

Ochroconis podocarpi



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Ochroconis podocarp Crous, sp. nov.

Etymology. Name refers to *Podocarpus*, the host genus from which this fungus was collected.

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

Mycelium consisting of smooth, pale brown to medium brown, septate, branched, 1.5–2 µm diam hyphae, giving rise to hyphal strands and hyphal coils. *Conidiophores* erect, 1-septate, unbranched, medium brown, smooth, subcylindrical, 5–16 × 2 µm. *Conidiogenous cells* terminal, medium brown, smooth, subcylindrical, 5–12 × 2 µm, with 1–4 terminal cylindrical denticles, 1–1.5 × 1 µm. *Conidia* solitary, medianly 1-septate, fusoid-ellipsoid to subcylindrical, apex obtuse, base with truncate scar, 0.5 µm diam, medium brown, verruculose, (6–)7–9(–10) × 2(–2.5) µm.

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

Typus. AUSTRALIA, New South Wales, Australian Botanic Garden, Mount Annan, on leaves of *Podocarpus grayae* (*Podocarpaceae*), 25 Nov. 2016, P.W. Crous (holotype CBS H-23267, culture ex-type CPC 32829 = CBS 143174, ITS, LSU and *tub2* sequences GenBank MG386032, MG386085 and MG386162, MycoBank MB823373).

Notes — The genus *Ochroconis* is characterised by olivaceous to brown colonies, pigmented conidiophores, and sympodial conidiogenesis with denticles that give rise to septate, pigmented, verruculose conidia. *Ochroconis podocarp* is phylogenetically closely related to, but distinct from *O. humicola* (CBS 116655 ex-type from peat soil, Canada), which is a species characterised by rapid growth, and conidiophores up to 300 µm in length (Giraldo et al. 2014).

Based on a megablast search using the ITS sequence, the closest matches in NCBI's GenBank nucleotide database were *Ochroconis bacilliformis* (GenBank KP798632; Identities 360/414 (87 %), 23 gaps (5 %)), *Ochroconis robusta* (GenBank KP798633; Identities 363/418 (87 %), 30 gaps (7 %)) and *Ochroconis constricta* (GenBank KX610329; Identities 335/383 (87 %), 13 gaps (3 %)). The highest similarities using the LSU sequence were *Ochroconis humicola* (GenBank KF156124; Identities 775/799 (97 %), 7 gaps (0 %)), *Ochroconis musae* (GenBank KT272088; Identities 816/852 (96 %), 4 gaps (0 %)) and *Ochroconis mirabilis* (GenBank KF282661; Identities 812/849 (96 %), 5 gaps (0 %)). The highest similarities using the *tub2* sequence were *Ochroconis longiphorum* (GenBank KF156182; Identities 374/461 (81 %), 8 gaps (1 %)), *Ochroconis macrozamia* (GenBank KF156191; Identities 375/467 (80 %), 19 gaps (4 %)) and *Ochroconis gamsii* (GenBank HQ877664; Identities 371/463 (80 %), 19 gaps (4 %)).

Colour illustrations. *Podocarpus grayae*; conidiophores and conidia. Scale bars = 10 µm.

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