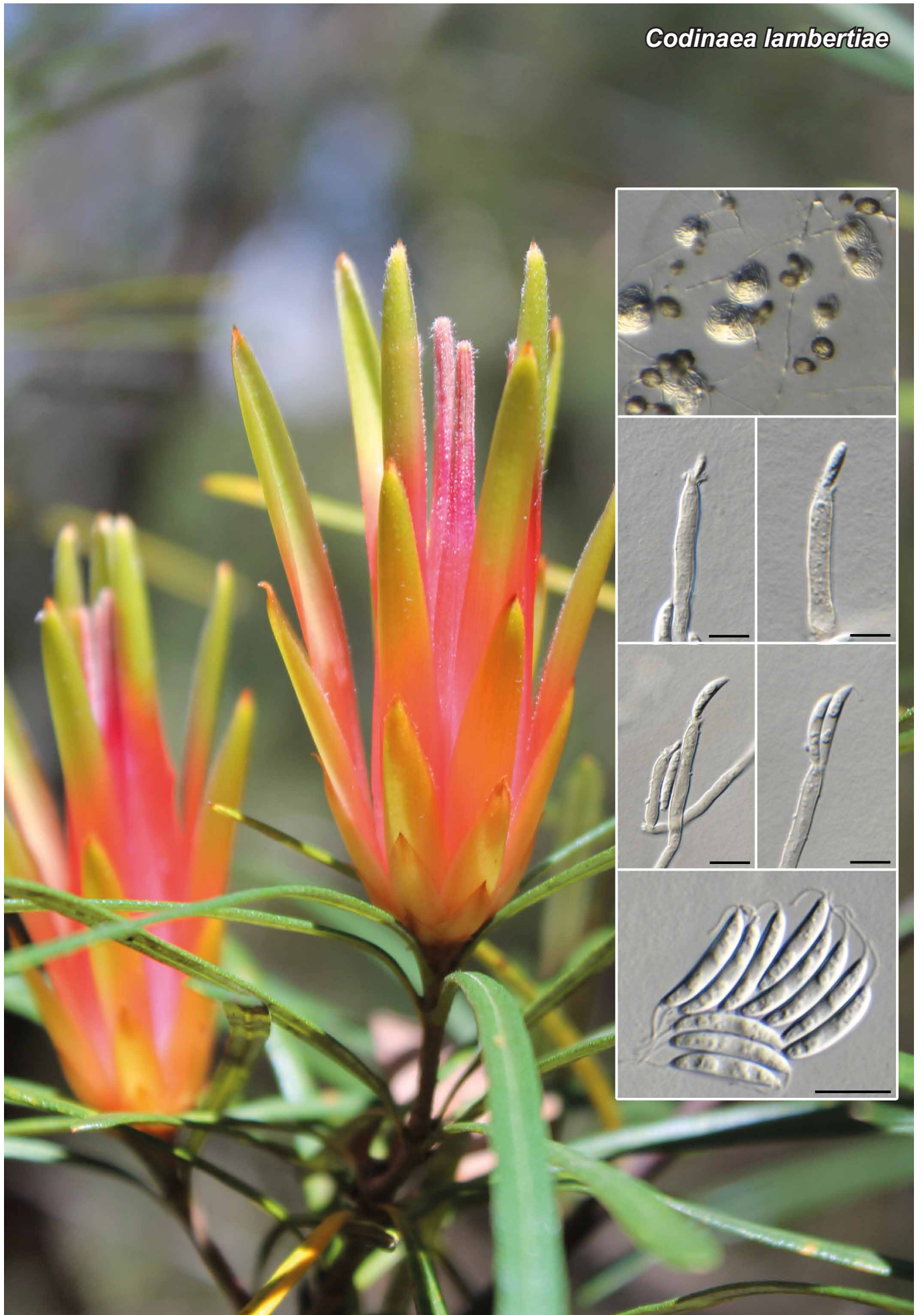


Codinaea lambertiae



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Codinaea lambertiae Crous, *sp. nov.*

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

Classification — *Chaetosphaeriaceae*, *Chaetosphaeriales*, *Sordariomycetes*.

Mycelium consisting of hyaline, smooth, septate, branched, 2–3 µm diam hyphae. *Conidiophores* solitary, arising from creeping hyphae, flexuous, 100–200 × 3 µm, multiseptate, becoming pale to medium brown in fertile region, mostly unbranched, rarely branched close to apex. *Conidiogenous cells* integrated, apical, rarely intercalary, subcylindrical, medium brown, smooth, 15–35 × 2.3–5 µm, phialidic with flared apical collarette, 3.5–4.5 µm diam. *Conidia* solitary, aggregating in slimy mass, hyaline, smooth, aseptate, curved, fusoid-ellipsoid, guttulate, apex subacutely rounded, base truncate, 1 µm diam, (13–)14–15(–18) × (2.5–)3 µm, with single appendage at each end, flexuous, unbranched, 5–8 µm long.

Culture characteristics — Colonies flat, spreading, with sparse aerial mycelium and feathery, lobate margins, reaching 30 mm diam after 2 wk at 25 °C. On MEA surface pale olivaceous grey, reverse smoke grey. On PDA surface and reverse smoke grey. On OA surface iron-grey.

Typus. AUSTRALIA, New South Wales, Fitzroy Falls, Morton National Park, on leaves of *Lambertia formosa* (*Proteaceae*), 26 Nov. 2016, P.W. Crous (holotype CBS H-23288, culture ex-type CPC 32289 = CBS 143419, ITS and LSU sequences GenBank MG386052 and MG386105, MycoBank MB823401).

Notes — *Codinaea* (setulate conidia) is distinguished from *Dictyochoaeta* (asetulate conidia) (Réblová & Winka 2000), and thus the present collection is described as a new species of *Codinaea*. Phylogenetically, *C. lambertiae* is part of the *C. simplex* species complex (Hughes & Kendrick 1968, Crous et al. 2014b), but appears to be distinct based on DNA sequence.

Based on a megablast search using the ITS sequence, the closest matches in NCBI's GenBank nucleotide database were *Dictyochoaeta simplex* (GenBank EF029193; Identities 506/514 (98 %), 1 gap (0 %)), *Dictyochoaeta fertilis* (GenBank AF178540; Identities 491/501 (98 %), 3 gaps (0 %)) and *Codinaea pini* (GenBank NR_137943; Identities 490/530 (92 %), 20 gaps (3 %)). The highest similarities using the LSU sequence were *Dictyochoaeta simplex* (GenBank AF178559; Identities 822/831 (99 %), no gaps), *Codinaea pini* (GenBank KP004493; Identities 826/838 (99 %), 1 gap (0 %)) and *Chaetosphaeria rivularia* (GenBank KR347357; Identities 810/838 (97 %), 1 gap (0 %)).

Colour illustrations. *Lambertia formosa*; conidiophores sporulating on PNA, conidiogenous cells and conidia. Scale bars = 10 µm.

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