

*Achaetomium lippiae*



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***Achaetomium lippiae*** M.G. Viana, C.C. Albuquerque, E.S. Santos, J.D.P. Bezerra & L.M. Paiva, *sp. nov.*

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

*Classification* — *Chaetomiaceae*, *Sordariales*, *Sordariomycetes*.

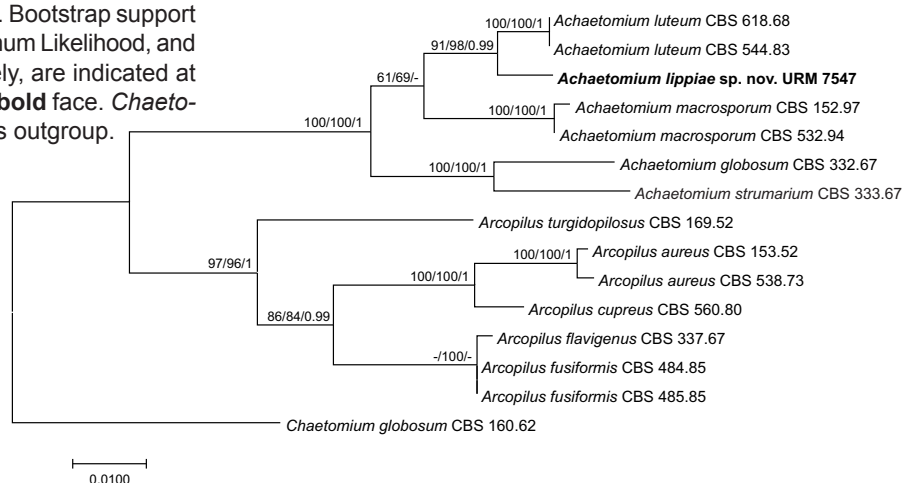
*Mycelium* subhyaline, septate, 2–3 µm wide hyphae. *Ascomata* superficial and immersed, solitary or gregarious, ostiolate, brown to dark brown, globose to subglobose, 122–160(–256) × 101.5–143(–212) µm. *Ascomatal wall* brown, *textura intricata* or *epidermoidea* in surface view. *Terminal* or *lateral hairs* not observed. *Asci* fasciculate, cylindrical to subcylindrical, 8-spored, soon evanescent, 35–60 × 8–9.5 µm, short-stipitate, without apical structures. *Paraphyses* and *periphyses* not observed. *Ascospores* 1-celled, brown to dark brown, limoniform, 10–16 × 5.5–6.5(–8) µm. *Chlamydospores* brown, globose to subglobose, terminal and intercalary, 10.5–14.5 × 8 µm. *Asexual morph* not observed.

*Culture characteristics* — Colonies covering Petri dishes after 2 wk at 25 °C. On PDA, colonies with cream to yellowish floccose aerial mycelium, reverse yellowish with centre pale brown. On MEA, colonies are similar to PDA with reverse yellowish to amber. On WA, colonies with sparse growth and whitish mycelium, reverse uncoloured.

*Typus.* BRAZIL, Rio Grande do Norte state, Mossoró municipality, Universidade do Estado do Rio Grande do Norte (S5°22'43.85" W37°30'12.25"), as endophyte from *Lippia gracilis* (*Verbenaceae*), Mar. 2015, M.G. Viana (holotype URM 90067, culture ex-type URM 7547, ITS, LSU and *BenA* sequences GenBank KY855413, KY855414 and KY855412, MycoBank MB820711).

*Notes* — According to morphological features and phylogenetic inferences, Wang et al. (2016a, b) demonstrated that *Achaetomium* is a monophyletic lineage in the family *Chaetomiaceae*. Based on our phylogenetic analyses using concatenated ITS, *BenA* and LSU sequences, *A. lippiae* is closely related to *A. luteum*. Based on a megablast search in GenBank, the ITS sequence of *A. lippiae* has 98 % (525/535) similarity to *A. luteum* (CBS 618.68; GenBank KX976571.1), 96 % (519/541) similarity to *A. macrosporum* (CBS 152.97; GenBank KX976573.1), and 95 % (519/541) similarity to *A. strumarium* (CBS 333.67; GenBank NR\_144811.1), amongst others. On its LSU sequence, *A. lippiae* is 99 % (792/797) similar to *A. strumarium* (CBS 333.67; GenBank AY681170.1), amongst others. The *BenA* sequence has 95 % (400/423) similarity to *A. luteum* (CBS 618.68; GenBank KX976912.1), 89 % (377/423) similarity to *A. macrosporum* (CBS 152.97; GenBank KX976914.1) and 86 % (420/487) similarity to *A. strumarium* (CBS 333.67; GenBank AY681238.1). Morphologically, *A. lippiae* is different from *A. strumarium* in size of the ascomata ((120–)160–300 µm diam vs 122–159(–256) µm diam in *A. lippiae*), number of ascomatal hairs (3 µm vs absent in *A. lippiae*), size of asci (48–78 × 7–11 µm vs 35–60 × 8–9.5 µm in *A. lippiae*) and ascospores ((10–)11–13(–13.5) × 6–7.5 µm vs 10–16 × 5.5–6.5(–8) µm in *A. lippiae*), and presence of chlamydospores (absent vs present in *A. lippiae*) (Cannon 1986). *Achaetomium lippiae* also differ from *A. luteum* in ascomata size (116.2–182.6 × 99.6–157.7 µm), asci (37–40.7 µm) and ascospores (8.8–10.3 × 3.7–6.6 µm) (Rai et al. 1964); and from *A. macrosporum* in ascomata size (140–290 × 110–210 µm), asci (55–80 × 12–19 µm) and ascospores (16.5–21.5 × 10–13.5 µm) (Cannon 1986).

Maximum likelihood tree obtained by phylogenetic analyses of the combined ITS and LSU rDNA and *BenA* sequences was conducted in MEGA v. 7 (Kumar et al. 2016). Bootstrap support values from Maximum Parsimony and Maximum Likelihood, and Bayesian posterior probabilities, respectively, are indicated at the nodes. The new species is indicated in **bold face**. *Chaetomium globosum* (CBS 160.62) was used as outgroup.



*Colour illustrations.* *Lippia gracilis* in the Universidade do Estado do Rio Grande do Norte. Ascomata, ascomatal wall, ascus, ascospores, and chlamydospore. Scale bars = 25 µm and 10 µm, respectively.

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