

Aquillomyces metrosideri



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***Aquilomyces metrosideri* Crous, sp. nov.**

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

Classification — *Morosphaeriaceae*, *Pleosporales*, *Dothi-deomycetes*.

Conidiomata solitary, brown, globose to pyriform, 150–200 µm diam, with central ostiole; wall of 6–8 layers of brown *textura angularis*. *Conidiophores* lining the inner cavity, reduced to conidiogenous cells or a supporting cell, branched at base, hyaline, smooth, subcylindrical, 10–15 × 3–4 µm. *Conidiogenous cells* terminal and intercalary, subcylindrical, hyaline, smooth, phialidic, 7–10 × 2.5–3.5 µm. *Conidia* solitary, hyaline, smooth, aseptate, subcylindrical with obtuse apex and truncate hilum, (3–)4(–5) × 1.5–2 µm.

Culture characteristics — Colonies flat, spreading, with moderate aerial mycelium and lobate, smooth margin, reaching 50 mm diam after 2 wk at 25 °C. On MEA, PDA and OA surface olivaceous grey, reverse iron-grey.

Typus. NEW ZEALAND, Devonport, Lake Road, from stem and internal discoloration of *Metrosideros* sp. (*Myrtaceae*), 4 Oct. 2019, K. Hofer (holotype CBS H-24414, culture ex-type CPC 38517 = T19_034621 = CBS 146782, ITS, LSU, *actA* and *cmdA* sequences GenBank MZ064416.1, MZ064473.1, MZ078144.1 and MZ078162.1, MycoBank MB 839503).

Notes — *Aquilomyces metrosideri* is related to the sterile endophyte *A. patris* (CBS 135661; Knapp et al. 2015). *Aquilomyces* is known to have a *massarina*-like sexual morph (Tanaka et al. 2015).

Based on a blastn search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Aquilomyces patris* (strain CBS 135661, GenBank NR_137961.1; Identities = 472/569 (83 %), 44 gaps (7 %)), *Aquilomyces rebunensis* (voucher HHUF 27556, GenBank NR_154664.1; Identities = 369/402 (92 %), five gaps (1 %)) and *Clypeoloculus towadaensis* (voucher HHUF 30145, GenBank NR_153865.1; Identities = 438/515 (85 %), 22 gaps (4 %)). Closest hits using the **LSU** sequence are *Clypeoloculus towadaensis* (strain HHUF 30145, GenBank NG_058722.1; Identities = 785/793 (99 %), no gaps), *Aquilomyces patris* (strain CBS 135661, GenBank NG_057057.1; Identities = 820/833 (98 %), four gaps (0 %)) and *Clypeoloculus microsporus* (strain HHUF 30143, GenBank NG_068960.1; Identities = 780/793 (98 %), two gaps (0 %)). Closest hits using the **actA** sequence had highest similarity to *Aquilomyces patris* (strain CBS 135662, GenBank KP184121.1; Identities = 224/237 (95 %), no gaps), *Exserohilum gedarefense* (strain CBS 504.90, GenBank LT838289.1; Identities = 188/258 (73 %), 21 gaps (8 %)) and *Setosphaeria rostrata* (strain BRIP 12090, GenBank LT837679.1; Identities = 184/256 (72 %), 20 gaps (7 %)). Closest hits using the **cmdA** sequence had highest similarity to *Aquilomyces patris* (strain CBS 135661, GenBank KP184154.1; Identities = 422/467 (90 %), four gaps (0 %)), *Darksidea delta* (strain CBS 135629, GenBank KP184144.1; Identities = 329/375 (88 %), 12 gaps (3 %)) and *Darksidea epsilon* (strain CBS 135658, GenBank KP184147.1; Identities = 327/375 (87 %), 12 gaps (3 %)).

Colour illustrations. Devonport, Lake Road, New Zealand. Conidiomata on PDA; conidiogenous cells giving rise to conidia; conidia. Scale bars = 200 µm (conidiomata), 10 µm (all others).

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