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Key words

ITS DNA barcodes
LSU
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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 podocarp* from *Podocarpus*, *Cercospora chrysanthemoides* from *Chrysanthemoides*, *Devriesia shakazulii* 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 phyllicae* from *Phyllica* (Tristan de Cunha, Inaccessible Island), *Passalora lobeliaefistulosis* from *Lobelia* (Brazil) and *Zymoseptoria verkleyi* from *Poa* (The Netherlands). *Valsalinicola* 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.

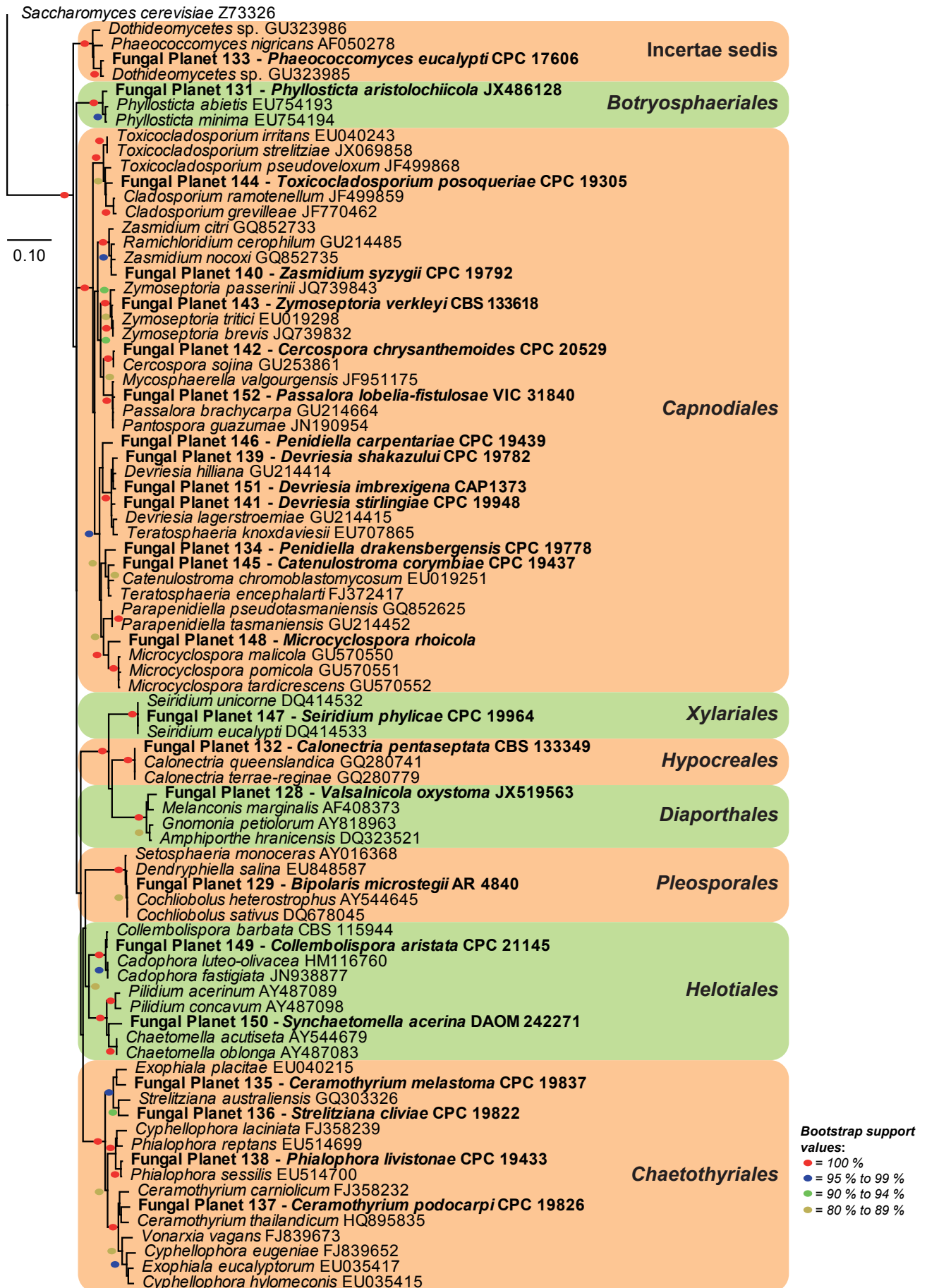
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Neighbour-joining tree obtained using a distance analysis with a general time reversible (GTR) substitution model on the partial 28S nrRNA gene alignment (817 nucleotides including alignment gaps) as implemented in PAUP v. 4.0b10 (Swofford 2003). Novel 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

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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 collarete. *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.

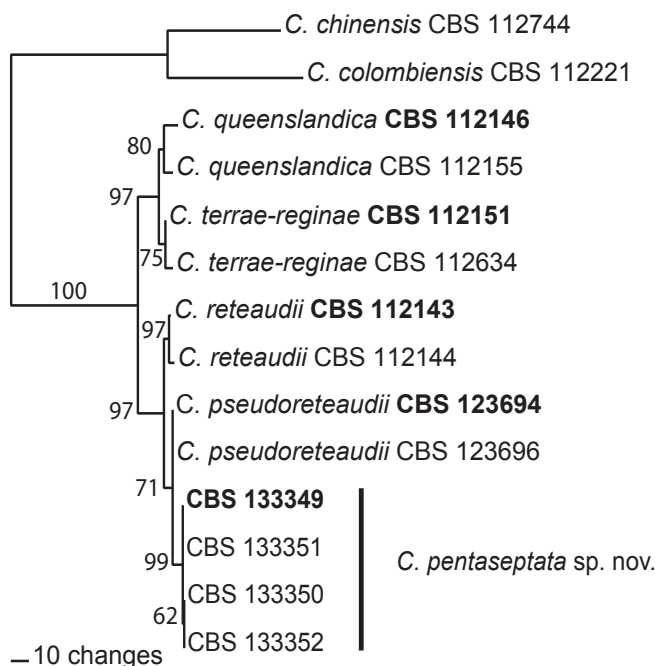
Typus. VIETNAM, Bavi, Hanoi, *Eucalyptus* hybrid, Sept. 2011, P.Q. Thu, holotype CBS H-21062, culture ex-type CBS 133349, β-tubulin (TUB) sequence GenBank JX855942, Histone H3 (HIS3) sequence GenBank JX855946, ITS sequence GenBank JX855950, LSU sequence GenBank JX855954 and translations elongation factor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

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

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**.



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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 collarete (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 CBSH-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 NCBI's 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 deniquatum* (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.



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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 NCBI's GenBank nucleotide database, the closest hits using the LSU sequence are *Seiridium eucalypti* (GenBank DQ414533; Identities = 833/833 (100 %), Gaps = 0/833 (0 %)), *Seiridium unicorn* (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 unicorn* (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.

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