Pseudocercospora parapseudarthriae
**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. Conidial pales 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, (27–)40–60(–75) × 2 µm diam, not thickened nor darkened, 3–6-septate, 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.

Notes — Crous & Braun (1996) provided a description based on the type specimen of *P. pseudarthria* (on *Pseudarthria vidica*, 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 schizolori* (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 cercid-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 varicolor* (GenBank GU384538; Identities = 299/313 (96 %), no gaps), *Pseudocercospora ravenalica* (GenBank GU384521; Identities = 295/314 (94 %), no gaps) and *Pseudocercospora ionicericola* (GenBank JQ324999; Identities = 476/508 (94 %), Gaps = 3/508 (0 %)).