

Didymocyrtis brachylaenae



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***Didymocyrtis brachylaenae* Crous, sp. nov.**

Etymology. Name refers to *Brachylaena*, the host genus from which this fungus was collected.

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

Conidiomata pycnidial, globose, brown, 200–350 µm diam, with central ostiole; wall of 3–6 layers of medium brown *textura angularis*. *Conidiophores* mostly reduced to conidiogenous cells lining the inner cavity, ampulliform to doliiform, 5–7 × 2.5–3.5 µm, proliferating percurrently at apex; a few conidiophores observed that are subcylindrical, branched, 1–2-septate, with terminal and intercalary conidiogenous cells. *Conidia* fusoid-ellipsoid to subcylindrical, widest in middle, 1(–3)-septate, apex subobtuse, base truncate, medium brown, smooth, granular, (8–)9–10(–13) × (2–)3 µm. *Spermatia* observed in same conidiomata as conidia, hyaline, smooth, aseptate, ellipsoid, 3–4.5 × 2 µm.

Culture characteristics — Colonies flat, spreading, with moderate aerial mycelium, covering dish after 2 wk at 25 °C. On MEA surface pale luteous, reverse umber. On PDA surface and reverse umber. On OA surface umber with patches of pale luteous.

Typus. SOUTH AFRICA, Eastern Cape Province, Haga Haga, on leaves of *Brachylaena discolor* (*Asteraceae*), 24 Dec. 2010, *M.J. Wingfield* (holotype CBS H-23565, culture ex-type CPC 32651 = CBS 144438, ITS, LSU, *rpb2* and *tub2* sequences GenBank MH327821.1, MH327857.1, MH327873.1 and MH327896.1, MycoBank MB825436).

Colour illustrations. *Brachylaena discolor* at Haga Haga; symptomatic leaf, conidiogenous cells and conidia, spermatia, and 1-septate conidia. Scale bars = 10 µm.

Notes — The genus *Diederichomyces* was established by Trakunyingcharoen et al. (2014) for several phoma-like lichenicolous species. *Diederichomyces* was, however, reduced to synonymy under *Didymocyrtis* by Ertz et al. (2015), which is an older name, and has priority. Although phylogenetically related to *D. cladoniicola*, *D. brachylaenae* is distinct in having conidia that are 1(–3)-septate. Furthermore, although they were neither described nor illustrated, original isolations of *D. brachylaenae* were from a phaeosphaeria-like sexual morph, which is also consistent with its phylogenetic position in the *Phaeosphaeriaceae*.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the ITS sequence had highest similarity to *Phaeosphaeria poagena* (GenBank KJ869114.1; Identities = 461/476 (97 %), 3 gaps (0 %)), *Phaeosphaeria podocarp* (GenBank NR_137933.1; Identities = 454/476 (95 %), 2 gaps (0 %)) and *Parastagonospora nodorum* (GenBank KM056326.1; Identities = 453/476 (95 %), 11 gaps (2 %)). Closest hits using the LSU sequence are *Didymocyrtis cladoniicola* (GenBank LN907456.1; Identities = 865/868 (99 %), no gaps), *Neosulcatispora agaves* (GenBank KT950867.1; Identities = 860/866 (99 %), no gaps) and *Phaeosphaeriopsis musae* (GenBank DQ885894.1; Identities = 864/872 (99 %), no gaps). Closest hits using the *rpb2* sequence had highest similarity to *Phaeosphaeria chiangraina* (GenBank KM434307.1; Identities = 511/597 (86 %), 2 gaps (0 %)), *Phaeosphaeria oryzae* (GenBank KM434306.1; Identities = 511/597 (86 %), 2 gaps (0 %)) and *Phaeosphaeria musae* (GenBank KM434304.1; Identities = 511/597 (86 %), 2 gaps (0 %)). Closest hits using the *tub2* sequence had highest similarity to *Stagonospora avenaria* f. sp. *avenaria* (GenBank AY870402.1; Identities = 902/968 (93 %), 12 gaps (1 %)), *Stagonospora avenae* f. sp. *triticea* (GenBank AY786330.1; Identities = 898/964 (93 %), 4 gaps (0 %)) and *Parastagonospora nodorum* (GenBank CP022806.1; Identities = 898/964 (93 %), 4 gaps (0 %)).