

Stagonospora lomandrae



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***Stagonospora lomandrae* Crous, sp. nov.**

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

Classification — *Massarinaceae*, *Pleosporales*, *Dothideomycetes*.

Conidiomata immersed, pycnidial, 200–300 µm diam, globose, brown, with central ostiole, 30–40 µm diam, substomatal; wall of 3–4 layers of brown *textura angularis*. *Conidiophores* reduced to conidiogenous cells lining the inner cavity, hyaline, smooth, ampulliform, phialidic with percurrent proliferation at apex, 8–12 × 4–6 µm. *Conidia* (18–)19–21(–22) × (5–)6 µm, solitary, hyaline, smooth, prominently guttulate, subcylindrical, straight, apex obtuse, base truncate, 2 µm diam, 2-septate, with a septum a third in from each end. *Microconidia* in same conidioma, hyaline, smooth, guttulate, ellipsoid, apex obtuse, base truncate. *Ascomata* similar to conidiomata in anatomy. *Pseudoparaphyses* intermingled among asci, hyaline, smooth, septate, branched, hyphae-like, 2–3 µm diam, constricted at septa. *Asci* 8-spored, bitunicate, fissitunicate, narrowly ellipsoid to slightly clavate, 60–80 × 15–17 µm. *Ascospores* triseriate, fusoid-ellipsoid, hyaline to pale brown with thin mucoid sheath, constricted at median septum, developing two additional septa in apical cell (which is swollen and wider than basal cell), and one septum in basal cell, (18–)20–25(–27) × (5–)7(–8) µm.

Culture characteristics — Colonies flat, spreading, with moderate to abundant aerial mycelium and smooth, lobate margins, covering dish after 2 wk at 25 °C. On MEA surface dirty white, reverse saffron. On PDA surface olivaceous grey, reverse luteous. On OA surface dirty white.

Typus. AUSTRALIA, New South Wales, Sussex Inlet, on leaves of *Lomandra longifolia* (*Asparagaceae*), 27 Nov. 2016, P.W. Crous (holotype CBS H-23307, culture ex-type CPC 32073 = CBS 143447, ITS, LSU, *rpb2* and *tef1* sequences GenBank MG386067, MG386120, MG386147 and MG386156, MycoBank MB823416).

Notes — *Stagonospora* was revised by Quaedvlieg et al. (2013). *Stagonospora lomandrae* is phylogenetically related to *S. pseudoperfecta* (ascospores 21–30.5 × 5–7 µm, 1-septate, with mucoid sheath, conidia aseptate, 21.5–26 × 4–5.5 µm; Tanaka et al. 2015) and *S. trichophorica* (conidia 1–3(–4)-septate, (12–)18–22(–25) × 4(–5) µm; Crous et al. 2014a), but is morphologically and phylogenetically distinct.

Based on a megablast search using the ITS sequence, the closest matches in NCBI's GenBank nucleotide database were *Stagonospora bicolor* (as *Saccharicola bicolor*; GenBank KP117300; Identities 485/497 (98 %), 4 gaps (0 %)), *S. trichophorica* (GenBank KJ869110; Identities 518/531 (98 %), 4 gaps (0 %)) and *S. pseudoperfecta* (GenBank AB809641; Identities 485/499 (97 %), 3 gaps (0 %)). The highest similarities using the LSU sequence *S. forlisesenensis* (GenBank KX655547; Identities 854/857 (99 %), no gaps), *S. pseudoperfecta* (GenBank AB807577; Identities 845/849 (99 %), no gaps) and *S. trichophorica* (GenBank KJ869168; Identities 836/840 (99 %), no gaps). The highest similarities using the *rpb2* sequence were distant hits with *Neottiosporina paspali* (GenBank GU371779; Identities 749/848 (88 %), 1 gap (0 %)), *Helminthosporium microsorum* (GenBank KY984390; Identities 718/848 (85 %), no gaps) and *H. quercinum* (GenBank KY984398; Identities 712/848 (84 %), no gaps). The highest similarities using the *tef1* sequence were distant hits with *H. oligosporum* (GenBank KY984451; Identities 226/269 (84 %), 12 gaps (4 %)), *H. tiliae* (GenBank KY984457; Identities 224/269 (83 %), 12 gaps (4 %)) and *H. quercinum* (GenBank KY984454; Identities 219/267 (82 %), 13 gaps (4 %)).

Colour illustrations. *Lomandra longifolia* at Sussex Inlet; ascomata sporulating on OA, asci and pseudoparaphyses, conidiogenous cells and conidia. Scale bars = 10 µm.

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