Camarosporium psoraleae
Camarosporium psoraleae Crous & M.J. Wingf., sp. nov.

Etymology. Named after the host from which it was isolated, Psoralea.

Conidiomata immersed to erumpent, solitary with central ostiole, globose, up to 400 µm diam; wall of 3–6 layers of brown *textura angularis*. Conidiophores reduced to conidiogenous cells. Conidiogenous cells lining the inner cavity, hyaline, smooth, phialidic with prominent periclinal thickening and thick channel (at times also with percurrent proliferation), globose to doliiform, 7–12 × 6–9 µm. Conidia brown, finely roughened, ellipsoid to ovoid, with obtuse ends, 1–3 transversely septate, developing 1–6 oblique to transverse septa, at times becoming constricted at primary septa, (12–)14–16(–18) × (8–)10(–11) µm. Paraphyses hyaline, hyphal-like, smooth, intermingled among conidiogenous cells, subcylindrical, base bulbous, tapering to obtuse apex, 1–4-septate, 5–7 µm diam at base, 2–3 µm diam at apex, 30–100 µm long, unbranched or branched at base, and anastomosing. Microconidiogenous cells intermingled among macroconidiogenous cells, hyaline, smooth, ampulliform to doliiform to irregular, mon- to polyphalidic, proliferating percurrently, or with periclinal thickening, 5–8 × 4–6 µm. *Microconidia* hyaline, smooth, guttulate, bacilliform to subcylindrical, apex obtuse, base truncate, 4–6 × 2–3 µm.

Culture characteristics — Colonies covering the dish in 2 wk, with sparse aerial mycelium. On MEA surface dirty white with cinnamon, reverse cinnamon. On OA surface cinnamon. On PDA surface cinnamon to buff, reverse buff.


Notes — Although the mode of conidiogenesis and the presence of paraphyses is different from that observed in the type species of *Camarosporium*, *C. propinquum* (Sutton 1980), the present taxon is best accommodated in this genus. Phylogenetically *C. phragmites* is closely related to *C. leucadendri*, though conidia of the latter are larger, (15–)16–19(–21) × (8–)9.5–11(–12) µm (Marincowitz et al. 2008a).

Based on a megablast search of NCBI s GenBank nucleotide database, the closest hits using the LSU sequence are *Microdiplodia hawaiiensis* (GenBank DQ885897; Identities = 896/897 (99 %), Gaps = 1/897 (0 %)), *Camarosporium leucadendri* (GenBank EU552106; Identities = 876/877 (99 %), no gaps) and *C. brabeji* (GenBank EU552105; Identities = 871/872 (99 %), Gaps = 1/872 (0 %)). Closest hits using the ITS sequence had highest similarity to *C. leucadendri* (GenBank EU552106; Identities = 559/561 (99 %), Gaps = 1/561 (0 %)), *C. mananes* (GenBank DQ885900; Identities = 557/561 (99 %), no gaps) and *Myrothecium verrucaria* (GenBank AB693919; Identities = 470/483 (97 %), Gaps = 2/483 (0 %)).