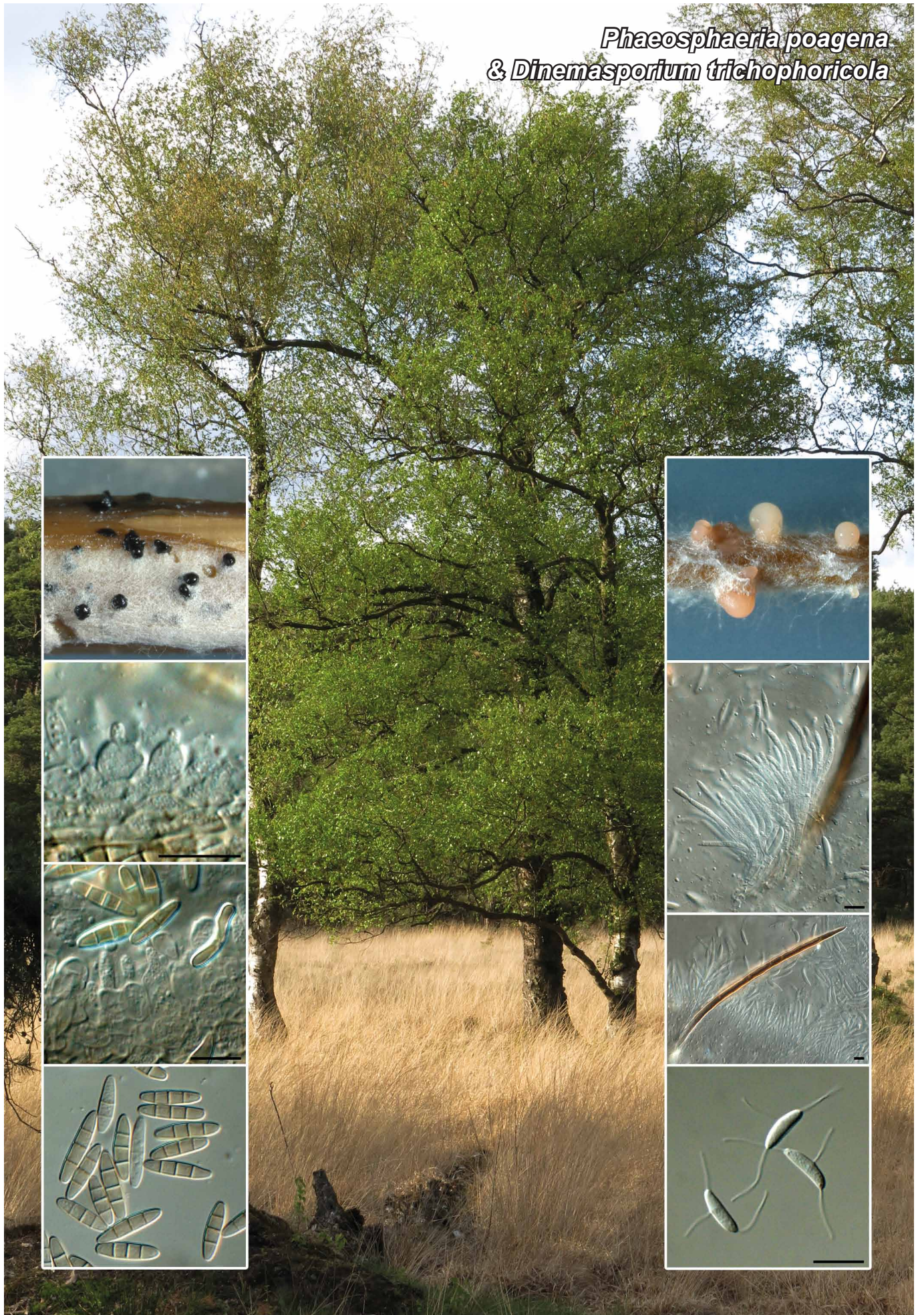


Phaeosphaeria poagena
& *Dinemasporium trichophoricola*



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

Conidiomata pycnidial, globose, black, erumpent, up to 250 µm diam, with central ostiole; wall of 2–3 layers of brown *textura angularis*. *Conidiophores* reduced to conidiogenous cells, hyaline, smooth, doliiiform, 7–10 × 4–5 µm, with prominent periclinal thickening, or tightly aggregated percurrent proliferations. *Conidia* solitary, brown, smooth, fusoid-ellipsoidal to subcylindrical, (1–)3-septate, becoming slightly constricted at septa, apex subobtusely, base truncate, (8–)12–14(–16) × (2.5–)3(–3.5) µm.

Culture characteristics — Colonies flat, spreading, erumpent in centre, with moderate aerial mycelium and even, smooth margins, reaching 40 mm diam after 2 wk at 25 °C. On OA and PDA surface pale olivaceous-grey, with luteous zones.

Typus. NETHERLANDS, Raalte, on *Poa* sp. (*Poaceae*), 2013, *W. Quaedvlieg* (holotype CBS H-21674, culture ex-type D791 = CBS 136771; ITS sequence GenBank KJ869114, LSU sequence GenBank KJ869172, TUB sequence GenBank KJ869242, MycoBank MB808889).

Notes — The present collection represents yet another novel *Phaeosphaeria* sp. from *Poa*, which is only known from its *Phaeoseptoria* morph. The asexual morph *Phaeoseptoria* is now treated as synonym of *Phaeosphaeria* (see Quaedvlieg et al. 2013). *Phaeosphaeria poagensis* is described as new as its small conidial dimensions do not correspond with any of the

asexual morphs recorded on *Poa* (Leuchtman 1984, Shoemaker & Babcock 1989, Quaedvlieg et al. 2013).

ITS. Based on a megablast search of NCBI GenBank nucleotide database, the closest hits using the ITS sequence are *Ascochyta manawaorae* (GenBank GU230751; Identities = 458/478 (96 %), Gaps = 4/478 (0 %)), *Parastagonospora nodorum* (GenBank KF512822; Identities = 475/499 (95 %), Gaps = 8/499 (1 %)) and *Phaeosphaeria oryzae* (GenBank KF251186; Identities = 483/521 (93 %), Gaps = 10/521 (1 %)).

LSU. Based on a megablast search of NCBI GenBank nucleotide database, the closest hits using the LSU sequence are *Phaeosphaeria oryzae* (GenBank GQ387591; Identities = 823/830 (99 %), Gaps = 2/830 (0 %)), *Phaeosphaeriopsis musae* (GenBank DQ885894; Identities = 823/830 (99 %), Gaps = 2/830 (0 %)) and *Vrystaatia aloecicola* (GenBank KF251781; Identities = 815/822 (99 %), Gaps = 2/822 (0 %)).

TUB. Based on a megablast search of NCBI GenBank nucleotide database, the closest hits using the TUB sequence are *Ophiostoma sparsiannulatum* (GenBank FJ907177; Identities = 183/217 (84 %), Gaps = 5/217 (2 %)), *Fusarium longipes* (GenBank GQ915443; Identities = 187/222 (84 %), Gaps = 7/222 (3 %)) and *Nectria antarctica* (GenBank HM484601; Identities = 187/224 (83 %), Gaps = 9/224 (4 %)).

Dinemasporium trichophoricola* Crous & Quaedvlieg, sp. nov.Etymology.* Named after the host genus from which it was collected, *Trichophorum*.

On autoclaved *Trichophorum* leaves on SNA. *Conidiomata* sporodochial, up to 350 µm diam; basal layer up to 35 µm thick. *Setae* brown, simple, septate, subulate with acute apex (obtuse when young), unbranched, thick-walled, 1–9-septate, 70–250 × 4–8 µm. *Conidiophores* up to 65 µm long, invested in mucus. *Conidiogenous cells* determinate, proliferating percurrently near apex, hyaline, smooth, subcylindrical to lageniform, 7–22 × 2–2.5 µm. *Conidia* hyaline, aseptate, thin-walled, smooth, granular, naviculate to fusiform or ellipsoid, gently curved or straight, apex obtuse to subobtusely rounded, base truncate, (8–)9–11(–13) × 2.5(–3) µm, with a single unbranched, flexuous, tubular appendage at each end; basal appendage excentric, apical and basal appendages 9–13 µm long; lateral appendages (2), inserted 4–6 µm below apex, 8–11 µm long.

Culture characteristics — Colonies flat, spreading, with sparse aerial mycelium and even, smooth margins, reaching 55 mm diam after 2 wk at 25 °C. On OA surface buff with patches of saffron. On PDA surface and reverse dirty white.

Typus. NETHERLANDS, Raalte, on *Trichophorum cespitosum* (*Cyperaceae*), 2013, *W. Quaedvlieg* (holotype CBS H-21675, culture ex-type D792 = CBS 136772; ITS sequence GenBank KJ869115, LSU sequence GenBank KJ869173, MycoBank MB808890).

Colour illustrations. Raalte, The Netherlands; conidiomata, conidiogenous cells and conidia of *Phaeosphaeria poagensis* (left column); conidiomata, conidiophores, setae and conidia of *Dinemasporium trichophoricola* (right column). Scale bars = 10 µm.

Notes — Based on DNA phylogenetic data, Crous et al. (2012b) concluded that conidial appendages as sole taxonomic character were of insufficient value to determine generic boundaries in these coelomycetous fungi, and subsequently reduced *Stauronema* to synonymy with *Dinemasporium*. *Dinemasporium trichophoricola* is comparable with two species, namely *D. indicum* (conidia 7–13 × 2–3 µm, terminal appendages 6.5–17 µm, lateral appendages 8–20 µm long, but 3–4 µm below apex) and *D. pseudoindicum* (conidia 9–13 × 3–4 µm, terminal appendages 9–22 µm, lateral appendages 10–17 µm long, but 4–6 µm below apex). *Dinemasporium trichophoricola* can be distinguished from both species based on its shorter appendages. Of interest is that conidiomatal setae were observed to form on OA, but not on *Trichophorum* leaves on SNA, while conidia again developed lateral appendages on *Trichophorum* leaves, but not on OA.

ITS. Based on a megablast search of NCBI GenBank nucleotide database, the closest hits using the ITS sequence are *Dinemasporium pseudoindicum* (GenBank JQ889277; Identities = 510/523 (98 %), Gaps = 9/523 (1 %)), *Dinemasporium strigosum* (GenBank JQ889286; Identities = 491/521 (94 %), Gaps = 17/521 (3 %)) and *Dinemasporium americana* (GenBank JQ889274; Identities = 470/499 (94 %), Gaps = 24/499 (4 %)).

LSU. Based on a megablast search of NCBI GenBank nucleotide database, the closest hits using the LSU sequence are *Dinemasporium pseudoindicum* (GenBank JQ889293; Identities = 670/674 (99 %), Gaps = 1/674 (0 %)), *Dinemasporium strigosum* (GenBank JQ889300; Identities = 669/674 (99 %), 1/674 (0 %)) and *Dinemasporium americana* (GenBank JQ889290; Identities = 669/674 (99 %), Gaps = 1/674 (0 %)).