

Phaeocercospora colophospermi



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Phaeocercospora Crous, gen. nov.

Etymology. *Phaeo* (= pigmented) and its morphological similarity to *Cercospora*.

Foliicolous, associated with leaf spots. *Caespituli* amphigenous, subepidermal, arising from subepidermal, globular fruiting bodies (immature structures with undefined white contents); wall of 2–3 layers of *textura angularis*, bursting through epidermis, forming grey sporodochia with densely aggregated conidiophores. *Conidiophores* subcylindrical to ampulliform, brown, finely verruculose, aggregated, 0–2-septate. *Conidiogenous*

cells terminal, brown, finely verruculose, ampulliform, tapering to a truncate apex, proliferating several times percurrently at apex (proliferations irregular, rough). *Conidia* solitary, brown, finely verruculose, guttulate, subcylindrical to narrowly obclavate, straight to mildly curved, apex subobtuse, base truncate with marginal frill, transversely septate; hila and scars not thickened, nor darkened or refractive.

Type species. *Phaeocercospora colophospermi*.
Mycobank MB800386.

Phaeocercospora colophospermi Crous, sp. nov.

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

Leaf spots amphigenous, brown, angular, vein-limited, 1–4 mm diam, with raised border. *Caespituli* amphigenous, subepidermal, arising from subepidermal, globular fruiting bodies up to 150 µm diam (immature structures with undefined white contents); wall of 2–3 layers of *textura angularis*, bursting through epidermis, forming grey sporodochia with densely aggregated conidiophores. *Conidiophores* subcylindrical to ampulliform, brown, finely verruculose, aggregated, 0–2-septate, 15–25 × 5–7 µm. *Conidiogenous cells* terminal, brown, finely verruculose, ampulliform, tapering to a truncate apex, 2.5–3.5 µm diam, proliferating several times percurrently at apex (proliferations irregular, rough), 12–20 × 5–7 µm. *Conidia* solitary, brown, finely verruculose, guttulate, subcylindrical to narrowly obclavate, straight to mildly curved, apex subobtuse, base truncate with marginal frill, 1–3-septate, (25–)45–55(–65) × (4.5–)5–6(–7) µm, up to 85 µm long in culture, and 3–5-septate; hila and scars not thickened, nor darkened or refractive.

Culture characteristics — (in the dark, 25 °C after 3 wk): Colonies erumpent, but not spreading, slow-growing, reaching 5 mm diam, lacking aerial mycelium, and with smooth, irregular margins. On MEA iron-grey on surface and in reverse; on OA iron-grey with diffuse red-brown pigment in agar; on PDA olivaceous grey with patches of pale olivaceous grey due to profuse sporulation.

Typus. SOUTH AFRICA, Mpumalanga, Kruger Game Reserve, Satara Rest Camp, on leaves of *Colophospermum mopane* (*Fabaceae*), 11 July 2011, P.W. Crous & K.L. Crous, holotype CBS H-20966, cultures ex-type CPC 19813, 19812 = CBS 132687, ITS sequence GenBank JX069870 and LSU sequence GenBank JX069854, MycoBank MB800387.

Notes — *Phaeocercospora* is reminiscent of the genera *Pseudocercospora*, *Scolecostigmia*, and *Cercostigmia*. However, *Scolecostigmia* (based on *S. mangiferae*) (Braun et al. 1999) clusters in a clade sister to *Pseudocercospora* s.str., and distant from *Phaeocercospora*. Although *Cercostigmia concentrica* (the type species of *Cercostigmia*) (Braun & Hill 2002) is not known from culture, other taxa with a similar morphology cluster in *Pseudocercospora* s.str., suggesting that *Cercostigmia* should be treated as synonym of *Pseudocercospora* (Crous et al. 2001, 2006). The *Dothistroma* clade is not well resolved, and other than *Dothistroma* and *Phaeocercospora*, also includes taxa with a *Passalora*-like morphology (scars and hila thickened, darkened and refractive).

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hit using the ITS sequence is *Mycosphaerella laricina* (GenBank EU167595; Identities = 519/562 (92 %), Gaps = 13/562 (2 %)), followed by *Passalora sequoiae* (GenBank GU214667; Identities = 519/563 (92 %), Gaps = 16/563 (3 %)), and *Passalora loranthei* (GenBank EU853479; Identities = 504/548 (92 %), Gaps = 16/548 (3 %)). Closest hits using the LSU sequence yielded highest similarity to *Passalora perplexa* (GenBank GU214459; Identities = 873/876 (99 %), Gaps = 0/876 (0 %)), *Mycosphaerella pini* (= *Dothistroma septosporum*, GenBank GU214427; Identities = 871/876 (99 %), Gaps = 0/876 (0 %)), and *Dothistroma pini* (GenBank GU214426; Identities = 870/876 (99 %), Gaps = 0/876 (0 %)).

Colour illustrations. *Colophospermum mopane* tree at Satara Rest Camp; symptomatic leaf; close-up of leaf spot; colony sporulating in culture; conidia and conidiogenous cells. Scale bar = 10 µm.