

Helminthosporium livistonae



Fungal Planet 758 – 13 July 2018

***Helminthosporium livistonae* Crous, sp. nov.**

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

Classification — *Massarinaceae*, *Pleosporales*, *Dothideo-myces*.

Mycelium consisting of hyaline, septate, branched, 2.5–3 µm diam hyphae. *Conidiophores* arising from superficial mycelium, erect, flexuous, medium brown, cylindrical, smooth to rough-walled, multiseptate, up to 500 µm tall, with obtuse apex, 4–6 µm diam. *Conidiogenous cells* integrated along length of conidiophore, terminal and intercalary, pores inconspicuous. *Conidia* subcylindrical, straight, medium brown, smooth, apex obtuse, base somewhat obconic, hilum thickened and darkened, 2–3 µm diam, (3–)4–6(–7)-distoseptate, (25–)40–55(–65) × (7–)8–9 µm; conidia solitary, terminal and lateral, or in short unbranched chains of up to three.

Culture characteristics — Colonies flat, spreading, surface folded, with moderate aerial mycelium and smooth, lobate margin, reaching 65 mm diam after 2 wk at 25 °C. On MEA surface dirty white, reverse sienna. On PDA surface saffron, reverse peach. On OA surface ochreous to salmon with diffuse salmon pigment.

Typus. AUSTRALIA, New South Wales, Murrumarang National Park, on leaves of *Livistona australis* (*Arecaceae*), 27 Nov. 2016, P.W. Crous (holotype CBS H-23589, culture ex-type CPC 32158 = CBS 144413, ITS and LSU sequences GenBank MH327795.1 and MH327831.1, MycoBank MB825400).

Notes — The *Helminthosporium* complex was recently treated by Voglmayr & Jaklitsch (2017). *Helminthosporium livistonae* must to be compared to *Exosporium livistonicola*, which is distinct in having inconspicuous conidiogenous loci, and conidia that are solitary, obclavate, 20–85 × 4–7 µm, 2–5-distoseptate (Braun et al. 2014, Videira et al. 2017). *Exosporium livistonae* is distinct in having obclavate conidia that are solitary, 5-distoseptate, (45–)60–70(–80) × (7–)8(–10) µm, with distinct scars on the conidiophores (Crous et al. 2011b); in addition, its LSU sequence (GenBank JQ044446.1) is only 85 % identical to that of *Helminthosporium livistonae* (760/891, 29 gaps).

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the ITS sequence had highest similarity to *Helminthosporium juglandinum* (GenBank NR_155197.1; Identities = 485/542 (89 %), 20 gaps (3 %)), *Helminthosporium quercinum* (GenBank NR_155198.1; Identities = 483/543 (89 %), 22 gaps (4 %)) and *Corynespora proliferata* (GenBank FJ852596.1; Identities = 482/543 (89 %), 23 gaps (4 %)). Closest hits using the LSU sequence are *Helminthosporium genistae* (GenBank KY984312.1; Identities = 855/885 (97 %), 2 gaps (0 %)), *Helminthosporium microsorum* (GenBank KY984329.1; Identities = 853/884 (96 %), no gaps) and *Helminthosporium quercinum* (GenBank KY984338.1; Identities = 852/884 (96 %), no gaps).

Colour illustrations. Symptomatic leaves of *Livistona australis*; conidiophores and conidia. Scale bars = 10 µm.

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