

*Mallocybe crassivelata*



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***Mallocybe crassivelata* Ferisin, Bizio, Esteve-Rav., Vizzini & Dovana, sp. nov.**

*Etymology.* From the Latin *crassus* (thick) and *velatus* (with a veil), referring to the presence of a thick, abundant veil on the pileus surface.

*Classification* — *Inocybaceae*, *Agaricales*, *Agaricomycetes*.

*Basidiomata* stipitate. *Pileus* 20–40 mm diam, at first convex, then appanate to plano-convex, without umbo, with an inflexed margin when young, fibrillose-tomentose to woolly-tomentose, sometimes scaly, when moist almost smooth; initially ochraceous yellow (Mu 10YR 6/6) to ochraceous brown (Mu 7.5Y 8/4), brown with an olivaceous tinge when moist, sometimes fulvous orange (Mu 7.5YR 3/6) at disc; in young basidiomes with a thick, white velipellis. *Lamellae* rather crowded to crowded ( $L = 48–85$ ), with lamellulae ( $l = 0–1$ ), adnexed to arcuate, sometimes subdecurrent, initially pale ochraceous with a faint olivaceous hue, then brown; edge whitish to concolourous, crenulate. *Stipe* 25–40 × 3–6 mm, cylindrical, solid, then becoming fistulose, pale yellow to concolourous with pileus in aged basidiomes; surface fibrillose, white towards the base for the presence of a white velipellis; white cortina present in young basidiomes. *Context* yellowish in pileus, somewhat and ochraceous brownish in stipe. *Smell* earthy sometimes mixed with a subspermatic component. *Taste* indistinct. *Basidiospores* (7.7–)8.3–8.7–9.2(–11.4) × (3.9–)4.7–5–5.2(–5.9)  $\mu\text{m}$ ,  $Q = (1.5–)1.67–1.76–1.85(–2.1)$ , smooth, yellowish, very variable in shape, ellipsoid to subphaseoliform, sometimes amygdaliform in side view with obtuse or sub-ogival apex; presence of anomalous long spores (over 11  $\mu\text{m}$ , probably discharged from bisporic basidia), walls up to 0.5  $\mu\text{m}$  thick. *Basidia* (20–)22.7–26.3(–27) × (7.7–)8.2–9.4(–9.9)  $\mu\text{m}$ , clavate to cylindrical, 4-spored, sometimes 1–2-spored, with inner olivaceous guttulae and brown necropigment, sterigmata up to 3  $\mu\text{m}$  long; sometimes they are rarely present on lamella edge. *Hymenophoral trama* regular, formed by cylindrical to ellipsoidal, 10–16  $\mu\text{m}$  wide elements, with a brownish wall; subhymenium consisting of up to 100  $\mu\text{m}$  long elements, 7–13  $\mu\text{m}$  wide. *Cheilocystidia* very numerous, (14.3–)18–28.2(–32.6) × (6.1–)7.9–11.4(–14.7)  $\mu\text{m}$ , hyaline, usually thin-walled, very variable in shape, cylindrical, oblong to clavate, with a few septa; mixed with basidia. *Pleurocystidia* absent. *Caulocystidia* present at stipe apex (1/4), at least partly catenulate with terminal element as true cystidium, from ellipsoid to ovoid, up to 25  $\mu\text{m}$  long. *Pileipellis* an undifferentiated cutis with some ascending hyphae; terminal elements cylindrical to subcylindrical, 50–110 × 7–14  $\mu\text{m}$ , with ochraceous-brown parietal pigment. *Clamp-connections* present.

*Habitat & Distribution* — Gregarious in deciduous (*Fagaceae*) or coniferous (*Picea abies*, *Pinus sylvestris*) forests. So far known from Italy, Slovenia and Spain.

*Colour illustrations.* Pregarje, Slovenia, *Fagus sylvatica* forest. *Mallocybe crassivelata* basidiomata in habitat; basidiospores; caulocystidia; basidia and cheilocystidia. Scale bars = 10  $\mu\text{m}$ .

*Typus.* SLOVENIA, Pregarje, 710 m asl, under *Fagus sylvatica*, 28 June 2014, G. Ferisin (holotype MCVE 29561; ITS and LSU sequences GenBank MN536812 and MN537138, MycoBank MB832767).

*Additional materials examined.* ITALY, Veneto, Belluno, Falcade, 1148 m asl, in *Picea abies* forest, 11 Oct. 2001, E. Bizio, MCVE 21499; ITS sequence GenBank MN536813. — SPAIN, Community of Galicia, Province of Orense, Cambela, 29TPG5280, 900 m asl, in *Castanea sativa* forest, 20 Oct. 1999, F. Esteve-Raventós, M. Villarreal & F.D. Calonge, AH 29788; ITS sequence GenBank MN536810; Community of Madrid, Rascafría, 24 June 1993, in mixed forest of *Quercus pyrenaica* and *Pinus sylvestris*, A. Guerra & G. Moreno, AH 46622; ITS sequence GenBank MN536811.

*Notes* — Terminology for descriptive terms is according to Kuyper (1986) and Vellinga (1988) and colour codes are taken from Munsell (1994). In our phylogeny *M. crassivelata* belongs to a well-supported clade (bootstrap support value = 88 %) together with *M. leucoloma*, *M. malenconii*, *M. myriadophylla* and three sequences of 'Uncultured *Inocybe* sp.' (GenBank JX630703, JX630710, JX630716) from the USA and associated with *Dryas integrifolia*. *Mallocybe crassivelata* shows, as major morphological features, a rather fleshy, predominately ochraceous basidioma, fibrillose-tomentose to woolly-tomentose pileus covered with a thick white velipellis, narrow subphaseoliform spores and an earthy smell (similar to that of *Inosperma cervicolor*) often associated to a subspermatic component, though in some collections (AH 29788) nearly indistinct. *Mallocybe leucoloma* differs from the new species mainly by a smaller and slender habit, different shape of cheilocystidia (often pyriform), sub-odourless context and being associated with dwarf *Salix* or *Dryas* (Kühner 1988). *Mallocybe malenconii* can easily be distinguished by its longer spores (9–12 × 4–5.5  $\mu\text{m}$ ) with mean  $Q$ -value of c. 1.95 (Vauras & Larsson 2011) and an indistinct smell (Heim 1931). Compared to *M. crassivelata*, *M. myriadophylla* has a pale grey cortina, very narrow and crowded lamellae (–4 mm wide), smell 'indistinct to somewhat fungoid and slightly metallic' and seems strictly associated with *Betula pendula* (Vauras & Larsson 2011). *Mallocybe hebelomoides* is characterised by a smaller size, broadly elliptical to subovoid spores with  $Q = 1.4–1.6$  and habitat under dwarf *Salix* species (Kühner 1988). Finally, *M. pallidotomentosa*, so far known only from Germany, is morphologically quite close to *M. crassivelata*, but differs mainly in growing under *Populus tremula* and *Betula* sp. (Ludwig 2017) and by a different ITS sequence (Ditte Bandini, pers. comm.).

**Supplementary material**

**FP1090** Maximum-likelihood analysis of the combined *nrITS* and *nrLSU* regions was performed with RAxML v. 8.2.11 (Stamatakis & Alachiotis 2010) using the GTR+G model in Geneious v. 11.1.4.

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