

Sporidesmium melaleucaae



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***Sporidesmiales* Crous, ord. nov.**

Classification — *Sporidesmiaceae*, *Sporidesmiales*, *Sordariomycetes*.

Mycelium consisting of hyaline, smooth, branched, septate hyphae, immersed or superficial. *Conidiophores* solitary or in clusters, erect, subcylindrical, unbranched, dark brown, septate. *Conidiogenous cells* terminal, medium brown, smooth, subcylindrical, holoblastic. *Conidia* dry, solitary, medium brown,

smooth, obclavate to cylindrical or fusoid, straight to flexuous, apex obtuse, base obconically truncate, distoseptate.

Type family. *Sporidesmiaceae* Fr.

Type genus. *Sporidesmium* Link.

Mycobank MB 825433.

Notes — The order *Sporidesmiales* presently only contains the genus *Sporidesmium*.

***Sporidesmium melaleucaae* Crous, sp. nov.**

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

Mycelium consisting of hyaline, smooth, branched, septate, 2–3 µm diam hyphae. *Conidiophores* solitary or in clusters, erect, subcylindrical, dark brown, 1–2-septate, 12–30 × 4–6 µm. *Conidiogenous cells* terminal, medium brown, smooth, subcylindrical, holoblastic, 5–20 × 4–5 µm. *Conidia* solitary, medium brown, smooth, obclavate, straight to flexuous, apex obtuse, base obconically truncate, 3.5–4 µm diam, 5–21-distoseptate, (45–)80–130(–170) × (8–)9–10(–11) µm.

Culture characteristics — Colonies erumpent, with sparse aerial mycelium and even lobate margin, reaching 10 mm diam after 2 wk at 25 °C. On MEA and PDA surface pale luteous, reverse luteous. On OA surface umber.

Typus. AUSTRALIA, New South Wales, Tulaswalla Creek, on *Melaleuca* sp. (*Myrtaceae*), 27 Nov. 2016, P.W. Crous (holotype CBS H-23567, culture ex-type CPC 32707 = CBS 144435, ITS and LSU sequences GenBank MH327817.1 and MH327853.1, MycoBank MB825434).

Additional material examined. AUSTRALIA, New South Wales, Tulaswalla Creek, on *Melaleuca* sp. (*Myrtaceae*), 27 Nov. 2016, P.W. Crous, CPC 32936, ITS and LSU sequences GenBank MH327818.1 and MH327854.1.

Notes — The genera *Sporidesmium* and *Ellisembia* are morphologically similar (Réblová 1999), and we choose to use the older name, *Sporidesmium*. Phylogenetically, *S. melaleucaae* is allied to *E. bambusicola*, which has obclavate to ellipsoid conidia, 9–11-distoseptate, 40–55 × 10–12 µm. Morphologically, *S. melaleucaae* is also similar to *E. bambusicola*, although it has much longer conidiophores (2–4-septate, 50–100 × 4–7 µm), and smaller conidia (60–130 × 13–15 µm) (Wu & Zhuang 2005).

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the ITS sequence of CPC 32707 had highest similarity to *Cataractispora appendiculata* (GenBank KU975063.1; Identities = 322/379 (85 %), 18 gaps (4 %)), *Submersisphaeria aquatica* (GenBank KU975067.1; Identities = 477/583 (82 %), 30 gaps (5 %)) and *Pseudoproboscispora caudae-suis* (GenBank KU975068.1; Identities = 481/589 (82 %), 37 gaps (6 %)). The ITS sequences of CPC 32707 and CPC 32936 differed with 1 nucleotide (564/565). Closest hits using the LSU sequence are *Ellisembia bambusicola* (GenBank DQ408562.1; Identities = 809/822 (98 %), no gaps), *Fluminicola thailandensis* (GenBank MF374368.1; Identities = 780/829 (94 %), 7 gaps (0 %)) and *Fluminicola saprotrophitica* (GenBank MF374367.1; Identities = 769/818 (94 %), 7 gaps (0 %)). The LSU sequences of CPC 32707 and CPC 32936 differed with 1 nucleotide (842/843).

Colour illustrations. Tulaswalla Creek; conidiophores, conidiogenous cells and conidia. Scale bars = 10 µm.

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