

Cylindromonium alloxyl



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Cylindromonium alloxyl Crous, *sp. nov.*

Etymology. Name refers to the host genus *Alloxylon* from which it was isolated.

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

Mycelium consisting of hyaline, smooth, septate, branched, 1.5–2 µm diam hyphae. *Conidiophores* solitary, subcylindrical, unbranched, hyaline, smooth, flexuous, erect, 1–2-septate, 30–60 × 2 µm. *Conidiogenous cells* integrated, terminal, hyaline, smooth, subcylindrical, 10–20 × 1.5–2 µm, phialidic, apex with periclinal thickening, lacking collarette. *Conidia* hyaline, smooth, medianly 1-septate, aggregating in cylindrical spore packets, subcylindrical with obtuse ends, (14–)15–17(–18) × 2–3 µm.

Culture characteristics — Colonies erumpent, spreading, surface folded, with moderate aerial mycelium and smooth, lobate margin, reaching 25 mm diam after 2 wk at 25 °C. On MEA and PDA surface and reverse saffron; on OA surface buff.

Typus. AUSTRALIA, New South Wales, Limpinwood Nature Reserve, Mt Merino, mycophilic on *Meliola* on leaves of *Alloxylon pinnatum* (*Proteaceae*), 26 May 2015, B.A. Summerell, HPC 2951 (holotype CBS H-24401, culture ex-type CPC 38159 = CBS 146806, ITS, LSU, *actA*, *his3*, *rpb2*, *tef1* (first and second part) and *tub2* sequences GenBank MW175339.1, MW175379.1, MW173093.1, MW173108.1, MW173114.1, MW173120.1, MW173128.1 and MW173133.1, MycoBank MB837829).

Notes — *Cylindromonium* was recently established as genus to accommodate acremonium-like taxa with unbranched, hyaline conidiophores, and cylindrical, 1-septate conidia (Crous et al. 2019a).

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Cylindromonium lichenicola* (strain CBS 188.70, GenBank MH859549.1; Identities = 540/591 (91 %), 18 gaps (3 %)), *Cylindromonium rhabdosporum* (strain CBS 438.66, GenBank MH858850.1; Identities = 538/590 (91 %), 18 gaps (3 %)), and *Phialoseptomonium eucalypti* (strain CBS 145542, GenBank NR_165572.1; Identities = 534/587 (91 %), 14 gaps (2 %)). Closest hits using the **LSU** sequence are *Cylindromonium lichenicola* (strain CBS 415.70A, GenBank MH871536.1; Identities = 588/608 (97 %), two gaps (0 %)), *Trichonectria rectipila* (strain CBS 132.87, GenBank NG_064146.1; Identities = 583/606 (96 %), two gaps (0 %)), and *Phialoseptomonium eucalypti* (strain CBS 145542, GenBank NG_067890.1; Identities = 571/596 (96 %), two gaps (0 %)). Closest hits using the **tef1** (second part) sequence had highest similarity to *Simplicillium aogashimaense* (strain JCM 18167, GenBank LC496904.1; Identities = 391/432 (91 %), two gaps (0 %)), *Simplicillium cylindrosporium* (strain JCM 18169, GenBank LC496906.1; Identities = 390/433 (90 %), two gaps (0 %)), and *Nectria marina* (strain MFLUCC 16-0544, GenBank MN433214.1; Identities = 389/432 (90 %), no gaps (0 %)). No significant hits were obtained when the **actA**, **his3**, **rpb2**, **tef1** (first part) and **tub2** sequences were used in blastn and megablast searches.

Colour illustrations. Rainforest at Limpinwood Nature Reserve (photo B. Summerell). Conidiophores sporulating on a sterile pine needle; conidiophores and conidiogenous cells giving rise to conidia; conidia. Scale bars = 10 µm.