

Beltraniopsis neolitseae
& *Acrodontium neolitseae*



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***Beltraniopsis neolitseae* Crous & Summerell, sp. nov.**

Etymology. Named after the host genus from which it was collected, *Neolitsea*.

Setae erect, dark brown, straight to somewhat flexuous, tapering to obtuse apex, 8–20-septate, 300–500 × 6–8 µm, with basal cell arising from superficial hyphae. *Conidiophores* arranged around base of setae, or occurring laterally on setae, pale brown to brown, smooth, flexuous when arising from hyphae, up to 80 µm tall, 3–5 µm diam, 3–5-septate. *Separating cells* ellipsoid to clavate, pale brown, smooth, 7–10 × 4–6 µm, with 1–3 terminal subdenticulate loci. On conidiophores separating cells usually originating from 1–2 supporting cells, medium to brown, 10–15 × 6–9 µm, with 1–4 terminal loci giving rise to separating cells. *Conidia* solitary, biconic, rostrate with short beak, aseptate, pale olivaceous-brown, smooth, with hyaline transverse band, usually only visible in older conidia, (27–)30–33(–35) × (6–)7–8(–9) µm.

Culture characteristics — Colonies covering dish within 2 wk at 22 °C, spreading, with sparse aerial mycelium and feathery margins. On PDA surface and reverse olivaceous-grey. On OA surface iron-grey. On MEA surface and reverse olivaceous-grey.

Typus. AUSTRALIA, New South Wales, Nightcap National Park, S28°38'41.3" E153°20'17.9", on *Neolitsea australiensis* (Lauraceae) leaves, 9 Mar. 2013, B.A. Summerell (holotype CBS H-21686, culture ex-type CPC 22168 = CBS 137974; ITS sequence GenBank KJ869126, LSU sequence GenBank KJ869183, MycoBank MB808901).

***Acrodontium neolitseae* Crous & Summerell, sp. nov.**

Etymology. Named after the host genus from which it was collected, *Neolitsea*.

Mycelium consisting of brown, septate, branched, smooth, 1.5–2 µm diam hyphae. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* pale brown, smooth, elongate ampulliform, slightly constricted at base, straight to flexuous, tapering towards subacutely rounded apex, proliferating sympodially, forming a rachis in upper two thirds of conidiogenous cell, 30–60 × 2–2.5 µm, loci inconspicuous warts, slightly thickened, 0.3 µm diam. *Conidia* solitary, pale brown, smooth, ellipsoid with obtuse apex, tapering in lower part to truncate hilum, 0.3–0.5 µm diam, slightly darkened, (2–)2.5–3(–3.5) × (1.5–)2(–2.5) µm.

Culture characteristics — Colonies reaching up to 15 mm diam after 2 wk at 22 °C, spreading, erumpent, folded, with moderate aerial mycelium, and even, lobate margins. On PDA surface pale olivaceous-grey in centre, olivaceous-grey in outer region, reverse olivaceous-grey. On OA and MEA pale olivaceous-grey in centre, olivaceous-grey in outer region and underneath.

Colour illustrations. Nightcap National Park, New South Wales, Australia; conidiophores and conidia of *Beltraniopsis neolitseae* in culture (left column); conidiophores and conidia of *Acrodontium neolitseae* (right column) in culture. Scale bars = 10 µm.

Notes — The genus *Beltraniopsis* is characterised by solitary, brown conidiophores with lobed foot cells that are fertile, with sympodial conidiogenesis, denticulate conidiogenous cells, separating cells, and brown, biconic conidia with an equatorial band of lighter pigment (Seifert et al. 2011). Using the key of Gusmão et al. (2000), *B. neolitsea* is most similar to *B. fabularis* (conidia 30–37 × 9 µm) but can be distinguished by having smaller conidia, separating cells and longer setae.

ITS. Based on a megablast search of NCBI GenBank nucleotide database, the closest hits using the ITS sequence are *Beltrania querna* (GenBank EF029240; Identities = 533/568 (94 %), Gaps = 12/568 (2 %)), *Menisporopsis theobromae* (GenBank GU905996; Identities = 451/484 (93 %), Gaps = 15/484 (3 %)) and *Beltraniella portoricensis* (GenBank GU905993; Identities = 448/482 (93 %), Gaps = 9/482 (1 %)).

LSU. Based on a megablast search of NCBI GenBank nucleotide database, the closest hits using the LSU sequence are *Subramaniomyces fusisaprophyticus* (GenBank EU040241; Identities = 763/780 (98 %), Gaps = 3/780 (0 %)), *Pseudomasaria carolinensis* (GenBank DQ810233; Identities = 761/779 (98 %), Gaps = 3/779 (0 %)) and *Parapleurotheciopsis inaequi-septata* (GenBank EU040235; Identities = 752/781 (96 %), Gaps = 4/781 (0 %)).

Typus. AUSTRALIA, New South Wales, Nightcap National Park, S28°38'41.3" E153°20'17.9", on *Neolitsea australiensis* (Lauraceae) leaves, 9 Mar. 2013, B.A. Summerell (holotype CBS H-21687, culture ex-type CPC 22172 = CBS 137975; ITS sequence GenBank KJ869127, LSU sequence GenBank KJ869184, MycoBank MB808902).

Notes — The genus *Acrodontium* was established by de Hoog (1972) and accommodates around 10 species being saprobic on wood, bark or leaves, or even being fungicolous (Seifert et al. 2011). Using the key of de Hoog (1972), *A. neolitsea* is most similar to *A. hydnicola*, except that conidiophores are not branched but reduced to solitary conidiogenous cells. *Acrodontium* represents yet another genus newly shown to belong to the *Mycosphaerellaceae*.

ITS. Based on a megablast search of NCBI GenBank nucleotide database, the closest hits using the ITS sequence are *Pseudocercospora fraxini* (GenBank GU214682; Identities = 547/550 (99 %), no gaps), *Acrodontium crateriforme* (GenBank FN666566; Identities = 481/484 (99 %), no gaps) and *Pseudotaeniolina globosa* (GenBank KC311489; Identities = 505/560 (90 %), Gaps = 15/560 (2 %)).

LSU. Based on a megablast search of NCBI GenBank nucleotide database, the closest hits using the LSU sequence are *Pseudocercospora fraxini* (GenBank GU214682; Identities = 843/843 (100 %), no gaps), *Phaeothecoidea melaleuca* (GenBank HQ599595; Identities = 814/842 (97 %), Gaps = 2/842 (0 %)) and *Phacellium paspali* (GenBank GU214669; Identities = 815/847 (96 %), Gaps = 6/847 (0 %)).