Spegazzinia bromeliacearum
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**Spegazzinia bromeliacearum** S.S. Nascimento & J.D.P. Bezerra, *sp. nov.*

*Etymology.* The name refers to the host plant family, Bromeliaceae.

*Classification.* — Didymosphaeriaceae, Pleosporales, Dothideomycetes.

*Hyphae.* Hyaline when young and becoming brown to dark brown with age, smooth to slightly verruculose, 2–3 μm wide. *Conidio- phores* straight or flexuous, smooth to slightly verruculose, pale brown, 0(–2)-septate, 17–32 × 2–3 μm. *Conidiogenous cells* monoblastic, ampulliform, smooth to slightly verruculose, (6.5–)7–8.5(–14) × (3–)4–5 μm. *Conidia* globose, initially hyaline to pale brown, becoming brown to dark brown with age, 4-celled, crossed-septate, (7.5–)11.5–19(–26.5) μm diam excluding the spines; old conidia conspicuously spinulate, with spines measuring up to 5 μm long, globose, (21–)26.5–28(–30.5) μm diam. *Fertile coils* observed.

*Culture characteristics.*—Colonies at 25 °C for 7 d in darkness. On PDA, colonies reaching 5 cm diam, flat, lightly velvety, surface smooth, olivaceous and reverse olivaceous to black, with whitish margins. On MEA, colonies growing up to 6 cm diam, greenish smooth, with whitish margins, flat, velvety, moderately dense, reverse brownish olivaceous to black. Conidia forming before 7 d.

*Typus.* Brazil, Pernambuco state, Buíque, Catimbau National Park (58°36'35" W37°14'40"), as endophyte from leaves of *Tilandsia catimbauensis* (Bromeliaceae), June 2015, K.T.L.S. Freire (holotype URM 93059, culture ex-type URM 8084, ITS and LSU sequences GenBank MK804501 and MK809513, MycoBank MB830761).

*Notes.* — The genus *Spegazzinia* was introduced by Saccardo (1880) and currently 27 records are listed in Index Fungorum and MycoBank (Feb. 2019). BLASTn searches using the *ITS* rDNA sequence from *S. bromeliacearum* demonstrated 92.41 % identity to *S. intermedia* (CBS 249.89, GenBank MH862171.1) and 88.52 % to *S. tessarthra* (MFLUCC 17-2249, GenBank MH071193.1), amongst others. The *LSU* rDNA sequence is 99.23 % identical to *Spegazzinia* sp. isolated as endophyte from *Camellia sinensis* var. *assamica* in Thailand (CMU328, GenBank MH734521.1) and 98.07 % to *S. intermedia* (CBS 249.89, GenBank MH873861.1). Morphologically, *S. bromeliacearum* resembles *S. intermedia*, but differs from it by the size of its conidiophores (up to 30 μm long and 1–4 μm wide) and conidia (18–28 μm diam) (Ellis 1976). The production of fertile coils in *S. bromeliacearum* has never been reported in any species of *Spegazzinia*.

Bayesian inference tree obtained by a phylogenetic analysis of the combined ITS and LSU rDNA sequences conducted in MrBayes on XSEDE in the CIPRES science gateway (Miller et al. 2010). The substitution model GTR+I+G was used for ITS and LSU alignments. Bayesian posterior probability values are indicated at the nodes. The new species is indicated in bold. Verrucoconiothyrium nitidae (CPC 25373) was used as outgroup.

Sandy S. Nascimento, Karla T.L.S. Freire, Thays G.L. Oliveira, Laura M. Paiva & Jadson D.P. Bezerra, Departamento de Micologia, Universidade Federal de Pernambuco, Recife, Brazil; e-mail: nascsandy@outlook.com, kkfreira@hotmail.com, thays.gabilins@hotmail.com, mesquitapaiva@terra.com.br & jadsondpb@gmail.com

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