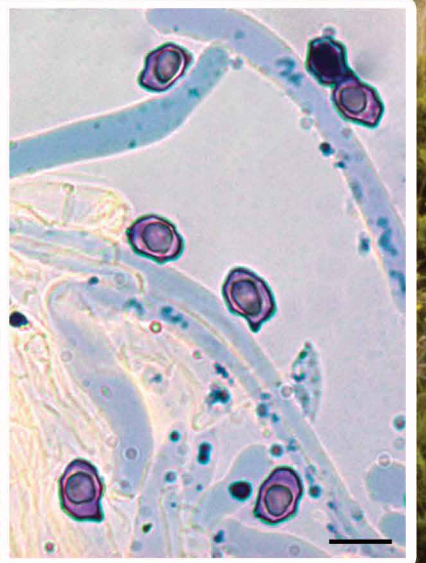


Entoloma yanacolor



Fungal Planet 728 – 13 July 2018

Entoloma yanacolor A. Barili, C.W. Barnes & Ordoñez, *sp. nov.*

Etymology. Named refers to the black colour of the fruiting body (*yana*) in the native Quichua Andean language.

Classification — *Entolomataceae*, *Agaricales*, *Agaricomycetes*.

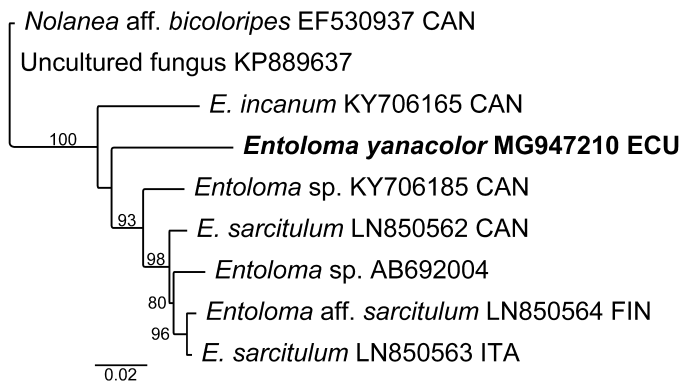
Basidiomata small, convex. *Pileus* 20 mm diam, smooth waxy surface, black, entire margin, slightly fleshy texture. *Lamellae* moderately close, adnate to adnate with decurrent teeth, whitish becoming pink with age, thick with entire and concolorous translucent edge. *Stipe* central, 23 × 2 mm, cylindrical, pale concolorous with pileus, smooth surface with white mycelium at the base. *Context* hollow, fragile. Indistinctive *odour* and taste. *Pileipellis* as a trichoderm, extended fusiform to subclaviform pileocystidia. *Lamellar trama* regular with cylindrical septate hyphae. *Basidia* 30–50 × 8–4 µm, claviform, 4-spored, *clamp connections* absent, fertile lamellae edge. *Basidiospores* 9–11 × 6.5–7.5 µm, ellipsoid, mostly with 6 angles, hyaline to pale pink, non-amyloid, non-dextrinoid, cyanophylic, metachromatic, *Q* = 1.5. *Pleurocystidia* subcylindrical, hyaline with thin wall. *Cheilocystidia* absent. *Caulocutis* as subtrichoderm with fusiform caulocystidia. *Clamp connections* absent.

Habitat — Gregarious on soil, among *Azorella* sp. in the Andean paramo.

Typus. ECUADOR, Chimborazo province, Sangay National Park, alt. 3770 m, May 2016, J. Flores (holotype QCAM6312, Fungarium QCAM, ITS-LSU sequence GenBank MG947210, MycoBank MB824642, TreeBASE Submission ID 22308).

Notes — *Entoloma yanacolor* is a small species of Collybioid habit, that belongs to subg. *Leptonia* and to sect. *Cyanula* (Boccardo et al. 2008), the only difference being it is glabrous and not fibrillous / tomentose. Morphologically *E. yanacolor* is very similar to *E. corvinum* (Breitenbach & Kränzlin 1991), differing only by the glabrous surface of the pileus and stipe. However, the DNA sequence analysis excludes it being that species.

The megablast search using the full ITS sequence of *E. yanacolor* was truncated due to a unique 14-base gap near the end of the ITS2, giving only 91 % coverage for the top seven hits. Therefore, 14 ambiguous (n) bases were inserted at the site of the gap, increasing the coverage of the top six megablast results to 100 %. The results of the adjusted megablast search of the NCBI GenBank nucleotide database showed *E. yanacolor* was distinct from other species presently available for the genus with the closest species based on ITS sequence being an *Entoloma* sp. (GenBank KY706185; Identities = 569/624 (91 %), 22 gaps (4 %), adjusted for the 14-base gap insert). The ITS phylogenetic tree includes the top eight megablast hits for the *E. yanacolor* sequence.



The phylogenetic tree was constructed using the Maximum Likelihood plugin PHYML in Geneious R9 (<http://www.geneious.com>; Kearsse et al. 2012), and the substitution model determined by jModelTest (Posada 2008) according to the Corrected Akaike Information Criterion (AICc). *Nolanea* aff. *bicoloripes* (GenBank EF530937) is the outgroup. Bootstrap support values ≥ 80 % are given above branches. The phylogenetic position of *E. yanacolor* is indicated in **bold**. The species name is followed by the GenBank accession number, and when the country of origin was indicated, the three letter United Nations country code was used, in order of appearance CAN: Canada, ECU: Ecuador, FIN: Finland, ITA: Italy.

Colour illustrations. Ecuador, Sangay National Park; basidiocarp; pleurocystidia; basidiospores in cresyl blue. Scale bars = 10 µm.

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