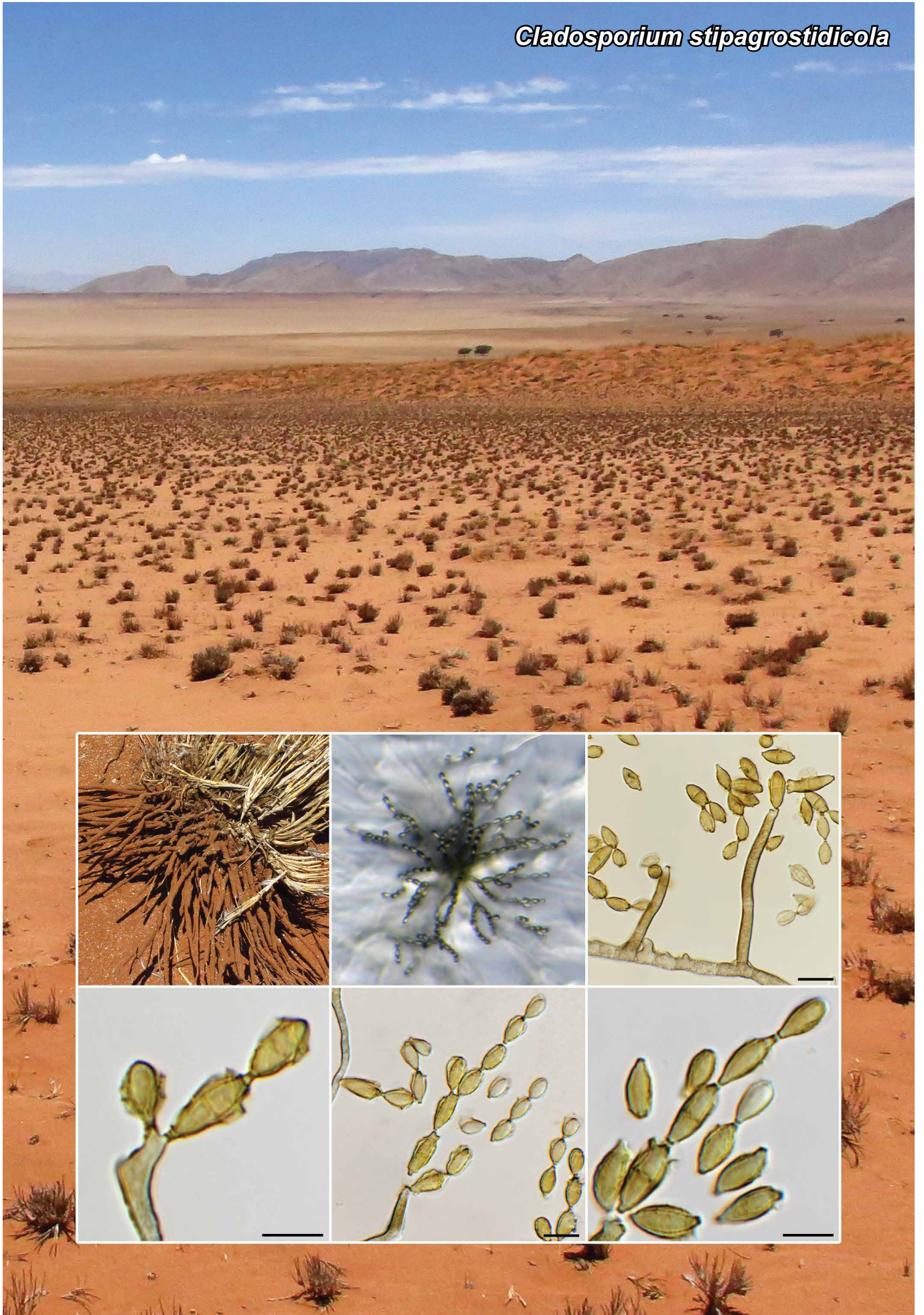


Cladosporium stipagrostidicola



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***Cladosporium stipagrostidicola* Crous, sp. nov.**

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

Classification — *Cladosporiaceae*, *Cladosporiales*, *Dothi-deomycetes*.

Mycelium consisting of pale brown to brown, finely verruculose, branched, septate, 2.5–3 µm diam hyphae. *Conidiophores* reduced to conidiogenous cells or macronematous, erect, straight to geniculate-sinuose, unbranched, subcylindrical, 10–70 × 3–4 µm, 1–4-septate, brown, smooth to verruculose. *Conidiogenous cells* integrated, terminal, subcylindrical, brown, smooth to verruculose, tapering at apex to 1–3 denticulate loci, thickened, darkened and refractive, 1.5–2 µm diam, 15–30 × 3–4 µm. *Conidia* occurring in dry, branched chains. *Secondary ramoconidia* fusoid-ellipsoid to subcylindrical, tapering at ends, golden brown, verruculose to prominently warty, 0–1(–2)-septate, 10–20 × 5–6(–7) µm; warts up to 2 µm diam; hila protruding, thickened, darkened, somewhat refractive, 1.5–2 µm diam; intermediate and terminal conidia aseptate, golden brown, verruculose to prominently warty, (8–)9–10(–11) × (4–)5(–6) µm; hila denticulate, thickened, darkened, refractive, 1.5–2 µm.

Culture characteristics — Colonies flat, spreading, with moderate aerial mycelium and feathery, lobate margin, reaching 16 mm diam after 2 wk at 25 °C. On MEA, PDA and OA surface and reverse iron-grey.

Typus. NAMIBIA, Saagberg dunes in the 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-24490, culture ex-type CPC 38936 = CBS 146978, ITS, LSU, *actA* and *tef1* (first part) sequences GenBank MZ064420.1, MZ064477.1, MZ078146.1 and MZ078223.1, MycoBank MB 839508).

Notes — *Cladosporium stipagrostidicola* resides in the *C. cladosporioides* species complex (Bensch et al. 2010, 2012, 2015, 2018), being related to *C. flabelliforme* and *C. flavovirens*. *Cladosporium flabelliforme* is distinct in having conidial chains characteristically spread in a fan-like manner, secondary ramoconidia 11–27 × (2–)2.5–3(–3.5) µm, 0(–1)-septate, small terminal conidia, obovoid or ellipsoid, 4.5–8 × 1.5–2.5 µm (Bensch et al. 2010). *Cladosporium flavovirens* is distinct from other species in that it has secondary ramoconidia 9–30 × 3.5–4 µm, 0–2-septate, and small terminal conidia, obovoidal to short ellipsoidal, 5–7 × 2.5–3 µm (Sandoval-Denis et al. 2016).

Colour illustrations. *Stipagrostis* tussocks in the Namib Sand Sea, Namibia. Roots of *Stipagrostis* cf. *ciliata* with rhizosheaths; conidiophores giving rise to conidial chains; ornamented conidia. Scale bars = 10 µm.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the ITS sequence had highest similarity to *Cladosporium delicatulum* (strain CL_FF_10_con, GenBank MT548673.1; Identities = 535/535 (100 %), no gaps), *Cladosporium perangustum* (strain CL2, GenBank MT466522.1; Identities = 535/535 (100 %), no gaps) and *Cladosporium cladosporioides* (strain CBS 127759, GenBank MH864765.1; Identities = 535/535 (100 %), no gaps). Closest hits using the LSU sequence are *Cladosporium asperulatum* (strain CBS 126340, GenBank NG_069955.1; Identities = 877/877 (100 %), no gaps), *Cladosporium australiense* (strain CBS 125984, GenBank NG_069941.1; Identities = 877/877 (100 %), no gaps) and *Cladosporium cladosporioides* (strain CBS 127339, GenBank MH875964.1; Identities = 877/877 (100 %), no gaps). Closest hits using the *actA* sequence had highest similarity to *Cladosporium ramotenellum* (strain CBS 145592, GenBank MT223748.1; Identities = 420/437 (96 %), no gaps), *Cladosporium myrtacearum* (strain CPC 16319, GenBank KT600605.1; Identities = 405/431 (94 %), four gaps (0 %)) and *Cladosporium rugulovarians* (strain CPC 18444, GenBank KT600656.1; Identities = 486/521 (93 %), three gaps (0 %)). Closest hits using the *tef1* sequence had highest similarity to *Cladosporium funiculosum* (strain CPC 22298, GenBank MF473409.1; Identities = 287/328 (88 %), 12 gaps (3 %)), *Cladosporium pseudocladosporioides* (strain SL1023, GenBank MH329203.1; Identities = 284/327 (87 %), 15 gaps (4 %)) and *Cladosporium ipereniae* (strain CPC 16238, GenBank KT600491.1; Identities = 325/378 (86 %), 15 gaps (3 %)).

Supplementary material

FP1195 Consensus phylogram (50 % majority rule) obtained from the maximum likelihood analysis with IQ-TREE v. 1.6.12 (Nguyen et al. 2015, Kalyaanamoorthy et al. 2017, Hoang et al. 2018) of the *Cladosporium* multi-gene (*actA* / *tef1*) nucleotide alignment. Bootstrap support values (> 69 % shown; only values > 94 % are significant) from 5000 ultrafast bootstrap replicates are shown at the nodes. Culture collection and GenBank accession (in superscript) numbers are indicated for all species and numbers in **bold** represent those cultures with a type status. The tree was rooted to *Cercospora beticola* (culture CBS 116456) and the species described here is highlighted with a coloured block and **bold** face. Alignment statistics: 67 strains including the outgroup; 661 characters including alignment gaps analysed: 429 distinct patterns, 250 parsimony-informative, 88 singleton sites, 323 constant sites. The best model identified for the entire alignment in IQ-TREE using the TESTNEWMERGE option was: TIM2+F+I+G4. The alignment and tree were deposited in TreeBASE (Submission ID 28129).

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