

*Diaporthe psoraleae*  
& *Diaporthe psoraleae-pinnatae*





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## *Diaporthe psoraleae* Crous & M.J. Wingf., *sp. nov.*

*Etymology.* Named after the host genus from which it was collected, *Psoralea*.

On PNA. *Conidiomata* pycnidial, globose, aggregated in a large stroma up to 600 µm diam, black, erumpent, exuding creamy conidial droplets from central ostioles; walls of 3–6 layers of medium brown *textura angularis*. *Conidiophores* hyaline, smooth, 1–2-septate, unbranched, densely aggregated, cylindrical, straight to sinuous, 25–40 × 4–6 µm. *Conidiogenous cells* 10–25 × 2.5–3.5 µm, phialidic, cylindrical, terminal, with slight taper towards apex, 1–2 µm diam, with visible periclinal thickening; collarette not observed. *Paraphyses* cylindrical, hyaline, smooth, 1–2-septate, up to 40 µm long, 1.5–2 µm diam. *Alpha conidia* aseptate, hyaline, smooth, guttulate, obovoid to fusoid-ellipsoid, tapering towards both ends, straight, widest just below apex, in upper third of conidium, apex obtuse, base rounded to obconically truncate, (11–)13–15(–16) × (4–)6–7(–8) µm. *Gamma conidia* not observed. *Beta conidia* not observed.

Culture characteristics — Colonies covering MEA and OA dishes after 2 wk, but only reaching 55 mm diam on PDA, margins feathery, uneven, with sparse aerial mycelium. On PDA surface and reverse amber; on MEA surface hazel in centre, sepia in outer region, brown-vinaceous underneath; on OA surface vinaceous-buff to isabelline.

*Typus.* SOUTH AFRICA, Western Cape Province, Betty's Bay, Harold Porter National Botanical Garden, on stems of *Psoralea pinnata* (*Fabaceae*), 28 Oct. 2012, M.J. Wingfield (holotype CBS H-21422, culture ex-type CPC 21634, 21635 = CBS 136412, ITS sequence GenBank KF777158, LSU

sequence GenBank KF777211, TEF sequence GenBank KF777245, TUB sequence GenBank KF777251, MycoBank MB805822).

Notes — No species of *Diaporthe* are presently known to occur on *Psoralea* in South Africa (Crous et al. 2000, Gomes et al. 2013). Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the LSU sequence are *Diaporthe eres* (GenBank AF362565; Identities = 873/875 (99 %), no gaps), *D. eucalyptorum* (GenBank JX069846; Identities = 878/881 (99 %), no gaps) and *D. musigena* (GenBank JF951158; Identities = 878/881 (99 %), no gaps). Closest hits using the ITS sequence had highest similarity to *D. cinerascens* (GenBank KC343050; Identities = 552/572 (97 %), Gaps = 3/572 (0 %)), *D. neotheicola* (GenBank KC145902; Identities = 575/598 (96 %), Gaps = 4/598 (0 %)) and *D. rhusicola* (GenBank JF951146; Identities = 553/576 (96 %), Gaps = 4/576 (0 %)). Closest hits using the TEF sequence had highest similarity to *D. neotheicola* (GenBank JQ809273; Identities = 390/460 (85 %), Gaps = 28/460 (6 %)), *D. oncostoma* (GenBank KC343888; Identities = 410/495 (83 %), Gaps = 22/495 (4 %)) and *D. vaccinii* (GenBank KC343954; Identities = 413/499 (83 %), Gaps = 23/499 (4 %)). Closest hits using the TUB sequence had highest similarity to *D. hickoriae* (GenBank KC344086; Identities = 645/690 (93 %), Gaps = 2/690 (0 %)), *D. stictica* (GenBank KC344180; Identities = 645/690 (93 %), Gaps = 3/690 (0 %)) and *D. foeniculacea* (GenBank KC344069; Identities = 640/691 (93 %), Gaps = 10/691 (1 %)).

## *Diaporthe psoraleae-pinnatae* Crous & M.J. Wingf., *sp. nov.*

*Etymology.* Named after the host from which it was collected, *Psoralea pinnata*.

On PNA. *Conidiomata* pycnidial, globose, up to 250 µm diam, black, erumpent, exuding creamy conidial droplets from central ostioles; walls of 3–6 layers of medium brown *textura angularis*. *Conidiophores* hyaline, smooth, 0–1-septate, unbranched, densely aggregated, cylindrical, straight to sinuous, 15–25 × 2.5–3.5 µm. *Conidiogenous cells* 8–15 × 2–3 µm, phialidic, cylindrical, terminal, with slight taper towards apex, 1–1.5 µm diam, with visible periclinal thickening; collarette slightly flared, up to 1 µm long when present. *Paraphyses* not observed. *Alpha conidia* aseptate, hyaline, smooth, guttulate, subcylindrical to fusoid-ellipsoid, tapering towards both ends, straight, apex obtuse, base subtruncate, (7–)9–10(–12) × (2–)2.5–3 µm. *Gamma conidia* not observed. *Beta conidia* not observed.

Culture characteristics — Colonies covering plates within 2 wk, spreading with sparse aerial mycelium. On MEA surface honey to buff, reverse honey with patches of cinnamon; on OA surface olivaceous-grey in centre, pale olivaceous-grey in outer region; on PDA honey on surface and reverse.

*Colour illustrations.* *Psoralea pinnata* dieback at Harold Porter National Botanical Garden, Betty's Bay, South Africa. Left column *Diaporthe psoraleae*: conidiomata on PNA; conidiogenous cells and alpha conidia. Right column *Diaporthe psoraleae-pinnatae*: conidioma on PNA; alpha conidia. Scale bars = 10 µm.

*Typus.* SOUTH AFRICA, Western Cape Province, Betty's Bay, Harold Porter National Botanical Garden, on stems of *Psoralea pinnata* (*Fabaceae*), 28 Oct. 2012, M.J. Wingfield (holotype CBS H-21423, culture ex-type CPC 21638, 21639 = CBS 136413, ITS sequence GenBank KF777159, LSU sequence GenBank KF777212, TUB sequence GenBank KF777252, MycoBank MB805823).

Notes — Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the LSU sequence are *Phaeocystostroma plurivorum* (GenBank FR748104; Identities = 880/884 (99 %), no gaps), *Diaporthe decedens* (GenBank AF408348; Identities = 874/878 (99 %), no gaps) and *Phomopsis viticola* (GenBank AF439635; Identities = 857/862 (99 %), no gaps). Closest hits using the ITS sequence had highest similarity to *D. helianthi* (GenBank AJ312349; Identities = 552/584 (95 %), Gaps = 13/584 (2 %)), *D. ambigua* (GenBank KC343010; Identities = 543/575 (94 %), Gaps = 11/575 (1 %)) and *Phomopsis limonii* (GenBank KC145856; Identities = 553/588 (94 %), Gaps = 11/588 (1 %)). Closest hits using the TUB sequence had highest similarity to *D. rhoina* (GenBank KC344157; Identities = 663/692 (96 %), Gaps = 2/692 (0 %)), *D. acerina* (GenBank KC343974; Identities = 639/706 (91 %), Gaps = 21/706 (2 %)) and *Diaporthe* cf. *nobilis* (GenBank KC344116; Identities = 636/703 (90 %), Gaps = 14/703 (1 %)).

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