



Boletus spp. sect. *boletus* –
morphology, ecology and
some applications

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Boletus spp. sect. *boletus* (true ceps) – common features

Common macroscopic features:

- flesh white (or pale yellow), specific (for the group s.l.) mild-tasting (specific odor for the section), flesh does not change color when exposed to air;
- stipe with enlarged base, clavate or very rarely cylindrical and with netted pattern, at least in the upper part;
- tubes are small, \pm white, cream, pale yellow, lemon yellow, olivaceous green to olivaceous brown for oldest individuals and respectively spores mass that are either yellow-brown or olive-brown, pores are concolour ;
- tubes are notched to the stipe;
- cap is usually dry, vary rare slightly viscous and cap cuticle can be detached hardly;
- very often „water painting “ spots on cap and \pm wrinkled surface toward the margin.

Common microscopic features:

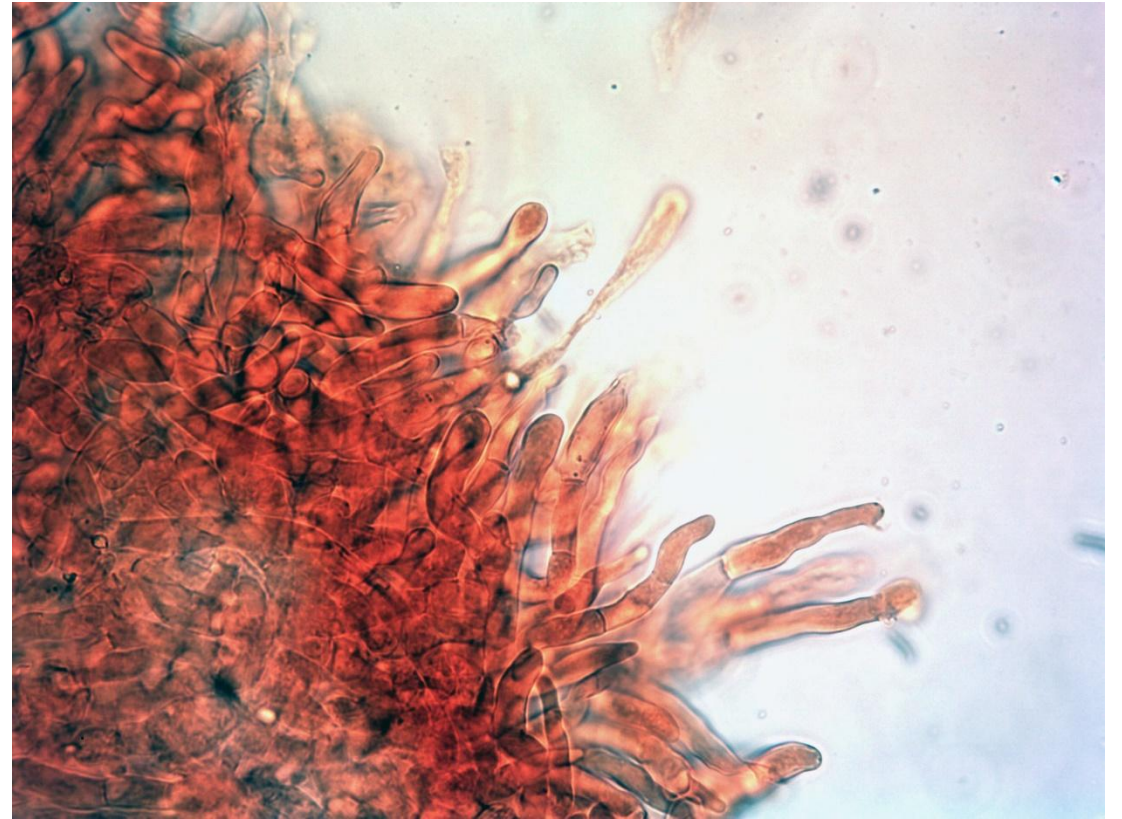
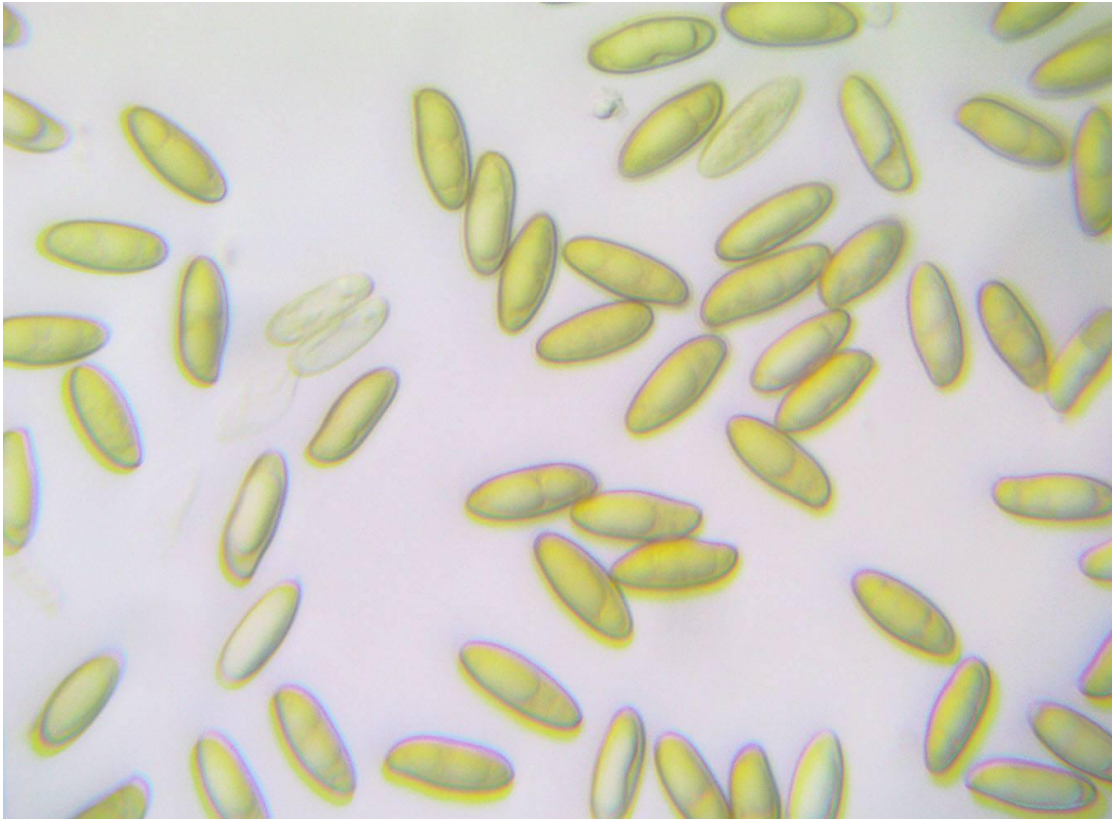
- hyphae of the flesh in the stipe base inamyloid with Melzer's reagent;
- pileipellis – trichoderm type of interwoven septate hyphae (perpendicular to the cap surface);
- cells of the hyphae are cylindrical, not encrusted.

Common ecological features:

- all of them participate in obligate, symbiotic ectomycorrhizal associations ;
- usually they form LD - ET of ectomycorrhiza (according to Agerer with most evolved type F rhizomorphs);
- most of them have a wide host range of photobionts;
- wide spread in northern hemisphere from subarctic to near equator.



Boletus spp. sect. *boletus* (true ceps) –
microscopic features



Boletus edulis Bull.

Boletus edulis Bull. – 52 forms, subs. and varieties
(according indexfungorum.org)

CAP: 12-25 cm, broadly hemispherical, then convex, flat convex or flat, ±viscid, darker in the center, paler towards the margin, beige, pale brown, hazel brown to dark brown (very rare).

STIPE: club-shaped, ±cylindrical, bulbously swollen or rooting, white or whitish to pale ochre, with ± white network, often buried in soil or forest litter (sometimes more than $\frac{2}{3}$). CAP diameter : STIPE length – 1:3 to 1:6 (very rare up to 1:8)
HYMENIUM: Tubes first whitish, then cream, pale yellow to yellow with olivaceous tint (comparing to other species from this section here is the lightest tubes). Small holes around pores.
Smell distinctive – like ceps but very delicate and weak comparing to other spp.

ECOLOGY: spruce - *Picea abies* (L.) H.Karst., pines (*Pinus* spp.); (*Fagus* spp. & *Betula* spp., *Cistus* spp. – another species probably?) Grows from beginning of summer to late autumn.



Boletus edulis Bull.



Boletus pinophilus Pilát & Dermek

***Boletus pinophilus* Pilát & Dermek.** – 5 forms and varieties (according indexfungorum.org)

CAP: 15-35 cm, widely hemispherical, later convex, flattened, rarely flat, usually wrinkled near margin, dry to slightly viscid, vinaceous brown to bricked brown (reddish and/or grayish tint).

STIPE: swollen, clavate, vary rare cylindrical, pale ochre to concolorous, but paler than cap – ochre instead reddish tint, with + white network.

HYMENIUM: Tubes first whitish, then cream, pale yellow to yellow with olivaceous tint. Smell not distinctive – like ceps.

ECOLOGY: spruce - *Picea abies* (L.) H.Karst., Scott pine (*Pinus sylvestris* L.) and *Pinus mugo* Turra but prefers *Pinus* spp.

Grow in late spring – late autumn – disappear during summer.

This is the biggest cep from the section.



Boletus pinophilus Pilát & Dermek



Boletus aureus Schaeff.

***Boletus aureus* Schaeff.**

CAP: 10-20 cm, widely hemispherical then convex, flat-convex, flat and sometimes flat-depressed, dry, velvety, later smooth, black brown, dark brown to chestnut brown, in young fruitbodies more or less uniformly colored, later with irregular paler brown, bronze or orange brown like „water painting“ spots.

STIPE: clavate or rarely cylindrical, beige ochre, orange brown to chestnut brown, rarely whitish, with fine network darker than stipe color, most clear in upper part.

HYMENIUM: Tubes whitish, then cream, pale yellow, lemon yellow, olivaceous green to olivaceous brown tint. Smell distinctive – very strong. (Strongest smell from this section)

ECOLOGY: *Quercus frainetto* Ten. and *Quercus cerris* L., rare other *Quercus* spp. or *Castanea sativa* Mill. (Fagaceae) This is the species with the most narrow host range and the most xerophytic one.



Boletus aureus Schaeff.



Boletus reticulatus Schaeff.

***Boletus reticulatus* Schaeff.**

CAP: 8 to 20 cm, widely hemispherical, then convex, flat convex or flat, dry or very rare slightly viscid, finely to coarsely cracked, pale ochre brown to brown, sometimes discoloured to ochraceous, greyish ochraceous or almost entirely whitish, often wrinkled at the margin.

STIPE: club-shaped or cylindrical, almost concolorous with the cap, with fine white network in upper part.

HYMENIUM: Tubes whitish, then cream, pale yellow, lemon yellow, olivaceous green to olivaceous brown tint. Smell not distinctive – like ceps.

ECOLOGY: *Quercus frainetto* Ten., *Quercus cerris* L. (rare than previous sp.), other *Quercus* spp. or *Castanea sativa* Mill. (Fagaceae), *Fagus* spp. (very often – probably another ecotype), ect. broad host range.

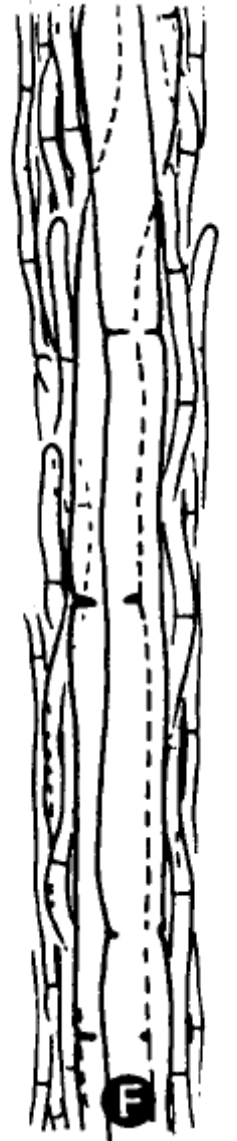
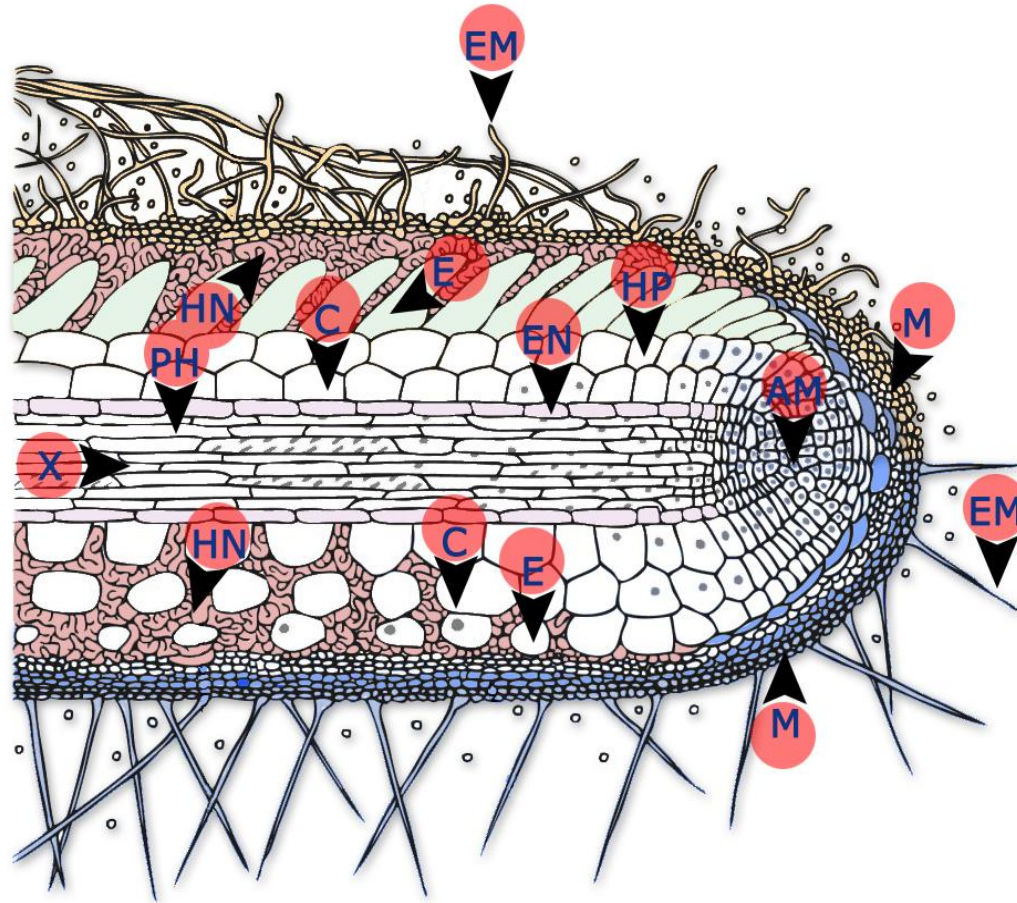


Boletus reticulatus Schaeff.

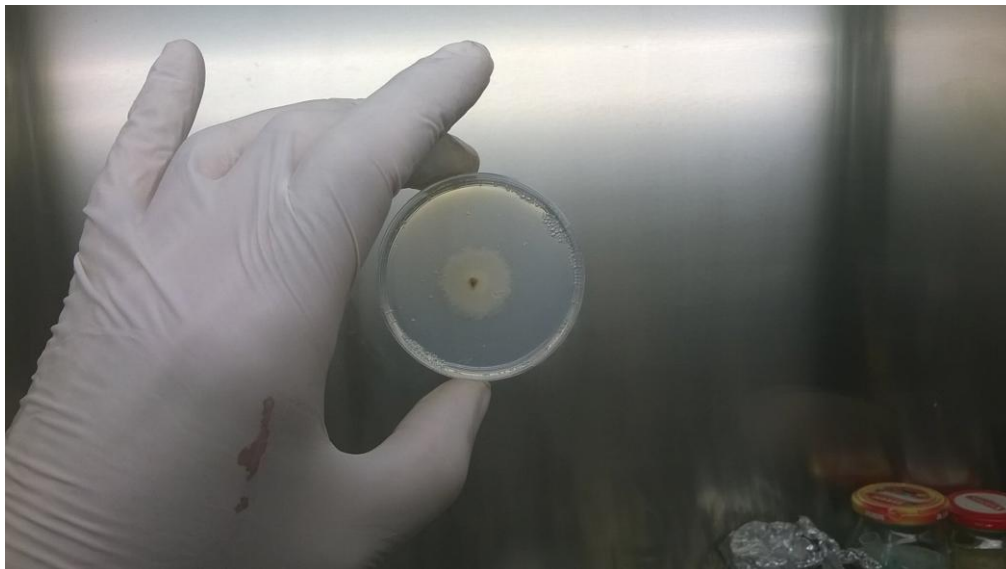
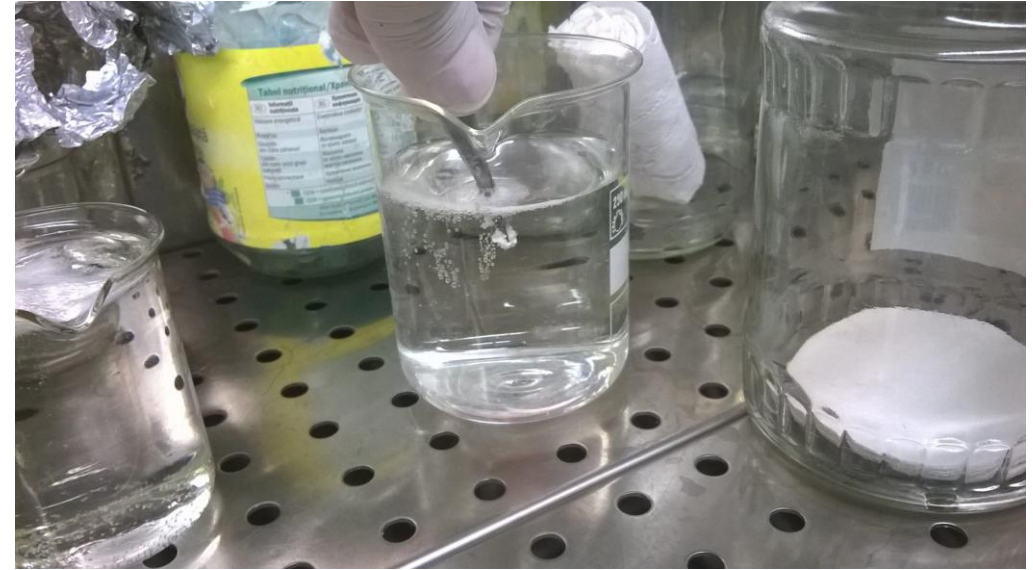
These images are taken from **boletales.com**, author of images – Boris Assyov from Institute of Biodiversity and Ecosystem Research, IBER at the Bulgarian Academy of Sciences, <http://www.iber.bas.bg/>



Ectotrophic status of *Boletus* spp.



Some applications



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GATTTGAGGTCAGAGTTCAAATGGTCCTA
ACCCTGCGCGTTTCGTCGGCCTCACGACCG
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GCGATTCACTGCTCACCTACACGCTCCN
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Descriptions

Sequences producing significant alignments:

Select: [All](#) [None](#) Selected:0

[Alignments](#) [Download](#) [GenBank](#) [Graphics](#) [Distance tree of results](#)

Description	Max score	Total score	Query cover	E value	Ident	Accession
<input type="checkbox"/> Boletus edulis isolate 2074 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene.	311	311	98%	2e-81	98%	KC750229.1
<input type="checkbox"/> Boletus edulis isolate 2037 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence	311	311	98%	2e-81	98%	HM579925.1
<input type="checkbox"/> Boletus edulis voucher 12524MK (H) 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal R	311	311	98%	2e-81	97%	GU198975.1
<input type="checkbox"/> Uncultured Boletus isolate 51/08 18S ribosomal RNA, internal transcribed spacer 1, 5.8S ribosomal RNA, internal transcribed spacer 2, and 28S ribosomal RNA gene, region	311	311	98%	2e-81	98%	FJ816721.1
<input type="checkbox"/> Boletus sp. YM709 genes for 18S rRNA, ITS1, 5.8S rRNA, ITS2 and 28S rRNA, partial and complete sequence	305	305	98%	1e-79	97%	AB848409.1
<input type="checkbox"/> Boletus edulis isolate B47 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, p	305	305	98%	1e-79	97%	KM401598.1
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<input type="checkbox"/> Boletus edulis strain BE102 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene.	305	305	98%	1e-79	97%	KJ920140.1
<input type="checkbox"/> Uncultured Boletus clone OTU_233k 5.8S ribosomal RNA gene, partial sequence; internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence	305	305	98%	1e-79	97%	KJ008809.1
<input type="checkbox"/> Boletus edulis genes for 18S rRNA, ITS1, 5.8S rRNA, ITS2, 28S rRNA, partial and complete sequence, specimen voucher: TNS:F55586	305	305	98%	1e-79	97%	AB821458.1
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<input type="checkbox"/> Boletus edulis isolate 2121 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene.	305	305	98%	1e-79	97%	KC750230.1
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<input type="checkbox"/> Boletus edulis isolate 2059 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene.	305	305	98%	1e-79	97%	KC750227.1
<input type="checkbox"/> Boletus edulis isolate 412 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, p	305	305	98%	1e-79	97%	KC750226.1
<input type="checkbox"/> Boletus edulis isolate 410 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, p	305	305	98%	1e-79	97%	KC750225.1

THANK YOU

ACKNOWLEDGEMENTS

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