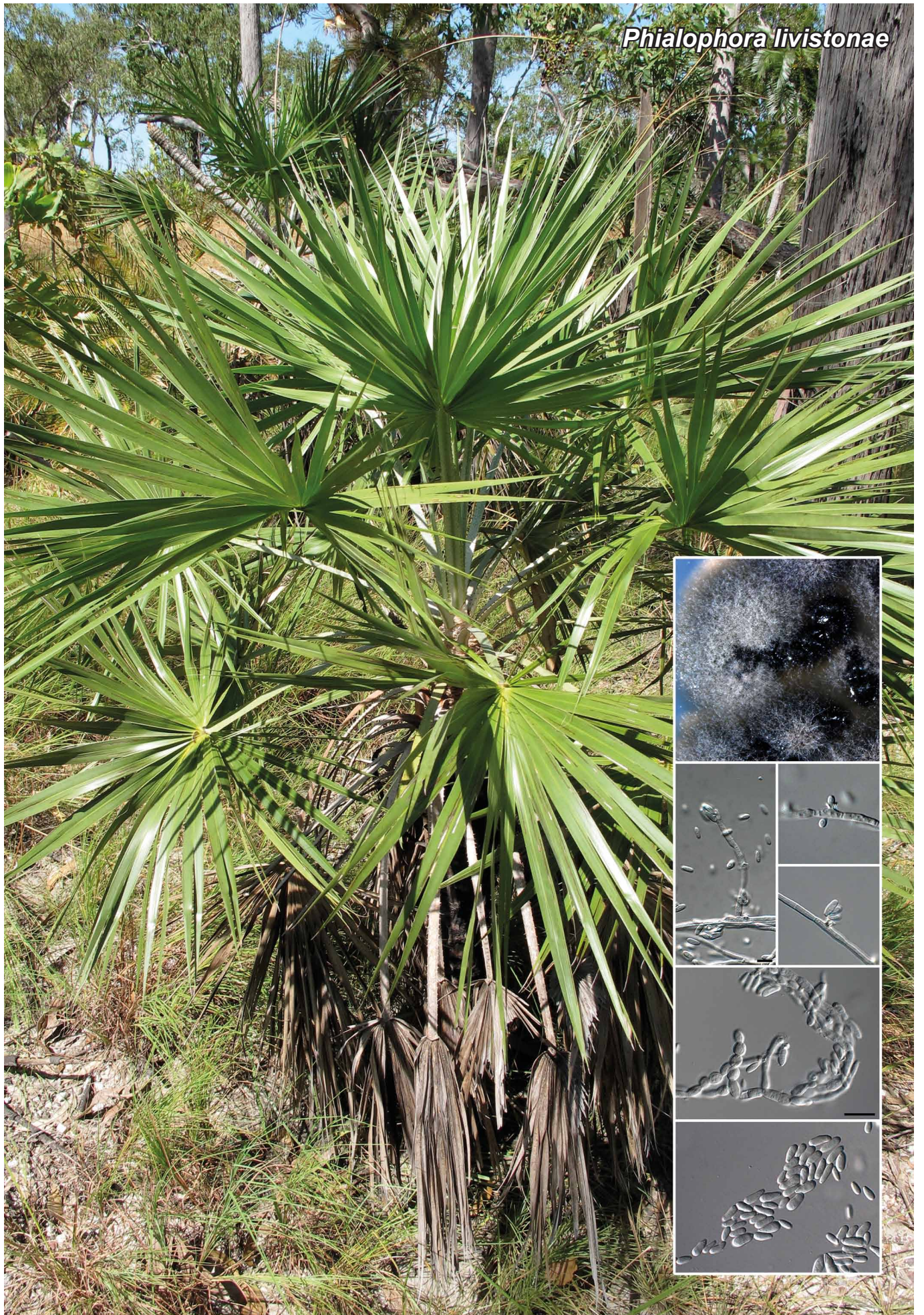


Phialophora livistonae



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Phialophora livistonae Crous & Summerell, *sp. nov.*

Etymology. Named after the host genus from which it was collected, *Livistona*.

Colonies on synthetic nutrient-poor agar. *Mycelium* consisting of spreading, septate, branched hyphae, smooth, pale brown, 2–3 µm diam. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* intercalary and integrated on hyphae, pale brown, subcylindrical to narrowly ellipsoid, at times erect on hyphae, ampulliform to doliiform, monophialidic, 4–10 × 3–4 µm; collarette flaring, 1–2 × 1–1.5 µm. *Conidia* solitary, hyaline to pale brown, smooth, clavate to fusoid-ellipsoid, apex obtuse, tapering to a truncate base, 0.5–1 µm diam, (4–)7–8(–10) × (2–)3(–3.5) µm; at times becoming 1-septate with age. *Chlamydospores* intercalary, pale brown to brown, smooth, globose to narrowly ellipsoid, 0–1-septate, 8–10 × 3–5 µm.

Culture characteristics — (in the dark, 25 °C after 2 wk): Colonies on potato-dextrose agar, malt extract agar and oat-meal agar erumpent, spreading, with even, smooth margin and sparse aerial mycelium; surface olivaceous-grey to iron-grey; reverse iron-grey; reaching 8 mm diam.

Typus. AUSTRALIA, Northern Territory, Litchfield National Park, S13°01.226' E130°56.349', on leaves of *Livistona humilis* (*Arecaceae*), 25 Apr. 2011, P.W. Crous & B.A. Summerell, holotype CBS H-21080, cultures ex-type CPC 19433 = CBS 133589, ITS sequence GenBank KC005774, LSU sequence GenBank KC005796, MycoBank MB801774.

Notes — Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the LSU sequence are *Phialophora sessilis* (GenBank FJ147173; Identities = 728/733 (99 %), Gaps = 1/733 (0 %)), *Cyphellophora eucalypti* (GenBank GQ303305; Identities = 859/882 (97 %), Gaps = 4/882 (0 %)) and *Cyphellophora fusarioides* (GenBank JQ766486; Identities = 745/766 (97 %), Gaps = 4/766 (1 %)). Closest hits using the ITS sequence had highest similarity to *Phialophora sessilis* (GenBank AB190381; Identities = 570/630 (90 %), Gaps = 27/630 (4 %)), *Cyphellophora eucalypti* (GenBank GQ303274; Identities = 536/622 (86 %), Gaps = 33/622 (5 %)) and *Phialophora olivacea* (GenBank AB190379; Identities = 544/633 (86 %), Gaps = 41/633 (6 %)). Although phylogenetically allied to *P. sessilis* (conidia 3 × 1.8 µm; de Hoog et al. 1999), conidia of *P. livistonae* are larger and easily distinguishable.

Colour illustrations. *Livistona humilis* growing in Litchfield National Park, Northern Territory; colony on synthetic nutrient-poor agar; hyphae, conidiogenous cells and conidia. Scale bars = 10 µm.

Pedro W. Crous & Johannes Z. Groenewald, CBS-KNAW Fungal Biodiversity Centre, P.O. Box 85167, 3508 AD Utrecht, The Netherlands;
e-mail: p.crous@cbs.knaw.nl & e.groenewald@cbs.knaw.nl
Brett A. Summerell, Royal Botanic Gardens and Domain Trust, Mrs. Macquaries Road, Sydney, NSW 2000, Australia;
e-mail: Brett.Summerell@rbgsyd.nsw.gov.au