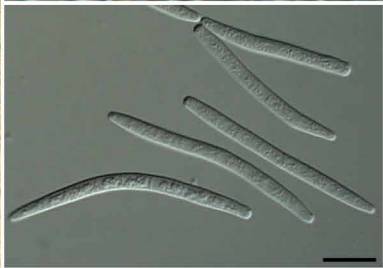
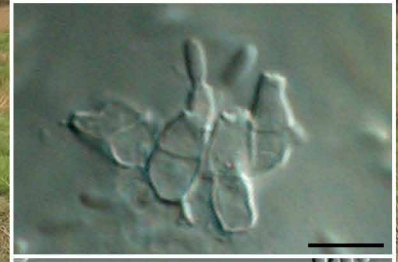


*Parastagonospora poagena*  
& *Pyrenochaetopsis poae*



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***Parastagonospora poagensis* Crous & Quaedvlieg, sp. nov.***Etymology.* Named after the host genus from which it was collected, *Poa*.

*Conidiomata* erumpent, globose, brown, up to 350 µm diam with central ostiole, exuding a pinkish conidial mass; wall of 2–3 layers of brown *textura angularis*. *Conidiophores* reduced to conidiogenous cells, hyaline, smooth, ampulliform to subcylindrical, proliferating inconspicuously percurrently near apex, 4–6 × 3–6 µm. *Conidia* solitary, subhyaline, smooth, granular, subcylindrical with taper in apical third to subobtuse apex, straight to gently curved, sigmoid, base truncate, 2.5–3 µm diam, 3–9-septate, (30–)40–55(–60) × (3–)3.5(–4) µm.

Culture characteristics — On OA flat, spreading with sparse aerial mycelium and even, smooth margins; surface dirty white with patches of pale olivaceous-grey, similar in reverse.

*Typus.* NETHERLANDS, Raalte, on *Poa* sp. (*Poaceae*), 2013, *W. Quaedvlieg* (holotype CBS H-21676, culture ex-type D800 = CBS 136776; ITS sequence GenBank KJ869116, LSU sequence GenBank KJ869174, MycoBank MB808891).

Notes — The genus *Parastagonospora* was recently introduced to accommodate several cereal pathogens that could not be placed in *Stagonospora* or *Phaeosphaeria* (Quaedvlieg

et al. 2013). Phylogenetically, *P. poagensis* is closely related to *P. avenae* (conidia (1–)3(–7)-septate, (17–)33(–46) × (2.5–)3.5(–4.5 µm); Bissett 1982), though it is distinct in its conidial morphology. Conidia of *P. poagensis* are much larger than that of *P. poae* (1-septate, 20–32 × 2–2.5 µm; Quaedvlieg et al. 2013).

**ITS.** Based on a megablast search of NCBI GenBank nucleotide database, the closest hits using the ITS sequence are *Phaeosphaeria avenaria* f. sp. *triticae* (GenBank EF452729; Identities = 553/561 (99 %), Gaps = 1/561 (0 %)), *Phaeosphaeria avenaria* (GenBank U77358; Identities = 552/560 (99 %), no gaps) and *Parastagonospora avenae* (GenBank KF251174; Identities = 536/544 (99 %), no gaps).

**LSU.** Based on a megablast search of NCBI GenBank nucleotide database, the closest hits using the LSU sequence are *Parastagonospora nodorum* (GenBank EU754175; Identities = 848/848 (100 %), no gaps), *Phaeosphaeria avenaria* f. sp. *triticae* (GenBank EF590322; Identities = 848/848 (100 %), no gaps) and *Phaeosphaeria nigrans* (GenBank KF251687; Identities = 828/828 (100 %), no gaps).

***Pyrenochaetopsis poae* Crous & Quaedvlieg, sp. nov.***Etymology.* Named after the host genus from which it was collected, *Poa*.

*Conidiomata* globose, erumpent, up to 250 µm diam with central ostiole, up to 35 µm diam; outer surface covered with brown, erect setate, smooth, septate, with apical taper towards obtuse ends, 1.5–3 µm diam; wall of 2–3 layers of brown *textura angularis*. *Conidiophores* reduced to conidiogenous cells, or with a single supporting cell, subcylindrical to ampulliform, hyaline, smooth, with periclinal thickening, 4–5 × 3–4 µm. *Conidia* solitary, hyaline, smooth, cylindrical with obtuse ends, eguttulate or with 1–2 small guttules, (3–)4–5(–7) × 1.5(–2) µm.

Culture characteristics — Colonies flat, spreading with sparse aerial mycelium and even, smooth margins. On OA surface olivaceous-grey. On MEA surface pale olivaceous-grey to olivaceous-grey, iron-grey in reverse.

*Typus.* NETHERLANDS, Raalte, on *Poa* sp. (*Poaceae*), 2013, *W. Quaedvlieg* (holotype CBS H-21677, culture ex-type CBS 136769 = D779; ITS sequence GenBank KJ869117, LSU sequence GenBank KJ869175, ACT sequence GenBank KJ869226, TUB sequence GenBank KJ869243, MycoBank MB808892).

Notes — The genus *Pyrenochaetopsis* (based on *P. leptospora*) was introduced to accommodate phoma-like species with setose pycnidia (de Gruyter et al. 2010). Within *Pyrenochaetopsis*, *P. poae* is closely allied to *P. leptospora* (conidia 4.5–7 × 1–2 µm; Boerema et al. 2004) and is best distinguished based on phylogenetic data.

**ITS.** Based on a megablast search of NCBI GenBank nucleotide database, the closest hits using the ITS sequence are *Pyrenochaetopsis leptospora* (GenBank JF740262; Identities

= 477/478 (99 %), no gaps), *Dokmaia monthadangii* (GenBank JN559405; Identities = 491/498 (99 %), no gaps) and *Peri-sporiopsis* aff. *meliioides* (GenBank FJ884130; Identities = 476/486 (98 %), Gaps = 1/486 (0 %)).

**LSU.** Based on a megablast search of NCBI GenBank nucleotide database, the closest hits using the LSU sequence are *Didymosphaeria futilis* (GenBank GU205219; Identities = 851/851 (100 %), no gaps), *Pyrenochaetopsis microspora* (GenBank GQ387631; Identities = 851/851 (100 %), no gaps) and *Pyrenochaetopsis leptospora* (GenBank GQ387628; Identities = 851/851 (100 %), no gaps).

**ACT.** Based on a megablast search of NCBI GenBank nucleotide database, the closest hits using the ACT sequence are *Phaeosphaeria nodorum* (GenBank XM\_001791742; Identities = 388/409 (95 %), no gaps), *Alternaria chlamydospora* (GenBank JQ671621; Identities = 466/512 (91 %), Gaps = 6/512 (1 %)) and *Embellisia eureka* (GenBank JQ671596; Identities = 454/500 (91 %), Gaps = 6/500 (1 %)). A blast2 comparison between the actin sequence of *Pyrenochaetopsis leptospora* strain CBS 101635 in Q-bank and our sequence revealed Identities = 252/265 (95 %), Gaps = 1/265 (0 %).

**TUB.** Based on a megablast search of NCBI GenBank nucleotide database, the closest hits using the TUB sequence are *Ulocladium multiforme* (GenBank JQ672002; Identities = 252/293 (86 %), Gaps = 12/293 (4 %)), *Ulocladium atrum* (GenBank JQ671998; Identities = 252/293 (86 %), Gaps = 12/293 (4 %)) and *Embellisia planifunda* (GenBank JQ671950; Identities = 252/295 (85 %), Gaps = 15/295 (5 %)). A similar search in the Q-bank fungal nucleotide database (www.q-bank.eu) revealed highest similarity with *Pyrenochaetopsis leptospora* (CBS 536.66; Identities = 322/327 (98 %), no gaps), *Pyrenochaetopsis microspora* (CBS 102876; Identities = 322/327 (98 %), no gaps) and *Pyrenochaetopsis decipiens* (CBS 343.85; Identities = 287/331 (87 %), Gaps = 4/331 (1 %)).

*Colour illustrations.* Raalte, The Netherlands; conidiomata, conidiogenous cell and conidia of *Parastagonospora poae* (left column); conidiomata, conidiogenous cells and conidia of *Pyrenochaetopsis poae* (right column). Scale bars = 10 µm.