

Chrysocrypta corymbiae



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***Chrysocrypta* Crous & Summerell, gen. nov.**

Etymology. *Chryso* (Greek) = orange, and *cryptos* (Greek) = hidden.

Conidiomata characteristic yellow-orange structures on leaf spots, eustromatic, separate, subepidermal, subglobose, opening by means of irregular rupture; wall of 3–6 layers of orange-brown *textura angularis*; conidiomata exuding slimy orange masses of conidia. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* lining the inner cavity of conidioma, hyaline, smooth, ampulliform, apex truncate, with

minute periclinal thickening, at times apical part elongated into a long neck. *Conidia* dimorphic, intermixed in same conidiomata. *Macroconidia* broadly ellipsoid to obovoid, hyaline, smooth, granular to guttulate, thick-walled, apex obtuse, base flattened. *Microconidia* hyaline, smooth, guttulate, fusoid-ellipsoid, apex acutely rounded, base truncate.

Type species. *Chrysocrypta corymbiae*.
MycoBank MB800379.

***Chrysocrypta corymbiae* Crous & Summerell, sp. nov.**

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

Leaf spots amphigenous, subcircular, 5–15 µm diam, grey-brown with raised, dark brown border. *Conidiomata* visible as characteristic yellow-orange structures on leaf spots, eustromatic, separate, subepidermal, subglobose, opening by means of irregular rupture; up to 400 µm diam in culture (on PNA); wall of 3–6 layers of orange-brown *textura angularis*; conidiomata exuding slimy orange masses of conidia. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* lining the inner cavity of conidioma, hyaline, smooth, ampulliform, 4–6 × 5–10 µm; apex truncate, 1.5 µm diam, with minute periclinal thickening, at times apical part elongated into a long neck, up to 15 µm long, 2–3 µm diam. *Conidia* dimorphic, intermixed in same conidiomata. *Macroconidia* broadly ellipsoid to obovoid, hyaline, smooth, granular to guttulate, thick-walled, apex obtuse, base flattened, 1–1.5 µm diam, (7–)8–9(–11) × (4–)5(–6) µm. *Microconidia* hyaline, smooth, guttulate, fusoid-ellipsoid, apex acutely rounded, base truncate, 1–1.5 µm diam, 5–7 × 2.5–3 µm.

Culture characteristics — (in the dark, 25 °C after 3 wk): Colonies spreading, flat, covering surface of dish, with sparse aerial mycelium. On MEA bright orange, reverse cinnamon; on OA cinnamon; on PDA surface dirty white with orange sporulation.

Colour illustrations. Termite mount and vegetation at Mary River Conservation Reserve; conidiomata sporulating on malt extract agar; conidiogenous cells and conidia. Scale bars = 10 µm.

Typus. AUSTRALIA, Northern Territory, Mary River National Park, Mary River Conservation Reserve, S12°54.130' E131°37.594', leaves of *Corymbia* sp., 24 Apr. 2011, P.W. Crous & B.A. Summerell, holotype CBS H-20963, cultures ex-type CPC 19279 = CBS 132528, ITS sequence GenBank JX069867 and LSU sequence GenBank JX069851, MycoBank MB 800380.

Notes — The *Cryphonectriaceae* was recently introduced as family for the *Cryphonectria-Endothia* stem canker pathogens occurring on woody hosts (Gryzenhout et al. 2006). In a recent paper by Vermeulen et al. (2011), reference is made to the fact that the family now includes 13 genera. However, this assumes that *Cryphonectriaceae* only occurs on stems of woody hosts, which is incorrect, as several genera are also well-established foliar pathogens of these hosts, e.g. *Foliocryphia* on *Eucalyptus coccifera* in Tasmania (Cheewangkoon et al. 2009), and *Aurantiosacculus* on various eucalypt species in Australia (Crous et al. 2012). *Chrysocrypta* is similar to *Foliocryphia*, but distinct in forming dimorphic conidia. The introduction of *Chrysocrypta* adds yet another genus to this family, which is associated with leaf spots on *Corymbia*.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hit using the ITS sequence is *Amphiportha leiphaemia* (GenBank AJ293882; Identities = 523/614 (85 %), Gaps = 44/614 (7 %)), followed by *Amphilogia gyrosa* (GenBank EF026147; Identities = 533/630 (85 %), Gaps = 49/630 (8 %)), and *Cryphonectria nitschkei* (GenBank GQ290656; Identities = 421/473 (89 %), Gaps = 27/473 (6 %)). Closest hits using the LSU sequence yielded highest similarity to species of *Harknessia*, e.g. *Harknessia renisporea* (GenBank JQ706237; Identities = 851/875 (97 %), Gaps = 6/875 (1 %)), *Foliocryphia eucalypti* (GenBank GQ303307; Identities = 847/875 (97 %), Gaps = 6/875 (1 %)), and *Endothia gyrosa* (GenBank DQ470972; Identities = 847/877 (97 %), Gaps = 10/877 (1 %)).

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