

Alternaria mirabibensis



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***Alternaria mirabibensis* Crous, sp. nov.**

Etymology. Name refers to the collection site, namely the Mirabib Rock in the Namib Desert, Namibia, where Stanley Kubrick filmed 'the dawn of mankind' in the movie '2001 - A Space Odyssey'.

Classification — *Pleosporaceae*, *Pleosporales*, *Dothideo-mycetes*.

Mycelium consisting of pale brown, smooth, branched, septate, 3–4 µm diam hyphae. **Conidiophores** erect, solitary, arising from superficial mycelium, 50–150 × 3–5 µm, 3–6-septate, branched or not, brown, smooth, subcylindrical, straight to flexuous. **Conidiogenous cells** terminal and intercalary, straight to geniculous-sinuuous, flexuous, 10–30 × 5–7 µm, with thickened, darkened, 1–2 terminal pores, 2–3 µm diam. **Conidia** occurring in branched chains, conidia brown, verruculose, guttulate, ovoid to ellipsoid, (23–)33–45(–50) × (13–)15–16(–17) µm (body excluding beak), with 3–6(–7) transverse septa, and (1–)2–3(–6) longitudinal or oblique septa, commonly forming a long terminal beak, 20–120 µm long, that becomes a secondary conidiophore, giving rise to terminal and lateral chains of conidia.

Culture characteristics — Colonies flat, spreading, with moderate aerial mycelium and smooth, lobate margin, reaching 40 mm diam on MEA, but covering dish on PDA and OA after 2 wk at 25 °C. On MEA surface folded, grey olivaceous, reverse isabelline; on PDA surface and reverse grey olivaceous; on OA surface grey olivaceous.

Typus. NAMIBIA, Gobabeb-Namib Research Institute, Mirabib, on plant litter, 19 Nov. 2019, P.W. Crous, HPC 3108 (holotype CBS H-24445, culture ex-type CPC 38838 = CBS 146826, ITS, LSU, *actA*, *chs-1*, *cmdA*, *gapdh*, *tef1* and *tub2* sequences GenBank MW175361.1, MW175401.1, MW173096.1, MW173101.1, MW173102.1, MW173104.1, MW173125.1 and MW173140.1, MycoBank MB837852).

Colour illustrations. View from top of Mirabib Rock, looking outwards across the Namib Desert. Conidiophores and conidiogenous cells giving rise to conidial chains. Scale bars = 10 µm.

Notes — *Alternaria mirabibensis* is closely related to *Alternaria burnsii* (CBS 130264) (Woudenberg et al. 2015, Nishikawa & Nakashima 2020), but is phylogenetically distinct.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Alternaria alternata* (strain KU20017.1, GenBank MT487794.1; Identities = 552/566 (98 %), two gaps (0 %)), *Alternaria arborescens* (strain ALT-14, GenBank MH879771.1; Identities = 552/566 (98 %), two gaps (0 %)), and *Alternaria burnsii* (strain CBS 130264, GenBank MH865506.1; Identities = 552/566 (98 %), two gaps (0 %)). Closest hits using the **LSU** sequence are *Alternaria multififormis* (strain CBS 102060, GenBank NG_069860.1; Identities = 870/871 (99 %), no gaps), *Alternaria terricola* (strain CBS 202.67, GenBank NG_069728.1; Identities = 870/871 (99 %), no gaps), and *Alternaria atra* (strain CBS 125894, GenBank MH875550.1; Identities = 870/871 (99 %), no gaps). Closest hits using the **actA** sequence had highest similarity to *Alternaria iridicola* (strain AC139, GenBank LC481866.1; Identities = 179/185 (97 %), no gaps), *Alternaria alternata* (strain LSA2, GenBank KY131956.1; Identities = 186/193 (96 %), no gaps), and *Alternaria tenuissima* (strain U-2, GenBank MN752246.1; Identities = 208/216 (96 %), no gaps). Closest hits using the **chs-1** sequence had highest similarity to *Alternaria novae-guineensis* (strain SCSJ08, GenBank MH793684.1; Identities = 233/242 (96 %), no gaps), *Alternaria solani* (strain NL03003, GenBank CP022032.1; Identities = 257/269 (96 %), no gaps), and *Alternaria radicina* (strain BMP0079, GenBank EU141977.1; Identities = 252/264 (95 %), no gaps). Closest hits using the **cmdA** sequence had highest similarity to *Alternaria alstroemeriae* (strain CBS 118809, GenBank MH175185.1; Identities = 579/639 (91 %), 15 gaps (2 %)), *Alternaria iridiaustralis* (strain CBS 118486, GenBank MH175191.1; Identities = 578/638 (91 %), 15 gaps (2 %)), and *Alternaria alternata* (strain 17MC, GenBank MG925134.1; Identities = 580/647 (90 %), 25 gaps (3 %)). Closest hits using the **gapdh** sequence had highest similarity to *Alternaria tenuissima* (strain GP4, GenBank MK451969.1; Identities = 553/577 (96 %), no gaps), *Alternaria longipes* (strain AXLY2019010, GenBank MN044655.1; Identities = 552/577 (96 %), no gaps), and *Alternaria alternata* (strain D11, GenBank MK732570.1; Identities = 552/577 (96 %), no gaps). Closest hits using the **tef1** sequence had highest similarity to *Alternaria alternata* (strain EGS 34-016, GenBank AH013339.2; Identities = 284/304 (93 %), no gaps), *Alternaria jacinthicola* (strain Mlb684, GenBank HQ413697.1; Identities = 293/317 (92 %), no gaps), and *Alternaria longipes* (strain KY_2019_012, GenBank MT548042.1; Identities = 247/273 (90 %), five gaps (1 %)). Closest hits using the **tub2** sequence had highest similarity to *Alternaria arborescens* (strain BAS_G1, GenBank MF070272.1; Identities = 282/289 (98 %), no gaps), *Alternaria tenuissima* (strain CBS 124278, GenBank MF070256.1; Identities = 282/289 (98 %), no gaps), and *Alternaria gaisen* (strain CBS 118488, GenBank MF070254.1; Identities = 282/289 (98 %), no gaps).

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