

*Hysterobrevium walvisbayicola*



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***Hysterobrevium walvisbayicola* Crous, sp. nov.**

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

*Classification* — *Hysteriaceae*, *Hysteriales*, *Dothideomycetes*.

*Conidiomata* pycnidial, brown, subglobose with central ostiole, 200–300 µm diam (larger on OA than on MEA), exuding a pink to creamy conidial mass. *Conidiophores* subcylindrical, hyaline, smooth, branched, 1–3-septate, 15–60 × 1.5–2 µm, some branches sterile, appearing as paraphyses. *Conidiogenous cells* terminal and intercalary, hyaline, smooth, subcylindrical, 7–20 × 1.5–2 µm, phialidic. *Conidia* solitary, hyaline, smooth, guttulate, subcylindrical with obtuse ends, aseptate, straight, 3–5 × 1.5–2 µm.

*Culture characteristics* — Colonies flat, spreading, with sparse aerial mycelium and smooth, lobate margin, reaching 20 mm diam after 2 wk at 25 °C. On MEA surface and reverse umber; on PDA surface ochreous with patches of umber, reverse ochreous; on OA surface ochreous to umber.

*Typus.* NAMIBIA, Walvis Bay, on leaves of unidentified tree, 19 Nov. 2019, P.W. Crous, HPC 3128 (holotype CBS H-24508, culture ex-type CPC 38948 = CBS 147003, ITS, LSU and *tef1* (first part) sequences GenBank MZ064428.1, MZ064485.1 and MZ093619.1, MycoBank MB 839517).

*Notes* — *Hysterobrevium walvisbayicola* is a phoma-like coelomycetous fungus that clusters in a complex of *Dothideomycetes* characterised by hysterothecial ascomata, namely *Gloniopsis*, *Hysterobrevium* and *Rhytidhysterion*. Although taxa in this complex are not known by their asexual morphs, Boehm et al. (2009) did record a coelomycetous asexual morph for *Hysterobrevium mori*. For the present, this species is best accommodated in *Hysterobrevium*.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Gloniopsis calami* (strain MFLUCC 10-0927, GenBank MN608546.1; Identities = 449/480 (94 %), 11 gaps (2 %)), *Rhytidhysterion rufulum* (strain CFE-147, GenBank MN653261.1; Identities = 441/471 (94 %), 12 gaps (2 %)) and *Gloniopsis leucaenae* (strain MFLUCC 17-2425, GenBank NR\_163334.1; Identities = 426/456 (93 %), 11 gaps (2 %)). Closest hits using the **LSU** sequence are *Hysterodifractum partisporum* (voucher HUEFS 42865, GenBank NG\_060652.1; Identities = 884/907 (97 %), two gaps (0 %)), *Hysterobrevium mori* (strain GKM 1214, GenBank GQ221895.1; Identities = 880/906 (97 %), one gap (0 %)) and *Gloniopsis subrugosa* (strain SMH557, GenBank GQ221896.1; Identities = 879/906 (97 %), one gap (0 %)). Distant hits obtained using the **tef1** sequence had highest similarity to *Gloniopsis subrugosa* (strain GKM 1214, GenBank GU397336.1; Identities = 401/499 (80 %), 22 gaps (4 %)) and *Hysterobrevium mori* (strain GKM 1013, GenBank GU397338.1; Identities = 402/500 (80 %), 31 gaps (6 %)).

*Colour illustrations.* Flamingos at Walvis Bay lagoon. Conidiomata on OA; conidiogenous cells giving rise to conidia; conidia. Scale bars = 10 µm.

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