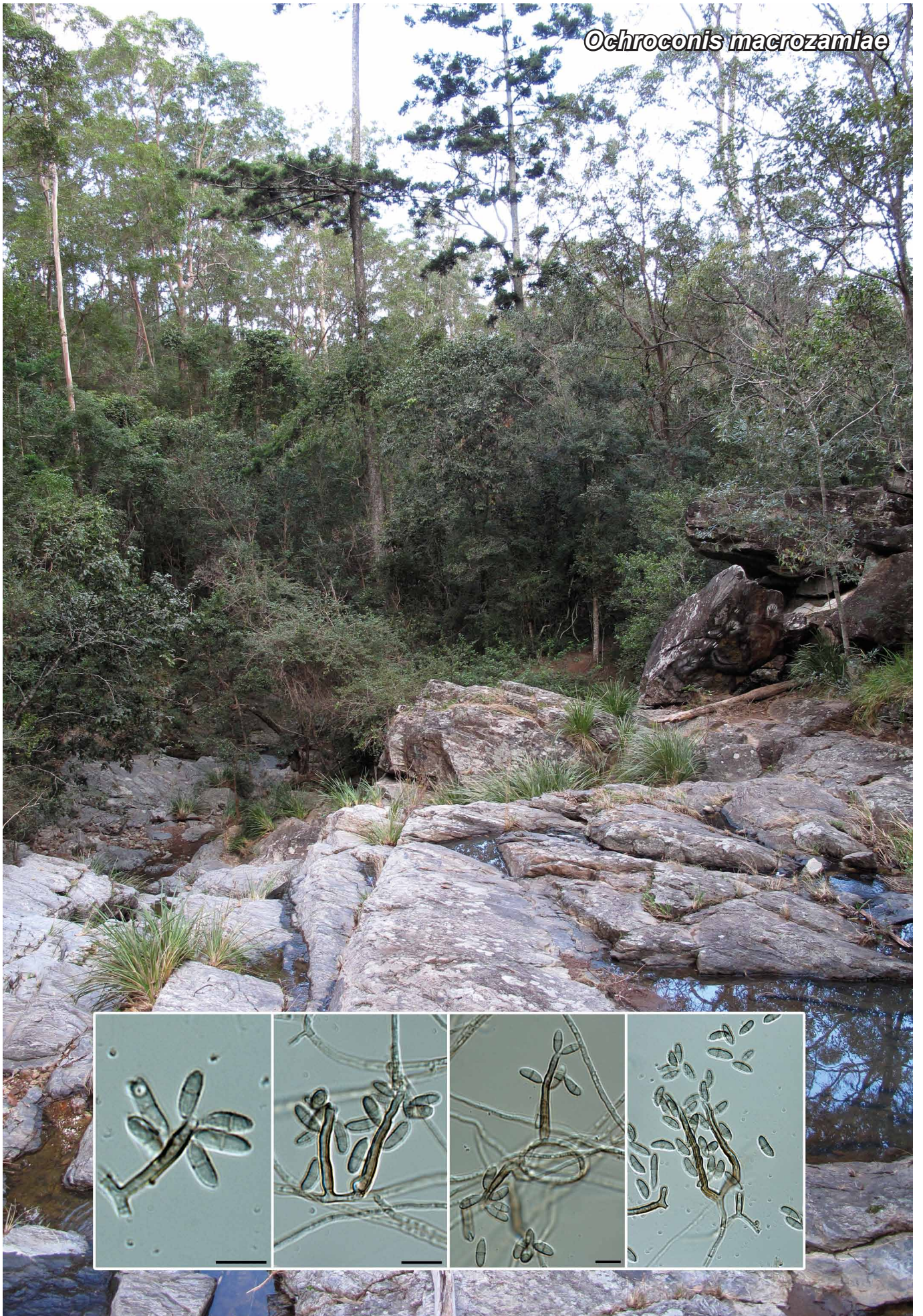


Ochroconis macrozamia



Fungal Planet 226 – 10 June 2014

Ochroconis macrozamia 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 geniculous-sinuuous, 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 sepia. On MEA surface isabelline with sepia margins, reverse dark brick.

Typus. AUSTRALIA, Queensland, Brisbane, Slaughter Falls, on *Macrozamia* (*Zamiaceae*) leaf litter, 16 July 2009, *P.W. Crous & R.G. Shivas* (holotype CBS H-21682, culture ex-type CPC 17262 = CBS 137971; ITS sequence GenBank KJ869123, LSU sequence GenBank KJ869180, MycoBank MB808897).

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 *Sym-poventuriaceae*. Of the species presently known in the genus, *O. macrozamia* 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.

Pedro W. Crous & Johannes Z. Groenewald, CBS-KNAW Fungal Biodiversity Centre, P.O. Box 85167, 3508 AD Utrecht, The Netherlands;
e-mail: p.crous@cbs.knaw.nl & e.groenewald@cbs.knaw.nl
Roger G. Shivas, Plant Pathology Herbarium, Department of Agriculture, Forestry and Fisheries, Dutton Park 4102, Queensland, Australia;
e-mail: roger.shivas@daff.qld.gov.au