





Fungal Planet 767 – 13 July 2018

***Lareunionomyces eucalypti* Crous, sp. nov.**

*Etymology.* Name refers to *Eucalyptus*, the host genus from which this fungus was collected.

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

*Conidiophores* solitary, erect, dark brown, finely roughened towards basal region, thick-walled, straight to slightly flexuous, unbranched, subcylindrical, arising from superficial hyphae, base lacking rhizoids, 60–160 × 5–6 µm, 2–7-septate. *Conidiogenous region* consisting of a penicillate series of branches. Primary branches brown, smooth, aseptate, subcylindrical to clavate, 6–15 × 4–5 µm. Secondary and tertiary branches pale brown, subcylindrical, smooth, 6–8 × 2–3 µm, giving rise to 1–4 conidiogenous cells. *Conidiogenous cells* subcylindrical, pale brown, smooth, 7–20 × 2–3 µm; apex proliferating inconspicuously percurrently, collarettes if present cylindrical, inconspicuous. *Conidia* aggregating in mucoid mass, hyaline, smooth, cylindrical, apex obtuse, base truncate, (3.5–)5–6(–7) × 2(–2.5) µm.

*Culture characteristics* — Colonies flat, spreading, with sparse aerial mycelium and smooth, lobate margin, reaching 7 mm diam after 2 wk at 25 °C. On MEA, PDA and OA surface umber, reverse sienna to umber, with diffuse umber pigment on OA.

*Typus.* AUSTRALIA, Victoria, Drummer Forest, on leaves of *Eucalyptus* sp. (*Myrtaceae*), 30 Nov. 2016, P.W. Crous (holotype CBS H-23578, culture ex-type CPC 32621 = CBS 144424, ITS, LSU, *rpb2*, *tef1* and *tub2* sequences GenBank MH327804.1, MH327840.1, MH327867.1, MH327878.1 and MH327889.1, MycoBank MB825413).

*Notes* — The monotypic genus *Lareunionomyces* was established for a genus of hyphomycetes occurring on leaves of *Syzygium jambos* in La Réunion (Crous et al. 2016b). *Lareunionomyces eucalypti* is allied to *L. syzygii*, but distinct from it in that the latter species has shorter conidiophores, 50–100 × 5–8 µm, up to 8 series of branches in the conidiogenous head, and smaller conidia, (3.5–)4(–5) × (1.5–)2 µm (Crous et al. 2016b). For details on *Neolauriomycetaceae* see *Neolauriomycetes eucalypti* in Fungal Planet 768.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the ITS sequence had highest similarity to *Lareunionomyces syzygii* (GenBank NR\_145315.1; Identities = 529/542 (98 %), 2 gaps (0 %)), *Neofabraea inaequalis* (GenBank NR\_155470.1; Identities = 498/545 (91 %), 14 gaps (2 %)) and *Phlyctema vagabunda* (GenBank KT923789.1; Identities = 497/546 (91 %), 17 gaps (3 %)). Closest hits using the LSU sequence are *Lareunionomyces syzygii* (GenBank KX228338.1; Identities = 861/875 (98 %), no gaps), *Exochalara longissima* (GenBank HQ609476.1; Identities = 856/875 (98 %), no gaps) and *Davidhawksworthia illicicola* (GenBank KU728555.1; Identities = 847/884 (96 %), 10 gaps (1 %)). Closest hits using the *rpb2* sequence had highest similarity to *Trichoderma cf. stilbohypoxyli* (GenBank EU241502.1; Identities = 214/265 (81 %), 4 gaps (1 %)), *Trichoderma hispanicum* (GenBank JN715600.1; Identities = 212/265 (80 %), 4 gaps (1 %)) and *Trichoderma paraviridescens* (GenBank KT343762.1; Identities = 213/267 (80 %), 4 gaps (1 %)). Closest hits using the *tef1* sequence had highest similarity to *Acephala applanata* (GenBank DQ274571.1; Identities = 217/251 (86 %), 9 gaps (3 %)), *Ulocladium alternariae* (GenBank AY375370.1; Identities = 219/255 (86 %), 8 gaps (3 %)) and *Cadophora viticola* (GenBank HQ661081.1; Identities = 206/236 (87 %), 7 gaps (2 %)). Closest hits using the *tub2* sequence had highest similarity to *Amorphotheca resiniae* (GenBank XM\_024862766.1; Identities = 679/776 (88 %), 2 gaps (0 %)), *Hymenoscyphus subsymmetricus* (GenBank KJ472286.1; Identities = 651/743 (88 %), 4 gaps (0 %)) and *Hymenoscyphus subpallenscens* (GenBank KJ472284.1; Identities = 638/733 (87 %), 2 gaps (0 %)).

*Colour illustrations.* *Eucalyptus* trees at Drummer Forest; conidiophores sporulating on SNA, showing conidiogenous cells and conidia. Scale bars = 10 µm.

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