



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 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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