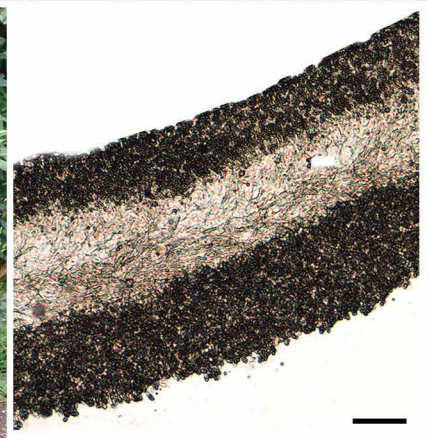


*Saproamanita quitensis*

Fungal Planet 749 – 13 July 2018

***Saproamanita quitensis*** E. Caicedo, A. Barili, C.W. Barnes & Ordoñez, *sp. nov.*

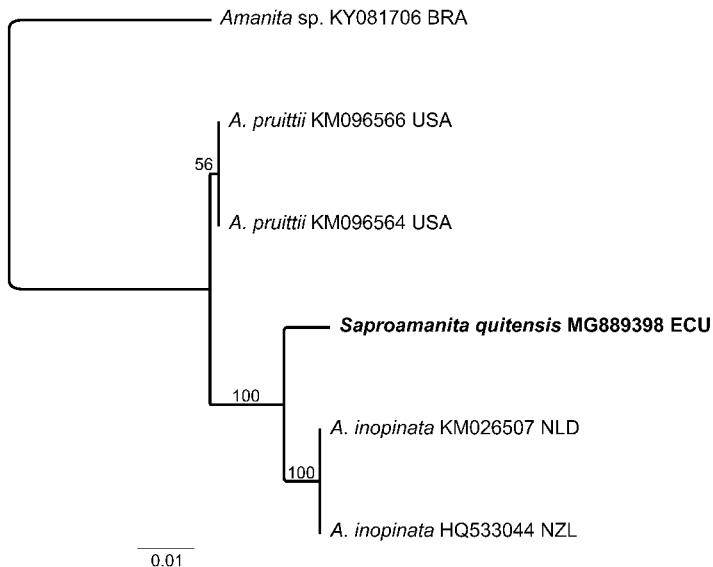
*Etymology.* Named reflects the locality where the species was collected.

*Classification* — *Amanitaceae*, *Agaricales*, *Agaricomycetes*.

*Basidiomata* small to medium size, pileus 90 mm diam, broadly convex, whitish, warts on the surface, margin whole, slightly revolute, rimose, thick texture, fleshy. *Warts* thick, dense, hard, scale-shaped, persistent, bigger and thicker towards the centre, pointy. Towards the margin warts thinner and truncated, from whitish to cream until dark brown on the tips, tending to get darker. *Lamellae* free, tall, ventricose, crowded, white with cream tones, slightly wavy margin and very finely serrate. *Stipe* 60 × 30 mm, short, thick, cylindrical with a slight wider base, white, smooth. *Annulus* remnant adhered, cream colour, disappears during drying process. *Volva* dissociated with reddish brown pearls. *Odour* not distinctive when fresh, strong fungal odour when dry. *Pileipellis* pseudocutis. *Lamellar trama* bilateral, divergent, with mostly clavate hyphae 9–14 µm wide, septate, thin cell wall, occasionally little differentiated filamentous hyphae. *Caulocutis* with acrophysalids, clavate hyphae with longitudinal clamp connections. *Veil trama* predominance of filamentous hyphae, ellipsoid and pyriform hyphae less abundant. *Basidia* 34–52.5 × 8–13.5 µm, four sterigmata, sometimes two, 3 µm long. Clamp connections occasionally present at the base. *Basidiospores* 6–12 × 6.5–9.5 µm, globose or rarely subglobose, apiculate, hyaline, thin cell wall or slightly thickened, amyloid, acyanophilic, non-metachromatic, Q = 1.04.

*Habitat* — Solitary, on the ground near *Polylepis racemosa* in an urban park.

*Typus.* ECUADOR, Pichincha province, Itchimbia Metropolitan Park, alt. 2882 m, Jan. 2017, E. Caicedo (holotype QCAM7047, ITS-LSU sequence GenBank MG889398, MycoBank MB824231, TreeBASE Submission ID 22306).



*Colour illustrations.* Ecuador, Itchimbia Metropolitan Park; close-up of basidiocarp; basidiocarp next to *Polylepis racemosa*; lamellar trama. Scale bar = 100 µm.

*Notes* — Phylogenetically, *Saproamanita quitensis* is distinct from other *Amanita* spp. available in the NCBI GenBank nucleotide database. The closest species based on a megablast search of the full ITS sequence is *Amanita inopinata*, currently *Saproamanita inopinata*, from the Netherlands (GenBank KM026507) and from New Zealand (GenBank HQ533044) both with 100 % coverage and a 97 % Identity score from 18 base differences and 9 gaps. Only one other species, *A. pruitii*, currently *Saproamanita pruitii* (Redhead et al. 2016), had 100 % coverage for the full ITS sequence in the megablast search, with a 96 % Identity score from 24 base differences and 10 gaps. Following the above-mentioned species, the highest megablast search was to an *Amanita* sp. (GenBank KY081706) from Brazil with 99 % coverage and an 88 % Identity score from 75 base differences and 22 gaps. The percent coverage of the full ITS in the megablast search dropped significantly thereafter.

According to the description of Tulloss (2009), *S. quitensis* belongs to the subgenus *Lepidella*, sect. *Lepidella*, subsect. *Vittadiniae*, and according to Tulloss (2003) it belongs to the stirps *Nauseosa* due to the presence of clamp connections at the base of the basidia, the spore morphology and the characteristics of the remnants of the universal veil on the stipe. Morphologically, the closest species based on the description of Tulloss (2003) is *A. nauseosa* but it differs notably by the larger pileus size, presence of umbo, and strong odour when fresh and dry. Other close species are *S. pruitii*, but it differs by the odour, and shape and size of basidiospores (Tulloss et al. 2014); *A. prairicola* differs by the presence of a persistent ring, and size and shape of the basidiospores, additionally the latter species belongs to the *Vittadinii* stirps (Tulloss 1998).

The phylogenetic tree was constructed using the Maximum Likelihood plugin PHYML in Geneious R9 (<http://www.geneious.com>; Kearse et al. 2012), and the substitution model determined by jModelTest (Posada 2008) according to Corrected Akaike Information Criterion (AICc). The genus *Amanita* is used based on current nomenclature in NCBI nucleotide database. *Amanita* sp. (GenBank KY081706) is the outgroup. Bootstrap support values ≥ 50 % are given above branches. The phylogenetic position of *S. quitensis* is indicated in **bold**. The species name is followed by the accession number, and the three letter United Nations country code, in order of appearance BRA: Brazil, USA: United States, ECU: Ecuador, NLD: Netherlands, NZL: New Zealand.

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