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# Type studies of *Cortinarius phaeopygmaeus* and *C. rusticellus*, and a new salicticolous species *C. chrysophilus*

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## Abstract

This article deals with the taxonomy of three species belonging to *Cortinarius* subgenus *Telamonia* section *Flexipedes*. The micromorphologies and mostly ITS gene regions were examined from the lectotypes and some syntypes of *Cortinarius phaeopygmaeus* J. Favre and *C. rusticellus* J. Favre. *Cortinarius phaeopygmaeus* appeared to be a previously unrecognized species. *Cortinarius rusticellus* is reduced to a synonym of *C. comatus* J. Favre. Its lectotype and protologue agreed with *C. comatus*. The syntype of *C. rusticellus* was conspecific with *C. lamoureae* Bon. *Cortinarius chrysophilus* is described as new from *Salix* vegetation on boreal seashores and in the alpine zone. It belongs to the *C. cucumisporus* complex.

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Fig. 1. *Cortinarius chrysophilus*. a holotype. b spores of holotype. c KK 313/17. d KK 48/22.

## Introduction

The genetic studies have been fundamental to understand the species of *Cortinarius* subgenus *Telamonia* (*Agaricales*). Notably, the public ITS (internal transcribed spacer) sequences of type specimens have proven to be crucial for the identifications. A large number of *Telamonia* type sequences have been published recently, especially by Liimatainen et al. (2017, 2020). Kokkonen (2020) concentrated on the *Telamonia* species growing with *Salix*. This study continued to clarify the taxonomy of some *Salix* associated species from section *Flexipedes* Kytöv., Niskanen & Liimat.

In the previous study of Kokkonen (2020), *C. rusticellus* J. Favre was interpreted as conspecific with *C. lamoureae* Bon on the basis of the literal descriptions (Favre 1955, Horak 1987), own collections and

the ITS sequence of the holotype of *C. lamoureae*. However, the ITS sequence gained from the lectotype of *C. rusticellus*, published later by Liimatainen et al. (2020), was nearly identical with the sequences of *C. comatus* J. Favre. The aim of this study was to clarify the identity of *C. rusticellus* based on morphological and possibly genetic studies of the lectotype and the syntype specimens. The lectotype was thought to be a possible mixed collection of two species. Another aim was to clarify the identity of *C. phaeopygmaeus* J. Favre. Favre's collections of *C. phaeopygmaeus* had not been analysed genetically before. Since its lectotype is scarce, several syntypes were loaned along with the lectotype for comparison. Thirdly, an anonymous group from the *C. cucumisporus* complex (Kokkonen 2020) is described as a new species, *C. chrysophilus*, with new data.

**Table 1.** Accession numbers of the *Cortinari* sequences submitted to GenBank in this study.

Species	Specimen	Accession number	ITS	RPB2
<i>C. chrysophilus</i>	KK 286/17		OQ079466	OQ095233
<i>C. chrysophilus</i>	KK 235/04		OQ079467	OQ095234
<i>C. chrysophilus</i>	KK 93/22 holotype		OQ079468	OQ095235
<i>C. chrysophilus</i>	KK 313/17			OQ095247
<i>C. comatus</i>	<i>C. phaeopygmaeus</i> syntype Favre 163-3		OQ079480	
<i>C. cucumisporus</i>	KK 1378/16			OQ095243
<i>C. cucumisporus</i>	KK 56/19			OQ095244
<i>C. aff. desertorum</i>	<i>C. phaeopygmaeus</i> syntype Favre 163a		OQ079478	
<i>C. aff. desertorum</i>	KK 160/06			OQ095248
<i>C. aff. desertorum</i>	KK 246/06			OQ095249
<i>C. cf. desertorum</i>	KK 355/17			OQ095260
<i>C. desertorum</i>	KK 293/17		OQ079471	OQ095238
<i>C. desertorum</i>	<i>C. phaeopygmaeus</i> syntype Favre 163d		OQ079479	
<i>C. desertorum</i>	KK 1377/16			OQ095246
<i>C. desertorum</i>	KK 710/18			OQ095252
<i>C. desertorum</i>	KK 66/19			OQ095253
<i>C. desertorum</i>	KK 835/18			OQ095254
<i>C. desertorum</i>	E. Campo 23.VIII.2006			OQ095255
<i>C. desertorum</i>	KK 106/08			OQ095256
<i>C. desertorum</i>	KK 351/17			OQ095257
<i>C. cf. diasemospermus</i>	KK 69/22		OQ079469	OQ095236
<i>C. cf. diasemospermus</i>	KK 61/22		OQ079470	OQ095237
<i>C. cf. diasemospermus</i>	KK 53/22		OQ079475	OQ095242
<i>C. cf. diasemospermus</i>	KK 538/07			OQ095250
<i>C. cf. diasemospermus</i>	KK 275/06			OQ095251
<i>C. cf. diasemospermus</i>	KK 235/06			OQ095258
<i>C. cf. diasemospermus</i>	KK 353/17			OQ095262
<i>C. diasemospermus</i>	KK 43/22		OQ079472	OQ095239
<i>C. diasemospermus</i>	KK 88/22		OQ079473	OQ095240
<i>C. diasemospermus</i>	KK 54/22		OQ079474	OQ095241
<i>C. diasemospermus</i>	KK 548/07			OQ095259
<i>C. diasemospermus</i>	KK 288/17			OQ095261
<i>C. lamoureae</i>	<i>C. rusticellus</i> syntype Favre 165b		OQ079477	
<i>C. phaeopygmaeus</i>	KK 645/18		OQ079465	OQ095232
<i>C. phaeopygmaeus</i>	<i>C. phaeopygmaeus</i> lectotype Favre 163c		OQ079476	
<i>C. phaeopygmaeus</i>	KK 723/03			OQ095245

## Materials and methods

The lectotype and four syntypes of *C. phaeopygmaeus* as well as the lectotype and the syntype of *C. rusticellus* were loaned from the Geneve herbarium (G). With both species, the specimens were first examined by microscope and then considered, whether to analyse them genetically. The new collections of *C. phaeopygmaeus* and *C. chrysophilus* are deposited in TUR.

The macroscopic descriptions are based on fresh fruitbodies, and the colour codes refer to Küppers (1999). The microscopic features were examined from dried specimens. Spores and lamellar hyphae were examined in Melzer's reagent and pileipellis hyphae in 10 % NH<sub>4</sub>OH. Spore measures excluded ornamentation and basidial lengths excluded sterigmata. The sizes of spores and basidia are given as length × width. The microscopic measures are reported as a range, except also as a 90 % confidence interval in case of the new species. The mean is underlined. The Q value is the ratio of spore length to spore width.

The molecular methods included both ITS and RPB2 (RNA polymerase II subunit) regions. The methods followed Kokkonen (2020) with the following exceptions. Both Illustra PuReTaq Ready-To-Go PCR Beads (Cytiva) and MyTaq Red Mix (Meridian Bioscience) were used for the PCR procedure. New RPB2 primers were designed for the old types: a forward primer RPB2-tel2F (5'-CGAGTYTGCCRAC-CRYTGTT-3') and a reverse primer RPB2-tel2R (5'-AACARYGGTYGGCARACTCG-3'). They were used with the primers RPB2-6F and RPB2-7R (Liu et al. 2000), but without success. Thus, only RPB2-6F and RPB2-7R were used for the published RPB2 sequences. All mentioned specimens were sequenced. The sequences were submitted to GenBank, except for few identical sequences. Their accession numbers are included in Table 1.

For the ITS and RPB2 phylogenetic trees, the sequences were aligned by MAFFT 7.0 (Kato 2013) and adjusted manually in AliView (Larsson 2014). The RPB2 sequences were aligned according to the codons. The alignments are in Electronic Supplementary Materials 1 and 2. The trees were obtained by maximum likelihood (ML) analyses in raxmlGUI 2.0.10 (Edler et al. 2021) with thorough bootstrap,

1000 replicates and GTRGAMMA model. They were edited in TreeGraph 2 (Stöver & Müller 2010) and GIMP 2.8. The trees include sequences from Kokkonen (2020) and the ITS sequence of the *C. rusticellus* lectotype was downloaded from GenBank (Liimatainen et al. 2020).

## Results

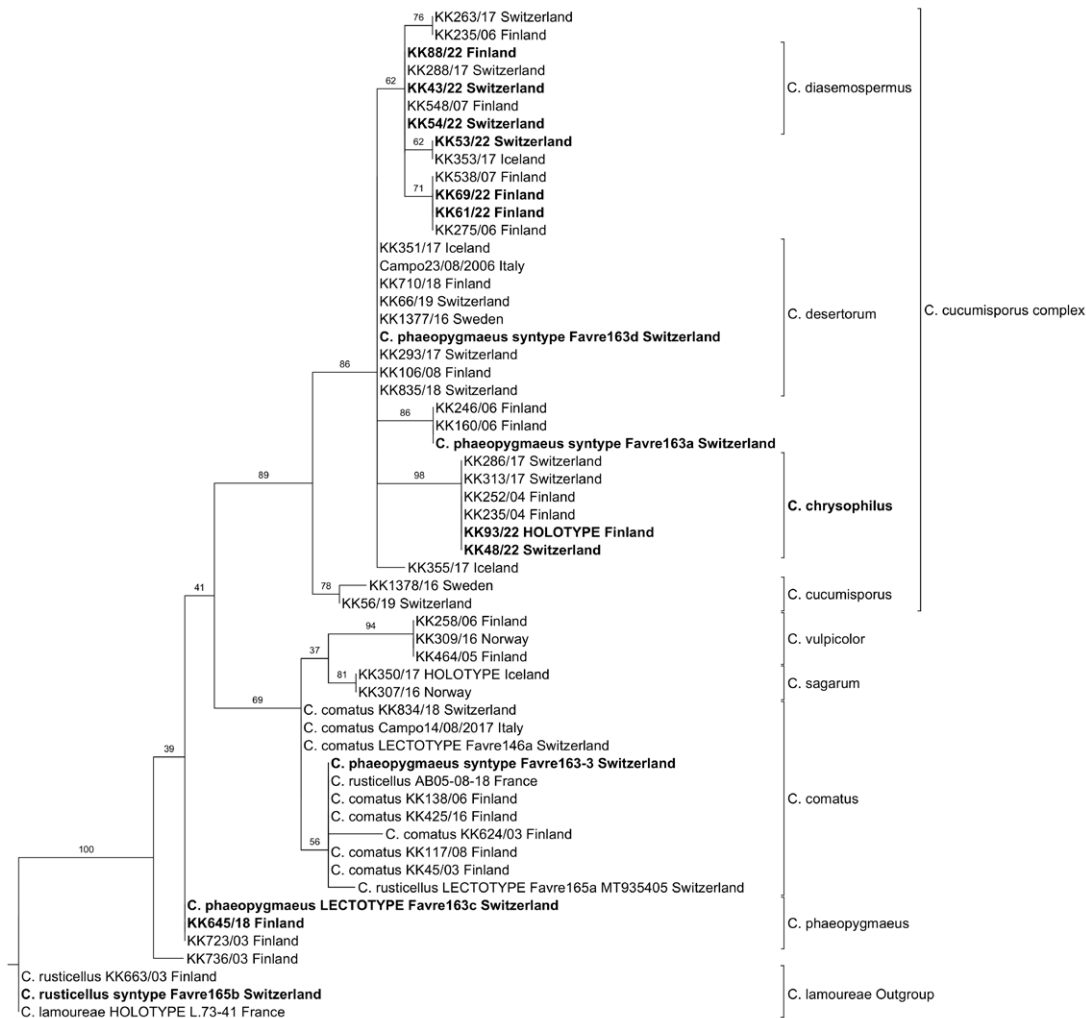
### Phylogeny

The ITS and RPB2 ML phylogenetic trees are presented in Figures 2 and 3. They include the new sequences from the material described by Favre and the *C. cucumisporus* complex. In both trees, the new species *C. chrysophilus* was highly supported. *Cortinarius desertorum* and *C. diasemospermus* groups of the ITS tree were scattered in the RPB2 tree. On the basis of the RPB2 tree these species seem conspecific. One reason for the different topology observed within the *C. cucumisporus* complex between the trees is probably the very small differences among the sequences, mostly 1–2 bases or indels. Also, ambiguous bases appeared more often in RPB2 sequences. Several clades of the *C. cucumisporus* complex were insignificantly supported in the RPB2 tree. A concatenated analysis was not tried, since ITS was regarded as more important than RPB2 for the species recognition and the trees were compared with each other. More gene regions should be analysed to clarify the species limits in the complex.

### Taxonomy

***Cortinarius phaeopygmaeus*** J. Favre, *Ergebn. Wiss. Unters. Schweiz. Natl. Parks* 5 (33): 204 (1955)

**LECTOTYPE:** *Cortinarius phaeopygmaeus* J. Favre, Switzerland, Graubünden, Val S-charl, Costainas, near d'Astras, alt. 2400 m, among *Salix herbacea*, 24.VIII.1947 J. Favre 163c (GK13506). – Half a fruitbody and few small pieces. Spores 9.6–10.5–11.6 × 6.0–6.3–6.8 μm, Q=1.48–1.66–1.83 (n=20); ellipsoid or cylindrical, without a suprahilar depression;



**Fig. 2.** A maximum likelihood tree of ITS sequences. Bootstrap values on branches. New sequences and the new species are highlighted. Log likelihood -1004.55.

weakly or rather weakly verrucose; moderately to rather strongly dextrinoid. Lamellar hyphae encrusted.

**SYNTYPE:** *Cortinarius phaeopygmaeus* J. Favre. Switzerland, Graubünden, near S-charl, Sesvenna, alt. 2550 m, among *Salix herbacea*, 24.VIII.1943 J. Favre 163a (GK13504). – Five fruitbodies in good condition. Spores 7.5–9.0–9.9 × 4.5–5.0–5.6 μm, Q=1.48–1.82–2.13 (n=20); ellipsoid, cylindrical or

subamygdaloid, suprahilar depression occasional; weakly verrucose; indextrinoid. Lamellar hyphae strongly encrusted. Three examined fruitbodies with similar morphology. Determined as *C. aff. desertorum* by ITS. RPB2 failed.

**SYNTYPE:** *Cortinarius phaeopygmaeus* J. Favre. Switzerland, Graubünden, west of Pass Taunter Pizza, near Pass dal Fuorn, alt.2650 m, among *Salix herbacea*, 5.IX.1953 J. Favre 163b (GK13505).



**Fig. 3.** A maximum likelihood tree of RPB2 sequences. Bootstrap values on branches. New sequences and the new species are highlighted. Log likelihood -1381.56.

– Specimen with ca. 11 fruitbodies in good condition. Spores  $8.7\text{--}10.1\text{--}11.6 \times 5.4\text{--}6.1\text{--}6.9 \mu\text{m}$ ,  $Q=1.43\text{--}1.66\text{--}1.98$  ( $n=15$ ); ellipsoid to amygdaloid; weakly or rather weakly verrucose; indextrinoid or weakly dextrinoid. Lamellar hyphae strongly encrusted. DNA analysis of ITS yielded a *Bovista* sequence. Determined as *C. comatus* by morphology. One deviating orange and more slender fruitbody had hyaline spores and is not *Cortinarius*.

**SYNTYPE:** *Cortinarius phaeopygmaeus* J. Favre. Switzerland, Valais, near Zermatt, between Riffelalp and Riffelberg, alt. 2200–2300 m, 5.VIII.1945, leg. S. Ruhlé, J. Favre 163d (GK13507). – Specimen with ca. 7 similar fruitbodies in good condition. Spores  $8.1\text{--}8.9\text{--}10.2 \times 4.9\text{--}5.3\text{--}5.7 \mu\text{m}$ ,  $Q=1.54\text{--}1.67\text{--}1.90$  ( $n=20$ ); amygdaloid to ellipsoid, rarely constricted near the apex; weakly or rather weakly verrucose;

indextrinoid or weakly dextrinoid. Lamellar hyphae encrusted. Determined as *C. desertorum* by ITS. RPB2 failed.

**SYNTYPE:** *Cortinarius phaeopygmaeus* J. Favre. Switzerland, Graubünden, Val dal Botsch, near Fuorn, alt. 2500 m, among *Salix herbacea*, 20.VIII.1950 J. Favre 163-3 (GK13510). – Five small fruitbodies. Spores  $8.5\text{--}10.2\text{--}11.1 \times 5.5\text{--}6.2\text{--}6.8 \mu\text{m}$ ,  $Q=1.39\text{--}1.67\text{--}2.00$  ( $n=20$ ); ellipsoid to amygdaloid, suprahilar depression rare; rather weakly to moderately verrucose; weakly dextrinoid. Lamellar hyphae strongly encrusted. Determined as *C. comatus* by ITS. RPB2 failed.

**COMMENTS:** All the examined syntypes were different species than the lectotype. The micromorphological features of the lectotype agreed with the protologue and the lectotype was well selected by

Horak (1987). *Cortinarius phaeopygmaeus* is genetically near e.g., *C. comatus* and *C. desertorum*, which species were among the syntypes. Contrary to Horak (1987), the syntype Favre 163a was not determined as a mixed collection.

No other *phaeopygmaeus* collections are known from the Alps by the author, but an anonymous GenBank sequence with only ITS2 is likely conspecific (MT095587, Arraiano-Castilho et al. 2020). It was the only match in GenBank. Three GenBank ITS sequences determined as *C. phaeopygmaeus* were different species. *Cortinarius phaeopygmaeus* occurs in the boreal zone. Two collections were found in boreal *Salix* thickets in Finland. They were determined by having identical sequences with the lectotype excluding the ambiguous bases. Another collection is mentioned in Kokkonen (2020) as *Cortinarius* sp. (p. 102, KK 723/03). Surprisingly, the RPB2 sequences of the boreal *phaeopygmaeus* collections and *C. vulpicolor* M.M. Moser & McKnight were nearly identical, deviating only by a heterozygous locus in *C. vulpicolor*, although their ITS sequences differed as much as five bases and two indels.

The boreal *phaeopygmaeus* specimens agree morphologically with the description of Favre and the lectotype, except that the colour of velum was not distinctly yellow brown but yellowish or whitish. The pilei were dark red brown, with or without a small umbo and up to 2.3 cm broad. The stipes were often flocculose and had sometimes a band. The smell was weak, vaguely reminiscent of Pelargonium. Both collections had weakly or rather weakly verrucose, ellipsoid, moderately to rather strongly dextrinoid spores. One of them had on average narrower spores with mean size  $10.4 \times 5.9 \mu\text{m}$  and mean  $Q=1.78$  ( $n=20$ ), and some spores were subamygdaloid. The mean spore size of the other was  $10.3 \times 6.3 \mu\text{m}$  with mean  $Q=1.65$  ( $n=20$ ). They were found from moist habitats with *Salix phylicifolia*.

**OTHER SPECIMENS EXAMINED:** Finland. Pohjois-Karjala. Nurmes, Valtimo, Haapakylä, mouth of the river Matkusjoki, thicket with *Salix phylicifolia* and *S. myrsinifolia*, 18.IX.2003 Kokkonen 723/03. Kainuu. Kuhmo, N of Koirakangas, moist brookside, under *S. phylicifolia*, near *Alnus incana*, 7.IX.2018 Kokkonen 645/18.

***Cortinarius comatus*** J. Favre, *Ergebn. Wiss. Unters. Schweiz. Natl. Parks* 5 (33): 202 (1955)

= ***Cortinarius rusticellus*** J. Favre, *Ergebn. Wiss. Unters. Schweiz. Natl. Parks* 5 (33): 204 (1955)

**LECTOTYPE:** *Cortinarius rusticellus* J. Favre. Switzerland, Graubünden, Alp Murter, National Park, alt. 2400 m, by *Salix retusa*, 26.VIII.1942 J. Favre 165a (GK13512). — Specimen with ca. 7 fruitbodies in more or less good condition. Pileus usually strongly fibrillose or squamulose. Spores  $9.5\text{--}10.4\text{--}13.0 \times 6.3\text{--}6.8\text{--}7.8 \mu\text{m}$ ,  $Q=1.35\text{--}1.53\text{--}1.76$  ( $n=20$ ); ellipsoid, rarely subamygdaloid or amygdaloid, rarely with a slight suprahilal depression; rather weakly verrucose, in one fruitbody apex often strongly verrucose; indextrinoid or very weakly dextrinoid. Lamellar hyphae encrusted and with dark flecks. Four examined fruitbodies, including one with a smoother pileus, had a similar micromorphology.

**SYNTYPE:** *Cortinarius rusticellus* J. Favre. Switzerland, Graubünden, Tarasp, Munt dalla Bescha, alt. 2500-2550 m, among *Salix herbacea*, 8.IX.1945 J. Favre 165b (GK13513). — Specimen with ca. 10 fruitbodies in good condition. Pileus more or less smooth. Spores  $9.7\text{--}10.8\text{--}12.6 \times 5.6\text{--}6.3\text{--}7.1 \mu\text{m}$ ,  $Q=1.47\text{--}1.72\text{--}1.95$  ( $n=40$  from 2 fruitbodies); ellipsoid to subamygdaloid, rarely with a slight suprahilal depression; moderately verrucose, often somewhat more strongly at apex; moderately dextrinoid. Lamellar hyphae encrusted. Two examined fruitbodies with a similar micromorphology. Determined as *Cortinarius lamoureae* Bon by ITS. RPB2 failed.

**COMMENTS:** The lectotype of *C. rusticellus* was sequenced by Liimatainen et al. (2020). Since this ITS sequence deviates only by one base from several *C. comatus* sequences including the ITS1 of the *C. comatus* lectotype (Kokkonen 2020 and Fig. 2), and its morphology agreed with both *C. comatus* and the description of *C. rusticellus* by Favre (1955), *C. rusticellus* is reduced to a synonym of *C. comatus*. These species were published at the same time. The spores of the *C. rusticellus* lectotype were on average larger than the spores of the *C. comatus* lectotype and most *C. comatus* specimens, but the spore size of *C. comatus* has varied much and has sometimes been

as large as in the *C. rusticellus* lectotype (Kokkonen 2020). Contrary to expectations, the *C. rusticellus* lectotype was not found to be a mixed collection, but the syntype was a different species, conspecific with *C. lamoureae*. Their spores differed clearly by dextrinoidity and the lectotype spores were wider.

The identity of *C. rusticellus* has been vague: it has been interpreted differently by mycologists and appeared unclear also to Favre, since the lectotype and the syntype were different species. Favre (1955) published spore drawings of both the lectotype and the examined syntype, but the announced spore size  $9\text{--}12 \times 6.5\text{--}7.5 \mu\text{m}$  agrees better with the lectotype, which is why the syntype is not selected as a new lectotype. Also, the description of pileus as coarsely fibrillose, nearly fluffy (Favre 1955) describes typical *C. comatus*. The spores of the *C. rusticellus* lectotype as published by Horak (1987) resemble the usual spores of *C. lamoureae*, since they are narrower and have a distinct suprahilar depression. The spores may not represent the lectotype.

***Cortinarius chrysophilus*** Kokkonen, sp. nov.  
Figure 1 and Kokkonen (2020) Figure 4h  
Mycobank MB847009

**ETYMOLOGY:** the name refers to the type locality “Golden Bay” and the yellow brown velum.

**TYPE:** Finland, Keski-Pohjanmaa, Raahe, Kultalanlahti, sandy sea shore with scattered *Salix* bushes, near *Salix phylicifolia*, among hay, herbs and mosses, 23.IX.2022 K. Kokkonen 93/22 (holotype TUR; isotype G).

**PILEUS** diameter 6–18 mm; convex, campanulate or applanate, with or without obtuse umbo, rarely margin slightly undulate; dark brown, dark red brown ( $S_{60}Y_{50-60}M_{50}$ ), rarely paler red brown, centre often blackish; when young entirely covered by yellow brown or brownish squamules or fibrils, later usually fibrillose only at margin, margin often with yellow brown or whitish velum remnants; hygrophane, turning yellow when drying, translucently striate at margin or not. **LAMELLAE** up to 2.5 mm broad; adnate or emarginate; distant or rather distant; dark brown, rather dark brown or red brown; edge even or fimbriate, concolorous. **STIPE** 14–32 mm long, 1–2 mm wide; equal, rarely slightly tapering downwards or base clavate; dark brown

or red brown, more rarely yellow brown or at times apex yellow brown, often darkening towards base, at times base blackish; covered with yellow brown, cream or whitish squamules or fibrils, rarely only delicately silky fibrillose. **CONTEXT** at pileus dark brown or black brown, at stipe dark brown or apex yellow brown and darkening towards base, base up to black brown. **SMELL** not distinctive.

**SPORES** (7.3)8.2–9.3–10.5(11.5)  $\times$  (4.5)4.7–5.1–5.6(5.8)  $\mu\text{m}$ , range of mean values  $8.9\text{--}9.7 \times 4.9\text{--}5.3 \mu\text{m}$ ,  $Q=(1.49)1.64\text{--}1.82\text{--}2.02(2.14)$ , range of mean  $Q$  values 1.72–1.87 (120 spores from 6 collections); ellipsoid, amygdaloid or fusoid, the predominant shape varies among specimens, often with a suprahilar depression; moderately to rather strongly verrucose, rarely rather weakly verrucose, verrucae usually larger at apex; rather weakly or weakly dextrinoid. **BASIDIA**  $23\text{--}30 \times 7\text{--}9 \mu\text{m}$  ( $n=16$ ), 4-spored. **LAMELLAR HYPHAE** strongly encrusted and with dark brown flecks. **PILEIPELLIS** hyphae 1.5–30  $\mu\text{m}$  wide, brown, coarsely encrusted, with dark brown crystals.

**HABITAT** boreal sandy sea shores and alpine zone. Connected with *Salix*: found near *Salix phylicifolia* and sometimes also *Alnus incana* in the boreal zone as well as near *Salix herbacea* or other low *Salix* in the alpine zone.

**DISTRIBUTION** known from two middle boreal sites in Finland and one alpine site in Switzerland.

**ADDITIONAL SPECIMENS EXAMINED:** Finland. Keski-Pohjanmaa. Kalajoki, Hiekkasärkät, near *Salix phylicifolia* and *Alnus incana*, 9.IX.2004 Kokkonen 235/04, 252/04. Switzerland. Graubünden. Scuol, Lai Sessenna, alt. 2660 m, near *Salix herbacea*, 17.VIII.2017 Kokkonen 286/17, 313/17, near *S. herbacea*, *S. reticulata* and *S. cf. helvetica*, 21.VIII.2022 Kokkonen 48/22.

**COMMENTS:** *Cortinarius chrysophilus* is characterized by small, dark brown fruitbodies with yellow brown or brownish fibrils or squamules at least when young, ellipsoid to amygdaloid spores with a suprahilar depression, and growth with *Salix*. It belongs genetically to the diverse *C. diasemospermus* coll. group within the *C. cucumisporus* complex (Kokkonen 2020). The species was delimited genetically: it was the most distant subgroup and was highly supported both by ITS and RPB2 as a separate species. The ITS sequence deviated 3–5 bases and 2–3 indels

from the types of *C. diasemospermus* Lamoure and *C. stenospermus* Lamoure, turned out to be a synonym of *C. desertorum* (Velen.) Garnier on the basis of the published type sequence of *C. desertorum* (Liimatainen et al. 2020). The type sequences of *C. stenospermus* and *C. desertorum* differ only by an indel. Also, other published *C. desertorum* synonyms with complete type sequences (Liimatainen et al. 2020) differed at least by 3 bases and 2 indels from *C. chrysophilus*.

*Cortinarius chrysophilus* may morphologically be confused with other species or subgroups within *C. diasemospermus* coll., most easily with *C. diasemospermus* s. str., which has sometimes been observed with yellow brown fibrils on stipe or on pileus and similar spores by the author. However, *C. desertorum* and others within *diasemospermus* coll. may also have sometimes a yellow brown or brownish velum. Two specimens representing *C. desertorum* and a subgroup of *C. diasemospermus* coll. were among the syntypes of *C. phaeopygmaeus*, which was described to have a yellow brown velum by Favre (1955). Further, the *C. desertorum* synonyms, *C. ammophilus* A. Pearson and *C. pertristis* J. Favre were described to have a pale brown or brown velum (Pearson 1946, Favre 1955). *Cortinarius chrysophilus* has never been observed with a Pelargonium smell unlike sometimes other fungi of this complex. Micromorphological differences were observed when compared to some subgroups: the spores of Groups 1 and 3 (Kokkonen 2020) were on average wider and the spores of Group 2 more strongly dextrinoid.

There exist also other similar looking small *Telamonia* species with *Salix*. *Cortinarius comatus* has also yellow brown squamules, but its spores are wider, and it has so far been found only from paludified *Salix* thickets in the boreal zone. The spores of *C. phaeopygmaeus* are wider, more weakly verrucose and more strongly dextrinoid. The spores of *C. lamoureae* are more strongly dextrinoid and usually wider. When compared to the common *C. saniosus*, *C. saniosus* has a yellower stipe, a smoother pileus, and more strongly dextrinoid, ellipsoid spores.

*Cortinarius desertorum* (Velen.) Garnier, Bibliographie des Cortinaires, D-O: 18 (1991). Basionym *Telamonia desertorum* Velen., Novitates Mycologicae: 110 (1939) = *Cortinarius stenospermus* Lamoure, Arctic Alpine Mycology. II: 255 (1987).

## Discussion

*Telamonia* species growing with *Salix* consist of species complexes, where the differences among closely related species are small (Kokkonen 2020). Also, the species may be difficult to delimit. This emphasizes care in morphological observations, genetic analyses and habitat information. The DNA studies have proven to be invaluable. In some cases, it seems impossible to identify species reliably based on morphology. Similar problems had mycologists in the past, which was revealed also in this study concerning Favre's collections of *C. phaeopygmaeus* and *C. rusticellus*. Type sequences are highly significant, and it is important to keep in mind that the type collections may consist of more than one species, too. New methods and large datasets are welcome for the study of this difficult subgenus.

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### Electronic supplementary materials

ESM1: Alignment of ITS sequences

ESM2: Alignment of RPB2 sequences