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***Beltrania pseudorhombica* Crous & Y. Zhang ter, sp. nov.**

Etymology. Named after this morphological similarity to *Beltrania rhombica*.

Setae erect, dark brown, thick-walled, indistinctly septate, straight to somewhat flexuous, tapering to an acute apex, up to 5-septate, 130–220 × 4–5 µm, with lobed basal cell, 10–12 µm diam. *Conidiophores* erect, unbranched, medium brown, smooth, 2–3-septate, 30–50 × 4–5 µm. *Conidiogenous cells* terminal, pale brown, smooth, polyblastic with several flat-tipped denticles, 1.5–2 µm. *Separating cells* pale brown, finely roughened, 7–12 × 5–6 µm, with several apical, flat-tipped denticles, 1 µm diam. *Conidia* solitary, biconic, pale brown, aseptate, with a distinct median transverse band of lighter pigment, (20–)22–25(–26) × (7–)8(–9) µm, apical appendage 7–11 × 1 µm, tapering to an acutely rounded tip.

Culture characteristics — Colonies reaching 70 mm diam after 2 wk at 22 °C. On MEA spreading, with fluffy aerial mycelium and lobate margins; surface and reverse dirty white. On OA surface iron-grey, outer region dirty white. On PDA surface and reverse dirty white.

Typus. CHINA, Beijing, Fragrant Hill, N39°59'18.4" E116°11'25", on needles of *Pinus tabulaeformis* (Pinaceae), 1 Sept. 2013, P.W. Crous & Y. Zhang (holotype CBS H-21717, culture ex-type CPC 23656 = CBS 138003; ITS sequence GenBank KJ869158, LSU sequence GenBank KJ869215, MycoBank MB808942).

Notes — The genus *Beltrania* is characterised by having pigmented, unbranched setae, and basal conidiophores that give rise to conidiogenous cells that proliferate sympodially by means of short protruding denticles, giving rise to separating cells and conidia that are brown, biconic, with an equatorial band of lighter pigment, and a single apical appendage (Seifert et al. 2011). *Beltrania pseudorhombica* differs from *B. rhombica* in having longer setae and shorter, narrower conidia (setae 200–300 µm long, conidia 15–30 × 7–14 µm; Ellis 1971).

ITS. Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the ITS sequence are *Beltrania rhombica* (GenBank GU797390; Identities = 502/508 (99 %), Gaps = 3/508 (0 %)), *Beltrania querna* (GenBank GU905994; Identities = 487/494 (99 %), Gaps = 1/494 (0 %)) and *Menisporopsis theobromae* (GenBank GU905996; Identities = 471/488 (97 %), Gaps = 4/488 (0 %)).

LSU. Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the LSU sequence are *Parapleurotheciopsis inaequiseptata* (GenBank EU040235; Identities = 794/814 (98 %), Gaps = 2/814 (0 %)), *Pseudomasaria carolinensis* (GenBank DQ810233; Identities = 792/812 (98 %), Gaps = 1/812 (0 %)) and *Subramaniomyces fusisaprophyticus* (GenBank EU040241; Identities = 791/813 (97 %), Gaps = 1/813 (0 %)).

***Chaetopsina beijingensis* Crous & Y. Zhang ter, sp. nov.**

Etymology. Named after the location where it was collected in China, Beijing.

Conidiophores erect, setiform, tapering towards acutely rounded apex, mostly flexuous, yellow-brown, turning red-brown in 3 % KOH, fertile in mid region, unbranched, verruculose, 200–350 × 8–13 µm, 12–16-septate, thick-walled (2 µm diam), base bulbous, up to 15 µm diam; fertile region consisting of irregularly branched, dense aggregated conidiogenous cells. *Conidiogenous cells* ampulliform to lageniform, hyaline, smooth, mono- to polyphialidic, 6–12(–20) × 3.5–5 µm. *Conidia* hyaline, smooth, guttulate, subcylindrical, aseptate, apex and base bluntly rounded, base rarely with flattened hilum, (11–)12–13(–14) × 2(–2.5) µm.

Culture characteristics — Colonies reaching 15 mm diam after 2 wk at 22 °C. On MEA spreading with sparse aerial mycelium; surface folded, margins smooth, even, umber. On OA salmon. On PDA umber in centre, dirty white in outer region.

Typus. CHINA, Beijing, Fragrant Hill, N39°59'18.4" E116°11'25", on needles of *Pinus tabulaeformis* (Pinaceae), 1 Sept. 2013, P.W. Crous & Y. Zhang (holotype CBS H-21718, culture ex-type CPC 23629 = CBS 138004; ITS sequence GenBank KJ869159, LSU sequence GenBank KJ869216, MycoBank MB808943).

Colour illustrations. *Pinus tabulaeformis* in China; setae, conidiophores and conidia of *Beltrania pseudorhombica* in culture (left column); conidiophores, setae and conidia of *Chaetopsina beijingensis* in culture (right column). Scale bars = 10 µm.

Notes — The genus *Chaetopsina* has nectria-like sexual morphs that are accommodated in *Chaetopsinectria* (Luo & Zhuang 2010). Several species have been reported from *Pinus* needles, the most common being *C. fulva* (conidia cylindrical, 8–12 × 1.5 µm; Kirk & Sutton 1985), while Crous et al. (2013b) also introduced *C. pini* (conidia (13–)15–16(–18) × 2(–2.5) µm) and *C. pinicola* (conidia (11–)13–15(–17) × 2(–2.5) µm) from Thailand. *Chaetopsina beijingensis* is similar to the two species described from Thailand, though it is distinguishable by having smaller conidia.

ITS. Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the ITS sequence are *Chaetopsina fulva* (GenBank GU075861; Identities = 499/510 (98 %), no gaps), *Chaetopsina pinicola* (GenBank KF777145; Identities = 573/597 (96 %), Gaps = 8/597 (1 %)) and *Cosmospora chaetopsinae* (GenBank GU075858; Identities = 470/510 (92 %), Gaps = 16/510 (3 %)).

LSU. Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the ITS sequence are *Chaetopsina fulva* (GenBank GU075867; Identities = 786/786 (100 %), no gaps), *Chaetopsina pinicola* (GenBank KF777201; Identities = 775/786 (99 %), no gaps) and *Chaetopsina pini* (GenBank KF777200; Identities = 772/786 (98 %), no gaps).