

Zasmidium gahniicola



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Zasmidium gahnii Crous, *sp. nov.*

Etymology. Name refers to *Gahnia*, the host genus from which this fungus was collected.

Classification — *Mycosphaerellaceae*, *Capnodiales*, *Dothideomycetes*.

Mycelium consisting of medium brown, verruculose, branched, septate, 2–2.5 µm diam hyphae. *Conidiophores* solitary, erect, straight to flexuous, 70–120 × 2–3.5 µm, thick-walled, dark brown, finely verruculose, 4–6-septate. *Conidiogenous cells* integrated, terminal, subcylindrical, medium brown, finely roughened, 15–40 × 3 µm; scars thickened, darkened, somewhat refractive, 1 µm diam, arranged in a rachis. *Conidia* solitary, verruculose, medium brown, subcylindrical, 1(–3)-septate, straight, apex obtuse, tapering in basal cell to truncate hilum, 1 µm diam, thickened, darkened, slightly refractive, (9–)13–18(–20) × (3.5–)4(–5) µm.

Culture characteristics — Colonies erumpent, spreading, surface folded, with moderate aerial mycelium and smooth, lobate margins, reaching 15 mm diam after 2 wk at 25 °C. On MEA, PDA and OA surface and reverse iron-grey.

Typus. AUSTRALIA, New South Wales, Barren Grounds Nature Reserve, on leaves of *Gahnia sieberiana* (*Cyperaceae*), 26 Nov. 2016, P.W. Crous (holotype CBS H-23286, culture ex-type CPC 32219 = CBS 143422, ITS and LSU sequences GenBank MG386050 and MG386103, MycoBank MB823399).

Notes — The only cercosporoid fungus known from *Gahnia* is *Zasmidium gahniae*, occurring on *G. lacera* and *G. setifolia* in New Zealand. It is characterised by having solitary, straight, cylindrical to narrowly obclavate, pluriseptate conidia (20–300 × 3–5 µm; Braun et al. 2014), and is thus quite distinct from those of *Z. gahnii*.

Based on a megablast search using the ITS sequence, the closest matches in NCBI's GenBank nucleotide database were *Zasmidium podocarp* (GenBank KY979766; Identities 507/531 (95 %), 2 gaps (0 %)), *Z. commune* (GenBank KY979762; Identities 504/533 (95 %), 6 gaps (1 %)) and *Z. strelitziae* (as *Ramichloridium strelitziae*; GenBank EU041803; Identities 499/532 (94 %), 5 gaps (0 %)). The highest similarities using the LSU sequence were *Z. velutinum* (as *Periconiella velutina*; GenBank EU041838; Identities 811/817 (99 %), no gaps), *Z. commune* (GenBank KY979820; Identities 804/810 (99 %), no gaps) and *Z. arcuata* (as *Periconiella arcuata*; GenBank EU041836; Identities 830/837 (99 %), no gaps).

Colour illustrations. *Gahnia sieberiana*; conidiophores sporulating on SNA, conidiogenous cells and conidia. Scale bars = 10 µm.

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