

*Coleophoma proteae*



Fungal Planet 118 – 4 June 2012

***Coleophoma proteae* Crous, sp. nov.**

*Etymology.* Named after the host genus from which it was isolated, *Protea*.

*Leaf spots* amphigenous, subcircular, up to 30 mm diam, brown, with concentric circles. *Conidiomata* immersed, subepidermal, amphigenous, globose, sporulating profusely on leaves (and in culture), with conidiomata arranged in concentric circles; up to 250 µm diam; wall of 2–6 layers of dark brown *textura angularis*. *Paraphyses* intermingled among conidiophores, hyaline, subcylindrical, 0–2-septate, up to 40 µm long, 2–3 µm diam, tapering towards obtusely rounded apex. *Conidiophores* hyaline, smooth, subcylindrical, 1–3-septate, 15–40 × 3–4 µm. *Conidiogenous cells* hyaline, smooth, subcylindrical, apical or lateral on conidiophores, 10–17 × 2.5–3.5 µm; tapering towards a truncate apex, 2–2.5 µm diam, with minute periclinal thickening. *Conidia* solitary, guttulate, hyaline, smooth, subcylindrical, apex obtuse, base tapered towards flattened scar, 1.5–2 µm diam, (11–)12–14(–17) × (3–)4(–5) µm.

*Culture characteristics* — (in the dark, 25 °C after 3 wk): Colonies erumpent, spreading with sparse aerial mycelium and feathery margins, reaching 25 mm diam. On MEA surface iron-grey, with patches of olivaceous grey, reverse iron-grey; on OA olivaceous grey; on PDA smoke grey, with patches of honey.

*Typus.* SOUTH AFRICA, Gauteng, Walter Sisulu National Botanical Gardens, on leaves of *Protea caffra* (*Proteaceae*), 5 July 2011, P.W. Crous, M.K. Crous & M. Crous, holotype CBS H-20962, cultures ex-type CPC 19715, 19714 = CBS 132532, ITS sequence GenBank JX069866 and LSU sequence GenBank JX069850, MycoBank MB800378.

*Notes* — The genus *Coleophoma* has pycnidial conidiomata with central ostioles, persistent, hyaline paraphyses, phialidic conidiogenous cells with periclinal thickening, and hyaline, cylindrical conidia. Although the genus *Coleophoma* was recently treated (Nag Raj 1978, Sutton 1980), no phylogenetic overview is presently available. Wu et al. (1996) provided a treatment of 22 taxa, accepting six species, a key to which is presented in Duan et al. (2007). Based on this key, *C. proteae* is most similar to *C. prunicola* (pathogenic to *Prunus*) and *C. fusiformis* (pathogenic to *Rhododendron*) (conidia 20–28 × 4.5–5.5 µm), but distinct in having somewhat smaller conidia. *Coleophoma proteae* was associated with serious leaf blight disease on *Protea caffra*. This is the first record of *Coleophoma* leaf disease on *Proteaceae*.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hit using the ITS sequence is *Coleophoma eucalyptorum* (GenBank JQ044430; Identities = 524/550 (95 %), Gaps = 6/550 (1 %)), followed by *Coleophoma empetri* (GenBank FJ480134; Identities = 511/533 (96 %), Gaps = 5/533 (1 %)), and *Neofabraea eucalypti* (GenBank GQ303279; Identities = 518/555 (93 %), Gaps = 12/555 (2 %)). Closest hits using the LSU sequence yielded highest similarity to *Coleophoma eucalyptorum* (GenBank JQ044449; Identities = 892/901 (99 %), Gaps = 2/901 (0 %)), *Coleophoma empetri* (GenBank FJ588252; Identities = 890/901 (99 %), Gaps = 2/901 (0 %)), and *Cryptosporiopsis actinidiae* (GenBank HM595594; Identities = 886/902 (98 %), Gaps = 4/902 (0 %)).

*Colour illustrations.* Symptomatic leaves of *Protea caffra* in Walter Sisulu National Botanical Gardens; conidiomata sporulating on oatmeal agar; conidiogenous cells, paraphyses and conidia. Scale bars = 10 µm.