

*Lareunionomyces eucalypticola*





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## *Lareunionomyces eucalypticola* Crous, sp. nov.

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

*Classification* — *Neolauriomycetaceae*, *Helotiales*, *Leotiomycetes*.

*Conidiophores* solitary, erect, dark brown, smooth, thick-walled, straight to slightly flexuous, subcylindrical, arising from superficial hyphae, base swollen with brown rhizoids, 150–250 × 5–9 µm, sparsely 2–3-septate. *Conidiogenous region* consisting of a penicillate series of branches. Primary branches brown, smooth, aseptate, subcylindrical to clavate, 9–15 × 5–7 µm. Secondary branches pale brown, subcylindrical, smooth, 7–10 × 4–6 µm. Tertiary branches 7–9 × 3–4 µm, and quaternary branches 6–9 × 3–4 µm, giving rise to 1–4 conidiogenous cells. *Conidiogenous cells* subcylindrical, pale brown, smooth, 12–15 × 1.5–2 µm, apex proliferating inconspicuously percurrently. *Conidia* forming in cylindrical, unbranched chains, eventually forming a mucoid mass, hyaline, smooth, cylindrical, apex obtuse, base truncate, 4–4.5(–6) × 2–2.5 µm.

*Culture characteristics* — Colonies erumpent, with folded surface, sparse aerial mycelium and smooth, lobate margin, reaching 8 mm diam after 2 wk at 25 °C. On MEA surface umber in middle, buff at margin, reverse umber. On PDA surface and reverse sepia. On OA surface umber.

*Typus.* COLOMBIA, San Bernardo, on leaves of *Eucalyptus grandis* (*Myrtaceae*), 3 June 2010, M.J. Wingfield, HPC 2497 (holotype CBS H-24240, culture ex-type CPC 36155 = CBS 146043, ITS, LSU, *rpb2* and *tef1* sequences GenBank MN562116.1, MN567624.1, MN556800.1 and MN556820.1, MycoBank MB832871).

*Notes* — *Lareunionomyces* was established for a genus of hyphomycetes that resembles *Sporendocladia*, except that it has a more intricate conidiogenous apparatus (Crous et al. 2016b). *Lareunionomyces eucalypticola* is phylogenetically related to *L. loeiensis* (on leaf litter, Thailand). The two species are easily distinguished based on their conidiophores, those of the latter being smaller, 90–150(–165) × 5–6.5 µm, and lacking rhizoids (Crous et al. 2018a).

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Lareunionomyces loeiensis* (strain BCC 84472, GenBank NR\_161149.1; Identities = 511/522 (98 %), 1 gap (0 %)), *Lareunionomyces eucalypti* (strain CPC 32621, GenBank NR\_160352.1; Identities = 526/543 (97 %), 3 gaps (0 %)), and *Lareunionomyces syzygii* (strain CBS 141326, GenBank NR\_145315.1; Identities = 532/553 (96 %), 3 gaps (0 %)). Closest hits using the **LSU** sequence are *Lareunionomyces loeiensis* (strain BCC 84472, GenBank MK047510.1; Identities = 863/871 (99 %), no gaps), *Lareunionomyces syzygii* (strain CBS 141326, GenBank NG\_058244.1; Identities = 878/891 (99 %), no gaps), and *Lareunionomyces eucalypti* (strain CPC 32621, GenBank NG\_064545.1; Identities = 854/867 (99 %), no gaps). Closest hits using the **rpb2** sequence had highest similarity to *Lareunionomyces eucalypti* (strain CPC 32621, GenBank MH327867.1; Identities = 713/790 (90 %), no gaps), *Neolauriomycetes eucalypti* (strain CPC 32623, GenBank MH327868.1; Identities = 753/901 (84 %), no gaps), and *Diplococcium spicatum* (strain CBS 852.73, GenBank EF204483.1; Identities = 695/895 (78 %), 26 gaps (2 %)). Closest hits using the **tef1** sequence had highest similarity to *Lareunionomyces eucalypti* (strain CPC 32621, GenBank MH327878.1; Identities = 431/519 (83 %), 28 gaps (5 %)), *Porodiplodia vitis* (strain CBS 144634, GenBank MK442707.1; Identities = 218/248 (88 %), 12 gaps (4 %)), and *Cadophora luteo-olivacea* (strain Clo-15, GenBank HQ661073.1; Identities = 218/251 (87 %), 10 gaps (3 %)).

*Colour illustrations.* *Eucalyptus grandis* trees. Sporulation on oatmeal agar; conidiophores with swollen bases; conidiogenous cells; conidia. Scale bars = 10 µm.

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