

*Diaporthe obtusifoliae*



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## *Diaporthe obtusifoliae* Crous, *sp. nov.*

*Etymology.* Named after the host species from which it was isolated, *Acacia obtusifolia*.

*Classification* — *Diaporthaceae*, *Diaporthales*, *Sordariomycetes*.

*Leaf spots* amphigenous, medium brown, circular with a raised margin, 1–4 mm diam, coalescing with age to form larger blotches. *Conidiomata* pycnidial, immersed, globose, 180–250 µm diam, medium brown, with central ostiole; wall of 4–6 layers of medium brown *textura angularis*. *Conidiophores* lining the inner cavity, hyaline, smooth, subcylindrical, branched, 1–2-septate, 25–40 × 4–6 µm. *Conidiogenous cells* terminal and intercalary, subcylindrical with slight apical taper, 10–25 × 3–5 µm; proliferating percurrently near apex. *Conidia* solitary, aseptate, ellipsoid, apex subobtuse, base with truncate hilum, 2 µm diam, slightly thickened and refractive; conidia hyaline, smooth, guttulate, becoming pale brown with age, (12–)14–16(–18) × (6–)6.5–7 µm.

*Culture characteristics* — Colonies flat, spreading, with moderate aerial mycelium and feathery, lobate margins, reaching 30 mm diam after 2 wk at 25 °C. On MEA surface pale olivaceous grey, reverse olivaceous grey. On PDA surface and reverse olivaceous grey. On OA surface pale olivaceous grey.

*Typus.* AUSTRALIA, New South Wales, Gnupa State Forest, on leaves of *Acacia obtusifolia* (*Fabaceae*), 29 Nov. 2016, P.W. Crous (holotype CBS H-23318, culture ex-type CPC 32336 = CBS 143449, ITS, LSU and *his3* sequences GenBank MG386072, MG386125 and MG386137, MycoBank MB823421).

*Notes* — Although *D. obtusifoliae* is morphologically distinct from the typical *Diaporthe* spp. by forming broadly ellipsoid conidia, it clusters within the genus. Based on morphology it is distinct from *D. acaciarum* (on *A. tortilis*, Tanzania, alpha conidia (6–)6.5–7(–7.5) × (2–)2.5(–3) µm; Crous et al. 2014b) and *D. acaciigena* (on *A. retinodes*, Australia, alpha conidia ellipsoid to subclavate, (9–)10–11(–12) × (4–)6–6.5(–7) µm; Crous et al. 2011). It is also distinct from *D. scobina*, to which it is most closely related (Gomes et al. 2013).

Based on a megablast search using the ITS sequence, the closest matches in NCBI's GenBank nucleotide database were *D. acaciigena* (GenBank NR\_137113; Identities 538/568 (95 %), 7 gaps (1 %)), *D. scobina* (GenBank KC343195; Identities 534/572 (93 %), 20 gaps (3 %)) and *D. padi* var. *padi* (GenBank KC343170; Identities 531/569 (93 %), 18 gaps (3 %)). The highest similarities using the LSU sequence were *D. perijuncta* (GenBank AF408356; Identities 829/835 (99 %), no gaps), *D. fusicola* (GenBank KY011836; Identities 825/832 (99 %), no gaps) and *D. ovoicicola* (GenBank KY011838; Identities 818/825 (99 %), no gaps). The highest similarities using the *his3* sequence were with *D. acaciigena* (GenBank KC343489; Identities 356/385 (92 %), 13 gaps (3 %)), *D. pustulata* (GenBank KC343671; Identities 349/382 (91 %), 10 gaps (2 %)) and *D. amygdali* (GenBank KP293563; Identities 349/384 (91 %), 10 gaps (2 %)).

*Colour illustrations.* Symptomatic leaves of *Acacia obtusifoliae*; leaf spots, conidiomata sporulating on PDA, conidiophores and conidia. Scale bars = 10 µm.

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