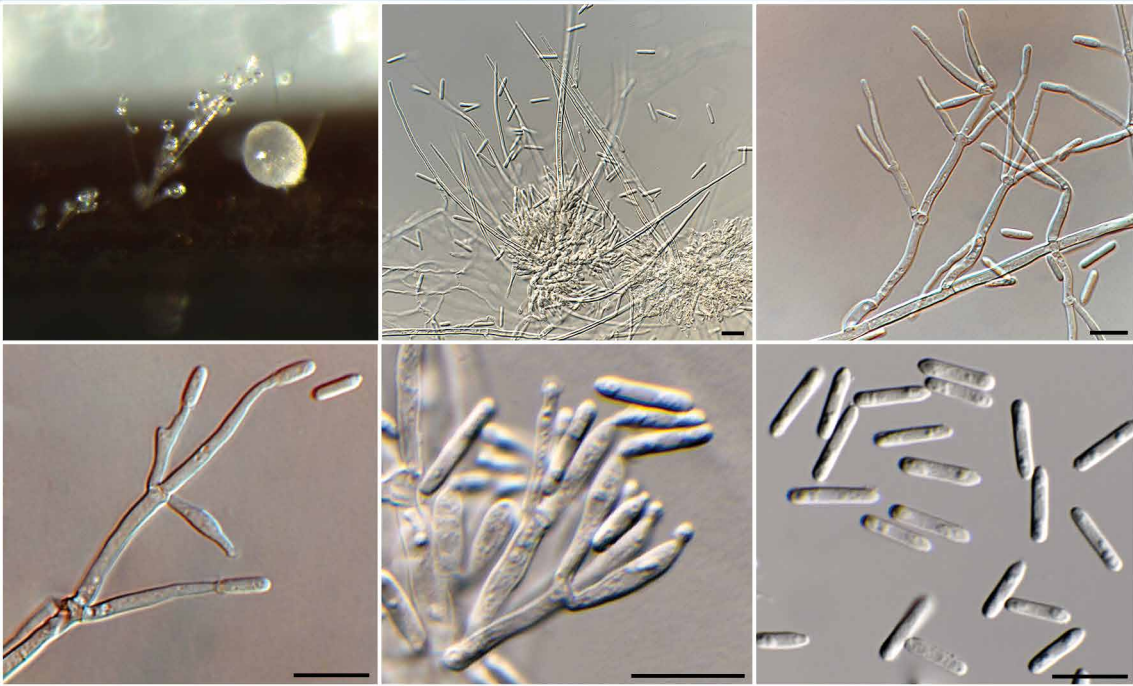


Volutella salvadorae



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***Volutella salvadorae* Crous, sp. nov.**

Etymology. Name refers to the host genus *Salvadora* from which it was isolated.

Classification — *Nectriaceae*, *Hypocreales*, *Sordariomycetes*.

Conidiophores dimorphic. Subverticillium-like conidiophores erect, solitary, at times aggregated into synnemata, subcylindrical, smooth, unbranched or branched below, 3–8-septate, 100–200 × 3–4 µm. *Conidiogenous cells* phialidic, hyaline, smooth, subcylindrical with apical taper, arranged in 2–3 whorls, 10–25 × 2–3 µm, with apical flared collarette, 1–2 µm long. *Conidia* solitary, cylindrical, apex obtuse, base tapering abruptly to truncate hilum, hyaline, smooth, guttulate, (6–)10–12(–15) × 2(–2.5) µm. *Conidiomata* sporodochial, white, with mucoid conidial mass, arising from submerged hyphae, forming a layer of branched, 2–3-septate conidiophores, subcylindrical, hyaline, smooth, 20–35 × 3–4 µm. *Conidiogenous cells* terminal and intercalary, hyaline, smooth, doliiform, phialidic with minute marginal frill, 6–11 × 3–4 µm. *Setae* arising throughout conidioma within conidiogenous apparatus, replacing phialides on conidiophore, thick-walled, hyaline, smooth, flexuous, sparingly septate, tapering to acutely rounded apex, 50–150 × 2.5–3 µm.

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

Typus. NAMIBIA, Walvis Bay, on stems of *Salvadora persica* (*Salvadoraceae*), 20 Nov. 2019, P.W. Crous, HPC 3120 (holotype CBS H-24534, culture ex-type CPC 39017 = CBS 147070, ITS, LSU, *actA*, *cmdA*, *rpb2*, *tef1* (first part) and *tub2* sequences GenBank MZ064450.1, MZ064507.1, MZ078155.1, MZ078168.1, MZ078209.1, MZ078234.1 and MZ078276.1, MycoBank MB 839537).

Notes — *Volutella salvadorae* is related to several species of *Volutella* (see Gräfenhan et al. 2011), including *V. consors* (setae 250–260 µm long, conidia (4.5–)5–7(–13) × 1.5–2.5(–3) µm; Samuels 1977), from which it is phylogenetically distinct.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Volutella consors* (strain CBS 139.79, GenBank KM231768.1; Identities = 544/566 (96 %), two gaps (0 %)), *Lauriomyces sakaeratensis* (voucher SFC 01642, GenBank KX649976.1; Identities = 547/571 (96 %), nine gaps (1 %)) and *Volutella citrinella* (strain DAOM 226720, GenBank HQ897821.1; Identities = 543/567 (96 %), five gaps (0 %)). Closest hits using the **LSU** sequence are *Volutella ciliata* (strain CBS 127312, GenBank MH875955.1; Identities = 796/803 (99 %), no gaps), *Volutella rosea* (strain CBS 128258, GenBank KM231634.1; Identities = 796/803 (99 %), no gaps) and *Volutella roseola* (strain CBS 377.55, GenBank MH869058.1; Identities = 792/800 (99 %), one gap (0 %)). Closest hits using the **actA** sequence had highest similarity to *Volutella consors* (strain CBS 122767, GenBank KM231160.1; Identities = 615/669 (92 %), ten gaps (1 %)), *Volutella ciliata* (strain CBS 483.61, GenBank KM231163.1; Identities = 609/693 (88 %), 34 gaps (4 %)) and *Volutella rosea* (strain CBS 128258, GenBank KM231162.1; Identities = 610/695 (88 %), 35 gaps (5 %)). Closest hits using the **cmdA** sequence had highest similarity to *Volutella consors* (strain CBS 122767, GenBank KM231333.1; Identities = 495/621 (80 %), 26 gaps (4 %)), *Volutella ciliata* (strain CBS 483.61, GenBank KM231336.1; Identities = 356/436 (82 %), 15 gaps (3 %)) and *Volutella rosea* (strain CBS 128258, GenBank KM231335.1; Identities = 358/439 (82 %), 19 gaps (4 %)). Closest hits using the **rpb2** sequence had highest similarity to *Volutella citrinella* (strain DAOM 226720, GenBank HQ897770.1; Identities = 724/829 (87 %), two gaps (0 %)), *Volutella consors* (strain CBS 328.77, GenBank HQ897716.1; Identities = 722/828 (87 %), no gaps) and *Volutella ciliata* (strain CBS 426.52, GenBank MH936691.1; Identities = 706/837 (84 %), six gaps (0 %)). Closest hits using the **tef1** sequence had highest similarity to *Volutella consors* (strain CBS 122767, GenBank KM231898.1; Identities = 383/476 (80 %), 28 gaps (5 %)), *Thelonectria jungneri* (strain G.J.S.10-127, GenBank KJ022367.1; Identities = 236/270 (87 %), 13 gaps (4 %)) and *Lanatonectria flavolanata* (strain 5622, GenBank HM054073.1; Identities = 233/267 (87 %), 14 gaps (5 %)). Closest hits using the **tub2** sequence had highest similarity to *Volutella consors* (strain CBS 122767, GenBank KM232025.1; Identities = 547/650 (84 %), 28 gaps (4 %)), *Volutella rosea* (strain CBS 128258, GenBank KM232027.1; Identities = 415/486 (85 %), 23 gaps (4 %)) and *Gliocladiopsis indonesiensis* (strain CBS 116090, GenBank JQ666132.1; Identities = 409/481 (85 %), 28 gaps (5 %)).

Colour illustrations. Walvis Bay, Namibia. Conidiophores on PNA and SNA; conidiogenous cells giving rise to conidia; 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