

*Leptosillia mayteni*



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## *Leptosillia mayteni* Crous, sp. nov.

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

**Classification** — *Leptosilliaceae*, *Xylariales*, *Sordariomycetes*.

*Conidiomata* solitary to aggregated, pycnidial, globose, brown, 180–200 µm diam, with central ostiole; wall of 6–8 layers of pale brown *textura angularis*. *Conidiophores* lining the inner cavity, hyaline, smooth, subcylindrical, 0–3-septate, branched at base or not, 7–30 × 1.5–2 µm. *Conidiogenous cells* hyaline, smooth, subcylindrical, 5–8 × 1.5 µm, proliferating percurrently at apex, at times with three conidia still attached to apex. *Conidia* hyaline, smooth, aseptate, bean-shaped, slightly curved, inequilateral, inner plane flat, outer plan convex, apex and base rounded toward inner plane, (4–)5(–6) × 1.5 µm.

**Culture characteristics** — Colonies erumpent, spreading, with moderate aerial mycelium and smooth, lobate margin, reaching 50 mm diam after 2 wk at 25 °C. On MEA surface dirty white, reverse cinnamon. On PDA surface and reverse cinnamon. On OA surface dirty white with diffuse cinnamon pigment.

**Typus.** SOUTH AFRICA, Western Cape Province, Knysna, Knysna area, on leaves of *Maytenus heterophylla* (*Celastraceae*), 23 Nov. 2018, F. Roets, HPC 2721 (holotype CBS H-24178, culture ex-type CPC 37000 = CBS 146079, ITS, LSU and *rpb2* sequences GenBank MN562131.1, MN567638.1 and MN556808.1, MycoBank MB832889).

**Notes** — The genus *Leptosillia* was recently treated by Voglmayr et al. (2019). Although *L. mayteni* was isolated from leaves, most species of *Leptosillia* are isolated from bark and twigs. Morphologically, the asexual morph of *L. mayteni* is most similar to that of *L. wienkampii*, conidia (5–)5.5–6.2(–7) × (1.4–)1.6–1.9(–2.1) µm, although the two species are phylogenetically quite distinct.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Leptosillia wienkampii* (as *Leptosillia* sp. HV-2019e, strain CRW, GenBank MK527865.1; Identities = 398/427 (93 %), 4 gaps (0 %)), *Liberomyces saliciphilus* (as *Sordariomycetes* sp. SP-2010b, strain H041, GenBank FR715510.1; Identities = 397/427 (93 %), 3 gaps (0 %)), and *Leptosillia slaptonensis* (as *Leptosillia* sp. HV-2019d, strain CRU1, GenBank MK527859.1; Identities = 389/428 (91 %), 5 gaps (1 %)). Closest hits using the **LSU** sequence are *Leptosillia slaptonensis* (as *Leptosillia* sp. HV-2019d, strain CRU2, GenBank MK527860.1; Identities = 822/842 (98 %), 3 gaps (0 %)), *Leptosillia wienkampii* (as *Leptosillia* sp. HV-2019e, strain CRW, GenBank MK527865.1; Identities = 808/828 (98 %), 2 gaps (0 %)), and *Leptosillia acerina* (as *Leptosillia* sp. HV-2019a, strain CRA2, GenBank MK527850.1; Identities = 818/839 (97 %), no gaps). No significant hits were obtained when the **rpb2** sequence was used in blastn and megablast searches.

**Colour illustrations.** Knysna forest with *Maytenus heterophylla* trees. Conidiophores with conidiogenous cells; conidia. Scale bars = 10 µm.

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