

*Periconia neobrittanica*



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## *Periconia neobrittanica* Crous, *sp. nov.*

*Etymology.* Name refers to its morphological similarity with *Periconia brittanica*.

*Classification* — *Periconiaceae*, *Pleosporales*, *Dothideomycetes*.

*Mycelium* consisting of brown, verruculose, branched, septate, 2–3 µm diam hyphae. *Conidiophores* dimorphic. *Microconidiophores* reduced to conidiogenous cells occurring directly on hyphae, tretic, giving rise to a single conidium, but at times also clusters of conidial chains occur. *Macroconidiophores* 100–300 × 10–17 µm, solitary, or in clusters of 2–3, arising from a brown stroma, subcylindrical, straight to flexuous, unbranched, dark brown, smooth, thick-walled, base swollen, 15–25 µm diam; stipe mostly aseptate, with 2–5 septa in upper conidiogenous region; primary branches subcylindrical, brown, verruculose, 0–1-septate, 10–25 × 7–10 µm. *Conidiogenous cells* terminal and intercalary, occurring in an apical chain on primary, or directly on conidiophore, 10–15 µm long, tretic. *Conidia* aseptate, spherical, pale to medium brown, with delicate spines, occurring in branched chains, (6–)8–10(–12) µm diam; conidiogenous apparatus usually unilateral on conidiophore.

*Culture characteristics* — Colonies flat, spreading, with sparse aerial mycelium and even margin, covering dish after 2 wk at 25 °C. On MEA, PDA and OA surface and reverse iron-grey.

*Typus.* USA, California, Davis, UC Davis, on leaves of *Melaleuca styphelioides* × *lanceolata* (*Myrtaceae*), 2 Apr. 2019, P.W. Crous, HPC 2897 (holotype CBS H-24203, culture ex-type CPC 37903 = CBS 146062, ITS and LSU sequences GenBank MN562149.1 and MN567656.1, MycoBank MB832909).

*Notes* — *Periconia* was treated by Tanaka et al. (2015). *Periconia neobrittanica* is similar to *P. britannica* in having unilateral conidiophores and micro- plus macroconidiophores. It is distinct in that it has larger conidia with delicate spines, and shorter conidiophores (Ellis 1976).

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Ascomycete* sp. (strain nasa64 from the Atacama desert in Chile, GenBank DQ683977.1; Identities = 528/528 (100 %), no gaps), *Periconia aquatica* (strain HKAS 92754, GenBank NR\_158841.1; Identities = 438/475 (92 %), 5 gaps (1 %)), and *Periconia submersa* (strain HKAS 92738, GenBank NR\_158842.1; Identities = 437/476 (92 %), 6 gaps (1 %)). The ITS sequence is 90 % (439/487, including 11 gaps) similar to *Noosia banksiae* (strain CPC 17282, GenBank JF951147.1), which represents the most similar species obtained when the LSU sequence was used in the megablast search. Closest hits using the **LSU** sequence are *Noosia banksiae* (strain CBS 129526, GenBank NG\_064279.1; Identities = 889/896 (99 %), no gaps), *Sporidesmium tengii* (strain voucher HKUCC 10837, GenBank DQ408559.1; Identities = 849/856 (99 %), 1 gap (0 %)), and *Periconia cyperacearum* (strain CPC 32138, GenBank NG\_064549.1; Identities = 888/896 (99 %), no gaps).

*Colour illustrations.* Branch of *Melaleuca styphelioides* × *lanceolata* in California. Conidiophores, conidiogenous cells and conidia. Scale bars = 10 µm.