

Scolecobasidium blechni



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Scolecobasidium blechni Crous, *sp. nov.*

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

Classification — *Sympoventuriaceae*, *Venturiales*, *Dothideomycetes*.

Mycelium consisting of medium brown, smooth, branched, septate, 1.5–2 µm diam hyphae, giving rise to hyphal coils. *Conidiophores* erect, solitary or at times two arising from the same basal cell, 2–3-septate, unbranched, straight to irregularly curved, brown, smooth, subcylindrical, 18–40 × 2.5–3 µm. *Conidiogenous cells* terminal, medium brown, smooth, subcylindrical, 8–22 × 2.5–3 µm with 1–4 terminal denticles, 1–1.5 × 1 µm. *Conidia* solitary, medianly 1-septate (or up to 3-septate), fusoid-ellipsoid to subcylindrical, curved to straight, apex obtuse, base with basal marginal frill, 0.5 µm long, medium brown, verruculose, (9–)11–12(–14) × (3–)3.5–4 µm.

Culture characteristics — Colonies flat, spreading, with moderate aerial mycelium and smooth, lobate margin, reaching 20 mm diam after 2 wk at 25 °C. On MEA, PDA and OA surface and reverse isabelline.

Typus. SOUTH AFRICA, Western Cape Province, Knysna, Knysna area, on leaves of *Blechnum capense* (*Blechnaceae*), 23 Nov. 2018, F. Roets, HPC 2704 (holotype CBS H-24181, culture ex-type CPC 37047 = CBS 146055, ITS, LSU, *tef1* and *tub2* sequences GenBank MN562134.1, MN567641.1, MN556826.1 and MN556843.1, MycoBank MB832892).

Notes — *Scolecobasidium* represents an older name for the genus commonly referred to as *Ochroconis* (Seifert et al. 2011). *Scolecobasidium blechni* is phylogenetically related to *Ochroconis cordanae* (conidia 1-septate, obovoidal to broadly fusiform, ((5–)7–9(–10) × (2.5–)3–3.5 µm; Samerpitak et al. 2014) and *O. macrozamia* ((5–)8–10(–12) × (3–)3.5(–4) µm; Crous et al. 2014), but is distinct based on its slightly longer conidia and DNA phylogeny.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Ochroconis cordanae* (strain CBS 101179, GenBank KF156020.1; Identities = 548/622 (88 %), 42 gaps (6 %)), *Ochroconis macrozamia* (strain CBS 102491, GenBank KF156021.1; Identities = 569/653 (87 %), 48 gaps (7 %)), and *Ochroconis musae* (strain CBS 145061, GenBank MK442605.1; Identities = 353/404 (87 %), 16 gaps (3 %)). Closest hits using the **LSU** sequence are *Ochroconis macrozamia* (strain CBS 102491, GenBank KF156152.1; Identities = 773/789 (98 %), 10 gaps (1 %)), *Ochroconis constricta* (strain CBS 269.61, GenBank MH869616.1; Identities = 828/869 (95 %), 13 gaps (1 %)), and *Ochroconis robusta* (strain NH673, GenBank LC469382.1; Identities = 820/860 (95 %), 11 gaps (1 %)). Closest hits using the **tef1** sequence had highest similarity to *Ochroconis macrozamia* (strain CBS 102491, GenBank KF155983.1; Identities = 370/419 (88 %), 20 gaps (4 %)), *Scolecobasidium variabile* (strain NBRC 32268, GenBank DQ307356.1; Identities = 229/257 (89 %), 6 gaps (2 %)), and *Ochroconis humicola* (strain NBRC 32054, GenBank AB564640.1; Identities = 380/473 (80 %), 4 gaps (9 %)). Closest hits using the **tub2** sequence had highest similarity to *Ochroconis macrozamia* (strain CBS 102491, GenBank KF156191.1; Identities = 405/438 (92 %), 1 gap (0 %)), *Acremonium exuviarum* (strain UAMH 9995, GenBank AY882947.1; Identities = 228/264 (86 %), 5 gaps (1 %)), and *Setophoma pseudosacchari* (strain CBS 145373, GenBank MK540176.1; Identities = 226/265 (85 %), 5 gaps (1 %)).

Colour illustrations. Knysna forest with *Blechnum capense* trees. Conidiophores with conidiogenous cells and conidia. Scale bars = 10 µm.

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