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 to be associated with *Lithocarpus* trees in subtropical China and resembling *C. salor*, but it differs from *C. salor* in the slender basidiomata and the narrower basidiospores, as well as in molecular sequence data. *Cortinarius tibeticisalor* were collected from eastern Tibetan Plateau, associated with *Abies*, it differs from other species within sect. *Delibuti* in 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.

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Introduction

Cortinarius (Pers.) Gray is an ectomycorrhizal fungal genus, associated with a wide host range of plants, 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 its species diversity is still unknown. Most of *Cortinarius* species were originally discovered from Europe and America, 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 to belong 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 to 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 *Cortinarius* species have been described from China (*Wei & Yao, 2013*; *Xie et al., 2019*; *Xie et al., 2020*; *Xie et al., 2021*; *Yuan et al., 2020*). Some glutinous violet *Cortinarius* specimens resembling *C. salor* were found during an 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 the subtropical areas with the evergreen broadleaf forests

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dominated by *Lithocarpus brevicaudatus*. Meanwhile, the collection sites in Tibet are the plateau-alpine areas with 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.

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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) $\geq$ 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 association with *Lithocarpus brevicaudatus*.

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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 a girdle on the upper part of the stipe, disappearing with age. Context whitish at the pileus, slightly with 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 within stipe. Odor not significant, taste mild.

Basidiospores 7.4–9.5 (10.6) × 6–7.7 (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, with hyphae 2–7 µm wide, yellowish to colorless in 5% KOH, with small encrusted spots, with some thick-walled hyphae. Hypodermium present; hypodermial 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, yellowish white (4A2) at base.

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 broadleaf forests, 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 the similarity 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

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robust, bluish gray to brown with olive tinge; veil glutinous, 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, wavy at margin of 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, 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 a girdle on the upper part of the stipe, dispearing with age. Context white with marbled violet tinge at first, slightly yellowish from the center of the pileus, then yellow at the stipe, especially at the middle. Odor weak when fresh, somewhat like honey when old or dry. Taste mild.

Basidiospores 9.0–12.0 (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 margin, yellowish brown (5D7-5E8) at centre; lamellae dark bluish gray (19E2-19F2); stipe bluish white at apex, light brown (6D6-6E7) to dark brown (6F4-6F8), white at base.

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

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- Pileus more or less violet to blue when young, 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 grayish 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, 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..... ***C. transiens***
- Pileus more orange tinge, basidiospores 7.5–9.5 × 6.5–7.5 µm..... ***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 is 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

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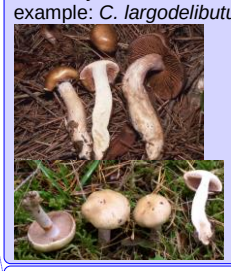

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批注 [I4]: Some species are not so obviously “grayish blue to olive brown”, for example: C. largodelibutus.

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the margin, while the centre is more olive gray to yellowish brown even in young specimens, the stipe is pale, and 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 is 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, larger 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, and 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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Acknowledgements

The authors are grateful to the anonymous reviewers for the constructive comments and suggestions on the manuscript. We also thank to Dr. Rong Xie and Ms. Hui-Juan Sun (Tibet Academy of Agricultural and Animal Husbandry Sciences) and Mr. Ju-Zuo Li (Life Science College, Northeast Normal University) for their kind help in the fieldwork.

References

Ariyawansa HA, Hyde KD, Jayasiri SC, Buyck B, Chethana KWT, Dai DQ, Dai YC, Daranagama DA, Jayawardena RS, Lücking R, Ghobad-Nejhad M, Niskanen T, Thambugala KM, Voigt K, Zhao RL, Li GJ, Doilom M, Boonmee S, Yang ZL, Cai Q, Cui YY, Bahkali AH, Chen J, Cui BK, Chen JJ, Dayarathne MC, Dissanayake AJ, Ekanayaka AH, Hashimoto A, Hongsanan S, Jones EBG, Larsson E, Li WJ, Li QR, Liu JK, Luo ZL, Maharachchikumbura SSN, Mapook A, McKenzie EHC, Norphanphoun C, Konta S, Pang KL, Perera RH, Phookamsak R, Phukhamsakda C, Pinruan U, Randrianjohany E, Singtripop C, Tanaka K, Tian CM, Tibpromma S, Abdel-Wahab MA, Wanasinghe DN, Wijayawardene NN, Zhang JF, Zhang H, Abdel-Aziz FA, Wedin M, Westberg M, Ammirati JF, Bulgakov TS, Lima DX, Callaghan TM, Callac P, Chang CH, Coca LF, Dal-Forno M, Dollhofer V, Fliegerová K, Greiner K, Griffith GW, Ho H-M, Hofstetter V, Jeewon R, Kang JC, Wen T-C, Kirk PM, Kytövuori I, Lawrey JD, Xing J, Li H, Liu ZY, Liu XZ, Liimatainen K, Lumbsch HT, Matsumura M, Moncada B, Nuankaew S, Parnmen S, de Azevedo Santiago A LCM, Sommai S, Song Y, de Souza CAF, de Souza-Motta CM, Su HY, Suetrong S, Wang Y, Wei SF, Wen TC, Yuan HS, Zhou LW, Réblová M, Fournier J, Camporesi E, Luangsa-ard JJ, Tasanathai K, Khonsanit A, Thanakitpipattana D, Somrithipol S, Diederich P, Millanes AM, Common RS, Stadler M, Yan JY, Li XH, Lee HW, Nguyen TTT, Lee HB, Battistin E, Marsico O, Vizzini A, Vila J, Ercole E, Eberhardt U, Simonini G, Wen HA, Chen XH, Miettinen O, Spirin V, Hernawati. 2015. Fungal diversity notes 111–252—taxonomic and phylogenetic contributions to fungal taxa. *Fungal diversity* 75:27–274 DOI 10.1007/s13225-015-0346-5.

Bidaud A, Moënne-Loccoz P, Reumaux P. 1992. *Atlas des Cortinaires* IV. Meyzieu: Éditions Fédération Mycologique Dauphiné-Savoie.

Bidaud A, Moënne-Loccoz P, Reumaux P. 1994. *Atlas des Cortinaires. Clé générale des sousgenres, sections, sous-sections et séries.* Meyzieu: Éditions Fédération Mycologique Dauphiné-Savoie.

Brandrud TE. 1996. *Cortinarius*, subgenus *Phlegmacium*, section *Phlegmacium* in Europe. A study of character variation and ecology including a numerical analysis of the *C. argutus* complex. *Mycological Research* 100(4):471–485 DOI 10.1016/S0953-7562(96)80146-8.

Brandrud TE, Lindström H, Marklund H, Melot J, Muskos S. 1989. *Cortinarius Flora Photographica* I. Sweden: Cortinarius HB.

Cadiñanos JA, Gomez MM, Ballarà J. 2016. *Cortinarius oreoborealis* y *C. pyrenaicus*, dos nuevas especies de la seccion *Myxacium*, subgenero *Myxacium* (Fr.) Trog ss. str. *Journal des JEC* 18:39–65.

Consiglio G, Antonini D, Antonini M. 2003. *Il Genere Cortinarius in Italia*, Parte prima. Luglio: Associazione Micologica Bresadola.

Consiglio G. 2012. *Il Genere Cortinarius in Italia*, Parte sesta. Luglio: Associazione Micologica Bresadola.

Dima B, Lindström H, Liimatainen K, Olson A, Soop K, Kytövuori I, Dahlberg A, Niskanen T. 2016. Typification of Friesian names in *Cortinarius* sections *Anomali*,

Spilomei and *Bolares*, and description of two new species from northern Europe. *Mycological Progress* 15(9):903–919 DOI 10.1007/s11557-016-1217-5.

Earle FS. 1902. A key to the North American species of *Cortinarius* I. *Torreya* 2(11):169–172 DOI 10.2307/40594021.

Feng B, Zhao Q, Xu JP, Qin J, Yang ZL. 2016. Drainage isolation and climate change-driven population expansion shape the genetic structures of *Tuber indicum* complex in the Hengduan Mountains region. *Scientific Reports* **6**:21811 DOI 10.1038/srep21811.

Fries EM. 1838. *Epicrisis Systematis Mycologici. seu synopsis hymenomycetum*. Uppsala.

Frøslev TG, Brandrud TE, Jeppesen TS. 2006. New species and combinations in *Cortinarius* subgenus *Phlegmacium* section *Calochroi*. *Mycotaxon* 97:367–377.

Gardes M, Bruns TD. 1993. ITS primers with enhanced specificity for basidiomycetes. Application to the identification of mycorrhizae and rusts. *Molecular Ecology* 2(2):113–118 DOI 10.1111/j.1365-294X.1993.tb00005.x.

Garnica S, Schön ME, Abarenkov K, Riess K, Liimatainen K, Niskanen T, Dima B, Soop K, Frøslev TG, Jeppesen TS, Peintner U, Kühnert-Finkernagel R, Brandrud TE, Saar G, Oertel B, Ammirati JF. 2016. Determining threshold values for barcoding fungi lessons from *Cortinarius* (Basidiomycota), a highly diverse and widespread ectomycorrhizal genus. *FEMS Microbiology Ecology* 92:fiw045 DOI 10.1093/femsec/fiw045.

Garnica S, Weiß M, Oertel B, Oberwinkler F. 2005. A framework for a phylogenetic classification in the genus *Cortinarius* (Basidiomycota, Agaricales) derived from morphological and molecular data. *Botany* 83(11):1457–1477 DOI 10.1139/b05-107.

Hall TA. 1999. BioEdit: A user-friendly biological sequence alignment editor and analysis program for windows 95/98/NT. *Nucleic Acids Symposium Series* 41(41):95–98 DOI 10.1021/bk-1999-0734.ch008.

Harrower E, Ammirati JF, Cappuccino AA, Ceska O, Kranabetter JM, Kroeger P, Lim S, Taylor T, Berbee ML. 2011. *Cortinarius* species diversity in British Columbia and molecular phylogenetic comparison with European specimen sequences. *Botany* 89(11):799–810 DOI 10.1139/b11-065.

Harrower E, Bougher NL, Henkel TW, Horak E, Matheny PB. 2015. Long-distance dispersal and speciation of Australasian and American species of *Cortinarius* sect. *Cortinarius*. *Mycologia* 107(4):697–709 DOI 10.3852/14-182.

Horak E. 1983. Mycogeography in the South Pacifc region: Agaricales, Boletales. *Australian Journal of Botany* 10:1–41 DOI 10.1071/BT8310001.

Kibby G. 2005. Fungal Portraits: No. 21: *Cortinarius betulinus*. *Field Mycology* 6(1):3–4 DOI 10.1016/S1468-1641(10)60282-4.

Kornerup A, Wanscher JHK. 1978. *The methuen handbook of colour*. London: Eyre Methuen Ltd. Reprint.

Li Y, Azbukina ZM. 2011. *Fungi of Ussuri river valley*. Beijing: Science Press.

Liimatainen K, Niskanen T, Dima B, Kytövuori I, Ammirati JF, Frøslev TG. 2014. The largest type study of Agaricales species to date: bringing identification and nomenclature of

Phlegmacium (*Cortinarius*) into the DNA era. *Persoonia* 33:98–140 DOI 10.3767/003158514X684681.

Moser M, Horak E. 1975. *Cortinarius* und nahe verwandte Gattungen in Südamerika. *Beihefte zur Nova Hedwigia* 52:1–628.

Niskanen T. 2008. *Cortinarius* subgenus *Telamonia* p.p. in North Europe. PhD. Thesis, University of Helsinki.

Niskanen T, Kytövuori I, Bendiksen E, Bendiksen K, Brandrud TE, Frøslev TG, Høiland K, Jeppesen TS, Liimatainen K, Lindström H. 2008. *Cortinarius* (Pers.) Gray. In: Knudsen H, Vesterholt J, ed. *Funga Nordica. Agaricoid, boletoid, clavarioid, cyphelloid and gastroid genera*. Copenhagen: Nordsvamp, 676–677.

Niskanen T, Kytövuori I, Liimatainen K, Ammirati JF. 2015. Nomenclatural novelties. *Index Fungorum* 256:1–2 http://www.indexfungorum.org/Publications/Index%20Fungorum%20no.256.pdf.

Nylander JAA, Zoology S, Posada D, Mrmodeltest R, Os F. 2008. MrModeltest 2.3 README, May 22 2008.

Orton PD. 1955. *Cortinarius* I. Leeds: The Naturalist.

Osmundson TW, Robert VA, Schoch CL, Baker LJ, Smith A, Robich G, Mizzan L, Garbelotto MM. 2013. Filling gaps in biodiversity knowledge for macrofungi: contributions and assessment of an herbarium collection DNA barcode sequencing project. *PLoS One* 8(4):e62419 DOI 10.1371/journal.pone.0062419.

Peintner U, Bougher NL, Castellano MA, Moncalvo JM, Moser MM, Trappe JM, Vilgalys R. 2001. Multiple origins of sequestrate fungi related to *Cortinarius* (Cortinariaceae). *American Journal of Botany* 88(12):2168–2179 DOI 10.2307/3558378.

Peintner U, Dresch P, Bellù F, Borghi E. 2014. *Cortinarius microglobisporus* (Basidiomycota), a new species with roundish spores related to *C. illuminus*. *Mycological Progress* 13(3):899–904 DOI 10.1007/s11557-014-0975-1.

Peintner U, Horak E, Moser MM, Vilgalys R. 2002. Phylogeny of *Rozites*, *Cuphocybe* and *Rapacea* inferred from ITS and LSU rDNA sequences. *Mycologia* 94(4):620–629 DOI 10.1080/15572536.2003.11833190.

Peintner U, Moncalvo JM, Vilgalys R. 2004. Toward a better understanding of the infrageneric relationships in *Cortinarius* (Agaricales, Basidiomycota). *Mycologia* 96(5):1042–1058 DOI 10.1080/15572536.2005.11832904.

Peintner U, Moser MM, Thomas KA, Manimohan P. 2003. First records of ectomycorrhizal *Cortinarius* species (Agaricales, Basidiomycetes) from tropical India and their phylogenetic position based on rDNA ITS sequences. *Mycological Research* 107(PT4):485–494 DOI 10.1017/S0953756203007585.

Ronquist F, Huelsenbeck JP. 2003. MrBayes 3: Bayesian phylogenetic inference under mixed models. *Bioinformatics* 19(12):1572–1574 DOI 10.1093/bioinformatics/btg180.

Sawyer NA, Chambers SM, Cairney JWG. 1999. Molecular investigation of genet distribution and genetic variation of *Cortinarius rotundisporus* in eastern Australian sclerophyll forests. *New Phytologist* 142(3):561–568 DOI 10.1046/j.1469-8137.1999.00417.x.

Shao LP, Xiang CT. 1997. *Forest Mushrooms of China*. Haerbin: Northeast Forestry University Press.

Silvestro D, Michalak I. 2012. RaxmlGUI: a graphical front-end for RAxML. *Organisms Diversity & Evolution* 12:335–337 DOI 10.1007/s13127-011-0056-0.

Soop K. 1990. Observationer av några intressanta *Cortinarius*-arter. *Agarica* 10/11(19/20):30–43.

Soop K. 2013. *Cortinarioid fungi of New Zealand*, 9th edn. Sweden: Éditions Scientrix.

Soop K. 2014. *Cortinarius in Sweden*, 14th edn. Sweden: Éditions Scientrix.

Soop K. 2016. A contribution to the study of the cortinarioid mycoflora of New Zealand, VII. *New Zealand Journal of Botany* 54(3):344–365 DOI 10.1080/0028825X.2016.1178149.

Soop K, Dima B, Cooper JA, Park D, Oertel B. 2019. A phylogenetic approach to a global supraspecific taxonomy of *Cortinarius* (Agaricales) with an emphasis on the southern mycota. *Persoonia* 42:261–290 DOI 10.3767/persoonia.2019.42.10.

Soop K, Wallace M, Dima B. 2018. New *Cortinarius* (Agaricales) species described from New Zealand. *New Zealand Journal of Botany* 56(2):163–182 DOI 10.1080/0028825X.2018.1436574.

Stamatakis A. 2014 RAxML version 8: a tool for phylogenetic analysis and post-analysis of large phylogenies. *Bioinformatics* 30:1312–1313 DOI 10.1093/bioinformatics/btu033.

Teasdale SE, Beulke AK, Guy PL, Orlovich DA. 2013. Environmental barcoding of the ectomycorrhizal fungus *Cortinarius*. Fungal Diversity 58(1):299–310 DOI 10.1007/s13225-012-0218-1.

Thompson JD, Gibson TJ, Plewniak F, Jeanmougin F, Higgins DG. 1997. The Clustal_X windows interface: flexible strategies for multiple sequence alignment aided by quality analysis tools. *Nucleic Acids Research* 25(24):4876–4882 DOI 10.1093/nar/25.24.4876.

Teng SC. 1963. *Fungi of China*. Beijing: Science Press.

Trog JG. 1844. Verzeichniss schweizerischer Schwämme, welche grösstentheils in der Umgebung von Thun gesammelt worden sind. *Mitteilungen der Naturforschenden Gesellschaft Bern* 1844(15-23):17–92.

Wang B, Qiu YL. 2006. Phylogenetic distribution and evolution of mycorrhizas in land plants. *Mycorrhiza* 16:299–363 DOI 10.1007/s00572-005-0033-6.

Wang K, Zhao MJ, Su JH, Yang L, Deng H, Wang YH, Wu HJ, Li Y, Wu HM, Wei XD, Wei TZ, Cai L, Yao YJ. 2020. The use of Checklist of Fungi in China database in the red list assessment of macrofungi in China. *Biodiversity Science* 28(1):74–98 DOI 10.17520/biods.2019163.

Wei TZ, Yao YJ. 2013. *Cortinarius korfii*, a new species from China. *Mycosystema* 32(3):557–562 DOI 10.13346/j.mycosystema.2013.03.017.

White TJ, Bruns T, Lee S, Taylor J. 1990. Amplification and direct sequencing of fungal ribosomal RNA genes for phylogenetics. In: Innis MA, Gelfand DH, Sninsky JJ, White TJ, ed. *PCR protocols: a guide to methods and amplifcations*. New York: Academic Press.

Wilson AW, Hosaka K, Mueller GM. 2017. Evolution of ectomycorrhizas as a driver of diversification and biogeographic patterns in the model mycorrhizal mushroom genus *Laccaria*. *New Phytologist* 213:1862–1873 DOI 10.1111/nph.14270.

Wright SH, Berch SM, Berbee ML. 2009. The effect of fertilization on the below-ground diversity and community composition of ectomycorrhizal fungi associated with western hemlock (*Tsuga heterophylla*). *Mycorrhiza* 19(4): 267-276 DOI 10.1007/s00572-008-0218-x.

Xie ML. 2018. Resources and taxonomy of *Cortinarius* in northeast of China. MA. Thesis, Jilin Agricultural University.

Xie ML, Li D, Wei SL, Ji RQ, Li Y. 2019. *Cortinarius subcaesiobrunneus* sp. nov., (Cortinariaceae, Agaricales) a new species from northwest China. *Phytotaxa* 392(3):217–224 DOI 10.11646/phytotaxa.392.3.4.

Xie ML, Wei TZ, Dima B, Fu YP, Ji RQ, Li Y. 2021. *Cortinarius khinganensis* (Agaricales), a new species of section *Illumini* from Northeast China. *Phytotaxa* 500(1): 1-10. DOI 10.11646/phytotaxa.500.1.1

Xie ML, Wei TZ, Fu YP, Li D, Qi LL, Xing PJ, Cheng GH, Ji RQ, Li Y. 2020. Three new species of *Cortinarius* subgenus *Telamonia* (Cortinariaceae, Agaricales) from China. *MycoKeys* 69:91–109 DOI 10.3897/mycokeys.69.49437.

Yuan HS, Lu X, Dai YC, Hyde KD, Kan YH, Kušan I, He SH, Liu NG, Sarma VV, Zhao CL, Cui BK, Yousaf N, Sun GY, Liu SY, Wu F, Lin CG, Dayarathne MC, Gibertoni TB, Conceição LB, Garibay-Orijel R, Villegas-Ríos M, Salas-Lizana R, Wei TZ, Qiu JZ, Yu ZF, Phookamsak R, Zeng M, Paloi S, Bao DF, Abeywickrama PD, Wei DP, Yang J, Manawasinghe IS, Harishchandra D, Brahmanage RS, de Silva NI, Tennakoon DS, Karunarathna A, Gaforov Y, Pem D, Zhang SN, de Azevedo Santiago ALCM, Bezerra JDP, Dima B, Acharya K, Alvarez-Manjarrez J, Bahkali AH, Bhatt VK, Brandrud TE, Bulgakov TS, Camporesi E, Cao T, Chen YX, Chen YY, Devadatha B, Elgorban AM, Fan LF, Du X, Gao L, Gonçalves CM, Gusmão LFP, Huanraluek N, Jadan M, Jayawardena RS, Khalid AN, Langer E, Lima DX, de Lima-Júnior NC, de Lira CRS, Liu JK, Liu S, Lumyong S, Luo ZL, Matočec N, Niranjan M, Oliveira-Filho JRC, Papp V, Pérez-Pazos E, Phillips AJL, Qiu PL, Ren YH, Ruiz RFC, Semwal KC, Soop K, de Souza CAF, Souza-Motta CM, Sun LH, Xie ML, Yao YJ, Zhao Q, Zhou LW. 2020. Fungal diversity notes 1277–1386: taxonomic and phylogenetic contributions to fungal taxa. *Fungal Diversity* 104:1–266 DOI 10.1007/s13225-020-00461-7.

Yuan ML, Sun PQ. 1995. Sichuan Mushroom. Chengdu: Sichuan Science and Technology Press.