

Neolauriomyces eucalypti



Fungal Planet 768 – 13 July 2018

***Neolauriomycetaceae* Crous, fam. nov.**

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

Conidiophores solitary, erect, subcylindrical, straight, slightly flexuous, unbranched, medium brown, smooth, septate, terminating in a phialide, or in a penicillate head: primary branches subcylindrical to doliiform, medium brown, smooth. Secondary branches doliiform to subcylindrical, medium brown, smooth, giving rise to phialides. *Conidiogenous cells* phialidic, ampulliform, medium brown, smooth, including the apical collarette,

cylindrical, medium brown. *Conidia* occurring in chains, unbranched, hyaline, smooth-walled, cylindrical, aseptate, ends truncate.

Type genus. *Neolauriomyces* Crous.
Mycobank MB825414.

Notes — The family *Neolauriomycetaceae* presently contains three genera, namely *Exochalara*, *Lareunionomyces* and *Neolauriomyces*.

***Neolauriomyces* Crous, gen. nov.**

Etymology. Named reflects a similarity to the genus *Lauriomyces*.

Conidiophores solitary, erect, subcylindrical, straight, slightly flexuous, unbranched, medium brown, smooth, septate. *Conidiogenous head* penicillate, primary branches subcylindrical to doliiform, medium brown, smooth. Secondary branches doliiform to subcylindrical, medium brown, smooth, giving rise to 1–2

phialides. *Conidiogenous cells* phialidic, ampulliform, medium brown, smooth, including the apical collarette, cylindrical, medium brown. *Conidia* occurring in long dry chains, unbranched, hyaline, smooth-walled, cylindrical, aseptate, ends truncate.

Type species. *Neolauriomyces eucalypti* Crous.
Mycobank MB825415.

***Neolauriomyces eucalypti* Crous, sp. nov.**

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

Conidiophores solitary, erect, subcylindrical, straight, slightly flexuous, unbranched, medium brown, smooth, 4–8-septate, 40–120 × 5–6 µm. *Conidiogenous head* penicillate, primary branches subcylindrical to doliiform, medium brown, smooth, 4–6 × 4–5 µm. Secondary branches doliiform to subcylindrical, medium brown, smooth, 3–5 × 4–5 µm, giving rise to 1–2 phialides. *Conidiogenous cells* phialidic, ampulliform, medium brown, smooth, 10–14 × 3–5 µm, including the apical collarette, cylindrical, medium brown, 4–7 × 1.5–2 µm. *Conidia* occurring in long dry chains (20–40), unbranched, hyaline, smooth-walled, cylindrical, aseptate, ends truncate, 4(–5) × 1.5 µm.

Culture characteristics — Colonies erumpent, spreading, with sparse aerial mycelium and smooth, lobate margin, reaching 12 mm diam after 2 wk at 25 °C. On MEA, PDA and OA surface and reverse amber.

Typus. AUSTRALIA, Victoria, Drummer Forest, on leaves of *Eucalyptus* sp. (*Myrtaceae*), 30 Nov. 2016, P.W. Crous (holotype CBS H-23577, culture ex-type CPC 32623 = CBS 144425, ITS, LSU, *rpb2*, *tef1* and *tub2* sequences GenBank MH327805.1, MH327841.1, MH327868.1, MH327879.1 and MH327890.1, MycoBank MB825416).

Additional material examined. AUSTRALIA, New South Wales, Nullica State Forest, on *Eucalyptus* leaf litter (*Myrtaceae*), 29 Nov. 2016, P.W. Crous, CPC 32613, ITS, LSU, *rpb2*, *tef1* and *tub2* sequences GenBank MH327806.1, MH327842.1, MH327869.1, MH327880.1 and MH327891.1.

Colour illustrations. Symptomatic *Eucalyptus* leaves; conidiophores sporulating on SNA, conidiogenous cells and long conidial chains. Scale bars = 10 µm.

Notes — Although *Neolauriomyces* resembles *Lauriomyces* morphologically (Crous et al. 2009), the genus *Neolauriomyces* is phylogenetically related to *Exochalara* and *Lareunionomyces*. *Exochalara* is quite distinct from *Neolauriomyces* in having solitary conidiophores with percurrent proliferation that terminate in a phialide giving rise to chains of conidia (Gams & Holubová-Jechová 1976). *Neolauriomyces* is also distinct from *Lareunionomyces* because its phialides are widely dispersed (not densely aggregated) and have prominently ampulliform phialides with long collarettes. Based on the *tef1* and *tub2* sequences, the two isolates of *Neolauriomyces eucalypti* considered in this study might actually represent two cryptic species but additional strains are required to resolve this question.

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 = 521/543 (96 %), 7 gaps (1 %)), *Neofabraea inaequalis* (GenBank NR_155470.1; Identities = 496/545 (91 %), 13 gaps (2 %)) and *Pseudofabraea citricarpa* (GenBank NR_154319.1; Identities = 491/539 (91 %), 14 gaps (2 %)). The ITS sequences of CPC 32613 and 32623 are identical (539/539). Closest hits using the LSU sequence are *Exochalara longissima* (GenBank HQ609476.1; Identities = 857/875 (98 %), no gaps), *Lareunionomyces syzygii* (GenBank KX228338.1; Identities = 846/875 (97 %), no gaps) and *Davidhawksworthia illicicola* (GenBank KU728555.1; Identities = 852/884 (96 %), 10 gaps (1 %)). The LSU sequences of CPC 32613 and 32623 are identical (875/875).

Pedro W. Crous & Johannes Z. Groenewald, Westerdijk Fungal Biodiversity Institute, P.O. Box 85167, 3508 AD Utrecht, The Netherlands; e-mail: p.crous@westerdijkinstitute.nl & e.groenewald@westerdijkinstitute.nl
Michael J. Wingfield, Forestry and Agricultural Biotechnology Institute (FABI), University of Pretoria, Pretoria 0002, South Africa; e-mail: mike.wingfield@fabi.up.ac.za
Treena I. Burgess & Giles E. St. J. Hardy, Centre for Phytophthora Science and Management, Murdoch University, 90 South Street, Murdoch, WA 6150, Australia; e-mail: tburgess@murdoch.edu.au & g-hardy@murdoch.edu.au