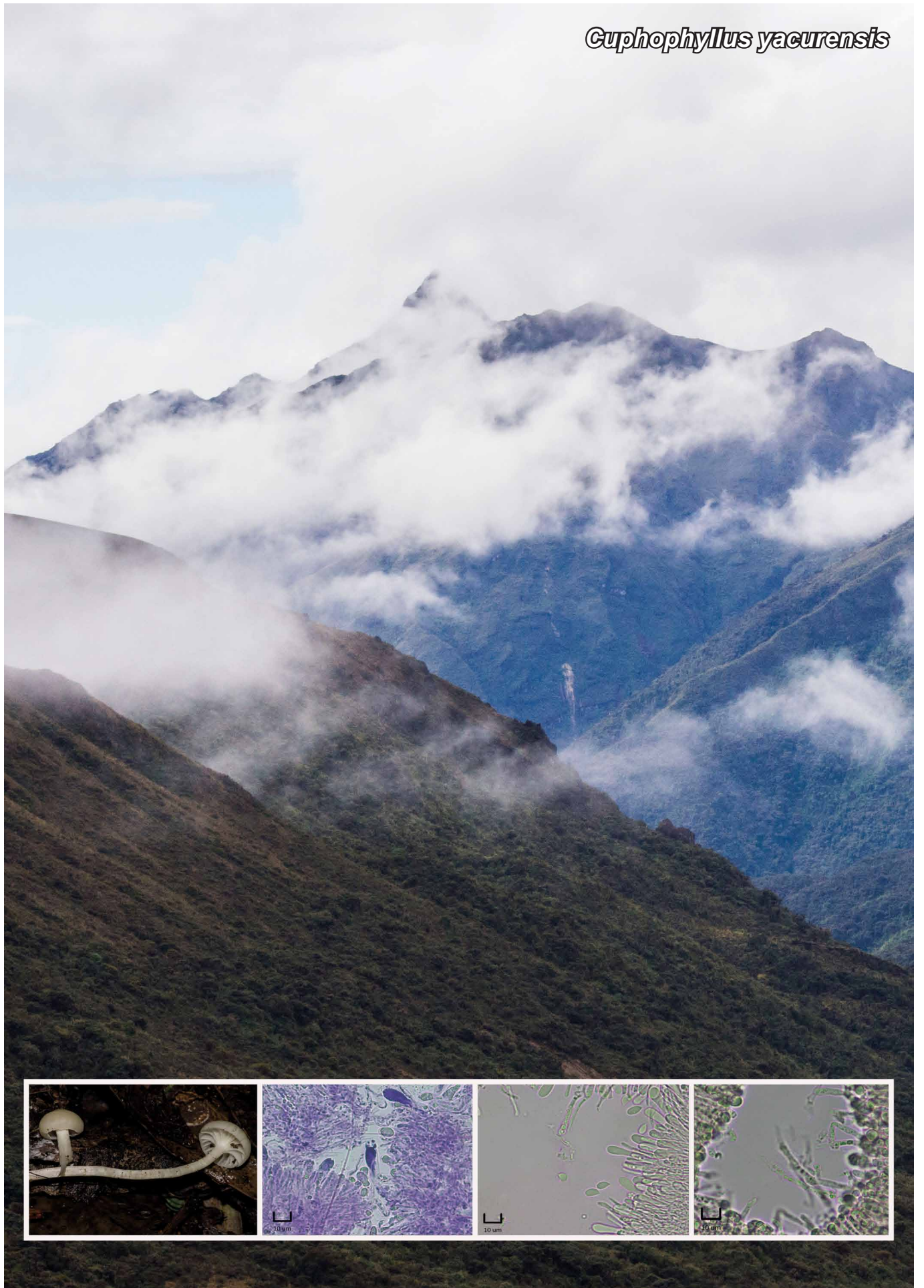


Cuphophyllus yacurensis



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Cuphophyllus yacurensis A. Barili, C.W. Barnes & Ordoñez, *sp. nov.*

Etymology. Name reflects the locality where the species was collected.

Classification — *Hygrophoraceae*, *Agaricales*, *Agaricomycetidae*, *Agaricomycetes*, *Basidiomycota*.

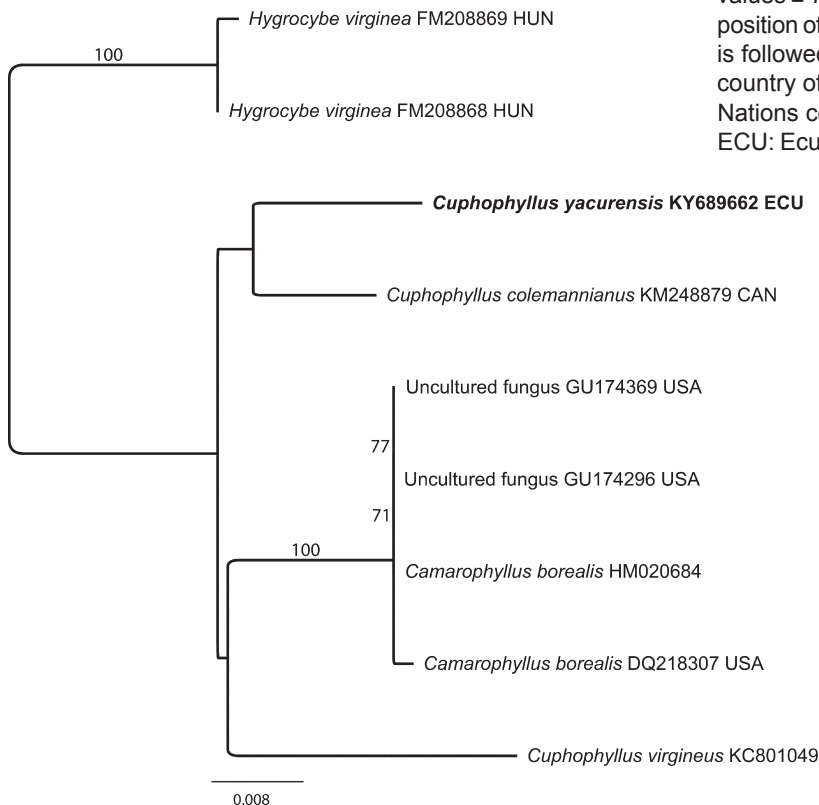
Basidiomata stipitate, pileus convex, 6 mm diam, white, surface smooth, dry, smooth margin. Texture slightly elastic, white, immutable. *Lamellae* white, thick, separate, decurrent, with lamellulae present, smooth margin. *Stipe* central, white, 40 × 1.5 mm, cylindrical, smooth, white cottony mycelia at the base. *Spore print* white. *Basidia* 32–37.5 × 7–7.5 μm, elongate, clavate, 2- and 4-spored, hyaline. *Clamp connections* present in the hymenium, lamellar trama irregular. *Pileipellis* as cutis. *Basidiospores* 8–9 × 5–5.5 μm, ellipsoid, amygdaloid, ovoid, smooth, non-amyloid, acyanophilic, non-dextrinoid, not metachromatic.

Habitat — Gregarious, on the ground, high montane forest.

Typus. ECUADOR, Zamora Chinchipe province, Yacuri National Park, alt. 3234 m, May 2015, A. Barilli (holotype QCAM 5891, Fungarium QCAM, ITS and LSU sequences GenBank KY689662 and KY780119, MycoBank MB820655, TreeBASE Submission ID 20679).

Notes — Phylogenetic analyses show *Cuphophyllus colemannianus* as the closest species to *C. yacurensis*, but several morphological differences were found. The pileus of *C. colemannianus* is larger (10–50 mm), pale brown, slimy surface, and striate margin, with intervenous lamellae, and larger basidia between 37–51 mm (Trudell & Ammirati 2009). A Blastn search was done with the complete ITS sequence of 634 bases of the *C. yacurensis* holotype (GenBank KY689662). The results showed the closest match to *C. colemannianus* from Canada (GenBank KM248879) with 97 % similarity from 21 base differences and 5 gaps. Following *C. colemannianus* in the Blastn search results were several uncultured fungi, *Camarophyllus borealis*, *Cuphophyllus virginea*, and two *Hygrocybe virginea* sequences. The phylogenetic analysis was done with the above-mentioned sequences and *Hygrocybe virginea* as the outgroup. The final alignment was trimmed to include ITS1 through ITS2 only and edited by hand for alignment errors.

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 the Corrected Akaike Information Criterion (AICc). *Hygrocybe virginea* (GenBank FM208869 and FM208868) is the outgroup. Bootstrap support values ≥ 70 % are given above the branches. The phylogenetic position of *C. yacurensis* is indicated in **bold**. The species name is followed by the GenBank accession number, and when the country of origin was indicated, also by the three letter United Nations country code, in order of appearance HUN: Hungary, ECU: Ecuador, CAN: Canada, USA: United States of America.



Colour illustrations. Ecuador, Yacuri National Park; basidia; basidiospores and clamp connection.

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