

Cortinarius glaucocelotus



Fungal Planet 1181 – 19 December 2020

Cortinarius glaucoelotus Brandrud, Dima, Krisai, Ballarà & Peintner, *sp. nov.*

Etymology. Name refers to bluish (glaucous) tinges on stipe and resemblance to *C. elotus* sensu Moser.

Classification — *Cortinariaceae*, *Agaricales*, *Agaricomycetes*.

Pileus 35–60(–80) mm diam, hemispherical, then plano-convex, glutinous, glabrous, often with coarse, radial innately fibrillose structure near margin, centre sometimes with whitish patches of universal veil remnants; initially olivaceous brown, often with greenish grey tinge at margin, more ochraceous brown-buff to brown at centre, exposed parts often becoming oxidised to warmer red-brown, even chestnut brown with age. *Lamellae* emarginate, 4–8 mm broad, greyish to faintly wax yellow-ochre tinged, paler towards margin, later greyish brown, edge even to slightly serrulate. *Stipe* 25–60 × 10–17 mm, with a distinctly (but not very broad) marginate bulb (bulb up to 27 mm wide), whitish, with a distinct and sometimes persistent lilac-amethyst zone at apex, with age brownish. Universal veil on bulb margin sparse, viscid, often difficult to distinguish from stipe surface, whitish (bluish tinges not seen), cortina abundant, whitish, soon brown from spores. *Context* whitish to cream, some with pale ochre grey hygrophanous streaks at stipe apex, cortex lilac at stipe apex, a few with vivid saffron yellow spots in base of bulb. *Odour* distinctly raphanoid (to earthy). *Taste* mild. *Spore print* dark (rusty) brown. *Basidiospores* (9.8–)10.9–11.9(–12.7) × (6.4–)6.7–7.5(–7.8) μm, av. = 11.40 × 7.07 μm, Q = (1.4–)1.5–1.7(–1.8), Q_{av} = 1.61 (type collection; n = 67); range of MVs from all collections 11.4–12.1 × 7.0–7.7 μm, av. = 11.81 × 7.37 μm, Q_{av} = 1.60; distinctly citriform to amygdaloid, strongly and coarsely, net-like verrucose, suprahilar plate indistinct, apiculus smooth. *Basidia* 4-spored, 9–11 μm wide. *Pileipellis* simplex, with gradual transition from erect-entangled-sinuuous, gelatinous, very narrow, 2–3 μm wide, pale yellow hyphae at surface, to more repent-parallel, slightly wider (3–4(–5)) μm hyphae basally. The basal epicutis with pale yellow brown hyphae, sometimes more strongly yellow to yellow brown, with some hyphae filled with amorphous-oleiferous golden brown pigment, pigment sometimes in lumps like staples of coins, hyphae sometimes forming subparallel, interconnected bundles. A few thicker (6–7 μm wide) hyphae with faintly thicker walls are sometimes seen basally, some of these might be distinctly zebra-striped encrusted.

Chemical reactions — KOH 20–30 % negative (slightly brownish) on pileipellis and bulb margin.

Habitat & Distribution — In calcareous *Abies* dominated forests, as well as calcareous *Picea* and *Pinus* forests. Very rare, but widely distributed in montane Europe (Pyrenees - The Alps - Caucasus), and into Asian Siberia. Result of nrDNA ITS sequencing verified the species from NE Spain (with *Pinus nigra* and *P. sylvestris*), E Austria (with *Abies alba* and some *Picea abies*), Russian W Caucasus (with *Abies nordmanniana* and

Colour illustrations. Austria, Schneebergdörfel, WU 42513, type locality. Spores and basidiomata (from WU 42513, holotype). Scale bar = 10 μm (spores).

some *Picea orientalis*) and Altai (Russian Siberia; with *Picea obovata*).

Typus. AUSTRIA, Lower Austria, Schneebergdörfel, 780 m asl, N47°46'45" E15°52'13", 9 Oct. 2017, T.E. Brandrud, I. Krisai-Greilhuber & H. Voglmayr (holotype TEB898-17 (O), isotypus WU 42513, ITS sequence GenBank MW135358, MycoBank MB837764).

Additional materials examined. AUSTRIA, Lower Austria, Schneebergdörfel NW, 9 Oct. 2017, T.E. Brandrud, I. Krisai-Greilhuber & H. Voglmayr, WU 42455 / TEB898b-17 (O), ITS sequence GenBank MW135357. – RUSSIA, Altai republic, Chuya river (Katun), NW of Uagan Unus, 22 Aug. 2001 (as '*C. elotus*'), M.M. Moser (IB 2001/0090), ITS-LSU sequence GenBank EU056953; Karachay-Cherkessia Republic (NW Caucasus), Kuzgynch river, Arkhyz W, 10 Oct. 2016, T.E. Brandrud & T. Svetasheva, TEB 635-16 (LE), ITS sequence GenBank MW135356. – SPAIN, Berguedà, Espunyola Can Gómira, 700–900 m asl, 8 Nov. 2014, J. Ballarà, JB-8525-14, ITS sequence GenBank MW135354.

Notes — *Cortinarius glaucoelotus* belongs to the Humolentes clade (within the Calochroi lineage), where it has a sister position to *C. pseudoglaucopus* and *C. praetermissus*. *Cortinarius pseudoglaucopus* is distributed both in Europe and North America, and shows a slight phylogeographical differentiation between these regions. The nrDNA ITS sequences generated from *C. glaucoelotus* differ from sequences of European *C. pseudoglaucopus* by 9–12 nucleotide and indel positions (98.35–98.02 % similarity). The two species have overlap in their distribution and similar habitat requirements: both are occurring in calcareous coniferous forests, but *C. glaucoelotus* is possibly more associated with *Abies* spp. They are co-occurring in W Caucasus and found in the same area and same kind of forests in E Austria and NE Spain. Morphologically, *C. glaucoelotus* and *C. pseudoglaucopus* are very similar, characterised e.g. by their initially olive brown pilei. Based on the material seen so far, it seems that *C. glaucoelotus* can be distinguished from *C. pseudoglaucopus* by the beautiful lilac-amethyst narrow zone at the stipe apex when young. However, we do not know if this lilac apex colour is constant. The bluish pigments in *C. pseudoglaucopus* are very variable, sometimes the stipe and context can be bluish-violet tinged when young, and the veil and bulb margin are often violaceous spotted when young. These bluish variants have usually rather dark pileus colours, as already indicated by Moser (1961). The bluish tinges on the bulb margin including the veil have not thus far been seen in *C. glaucoelotus*. It is also possible that *C. glaucoelotus* on average has more olive greenish tinges on the pileus margin when (very) young, but this needs further confirmation.

(text continues on Supplementary material page FP1181)

Supplementary material

FP1181 Phylogenetic tree of the Humolentes clade within sect. *Calochroi* derived from a Maximum Likelihood analysis based on nrITS1-5.8S-ITS2, partial nrLSU and binary data from indel coding with FastGap v. 1.2 (Borchsenius 2009). Analysis was performed in raxmlGUI v. 1.5.2 (Silvestro & Michalak 2012) using the GTRGAMMA substitution model for the partitioned (ITS1-5.8S-ITS2 and LSU) nucleotide data and the default setting for binary (indel) data. ML bootstrap support (BS) values are shown at the nodes (BS > 70 %). Sequences generated for this study are highlighted in **bold** face.

Bálint Dima, Department of Plant Anatomy, Institute of Biology, Eötvös Loránd University, Pázmány Péter sétány 1/C, H-1117, Budapest, Hungary; e-mail: cortinarius1@gmail.com

Tor Erik Brandrud, Norwegian Institute for Nature Research, Gaustadalléen 21, NO-0349 Oslo, Norway; e-mail: tor.brandrud@nina.no

Irmgard Krisai-Greilhuber, Department of Botany and Biodiversity Research, University of Vienna, Rennweg 14, 1030 Wien, Austria; e-mail: irmgard.greilhuber@univie.ac.at

Josep Ballarà, C/ Tossalet de les Forques, 44, E-08600, Berga, Catalonia, Spain; e-mail: josep.cortinarius@gmail.com

Ursula Peintner, Institute of Microbiology, University of Innsbruck, Technikerstrasse 25, 6020 Innsbruck, Austria; e-mail: Ursula.Peintner@uibk.ac.at