

Graminopassalora geissorhizae



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***Graminopassalora geissorhizae* Crous, sp. nov.**

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

Classification — *Mycosphaerellaceae*, *Mycosphaerellales*, *Dothideomycetes*.

Sporulating on SNA. *Conidiophores* medium brown, smooth, fasciculate, arising from a brown stroma of pseudoparenchymatal cells, subcylindrical, branched, 3–7-septate, up to 160 µm tall, 4–6 µm diam. *Conidiogenous cells* medium brown, smooth, integrated, subcylindrical, terminal and intercalary, 20–80 × 4–6 µm, with one to several loci, thickened, darkened, refractive, 2–3(–4) µm diam. *Conidia* solitary, medium brown, smooth to finely verruculose, subcylindrical, straight, apex subobtuse, base truncate, guttulate, 1–3-septate, (35–)40–55(–70) × (5–)6–7 µm; hila thickened, darkened and refractive, (2–)3–4 µm diam.

Culture characteristics — Colonies erumpent, spreading, with moderate aerial mycelium and lobed, feathery margin, reaching 15 mm diam after 2 wk at 25 °C. On MEA, PDA and OA surface and reverse olivaceous grey.

Typus. SOUTH AFRICA, Western Cape Province, Nieuwoudtville, Matjiesfontein, on leaves of *Geissorhiza splendidissima* (*Iridaceae*), 2018, *P.W. Crous*, HPC 3065 (holotype CBS H-24426, culture ex-type CPC 38623 = CBS 146788, ITS, LSU and *rpb2* sequences GenBank MW175336.1, MW175376.1 and MW173111.1, MycoBank MB837823).

Notes — *Graminopassalora*, based on *G. graminis*, is a monotypic genus occurring on members of *Poaceae*, with conidia 15–60 × 5–14 µm, (0–)1(–3)-septate (Braun et al. 2015, Videira et al. 2017). *Graminopassalora graminis* is widespread on a wide range of grasses, and Deighton (1967) considered *G. graminis* an aggregate species, possibly composed of several taxa. *Graminopassalora geissorhizae* is the first member of the genus known from *Iridaceae*.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Graminopassalora graminis* (strain MAFF 510604, GenBank MF951321.1; Identities = 383/411 (93 %), three gaps (0 %)), *Pseudocercospora ocimi-basilici* (strain ICMP 21324, GenBank MK210535.1; Identities = 377/407 (93 %), two gaps (0 %)), and *Pseudocercospora ocimicola* (strain CPC 10283, GenBank GU214678.1; Identities = 377/407 (93 %), two gaps (0 %)). Closest hits using the **LSU** sequence are *Graminopassalora graminis* (strain CBS 113303, GenBank GU214666.1; Identities = 840/848 (99 %), no gaps), *Ramulariopsis pseudoglycines* (strain CPC 18242, GenBank NG_059693.1; Identities = 829/848 (98 %), no gaps), and *Cercospora virgaureae* (strain CPC 11461, GenBank KX286977.1; Identities = 829/848 (98 %), no gaps). Closest hits using the **rpb2** sequence had highest similarity to *Zasmidium scaevolicola* (strain CBS 127009, GenBank MF951726.1; Identities = 700/875 (80 %), 25 gaps (2 %)), *Zasmidium citri-griseum* (strain CBS 122455, GenBank MF951695.1; Identities = 705/903 (78 %), 26 gaps (2 %)), and *Zasmidium hakeicola* (strain CBS 144590, GenBank MK442687.1; Identities = 665/860 (77 %), 13 gaps (1 %)).

Colour illustrations. *Geissorhiza splendidissima* with infected leaves. Conidiophores on SNA; conidiogenous cells giving rise to conidia. Scale bars = 10 µm.