Myrtacremonium eucalypti
Fungal Planet 563 – 20 June 2017

**Myrtacremonium** Crous, *gen. nov.*

*Etymology.* Name reflects the host family *Myrtaceae,* and the fact that the fungus has an acremonium-like morphology.

*Classification.* *Niessliaceae,* *Hypocreales,* *Sordariomycetes.*

*Mycelium* consisting of hyaline, smooth, septate, branched, hyphae. *Conidiophores* solitary, erect, straight to flexuous, hyaline, smooth, with basal septum. *Conidiogenous cells* terminal, integrated, hyaline, smooth, thick-walled at base, subcylindrical; apex phialidic, with minute flared collarette. *Conidia* solitary, but accumulating in slimy mass, hyaline, smooth, subcylindrical, straight with obtuse ends.

*Type species.* *Myrtacremonium eucalypti* Crous.
MycoBank MB820937.

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**Myrtacremonium eucalypti** Crous, *sp. nov.*

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

*Mycelium* consisting of hyaline, smooth, septate, branched, 1.5–2 μm diam hyphae. *Conidiophores* solitary, erect, straight to flexuous, hyaline, smooth, with basal septum, 20–60 × 2–3 μm. *Conidiogenous cells* terminal, integrated, hyaline, smooth, thick-walled at base, subcylindrical, 15–55 × 2–2.5 μm; apex phialidic, 1–1.5 μm diam with minute flared collarette. *Conidia* solitary, but accumulating in slimy mass, hyaline, smooth, subcylindrical, straight with obtuse ends, (5–)6–7(–8) × 1.5 μm.

*Culture characteristics.* — Colonies flat, spreading, reaching 10–20 mm diam after 2 wk at 25 °C, with sparse aerial mycelium, folded surface, and smooth, lobed margins. On MEA surface and reverse buff. On OA surface pale luteous to luteous. On PDA surface and reverse pale luteous.

*Typus.* **Australia,** Western Australia, Perth, on leaves of *Eucalyptus globulus* (*Myrtaceae*), 21 Sept. 2015, *P.W. Crous* (holotype CBS H-23123, culture ex-type CPC 29272 = CBS 142161, ITS, LSU, and tub2 sequences GenBank KY979741, KY979796, and KY979912, MycoBank MB820938).

*Notes.* *Myrtacremonium* is a new genus in the Acremonium complex (Gräfenhan et al. 2011, Lombard et al. 2015). Phylogenetically, it is related to *Eucasphaeria* (e.g. *E. rustici,* LSU GenBank KY173501; Identities = 767/785 (98 %), 2 gaps (0 %)), *Niesslia* (e.g. *N. exilis,* LSU GenBank AY489718; Identities = 782/798 (98 %), 2 gaps (0 %)), and *Rosasphaeria* (e.g. *R. moravica,* LSU GenBank JF440985; Identities = 782/798 (98 %), 2 gaps (0 %)), although it appears to cluster apart (only distant hits were also obtained when the ITS sequences were compared).

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*Colour illustrations.* *Eucalyptus globulus*; colony on SNA, conidiophores and conidia. Scale bars = 10 μm.

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