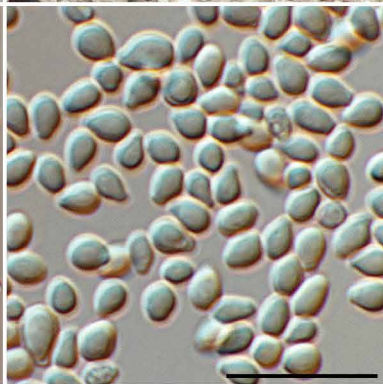
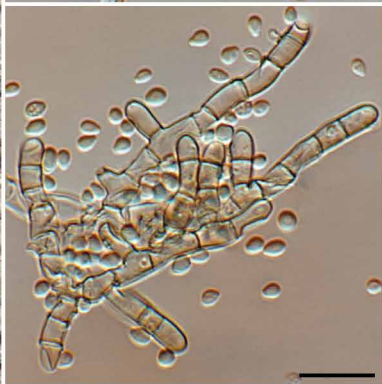
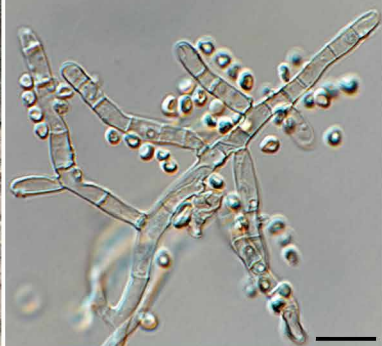
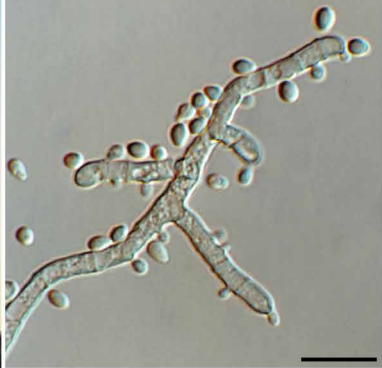


Sordaria equicola



Fungal Planet 1207 – 13 July 2021

***Sordaria equicola* Crous, sp. nov.**

Etymology. Name refers to the substrate from which it was isolated, on zebra (*Equus zebra hartmannae*) dung.

Classification — *Sordariaceae*, *Sordariales*, *Sordariomycetes*.

Mycelium consisting of smooth, pale brown, branched, septate, 1.5–2 µm diam hyphae. *Conidiophores* solitary, erect, arising from superficial hyphae, bearing a mucoid, crystalline conidial mass, subcylindrical, pale brown, smooth, branched, septate, appearing tuft-like, with numerous lateral branches, 3–4 µm diam, up to 80 µm tall. *Conidiogenous cells* integrated, terminal and intercalary, occurring throughout conidiophore as small phialidic openings, 1 µm diam, up to 0.5 µm tall, inconspicuous collarettes, not flared, conidiogenous cells 3–10 µm long, 3–4 µm diam. *Conidia* solitary, hyaline, smooth, aseptate, pyriform, apex subobtuse, base truncate, (3–)4(–4.5) × (2–)2.5(–3) µm.

Culture characteristics — Colonies flat, spreading, with moderate to abundant aerial mycelium and smooth, even margin, covering dish after 2 wk at 25 °C. On MEA, PDA and OA surface and reverse olivaceous grey.

Typus. NAMIBIA, Gravel plains north-east of Gobabeb - Namib Research Institute, on zebra (*Equus zebra hartmannae*) dung, 20 Nov. 2019, P.W. Crous, HPC 3103 (holotype CBS H-24504, culture ex-type CPC 38993 = CBS 146992, ITS, LSU, *actA*, *rpb2*, *tef1* (first part) and *tub2* sequences GenBank MZ064435.1, MZ064492.1, MZ078151.1, MZ078202.1, MZ078226.1 and MZ078267.1, MycoBank MB 839522).

Notes — *Sordaria* produces perithecia with asci containing eight uniseriate ascospores that are obovoid or subglobose, aseptate, smooth-walled, dark brown to black, pitted, reticulate or striate, with various appendages or sheaths (Guarro et al. 2012). *Sordaria equicola* is related to *S. fimicola*, a species commonly found in the feces of herbivores. *Sordaria equicola* is only known from its asexual morph, making a morphological comparison with other species impossible.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Sordaria fimicola* (strain KoRLI047353, GenBank MN341415.1; Identities = 569/573 (99 %), one gap (0 %)), *Asordaria humana* (strain CBS 416.82, GenBank MH861509.1; Identities = 569/573 (99 %), one gap (0 %)) and *Sordaria macrospora* (strain CBS 346.62, GenBank MH858175.1; Identities = 569/573 (99 %), one gap (0 %)). Closest hits using the **LSU** sequence are *Sordaria lappae* (strain CBS 154.97, GenBank MH874251.1; Identities = 807/808 (99 %), no gaps), *Asordaria humana* (strain CBS 416.82, GenBank MH873255.1; Identities = 807/808 (99 %), no gaps) and *Sordaria islandica* (strain CBS 512.77, GenBank MH872859.1; Identities = 807/808 (99 %), no gaps). Closest hits using the **actA** sequence had highest similarity to *Sordaria macrospora* (strain k-hell, GenBank XM_024655553.1; Identities = 398/405 (98 %), no gaps), *Neurospora crassa* (strain OR74A, GenBank XM_011396324.1; Identities = 394/405 (97 %), no gaps) and *Neurospora tetrasperma* (strain FGSC 2508, GenBank XM_009849372.1; Identities = 393/405 (97 %), no gaps). Closest hits using the **rpb2** sequence had highest similarity to *Sordaria fimicola* (strain CBS 723.96, GenBank DQ368647.1; Identities = 844/882 (96 %), no gaps), *Neurospora pannonica* (strain TRTC51327, GenBank AY780185.1; Identities = 863/902 (96 %), no gaps) and *Sordaria clematidis* (voucher MFLU 16-2138, GenBank MT394717.1; Identities = 803/842 (95 %), no gaps). Closest hits using the **tef1** sequence had highest similarity to *Pseudoneurospora* sp. (strain FMR 12156, GenBank HG326875.1; Identities = 447/494 (90 %), 15 gaps (3 %)), *Pseudoneurospora amorphoporcata* (strain CBS 626.80, GenBank FR774344.1; Identities = 440/487 (90 %), 16 gaps (3 %)) and *Neurospora pannonica* (strain FGSC 7221, GenBank FR774377.1; Identities = 425/483 (88 %), 17 gaps (3 %)). Closest hits using the **tub2** sequence had highest similarity to *Asordaria tenerifae* (strain CBS 264.86, GenBank AY681206.1; Identities = 447/480 (93 %), three gaps (0 %)), *Pseudoneurospora amorphoporcata* (strain CBS 626.80, GenBank FR774294.1; Identities = 436/469 (93 %), seven gaps (1 %)) and *Sordaria lappae* (strain CBS 154.97, GenBank AY681205.1; Identities = 448/482 (93 %), eight gaps (1 %)).

Colour illustrations. Zebras (*Equus zebra hartmannae*) in Namib Desert. Zebra dung; hyphae giving rise to conidia on SNA. Scale bars = 10 µm.

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