

*Cyphellophora goniomatis*





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## *Cyphellophora goniomatis* Crous, *sp. nov.*

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

*Classification* — *Cyphellophoraceae*, *Chaetothyriales*, *Eurotiomycetes*.

*Mycelium* consisting of pale brown, smooth, septate, branched, 2–3 µm diam hyphae. *Conidiophores* reduced to conidiogenous loci on hyphae, pale brown, smooth, phialidic, collarettes flared, 2–2.5 µm diam, loci 1–1.5 µm diam. *Conidia* aggregating in mucoid droplets, pale brown, smooth, guttulate, fusoid, inner plane flat, outer plane convex, apex subobtuse, tapering toward inner plane, base truncate, 1 µm diam, (0–)1(–3)-septate, (10–)15–18(–20) × (1.5–)2(–2.5) µm.

*Culture characteristics* — Colonies flat, spreading, surface folded, with moderate aerial mycelium and smooth, lobate margin, reaching 30 mm diam after 2 wk at 25 °C. On MEA, PDA and OA surface and reverse olivaceous grey.

*Typus.* SOUTH AFRICA, Western Cape Province, Knysna, Knysna area, on leaves of *Gonioma kamassi* (*Apocynaceae*), 23 Nov. 2018, *F. Roets*, HPC 2698 (holotype CBS H-24180, culture ex-type GPC 37032 = CBS 146077, ITS, LSU, *actA*, *tef1* and *tub2* sequences GenBank MN562133.1, MN567640.1, MN56789.1, MN56825.1 and MN56842.1, MycoBank MB832891).

*Notes* — *Cyphellophora* is characterised by pigmented phialides occurring directly on hyphae or occasionally on flask-shaped conidiogenous cells, and producing small clusters of olivaceous, septate, mostly curved conidia (Cheewangkoon et al. 2009, Crous et al. 2019b). *Cyphellophora goniomatis* is phylogenetically related to *C. guyanensis* (from angiosperm, French Guyana, conidia (2–)3–6-septate, (18–)19.7–28(–29) × 1.5–2 µm; Decock et al. 2003), although it has smaller conidia.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Cyphellophora guyanensis* (strain MUCL 43737, GenBank GU225943.1; Identities = 564/578 (98 %), 3 gaps (0 %)), *Exophiala spinifera* (strain CBS 126014, GenBank KF928476.1; Identities = 532/549 (97 %), 4 gaps (0 %)), and *Cyphellophora eucalypti* (strain CBS 124764, GenBank GQ303274.1; Identities = 592/611 (97 %), 5 gaps (0 %)). Closest hits using the **LSU** sequence are *Cyphellophora guyanensis* (strain CBS 129342, GenBank MH876666.1; Identities = 837/841 (99 %), 1 gap (0 %)), *Cyphellophora eucalypti* (strain CBS 124764, GenBank KC455254.1; Identities = 835/841 (99 %), 1 gap (0 %)), and *Cyphellophora artocarp*i (strain CHCJHB-JBLM, GenBank KP122930.1; Identities = 756/762 (99 %), no gaps). Closest hits using the **actA** sequence had highest similarity to *Cyphellophora eucalypti* (strain CBS 124764, GenBank JQ325009.1; Identities = 511/528 (97 %), no gaps), *Scolecotigmina mangiferae* (strain CBS 125467, GenBank GU320566.1; Identities = 510/527 (97 %), no gaps), and *Ophionectria trichospora* (strain CBS 314.75, GenBank KM231181.1; Identities = 517/539 (96 %), 1 gap (0 %)). No significant hits were obtained when the **tef1** sequence was used in blastn and megablast searches. Closest hits using the **tub2** sequence had highest similarity to *Cyphellophora guyanensis* (strain CBS 125756, GenBank JQ766338.1; Identities = 358/377 (95 %), no gaps), *Cyphellophora artocarp*i (strain CHCJHBJBLM, GenBank KP122925.1; Identities = 362/390 (93 %), 1 gap (0 %)), and *Ophionectria trichospora* (strain CBS 314.75, GenBank KM232047.1; Identities = 228/252 (90 %), 6 gaps (2 %)).

*Colour illustrations.* Knysna forest with *Gonioma kamassi* trees. Conidiogenous cells; conidia. Scale bars = 10 µm.

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