

Paramyrothecium salvadorae



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***Paramyrothecium salvadorae* Crous, sp. nov.**

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

Classification — *Stachybotryaceae*, *Hypocreales*, *Sordariomycetes*.

Conidiomata sporodochial with green mucoid conidial mass, stromatic, superficial, cupulate, separate or gregarious, 30–120 µm diam. *Setae* arising from stroma, hyaline, smooth, 5–10-septate, straight to flexuous, 100–200 × 2.5–3 µm; apices subacutely rounded. *Conidiophores* penicillate with branched conidiogenous apparatus; stipes hyaline, smooth, subcylindrical, septate, 20–40 × 3–4 µm; primary branches aseptate, smooth, 10–20 × 2.5–3 µm; secondary branches aseptate, smooth, 5–10 × 2.5–3 µm, terminating in a whorl of 3–6 *conidiogenous cells*, phialidic, subcylindrical, hyaline, 8–15 × 2–2.5 µm, smooth, straight to curved with conspicuous colarettes and periclinal thickening. *Conidia* aseptate, hyaline to olivaceous, subcylindrical, (8–)10–12(–13) × 2–2.5 µm, with obtuse ends.

Culture characteristics — Colonies flat, spreading, surface with concentric zone lines, with moderate aerial mycelium and smooth, even margin, reaching 38 mm diam after 2 wk at 25 °C. On MEA, PDA and OA surface dirty white, reverse buff.

Typus. NAMIBIA, Walvis Bay, on twigs of *Salvadora persica* (*Salvadoraceae*), 20 Nov. 2019, P.W. Crous, HPC 3120 (holotype CBS H-24538, culture ex-type CPC 39071 = CBS 147074, ITS, LSU, *rpb2*, *tef1* (second part) and *tub2* sequences GenBank MZ064453.1, MZ064510.1, MZ078210.1, MZ078254.1 and MZ078277.1, MycoBank MB 839539).

Notes — *Paramyrothecium salvadorae* is related to *P. roridum* (conidia subcylindrical to ellipsoidal, (5–)6.5–7.5(–8) × 2 µm; Lombard et al. 2016), from which it is morphologically and phylogenetically distinct.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Paramyrothecium roridum* (as *Myrothecium roridum*; strain MA-20, GenBank JF724152.1; Identities = 579/584 (99 %), three gaps (0 %)), *Paramyrothecium terrestris* (strain CBS 564.86, GenBank NR_145078.1; Identities = 574/581 (99 %), one gap (0 %)) and *Myrothecium lachastrae* (strain IMI 273160, GenBank AY254159.1; Identities = 570/578

(99 %), two gaps (0 %)). Closest hits using the **LSU** sequence are *Paramyrothecium nigrum* (strain CBS 116537, GenBank NG_069341.1; Identities = 811/812 (99 %), no gaps), *Paramyrothecium foliicola* (strain CBS 419.93, GenBank KU846323.1; Identities = 811/812 (99 %), no gaps) and *Paramyrothecium viridisporum* (strain CBS 873.85, GenBank NG_069344.1; Identities = 810/812 (99 %), no gaps). Closest hits using the **rpb2** sequence had highest similarity to *Paramyrothecium* sp. (strain MU6, GenBank MN397961.1; Identities = 682/714 (96 %), no gaps), *Paramyrothecium roridum* (strain CBS 372.50, GenBank KU846362.1; Identities = 671/714 (94 %), no gaps) and *Paramyrothecium foliicola* (strain CBS 419.93, GenBank KU846355.1; Identities = 668/714 (94 %), no gaps). Closest hits using the **tef1** sequence had highest similarity to *Paramyrothecium roridum* (as *Myrothecium roridum*; strain 781, GenBank JF724132.1; Identities = 430/435 (99 %), no gaps), *Striaticonidium cinctum* (as *Myrothecium cinctum*; strain ATCC 22270, GenBank AY489605.1; Identities = 440/451 (98 %), no gaps) and *Myrothecium inundatum* (strain IMI 158855, GenBank AY489626.1; Identities = 434/454 (96 %), no gaps). Closest hits using the **tub2** sequence had highest similarity to *Paramyrothecium roridum* (strain AGR1reis1, GenBank MH824740.1; Identities = 287/293 (98 %), no gaps), *Paramyrothecium foliicola* (strain CBS 113121, GenBank KU846411.1; Identities = 278/293 (95 %), no gaps) and *Paramyrothecium terrestris* (strain CBS 564.86, GenBank KU846420.1; Identities = 277/294 (94 %), one gap (0 %)).

Also see the phylogenetic tree provided with the supplementary material FP1194.

Supplementary material

FP1221 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 *Paramyrothecium* and related genera multigene (ITS / *tub2* / *cmdA* / *rpb2*) nucleotide alignment derived from the datasets of Lombard et al. (2016). GenBank accession numbers for the sequences used can also be obtained from Lombard et al. (2016). Bootstrap support values (> 69 % shown; only values > 94 % are significant) from 5 000 ultrafast bootstrap replicates are shown at the nodes. Culture collection numbers are indicated for all species and numbers in **bold** represent those cultures with a type status. The tree was rooted to *Fusarium sambucinum* (culture CBS 146.95) and the species described here is highlighted with a coloured block and **bold** face. Alignment statistics: 47 strains including the outgroup; 2415 characters including alignment gaps analysed: 900 distinct patterns, 651 parsimony-informative, 252 singleton sites, 1512 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).

Colour illustrations. Namib Desert, with mycologists in the distance. Sporodochial conidiomata on OA; conidiogenous cells giving rise to conidia; conidia. Scale bars = 10 µm.

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