

Acrodontium burrowsianum



Fungal Planet 1200 – 13 July 2021

***Acrodontium burrowsianum* Crous, sp. nov.**

Etymology. Named for John and Sandy Burrows, two remarkable botanists who are instrumental in maintaining the Buffelskloof Research Centre, Mbombela, South Africa.

Classification — *Teratosphaeriaceae*, *Mycosphaerellales*, *Dothideomycetes*.

Mycelium consisting of hyaline, septate, branched, smooth, 1–1.5 µm diam hyphae. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* pale brown, smooth, thin-walled, subulate to slightly ampulliform, at times with basal septum, flexuous, proliferating sympodially and forming a rachis in upper region, (15–)20–30(–40) × 2–3 µm with multiple loci, slightly thickened, not darkened. *Conidia* hyaline, thin-walled, smooth, solitary, aseptate, ellipsoid, apex obtuse, 3–4 × 1.5–2 µm; hilum slightly thickened, not darkened.

Culture characteristics — Colonies erumpent, spreading, surface folded, with moderate aerial mycelium and smooth, lobate margin, reaching 30 mm diam after 2 wk at 25 °C. On MEA and PDA surface smoke grey, reverse isabelline; on OA surface smoke grey with diffuse hazel pigment.

Typus. SOUTH AFRICA, Mpumalanga, Mbombela, Buffelskloof Nature Reserve, on leaves of unidentified *Poaceae*, 23 Nov. 2018, P.W. Crous, HPC 3155 (holotype CBS H-24507, culture ex-type CPC 38912 = CBS 147002, ITS, LSU, *actA*, *gapdh*, *his3*, *rpb2* and *tef1* (first part) sequences GenBank MZ064425.1, MZ064482.1, MZ078149.1, MZ078179.1, MZ078181.1, MZ078199.1 and MZ078225.1, MycoBank MB 839513).

Notes — *Acrodontium* was introduced by De Hoog (1972), with type species *A. crateriforme* (CBS 144.33; conidia (3–)3.5–4.5(–5) × (1.5–)2–3(–4) µm. The genus was recently revised by Videira et al. (2016), who resolved its higher order phylogeny as belonging to *Teratosphaeriaceae*. *Acrodontium burrowsianum* is related to *A. crateriforme*, but has smaller conidia.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Acrodontium crateriforme* (strain CBS 144.33, GenBank NR_152320.1; Identities = 457/459 (99 %), no gaps), *Pseudocercospora fraxini* (strain LCM 896.01, GenBank MF495428.1; Identities = 547/549 (99 %), no gaps) and *Acrodontium neolitseeae* (strain CBS 137975, GenBank NR_168148.1; Identities = 543/548 (99 %), no gaps). Closest hits using the **LSU** sequence are *Acrodontium crateriforme* (strain CBS 144.33, GenBank NG_057108.1; Identities = 859/859 (100 %), no gaps), *Acrodontium neolitseeae* (strain CBS 137975, GenBank KJ869184.1; Identities = 843/843 (100 %), no gaps) and *Neophaeothecoidea proteae* (strain CBS 114129, GenBank MH874518.1; Identities = 850/880 (97 %), two gaps (0 %)). Closest hits using the **actA** sequence had highest similarity to *Acrodontium crateriforme* (strain CPC 25894, GenBank KX287559.1; Identities = 521/530 (98 %), no gaps), *Ramularia lethalis* (strain CPC 25910, GenBank KX287754.1; Identities = 453/500 (91 %), eight gaps (1 %)) and *Pantospora chromolaenae* (strain CBS 145563, GenBank MK876459.1; Identities = 467/523 (89 %), 11 gaps (2 %)). Closest hits using the **gapdh** sequence had highest similarity to *Acrodontium crateriforme* (strain CPC 25894, GenBank KX288124.1; Identities = 507/516 (98 %), no gaps), *Teratoramularia persicariae* (strain CPC 11408, GenBank KX288384.1; Identities = 281/314 (89 %), no gaps) and *Ramularia calcea* (strain CBS 101613, GenBank KP894547.1; Identities = 295/337 (88 %), four gaps (1 %)). Closest hits using the **his3** sequence had highest similarity to *Acrodontium crateriforme* (strain CPC 11519, GenBank KX288728.1; Identities = 316/323 (98 %), one gap (0 %)), *Ramularia major* (strain CPC 12542, GenBank KX288922.1; Identities = 303/330 (92 %), 11 gaps (3 %)) and *Ramularia cynarae* (strain CPC 25897, GenBank KX288847.1; Identities = 303/330 (92 %), 11 gaps (3 %)). Closest hits using the **rpb2** sequence had highest similarity to *Acrodontium crateriforme* (strain CBS 840.71, GenBank KX288402.1; Identities = 843/847 (99 %), no gaps), *Teratosphaeria sieberi* (strain CPC 32099, GenBank MH327872.1; Identities = 380/478 (79 %), eight gaps (1 %)) and *Teratosphaeria henryi* (strain CBS 145539, GenBank MK876492.1; Identities = 377/477 (79 %), six gaps (1 %)). Closest hits using the **tef1** sequence had highest similarity to *Acrodontium crateriforme* (strain CPC 11509, GenBank GU384425.1; Identities = 266/275 (97 %), no gaps).

Colour illustrations. Unidentified *Poaceae* at Buffelskloof Nature Reserve. Conidiogenous cells on SNA; conidia. Scale bars = 10 µm.

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