Ochroconis macrozamiae
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**Ochroconis macrozamiae** Crous & R.G. Shivas, *sp. nov.*

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

*Mycelium* consisting of septate, branched, red-brown, smooth, 1.5–2 μm diam hyphae. *Conidiophores* erect, thick-walled, red-brown, straight to geniculose-sinuous, subcylindrical, 1–2-septate, 20–30 × 2.5–3 μm, solitary, tapering towards bluntly rounded conidiogenous cell, 10–12 × 2.5–3 μm, forming a rachis with minute denticles, 0.5 μm diam. *Conidia* red-brown, verruculose, constricted at median septum, broadly fusiform, mostly straight, with rounded apex and truncate, darkened base, 1 μm diam, (5–)8–10(–12) × (3–)3.5(–4) μm.

Culture characteristics — Colonies reaching 8 mm diam after 2 wk at 22 °C, erumpent, spreading, with moderate aerial mycelium and smooth, catenate margins. On PDA surface and reverse isabelline. On OA surface isabelline to sepiol, On MEA surface isabelline with sepiol margins, reverse dark brick.


Notes — Although commonly isolated from litter, species of *Ochroconis* are frequently associated with disease in cold-blooded animals. The genus *Ochroconis* was recently revised by Samerpitak et al. (2014) and shown to belong to the *Sympoventuriaceae.* Of the species presently known in the genus, *O. macrozamiae* is phylogenetically related to *O. gamsii* (conidia 6–9 × 2.4–2.8 μm; de Hoog 1985), but can be distinguished based on its larger conidia.

*ITS.* Based on a megablast search of NCBI’s GenBank nucleotide database, the closest hits using the ITS sequence are *Ochroconis gamsii* (GenBank HQ667520; Identities = 535/560 (96 %), Gaps = 15/560 (2 %)), *Ochroconis constricta* (GenBank AB161063; Identities = 432/446 (97 %), Gaps = 4/446 (1 %)) and *Ochroconis tshawytschae* (GenBank AB161066; Identities = 438/471 (93 %), Gaps = 10/471 (2 %)).

*LSU.* Based on a megablast search of NCBI’s GenBank nucleotide database, the closest hits using the LSU sequence are *Ochroconis gamsii* (GenBank AB161064; Identities = 592/611 (97 %), Gaps = 2/611 (0 %)), *Ochroconis humicola* (GenBank AB564618; Identities = 854/896 (95 %), Gaps = 6/896 (0 %)) and *Ochroconis tshawytschae* (GenBank KF282665; Identities = 816/859 (95 %), Gaps = 8/859 (0 %)).

*Colour illustrations.* Slaughter Falls, Brisbane, Australia; conidiophores and conidia in culture. Scale bars = 10 μm.