

Keissleriella poagens



Fungal Planet 216 – 10 June 2014

***Keissleriella poagensis* Crous & Quaedvlieg, sp. nov.**

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

Ascomata pseudothecial, brown, erumpent to superficial, solitary, globose, up to 250 µm diam, with central ostiole; ostiole surrounded by aseptate, subcylindrical, thick-walled, dark brown setae that taper slightly to a subobtuse apex, up to 60 µm long with bulbous base, 5–8 µm diam; ascomatal wall of 3–6 layers of medium brown *textura angularis* to *globulosa*. *Asci* 8-spored, 70–140 × 10–12 µm, cylindro-clavate, stipitate, bitunicate, fissitunicate, apex obtuse, with well-defined apical chamber. *Pseudoparaphyses* cellular, filamentous, septate, anastomosing, embedded in mucilage, 2–3 µm diam, extending above the asci. *Ascospores* biseriolate in asci, fusoid-ellipsoidal, 3-septate, constricted at septa, hyaline with subacute ends, surrounded by a mucilaginous sheath, 2–5 µm diam, (20–)21–23(–25) × (4–)4.5–5 µm.

Culture characteristics — Colonies erumpent, spreading, reaching 15 mm diam after 2 wk at 25 °C, with moderate aerial mycelium and lobate, smooth to feathery margins. On MEA surface pale olivaceous-grey, reverse umber. On OA surface dirty white with patches of pale olivaceous-grey. On PDA surface smoke-grey, reverse buff.

Typus. NETHERLANDS, Raalte, on *Poa* sp. (*Poaceae*), 2013, W. Quaedvlieg (holotype CBS H-21672, culture ex-type D775 = CBS 136767; ITS sequence GenBank KJ869112, LSU sequence GenBank KJ869170, MycoBank MB808887).

Notes — *Keissleriella poagensis* is phylogenetically closely allied to the genus *Keissleriella*, but morphologically different (Zhang et al. 2012b), in that we did not observe a papilla (then again, we studied it in culture not on host material) and ascospores were 3-septate. In agreement with *Keissleriella* are the brown setae surrounding the ostiole and the ascospores surrounded by a sheath. Presently, it seems best to place this species in *Keissleriella*, until more collections have been added to the *Lentitheciaceae*, which is a rather poorly known family.

ITS. Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the ITS sequence are *Coniothyrium fuckelii* (GenBank HQ832837; Identities = 330/362 (91 %), Gaps = 9/362 (2 %)), *Paraphaeosphaeria sporulosa* (GenBank JX496227; Identities = 329/362 (91 %), Gaps = 9/362 (2 %)) and *Coniothyrium nitidae* (GenBank GU355659; Identities = 335/369 (91 %), Gaps = 16/369 (4 %)).

LSU. Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the LSU sequence are *Pleurophoma pleurospora* (GenBank JF740327; Identities = 678/687 (99 %), Gaps = 2/687 (0 %)), *Keissleriella cladophila* (GenBank JX681090; Identities = 676/686 (99 %), no gaps) and *Keissleriella genistae* (GenBank GU205222; Identities = 676/686 (99 %), no gaps).

Colour illustrations. Raalte, The Netherlands; ascomata, setae, asci and ascospores in culture. Scale bars = 10 µm.