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RESEARCH ARTICLE

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P.W. Crous[1], R.G. Shivas[2], M.J. Wingfield[3], B.A. Summerell[4], A.Y. Rossman[5], J.L. Alves[6], G.C. Adams[7], R.W. Barreto[6], A. Bell[8], M.L. Coutinho[9], S.L. Flory[10], G. Gates[11], K.R. Grice[12], G.E.St.J. Hardy[13], N.M. Kleczewski[14], L. Lombard[1], C.M.O. Longa[15], G. Louis-Seize[16], F. Macedo[9], D.P. Mahoney[8], G. Maresi[17], P.M. Martin-Sanchez[18], L. Marvanová[19], A.M. Minnis[20], L.N. Morgado[21], M.E. Noordeloos[21], A.J.L. Phillips[22], W. Quaedvlieg[1], P.G. Ryan[23], C. Saiz-Jimenez[18], K.A. Seifert[16], W.J. Swart[24], Y.P. Tan[2], J.B. Tanney[16], P.Q. Thu[25], S.I.R. Videira[1], D.M. Walker[26], J.Z. Groenewald[1]

Key words

ITS DNA barcodes
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Abstract Novel species of microfungi described in the present study include the following from Australia: *Catenulostroma corymbiae* from *Corymbia, Devriesia stirlingiae* from *Stirlingia*, *Penidiella carpentariae* from *Carpentaria, Phaeococcomyces eucalypti* from *Eucalyptus*, *Phialophora livistonae* from *Livistona*, *Phyllosticta aristolochiicola* from *Aristolochia, Clitopilus austroprunulus* on sclerophyll forest litter of *Eucalyptus regnans* and *Toxicocladosporium posoqueriae* from *Posoqueria*. Several species are also described from South Africa, namely: *Ceramothyrium podocarpi* from *Podocarpus*, *Cercospora chrysanthemoides* from *Chrysanthemoides*, *Devriesia shakazului* from *Aloe*, *Penidiella drakensbergensis* from *Protea*, *Strelitziana cliviae* from *Clivia* and *Zasmidium syzygii* from *Syzygium*. Other species include *Bipolaris microstegii* from *Microstegium* and *Synchaetomella acerina* from *Acer* (USA), *Brunneiapiospora austropalmicola* from *Rhopalostylis* (New Zealand), *Calonectria pentaseptata* from *Eucalyptus* and *Macadamia* (Vietnam), *Ceramothyrium melastoma* from *Melastoma* (Indonesia), *Collembolispora aristata* from stream foam (Czech Republic), *Devriesia imbrexigena* from glazed decorative tiles (Portugal), *Microcyclospora rhoicola* from *Rhus* (Canada), *Seiridium phylicae* from *Phylica* (Tristan de Cunha, Inaccessible Island), *Passalora lobeliae-fistulosis* from *Lobelia* (Brazil) and *Zymoseptoria verkleyi* from *Poa* (The Netherlands). *Valsalnicola* represents a new ascomycete genus from *Alnus* (Austria) and *Parapenidiella* a new hyphomycete genus from *Eucalyptus* (Australia). Morphological and culture characteristics along with ITS DNA barcodes are also provided.

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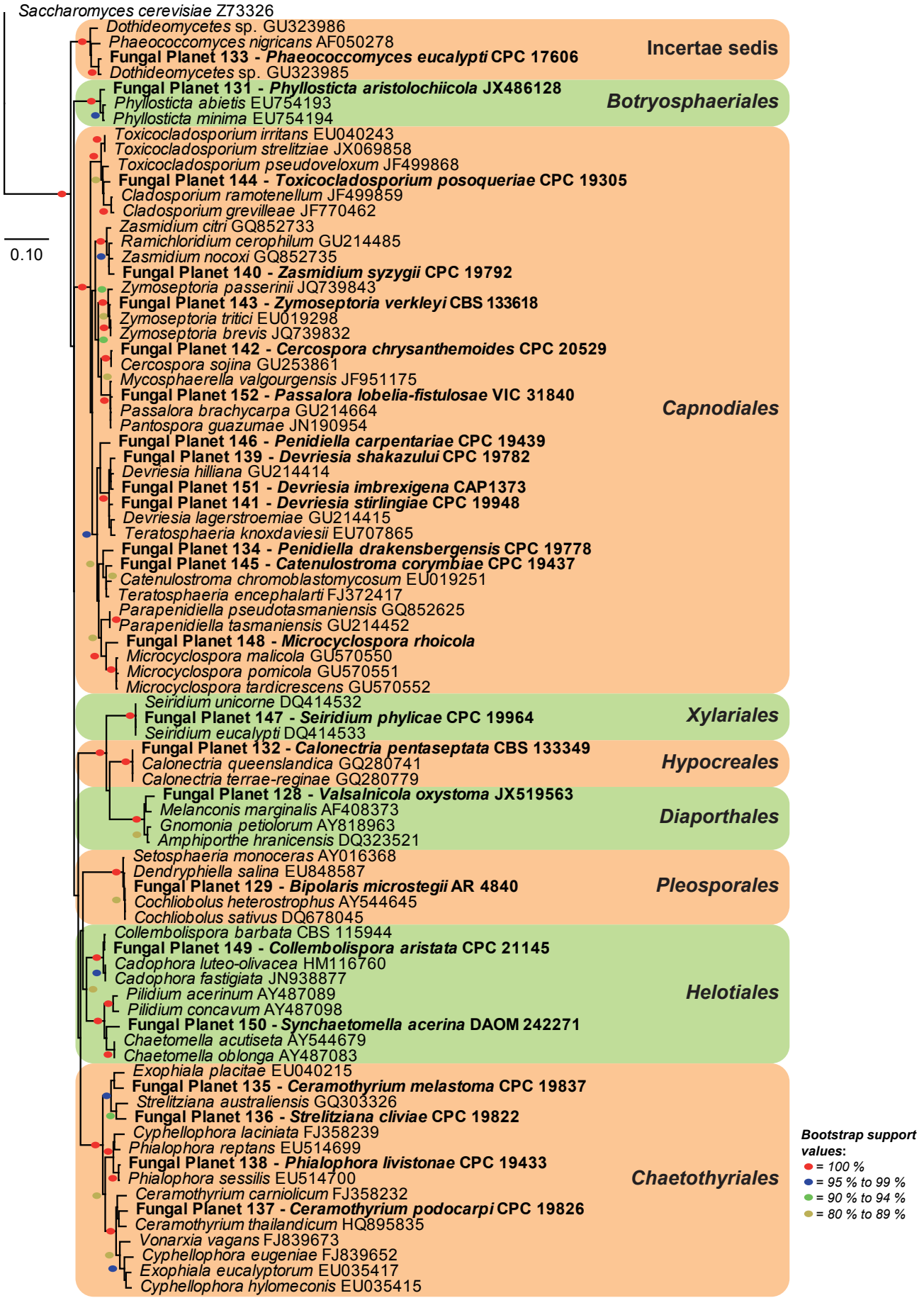
[1] CBS-KNAW Fungal Biodiversity Centre, Uppsalalaan 8, 3584 CT Utrecht, The Netherlands; corresponding author e-mail: p.crous@cbs.knaw.nl.
[2] Biosecurity Queensland, Ecosciences Precinct, Level 2C East, GPO Box 267, Brisbane 4001, Queensland, Australia.
[3] Forestry and Agricultural Biotechnology Institute, University of Pretoria, South Africa.
[4] Royal Botanic Gardens and Domain Trust, Mrs. Macquaries Road, Sydney, NSW 2000, Australia.
[5] Systematic Mycology & Microbiology Laboratory, USDA-ARS, Rm. 246, B010A, 10300 Baltimore Ave., Beltsville, MD 20705, USA.
[6] Universidade Federal de Viçosa UFV, Campus Universitário, 36570-00, Viçosa, Brazil.
[7] Department of Plant Pathology, University of Nebraska, Lincoln, NE 68583, USA.
[8] Gurney Road 45, Lower Hutt, New Zealand.
[9] REQUIMTE – CQFB and Departamento de Conservação e Restauro, Faculdade de Ciências e Tecnologia, Universidade Nova de Lisboa, Monte de Caparica, 2829-516 Caparica, Portugal.
[10] Agronomy Department, University of Florida, Gainesville, FL 32611, USA.
[11] School of Plant Science, University of Tasmania, Hobart, Australia.
[12] Agri-Science Queensland, PO Box 1054, Mareeba 4880, Queensland, Australia.
[13] School of Biological Sciences and Biotechnology, Murdoch University, Murdoch, Western Australia, 6150.
[14] Department of Botany and Plant Pathology, Purdue University, Southwest Purdue Agricultural Program, 4369 North Purdue Rd., Vincennes, IN 47591, USA.
[15] FEM-IASMA – Research and Innovation Centre, Sustainable Agro-Ecosystems and Bioresources Department. Via E. Mach 1, 38010 San Michele all'Adige (TN), Italy.
[16] Biodiversity (Mycology & Botany), Agriculture & Agri-Food Canada, 960 Carling Ave., Ottawa, Ontario K1A 0C6, Canada.
[17] IASMA - Centre for Technology Transfer, Via E. Mach 1, 38010 San Michele all'Adige (TN), Italy.
[18] Instituto de Recursos Naturales y Agrobiologia, IRNAS-CSIC, Av. Reina Mercedes 10, 41012 Sevilla, Spain.
[19] Czech Collection of Microorganisms, Institute of Experimental Biology, Faculty of Science, Masaryk University, Tvrdého 14, 602 00 Brno, Czech Republic.
[20] Center for Forest Mycology Research, Northern Research Station, USDA-Forest Service, One Gifford Pinochet Dr., Madison, WI 53726, USA.
[21] National Herbarium of the Netherlands, Naturalis Biodiversity Center, Leiden University, P.O. Box 9514, 2300 RA Leiden, The Netherlands.
[22] CREM, Departamento de Ciências da Vida, Faculdade de Ciências e Tecnologia, Universidade Nova de Lisboa, Monte de Caparica, 2829-516 Caparica, Portugal.
[23] Percy FitzPatrick Institute of African Ornithology, University of Cape Town, Rondebosch 7701, South Africa.
[24] Department of Plant Pathology, University of the Free State, P.O. Box 339, Bloemfontein 9300, South Africa.
[25] Forest Science Institute of Vietnam, Dong Ngac, Tu Liem, Hanoi, Vietnam.
[26] Department of Natural Sciences, The University of Findlay, Findlay, OH 45840, USA.



Neighbour-joining tree obtained using a distance analysis with a general time reversible (GTR) substitution model on the partial 28S nrRNA gene alignment (817 nucleotides including alignment gaps) as implemented in PAUP v. 4.0b10 (Swofford 2003). Novel species are indicated in a **bold** font and the orders are indicated on the right-hand side of the figure. The scale bar indicates the number of substitutions per site and the bootstrap support values (based on 1 000 replicates) are shown by colour-coded dots for values > 79 % (see legend on figure). The tree was rooted to a sequence of *Saccharomyces cerevisiae* (GenBank Z73326.)


Calonectria pentaseptata

Fungal Planet 132 – 20 December 2012

Calonectria pentaseptata L. Lombard, M.J. Wingf., P.Q. Thu & Crous, *sp. nov*.

Etymology. Name refers to the 5-septate macroconidia produced by this fungus.

Sexual morph unknown. *Conidiophores* consisting of a stipe bearing a suit of penicillate fertile branches, a stipe extension, and terminal vesicle; stipe septate, hyaline, smooth 47–133 × 6–10 µm; stipe extension septate, straight to flexuous, 168–350 µm long, 3–6 µm wide at the apical septum, terminating in a narrowly clavate vesicle, 2–6 µm diam. *Conidiogenous apparatus* 70–99 µm long, 23–90 µm wide; primary branches 0–1-septate, 19–31 × 4–7 µm; secondary branches aseptate, 16–34 × 4–7 µm; tertiary branches aseptate, 14–22 × 4–6 µm, each terminal branch producing 1–3 phialides; phialides cylindrical to allantoid, obpyriform when carried singly, hyaline, aseptate, 15–24 × 4–6 µm; apex with minute periclinal thickening and inconspicuous collarette. *Macroconidia* cylindrical, rounded at both ends, straight, (75–)87–109(–115) × (5–)6–8(–10) µm (av. = 98 × 7 µm), 5(–8)-septate, lacking a visible abscission scar, held in parallel cylindrical clusters by colourless slime. *Megaconidia* and *microconidia* not seen.

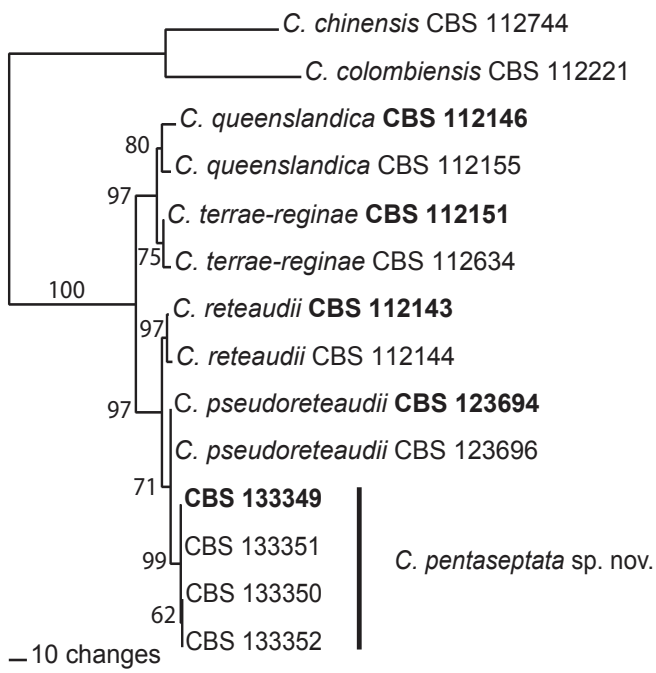
Culture characteristics — (in the dark, 24 °C after 1 wk): Colonies fast growing, with optimum growth at 24 °C on MEA; surface sienna to dark brick, reverse sepia-brown; abundant aerial mycelium and sporulation; chlamydospores extensive throughout the medium, forming microsclerotia.

Typus. Vietnam, Bavi, Hanoi, *Eucalyptus* hybrid, Sept. 2011, P.Q. Thu, holotype CBS H-21062, culture ex-type CBS 133349, β-tubulin (TUB) sequence GenBank JX855942, Histone H3 (HIS3) sequence GenBank JX855946, ITS sequence GenBank JX855950, LSU sequence GenBank JX855954 and translations elongation factor 1-alpha (TEF1-α) sequence GenBank JX855958, MycoBank MB801468.

Other specimens examined. Vietnam, Bavi, Hanoi, *Macadamia* sp., Sept. 2011, P.Q. Thu, CBS 133351, TUB sequence GenBank JX855944, HIS3 sequence GenBank JX855948, ITS sequence GenBank JX855952, LSU sequence GenBank JX855956 and TEF1-α sequence GenBank JX855960; ibid., *E. urophylla*, Sept. 2011, P.Q. Thu, CBS 133350, TUB sequence GenBank JX855943, HIS3 sequence GenBank JX855947, ITS sequence GenBank JX855951 and TEF1-α sequence GenBank JX855959; ibid., *Eucalyptus* hybrid, Sept. 2011, P.Q. Thu, CBS 133352, TUB sequence GenBank JX855945, HIS3 sequence GenBank JX855949, ITS sequence GenBank JX855953 and TEF1-α sequence GenBank JX855961.

Notes — *Calonectria pentaseptata* resides in the *C. reteaudii* species complex (Kang et al. 2001, Lombard et al. 2010a, b, c) based on morphological characteristics supported by phylogenetic inference. The macroconidia of *C. pentaseptata* (av. = 98 × 7 µm) are smaller than those of *C. pseudoreteaudii* (av. = 104 × 8 µm), and larger than those of *C. queenslandica* (av. = 69 × 6 µm), *C. reteaudii* (av. = 84 × 6.5 µm) and *C. terrae-reginae* (av. = 76 × 6 µm) (Lombard et al. 2010c). As with *C. queenslandica* and *C. terrae-reginae*, *C. pentaseptata* failed to produce microconidiophores and microconidia, distinguishing this fungus from *C. pseudoreteaudii* and *C. reteaudii*, which readily form these structures in culture (Lombard et al. 2010a, b, c).

One of two equally most parsimonious trees (TI = 380, CI = 0.942, RI = 0.921, RC = 0.868) obtained from a heuristic search with 1 000 random taxon additions of the combined sequences of TUB, HIS3 and TEF1-α sequence alignments of the *C. reteaudii* complex using PAUP v. 4.0b10. The bootstrap support values from 1 000 replicates are shown at the nodes. The tree was rooted to *C. chinensis* (CBS 112744) and *C. colombiensis* (CBS 112221). The ex-type strains are printed in **bold**.



Colour illustrations. *Eucalyptus* plantation in Vietnam; conidiophore; clavate vesicles; conidiogenous apparatus; conidia. Scale bars = 10 µm.

Lorenzo Lombard & Pedro W. Crous, CBS-KNAW Fungal Biodiversity Centre, P.O. Box 85167, 3508 AD Utrecht, The Netherlands; e-mail: l.lombard@cbs.knaw.nl & p.crous@cbs.knaw.nl
Pham Q. Thu, Forest Science Institute of Vietnam, Dong Ngac, Tu Liem, Hanoi, Vietnam; e-mail: vkhln@vista.gov.vn
Michael J. Wingfield, Forestry and Agricultural Biotechnology Institute, University of Pretoria, South Africa; e-mail: mike.wingfield@fabi.up.ac.za


Ceramothyrium melastoma

Fungal Planet 135 – 20 December 2012

Ceramothyrium melastoma Crous & M.J. Wingf., *sp. nov*.

Etymology. Named reflects the host genus, *Melastoma*.

Description of colonies sporulating on synthetic nutrient-poor agar (SNA). *Mycelium* consisting of pale brown, septate, branched, finely verruculose, 2–3 µm diam hyphae. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* integrated, lateral on hyphae, phialidic with small collarette (flaring or not), 2 µm wide, 1–1.5 µm high. *Conidia* pale brown to subhyaline, subcylindrical to obclavate, apex subobtuse, base tapering, truncate, 1–12-septate, but commonly forming lateral branches as in *Stanhughesia* morphs of *Ceratothyrium* (especially on potato-dextrose agar (PDA) and malt extract agar (MEA), but less so on SNA), conidial body (25–)40–60(–90) × (2.5–)3 µm, lateral branches 7–25 × 2.5–3 µm. *Triposporium* morph on PDA and MEA: *central conidial body* 15–30 µm long, 3–4 µm wide at clavate apex, giving rise to two apical, lateral branches that angle upwards, of unequal length, lateral arms 15–35 × 2.5–3 µm; constricted at septa where lateral arms join the conidial body.

Culture characteristics — (in the dark, 25 °C after 2 wk): Colonies on MEA, PDA and oatmeal agar erumpent, spreading, with smooth, even margin and sparse aerial mycelium. Surface pale olivaceous-grey, reverse olivaceous-grey, reaching 5 mm diam.

Typus. Indonesia, North Sumatra, Lake Toba, on leaves of *Melastoma* sp. (*Melastomataceae*), 20 Aug. 2011, *M.J. Wingfield*, holotype CBS H-21077, culture ex-type CPC 19837 = CBS 133576, ITS sequence GenBank KC005771, LSU sequence GenBank KC005793, MycoBank MB801771.

Notes — Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the LSU sequence are *Phaeococcomyces catenatus* (GenBank AF050277; Identities = 847/875 (97 %), Gaps = 0/875 (0 %)), *Exophiala placitae* (GenBank EU040215; Identities = 841/871 (97 %), Gaps = 0/871 (0 %)), and *Sarcinomyces petricola* (GenBank FJ358249; Identities = 835/865 (97 %), Gaps = 0/865 (0 %)). Closest hits using the ITS sequence had highest similarity to *Trichomerium deniqulatum* (GenBank JX313654; Identities = 559/664 (84 %), Gaps = 38/664 (6 %)), *Phaeococcomyces chersonesos* (GenBank AJ507323; Identities = 534/641 (83 %), Gaps = 43/641 (7 %)), and *Trichomerium gleosporum* (GenBank JX313656; Identities = 417/480 (87 %), Gaps = 18/480 (4 %)). *Ceramothyrium melastoma* clusters in a basal lineage to the *Chaetothyriales*, and renders *Ceramothyrium* paraphyletic. For a discussion on *Ceramothyrium*, see Fungal Planet 137.

Colour illustrations. Flower and leaves of *Melastoma* sp.; colonies growing on synthetic nutrient-poor agar; conidiogenous cells giving rise to conidia, which become star-shaped with age. Scale bars = 10 µm.

Pedro W. Crous & Johannes Z. Groenewald, CBS-KNAW Fungal Biodiversity Centre, P.O. Box 85167, 3508 AD Utrecht, The Netherlands;
e-mail: p.crous@cbs.knaw.nl & e.groenewald@cbs.knaw.nl
Michael J. Wingfield, Forestry and Agricultural Biotechnology Institute, University of Pretoria, South Africa;
e-mail: mike.wingfield@fabi.up.ac.za


Seiridium phylicae

Fungal Planet 147 – 20 December 2012

Seiridium phylicae Crous & M.J. Wingf., *sp. nov*.

Etymology. Name refers to the host genus, *Phylica*.

Caulicolous. *Conidiomata* stromatic, pycnidia, scattered to aggregated, erumpent, conical, up to 350 µm diam, uniloculate, dark brown to black, opening by irregular rupture; basal stroma of dark brown *textura angularis*. *Conidiophores* lining cavity, filamentous, creating impression of paraphyses, septate, branched, hyaline, smooth, up to 80 µm long, and 3.5 µm wide. *Conidiogenous cells* subcylindrical, terminal and lateral, integrated, smooth, hyaline, 10–20 × 1.5–3 µm; proliferating percurrently. *Conidia* fusoid to ellipsoid, dark to golden brown, granular, 5-septate, not constricted at septa, with visible central septal pore, (23–)28–30(–35) × (9–)10(–11) µm; basal cell conical with truncate hilum, pale brown to hyaline, 3–5 µm long; 4 median cells doliiform to subcylindrical, brown, with wall and septa being darker, cells together 17–23 µm long; apical cell broadly conical, apex rounded, hyaline, 2–4 µm long. Apical appendages tubular, unbranched, eccentric, 6–8 µm long; basal appendages unbranched, centric, 2–5 µm long.

Culture characteristics — (in the dark, 24 °C after 2 wk): Colonies erumpent, spreading, with moderate aerial mycelium and even, lobate margins. On malt extract agar surface pale olivaceous-grey, with patches of dirty white; reverse cinnamon. On potato-dextrose agar surface dirty white with patches of black sporulation; reverse dirty white. On oatmeal agar surface pale grey-olivaceous with patches of dirty white, reaching 30 mm diam.

Typus. UK, British Overseas Territory of Saint Helena, Ascension and Tristan da Cunha, Inaccessible Island, Blenden Hall, S37°17'41" W12°42'08", stems of *Phylica arborea* (*Rhamnaceae*), Sept. 2011, *P.G. Ryan*, holotype CBS H-21089, cultures ex-type CPC 19962–19965 (CPC 19964 = CBS 133587), β-tubulin (TUB) sequence GenBank KC005819–KC005821, TEF1-α sequences GenBank KC005815–KC005817, ITS sequences GenBank KC005785–KC005785, LSU sequences GenBank KC005807–KC005810, MycoBank MB801788.

Notes — Conidia of *Seiridium cardinale* are 21–30 × 8–10 µm, with basal appendage being 1 µm long when present, and apical appendage 0.5–1.5 µm (Sutton 1980), which clearly distinguishes it from *Seiridium phylicae*. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the LSU sequence are *Seiridium eucalypti* (GenBank DQ414533; Identities = 833/833 (100 %), Gaps = 0/833 (0 %)), *Seiridium unicorne* (GenBank DQ414532; Identities = 833/833 (100 %), Gaps = 0/833 (0 %)) and *Lepteutypa cupressi* (GenBank AF382379; Identities = 872/875 (99 %), Gaps = 3/875 (0 %)). Closest hits using the ITS sequence had highest similarity to *Seiridium cardinale* (GenBank AF409995; Identities = 552/558 (99 %), Gaps = 2/558 (0 %)), *Seiridium cupressi* (GenBank FJ430600; Identities = 558/567 (98 %), Gaps = 4/567 (1 %)) and *Seiridium unicorne* (GenBank AF377299; Identities = 567/578 (98 %), Gaps = 2/578 (0 %)). Closest hits using the TUB sequence had highest similarity to *Seiridium cardinale* (GenBank DQ926973; Identities = 353/366 (96 %), Gaps = 3/366 (1 %)) and *Seiridium cupressi* (GenBank AF320495; Identities = 385/401 (96 %), Gaps = 2/401 (0 %)). Only distant hits (e.g. Identities = 218/249 (88 %), Gaps = 12/249 (5 %)) with *Pestalotiopsis* spp. were obtained when the TEF sequences were used in a megablast search.

Colour illustrations. *Phylica arborea* growing on Inaccessible Island; colony on synthetic nutrient-poor agar; conidiophores, conidiogenous cells and conidia. Scale bars = 10 µm.

Pedro W. Crous & Johannes Z. Groenewald, CBS-KNAW Fungal Biodiversity Centre, P.O. Box 85167, 3508 AD Utrecht, The Netherlands;
e-mail: p.crous@cbs.knaw.nl & e.groenewald@cbs.knaw.nl
Peter G. Ryan, Percy FitzPatrick Institute of African Ornithology, University of Cape Town, Rondebosch 7701, South Africa;
e-mail: pryan31@gmail.com
Michael J. Wingfield, Forestry and Agricultural Biotechnology Institute, University of Pretoria, South Africa;
e-mail: mike.wingfield@fabi.up.ac.za

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