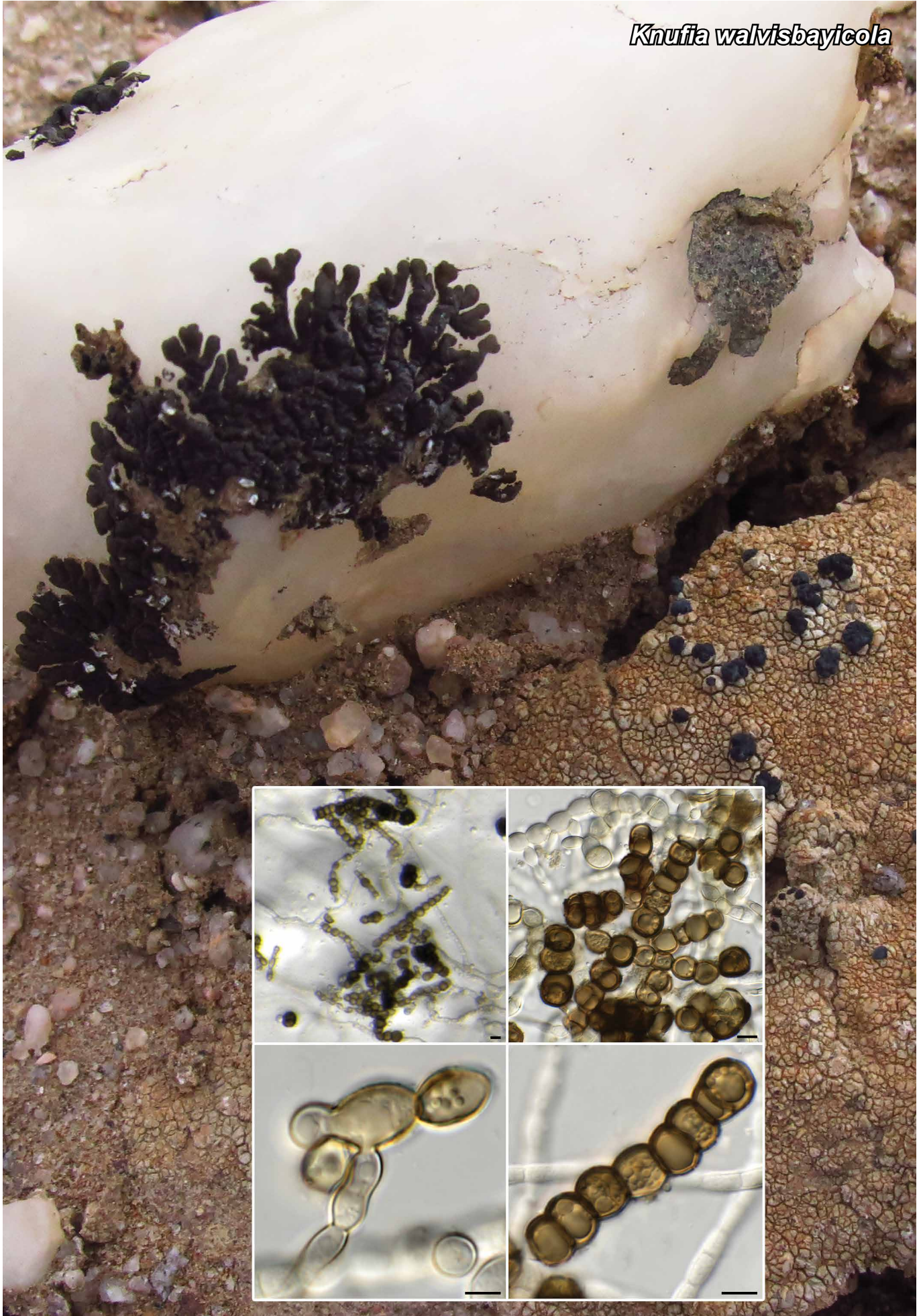


*Knuffia walvisbayicola*



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***Knufia walvisbayicola* Crous, sp. nov.**

*Etymology.* Name refers to Walvis Bay, Namibia, where it was collected.

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

*Mycelium* consisting of pale to dark brown hyphae, smooth, septate, branched, frequently constricted at septa, 3–4 µm diam. *Conidia* chlamydospore-like propagules, medium to dark brown, subcylindrical to elongated ellipsoid-ovoid, brown, warty, guttulate, thick-walled, with 2 to numerous transverse and 1–6 oblique or vertical septa, (20–)35–80(–170) × (9–)11–18(–30) µm.

*Culture characteristics* — Colonies erumpent, spreading, with sparse aerial mycelium and smooth, lobate margin, reaching 8 mm diam after 2 wk at 25 °C. On MEA surface and reverse umber; on PDA surface and reverse olivaceous grey; on OA surface umber.

*Typus.* NAMIBIA, Walvis Bay, from hypolith under a quartz stone, 19 Nov. 2019, P.W. Crous, HPC 3101 (holotype CBS H-24501, culture ex-type CPC 38988 = CBS 146989, ITS, LSU, *rpb1*, *tef1* (second part) and *tub2* sequences GenBank MZ064433.1, MZ064490.1, MZ078188.1, MZ078251.1 and MZ078265.1, MycoBank MB 839520).

*Additional material examined.* NAMIBIA, Walvis Bay, from hypolith under a quartz stone, 19 Nov. 2019, P.W. Crous, HPC 3101, culture CPC 38984 = CBS 146990, ITS, LSU, *rpb1*, *tef1* (second part) and *tub2* sequences GenBank MZ064434.1, MZ064491.1, MZ078189.1, MZ078252.1 and MZ078266.1.

*Notes* — *Knufia walvisbayicola* is related to *K. marmoricola* (from marble stone, Vatican City; endoconidia 4.4–5.0 µm diam; Isola et al. 2016), from which it is phylogenetically and morphologically distinct.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the ITS sequence of CPC 38988 had highest similarity to *Knufia marmoricola* (strain PiN-A2, GenBank KY887804.1; Identities = 483/505 (96 %), nine gaps (1 %)), *Knufia petricola* (strain 2Y43B, GenBank MT126632.1; Identities = 464/486 (95 %), ten gaps (2 %)) and *Knufia perforans* (strain CBS 885.95, GenBank NR\_121502.1; Identities = 569/596 (95 %), nine gaps (1 %)). The ITS sequences of CPC 38988 and 38984 differ by an extra thymine nucleotide at two alignment positions (624/626 (99 %)). Closest hits using the LSU sequence of CPC 38988 are *Knufia* sp. MV-2018 (strain MLT-8, GenBank MT636937.1; Identities = 850/852 (99 %), no gaps), *Knufia marmoricola* (strain CCFEE 5716, GenBank KR781074.1; Identities = 855/858 (99 %), no gaps) and *Knufia perforans* (strain CBS 885.95, GenBank NG\_042586.1; Identities = 855/858 (99 %), no gaps). The LSU sequences of CPC 38988 and 38984 are identical (796/796 (100 %)). Closest hits using the *rpb1* sequence of CPC 38988 had highest similarity to *Knufia* sp. LS-2015b (strain CGMCC 3.17226, GenBank KP226509.1; Identities = 565/593 (95 %), no gaps), *Knufia petricola* (strain CBS 726.95, GenBank KC978743.1; Identities = 575/631 (91 %), no gaps) and *Glyphium elatum* (strain CBS 268.34, GenBank FJ941902.1; Identities = 479/518 (92 %), no gaps). The *rpb1* sequences of CPC 38988 and 38984 are identical (682/682 (100 %)). Closest hits using the *tef1* sequence of CPC 38988 had highest similarity to *Knufia* sp. LS-2015b (strain CGMCC 3.17301, GenBank KP175012.1; Identities = 881/917 (96 %), no gaps), *Knufia petricola* (strain A95, GenBank MT859426.1; Identities = 895/953 (94 %), no gaps) and *Knufia epidermidis* (strain CGMCC 3.17300, GenBank KP175014.1; Identities = 837/918 (91 %), two gaps (0 %)). Distant hits obtained using the *tub2* sequence of CPC 38988 had highest similarity to *Phialophora americana* (strain CBS 102234, GenBank KU306351.1; Identities = 207/253 (82 %), nine gaps (3 %)), *Knufia peltigerae* (strain CGMCC 3.17283, GenBank KP226562.1; Identities = 173/204 (85 %), two gaps (0 %)) and '*Anthracinomyces ramosus*' (strain CGMCC 3.16367, GenBank KP226556.1; Identities = 175/207 (85 %), three gaps (1 %)). The *tub2* sequences of CPC 38988 and 38984 differ with three independent substitutions (573/576 (99 %)).

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

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