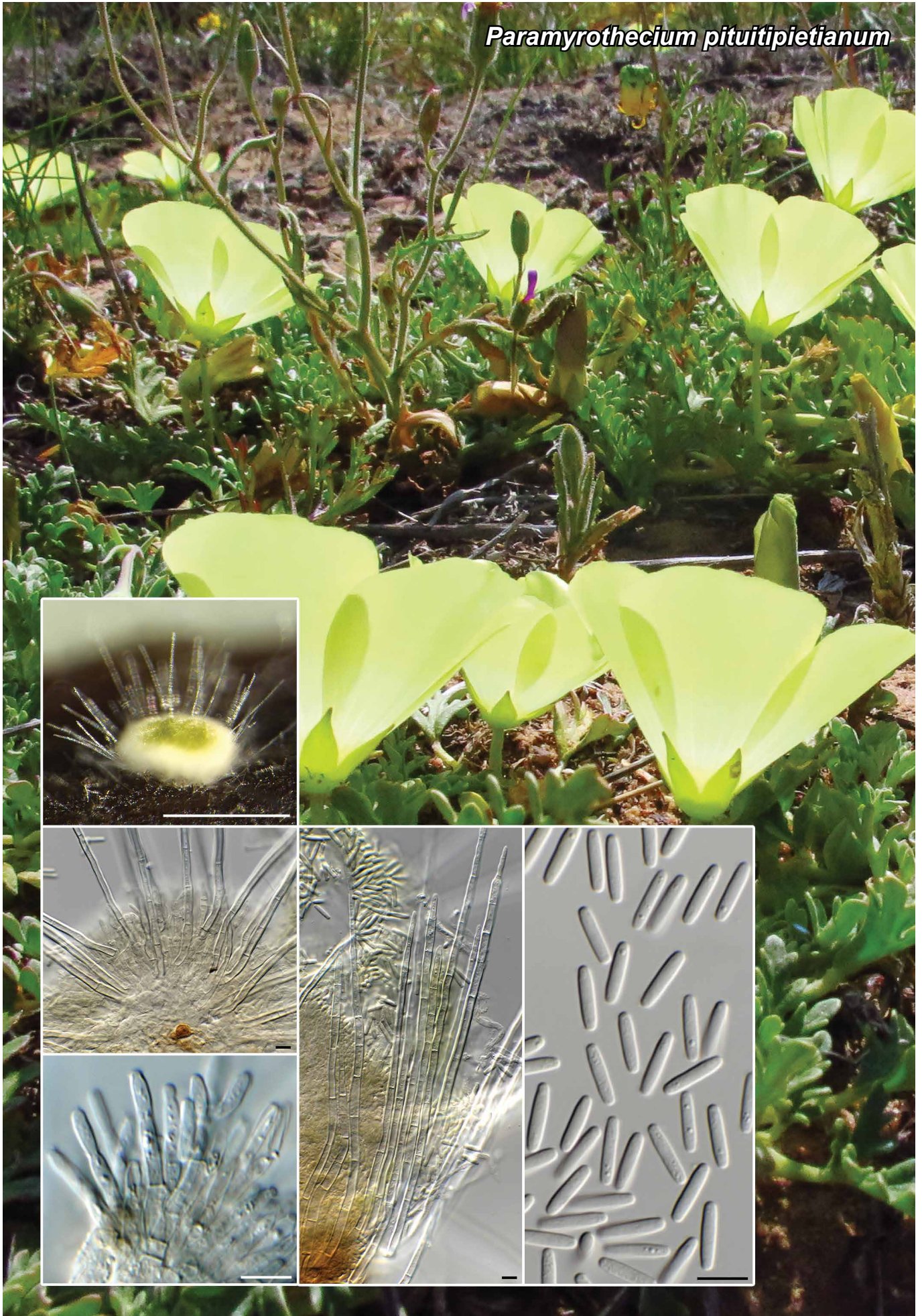


*Paramyrothecium pituitipietianum*





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***Paramyrothecium pituitipietianum* Crous, sp. nov.**

**Etymology.** Composed of pituita (= mucus, snot) and the name Piet (referring to 'Pietsnot' = Snotty Pete, the common South African name of *Grieliu* *humifusum*).

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

**Conidiomata** sporodochial, stromatic, superficial, cupulate, separate to gregarious, oval, 200–350 µm diam with a white, setose fringe surrounding the dark green mucoid conidial mass. **Stroma** well-developed of hyaline *textura angularis*. **Setae** thick-walled, 7–10-septate, straight to flexuous, hyaline, 100–300 × 4–5 µm, tapering to obtuse apex. **Conidiophores** penicillately branched, hyaline, smooth, 2–4-septate, 20–35 × 3–4 µm. **Conidiogenous cells** phialidic, hyaline, smooth, subcylindrical, tapering at tip, 10–15 × 2–2.5 µm. **Conidia** aseptate, subcylindrical, straight, pale green, smooth, guttulate, ends obtuse, (7–)9–10(–12) × (2–)2.5 µm.

**Culture characteristics** — Colonies flat, spreading, with moderate aerial mycelium and smooth, even margin, reaching 35 mm diam after 2 wk at 25 °C. On MEA surface folded, buff, reverse luteous; on PDA surface and reverse buff; on OA surface cinnamon.

**Typus.** SOUTH AFRICA, Western Cape Province, Nieuwoudtville, on stems of *Grieliu* *humifusum* (*Neuradaceae*), 2018, P.W. Crous, HPC 3057 (holotype CBS H-24435, culture ex-type CPC 38688 = CBS 146817, ITS, LSU, *cmdA*, *tef1* and *tub2* sequences GenBank MW175358.1, MW175398.1, MW173100.1, MW173124.1 and MW173139.1, MycoBank MB837849).

**Notes** — Lombard et al. (2016) distinguished *Paramyrothecium* from *Myrothecium* s.str. and the other myrothecium-like genera by their septate, thin-walled setae surrounding the sporodochia. *Paramyrothecium pituitipietianum* is closely related to *P. parvum* (conidia 4–5 × 1–2 µm) and *P. telicola* (conidia (7–)7.5–8.5(–9) × 1–3 µm; Lombard et al. 2016).

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Paramyrothecium parvum* (strain CBS 257.35, GenBank NR\_145076.1; Identities = 577/589 (98 %), one gap (0 %)), *Paramyrothecium roridum* (as *Myrothecium roridum*; strain BBA 62764, GenBank AJ301993.1; Identities = 589/602 (98 %), one gap (0 %)), and *Paramyrothecium acadiense* (strain CBS 123.96, GenBank KU846288.1; Identities = 576/589 (98 %), one gap (0 %)). Closest hits using the **LSU** sequence are *Paramyrothecium nigrum* (strain CBS 116537, GenBank NG\_069341.1; Identities = 826/827 (99 %), no gaps), *Paramyrothecium foliicola* (strain CBS 419.93, GenBank KU846323.1; Identities = 826/827 (99 %), no gaps), and *Paramyrothecium roridum* (strain CBS 372.50, GenBank MH868182.1; Identities = 845/847 (99 %), no gaps). Closest hits using the **cmdA** sequence had highest similarity to *Paramyrothecium tellicola* (strain CBS 478.91, GenBank KU846272.1; Identities = 488/600 (81 %), 17 gaps (2 %)), *Paramyrothecium sinense* (strain ZSY8, GenBank MH885437.1; Identities = 470/578 (81 %), 19 gaps (3 %)), and *Xepicula crassiseta* (strain CBS 392.71, GenBank KU847222.1; Identities = 494/608 (81 %), 30 gaps (4 %)). Distant hits using the **tef1** sequence had highest similarity to *Neomyrothecium humicola* (strain CBS 310.96, GenBank KU846527.1; Identities = 207/229 (90 %), six gaps (2 %)), *Gregatothecium humicola* (strain CBS 205.96, GenBank KU846402.1; Identities = 212/237 (89 %), ten gaps (4 %)), and *Brevistachys ossiformis* (strain CPC 16031, GenBank KU846092.1; Identities = 209/234 (89 %), nine gaps (3 %)). Closest hits using the **tub2** sequence had highest similarity to *Paramyrothecium* sp. 2 MP-2020 (strain 18ALOM016, GenBank MT671910.1; Identities = 324/330 (98 %), no gaps), *Paramyrothecium terrestris* (strain CBS 564.86, GenBank KU846420.1; Identities = 310/343 (90 %), seven gaps (2 %)), and *Paramyrothecium acadiense* (strain CBS 123.96, GenBank KU846405.1; Identities = 308/342 (90 %), six gaps (1 %)).

**Colour illustrations.** Characteristic yellow flowers of *Grieliu* *humifusum*. Conidioma on PNA (scale bar = 350 µm); setae; conidiogenous cells; conidia (scale bars = 10 µm).