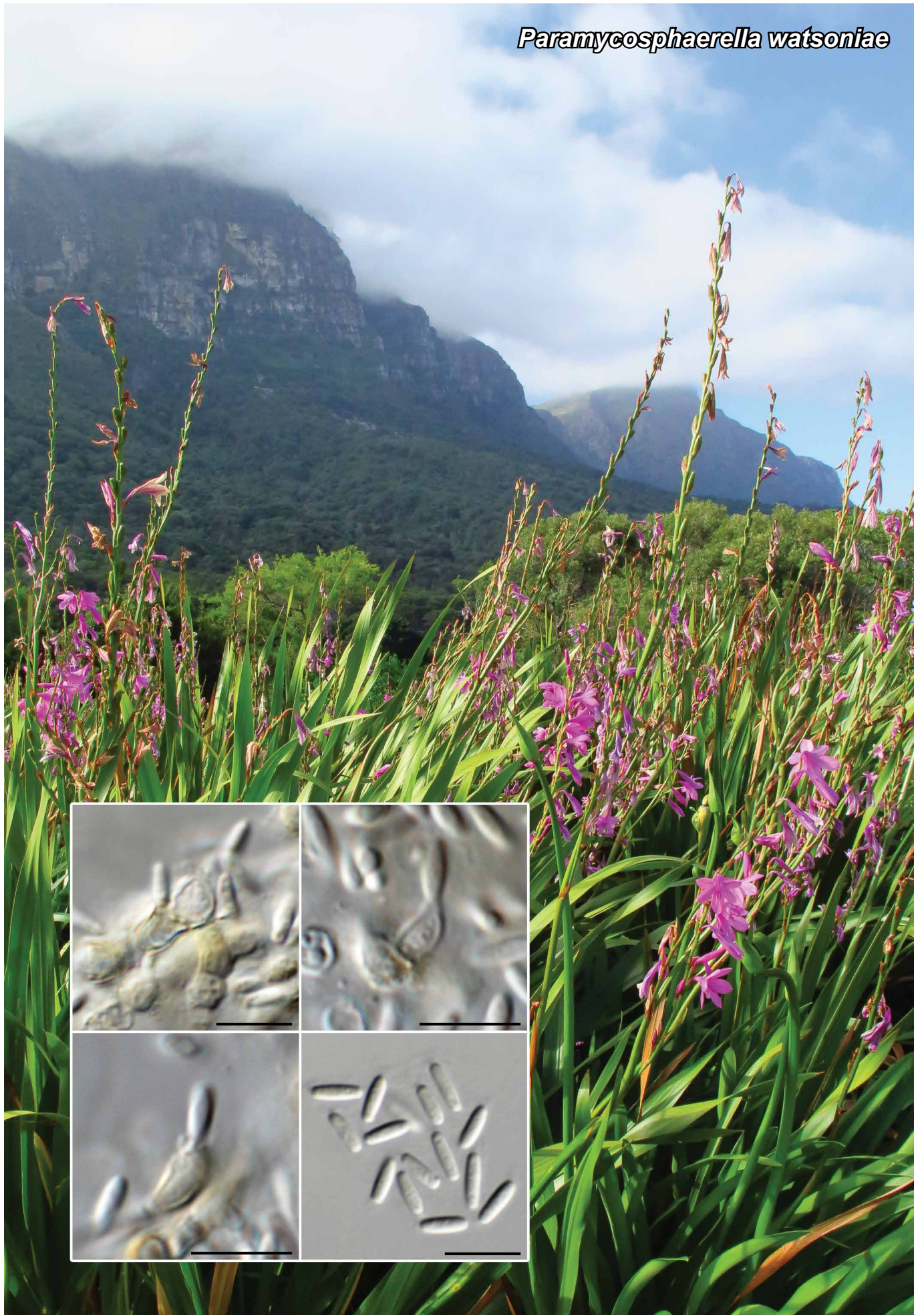


Paramycosphaerella watsoniae



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Paramycosphaerella watsoniae Crous, *sp. nov.*

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

Classification — *Mycosphaerellaceae*, *Capnodiales*, *Dothi-deomycetes*.

Conidiomata pycnidial, globose, brown, 200–250 µm diam, with central ostiole; wall of 3–6 layers of brown *textura angularis*. *Conidiophores* lining the inner cavity, reduced to conidiogenous cells, or 0–2-septate, subhyaline, smooth, branched, 4–24 × 3–4 µm. *Conidiogenous cells* terminal and intercalary, subhyaline, smooth, 4–5 × 3–4 µm, subcylindrical with periclinal thickening. *Conidia* solitary, hyaline, smooth, guttulate, aseptate, fusoid-ellipsoid, apex obtuse, base truncate, 0.5 µm diam, (3.5–)4–5(–6) × 2 µm.

Culture characteristics — Colonies flat, spreading, with sparse to moderate aerial mycelium and smooth, lobate margin, reaching 50 mm diam after 2 wk at 25 °C. On MEA surface honey, reverse isabelline to hazel. On PDA surface and reverse olivaceous grey. On OA surface rosy vinaceous.

Typus. SOUTH AFRICA, Western Cape Province, Cape Town, Kirstenbosch, on leaf spots of *Watsonia* sp. (*Iridaceae*), 2016, M.J. Wingfield, HPC 2757 (holotype CBS H-24193, culture ex-type CPC 37392 = CBS 146064, ITS, LSU, *actA*, *cmdA* and *rpb2* sequences GenBank MN562146.1, MN567653.1, MN556790.1, MN556795.1 and MN556814.1, MycoBank MB832906).

Notes — *Paramycosphaerella* is a mycosphaerella-like genus that lacks a *Ramularia* asexual morph as in *Mycosphaerella* s.str. (Crous et al. 2013b, Videira et al. 2017). *Paramycosphaerella watsoniae* is closely related but phylogenetically distinct from *P. sticheri* (on fronds of *Sticherus penniger*, Brazil; only known from its sexual morph; Guatimosim et al. 2016).

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Paramycosphaerella sticheri* (strain COAD 1422, GenBank NR_155660.1; Identities = 489/518 (94 %), 5 gaps (0 %)), *Paramycosphaerella wachendorffiae* (strain CBS 129579, GenBank MH865448.1; Identities = 508/542 (94 %), 7 gaps (1 %)), and *Pseudozasmidium vietnamense* (as *Mycosphaerella vietnamensis*, strain CMW37695, GenBank JQ732923.1; Identities = 461/501 (92 %), 13 gaps (2 %)). Closest hits using the **LSU** sequence are *Paramycosphaerella brachystegiae* (strain CBS 136436, GenBank NG_058048.1; Identities = 844/848 (99 %), no gaps), *Paramycosphaerella dicranopteridis-flexuosae* (strain CPC 24743, GenBank NG_059577.1; Identities = 803/808 (99 %), 1 gap (0 %)), and *Paramycosphaerella marksii* (strain CPC 11222, GenBank GU214447.1; Identities = 842/848 (99 %), no gaps). Closest hits using the **actA** sequence had highest similarity to *Paramycosphaerella intermedia* (strain CBS 114356, GenBank KF903466.1; Identities = 505/552 (91 %), 13 gaps (2 %)), *Paramycosphaerella marksii* (strain CBS 110750, GenBank KF903404.1; Identities = 503/552 (91 %), 14 gaps (2 %)), and *Hyalozasmidium aerohyalinosporum* (strain CBS 125011, GenBank KF903576.1; Identities = 501/553 (91 %), 20 gaps (3 %)). Closest hits using the **cmdA** sequence had highest similarity to *Hyalozasmidium aerohyalinosporum* (strain CBS 125011, GenBank KF902788.1; Identities = 270/294 (92 %), no gaps), *Paramycosphaerella intermedia* (strain CBS 114356, GenBank KF902579.1; Identities = 266/293 (91 %), no gaps), and *Virospora irregularis* (strain CBS 123242, GenBank KF902543.1; Identities = 266/294 (90 %), no gaps). No significant hits were obtained when the **rpb2** sequence was used in blastn and megablast searches.

Colour illustrations. *Watsonia* sp. at the foot of Table Mountain. Conidiophores with conidiogenous cells; conidia. Scale bars = 10 µm.

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