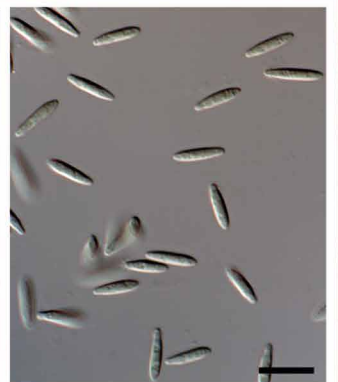
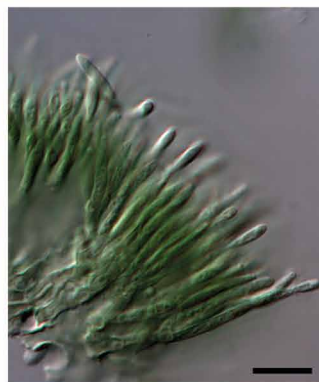
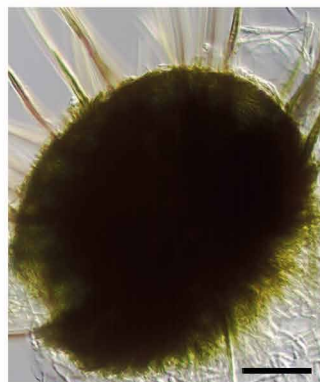
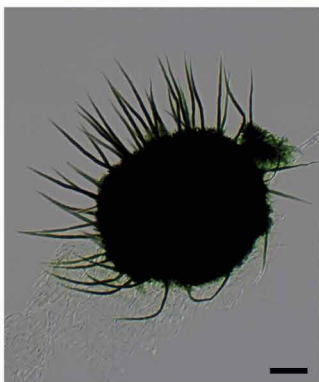


Alfaria dactylis



Fungal Planet 717 – 13 July 2018

***Alfaria dactylis* Valenz.-Lopez, Cano, Guarro & Stchigel, sp. nov.**

Etymology. From Latin *dactylus*, date, due to the nature of the substrate (date, the fruit of *Phoenix dactylifera*) from which the fungus was isolated.

Classification — *Stachybotryaceae*, *Hypocreales*, *Sordariomycetes*.

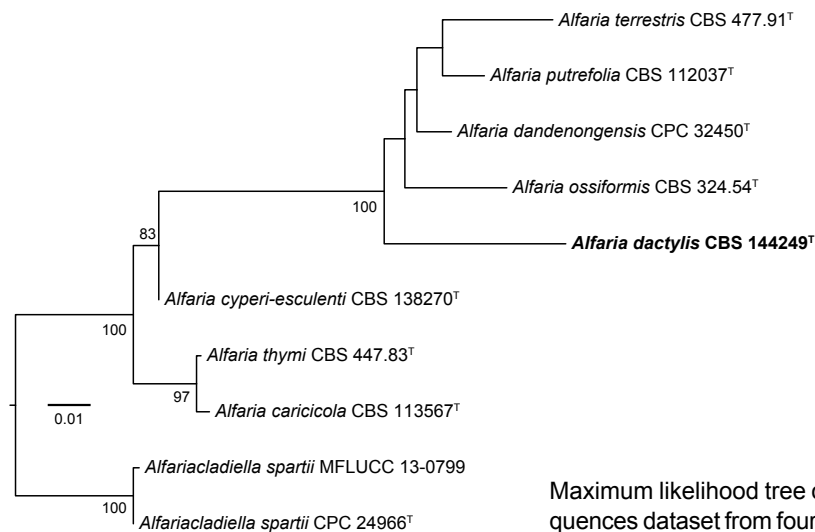
Hyphae hyaline to pale green, smooth- and thin- to thick-walled, septate, 2.5–5 µm wide. **Conidiomata** discrete, cupulate, stromatic, unilocular, non-ostiolate, superficial, solitary or confluent, greenish black, covered by setae, broadly lenticular, 177–275 × 133–242 µm, filled with black mass of slimy conidia; **conidioma wall** 10–27 µm broad, pseudoparenchymatous, of *textura globulosa* and *textura angularis*, composed of 2–4 layers of pale green to dark green, globose to flattened polygonal cells of 5–7.5 µm diam; **setae** greenish black, smooth- and thick-walled, multi-septate, unbranched, straight, narrowing towards the acute apices, 60–200 µm long, 4–8 µm wide at the base. **Conidiophores** densely aggregated, arising from the basal part of the locule, unbranched or branched at the base with 2–4 supporting cells, pale green, smooth-walled, up to 47 µm long, bearing 1–3 conidiogenous cells. **Conidiogenous cells** phialidic, cylindrical, elongate, hyaline to pale green, smooth-walled, 7–16 × 1.5–2.5 µm. **Conidia** hyaline to pale green, aseptate, smooth- and thin-walled, guttulate, lanceolate, 8.5–11.5 × 2–2.5 µm, with an obtuse apex and truncate at the base.

Culture characteristics — Colonies on OA reaching 19–21 mm diam after 7 d at 25 ± 1 °C, margin regular, flattened, with sparse aerial mycelium, surface white (M. 4A1); reverse white (M. 4A1). Colonies on MEA reaching 18–20 mm diam after 7 d at 25 ± 1 °C, margin regular, flattened, covered by dense white felty aerial mycelia, surface white (M. 4A1) to pale yellow (M. 4A3); reverse white (M. 4A1) to yellowish orange (M. 4A6). NaOH test negative.

Typus. SPAIN, Tarragona, from palm fruit of *Phoenix dactylifera* (*Areaceae*), Feb. 2017, coll. I.A. Iturrieta-González, isol. N. Valenzuela-Lopez (holotype CBS H-23398, cultures ex-type FMR 16398 = CBS 144249, ITS, LSU, *tub2* and *tef-1α* sequences GenBank LT984556, LT984557, LT984555 and LT984553, MycoBank MB824149).

Notes — *Alfaria dactylis* is characterised by the production of large, lanceolate, pale green conidia and discrete, cupulate, stromatic conidiomata covered by abundant setae, being morphologically similar to *A. dandenongensis* but differing in aspect of their conidia (cylindrical, granular and verruculose in *A. dandenongensis*) and setae (smooth-walled in *A. dactylis* vs verruculose in *A. dandenongensis*) (Crous et al. 2017). Despite the fact of *A. dactylis* is phylogenetically closely related to *A. ossiformis*, it is morphologically distinct from the latter species by its setose conidiomata (lacking of setae in *A. ossiformis*) (Lombard et al. 2016).

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hit using the LSU sequence is *A. ossiformis* CBS 324.54 (GenBank KU845993; Identities = 810/810 (100 %), no gaps). Closest hits using the ITS sequence are *A. putrefolia* CBS 112037 (GenBank KU845985; Identities = 533/544 (98 %), 6 gaps (1 %)) and *A. ossiformis* CBS 324.54 (GenBank NR_145068; Identities = 534/547 (98 %), 7 gaps (1 %)). The closest hits using the *tub2* sequence are *C. terrestris* CBS 477.91 (GenBank KU846019; Identities = 288/308 (94 %), 4 gaps (1 %)) and *C. putrefolia* CBS 112038 (GenBank KU846017; Identities = 285/307 (93 %), 2 gaps (0 %)). The closest hits using the *tef-1α* sequence are *A. terrestris* CBS 127305 (GenBank KU846012; Identities = 315/362 (87 %), 14 gaps (3 %)) and *A. ossiformis* CBS 324.54 (GenBank KU846009; Identities = 313/360 (87 %), 17 gaps (4 %)).



Colour illustrations. Tarragona, Spain; colony on MEA and OA after 14 d at 25 ± 1 °C; conidiomata under the stereomicroscope; cupulate stromatic conidiomata, conidiophores, conidiogenous cells and conidia. Scale bars = 50 µm (conidiomata), 10 µm (conidiophores and conidia).

Maximum likelihood tree obtained from the combined DNA sequences dataset from four loci (ITS, LSU, *tef-1α* and *tub2*) of our isolate and sequences retrieved from the GenBank database. Ex-type strains of the different species are indicated with ^T. The new species proposed in this study is indicated in **bold**. The RAxML v. 8.2.10 (Stamatakis 2014) bootstrap support values (≥ 70 %) are provided at the nodes. *Alfariacладиella spartii* CPC 24966 and MFLUCC 13-0799 were used as outgroup.

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