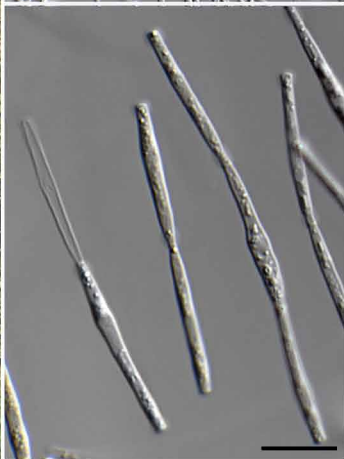
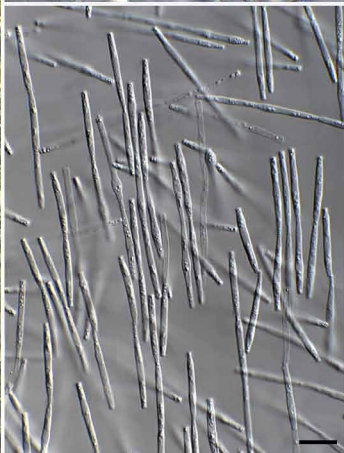


Yuccamyces citri



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Yuccamyces citri Crous, *sp. nov.*

Etymology. Name refers to *Citrus*, the host genus from which this fungus was collected.

Classification — *Incertae sedis*, *Patellariales*, *Dothideomycetes*.

Conidiophores erect, aggregated in penicillate tufts, forming upright sporodochia, hyaline, smooth, individually hyaline, but sporodochia distinctly pink in colour; conidiophores subcylindrical, septate, branched, up to 150 µm tall, 3–6-septate, 3–4 µm diam. *Conidiogenous cells* terminal and intercalary, subcylindrical, smooth, 15–25 × 2.5–3 µm, proliferating sympodially at apex. *Conidia* in slimy, branched chains, hyaline, smooth, guttulate, subcylindrical but widest in middle of each cell, and with characteristic taper toward septum, 1–2-septate, individual cells 15–20 × 2–3 µm, 1-septate, conidia 32–45 µm long, 2-septate conidia 55–65 µm long; conidia anastomosing with age.

Culture characteristics — Colonies flat, spreading, with sparse aerial mycelium and feathery margins, reaching 50 mm diam after 1 mo at 25 °C. On MEA, PDA and OA surface chestnut, reverse fuscous black.

Typus. ITALY, Catania, Mascali, on leaf litter of *Citrus limon* (*Rutaceae*), 30 Jan. 2016, V. Guarnaccia (holotype CBS H-23280, culture ex-type CPC 30046 = CBS 143161, ITS and LSU sequences GenBank MG386043 and MG386096, MycoBank MB823390).

Notes — *Yuccamyces citri* is very similar to the type of the genus, *Y. purpureus* (on *Flacourtia indica*, India; colonies become pinkish purple due to the accumulation of conidia; Dyko & Sutton 1979). In *Y. citri*, sporodochia also turn pink at maturity (similar to that of the type), but conidia are shorter and wider (55–65 × 2–3 µm) than those of *Y. purpureus* (46–72 × 1.5–2 µm). Dyko & Sutton (1979) speculated that the genus is a basidiomycete, but *Yuccamyces* is related to *Hysteropatella* (*Patellariaceae*).

Based on a megablast search using the ITS sequence, the closest matches in NCBI's GenBank nucleotide database were *Yuccamyces pilosus* (GenBank MG386044; Identities 685/789 (87 %), 51 gaps (6 %)), *Neodactylaria obpyriformis* (GenBank LT839090; Identities 334/386 (87 %), 13 gaps (3 %)), *Neoscytalidium dimidiatum* (GenBank FM211429; Identities 478/595 (80 %), 45 gaps (7 %)) and *Neofusicoccum mediterraneum* (GenBank GU799463; Identities 401/483 (83 %), 32 gaps (6 %)). The highest similarities using the LSU sequence were *Yuccamyces pilosus* (GenBank MG386097; Identities 813/853 (95 %), 3 gaps (0 %)), *Hysteropatella elliptica* (GenBank KM220948; Identities 805/853 (94 %), 3 gaps (0 %)), *Hysteropatella prostii* (GenBank KT876980; Identities 805/853 (94 %), 3 gaps (0 %)) and *Hysteropatella clavisporea* (GenBank AY541493; Identities 805/853 (94 %), 3 gaps (0 %)).

Colour illustrations. *Citrus limon* tree growing in Italy; conidiomata sporulating on PDA, conidiophores and conidia. Scale bars = 10 µm.