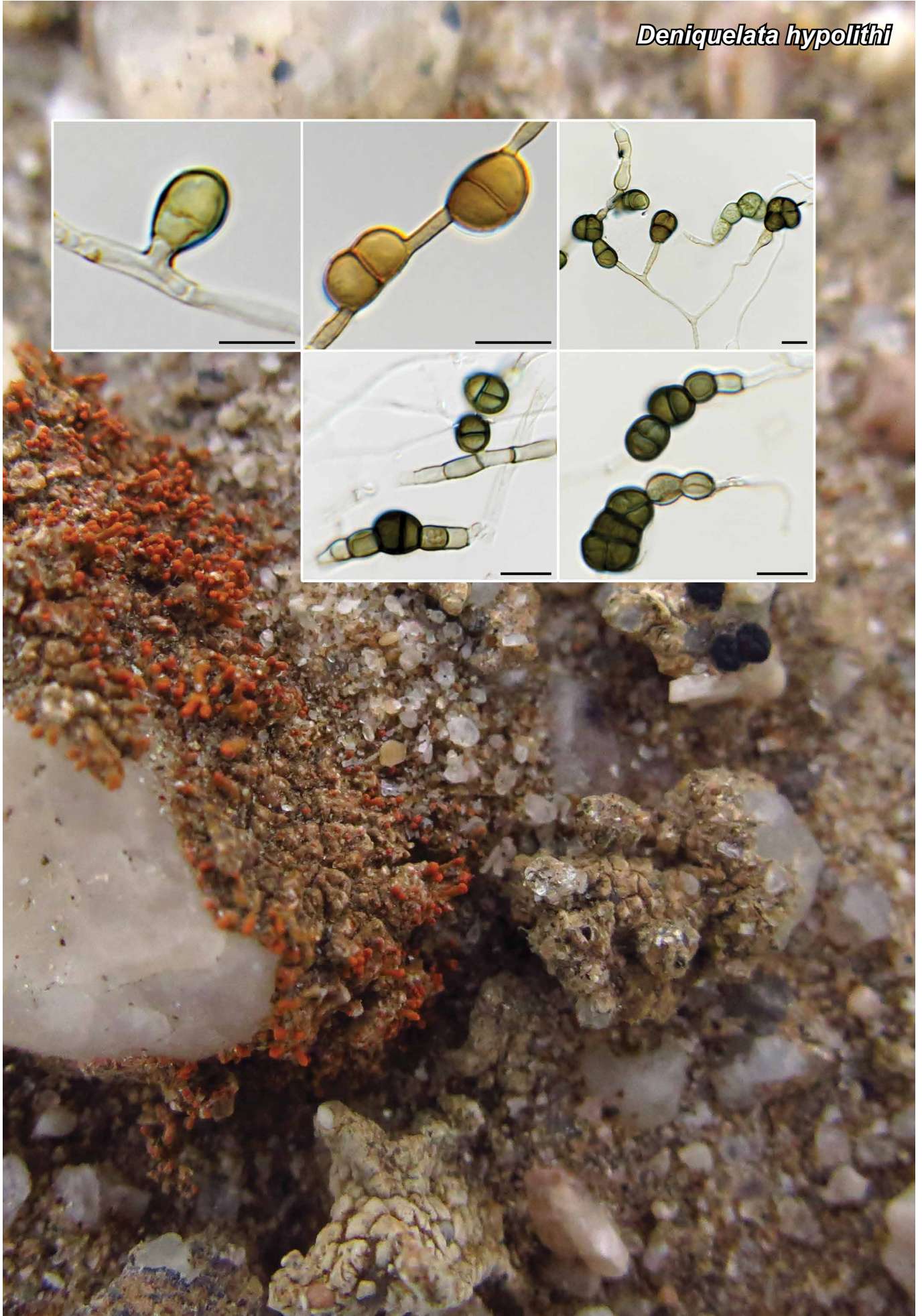


Deniquelata hypolithi



Fungal Planet 1204 – 13 July 2021

***Deniquelata hypolithi* Crous, sp. nov.**

Etymology. Name refers to the fact that it was isolated from a hypolith, under a rock.

Classification — *Didymosphaeriaceae*, *Pleosporales*, *Dothi-deomycetes*.

Mycelium consisting of pale olivaceous to subhyaline, smooth, branched, septate, 2–3 µm diam hyphae. *Conidiophores* when present reduced to conidiogenous cells, erect, pale brown, subcylindrical, 4–20 × 3–4 µm. *Conidia* as intercalary chains in hyphae, or terminal on conidiogenous cells, solitary, or in short chains disarticulating at maturity, or hyphae disintegrate, leaving conidial propagules which are alternaria-like in appearance. *Conidia* brown, smooth, thick-walled, subglobose to pyriform to ellipsoid, guttulate, with 1–3 transverse and 0–2 vertical or oblique septa, (7–)10–12(–17) × (7–)9–10(–11) µm.

Culture characteristics — Colonies flat, spreading, with moderate aerial mycelium and smooth, even margin, reaching 50 mm diam after 2 wk at 25 °C. On MEA, PDA and OA surface smoke grey, reverse umber to isabelline.

Typus. NAMIBIA, Walvis Bay, from hypolith under a quartz stone, 19 Nov. 2019, P.W. Crous, HPC 3101 (holotype CBS H-24500, culture ex-type CPC 38968 = CBS 146988, ITS, LSU, *actA*, *rpb2* and *tef1* (second part) sequences GenBank MZ064429.1, MZ064486.1, MZ078150.1, MZ078201.1 and MZ078250.1, MycoBank MB 839518).

Notes — *Deniquelata* was established for a genus of *Dothi-deomycetes* with pseudothecia giving rise to bitunicate asci with pseudoparaphyses and brown, muriform ascospores (Ariyawansa et al. 2013). *Deniquelata hypolithi* is the first asexual morph linked to a species of *Deniquelata*.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Deniquelata barringtoniae* (strain MFLUCC 11-0422, GenBank NR_111779.1; Identities = 669/691 (97 %), 13 gaps (1 %)), *Deniquelata quercina* (strain 1050-SAB SA5 1, GenBank MT820404.1; Identities = 649/681 (95 %), 14 gaps (2 %)) and *Didymocrea leucaenae* (strain MFLUCC 17-0896, GenBank NR_164298.1; Identities = 477/523 (91 %), 14 gaps (2 %)). Closest hits using the **LSU** sequence are *Deniquelata quercina* (strain 1050-SAB SA5 1, GenBank MT808605.1; Identities = 789/799 (99 %), one gap (0 %)), *Deniquelata barringtoniae* (strain MFLUCC 16-0271, GenBank MH260291.1; Identities = 805/816 (99 %), four gaps (0 %)) and *Neokalmusia thailandica* (strain MFLUCC 16-0399, GenBank KY706131.1; Identities = 778/814 (96 %), three gaps (0 %)). Distant hits obtained using the **actA** sequence had highest similarity to *Parastagonospora nodorum* (strain LDN03-Sn4, GenBank CP022803.1; Identities = 457/505 (90 %), five gaps (0 %)), *Setosphaeria rostrata* (strain BRIP 11426, GenBank LT837589.1; Identities = 474/534 (89 %), 15 gaps (2 %)) and *Setosphaeria minor* (strain BRIP 14612, GenBank LT837609.1; Identities = 471/531 (89 %), nine gaps (1 %)). Closest hits using the **rpb2** sequence had highest similarity to *Deniquelata vittalii* (strain PUFD39, GenBank MF168942.1; Identities = 744/823 (90 %), no gaps), *Didymocrea leucaenae* (strain MFLUCC 17-0896, GenBank MK434905.1; Identities = 733/823 (89 %), no gaps) and *Pseudopithomyces karoo* (strain MUCL 9365, GenBank LK936424.1; Identities = 766/905 (85 %), four gaps (0 %)). Closest hits using the **tef1** sequence had highest similarity to *Pseudopithomyces entadae* (strain MFLUCC 17-0917, GenBank MK360083.1; Identities = 889/920 (97 %), no gaps), *Tremateia murispora* (strain GZCC 18-2787, GenBank MK986482.1; Identities = 902/934 (97 %), no gaps) and *Tremateia chromolaenae* (strain MFLUCC 17-1425, GenBank MT235778.1; Identities = 882/915 (96 %), two gaps (0 %)). The *tef1* sequences of CPC 38988 and 38984 differ by a single substitution (935/936 (99 %)).

Colour illustrations. Quartz stones with lichen and hypolith growth. Hyphae giving rise to conidia. 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