

*Stagonospora trichophoricola*



Fungal Planet 214 – 10 June 2014

***Stagonospora trichophorica* Crous & Quaedvlieg, sp. nov.**

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

*Conidiomata* erumpent, globose, up to 300 µm diam, dark brown, glabrous, with central ostiole, up to 15 µm diam, separate on PNA but in clusters on OA. *Conidiophores* reduced to conidiogenous cells, hyaline, smooth, ampulliform, proliferating percurrently, 5–10 × 3–5 µm. *Conidia* hyaline, smooth, guttulate, fusoid-ellipsoidal with obtuse ends, 1–3(–4)-septate, constricted at septa, (12–)18–22(–25) × 4(–5) µm.

*Culture characteristics* — On SNA forming clusters of globose, dark brown chlamydospores, thick-walled, verruculose, up to 30 µm diam after 2 wk at 22 °C. Colonies spreading, flat with moderate aerial mycelium. Surface smoke-grey on OA and MEA, reverse iron-grey.

*Typus.* NETHERLANDS, Rozendaal, on *Trichophorum cespitosum* (*Cyperaceae*), 2013, *W. Quaedvlieg* (holotype CBS H-21670, culture ex-type D652 = CBS 136764; ITS sequence GenBank KJ869110, LSU sequence GenBank KJ869168, RPB2 sequence GenBank KJ869232, MycoBank MB808885).

*Notes* — The genus *Saccharicola* (*Massarinaceae*) was established by Eriksson & Hawksworth (2003) to accommodate *Leptosphaeria bicolor* and *L. taiwanensis*, with a note that they have stagonospora-like asexual morphs. The present collection from *Trichophorum cespitosum* is a typical *Stagonospora*, and appears to be phylogenetically closely related to *Saccharicola*, which probably is the sexual morph of *Stagonospora* s.str. (*Massarinaceae*; Quaedvlieg et al. 2013). We have not managed to find species of *Stagonospora* spp. described from *Trichophorum*, and *S. trichophorica* is morphologically and phylogenetically distinct from the species treated by Quaedvlieg et al. (2013).

*ITS.* Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the ITS sequence are *Saccharicola bicolor* (GenBank AF455415; Identities = 481/485 (99 %), Gaps = 1/485 (0 %)), *Saccharicola taiwanensis* (GenBank AF439462; Identities = 456/471 (97 %), Gaps = 1/471 (0 %)) and *Stagonospora perfecta* (GenBank KF251258; Identities = 468/485 (96 %), Gaps = 2/485 (0 %)).

*LSU.* Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the LSU sequence are *Neottiosporina paspali* (GenBank EU754172; Identities = 833/838 (99 %), no gaps), *Stagonospora pseudovitensis* (GenBank KF251765; Identities = 829/835 (99 %), no gaps) and *Stagonospora* cf. *paludosa* (GenBank KF251757; Identities = 829/835 (99 %), no gaps).

*RPB2.* Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the RPB2 sequence are *Neottiosporina paspali* (GenBank GU371779; Identities = 205/219 (94 %), no gaps), *Stagonospora duoseptata* (GenBank KF252260; Identities = 225/243 (93 %), no gaps) and *Stagonospora pseudocaricis* (GenBank KF302395; Identities = 224/250 (90 %), no gaps).

*Colour illustrations.* Landscape in Rozendaal, The Netherlands; conidiomata and conidia in culture. Scale bars = 10 µm.