Cylindrium grande
Cylindrium grande Crous & Carnegie, sp. nov.

Etymology. Name refers to *Eucalyptus grandis*, the host species from which this fungus was first isolated.

Classification — *Cylindriaceae*, *Hypocreales*, *Sordariomycetes*.

Myelium consisting of branched, septate, hyaline, 1.5–2.5 μm diam hyphae that form large, black, globose to lobed fertile structures up to 500 μm long on SNA, MEA, PDA and OA. *Conidiomata* sporodochial, sporulating on SNA, brown, 80–200 μm diam. *Conidiophores* arising from a pale brown stroma, smooth, pale brown, subcylindrical, branched below, 1–3-septate, 20–30 × 4–6 μm. *Conidiogenous cells* integrated, pale brown, smooth, subcylindrical to somewhat ampulliform, proliferating sympodially, terminal and intercalary, 15–20 × 2–4 μm; scars inconspicuous. *Conidia* solitary, subcylindrical, straight, aseptate, hyaline, smooth, apex obtuse, base bluntly rounded to truncate, (13–)18–20 (–22) × (2–)2.5–3 μm.

Culture characteristics — Colonies flat, spreading, with rounded to truncate, (13–)18–20 (–22) × (2–)2.5–3 μm. × 2–4 μm; scars inconspicuous. *Conidia* solitary, subcylindrical, straight, aseptate, hyaline, smooth, apex obtuse, base bluntly rounded to truncate, (13–)18–20 (–22) × (2–)2.5–3 μm. × 2–4 μm; scars inconspicuous. *Conidia* solitary, subcylindrical, straight, aseptate, hyaline, smooth, apex obtuse, base bluntly rounded to truncate, (13–)18–20 (–22) × (2–)2.5–3 μm.

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Notes — *Cylindrium* was treated by Crous et al. (2018b). *Cylindrium grande* is phylogenetically related to *C. elongatum* (on *Quercus* leaf litter; conidia 15–18 × 2 mm; Ellis & Ellis 1997), but the latter has smaller conidia.

Based on a megablast search of NCBI’s GenBank nucleotide database, the closest hits using the ITS of *C. grande* sequence had highest similarity to *Cylindrium elongatum* (GenBank KM231852; Identities = 528/544 (97 %), 3 gaps (0 %)), *Cylindrium syzygii* (GenBank NR_157430.1; Identities = 519/545 (95 %), 16 gaps (2 %)) and *Cylindrium algarvense* (GenBank NR_132637; Identities = 495/528 (94 %), 14 gaps (2 %)). The ITS sequences of *C. grande* and *C. elongatum* are 537/541 (99 %, including one gap) similar. Closest hits using the LSU sequence of *C. grande* are *Tristriatiperidium microsporum* (GenBank KT696539; Identities = 732/736 (99 %), no gaps), *Cylindrium syzygii* (as *Pseudoidriella syzygii*, GenBank JQ044441; Identities = 833/839 (99 %), 1 gap) and *Cylindrium purgamentum* (GenBank KY173525; Identities = 813/820 (99 %), 1 gap). The LSU sequences of *C. grande* and *C. elongatum* are 827/833 (99 %, including one gap) similar. Closest hits using the actA sequence of *C. grande* had highest similarity to *Cylindrium elongatum* (GenBank KM231264; Identities = 616/672 (92 %), 16 gaps (2 %)) and *Cylindrium aeuriginosum* (GenBank KM231265; Identities = 515/560 (92 %), 16 gaps (2 %)). The actA sequences of *C. grande* and *C. elongatum* are 631/667 (95 %, including three gaps) similar.

Closest hits using the cmdA sequence of *C. grande* had highest similarity to *Cylindrium elongatum* (GenBank KM231448; Identities = 557/692 (80 %), 42 gaps (6 %)) and *Cylindrium aeuriginosum* (GenBank KM231450; Identities = 492/604 (81 %), 35 gaps (6 %)). The cmdA sequences of *C. grande* and *C. elongatum* are 645/727 (89 %, including 16 gaps) similar. Closest hits using the rpb2 sequence of *C. grande* had highest similarity to *Cylindrium elongatum* (GenBank KM232428; Identities = 707/801 (88 %), 8 gaps (0 %)) and *Cylindrium aeuriginosum* (GenBank KM232430; Identities = 748/859 (87 %), 3 gaps (0 %)). The rpb2 sequences of *C. grande* and *C. elongatum* are 798/864 (92 %, no gaps) similar. Closest hits using the tef1 sequence of *C. grande* had highest similarity to *Cylindrium elongatum* (GenBank KM231988; Identities = 358/408 (88 %), 20 gaps (4 %)). The tef1 sequences of *C. grande* and *C. elongatum* are 414/469 (88 %, including 10 gaps) similar. Closest hits using the tub2 sequence of *C. grande* had highest similarity to *Cylindrium elongatum* (GenBank KM232123.1; Identities = 521/640 (81 %), 29 gaps (4 %)).

Colour illustrations. *Eucalyptus dunnii* forest. Sporodochium on pine needle agar; conidiogenous cells and conidia. Scale bars = 500 μm (sporodochium), 10 μm (all others).