Cortinarius subsalor and *C. tibeticisalor* spp. nov., two new species from the section *Delibuti* from China (#61287)

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Cortinarius subsalor and *C. tibeticisalor* spp. nov., two new species from the section *Delibuti* from China

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Cortinarius subsalor and *C. tibeticisalor* belonging to the section *Delibuti*, are described from China as new to science. *Cortinarius subsalor* has been found associated with *Lithocarpus* trees in subtropical China and resembles *C. salor*, but it differs with *C. salor* by the slender basidiomata and the narrower basidiospores, as well as molecular sequence data. *Cortinarius tibeticisalor* were collected from eastern Tibetan Plateau associated with *Abies*, differs from other species in sect. ~~*Delibuti* by the olive tinge of mature or dried basidiomata and bigger basidiospores.~~ The molecular data also support *C.subsalor* and *C.tibeticisalor* as new species. The phylogenetic analyses and biogeography of sect. *Delibuti* are discussed and a key to the species of this section currently known in the world is provided.

Cortinarius subsalor and *C. tibeticisalor* spp. nov., two new species from the section *Delibuti* from China

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Abstract

Cortinarius subsalor and *C. tibeticisalor* belonging to the section *Delibuti*, are described from China as new to science. *Cortinarius subsalor* has been found associated with *Lithocarpus* trees in subtropical China and resembles *C. salor*, but it differs with *C. salor* by the slender basidiomata and the narrower basidiospores, as well as molecular sequence data. *Cortinarius tibeticisalor* were collected from eastern Tibetan Plateau associated with *Abies*, differs from other species in sect. ~~*Delibuti* by the olive tinge of mature or dried basidiomata and bigger basidiospores~~. The molecular data also support *C.subsalor* and *C.tibeticisalor* as new species. The phylogenetic analyses and biogeography of sect. *Delibuti* are discussed and a key to the species of this section currently known in the world is provided.

Introduction

Cortinarius (Pers.) Gray is an ectomycorrhizal fungal genus, associated with a wide host ranges such as Betulaceae, Caesalpiniaceae, Cistaceae, Dipterocarpaceae, Fagaceae, Myrtaceae, Pinaceae, Rhamnaceae, Rosaceae, Salicaceae and some herbaceous plants (*Frøslev, Brandrud & Jeppesen, 2006*; *Niskanen, 2008*). The genus is distributed worldwide. Even though it is the largest genus among macrofungi, but species diversity is still unknown. Most of *Cortinarius* species were originally discovered from Europe and America continent, and rarely in Asia and Africa (*Horak, 1983*; *Xie et al., 2020*).

Cortinarius sect. *Delibuti* (Fr.) Sacc. with characteristics of viscid pileus and stipe, have usually been considered as a section in subg. *Myxacium* (Fr.) Trog (*Trog, 1844*; *Earle, 1902*; *Orton, 1955*; *Brandrud et al., 1989*; *Consiglio, Antonini & Antonini, 2003*). *Delibuti* species can easily be distinguished by the anomaloid appearances, mild taste and subglobose basidiospores from other myxacioid species (*Orton, 1955*; *Soop, 2014*). Section *Delibuti* was also considered belonging to subg. *Phlegmacium* (Fr.) Trog (*Bidaud, Moënne-Loccoz & Reumaux, 1992*; *Bidaud, Moënne-Loccoz & Reumaux, 1994*). Recently, *Soop et al.* (*2019*) treated sect. *Delibuti* among anomaloid sections, not in myxacioid sections based on the shared characters of sect. *Delibuti* and sect. *Anomali* Konrad & Maubl., together with the close relationship in the phylogenetic analyses. In the past, numeral species were assigned to section *Delibuti* (*Fries, 1838*; *Earle, 1902*; *Bidaud, Moënne-Loccoz & Reumaux, 1992*; *Soop, 2013*; *Soop, 2014*), however most species have been confirmed not belong to this section (*Orton, 1955*; *Consiglio, 2012*; *Dima et al., 2016*; *Soop et al., 2019*). *Soop et al.* (*2019*) defined only ten species in sect. *Delibuti*, but the phylogenetic analyses verified and showed that there can still be some undescribed species in this section (*Harrower et al., 2011*; *Garnica et al., 2016*; *Soop et al., 2019*). In China, four *Delibuti* species, *C. betulinus* J. Favre, *C. delibutus* Fr., *C. illibatus* Fr., and *C. salor* Fr., were reported (e.g. *Teng, 1963*; *Yuan & Sun, 1995*; *Shao & Xiang, 1997*; *Li & Azbukina, 2011*; *Xie, 2018*; *Wang et al., 2020*), but none of them have been confirmed by molecular sequence data, thus their occurrence in China is yet controversial.

We have conducted taxonomic and phylogenetic studies of *Cortinairus* in China. Several new *Cortinairus* species have been described from China (*Wei & Yao, 2013*; *Xie et al., 2019*; *Xie et al., 2020*; *Xie et al., 2021*; *Yuan et al., 2021*). Some glutinously violet *Cortinarius* specimens resemble *C. salor* were found during intensive field work and later, during the identification process they turned out to be new species which we describe here based on morphological and ecological characteristics, as well as phylogenetic analyses evidences. We also discuss the phylogenetic relationship and biogeography of sect. *Delibuti*. An identification key to the known species of sect. *Delibuti* is provided.

Materials & Methods

Specimens and morphological description

Specimens were collected from Zhejiang Province and Tibet Autonomous Region, respectively. The collection sites in Zhejiang are subtropical areas with the evergreen broadleaved forests dominated by *Lithocarpus brevicaudatus*. Meanwhile, the collection sites in Tibet are plateau-alpine areas, and these coniferous forests dominated by *Abies georgei* var. *smithii*. Fresh basidiomata were photographed in the field. Macroscopic characteristics were measured and recorded from every basidiomata, color codes follow *Kornerup & Wanscher* (*1978*). Microscopic features were examined and described in 5% KOH, Congo Red or Melzer's reagent and observed under a Zeiss AX10 light microscope. Thirty to forty mature basidiospores were measured (excluding apiculus and ornamentation) per collection. The length/width ratio (Q) was calculated for individual basidiospores. $X_{av.}$ and $Q_{av.}$ refer to the average value of basidiospores of each specimen. Voucher specimens deposited in the Herbarium of Mycology, Jilin Agricultural University (HMJAU), Changchun, China.

Phylogenetic reconstruction

DNA extraction, PCR amplifications, and sequencing methods followed *Xie et al.* (*2019*). The primers ITS1F and ITS4 were used in both PCR and sequencing reactions for the nrDNA ITS region with (*White et al., 1990*; *Gardes & Bruns, 1993*). The newly generated ITS sequences were submitted to GenBank. The ITS sequences for the phylogenetic analyses were selected based on results of BLASTn (> 90% identity) in GenBank and UNITE and followed the publication by *Garnica et al.* (*2016*) and *Soop et al.* (*2019*). Two species in section *Cyanites* Nespiak were chosen as outgroup followed *Xie et al.* (*2021*).

Sequences (*Table 1*) for the phylogenetic analyses were aligned and edited with BioEdit 7.1.3.0 and Clustal X (*Tompson et al., 1997*; *Hall, 1999*). For phylogenetic analyses, Bayesian Inference (BI) and Maximum Likelihood (ML) methods were implemented in this study. MrModeltest 2.3 was used to calculate the best model (HKY+I+G) for Bayesian Inference (BI) analysis (*Nylander et al., 2008*). BI analysis was performed with MrBayes 3.2.6 (*Ronquist & Huelsenbeck, 2003*). Markov Chains Monte Carlo (MCMC) chains were run for 500 000 generations, sampling every 100th at which point the average standard deviation of split frequencies was 0.009032. A The 50% majority rule consensus tree of the BI trees sampled in the MCMC analyses and posterior probability values were estimated from the samples after discarding the first 25% (1250) of sampled trees. The ML analysis was performed with RAxML (*Stamatakis, 2014*) and implemented in raxmlGUI (*Silvestro & Michalak, 2012*). All parameters in the ML analysis were kept as defaults, except for choosing GTRGAMMA as the model of sequence evolution. For testing the support of the branches, rapid bootstrap analysis with 1,000 replicates was chosen. The phylogenetic trees were visualized in FigTree 1.4.3. The Bayesian posterior probabilities values (BPP) ≥ 0.95 and ML bootstrap values (ML) ≥ 75% are shown on the branches at the nodes (BPP/ML).

Nomenclature

The electronic version of this article in Portable Document Format (PDF) will represent a published work according to the International Code of Nomenclature for algae, fungi, and plants, and hence the new names contained in the electronic version are effectively published under that

Code from the electronic edition alone. In addition, new names contained in this work have been submitted to MycoBank from where they will be made available to the Global Names Index. The unique MycoBank number can be resolved and the associated information viewed through any standard web browser by appending the MycoBank number contained in this publication to the prefix "http://www.mycobank.org/MycoTaxo.aspx?Link=T&Rec=". The online version of this work is archived and available from the following digital repositories: PeerJ, PubMed Central, and CLOCKSS.

Results

Phylogenetic analyses

The alignment contained 67 ITS sequences with 785 nucleotide sites, include 260 informative sites (see Supplemental Material). The BI and ML trees showed similar topologies and ML tree was selected as the representative phylogeny (*Figure 1*). The phylogenetic analyses showed 11 sections including section *Cyanites* outgroup, in addition one singleton species from Argentina, and two singletons from New Zealand. Every section formed separate monophyletic lineages with strong statistical support. Section *Delibuti* formed a distinct clade (BPP = 0.96) separated from other sections. Section *Delibuti* split into five main clades based on the analyses of ITS sequences. Clade A and B consist of Australasian species. Clade C is a clade including our new species from the Tibetan Plateau. Clade D consist of the species distributed in Europe, Asia and North and South America. Clade E represents the species in the Northern Hemisphere. *Cortinarius subsalor* (BPP/ML = 1.00/100%, clade E) and *C. tibeticisalor* (BPP/ML = 1.00/100%, clade C) formed a dinstinct lineages with high statistical support, respectively. Furthermore, *C. subsalor* formed a sister relationship with the European *C. salor* (BPP = 0.97, clade E).

Taxonomy

***Cortinarius subsalor* M.L. Xie, T.Z. Wei & Y. Li, sp. nov.**

MycoBank No. MB839320

(*Fig. 2*)

Etymology. The name refers to the similar species *Cortinarius salor*.

Holotype. CHINA. Zhejiang: Baishanzu Mountain, Qingyuan county, on moist soil under *Lithocarpus brevicaudatus* (Fagaceae) forest with scattered Theaceae and *Rhododendron*, 27°45´44" N, 119°11´50" E, ASL 1510 m, 20 July 2020, Jun-Liang Chen, *QY-0235(1192-1198)* (HMJAU48759), GenBank: MW911734.

Diagnosis. Pileus hemispherical to plane, violet, glutinous; lamellae violet at first, then pale grayish violet; stipe slender, pale violet, then brown; glutinous veil violet. Basidiospores on average 8.0–8.3 × 6.9–7.0 µm, subglobose to broadly ellipsoid. Differing from other species in sect. *Delituti* by the violet color of basidiomata, the distribution of subtropical China and associated with *Lithocarpus brevicaudatus*.

Description

Pileus 20–50 mm, hemispherical at first, then convex to applanate; bluish violet (18B6-18C7) at first, purple (15B6-15C7) to purplish red (14A6-14B7) at the centre, then grayish violet (17B4-17C5), pale violet (19A3) at the margin; surface glutinous. Lamellae emarginate; moderately crowded; violet (17B6) when young, then grayish violet (17B4-17C5) to pale grayish violet (15B1-15C2); edge almost even. Stipe slender, 35–65 mm long, 3–7 mm thick, clavate at base (up to 14 mm); pale violet to grayish violet (19A3-19B5), later whitish, lightly brown to brown (7D6-7E7); surface with viscid universal veil, basal mycelium white with bluish tinge. Universal veil viscid, violet, remnants forming girdle on the upper part of the stipe, disappearing with age. Context whitish at the pileus, slightly yellowish tinge at the center, pale violet tinge extend outward, hygrophanous near lamellae; white with pale violet tinge at the apex of the stipe, yellow at the lower part; somewhat hollow at the stipe. Odour not significant, taste mild.

Basidiospores 7.4–9.5 (10.6) × 6–7.[illegible] (8.7) µm, Q = 1.10–1.29, $X_{av.}$ = 8.0–8.3 × 6.9–7.0 µm, $Q_{av.}$ = 1.20, subglobose to broadly ellipsoid, moderately coarsely verrucose, moderately dextrinoid. Basidia 4-spored. Lamellar edges fertile. Pileipellis: epicutis strongly gelatinous, about 180–250 µm thick, hyphae 2–7 µm wide, yellowish to colorless in 5% KOH, with small encrusted spots, with some thick-walled hyphae. Hypodermium present, hyphae 4–10 µm wide, cylindrical, almost colorless in 5% KOH, smooth. Clamp connections present.

Exsiccatae. Pileus grayish violet (19B3-19C4) at the margin, light brown to dark brown (6D6-6F8) at the centre; lamellae rust brown (6E8); stipe brown (6D7-6E7), lighter downwards, base yellowish white (4A2).

ITS sequence. The ITS sequence (MW911734, holotype) distinct from other members of sect. *Delibuti* and deviating from them by at least 22 substitutions and indel positions.

Ecology and distribution. In subtropical evergreen broadleaved forest, associated with *Lithocarpus brevicaudatus* (Fagaceae). Known from Zhejiang and Hunan province of China.

Additional specimens examined. CHINA. Zhejiang: Baishanzu Mountain, Qingyuan county, on moist soil under *Lithocarpus brevicaudatus* (Fagaceae) forest with scattered Theaceae and *Rhododendron*, 27°45′55″ N, 119°11′0″ E, ASL 1500 m, 20 August 2020, Meng-Le Xie, *20xml12101* (HMJAU48758), GenBank: MW911733.

***Cortinarius tibeticisalor* M.L. Xie, T.Z. Wei & Y. Li, sp. nov.**

MycoBank No. MB839321

(*Fig. 3*)

Etymology. The name refers to the Tibetan Plateau, the type locality, and similar with *C. salor*.

Holotype. CHINA. Tibet Autonomous Region: Sejila Mountain, Linzhi city, on moist soil in *Abies* forest with scattered *Rhododendron*, 29°35′26″ N, 94°35′53″ E, ASL 4120 m, 5 September 2020, Meng-Le Xie, *20xml12416* (HMJAU48764), GenBank: MW911729.

Diagnosis. Pileus hemispherical to applanate, violet, glutinous, margin wavy, somewhat olive when mature; lamellae for a long time violet, then pale grayish violet to violet gray; stipe robust, bluish gray to brown with olive tinge; glutinous veil violet. Basidiospores on average 10.3–10.8 × 8.7–8.9 µm, subglobose to broadly ellipsoid, rarely ellipsoid. Differing from other species in sect. *Delituti* by the olive tinge of basidiomata and the large basidiospores.

Description

Pileus 50–85 mm, hemispherical at first, then convex to plane, sometimes slightly depressed, margin wavy in mature basidiomata; violet (17C7) at first, especially at the centre, paler violet towards the margin, then grayish orange (5B5) to brown (5D6-5E7) with olive tinge, dark at the centre; surface glutinous. Lamellae emarginate; moderately crowded; persistently violet (17C7), then grayish violet (19B4-19C6) to violet gray (19B2); edge uneven, with slightly serrate. Stipe 85–120 mm long, 10–15 mm thick, clavate at base (up to 23 mm); surface with viscid bluish gray (19B2) universal veil remnants, then becoming yellow to brown with olive tinge (4B6-4D7), grayish violet (19B4-19C6) at the apex; basal mycelium white. Universal veil viscid, violet, remnants forming girdle on the upper part of the stipe, dispearing with age. Context white with marbled violet tinge at first, slightly yellowish tinge from the center of the pileus, then yellow at the stipe, especially at the middle. Odour weakly when fresh, somewhat like honey when old or dry. Taste mild.

Basidiospores 9.0–[illegible]) (13.5) × 7.7–10. 6 µm, Q = 1.10–1.39, $X_{av.}$ = 10.3–10.8 × 8.7–8.9 µm, $Q_{av.}$ = 1.20–1.23, subglobose to broadly ellipsoid, rarely ellipsoid, moderately coarsely verrucose, weakly dextrinoid. Basidia 4-spored. Lamellar edges fertile, with narrow clavate cells. Pileipellis: epicutis strongly gelatinous, about 300–410 µm thick, hyphae 3–8 µm wide, with yellowish intracellular pigment in 5% KOH, smooth. Hypodermium present, hyphae 7–15 µm wide, irregular, almost colorless in 5% KOH, smooth. Clamp connections present.

Exsiccatae. Pileus olive brown (4E6-4F7) at the margin, yellowish brown (5D7-5E8) at the centre; lamellae dark bluish gray (19E2-19F2); stipe bluish white at the apex, light brown (6D6-6E7) to dark brown (6F4-6F8), base white.

ITS sequence. The ITS sequence (MW911729, holotype) distinct from other members of sect. *Delibuti* and deviating from them by at least 40 substitutions and indel positions.

Ecology and distribution. In plateau-alpine coniferous forests, associated with *Abies* (Pinaceae) trees. Known from Tibetan Plateau of China.

Additional specimens examined. CHINA. Tibet Autonomous Region: Sejila Mountain, Linzhi city, on moist soil under *Abies* forest with scattered *Rhododendron*, 29°35′25″ N, 94°35′55″ E, ASL 4170 m, 28 August 2019, Meng-Le Xie, *19xml10976* (HMJAU48761), GenBank MW911731, *19xml10981* (HMJAU48762), GenBank MW911732; Sejila Mountain, Linzhi city, on moist soil under *Abies* forest with scattered *Rhododendron*, 29°35′26″ N, 94°35′53″ E, ASL 4120 m, 5 September 2020, Meng-Le Xie, *20xml12395* (HMJAU48763), GenBank: MW911730.

Key to species of sect. *Delibuti*

1 Distributed in Northern Hemisphere 2

- Distributed in Southern Hemiphere 9

2. Pileus usually yellowish to ochraceous without blue 3

- Pileus violet to blue, sometimes partly yellow 4

3. Lamellae usually blue when young, veil yellowish .... ***C. delibutus***

- Lamellae pinkish ochraceous clay, veil not yellowish .... ***C. illibatus***

4. Pileus frankly blue when young, stipe bluish, veil violet 5

- Pileus greish blue to olive brown, stipe pale, veil different 7

5. Basidiomata usually small, lamellae violet, then grayish to brownish, stipe usually slender (< 10 mm), base white with bluish tinge, basidiospores on average 8.0–8.3 × 6.9–7.0 µm, subglobose to broadly ellipsoid, distributed in subtropical China, associated with *Lithocarpus brevicaudatus* .... ***C. subsalor***

- Basidiomata usually bigger, lamellae persistently lilaceous or bluish, the stipe usually more robust (> 10 mm thick) 6

6. Pileus usually staining buff or fading from the centre, stipe base usually grayish brown, basidiospores 7–9 × 6–8 µm, globose to subglobose, distributed in Europue, associated with deciduous and coniferous trees .... ***C. salor***

- Pileus usually olive brown when mature, stipe base usually white, basidiospores 10.3–10.8 × 8.7–8.9 µm, subglobose to broadly ellipsoid, rarely ellipsoid, distributed in Tibetan Plateau of China, associated with *Abies* .... ***C. tibeticisalor***

7. Basidiomata small, pileus yellow to olive-ochre at the centre, grayish blue towards the margin, soon fading, veil yellow, basidiospores 7.5–9.5 × 6.5–7.5 µm, subglobose, associated with *Betula* ……..……. ***C. betulinus***

- Basidiomata robust, associated with *Picea* 8

8. Pileus olive brown with a violet margin, veil olive brown, basidiospores 8–10 × 7–8 µm, globose .... ***C. transiens***

- Pileus more orange tinge, basidiospores 7.5–9.5×6.5–7.5 µm, subglobose ...... ***C. largodelibutus***

9. Associated with *Nothofagus* 10

- Associated with Myrtaceae trees 11

10. Pileus viscid, blue-green to aerugineous, stipe blue green, basidiospores 6.5–8.5 × 6–7 µm, subglobose, destributed in Australasia .... ***C. tessiae***

- Pileus glutinous, greyish yellow to greyish orange, stipe violet, then becoming white to pale brownish, basidiospores ellipsoid, destributed in North and South America .... ***C. illitus***

11. Basidiomata distinctly viscid to glutinous, mainly greyish blue-green, basidiospores 7–9 × 7–8 µm, globose to subglobose .... ***C. rotundisporus***

- Basidiomata weakly viscid, stipe often dry, mainly yellow-green to olive, Veil orange to ochraceous, basidiospores 6–7.5 × 5.5–6.5 µm, subglobose .... ***C. calaisopus***

Discussion

Cortinarius subsalor is similar with *C. betulinus*, *C. salor* and *C. transiens* (Melot) Soop due to the bluish tinge of the basiodiomata. However, *C. betulinus* is usually grayish blue at the margin of pileus and soon fading, the stipe often pale and the veil usually is yellow (*Kibby, 2005*; *Niskanen et al., 2008*; *Soop, 2014*). The pileus of *C. transiens* is often with a violet tone towards the margin, while the centre is more olive gray to yellowish brown even in young specimens, the stipe is pale, as well as the gelatinous veil is olive brown (*Soop, 1990*; *Soop, 2014*). In China sometimes some bluish myxacioid species have been misidentified as *C. salor* (MHHNU30409, GenBank: MK250915), collected from Hunan Province. Our phylogenetic analyses showed that this sequence belong to the new species *C. subsalor*. *Cortinarius salor* has persitently lilaceous lamellae, the stipe more robust (> 10 mm thick) and the base is more grayish brown, the the basidiospores are rounder (7–9 × 6–8 µm), and it occurs in European woodlands (*Orton, 1955*; *Consiglio, Antonini & Antonini, 2003*; *Soop, 2014*). Based on these features, *C. salor* can be distinguished from the Asian *C. subsalor*.

Cortinarius tibeticisalor is characterized by the basidiomata usually violet when young, then grayish orange to brown with an olive tinge, large basidiospores and a restricted distribution in the Tibetan Plateau. *Cortinarius tibeticisalor* is similar to *C. salor* in young stage, however, the basidiospores (7–9 × 6–8 µm) of *C. salor* are significantly smaller and rounder, as well as the basidiomata never have olive tinge (*Orton, 1955*; *Consiglio, Antonini & Antonini, 2003*; *Soop, 2014*).

According to our phylogenetic analyses, sect. *Delibuti* demonstrates a widely distributed lineage of *Cortinarius*, in both the Northern and Southern Hemispheres. This bihemispherical distribution is also seen in several other lineages in *Cortinarius*, such as *Anomali*, *Bolares*, *Camphorati*, *Defibulati*, *Illumini*, and *Vibratiles*, which result is in concordance with other papers (e.g. *Harrower et al., 2015*; *Garnica et al., 2016*; *Soop et al., 2019*). The nrDNA ITS region is not suitable to draw conclusions for comprehensive phylogenetic evaluation, however, there are some interesting patterns indicated in sect. *Delibuti* to be further discussed. The basal lineages (clade A and B) of *Delibuti* are solely distributed in the Australasia showing a presumable origin of the section in Australasia. Interestingly, the clade D contains species from multiple continents in the Northern and Southern Hemispheres. Some species distributed in Asia (*Cortinarius* sp., LC175538), in Europe (*Cortinarius* sp., JF907917), and in South America, like *Cortinarius* sp. (MF599228) from Colombia and *C. illitus* M.M. Moser & E. Horak, originally described from Argentina (*Moser & Horak, 1975*), but also found in North America (according to the sequences in GenBank).These patterns could explain that the evolution of sect. *Delibuti* is limited to the ectomycorrhizal host specificity, as well as geographic barriers (*Wang & Qiu, 2006*; *Brandrud, 1996*; *Wilson et al., 2017*; *Feng et al., 2016*). The evolution and origin of sect. *Delibuti*, even of genus *Cortinarius* will be a subject for future research.

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Figure 1

ML phylogram inferred from nrDNA ITS sequence data.

The tree is rooted with sect. *Cyanites*. The Bayesian posterior probabilities (BPP) ≥ 0.95 and ML bootstrap values (ML) ≥ 75% are shown on the branches (BPP/ML). New species is marked by blue bold.

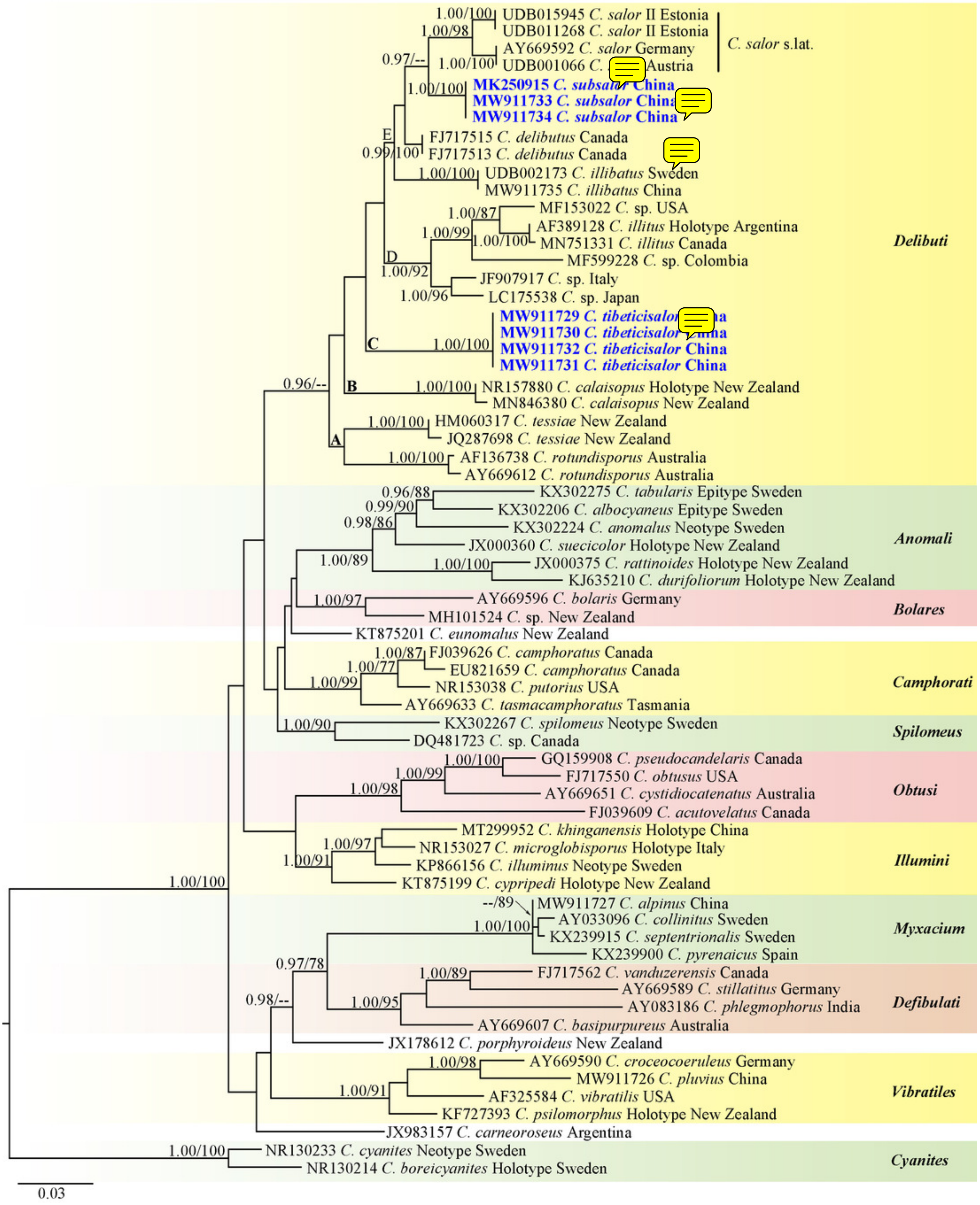
1.00/100
UDB015945 C. salor II Estonia
1.00/98
UDB011268 C. salor II Estonia
AY669592 C. salor Germany
0.97/--
1.00/100
UDB001066 C. Austria
C. salor s.lat.
1.00/100
MK250915 C. subsal China
MW911733 C. subsalor China
MW911734 C. subsalor China
E
FJ717515 C. delibutus Canada
0.99/100
FJ717513 C. delibutus Canada
1.00/100
UDB002173 C. illibatus Sweden
MW911735 C. illibatus China
1.00/87
MF153022 C. sp. USA
AF389128 C. illitus Holotype Argentina
1.00/99
1.00/100
MN751331 C. illitus Canada
Delibuti
D
MF599228 C. sp. Colombia
1.00/92
JF907917 C. sp. Italy
1.00/96
LC175538 C. sp. Japan
MW911729 C. tibeticisalor a
MW911730 C. tibeticisalor na
C
1.00/100
MW911732 C. tibeticisalor China
MW911731 C. tibeticisalor China
0.96/--
B
1.00/100
NR157880 C. calaisopus Holotype New Zealand
MN846380 C. calaisopus New Zealand
1.00/100
HM060317 C. tessiae New Zealand
A
JQ287698 C. tessiae New Zealand
1.00/100
AF136738 C. rotundisporus Australia
AY669612 C. rotundisporus Australia
0.96/88
KX302275 C. tabularis Epitype Sweden
0.99/90
KX302206 C. albocyaneus Epitype Sweden
0.98/86
KX302224 C. anomalus Neotype Sweden
Anomali
JX000360 C. suecicolor Holotype New Zealand
1.00/89
1.00/100
JX000375 C. rattinoides Holotype New Zealand
KJ635210 C. durifoliorum Holotype New Zealand
1.00/97
AY669596 C. bolaris Germany
Bolares
MH101524 C. sp. New Zealand
KT875201 C. eunomalus New Zealand
1.00/87
FJ039626 C. camphoratus Canada
1.00/77
EU821659 C. camphoratus Canada
1.00/99
NR153038 C. putorius USA
Camphorati
AY669633 C. tasmacamphoratus Tasmania
1.00/90
KX302267 C. spilomeus Neotype Sweden
Spilomeus
DQ481723 C. sp. Canada
1.00/100
GQ159908 C. pseudocandelaris Canada
1.00/99
FJ717550 C. obtusus USA
1.00/98
AY669651 C. cystidiocatenatus Australia
Obtusi
FJ039609 C. acutovelatus Canada
MT299952 C. khinganensis Holotype China
1.00/97
NR153027 C. microglobisporus Holotype Italy
1.00/91
KP866156 C. illuminus Neotype Sweden
Illumini
1.00/100
KT875199 C. cypripedi Holotype New Zealand
--/89
MW911727 C. alpinus China
1.00/100
AY033096 C. collinitus Sweden
Myxacium
KX239915 C. septentrionalis Sweden
KX239900 C. pyrenaicus Spain
0.97/78
1.00/89
FJ717562 C. vanduzerensis Canada
AY669589 C. stillatitus Germany
0.98/--
1.00/95
AY083186 C. phlegmophorus India
Defibulati
AY669607 C. basipurpureus Australia
JX178612 C. porphyroideus New Zealand
1.00/98
AY669590 C. croceocoeruleus Germany
MW911726 C. pluvius China
1.00/91
AF325584 C. vibratilis USA
Vibratiles
KF727393 C. psilomorphus Holotype New Zealand
JX983157 C. carneoroseus Argentina
1.00/100
NR130233 C. cyanites Neotype Sweden
Cyanites
NR130214 C. boreicyanites Holotype Sweden
0.03

Figure 2

Cortinarius susalor.

(A) HMJAU48759 (**Holotype**). (B) HMJAU48758. (C) Basidiospores (HMJAU48759). (D) Pileipellis (HMJAU48759). (Photos: M.L. Xie, J.L. Chen).

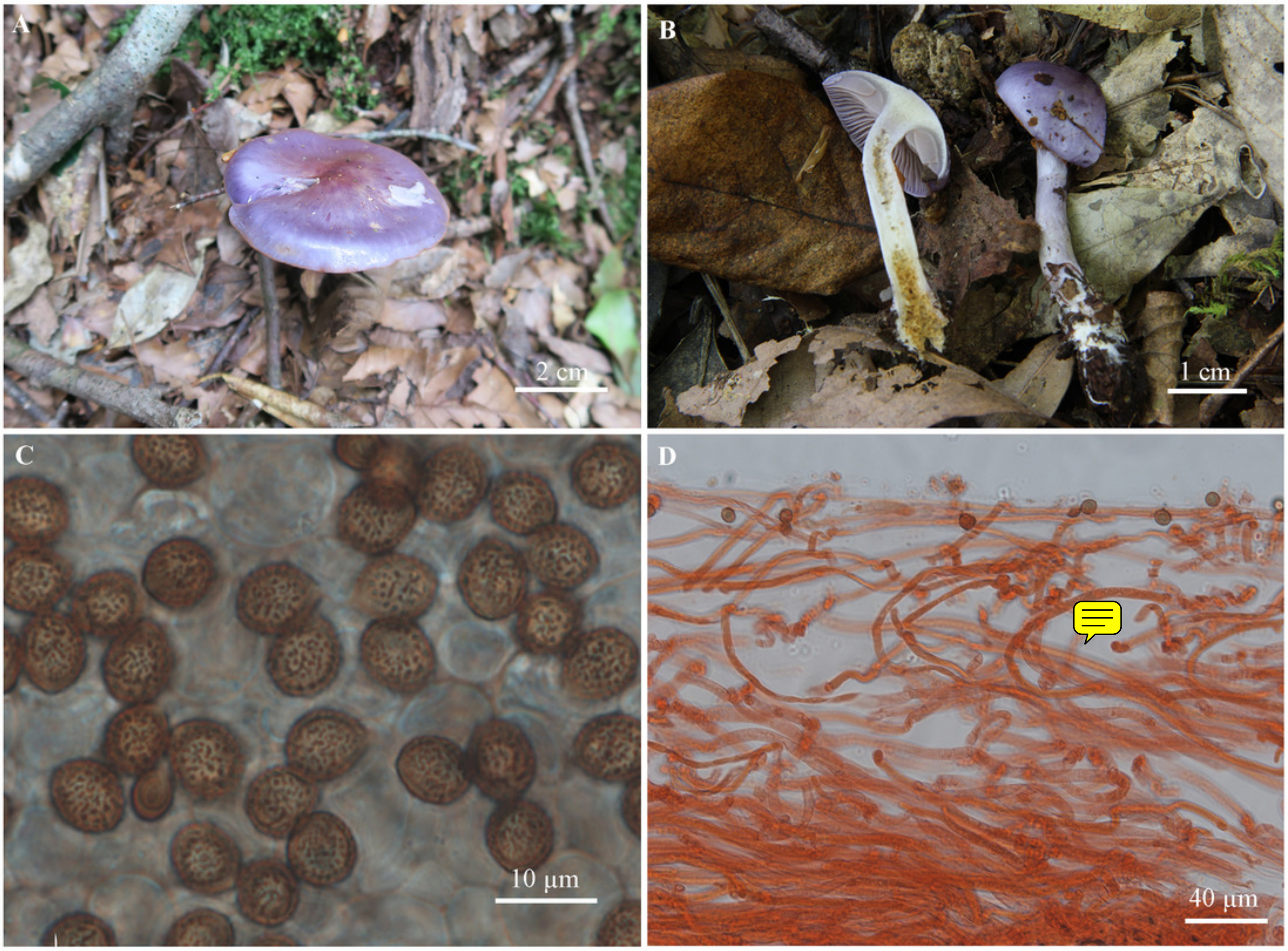

Figure 3

Cortinarius tibeticisalor.

(A) HMJAU48764 (**Holotype**). (B) HMJAU48762. (C) Basidiospores (HMJAU48764). (D) Pileipellis (HMJAU48764). (Photos: M.L. Xie).

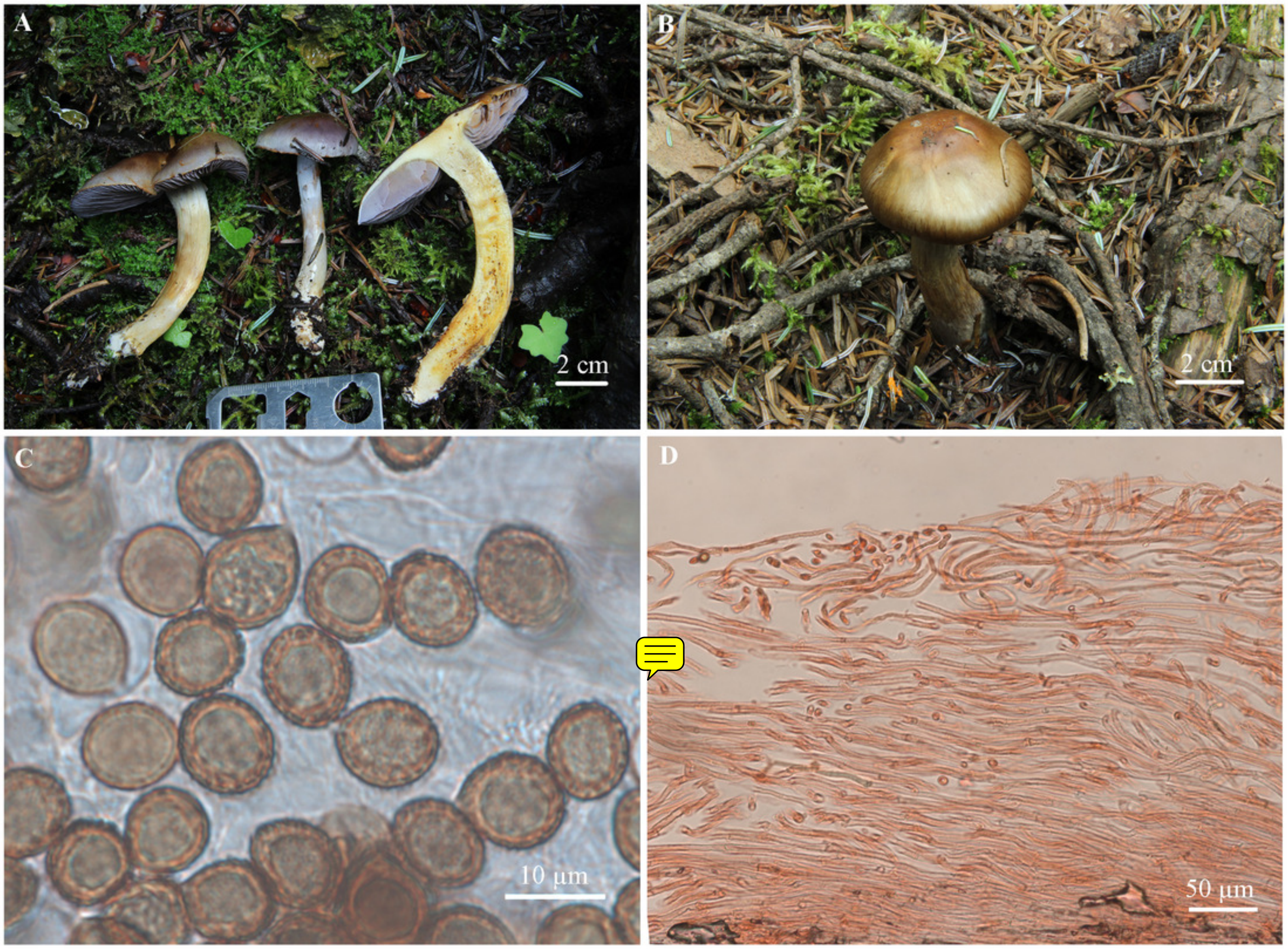

Table 1(on next page)

ITS sequences used in the phylogenetic analyses.

New species is in bold.

TABLE 1 ITS sequences used in the phylogenetic analyses. New species is in bold.

Species	**Voucher**	**Locality**	**Accession No.**	**References**
C. acutovelatus	F16388 (UBC)	Canada	FJ039609	*Harrower et al.* (*2011*)
C. albocyaneus Epitype	CFP1177 (S)	Sweden, Jämtland	KX302206	*Dima et al.* (*2016*)
C. alpinus	HMJAU44407	China, Neimenggu	MW911727	This study
C. anomalus Neotype	CFP1154 (S)	Sweden, Ångermanland	KX302224	*Dima et al.* (*2016*)
C. basipurpureus	PERTH 04259629	Australia	AY669607	*Garnica et al.* (*2005*)
C. bolaris	TUB 0118524	Germany	AY669596	*Garnica et al.* (*2005*)
C. boreicyanites Holotype	CFP931 (S)	Sweden, Jämtland	NR130214	*Liimatainen et al.* (*2014*)
C. calaisopus	60224 (OTA)	New Zealand	MN846380	GenBank
C. calaisopus Holotype	PDD 94050	New Zealand, Dunedin	NR157880	GenBank
C. camphoratus	DAVFP26155	Canada	EU821659	*Harrower et al.* (*2011*)
C. camphoratus	SMI193	Canada	FJ039626	*Harrower et al.* (*2011*)
C. carneoroseus	EN76 (CORD)	Argentina	JX983157	GenBank
C. collinitus	IB 19940257	Sweden	AY033096	*Peintner et al.* (*2002*)
C. croceocoeruleus	TUB 011833	Germany	AY669590	*Garnica et al.* (*2005*)
C. cyanites Neotype	AT2005069 (UPS)	Sweden, Uppland	NR130233	*Liimatainen et al.* (*2014*)
C. cypripedi Holotype	PDD 107723	New Zealand, Otago	KT875199	*Soop* (*2016*)
C. cystidiocatenatus	HO A20518A6	Australia, Tasmania	AY669651	*Garnica et al.* (*2005*)
C. delibutus	F17048 (UBC)	Canada	FJ717515	*Harrower et al.* (*2011*)
C. delibutus	SAT01-301-12	USA	FJ717513	*Harrower et al.* (*2011*)
C. durifoliorum Holotype	PDD 101829	New Zealand, Westland	KJ635210	*Soop, Wallace & Dima* (*2018*)
C. eunomalus	PDD 107706	New Zealand	KT875201	GenBank
C. illibatus	HMJAU48760	China, Heilongjiang	MW911735	This study
C. illibatus	AT2004220 (UPS)	Sweden	UDB002173	UNITE
C. illitus Holotype	IB 19630414	Argentina	AF389128	*Peintner, Moncalvo & Vilgalys*
C. illitus	MQ19-CMMF003109	Canada, Quebec	MN751331	GenBank
C. illuminus Neotype	F44877 (S)	Sweden	KP866156	*Niskanen et al.* (*2015*)
C. khinganensis Holotype	HMJAU44507	China, Neimenggu	MT299952	*Xie et al.* (*2021*)
C. microglobisporus	IB 20110123	Italy	NR153027	*Peintner et al.* (*2014*)
C. obtusus	SAT00-298-30	USA	FJ717550	*Harrower et al.* (*2011*)
C. phlegmophorus	Typus-M3	India	AY083186	*Peintner et al.* (*2003*)
C. pluvius	HMJAU44391	China, Neimenggu	MW911726	This study
C. porphyroideus	61406 (OTA)	New Zealand	JX178612	*Teasdale et al.* (*2013*)
C. pseudocandelaris	F17165 OC93 (UBC)	Canada, BC	GQ159908	*Harrower et al.* (*2011*)
C. psilomorphus Holotype	PDD 103885	New Zealand	KF727393	*Soop* (*2016*)
C. putorius Holotype	TN 07-411 (H)	USA	NR153038	*Ariyawansa et al.* (*2015*)
C. pyrenaicus	JB-8573/15	Spain, Gisclareny	KX239900	*Cadiñanos, Gomez & Ballarà* (*2016*)
C. rattinoides Holotype	PDD 88283	New Zealand	JX000375	GenBank
C. rotundisporus	PERTH 05255074	Australia	AY669612	*Garnica et al.* (*2005*)
C. rotundisporus	G12	Australia	AF136738	*Sawyer, Chambers & Cairney* (*1999*)
C. salor	IB 19940297	Austria	UDB001066	*Peintner et al.* (*2001*)
C. salor	TUB 011838	Germany	AY669592	*Garnica et al.* (*2005*)
C. salor Ⅱ	TUF106868	Estonia	UDB011268	UNITE

C. salor Ⅱ	TAAM128516	Estonia	UDB015945	UNITE
C. septentrionalis	ARAN Fungi03516	Sweden, Harjedalen	KX239915	*Cadiñanos, Gomez & Ballarà* (*2016*)
C. spilomeus Neotype	TEB CFP1137 (S)	Sweden	KX302267	*Dima et al.* (*2016*)
C. stillatitus	TUB 011587	Germany	AY669589	*Garnica et al.* (*2005*)
C. subsalor	**HMJAU48758**	**China, Zhejiang**	**MW911733**	**This study**
C. subsalor	**HMJAU48759**	**China, Zhejiang**	**MW911734**	**This study**
C. subsalor	**MHHNU 30409**	**China, Hunan**	**MK250915**	**GenBank**
C. suecicolor Holotype	PDD 74698	New Zealand	JX000360	GenBank
C. tabularis Epitype	CFP949 (S)	Sweden	KX302275	*Dima et al.* (*2016*)
C. tasmacamphoratus	HO A20606A0	Tasmania	AY669633	*Garnica et al.* (*2005*)
C. tessiae	PDD 94054	New Zealand, Dunedin	JQ287698	GenBank
C. tessiae	PDD 72611	New Zealand	HM060317	GenBank
C. tibeticisalor	**HMJAU48761**	**China, Tibet**	**MW911731**	**This study**
C. tibeticisalor	**HMJAU48762**	**China, Tibet**	**MW911732**	**This study**
C. tibeticisalor	**HMJAU48763**	**China, Tibet**	**MW911730**	**This study**
C. tibeticisalor	**HMJAU48764**	**China, Tibet**	**MW911729**	**This study**
C. vanduzerensis	VMS28	Canada	FJ717562	*Harrower et al.* (*2011*)
C. vibratilis	IB 19970078	USA	AF325584	*Peintner et al.* (*2001*)
C. sp.	CSU CO 2476	Colombia, Antioquia	MF599228	GenBank
C. sp.	FLAS-F-60161	USA	MF153022	GenBank
C. sp.	YM714	Japan, Hokkaido	LC175538	GenBank
C. sp.	1780	Italy	JF907917	*Osmundson et al.* (*2013*)
C. sp.	SWUBC500	Canada	DQ481723	*Wright, Berch & Berbee* (*2009*)
C. sp.	PDD 72685	New Zealand	MH101524	GenBank