

Phaeosphaeria caricis-sectae



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***Phaeosphaeria caricis-sectae* Crous, sp. nov.**

Etymology. Name refers to the host *Carex secta*, which is indigenous to New Zealand.

Classification — *Phaeosphaeriaceae*, *Pleosporales*, *Dothi-deomycetes*.

Conidiomata pycnidial, solitary, immersed in agar, globose, brown to dark brown, pycnidial with central ostiole, 250–350 µm diam; wall of 6–8 layers of brown *textura angularis*. *Conidiophores* reduced to conidiogenous cells lining the inner cavity, hyaline, smooth, doliiform to globose, holoblastic, 4–8 × 5–7 µm. *Conidia* solitary, subcylindrical, variously curved, apex obtuse, base truncate, guttulate, medium brown, smooth, (1–)3(–4)-septate, (20–)25–30(–36) × (2–)2.5–3 µm.

Culture characteristics — Colonies flat, spreading, with moderate aerial mycelium and lobate, even margin, reaching 45 mm diam after 2 wk at 25 °C. On MEA and PDA surface honey, reverse isabelline; on OA surface buff.

Typus. NEW ZEALAND, Auckland Airport, from leaf spots of *Carex secta* (*Cyperaceae*), 27 Aug. 2019, *C. Inglis* (holotype CBS H-24442, culture ex-type CPC 38771 = T19_05742B = CBS 146823, ITS, LSU, *rpb2*, *tef1* (first part) and *tub2* sequences GenBank MZ064413.1, MZ064470.1, MZ078195.1, MZ078221.1 and MZ078258.1, MycoBank MB 839500).

Notes — *Phaeosphaeria* (based on *P. oryzae*) has *Phaeoseptoria* asexual morphs (Quaedvlieg et al. 2013). Several species of *Phaeosphaeria* occurring on *Carex* mainly from Europe and North America were treated by Shoemaker & Babcock (1989), but these are all known from their sexual morphs, making it impossible to make a morphological comparison with the asexual *P. caricis-sectae*, which occurs on *Carex secta*, a host endemic to New Zealand. Three species of *Phaeoseptoria* are known from *Carex*, namely *P. caricis* (conidia 70–80 × 7 µm, 7–10-septate), *P. caricicola* (conidia 35–55 × 4 µm, 7-septate) and *P. festucae* (conidia 50–85 × 2.8–4.8 µm, 8–11-septate (Erdoğan & Özbek 2017), which are clearly distinct from *P. caricis-sectae*.

Colour illustrations. *Carex secta*. Conidioma on PDA; conidiogenous cells giving rise to conidia; conidia. Scale bars = 300 µm (conidioma), 10 µm (all others).

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Phaeosphaeria sinensis* (strain MFLUCC 18-1552, GenBank NR_163350.1; Identities = 462/482 (96 %), one gap (0 %)), *Phaeosphaeria oryzae* (strain 9Y-G19a, GenBank MT131346.1; Identities = 496/518 (96 %), six gaps (1 %)) and *Hendersonia sabaleos* (strain CBS 889.68, GenBank MH859244.1; Identities = 518/541 (96 %), four gaps (0 %)). Closest hits using the **LSU** sequence are *Phaeosphaeria sinensis* (strain MFLUCC 18-1552, GenBank NG_070076.1; Identities = 840/844 (99 %), no gaps), *Phaeosphaeria oryzae* (strain CBS 110110, GenBank NG_069025.1; Identities = 840/844 (99 %), no gaps) and *Phaeosphaeria musae* (strain CBS 120026, GenBank DQ885894.1; Identities = 840/844 (99 %), no gaps). Closest hits using the **rpb2** sequence had highest similarity to *Parastagonospora nodorum* (strain UTHSC DI16-240, GenBank LT797006.1; Identities = 831/902 (92 %), no gaps), *Didymocyrtis cladoniicola* (strain UTHSC DI16-313, GenBank LT797037.1; Identities = 808/931 (87 %), six gaps (0 %)) and *Phaeosphaeria oryzae* (strain MFLUCC 11-0170, GenBank KM434306.1; Identities = 627/679 (92 %), no gaps). No significant hits were obtained when the **tef1** sequence was used in blastn and megablast searches. Closest hits using the **tub2** sequence had highest similarity to *Neosulcatispora strelitziae* (strain CPC 25657, GenBank KX228380.1; Identities = 434/476 (91 %), 14 gaps (2 %)), *Phaeosphaeria podocarp* (strain CBS 138903, GenBank KP004508.1; Identities = 429/481 (89 %), 18 gaps (3 %)) and *Paraphoma vinacea* (strain UMPV001, GenBank KU176892.1; Identities = 284/320 (89 %), six gaps (1 %)).

Supplementary material

FP1188 Consensus phylogram (50 % majority rule) obtained from the maximum likelihood analysis with IQ-TREE v. 1.6.12 (Nguyen et al. 2015, Kalyaanamoorthy et al. 2017, Hoang et al. 2018) of the *Phaeosphaeriaceae* multigene (ITS / LSU) nucleotide alignment derived from that of Tennakoon et al. (2020). Bootstrap support values (> 69 % shown; only values > 94 % are significant) from 5 000 ultrafast bootstrap replicates are shown at the nodes. GenBank accession (superscript; only those not listed in Tennakoon et al. 2020 are shown) and/or culture collection/voucher numbers are indicated for all species. The tree was rooted to *Leptosphaeria doliolum* (culture CBS 505.75) and the species described here is highlighted with a coloured block and **bold** face. Alignment statistics: 58 strains including the outgroup; 1 479 characters including alignment gaps analysed; 556 distinct patterns, 319 parsimony-informative, 92 singleton sites, 1 068 constant sites. The best models identified in IQ-TREE were: TIM2+F+I+G4 (ITS), K2P+I+G4 (LSU). The alignment and tree were deposited in TreeBASE (Submission ID 28129).

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