Colletotrichum cobbittiense
**Colletotrichum cobbittiense** S. Luo, G. Dong & P. Wong, *sp. nov.*

**Etymology.** Named after the location, Cobbitty, where it was found.

**Classification.** *Glomerellaceae, Glomerellales, Sordariomycetes.*


Culture characteristics — Colonies on PDA reaching 55 mm diam in 5 d at 25 °C in the dark; moderate white aerial mycelium, becoming grey to dark grey at the centre or in patches, with moderate sporulation on cream to pale brown conidiomata. Reverse grey to dark grey at centre and in patches, with rounded ends, sometimes tapering to a rounded end or narrowed at the centre, (11–)12(–17) × (4–)5(–6) μm. Appressoria single or in clusters, pale to dark brown, smooth-walled, subglobose to ellipsoidal or broadly cylindrical, sometimes tapering to apex, with entire, undulate or lobate margin, 8–18 × 4–8 μm.

Notes — Leaf spots were observed on the leaves of a *Cordyline* interspecific hybrid (*C. stricta × C. australis*) tree in the garden of the Plant Breeding Institute, Cobbitty, New South Wales, Australia. The leaf lesions were characterised by bleached centres and diffuse brownish margins around the lesions (see photo plate). The leaf spots were generally small (5–10 mm) and discrete. This pathogen has not been previously recorded in Australia (Shivas et al. 2016).

Phylogenetic analyses based on sequence data from six loci (ACT, CHS-1, GAPDH, HIS3, ITS and TUB2) place the fungus in the Kahawae clade of the *gloeosporioides* complex (Weir et al. 2012). It is closest to *C. ti* but differs in having smaller conidia (mean length of 12 μm vs 16 μm), a growth rate of about twice as fast on PDA (55 mm diam after 5 d vs 50–55 mm after 10 d) and in not producing ascomata in culture. *Colletotrichum ti* has only been found in New Zealand on *Cordyline* while *C. cobbittiense* was isolated from lesions on leaves of a *Cordyline* interspecific hybrid (*C. stricta × C. australis*).

Multilocus phylogenetic tree inferred from the combined ACT, CHS-1, GAPDH, HIS3, ITS and TUB2 sequence alignment. The evolutionary analyses were conducted in MEGA v. 7 (Kumar et al. 2016) using the Maximum Likelihood method based on the Kimura 2-parameter model. The tree was rooted to *C. cymbidicola* IMI: 347923*. Ex-type strains are marked with an asterisk (*).


colour illustrations. Cordyline trees; leaf spot symptom on a *Cordyline* interspecific hybrid (*C. stricta × C. australis*); conidiophores and conidia; appressoria adhering to the plastic surface of agar plate. Scale bars (from left to right) = 10 mm, 10 μm, 10 μm.