

*Pseudophialophora sorghi*



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***Pseudophialophora sorghi*** R.J.V. Oliveira, C.M. Gonç., G.A. Silva & J.L. Bezerra,  
*sp. nov.*

*Etymology.* Name refers to the host plant, *Sorghum bicolor*, from which this fungus was isolated as endophyte.

*Classification* — *Magnaporthaceae*, *Magnaporthales*, *Sordariomycetes*.

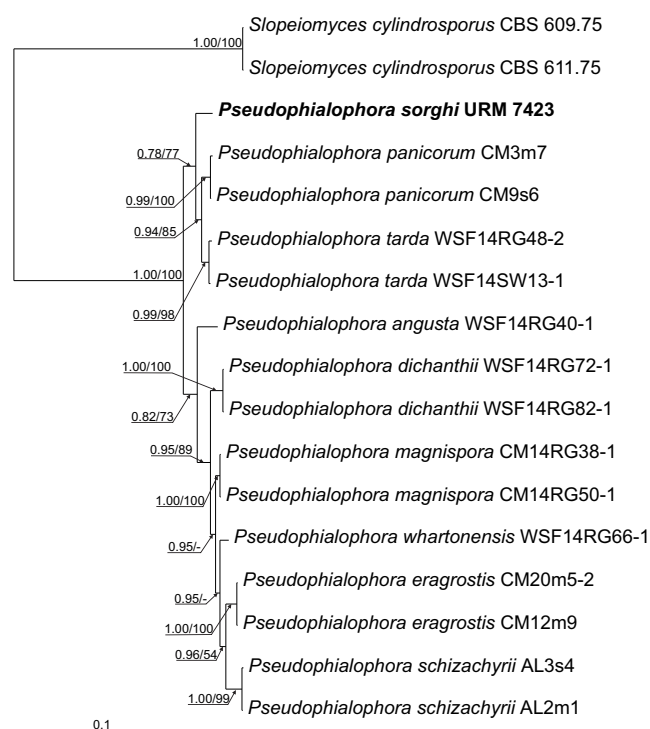
*Hyphae* hyaline, septate, branched, sometimes forming sterile coils. *Conidiophores* micronematous, simple or branched, hyaline, septate, non-constricted, cylindrical, straight to flexuous, apex attenuated, base not inflated. *Conidiogenous cells* polyphialidic, hyaline, simple or branched, attenuated, 4–22 × 3.5 µm. *Chlamydospores* intercalary, globose to subglobose. *Anastomosis* sometimes observed between conidiogenous cells and between conidia. *Conidia* aggregated in slimy heads, oblong ellipsoidal to ellipsoidal, aseptate, hyaline, smooth, 5–8.5 × 2–3 µm.

*Culture characteristics* — Colonies on PDA growing up to 1.2 cm diam after 7 d in the dark at 25 °C, dark grey, surface pale grey, aerial mycelia whitish to pale grey, reverse dark grey.

*Typus.* BRAZIL, Pernambuco, Serra Talhada (S07°59'00" W38°19'16"), as endophyte in roots of *Sorghum bicolor* (*Poaceae*), Dec. 2014, R.J.V. Oliveira (holotype as metabolically inactive culture, URM 7423, ITS, LSU, *rpb1* and *tef1* sequences GenBank KY421938, KY421941, KY421944 and KY421942, MycoBank MB819580).

*Notes* — The phylogenetic analyses of the four-gene dataset (*tef1*, *rpb1*, ITS and LSU rDNA) showed that *Pseudophialophora sorghi* formed a distinct clade with other species of *Pseudophialophora* with high support values. On ITS *P. sorghi* is 96 % (456/474) similar to *P. panicorum* (strain CM3m7, GenBank KF689652) and 96 % (443/463) to *P. tarda* (strain WSF14RG48-2, GenBank KP769840). The LSU sequence is 99 % (564/568) similar to *P. panicorum* (strain CM3m7, GenBank KF689642) and 99 % (566/568) to *P. tarda* (strain WSF14RG48-2, GenBank KP769832). The *rpb1* sequence is 99 % (602/608) similar to *P. panicorum* (strain CM9s6, GenBank KF689621) and 99 % (603/608) to *P. tarda* (strain WSF14RG48-2, GenBank KP784823). The *tef1* sequence is 99 % (884/893) similar to *P. panicorum* (strain CM3m7, GenBank KF689632) and 99 % (883/893) to *P. tarda* (strain WSF14SW13-1, GenBank KP784830). In the phylogenetic analysis *P. sorghi* is nearest to *P. panicorum* and *P. tarda*. However, colonies of *P. sorghi* are dark grey while *P. tarda* presents colonies yellowish and *P. panicorum* presents colonies yellow-green. Furthermore, conidia of *P. sorghi* (5–8.5 × 2–3 µm) are slightly smaller than conidia of *P. tarda* (7.5–9.5 × 2.5–3.5 µm) and conidia of *P. panicorum* (7.5–11.5 × 3.5–5 µm) (Luo et al. 2014, 2015). Anastomosis between conidiogenous cells and between conidia of *P. sorghi* were sometimes observed. This has never been reported in any species of *Pseudophialophora*.

*Colour illustrations.* *Sorghum bicolor* in the Instituto Agronômico de Pernambuco, Serra Talhada, Brazil; conidiophores; conidia, chlamydospores, sterile coils, anastomosis between conidiogenous cells, conidia and between hyphae. Scale bars = 20 µm.



Phylogenetic tree of the *Pseudophialophora* constructed using concatenated *tef1*, *rpb1*, ITS and LSU sequences. *Slopeiomyces cylindrosporus* (CBS 609.75 and CBS 611.75) was used as outgroup. Support values are from Bayesian inference and Maximum Likelihood (ML) analyses, respectively. The new species is in **bold** face. Support values of at least 50 % are shown at nodes.

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