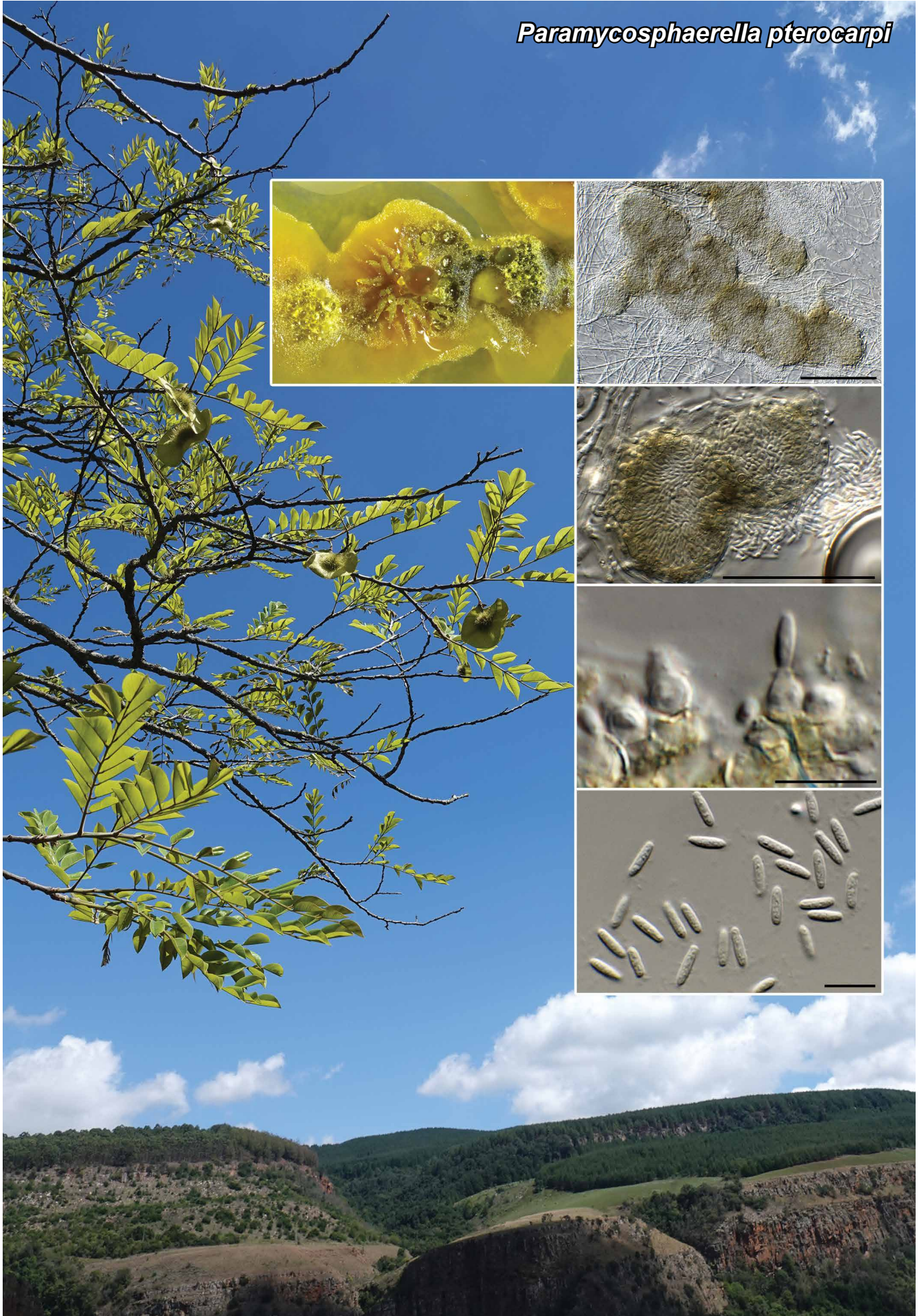


Paramycosphaerella pterocarpi



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Paramycosphaerella pterocarp Crous, *sp. nov.*

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

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

On SNA: *Conidiomata* solitary, erumpent, subglobose, brown, 30–100 µm diam with central ostiole, solitary or in chains, linked by a brown stroma; wall of 2–4 layers of brown *textura angularis*. *Conidiophores* reduced to conidiogenous cells, in dense clusters, hyaline, smooth to pale brown, verruculose, ampulliform, 3–6 × 2.5–3 µm, phialidic with periclinal thickening, with age developing percurrent proliferations. *Conidia* exuding from conidioma in mucoid droplets, aseptate, smooth, hyaline, subcylindrical, guttulate to granular, apex subobtuse, base truncate, (4–)6–7 × (1.5–)2 µm.

Culture characteristics — Colonies erumpent, spreading, surface folded, with moderate aerial mycelium and smooth, lobate margin, reaching 12 mm diam after 2 wk at 25 °C. On MEA surface and reverse greenish olivaceous with patches of pale mouse grey; on PDA surface and reverse luteous with patches of greenish olivaceous; on OA surface pale mouse grey.

Typus. SOUTH AFRICA, Mpumalanga, Mbombela, Buffelskloof Nature Reserve, on leaves of *Pterocarpus angolensis* (*Fabaceae*), Nov. 2018, *P.W. Crous*, HPC 3137 (holotype CBS H-24535, culture ex-type CPC 39035 = CBS 147071, ITS, LSU, *actA*, *cmdA*, *rpb2*, *tef1* (first part) and *tub2* sequences GenBank MZ064449.1, MZ064506.1, MZ078154.1, MZ078167.1, MZ078208.1, MZ078233.1 and MZ078275.1, MycoBank MB 839536).

Notes — *Paramycosphaerella pterocarp* is related to *Paramycosphaerella watsoniae* (conidia aseptate, fusoid-ellipsoid, (3.5–)4–5(–6) × 2 µm; Crous et al. 2019d), but can be distinguished based on its morphology, and phylogeny.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Paramycosphaerella watsoniae* (strain CPC 37392, GenBank NR_166341.1; Identities = 520/528 (98 %), one gap (0 %)), *Paramycosphaerella sticheri* (strain CPC 24720, GenBank NR_155660.1; Identities = 485/511 (95 %), two gaps (0 %)) and *Paramycosphaerella wachendorffiae* (strain CPC 18338, GenBank NR_156547.1; Identities = 481/516 (93 %), eight gaps (1 %)). Closest hits using the **LSU** sequence are *Paramycosphaerella brachystegiae* (strain CBS 136436, GenBank NG_058048.1; Identities = 864/866 (99 %), no gaps), *Paramycosphaerella watsoniae* (strain CPC 37392, GenBank NG_068339.1; Identities = 846/848 (99 %), no gaps) and *Paramycosphaerella dicranopteridis-flexuosae* (strain CPC 24743, GenBank NG_059577.1; Identities = 805/808 (99 %), one gap (0 %)). Closest hits using the **actA** sequence had highest similarity to *Paramycosphaerella watsoniae* (strain CBS 146064, GenBank MN556790.1; Identities = 552/584 (95 %), five gaps (0 %)), *Mycosphaerella musae* (strain CIRADCOK 003, GenBank MW070786.1; Identities = 524/580 (90 %), five gaps (0 %)) and *Paramycosphaerella intermedia* (strain CBS 114356, GenBank KF903466.1; Identities = 491/538 (91 %), four gaps (0 %)). Closest hits using the **cmdA** sequence had highest similarity to *Paramycosphaerella watsoniae* (strain CBS 146064, GenBank MN556795.1; Identities = 405/428 (95 %), no gaps), *Hyalozasmidium aerohyalinosporum* (strain CBS 125011, GenBank KF902788.1; Identities = 269/294 (91 %), no gaps) and *Nothopassalora personata* (strain IRAN 3479C, GenBank MN422408.1; Identities = 278/309 (90 %), no gaps). Closest hits using the **rpb2** sequence had highest similarity to *Paramycosphaerella watsoniae* (strain CBS 146064, GenBank MN556814.1; Identities = 733/793 (92 %), no gaps), *Virosphaerella pseudomarksii* (strain CBS 123241, GenBank MF951686.1; Identities = 679/864 (79 %), 26 gaps (3 %)) and *Mycosphaerelloides madeirae* (strain CBS 115936, GenBank KX288443.1; Identities = 635/824 (77 %), ten gaps (1 %)). Distant hits obtained using the **tef1** sequence had highest similarity to *Mycosphaerella musae* (strain CIRAD-MTQ 1241, GenBank MW071103.1; Identities = 315/381 (83 %), 24 gaps (6 %)), *Brunneosphaerella nitidae* (strain CPC 15231, GenBank JN712581.1; Identities = 313/380 (82 %), 30 gaps (7 %)) and *Brunneosphaerella protearum* (strain CPC 18328, GenBank JN712585.1; Identities = 307/378 (81 %), 27 gaps (7 %)). Closest hits using the **tub2** sequence had highest similarity to *Paramycosphaerella intermedia* (strain CBS 114356, GenBank KF902845.1; Identities = 275/329 (84 %), 12 gaps (3 %)), *Paramycosphaerella marksii* (strain CBS 110920, GenBank KF902848.1; Identities = 270/328 (82 %), ten gaps (3 %)) and *Zasmidium podocarp* (strain CBS 142529, GenBank KY979930.1; Identities = 307/383 (80 %), 21 gaps (5 %)).

Colour illustrations. Buffelskloof Nature Reserve. Conidiomata on PDA; conidiogenous cells giving rise to conidia; conidia. Scale bars = 100 µm (conidiomata), 10 µm (all others).

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