

Ochroconis musicola



Fungal Planet 783 – 13 July 2018

***Ochroconis musicola* Crous, sp. nov.**

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

Classification — *Sympoventuriaceae*, *Venturiales*, *Dothideo-mycetes*.

On OA. *Ascomata* occurring in clusters, globose, 50–100 µm diam, brown, surface smooth, lacking appendages; wall of 4–8 layers of brown *textura angularis*. *Asci* bitunicate, obovoid, 8-spored, with well-defined apical chamber, 2–3 µm diam, 25–40 × 15–18 µm. *Ascospores* fusoid-ellipsoid, guttulate, initially hyaline, but becoming pale brown with age, straight to slightly curved, initially medianly septate, prominently constricted at septum, later developing a septum in each of the two cells, widest just above median septum, encased in a mucoid sheath, up to 3.5 µm diam, (15–)19–22(–26) × (4–)5(–6) µm. Isolates only formed the sexual morph in culture.

Culture characteristics — Colonies erumpent, spreading, with moderate aerial mycelium on OA and PDA (abundant on MEA), and even, smooth margin, reaching 30 mm diam after 2 wk at 25 °C. On MEA and PDA surface isabelline, reverse brown vinaceous. On OA surface brown vinaceous.

Typus. MALAYSIA, on leaves of *Musa* sp. (*Musaceae*), 2010, P.W. Crous (holotype CBS H-23562, culture ex-type CPC 32927 = CBS 144441, ITS, LSU, *rpb2*, *tef1* and *tub2* sequences GenBank MH327824.1, MH327860.1, MH327876.1, MH327887.1 and MH327898.1, MycoBank MB825439).

Notes — The genus *Ochroconis* was recently revised by Samerpitak et al. (2013), who also linked the first sexual morph to the genus, namely *O. sexualis*. Morphologically, *O. musicola* is quite distinct from *O. sexualis*, as the latter species has ascomata with appendages, and smaller ascospores (8–10 × 2.5–3.5 µm) that lack a mucoid sheath. *Ochroconis musicola* is also phylogenetically distinct and related to *O. constricta*.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the ITS sequence had highest similarity to *Ochroconis constricta* (GenBank KX610329.1; Identities = 429/514 (83 %), 39 gaps (7 %)), *Scolecobasidium dendroides* (GenBank FJ914704.1; Identities = 425/512 (83 %), 36 gaps (7 %)) and *Ochroconis dracaenae* (GenBank NR_145404.1; Identities = 422/512 (82 %), 33 gaps (6 %)). Closest hits using the LSU sequence are *Ochroconis podocarp*i (GenBank MG386085.1; Identities = 786/835 (94 %), 6 gaps (0 %)), *Ochroconis macrozamia*e (GenBank KJ869180.1; Identities = 814/866 (94 %), 13 gaps (1 %)) and *Ochroconis musae* (GenBank KT272083.1; Identities = 817/872 (94 %), 8 gaps (0 %)). Closest hits using the *rpb2* sequence had highest similarity to *Ochroconis lascauxensis* (GenBank HE575203.1; Identities = 752/899 (84 %), no gaps), *Scolecobasidium terreum* (GenBank FR832487.1; Identities = 737/887 (83 %), 1 gap (0 %)) and *Mycosium cirrhosum* (GenBank KR349124.1; Identities = 732/908 (81 %), 2 gaps (0 %)). No significant hits were obtained when the *tef1* and *tub2* sequences were used in BLASTn and megablast searches.

Colour illustrations. Symptomatic leaves of *Musa* sp. in Malaysia; ascomata sporulating on OA (scale bars = 100 µm), asci and ascospores with sheaths (scale bars = 10 µm).