

*Didymella cari*

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***Didymella cari* Armstrong-Cho, Banniza & Crous, sp. nov.**

*Etymology.* Name refers to *Carum*, one of the host genera from which this fungus was collected.

*Classification* — *Didymellaceae*, *Pleosporales*, *Dothideomycetes*.

On PDA. *Conidiomata* separate, globose, brown, pycnidial, 200–350 µm diam, with central ostiole; wall of 3–6 layers of brown *textura angularis*. *Conidiophores* reduced to conidiogenous cells lining the inner cavity, hyaline, smooth, ampulliform to globose, holoblastic, (9–)12–16 × (9–)12–13 µm. *Conidia* solitary, hyaline, smooth, guttulate, subcylindrical, straight to curved, apex obtuse, base truncate, 2.5–4 µm diam, (0–)1(–2)-septate, (1-septate conidia with septum above median), (8–)21–26(–31) × (4–)6(–7) µm.

*Culture characteristics* — Colonies covering dish in 2 wk with fluffy to moderate aerial mycelium. On MEA surface sienna, reverse fulvous. On PDA surface pale olivaceous grey to olivaceous grey, reverse iron-grey. On OA surface pale luteous to buff.

*Typus.* CANADA, Saskatchewan, Choiceland, on living flower of *Carum carvi* (*Apiaceae*), 2015, *C. Armstrong-Cho* (holotype CBS H-23594, cultures ex-types CPC 33112 = CBS 144497 = A27, ITS, LSU, *actA* and *tub2* sequences GenBank MH327825.1, MH327861.1, MH327865.1 and MH327899.1, MycoBank MB825440).

*Additional material examined.* CANADA, Saskatchewan, Choiceland, on living flower of *Coriandrum sativum* (*Apiaceae*), 2015, *C. Armstrong-Cho*, CPC 33113 = CBS 144498 = A74, ITS, LSU, *actA* and *tub2* sequences GenBank MH327826.1, MH327862.1, MH327866.1 and MH327900.1; Lemberg, on living flower of *Carum carvi*, 2015, *C. Armstrong-Cho*, CPC 33114 = CBS 144499 = A122F, ITS, LSU and *tub2* sequences GenBank MH327827.1, MH327863.1 and MH327901.1; Lorie, on living stem of *Carum carvi*, 2016, *C. Armstrong-Cho*, CPC 33115 = CBS 144500 = A355, ITS sequence GenBank MH327828.1.

*Colour illustrations.* Coriander blossom blight; sporulation on caraway blossom (scale bar = 1 mm), conidia, and conidiogenous cells (right) (scale bars = 10 µm).

*Notes* — *Didymella cari* was isolated from blossom blight symptoms on coriander and caraway in Western Canada. Pathogenicity trials on coriander and caraway flowers showed that the isolates were pathogenic on both substrates. Phoma-like species reported from these hosts in the past include *Subplenodomus apiicola* from Brazil, *Phoma exigua* var. *exigua* from Poland and *Phoma multirostrata* from Australia (Mendes et al. 1998, Machowicz-Stefaniak et al. 2008, Golzar et al. 2015), which are clearly distinct based on their morphology (Boerema et al. 2004). Another taxon to consider is *Ascochyta carvi* (on leaves, stems and seeds of *Carum carvi* occurring in the former Czechoslovakia), although conidia of the latter species are significantly smaller, 0–1(–2)-septate, (6–)8–12(–14) × 2.5–4.5 µm (Ondrej 1983).

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the ITS sequence of CPC 33112 had highest similarity to *Didymella macrostoma* (GenBank KY367515.2; Identities = 478/485 (99 %), no gaps) and *D. glomerata* (GenBank KT223334.1; Identities = 478/485 (99 %), no gaps), from which *D. cari* can easily be distinguished based on its conidial dimensions (Chen et al. 2015, 2017). The ITS sequences of CPC 33112–33115 were identical, but that of CPC 33114 differed with one nucleotide from the rest. Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the LSU sequence of CPC 33112 had highest similarity to *D. macrostoma* (GenBank GU238096.1; Identities = 1226/1230 (99 %), 2 gaps (0 %)) and *D. tanacetii* (GenBank KT287040.1; Identities = 1225/1230 (99 %), 2 gaps (0 %)), *D. rosea* (GenBank KT287017.1; Identities = 1225/1230 (99 %), 2 gaps (0 %)). Except for two nucleotide changes, the LSU sequences of CPC 33112–33114 were identical. Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the *actA* sequence of CPC 33112 had highest similarity to *D. macrostoma* (GenBank KT309303.2; Identities = 210/238 (88 %), 2 gaps (0 %)), *D. tanacetii* (GenBank KT286999.1; Identities = 206/237 (87 %), no gaps) and *D. pedeiaae* (GenBank KT309272.2; Identities = 206/237 (87 %), no gaps). The *actA* sequences of CPC 33112 and CPC 33113 were identical. Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the *tub2* sequence of CPC 33112 had highest similarity to *D. negriana* (GenBank KY632664.1; Identities = 279/300 (93 %), no gaps), *Stagonosporopsis heliopsisidis* (GenBank KX928776.1; Identities = 277/298 (93 %), no gaps) and *Phoma adonidicola* (GenBank JQ934842.1; Identities = 275/296 (93 %), no gaps). The *tub2* sequences of CPC 33112–33114 were identical.