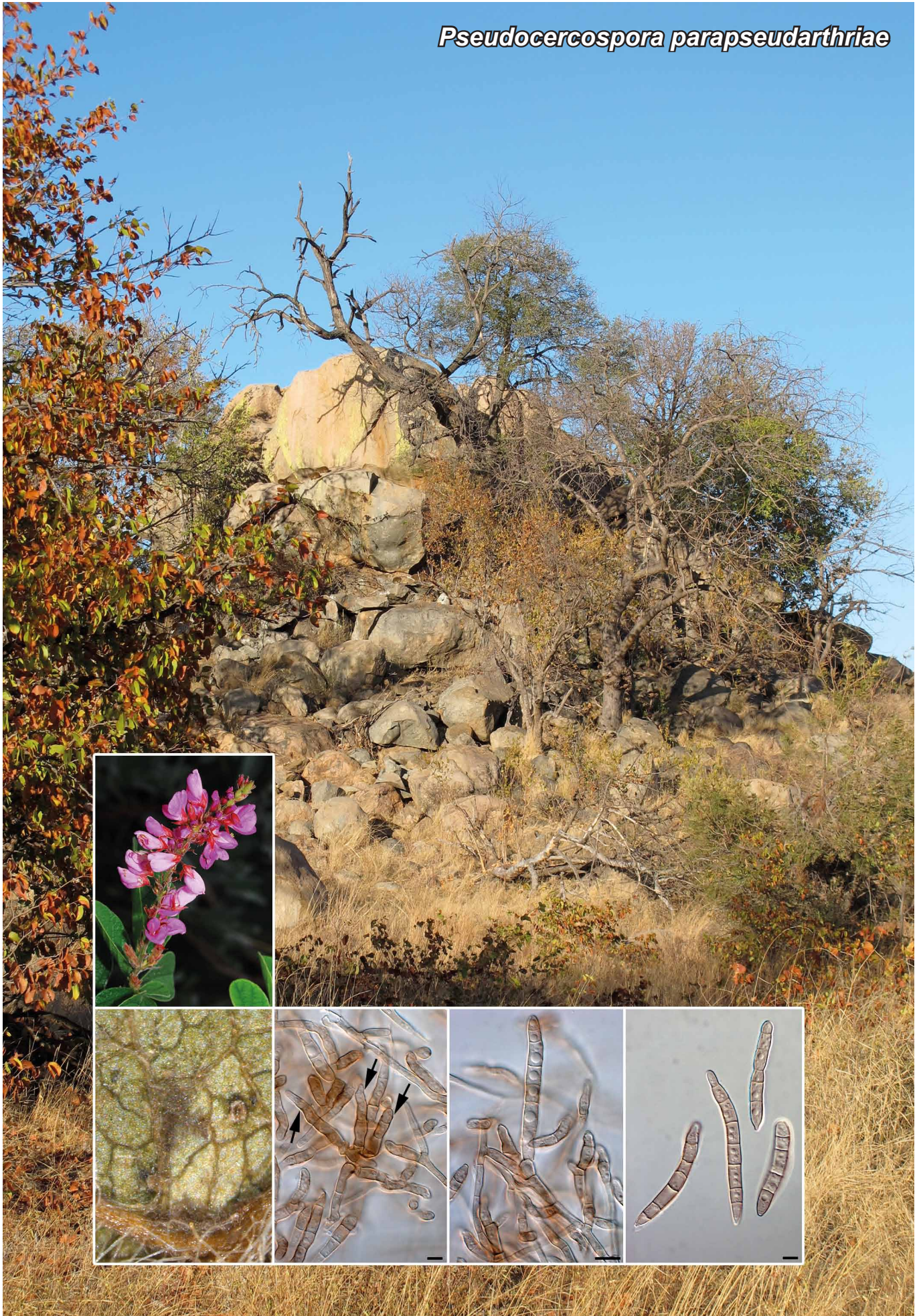


*Pseudocercospora parapseudarthriae*





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***Pseudocercospora parapseudarthriae* Crous & A.R. Wood, sp. nov.**

*Etymology.* Named for its morphological similarity to *Pseudocercospora pseudarthria*.

*Leaf spots* amphigenous, chlorotic yellow, becoming pale brown, subcircular to irregular, 1–10 mm diam with diffuse margins. Sporulation hypophyllous, frequently associated with raised leaf veins. *Mycelium* consisting of smooth, septate, branched, pale brown, 3–4 µm diam hyphae, giving rise to conidiophores. *Conidiophores* creeping, branching, up to 100 µm long, 4–5 µm diam. *Conidiogenous cells* terminal and lateral, subcylindrical to clavate, pale brown, smooth, guttulate, 10–20 × 4–5 µm, proliferating sympodially and percurrently near apex. *Conidia* pale to medium brown, guttulate, finely roughened, subcylindrical, apex bluntly rounded, basal cell tapering abruptly to a truncate base, 2 µm diam, not thickened nor darkened, 3–6-septate, (27–)40–60(–75) × (5–)6(–7) µm.

*Culture characteristics* — Colonies erumpent, spreading, with moderate aerial mycelium and smooth, lobate margins, reaching 20 mm diam after 2 wk at 22 °C. On PDA, OA and MEA surface olivaceous-grey in middle, iron-grey in outer region, and in reverse.

*Typus.* SOUTH AFRICA, KwaZulu-Natal, Hilton, Doreen Clarke Nature Reserve, S29°34' E30°17', on leaves of *Pseudarthria hookeri* (*Leguminosae*), 5 Mar. 2013, A.R. Wood (holotype of *P. parapseudarthriae* CBS H-21710, culture ex-type CPC 23449 = CBS 137996; ITS sequence GenBank KJ869151, LSU sequence GenBank KJ869208, ACT sequence GenBank KJ869229, TEF sequence GenBank KJ869238, MycoBank MB808933).

*Other specimens examined.* SOUTH AFRICA, Mpumalanga, Nelspruit, Schagen, on leaves of *Pseudarthria hookeri*, L.C.C. Liebenberg, 13 July 1936, PREM 32886. — SRI LANKA (CEYLON), Peradeniya, on *Pseudarthria vicida*, 20 Dec. 1913, T. Petch No. 4096, holotype of *P. pseudarthria* K (M).

*Colour illustrations.* Scenic outcrop in Mpumalanga, South Africa; plant host, conidiophore fascicles on leaves, conidiophores and conidia in vivo. Scale bars = 10 µm.

*Notes* — Crous & Braun (1996) provided a description based on the type specimen of *P. pseudarthria* (on *Pseudarthria vicida*, Sri Lanka) and concluded that it was the same fungus as observed in South Africa on *Pseudarthria hookeri*. The fresh collection obtained here allowed us to again re-examine these collections, and led to the conclusion that although similar, the collections on *P. hookeri* represent a different taxon with longer conidiophores and conidia.

*ITS.* Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the ITS sequence are *Pseudocercospora schizolobii* (GenBank DQ885903; Identities = 535/537 (99 %), no gaps), *Pseudocercospora cydoniae* (GenBank EF535716; Identities = 503/505 (99 %), Gaps = 1/505 (0 %)) and *Pseudocercospora flavomarginata* (GenBank GU269799; Identities = 498/500 (99 %), no gaps).

*LSU.* Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the ITS sequence are *Pseudocercospora timorensis* (GenBank KC677937; Identities = 811/811 (100 %), no gaps), *Pseudocercospora mombin* (GenBank KC677935; Identities = 811/811 (100 %), no gaps) and *Pseudocercospora jahnii* (GenBank KC677933; Identities = 811/811 (100 %), no gaps).

*ACT.* Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the ACT sequence are *Pseudocercospora madagascariensis* (GenBank JX902140; Identities = 531/537 (99 %), no gaps), *Pseudocercospora cruenta* (GenBank JQ325012; Identities = 580/588 (99 %), no gaps) and *Pseudocercospora cercidis-chinensis* (GenBank JX902131; Identities = 529/537 (98 %), no gaps).

*TEF.* Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the TEF sequence are *Pseudocercospora variicolor* (GenBank GU384538; Identities = 299/313 (96 %), no gaps), *Pseudocercospora ravenalicola* (GenBank GU384521; Identities = 295/314 (94 %), no gaps) and *Pseudocercospora lonicericola* (GenBank JQ324999; Identities = 476/508 (94 %), Gaps = 3/508 (0 %)).