hern.-Rest., *sp. nov.*

Etymology. From the Latin *tri*- three, and *sororum*- sisters. Named for the three sisters Jikke, Anoek and Elke Verhulst, who collected the soil sample from which the fungus was isolated.

Description on OA. *Conidiomata* sporodochial, scattered to gregarious, superficial, hyaline becoming brown with age, globose, setose with a central white conidial mass on OA (and PNA), basal stroma of *textura angularis*. *Setae* arising from outer elements of the stroma, abundant, basal cell pale brown, other cells brown to dark brown, subulate to subcylindrical, apex rounded, verrucose to warty, straight to flexuous, multiseptate, 133–163 µm long, 3.5–5.5 µm wide base, 1–2 µm wide at apex. *Conidiophores* arising from the stroma in a dense layer, unbranched, cylindrical, septate, hyaline to pale brown toward the apex, 30–72 × 2–2.5 µm. *Conidiogenous cells* integrated, terminal, lageniform to subcylindrical, phialidic with a collarette, hyaline to pale brown, 7.5–15.5 µm long, 2–3 µm wide at base, 1 µm wide at apex. *Conidia* cylindrical to ellipsoidal, 5–7 × 1–2 µm, or obovoid, 5–8 × 2–3 µm, curved at the apex, aseptate, smooth.

Culture characteristics — Colonies on OA after 1 wk at 25 °C reaching 10 mm diam, flat, spreading, with sparse aerial mycelium. Sporulation appears first in the centre of the colony, later present over the whole colony.

Typus. The Netherlands, Amersfoort, isolated from soil, Mar. 2017, *J.*, *A. & E. Verhulst* (holotype CBS H-23230, culture ex-type CBS 143234; ITS and LSU sequences GenBank MG022181 and MG022160, MycoBank MB823033).

Colour illustrations. Garden where the soil sample was collected; conidiomata overview on OA, setose conidiomata, conidiogenous cells, setae and conidia. Scale bars = 10 µm.

Notes — This new genus is similar to *Dinemasporium*, *Brunneodinemasporium*, *Pseudolachnea* (Crous et al. 2012) and *Vermiculariopsiella* (Seifert et al. 2011) in producing setose conidiomata with phialidic conidiogenous cells. However, *Verhulstia* is distinguished from all of them in having hyaline, lageniform conidiogenous cells that eventually become brown with age, with a conspicuous collarette and conidia without setulae. Furthermore, the strain CBS 143234 was phylogenetically placed in *Chaetosphaeriaceae*, in a separate branch close to species of *Chaetosphaeria* with low support.

Margarita Hernández-Restrepo, Westerdijk Fungal Biodiversity Institute, P.O. Box 85167,
3508 AD Utrecht, The Netherlands; e-mail: m.hernandez@westerdijkinstitute.nl


Striaticonidium deklijnearum

Fungal Planet 709 – 20 December 2017

Striaticonidium deklijnearum L. Lombard, *sp. nov.*

Etymology. Named for Lola and Nieve de Klijne, who collected the sample. This species was discovered during a Citizen Science project in the Netherlands, 'Wereldfaam, een schimmel met je eigen naam', describing novel fungal species isolated from Dutch soils.

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

Conidiomata sporodochial, stromatic, superficial, scattered or gregarious, oval to irregular in outline, 80–140 µm diam, 50–100 µm deep, with a white setose-like fringe surrounding an olivaceous green agglutinated slimy mass of conidia. *Stroma* poorly developed, hyaline, of a *textura angularis*. *Setae* sparse, sinuous, unbranched, hyaline to subhyaline, verrucose, 30–50 µm long, 2 µm wide, terminating in a blunt apex. *Conidiophores* arising from the basal stroma, consisting of a stipe and a penicillately branched conidiogenous apparatus; stipes unbranched hyaline, smooth, septate, 10–24 × 2–3 µm; primary branches aseptate, unbranched, smooth, 8–11 × 2–3 µm; secondary branches aseptate, unbranched, smooth, 9–13 × 2 µm; terminating in a whorl of 2–4 conidiogenous cells; conidiogenous cells phialidic, cylindrical to subcylindrical, hyaline, smooth, straight to slightly curved, 8–15 × 2–3 µm, with conspicuous collarettes and periclinical thickenings. *Conidia* aseptate, longitudinally striate, olivaceous green to brown, fusiform to ellipsoidal to undulate, (5–)6–8(–9) × 2–3 µm (av. 7 × 2 µm), with a distinct apical hilum.

Culture characteristics — Colonies on PDA, OA and CMA with abundant white aerial mycelium with sporodochia forming on the surface of the medium, covered by slimy olivaceous green conidial masses, reverse on PDA pale luteous.

Typus. The Netherlands, Ravenswaaij, from soil, Mar. 2017, *L. & N. de Klijne* (holotype CBS H-23235, culture ex-type CBS 143232 = JW17002; ITS, LSU, *tef1* and *tub2* sequences GenBank MG386077, MG386130, MG386158 and MG386171, MycoBank MB823349).

Notes — Lombard et al. (2016) introduced the genus *Striaticonidium* to accommodate myrothecium-like species characterised by longitudinally striate conidia. *Striaticonidium deklijnearum* is most similar to *S. cinctum*, but can be distinguished by having slightly smaller conidia ((5–)6–8(–9) × 2–3 µm (av. 7 × 2 µm)) compared to those of *S. cinctum* ((6–)7–9 × 2–3 µm (av. 8 × 3 µm); Lombard et al. 2016). Furthermore, the setae of *S. cinctum* (up to 120 µm long; Lombard et al. 2016) are longer than those of *S. deklijnearum* (up to 50 µm).

Based on megablast searches using the ITS sequences of the ex-type culture, the best matches were to *S. synnematum* (GenBank KU847242; Identities = 542/553 (98 %), 4 gaps (0 %)), and *S. cinctum* (GenBank KU847263; Identities = 541/552 (98 %), 1 gap (0 %)). Based on megablast searches using the *tef1* sequences of the ex-type culture, the best matches were to *S. cinctum* (GenBank KU847309; Identities 501/513 (98 %), 4 gaps (0 %)), and *S. humicola* (GenBank KU847312; Identities 215/245 (88 %), 5 gaps (2 %)). Based on megablast searches using the *tub2* sequences of the ex-type culture, the best matches were to *S. cinctum* (GenBank KU847327; Identities 362/372 (97 %), 2 gaps (0 %)), and *S. synnematum* (GenBank KU847332; Identities 352/371 (95 %), 1 gaps (0 %)).

Colour illustrations. Garden where the soil sample was collected; conidiophores, setae and conidia. Scale bars = 10 µm.

Lorenzo Lombard, Westerdijk Fungal Biodiversity Institute, P.O. Box 85167, 3508 AD Utrecht, The Netherlands;
e-mail: l.lombard@westerdijkinstitute.nl


Umbelopsis wiegerinckiae

Fungal Planet 710 – 20 December 2017

Umbelopsis wiegerinckiae Sandoval-Denis, *sp. nov.*

Etymology. Named for Frederique Madeleine Wiegerinck, who collected this sample. This species was discovered during a Citizen Science project in the Netherlands, 'Wereldfaam, een schimmel met je eigen naam', describing novel fungal species isolated from Dutch soils.

Classification — *Umbelopsidaceae*, *Umbelopsidales*, *Incertae sedis*, *Mucoromycotina*, *Zygomycota*.

Sporangiophores mainly umbellately branched, arising from a swollen portion of the subtended stalk 6.5–10 µm diam, (9.5–)28.5–193.5(–294.5) × (3–)4–5 µm, rarely unbranched, tapering slightly toward the apex, hyaline, smooth- and thick-walled, 0–1-septate, often with one septum 10–20 µm below the columella level. *Sporangia* globose to subglobose, (10–)13–18.5(–20.5) µm diam, pink, coral to red coloured, multi-spored; walls thin and deliquescent, leaving a small pale red coloured collarette. *Columellae* subglobose, globose to sphaeropedunculate, (3.5–)4 × 6(–7) µm diam. *Sporangiospores* ovoid, short ellipsoidal, oblong with rounded apices to ossiform, (3–)3.5–4.5(–5) × 2–2.5(–3.5) µm, pale red in mass, smooth- and thin-walled. *Chlamydospores* subglobose, globose to obovoid, (5–)6 × 10 µm diam, subhyaline to pale golden brown, formed singly and abundantly on the substrate mycelium, intercalary or on short stalks, smooth- and thick-walled.

Culture characteristics — Colonies on SNA reaching 20–23 mm diam in 7 d at 25 °C. Colony surface buff to rosy buff, flat, feathery, short wholly to floccose; margins highly irregular, rhizoid with abundant submerged mycelium. Reverse buff to rosy buff, without diffusible pigments. On MEA reaching 52–57 mm diam in 7 d at 25 °C. Colony surface rosy buff, brick to fawn coloured, flat to raised, forming concentric rings, velvety to felty; margins regular. Reverse cinnamon to brick coloured, without diffusible pigments. On PDA reaching 41–50 mm diam in 7 d at 25 °C. Colony surface pale luteous, with rust to brick centre, flat, velvety to felty forming inconspicuous concentric rings; aerial mycelium abundant; colony margins regular. Reverse pale luteous to straw, without diffusible pigments. On OA reaching 30–36 mm diam in 7 d. Colony colour peach to coral, salmon at the centre and white at the periphery, flat to raised, velvety to felty, dusty at the centre; aerial mycelium abundant, short and dense; margins regular. Reverse pale luteous, without diffusible pigments.

Typus. The Netherlands, Amersfoort, from garden soil, Feb. 2017, *F.M. Wiegerinck* (holotype CBS H-23227, culture ex-type CBS 143184; ITS, LSU and *actA* sequences GenBank LT904721, LT904722 and LT904705, MycoBank MB822627).

Colour illustrations. Background, collection site (Wiegerinck family's garden); umbellately branched sporangiophores emerging from the agar surface; collapsed sporangium showing the columella shape and membrane remnants of the sporangium membrane (collarette); sporangiophores; chlamydospores; sporangiospores. Scale bars = 10 µm.

Notes — Using ITS, LSU and *actA* sequences *Umbelopsis wiegerinckiae* nests within a group of *Umbelopsis* spp. characterised by having pink to red multi-spored sporangia forming mostly irregularly shaped sporangiospores such as *U. angularis* (angular spores), *U. gibberispora* (hump-shaped spores) and *U. swartii*/*U. westeae* (appendaged spores) (Meyer & Gams 2003). Three exceptions are known to occur in this group, forming oval to ellipsoidal spores (*U. fusiformis*, *U. ramanniana* and the new species *U. wiegerinckiae* described here). However, *U. wiegerinckiae* can be easily distinguished from *U. fusiformis* by having subglobose to globose sporangia with a conspicuous columella, whereas the latter species is characterized by fusiform sporangia lacking a columella (Sugiyama et al. 2003); and is distinguished from *U. ramanniana* by its ovoid to oblong and rounded spores (vs ellipsoid in the later species). However, the current concept of *U. ramanniana* remains unresolved, and it is thought to correspond to a complex of cryptic species (Meyer & Gams 2003, Sugiyama et al. 2003). Another species morphologically close to *U. wiegerinckiae* is *U. vinacea*, especially when cultural characteristics and chlamydospores are compared. Nevertheless, the former species produces angular spores and lacks columellae (Meyer & Gams 2003).

Marcelo Sandoval-Denis, Westerdijk Fungal Biodiversity Institute, P.O. Box 85167,
3508 AD Utrecht, The Netherlands; e-mail: m.sandoval@westerdijkinstitute.nl


Vandijckella johannae

Fungal Planet 711 – 20 December 2017

Vandijckellaceae Sandoval-Denis, *fam. nov.*

Classification — *Vandijckellaceae*, *Helotiales*, *Leotiomycetes*.

Colonies buff to ochreous, flat and radially folded with abundant aerial mycelium commonly aggregated forming hyphal ropes. *Mycelium* hyaline, septate, branched and smooth. *Conidiophores* simple, determinate, commonly reduced to conidiogenous cells borne directly on the aerial hyphae or rarely on a basal cell. *Conidiogenous cells* phialidic, hyaline and smooth-walled. *Conidia* clavate to cylindrical, rounded, smooth- and thin-walled, borne in chains.

Type genus. *Vandijckella* Sandoval-Denis.
MycoBank MB823486.

Vandijckella Sandoval-Denis, *gen. nov*.

Etymology. Named in honour of the president of the Royal Dutch Academy of Arts and Sciences (KNAW), José F.T.M. van Dijck. This species was discovered during a Citizen Science project in the Netherlands, 'Wereldfaam, een schimmel met je eigen naam', describing novel fungal species isolated from Dutch soils.

Mycelium hyaline, septate, smooth- and thin-walled, commonly aggregated to form ropes. *Conidiophores* monomorphic, smooth- and thin-walled, mononematous, short, simple and determinate, often reduced to conidiogenous cells. *Conidiogenous cells* hyaline, smooth- and thin-walled, borne laterally on aerial hyphae, monophialidic, ampulliform, with a conspicuous and long collarette at the apical conidiogenous locus. *Conidia* clavate, short cylindrical to oblong with rounded apices, straight, smooth- and thin-walled, grouping in a chain that easily detaches. *Sexual morph* unknown.

Type species. Vandijckella johannae Sandoval-Denis.
MycoBank MB822625.

Vandijckella johannae Sandoval-Denis, *sp. nov.*

Etymology. Linking the first female professor of the Netherlands, Johanna Westerdijk (10 Feb. 1917), to the first female president of the KNAW, José F.T.M. van Dijck (18 May 2015) – two phenomenal individuals, with a great legacy.

Conidiophores simple, mostly reduced to monophialides borne singly and laterally on the aerial hyphae or more commonly from hyphal ropes; rarely borne singly on swollen basal cells, 5–8.5 µm diam, (10.5–)11–51.5(–60) × 2.5–4(–5) µm, smooth and thin-walled. *Conidiogenous cells* ampulliform, lageniform to wide subulate, hyaline, (10.5–)13–17.5(–18) × 3–3.5(–4) µm, smooth- and thin-walled with discreet periclinal thickening and a conspicuous apical collarette, 3.5–4.5(–5) × 2–3.5 µm. *Conidia* catenulate, unicellular, clavate, cylindrical to oblong, often tapering toward the base, hyaline, (3.5–)4–5(–6) × (1–)2–2.5 µm.

Culture characteristics — Colonies on MEA reaching 30–35 mm diam in 7 d at 25 °C. Colony surface ochreous to buff at the centre with sienna to umber periphery, flat with raised centre and radially folded, velvety to dusty, sporulation abundant from copious aerial mycelium; margins regular, entire to undulate. Reverse sienna to luteous, becoming umber to olivaceous, without diffusible pigments. On OA reaching 25–35 mm diam in 7 d at 25 °C. Colony surface white to buff, with white margins, flat with scarce white aerial mycelium forming faint radial striations, membranous to velvety; margin regular and complete. Reverse white, umber at the centre, without diffusible pigments. On PDA reaching 33–40 mm diam in 7 d at 25 °C. Colony surface white, straw to umber coloured, raised and radially folded with flat margins, membranous at first becoming velvety to felty with the production of abundant floccose aerial mycelium, densely sporulating; margins regular with abundant submerged mycelium. Reverse white with umber to olivaceous centre, without diffusible pigments.

Typus. The Netherlands, Amsterdam, from garden soil, Feb. 2017, *J.F.T.M. van Dijck* (holotype CBS H-23223, culture ex-type CBS 143182; ITS, LSU, *rpb2* and *tub2* sequences GenBank LT904725, LT904726, LT904707 and LT904703, MycoBank MB822626).

Colour illustrations. Background, garden and collector (José F.T.M. van Dijck); conidiophores, conidiogenous cells and conidia. Scale bars = 5 µm.

Additional material examined. The Netherlands, Amsterdam, from garden soil, Feb. 2017, *J.F.T.M. van Dijck*, CBS 143181; ITS, LSU, *rpb2* and *tub2* sequences GenBank LT904723, LT904724, LT904706 and LT904702; *ibid*., CBS 143183; ITS, LSU, *rpb2* and *tub2* sequences GenBank LT904727, LT904728, LT904708 and LT904704.

Notes — Ribosomal DNA sequences related *Vandijckella johannae* to the *Dermataceae* and *Helotiaceae*, helotialean families including a heterogeneous assembly of asexual and sexual morphs, mostly plant pathogenic or saprobic species (Zhang & Wang 2015). However, the genus *Vandijckella* nested in an undefined clade well differentiated from the currently known families of the *Helotiales*, for which the family *Vandijckellaceae* is introduced. The new family is phylogenetically related to representatives from known polyphyletic genera, mostly discomycetes of uncertain association but previously assigned to the *Calloriceae*, *Dermataceae*, *Helotiaceae* or *Hyaloscyphaceae* s.lat. (Baschien et al. 2013, Baral & Haelewaters 2015). Moreover, the currently accepted families in *Helotiales* have been demonstrated to be polyphyletic by morphological and molecular data (Schoch et al. 2009, Zhang & Wang 2015). The new species *Vandijckella johannae* resembles the recently described genus *Davidhawksworthia* (Crous & Groenewald 2016), which is genetically closely related, both genera producing more or less cylindrical, aseptate conidia on ampulliform, somewhat swollen phialides. Nevertheless, *V. johannae* is distinguished by having monomorphic conidiophores bearing single phialides, and short cylindrical conidia formed in chains; vs dimorphic conidiophores (phialides borne on erect, penicillate conidiophores or as multiple phialides on a basal cell) and long cylindrical conidia (18–20(–22) µm long) of *Davidhawksworthia ilicicola*, the only species of that genus (Crous & Groenewald 2016). Another taxon phylogenetically closely related to *V. johannae* is *Mycoarthris corallina* (Marvanová et al. 2002), a fungus also forming chains of elongated cylindrical conidia. It is, however, morphologically dissimilar by producing polyblastic conidiogenous cells, with sympodial elongations.

Marcelo Sandoval-Denis & Alejandra Giraldo, Westerdijk Fungal Biodiversity Institute, P.O. Box 85167,
3508 AD Utrecht, The Netherlands; e-mail: m.sandoval@westerdijkinstitute.nl & a.giraldo@westerdijkinstitute.nl


Fusarium petersiae

Fungal Planet 712 – 20 December 2017

Fusarium petersiae L. Lombard, *sp. nov*.

Etymology. Named for Danique Peters, who collected this sample. This species was discovered during a Citizen Science project in the Netherlands, 'Wereldfaam, een schimmel met je eigen naam', describing novel fungal species isolated from Dutch soils.

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

On SNA, hyphae hyaline, smooth, 1–12 µm wide and chlamydospores absent. Sporulation abundant only from sporodochia and no conidiophores observed on the aerial mycelium. *Sporodochia* salmon to orange coloured, formed abundantly only on the surface of carnation leaves under 12 / 12 h cool fluorescent light/dark cycle at 25 °C after 5–7 d. *Conidiophores* in sporodochia 15–30 µm tall, densely and irregularly branched, bearing apical whorls of 2–4 monophialides; *sporodochial monophialides* subcylindrical, 10–14 × 2–4 µm, smooth, thin-walled, with a minute apical collarette. *Sporodochial conidia* (macroconidia) falcate, curved, with a papillate and curved apical cell, and tapering towards a foot-like basal cell, (3–)4(–5)-septate, often showing one or more empty cells, smooth, hyaline, thin-walled. Three-septate conidia (26–)28.5–33.5(–35) × (3–)3.5–4 µm (av. 31 × 4 µm); four-septate conidia (29–)31–35(–39) × (3–)3.5–4.5(–5) µm (av. 33 × 4 µm); five-septate conidia (32–)33–37(–39) × (3–)3.5–4 µm (av. 35 × 4 µm).

Culture characteristics — Colonies on PDA growing in the dark with an average radial growth rate of 3–3.5 mm/d at 24 °C, reaching 35–45 mm diam in 7 d. Colony surface buff to honey with rosy buff to brick margins, raised, velvety to felty with abundant floccose aerial mycelium; colony margins irregular and undulate. Reverse dark vinaceous to sepia with diffuse cinnamon pigment throughout the medium with abundant chlamydospores in the medium and aerial mycelium.

Typus. The Netherlands, Arnhem, from soil, Mar. 2017, *D. Peters* (holotype CBS H-23233, culture ex-type CBS 143231 = JW14004; ITS, LSU, *rpb1*, *rpb2* and *tef1* sequences GenBank MG386078, MG386131, MG386138, MG386149 and MG386159, MycoBank MB823350); *ibid*., JW14005; ITS, LSU, *rpb1*, *rpb2* and *tef1* sequences GenBank MG386079, MG386132, MG386139, MG386150 and MG386160.

Colour illustrations. Garden were the soil sample was collected; conidial spore masses, conidiophores, conidia (older conidia developing chlamydospores). Scale bars = 10 µm.

Notes — Based on sequence comparisons of the *rpb1*, *rpb2* and *tef1* sequences with those available in the Fusarium-ID (Geiser et al. 2004) and Fusarium MLST (http://www.cbs.knaw.nl/fusarium/; O'Donnell et al. 2010) sequence databases as recommended by O'Donnell et al. (2015), *F. petersiae* is a new member of the *F. tricinctum* species complex, closely related to *F. flocciferum* and *F. torulosum*. *Fusarium petersiae* can be distinguished from *F. flocciferum* (Booth 1971) by the formation of sporodochia, up to 5-septate macroconidia, and lack of conidiophores formed on the aerial mycelium. *Fusarium flocciferum* is characterised by the lack of sporodochia in culture, but produce abundant (up to 3-septate) macroconidia on conidiophores carried on the aerial mycelium (Booth 1971). *Fusarium torulosum* is very slow growing, usually producing only 5-septate macroconidia, and sometimes 0–1-septate microconidia (Nirenberg 1995) with sporulation also occurring on the aerial mycelium (Leslie & Summerell 2006).

Lorenzo Lombard, Westerdijk Fungal Biodiversity Institute, P.O. Box 85167, 3508 AD Utrecht, The Netherlands;
e-mail: l.lombard@westerdijkinstitute.nl


Plectosphaerella niemeijerarum

Fungal Planet 713 – 20 December 2017

Plectosphaerella niemeijerarum L. Lombard, *sp. nov*.

Etymology. Named for Flora and Rosalie Niemeijer, who collected this sample. This species was discovered during a Citizen Science project in the Netherlands, 'Wereldfaam, een schimmel met je eigen naam', describing novel fungal species isolated from Dutch soils.

Classification — *Plectosphaerellaceae*, *Glomerellales*, *Sordariomycetes.*

Conidiophores solitary, unbranched, hyaline, smooth, thin-walled. *Conidiogenous cells* phialidic, determinate or forming laterally, hyaline, smooth, with a single basal septum, widest at the base, straight to sinuous, gradually tapering to the apex, 10–48 × 2–3 µm, with periclinal wall thickening and cylindrical collarette. *Conidia* aggregate in slimy heads, fusiform to ellipsoid, tapering to rounded apex and base, hyaline, smooth, 0–1-septate, with a minute apiculus at either end, (3–)4–6 × 2–3 µm (av. 5 × 2 µm).

Culture characteristics — Colonies on PDA white, mycelium appressed, slimy, with sparse aerial mycelium. Aerial mycelium white, fluffy.

Typus. The Netherlands, Nieuwegein, from soil, Feb. 2017, *F. & R. Niemeijer* (holotype CBS H-23234, culture ex-type CBS 143233 = JW5012; ITS, LSU, *tef1* and *tub2* sequences GenBank MG386080, MG386133, MG386161 and MG386172, MycoBank MB823351).

Colour illustrations. Garden from which the soil sample was collected; conidiophores and conidia. Scale bars = 10 µm.

Notes — *Plectosphaerella niemeijerarum* is phylogenetically closely related to *P. plurivora* (on asparagus, Italy; conidia 4.5–10.5 × 2–5 µm; Carlucci et al. 2012), but morphologically distinct in having smaller conidia, (3–)4–6 × 2–3 µm (av. 5 × 2 µm).

Based on megablast searches using the ITS sequence of the ex-type culture, the best matches were to *Plectosphaerella* sp. (GenBank KX359601; Identities = 583/584 (99 %), no gaps) and *P. cucumerina* (GenBank KP068972; Identities = 554/555 (99 %), no gaps). Based on megablast searches using the *tef1* sequence of the ex-type culture, the best matches were to *P. plurivora* (GenBank KY421323; Identities 252/262 (96 %), 2 gaps (0 %)) and *P. pauciseptata* (GenBank KY421322; Identities 250/262 (95 %), 2 gaps (0 %)). Based on megablast searches using the *tub2* sequence of the ex-type culture, the best matches were to *P. plurivora* (GenBank KY421303; Identities 316/325 (97 %), 4 gaps (1 %)) and *P. oligotrophica* (GenBank JX508814; Identities 341/379 (90 %), 9 gaps (2 %)).

Lorenzo Lombard, Westerdijk Fungal Biodiversity Institute, P.O. Box 85167, 3508 AD Utrecht, The Netherlands;
e-mail: l.lombard@westerdijkinstitute.nl


Talaromyces annesophieae

Fungal Planet 714 – 20 December 2017

Talaromyces annesophieae Houbraken, *sp. nov.*

Etymology. *annesophieae*, refers to the name of the collector of the ex-type strain, Anne-Sophie den Boer. This species was discovered during a Citizen Science project in the Netherlands, 'Wereldfaam, een schimmel met je eigen naam', describing novel fungal species isolated from Dutch soils.

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

Conidiophores biverticillate, occasionally with an additional branch. *Stipes* smooth-walled, 100–150 × 2–3 µm, non-vesiculate. *Metuale* 4–6, 10–13 × 2–3 µm. *Phialides* 4–7 per stipe, lanceolate, 9–12 × 2–3 µm. *Conidia* smooth-walled, broadly ellipsoidal, 2–3 × 2–2.5 µm. *Ascomata* or *sclerotia* not observed.

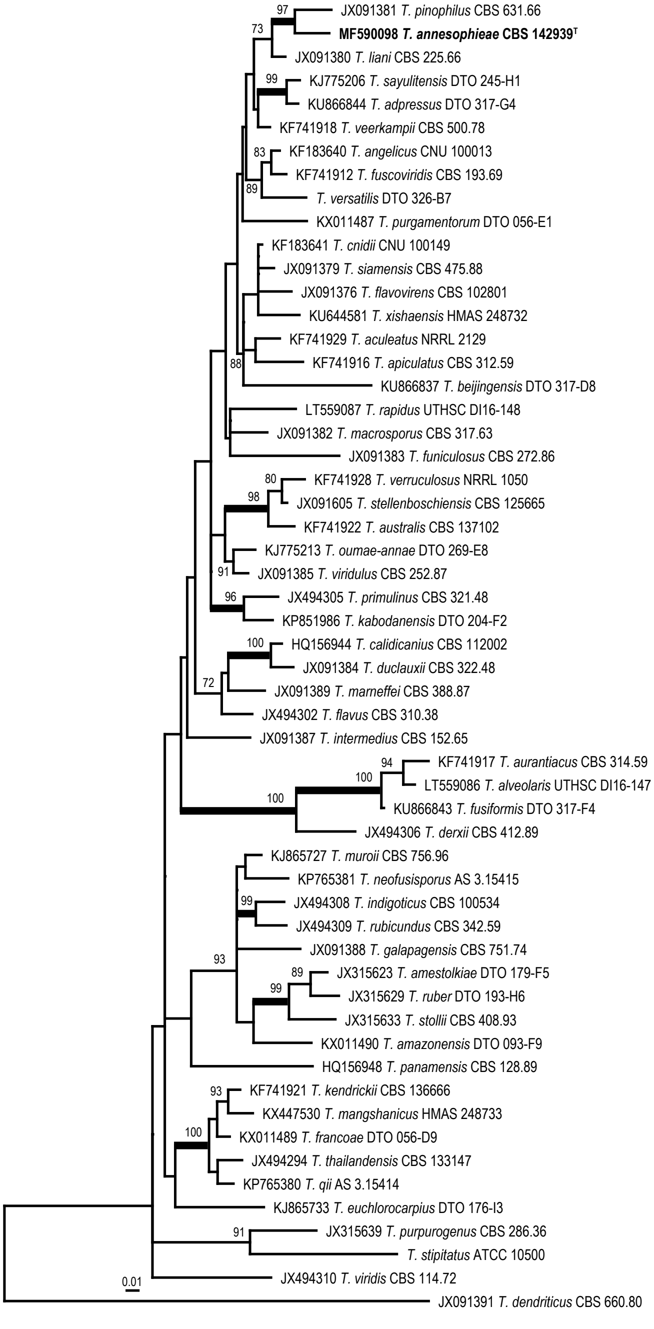
Culture characteristics — CYA, 25 °C, 7 d: Colonies raised in centre, weakly radially sulcate; margins irregular, lobate; mycelium white to pale yellow; texture velvety, velvety to granular in centre; sporulation weak; conidial colour *en masse* indeterminate; exudates droplets present, large, clear; soluble pigment absent; reverse pinkish brown. MEA, 25 °C, 7 d: Colonies plane, slightly raised in centre, non-sulcate; margins entire; mycelium white with yellow mycelium covering the colony; texture velvety, floccose in centre; sporulation strong; conidial colour *en masse* dull green; exudates absent; soluble pigment absent; reverse brown. YES, 25 °C, 7 d: Colonies raised in centre, non-sulcate; margins entire; mycelium pale yellow; sporulation absent, conidia *en masse* indeterminate; exudate absent; soluble pigment absent; reverse orange-brown in centre, yellow-brown near colony edge. DG18, 25 °C, 7 d: Colonies plane, non-sulcate; margins entire; mycelium white to pale yellow; texture velvety; sporulation moderate; conidial colour *en masse* dull to grey green; exudate absent; soluble pigment absent; reverse pale yellow. OA, 25 °C, 7 d: Colonies plane, non-sulcate; margins entire; mycelium yellow; texture velvety, slightly floccose in centre; sporulation strong; conidial colour *en masse* dark green; exudate present as clear droplets; soluble pigment absent; reverse indeterminate. CREA, 25 °C, 7 d: poor growth, acid and base compounds not produced. Ehrlich reaction negative.

The phylogenetic tree based on partial β-tubulin sequences was inferred using a maximum likelihood analysis in the MEGA 6 v. 6.06 software package. The Hasegawa-Kishino-Yano model with gamma distributed (+G) and invariant sites (+I) was the most suitable and therefore selected. Bootstrap support values are indicated at the nodes (1 000 bootstraps) and values below 70 % are not shown. The scale bar indicates the expected number of changes per site.

Colour illustrations. Background, collection site (backyard) and collector (Anne-Sophie den Boer); detail of colony on MEA showing yellow mycelium covering colony; conidia and conidiophores. Scale bars = 10 µm.

Typus. The Netherlands, Gelderland, ex soil, Mar. 2017, *A.-S. den Boer* (holotype CBS H-23216, culture ex-type = CBS 142939 = DTO 377-F3 = JW9011; ITS, *BenA* and *CaM* sequences GenBank MF574592, MF590098 and MF590104, MycoBank MB823027).

Notes — *Talaromyces annesophieae* is phylogenetically most closely related to *T. pinophilus*. *Talaromyces pinophilus* grows faster than *T. annesophieae* on the agar media MEA, CYAS and YES. The most striking difference is the ability of *T. pinophilus* to grow on CYA incubated at 37 °C (25–40 mm) (Yilmaz et al. 2014), while *T. annesophieae* is unable to grow at this temperature.



Jos Houbraken, Westerdijk Fungal Biodiversity Institute, P.O. Box 85167, 3508 AD Utrecht, The Netherlands;
e-mail: j.houbraken@westerdijkinstitute.nl


Collariella hilkhuijsenii

Fungal Planet 715 – 20 December 2017

Collariella hilkhuijsenii X. Wei Wang, *sp. nov.*

Etymology. Named for Joost Hilkhuijsen, who collected this specimen. This species was discovered during a Citizen Science project in the Netherlands, 'Wereldfaam, een schimmel met je eigen naam', describing novel fungal species isolated from Dutch soils.

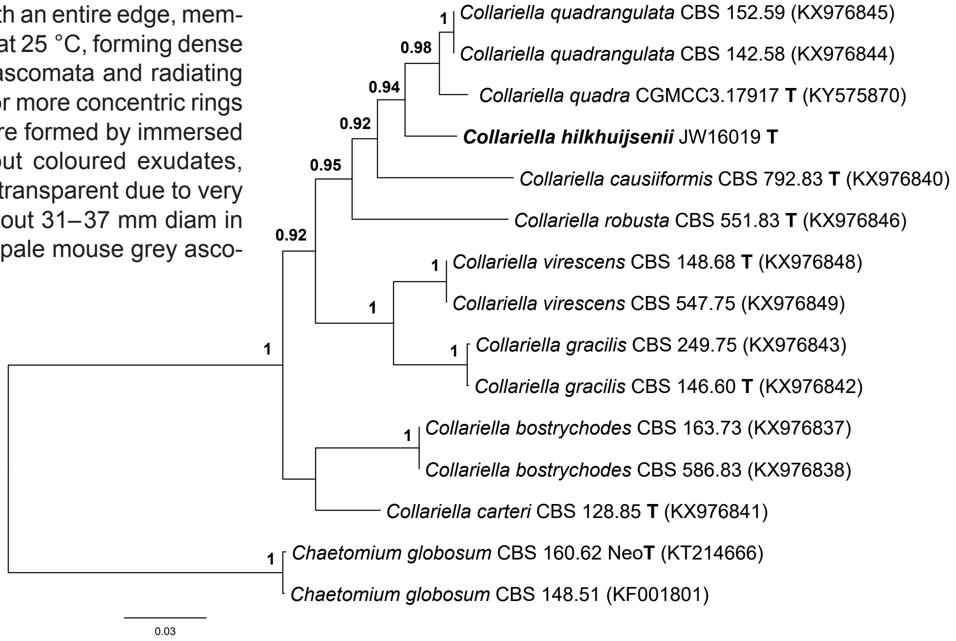
Classification — *Chaetomiaceae*, *Sordariales*, *Sordariomyces*.

Ascomata superficial, pale mouse grey in reflected light owing to ascomatal hairs, obovate to turbinate or ellipsoidal, 250–350 µm high (including the collar), 190–300 µm diam, with a wide ostiole around a darkened collar, 25–50 µm high and 110–180 µm wide. *Ascomatal wall* brown, *textura globulosa* to *angularis* in surface view, and often with cells arranged in a petaloid pattern around the bases of lateral hairs. *Terminal hairs* arising from the apical collar, conspicuously rough, dark brown, septate, erect in the lower part, 3–5.5 µm near the base, spirally coiled in the upper part. *Lateral hairs* seta-like, tapering and fading towards the tips. *Asci* fasciculate, clavate or fusiform, spore-bearing part 20–29 × 7–10.5 µm, stalks 12–25 µm long, with 8 irregularly-arranged ascospores, evanescent. *Ascospores* olivaceous when mature, limoniform, bilaterally flattened, (5.5–)6–6.5(–7) × 5–6 × 4–4.5(–5) µm, with an apical germ pore. *Asexual morph* unknown.

Culture characteristics — Colonies on OA with an entire edge, about 32–38 mm diam in 7 d at 25 °C, forming pale mouse grey ascomata, without aerial hypha, without coloured exudates, reverse uncoloured. Colonies on CMA similar to those on OA, but forming denser ascomata, and some ascomata developed slower. Colonies on MEA with an entire edge, membranous, about 35–41 mm diam in 7 d at 25 °C, forming dense and pale mouse grey to mouse grey ascomata and radiating furrows in the central part, with seven or more concentric rings around the mass of ascomata which are formed by immersed hyphae, without aerial hyphae; without coloured exudates, reverse uncoloured. Colonies on PCA transparent due to very spare mycelia, with an entire edge, about 31–37 mm diam in 7 d at 25 °C, forming relatively sparse pale mouse grey ascomata, without aerial hypha, without coloured exudates, reverse uncoloured.

Typus. The Netherlands, Reeuwijk, from garden soil, Feb. 2017, *J. Hilkhuijsen* (holotype CBS H-23232, culture ex-type CBS 143305 = JW16019; ITS, LSU, *tub2* and *rpb2* sequences GenBank MG432011, MG432012, MF716586 and MF716587, MycoBank MB823460).

Notes — This species appears morphologically similar to *Collariella bostrychodes*, but can be distinguished by smaller ascospores and thinner terminal ascomatal hairs compared to the ascospores (6–7 × 5.5–6.5 × 4.5–5.5 µm) and the terminal hairs (4–7 µm near the base) of *C. bostrychodes*. Phylogenetically, this species is close to *C. quadrangulata* that has quadrangular ascospores.



Consensus phylogram resulting from a Bayesian analysis of partial sequences of *rpb2* region from representative strains of *Collariella* species. The sequences were aligned using MAFFT v. 7 (Katoh & Standley 2013) and included 852 nucleotides. GTR+I+G was used as the best nucleotide substitution model and the phylogenetic tree was generated under MrBayes v. 3.2.1 (Ronquist & Huelsenbeck 2003). *Chaetomium globosum* (*Chaetomiaceae*, *Sordariales*) was used as the outgroup taxon.

Colour illustrations. Background, collection site (backyard) and collector (Joost Hilkhuijsen); ascomata with spirally coiled ascomatal hairs (scale bar = 100 µm), ascomatal wall, asci, part of a terminal ascomatal hair and ascospores (scale bars = 10 µm).

X.W. Wang, State Key Laboratory of Mycology, Institute of Microbiology, Chinese Academy of Sciences, No. 3,
1st Beichen West Road, Chaoyang District, Beijing 100101, China;
e-mail: wangxw@im.ac.cn

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