Diaporthe polincianellae
Diaporthe poincianellae T.G.L Oliveira, O.M.C. Magalhães & J.D.P. Bezerra, sp. nov.

Etymology. Name refers to Poiicinanella, the host plant genus from which it was isolated.

Classification — Diaporthaceae, Diaphathales, Sordariomycetes.

Conidiomata pycnidial in culture, globose to subglobose with thin wall, solitary or aggregated, dark brown to black, (212–)265–350 × (180–)265–318 μm, with cream to yellowish conidial drops exuding from the ostioles. Conidiogenous cells phialidic, hyaline, occasionally branched, straight to sinuous, slightly tapering towards the apex and slightly curved, 10.5–12.5 × 2–2.2 μm. Alpha conidia aseptate, hyaline, smooth, guttulate, fusoid to ellipsoidal, slightly tapered towards the rounded end, truncated base, 5.5–7.5(–8.5) × 3–3.5 μm. Beta conidia not observed. Sexual morph not observed.

Culture characteristics — On PDA at 25 °C in darkness, 8 cm diam after 15 d, colony initially white greyish, becoming yellowish, fluffy and whitish aerial mycelium. Reverse dark brown to black. Pycnidia forming after 15 d. On MEA at 25 °C in darkness, colony initially white to greyish, becoming yellowish, fluffy and whitish aerial mycelium, with slow growth reaching 5.5 cm diam after 15 d. Reverse dark brown to black with small whitish parts. Pycnidia forming after 15 d.

Type. Brazil, Paraíba state, Santa Teresinha, Tamanduá farm (S07°1.524’35.46”/W37°41.27’02.70”), as endophyte from branches of Poiicinanella pyramidalis (Fabaceae), May 2013, J.D.P. Bezerra (holotype URM 19176, culture ex-type URM 7932, ITS, LSU, CaM, his3, tef1-α and tub2 sequences GenBank MH989509, MH989513, MH989540, MH989539, MH989538 and MH989537, MycoBank M5827977).

Notes — The genus Diaporthe has been extensively reviewed and several new species have been included in it (Marin-Felix et al. 2019). BLASTn searches using ITS sequence of Diaporthe poincianellae demonstrated 99 % similarity to D. velutina (GenBank NR_152470.1), amongst others. The LSU sequence is 99 % similar to D. phragmitis (GenBank MH878644.1), amongst others. The CaM sequence has 93 % similarity to D. anacardii (GenBank KC343266.1). The his3 sequence is 94 % similar to D. inconspicua and D. pseudoinconspicua (e.g., GenBank KC343607.1 and MH122517.1). Based on the tef1 sequence D. poincianellae is 88 % similarity to D. velutina (GenBank KX999178.1), and based on tub2 sequence it is 95 % similar to D. cissampeli (GenBank KX228384.1). Morphologically, D. poincianellae differs from D. velutina based on the size of pycnidia (69–428 μm diam), conidiomata (10–23 × 1–2.5 μm), alpha conidia sometimes clavate (5.5–10 × 2–2.5 μm) and by the presence of beta conidia (Gao et al. 2017). Furthermore, D. poincianellae also differs from D. cissampeli by the size of its pycnidia (up to 200 μm diam), conidiogenous cells phialidic (10–15 × 1–2 μm) and alpha conidia subcylindrical (7.5–12 × 2–3 μm) (Crous et al. 2016b).

Bayesian inference tree obtained by a phylogenetic analysis of the combined ITS rDNA, tef1-α and tub2 sequences conducted in MrBayes on XSEDE in the CIPRES science gateway (Miller et al. 2010). The substitution model K80+I+G was used for ITS and HKY+G for tef1-α and tub2 alignments. Bayesian posterior probability values are indicated at the nodes. The new species is indicated in bold face. Diaporthella corylina (CBS 121124) was used as outgroup.

Colour illustrations. Brazilian tropical dry forest; conidiomata pycnidial; alpha conidiophores and conidia. Scale bars = 10 μm.