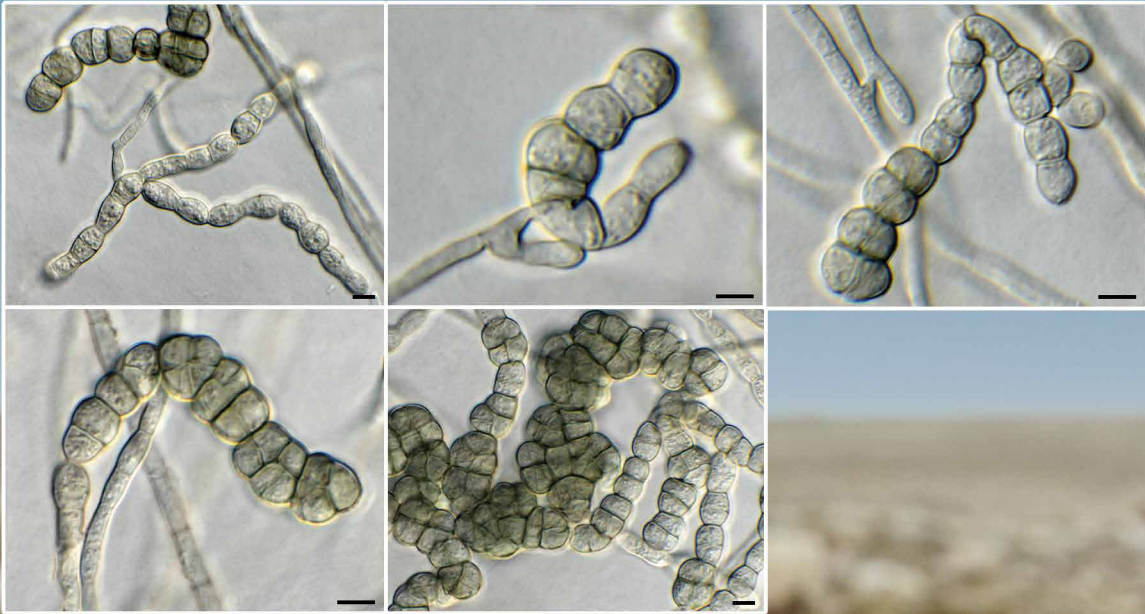


*Knufia hypolithi*

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## *Knufia hypolithi* Crous, sp. nov.

*Etymology.* Name refers to the fact that it was isolated from a hypolith, under a quartz stone.

*Classification* — *Trichomeriaceae*, *Chaetothyriales*, *Eurotiomycetes*.

*Mycelium* consisting of pale brown, smooth, septate, branched, 2–3 µm diam hyphae. *Chlamydo-spore-like propagules* intercalary, but commonly as terminal ends of hyphae, subcylindrical to ovoid-ellipsoid, dark brown, smooth-walled, with 3 to numerous constricted transverse septa, and several vertical or oblique septa, 15–80 × 10–25 µm.

*Culture characteristics* — Colonies flat, spreading, with moderate aerial mycelium and smooth, even margin, reaching 18 mm diam after 2 wk at 25 °C. On MEA, PDA and OA surface and reverse olivaceous grey.

*Typus.* NAMIBIA, Walvis Bay, from hypolith under a quartz stone, 19 Nov. 2019, P.W. Crous, HPC 3101 (holotype CBS H-24503, culture ex-type CPC 38987 = CBS 146991, ITS and LSU sequences GenBank MZ064430.1 and MZ064487.1, MycoBank MB 839519).

*Additional materials examined.* NAMIBIA, Walvis Bay, from hypolith under a rock, 19 Nov. 2019, P.W. Crous, cultures CPC 38983, 38985, ITS and LSU sequences GenBank MZ064431.1–MZ064432.1 and MZ064488.1–MZ064489.1.

*Colour illustrations.* Quartz stones and pebbles with lichen and hypolith growth. Hyphae giving rise to chlamydo-spore-like propagules. Scale bars = 10 µm.

*Notes* — *Knufia* is ecologically diverse, including species that are rock-inhabiting (Tsuneda et al. 2011), lichenicolous (Untereiner et al. 2011), opportunistic human pathogens (Li & Chen 2010), insect associates (He et al. 2013) and plant pathogens (Tsuneda & Currah 2005). *Knufia hypolithi* is related to '*Phialocephala fluminis*', from which it is morphologically and phylogenetically distinct.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Phialocephala fluminis* (strain WPF-48-12G, GenBank KT000162.1; Identities = 544/551 (99 %), five gaps (0 %)), *Phialocephala fluminis* (strain CBS 351.85, GenBank MH861889.1; Identities = 594/619 (96 %), nine gaps (1 %)) and *Knufia perfecta* (strain IRAN 2553C, GenBank MF062036.1; Identities = 519/562 (92 %), 21 gaps (3 %)). The ITS sequences of CPC 38983, 38985 and 38987 are identical (616/616 nucleotides). Closest hits using the **LSU** sequence are *Phialocephala fluminis* (strain CBS 351.85, GenBank MH873578.1; Identities = 845/855 (99 %), two gaps (0 %)), *Knufia perforans* (strain CBS 885.95, GenBank NG\_042586.1; Identities = 827/845 (98 %), two gaps (0 %)) and *Knufia* sp. MV-2018 (strain MLT-8, GenBank MT636937.1; Identities = 817/836 (98 %), two gaps (0 %)). The LSU sequences of CPC 38983, 38985 and 38987 are identical (814/814 nucleotides).

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