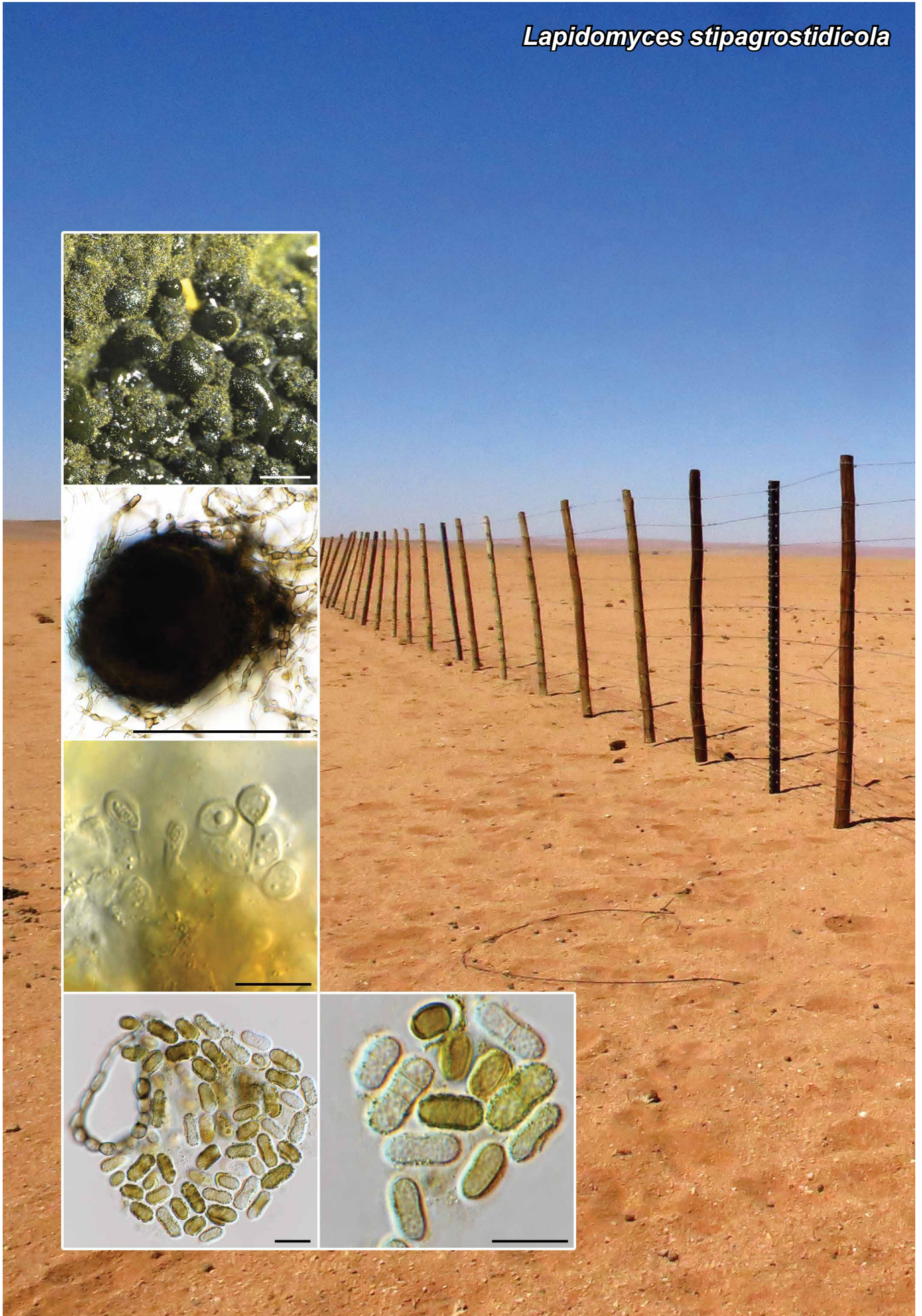


Lapidomyces stipagrostidicola



Fungal Planet 1202 – 13 July 2021

***Lapidomyces stipagrostidicola* Crous, sp. nov.**

Etymology. Name refers to the host genus *Stipagrostis* cf. *ciliata* from which it was isolated.

Classification — *Teratosphaeriaceae*, *Mycosphaerellales*, *Dothideomycetes*.

Conidiomata pycnidial, brown, erumpent, 50–300 µm diam with central ostiole exuding a brown mucoid conidial mass. *Conidiophores* reduced to conidiogenous cells lining inner cavity. *Conidiogenous cells* phialidic, hyaline, smooth, doliform to ovoid, 4–5 × 3.5–5 µm. *Conidia* occurring in unbranched chains, encased in a mucoid sheath encapsulating the conidiogenous cell and conidial chain, medium brown, verruculose, prominently warty, initially joined via a narrow isthmus, ellipsoid to subcylindrical with obtuse ends, 0(–3)-septate, (9–)11–13(–17) × (4–)5–6(–7) µm.

Culture characteristics — Colonies erumpent, spreading, surface folded, with moderate aerial mycelium and smooth, lobate margin, reaching 15 mm diam after 2 wk at 25 °C. On MEA, PDA and OA surface and reverse iron-grey.

Typus. NAMIBIA, boundary fence of Namib-Naukluft Park, east of Gobabeb Namib Research Institute, on leaves of *Stipagrostis* cf. *ciliata* (*Poaceae*), 20 Nov. 2019, P.W. Crous, HPC 3098 (holotype CBS H-24491, culture ex-type CPC 38938 = CBS 146979, ITS, LSU, *rpb2* and *tub2* sequences GenBank MZ064427.1, MZ064484.1, MZ078200.1 and MZ078264.1, MycoBank MB 839516).

Notes — *Lapidomyces* was established for a genus of dematiaceous hyphomycetes. Although the present species was isolated having a cladosporium-like morphology *in vivo*, it only formed a coelomycetous synasexual morph *in vitro*. It is related to *Lapidomyces hispanicus*, a sterile hyphomycete with dark brown hyphae, constricted at their septa (Egidi et al. 2014, Crous et al. 2019b).

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Lapidomyces hispanicus* (strain CBS 118355, GenBank NR_144960.1; Identities = 448/471 (95 %), six gaps (1 %)), *Phaeotheoidea melaleuca* (strain CPC 17223, GenBank HQ599594.1; Identities = 509/543 (94 %), nine gaps (1 %)) and *Camarosporula persooniae* (strain CBS 116258, GenBank JF770449.1; Identities = 513/549 (93 %), 13 gaps (2 %)). Closest hits using the **LSU** sequence are *Lapidomyces hispanicus* (strain CBS 118764, GenBank KF310016.1; Identities = 759/764 (99 %), no gaps), *Phaeotheoidea melaleuca* (strain CPC 17223, GenBank HQ599595.1; Identities = 827/843 (98 %), two gaps (0 %)), *Xenoconiothyrium catenata* (strain CMW 22113, GenBank JN712570.1; Identities = 831/849 (98 %), two gaps (0 %)) and *Camarosporula persooniae* (strain CBS 116258, GenBank JF770461.1; Identities = 829/849 (98 %), two gaps (0 %)). Distant hits obtained using the **rpb2** sequence had highest similarity to *Capnodium salicinum* (strain CBS 131.34, GenBank KT216553.1; Identities = 196/255 (77 %), 12 gaps (4 %)), *Lecanosticta jani* (strain Guat.267.44.N1, GenBank MK015342.1; Identities = 211/280 (75 %), 11 gaps (3 %)) and *Lecanosticta brevispora* (strain CMW46503, GenBank MK015309.1; Identities = 189/248 (76 %), nine gaps (3 %)). Closest hits using the **tub2** sequence had highest similarity to *Lapidomyces hispanicus* (strain TRN500, GenBank KF546778.1; Identities = 315/383 (82 %), five gaps (1 %)), *Petrophila incerta* (strain TRN139b, GenBank KF546769.1; Identities = 305/372 (82 %), 16 gaps (4 %)) and *Cladospodium sphaerospermum* (strain 18ESMA010, GenBank MT881938.1; Identities = 293/357 (82 %), 21 gaps (5 %)).

Colour illustrations. Namib Desert, eastern boundary fence of the Namib-Naukluft Park. Conidiomata on SNA; conidioma; conidiogenous cells giving rise to conidia; conidia. Scale bars = 300 µm (conidiomata), 10 µm (all others).

Pedro W. Crous & Johannes Z. Groenewald, Westerdijk Fungal Biodiversity Institute, P.O. Box 85167, 3508 AD Utrecht, The Netherlands; e-mail: p.crous@wi.knaw.nl & e.groenewald@wi.knaw.nl
 Neriman Yilmaz, Department of Biochemistry, Genetics and Microbiology, Forestry and Agricultural Biotechnology Institute (FABI), Faculty of Natural and Agricultural Sciences, University of Pretoria, Private Bag X20, Hatfield 0028, Pretoria, South Africa; e-mail: neriman.yilmazvisagie@fabi.up.ac.za
 Don Cowan, Centre for Microbial Ecology and Genomics, Department of Biochemistry, Genetics and Microbiology, University of Pretoria, Private Bag X20, Hatfield 0028, Pretoria, South Africa; e-mail: don.cowan@up.ac.za
 Gillian Maggs-Kölling, Gobabeb-Namib Research Institute, Walvis Bay, Namibia; e-mail: gillian@gobabeb.org