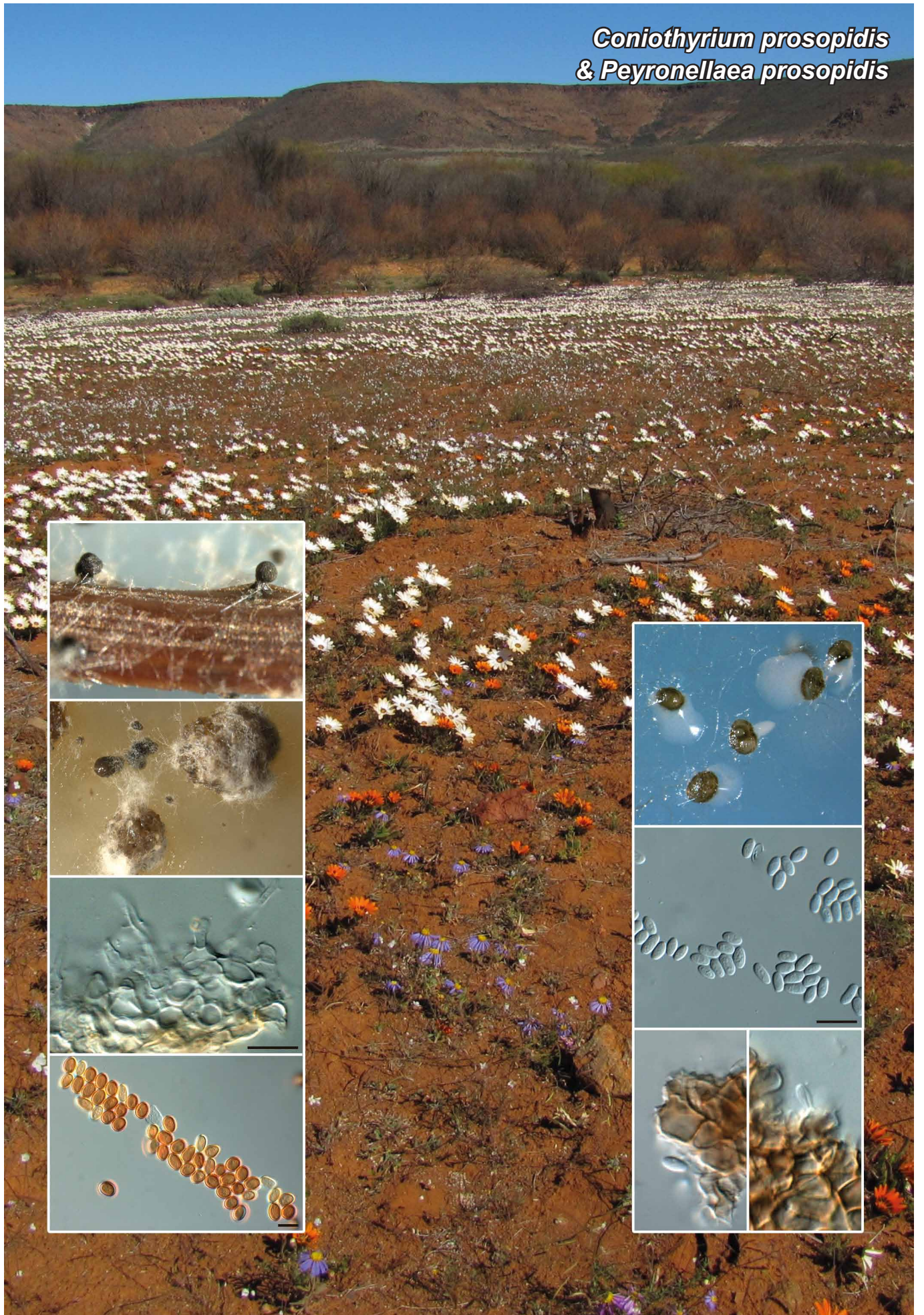


*Coniothyrium prosopidis*  
& *Peyronellaea prosopidis*





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## *Coniothyrium prosopidis* Crous & A.R. Wood, *sp. nov.*

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

*Conidiomata* immersed to erumpent, globose, up to 150 µm diam, brown with central ostiole, up to 80 µm diam; exuding a black conidial mass; wall of 3–6 layers of brown *textura angularis*. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* lining the inner cavity, ampulliform, hyaline, smooth, 5–8 × 4–5 µm; proliferating via periclinal thickening or with inconspicuous percurrent proliferation near apex. *Conidia* solitary, ellipsoid to globose, thin-walled but appearing thick-walled with age, brown, smooth, granular, (7–)8–9(–10) × (4–)5–6(–7) µm.

*Culture characteristics* — Colonies covering dish in 2 wk, with moderate to sparse aerial mycelium. On PDA surface and reverse olivaceous-grey; on OA surface iron-grey; on MEA surface olivaceous-grey, reverse iron-grey.

*Typus.* SOUTH AFRICA, Northern Cape Province, Calvinia, associated with a bark disease on *Prosopis* sp. (*Fabaceae*), Sept. 2012, A. Wood (holotype CBS H-21424, culture ex-type CPC 21699 = CBS 136415; additional collections studied, CPC 21701, 21703, 21705, 21708; ITS sequence GenBank KF777149–KF777153, LSU sequence GenBank KF777204–KF777206, MycoBank MB805824).

*Notes* — Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the LSU sequence of CPC 21699 are *Phoma aliena* (GenBank KC311486; Identities = 910/911 (99 %), no gaps), *Ascochyta pisi* (GenBank DQ678070; Identities = 910/911 (99 %), no gaps) and *Phoma negriana* (GenBank GU238117; Identities = 874/875 (99 %), no gaps). Closest hits using the ITS sequence of CPC 21699 had highest similarity to *Coniothyrium nitidae* (GenBank JN712453; Identities = 653/663 (98 %), Gaps = 1/663 (0 %)), *Microsphaeropsis proteae* (GenBank JN712497; Identities = 652/667 (98 %), Gaps = 6/667 (0 %)) and *Ascochyta pisi* var. *psii* (GenBank EU167557; Identities = 657/677 (97 %), Gaps = 7/677 (1 %)). *Coniothyrium prosopidis* is allied to *C. nitidae*, but neither belong to *Coniothyrium* s.str. (Aveskamp et al. 2010).

## *Peyronellaea prosopidis* Crous & A.R. Wood, *sp. nov.*

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

*Conidiomata* pycnidial, brown, immersed to superficial, globose, up to 200 µm diam, with 1–3 ostioles, 10–15 µm diam; wall of 3–5 layers of brown *textura angularis*. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* lining the inner cavity, hyaline, smooth, ampulliform to doliiform, 4–8 × 5–6 µm; apex with minute periclinal thickening. *Conidia* hyaline, smooth, granular, ellipsoid, aseptate, thin-walled, ends obtusely rounded, (5–)5.5–6(–7) × (2.5–)3(–3.5) µm. *Chlamydospores* intercalary on hyphae, arranged in chains, globose, brown, 5–9 µm diam.

*Culture characteristics* — Colonies covering dish in 2 wk, with moderate to fluffy aerial mycelium. On PDA surface and reverse iron-grey; on OA surface iron-grey with patches of pale olivaceous-grey due to fluffy aerial mycelium; on MEA surface pale olivaceous-grey with patches of olivaceous-grey, reverse iron-grey.

*Typus.* SOUTH AFRICA, Western Cape Province, Calvinia, associated with a stem disease of *Prosopis* sp. (*Fabaceae*), Sept. 2012, A. Wood (holotype CBS H-21425, culture ex-type CPC 21698 = CBS 136414, ITS sequence GenBank KF777180, LSU sequence GenBank KF777232, MycoBank MB805825); CPC 21704 = CBS 136550, ITS sequence GenBank KF777181, LSU sequence GenBank KF777233.

*Colour illustrations.* *Prosopis* sp. dieback in Calvinia, South Africa. Left column *Coniothyrium prosopidis*: conidiomata on PNA and PDA; conidiogenous cells, conidia. Right column *Peyronellaea prosopidis*: conidiomata on SNA; conidia and conidiogenous cells. Scale bars = 10 µm.

*Notes* — Several small-spored coelomycetes have in recent years been collected from *Prosopis*, some of which, like *Prosopidicola mexicana*, showed potential to be evaluated as biocontrol agent of this invasive weed (Lennox et al. 2004). Likewise *Peyronellaea prosopidis* was also isolated from stem lesions on *Prosopis*, although its potential as biocontrol agent has yet to be investigated.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the LSU sequences are *Phoma pedeiaae* (GenBank GU238127; Identities = 875/875 (100 %), no gaps), *Phoma dimorpha* (GenBank GU238068; Identities = 875/875 (100 %), no gaps) and *Peyronellaea coffeae-arabicae* (GenBank GU238006; Identities = 875/875 (100 %), no gaps). Closest hits using the ITS sequences had highest similarity to *Scytalidium acidophilum* (GenBank HQ213804; Identities = 500/500 (100 %), no gaps), *Phoma pomorum* (GenBank AY904062; Identities = 500/500 (100 %), no gaps) and *Phoma glomerata* (GenBank AY183371; Identities = 500/500 (100 %), no gaps). Based on a search with the ITS sequences in Q-Bank ([www.q-bank.eu](http://www.q-bank.eu)), the sequences were identical to diverse strains of *Peyronellaea pomorum* var. *pomorum* (Identities = 483/483 (100 %), no gaps).