

Septoriella callistemonis



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***Septoriella callistemonis* Crous, sp. nov.**

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

Classification — *Phaeosphaeriaceae*, *Pleosporales*, *Dothideomycetes*.

Conidiomata immersed, globose, brown, pycnidial, 250–350 µm diam, with central ostiole; wall of 6–8 layers of brown *textura angularis*. *Conidiophores* reduced to conidiogenous cells lining the inner cavity, hyaline, smooth, phialidic, at times sympodial, 5–10 × 3–4 µm. *Conidia* solitary, subcylindrical, variously curved to straight, apex obtuse, base truncate, brown, smooth, guttulate, (3–)7-septate, (35–)52–65(–67) × 3 µm.

Culture characteristics — Colonies flat, spreading, with moderate aerial mycelium and smooth, lobate margin, covering dish after 2 wk at 25 °C. On MEA, PDA and OA surface and reverse olivaceous grey.

Typus. NEW ZEALAND, Tauranga port, from leaf spots of *Callistemon* sp. (*Myrtaceae*), 22 Aug. 2019, C. Inglis (holotype CBS H-24441, culture ex-type CPC 38761 = T19_05745B = CBS 146822, ITS, LSU, *rpb2*, *tef1* (first part) and *tub2* sequences GenBank MZ064412.1, MZ064469.1, MZ078194.1, MZ078220.1 and MZ078257.1, MycoBank MB 839499).

Notes — Species of *Septoriella* are mostly saprobic or weakly aggressive pathogens of grasses, and thus the occurrence of *S. callistemonis* (on *Callistemon*) is surprising. It is related to several known species (Crous et al. 2019b, Marin-Felix et al. 2019a) from which it can be distinguished based on conidial dimensions and septation.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Phaeosphaeria typharum* (strain CBS 305.71, GenBank KY090643.1; Identities = 582/593 (98 %), two gaps (0 %)), *Septoriella allojunci* (strain MFLUCC 15-0701, GenBank KU058718.1; Identities = 577/590 (98 %), two gaps (0 %)) and *Phaeosphaeria eustoma* (strain CBS 337.86, GenBank AJ496629.1; Identities = 568/581 (98 %), two gaps (0 %)). Closest hits using the **LSU** sequence are *Septoriella oudemansii* (strain CBS 138012, GenBank MH878140.1; Identities = 801/803 (99 %), no gaps), *Phaeosphaeria fuckelii* (strain CBS 388.86, GenBank MH873665.1; Identities = 801/803 (99 %), no gaps) and *Loratospora luzulae* (strain MFLUCC 14-0826, GenBank NG_069310.1; Identities = 800/803 (99 %), no gaps). Closest hits using the **rpb2** sequence had highest similarity to *Septoriella tridentina* (strain MFLUCC 15-0474, GenBank KX891170.1; Identities = 835/893 (94 %), one gap (0 %)), *Phaeosphaeria ammophilae* (strain CBS 114595, GenBank GU371724.1; Identities = 814/876 (93 %), one gap (0 %)) and *Dactylidina dactylidis* (strain MFLUCC 14-0966, GenBank MG829253.1; Identities = 834/908 (92 %), one gap (0 %)). Closest hits using the **tef1** sequence had highest similarity to *Septoriella pseudophragmitis* (strain CBS 145417, GenBank MK559452.1; Identities = 381/418 (91 %), 22 gaps (5 %)), *Septoriella hollandica* (strain CBS 145374, GenBank MK540160.1; Identities = 371/422 (88 %), 19 gaps (4 %)) and *Septoriella germanica* (strain CBS 145372, GenBank MK540159.1; Identities = 363/415 (87 %), 20 gaps (4 %)). Closest hits using the **tub2** sequence had highest similarity to *Septoriella pseudophragmitis* (strain CBS 145417, GenBank MK559451.1; Identities = 309/324 (95 %), one gap (0 %)), *Septoriella hollandica* (strain CBS 145374, GenBank MK540175.1; Identities = 300/319 (94 %), one gap (0 %)) and *Alternaria eryngii* (strain EGS 41-005, GenBank JQ672007.1; Identities = 295/328 (90 %), five gaps (1 %)).

Colour illustrations. *Callistemon* sp. Conidiogenous cells giving rise to conidia; conidia. Scale bars = 10 µm.

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