

Distoseptispora caricis



Fungal Planet 972 – 18 December 2019

Distoseptispora caricis Crous, sp. nov.

Etymology. Name refers to the host genus *Carex* from which it was isolated.

Classification — *Distoseptisporaceae*, *Distoseptisporales*, *Sordariomycetes*.

Mycelium consisting of pale brown, smooth, septate, branched, 1.5–2 µm diam hyphae. *Conidiophores* erect, subcylindrical, dark brown, smooth, 2–4-septate, 35–90 × 6–7 µm. *Conidiogenous cells* integrated, terminal, cylindrical, brown, smooth, monoblastic, 13–16 × 5–6 µm. *Conidia* solitary, obclavate, brown, smooth, 5–10-distoseptate, septa with central pore, wall thick, tapering abruptly at base; basal cell pale brown, with truncate hilum, 3.5–4 µm diam; apex obtuse, but in culture developing further, becoming elongated, flexuous, 3–4-euseptate, frequently with visible mucoid appendage surrounding conidial apex, conidia (55–)65–85(–100) × 15–16(–17) µm.

Culture characteristics — Colonies erumpent, spreading, with moderate aerial mycelium and feathery margin, reaching 6 mm diam after 2 wk at 25 °C. On MEA, PDA and OA surface and reverse olivaceous grey.

Typus. THAILAND, Chiang Mai, on leaves of *Carex* sp. (*Cyperaceae*), 2008, P.W. Crous, HPC 2251 (holotype CBS H-24238, cultures ex-type CPC 36498 = CBS 146041, CPC 36442 = CBS 146040, ITS, LSU and *rpb2* sequences GenBank MN562124.1–MN562125.1, MN567632.1 (CPC 36498) and MN556805.1–MN556806.1, MycoBank MB832882).

Notes — *Distoseptispora* has macronematous, septate, unbranched, brown conidiophores, terminal, blastic conidiogenous cells and olivaceous to brown, septate conidia (Su et al. 2016). The genus presently includes 18 species, of which *D. caricis* is phylogenetically most closely related to *D. tectonigena* (148–225(–360) × 11–12 µm, cylindrical-obclavate, 20–46-distoseptate) and *D. multiseptata* (95–290 × 11–20 µm, obclavate, rostrate, dark-olivaceous green, multi-distoseptate). Morphologically it is quite distinct, having smaller conidia.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the ITS sequence of CPC 36442 had highest similarity to *Distoseptispora tectonigena* (strain MFLUCC 12-0292, GenBank NR_154018.1; Identities = 355/411 (86 %), 16 gaps (3 %)), *Distoseptispora multiseptata* (voucher MFLU 15-1144, GenBank NR_154017.1; Identities = 345/402 (86 %), 16 gaps (3 %)), and *Arthrospis truncata* (strain CBS 584.82, GenBank NR_159641.1; Identities = 323/378 (85 %), 18 gaps (4 %)). The ITS sequences of CPC 36442 and 36498 are identical (607/607 bases). Closest hits using the LSU sequence of CPC 36498 are *Ellisembia leonensis* (voucher HKUCC 10822, GenBank DQ408566.1; Identities = 828/847 (98 %), 1 gap (0 %)), *Distoseptispora* sp. DB-2019c (strain MFLUCC 18-0376, GenBank MN163017.1; Identities = 824/850 (97 %), no gaps), and *Distoseptispora dehongensis* (as *Distoseptispora* sp. SNZ-2018a, strain KUMCC 18-0090, GenBank MK079662.1; Identities = 774/809 (96 %), 6 gaps (0 %)). Closest hits using the *rpb2* sequence had highest similarity to *Ellisembia leonensis* (voucher HKUCC 10822, GenBank DQ435089.1; Identities = 732/830 (88 %), no gaps), *Penicillium vanluykii* (strain DTO 148I2, GenBank JX996615.1; Identities = 256/318 (81 %), 6 gaps (1 %)), and *Trichoderma longibrachiatum* (strain GJS 01-121, GenBank JN175507.1; Identities = 251/312 (80 %), no gaps). The *rpb2* sequences of CPC 36442 and 36498 differ with a single nucleotide (843/844 bases similar).

Colour illustrations. Garden in Thailand where *D. caricis* was collected. Conidiogenous cells and conidia. Scale bars = 10 µm.