Two new *Cortinarius* species in subgenus *Leprocybe* from Southwest China (#92333)

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Two new *Cortinarius* species in subgenus *Leprocybe* from Southwest China

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Two new *Cortinarius* species in subgenus *Leprocybe*, *C. henduanensis* and *C. yadingensi*s, are proposed based on a combination of morphological and molecular evidences. *Cortinarius henduanensis* has distinct olive tinged basidiomata, squamulose pileus, and small, subglobose to broadly ellipsoid basidiospores. *Cortinarius yadingensis* has squamulose pileus and stipe, subglobose to broadly ellipsoid basidiospore with strongly warts. Both of the two new species were found from Southwest China. The morphological characteristics of subgenus *Leprocybe* are also discussed.

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Abstract

Two new *Cortinarius* species in subgenus *Leprocybe*, *C. henduanensis* and *C. yadingensis*, are proposed based on a combination of morphological and molecular evidences. *Cortinarius henduanensis* has distinct olive tinged basidiomata, squamulose pileus, and small, subglobose to broadly ellipsoid basidiospores. *Cortinarius yadingensis* has squamulose pileus and stipe, subglobose to broadly ellipsoid basidiospore with strongly warts. Both of the two new species were found from Southwest China. The morphological characteristics of subgenus *Leprocybe* are also discussed.

Keywords: Basidiomycota; China; phylogeny; new taxa; taxonomy

Introduction

Cortinarius (Pers.) Gray is the largest genus in Agaricales (Basidiomycota) and distinguished from other agarics by its arachnoid partial veil, together with rust brown and verrucose basidiospores (Moser & Horak,1975). It is an extremely complex genus with more than 5800 names documented in Index Fungorum (http://www.indexfungorum.org/Names/Names.asp), and most of them were reported from Europe and North America. However, its diversity and distribution in Asia are still poorly understood.

Moser (1969) proposed subgen. *Leprocybe* M.M. Moser with five sections, sect. *Bolares* Kühner & Romagn. ex M.M. Moser, sect. *Brunneotincti* Kühner & Romagn. ex M.M. Moser, sect. *Leprocybe* M.M. Moser, sect. *Limonii* M.M. Moser ex Nezdojm. and sect. *Orellani* M.M. Moser. *Cortinarius* species with fluorescence reaction under ultraviolet light, e.g. *C. cotoneus* Fr., *C. limonius* (Fr.) Fr., *C. orellanus* Fr. and *C. venetus* (Fr.) Fr., were placed in the genus, and *C. cotoneus* was designated as type species. Peintner et al. (2004) found subgen. *Leprocybe* is non-monophyletic base on molecular phylogenetic analysis, and similar result was obtained by Harrower et al. (2011). Soop (2019) proposed two new sections of the subgenus, sect. *Persplendidi* Soop & Dima and sect. *Veronicae* Soop. Base on morphological and molecular data, Ammirati et al. (2021) proposed three new sections (sect. *Fuscotomentosi* Niskanen, Liimat. & Ammirati, sect. *Melanoti* Niskanen, Liimat. & Ammirati and sect. *Squamiveneti* Niskanen, Liimat. & Ammirati) and 11 new species from North America. The paper also validated sect. *Veneti* Bellanger, Niskanen, Ammirati & Liimat., which was proposed by Konrad & Maublanc (1937), and designated neo- or epitypes for four species. Bidaud et al. (2021) reported 11 species of the subgenus (included three new species) from Mediterranean, and confirmed 23 synonymies. Liimatainen et al. (2022) re-defined subgen. *Leprocybe* base on result from analysis of five genes, and seven sections, such as sect. *Fuscotomentosi*, sect. *Leprocybe*, sect. *Melanoti*, sect. *Persplendidi*, sect. *Squamiveneti*, sect. *Veneti* and sect. *Veronicae*, were included in the subgenus, sect. *Limonii* was placed in a new genus, *Aureonarius* Niskanen & Liimat.

In China, Keissler & Hohwag (1937) firstly reported *C. cotoneus* from Yunnan Province. Shao & Xiang (1997) documented *C. venetus* from Heilongjiang Province. Xie (2022) reported *Cortinarius nigrosquamosus* from Yunnan. In a survey of *Cortinarius* species in southwest of China, two undescribed species of subgenus *Leprocybe* was found base on morphology and phylogenetic analysis. The paper described the two new species and illustrated with both macro-morphology and microscopic characteristics.

Materials & Methods

Morphological study

Specimens were collected from Xizang Autonomous Region, Sichuan Province and Yunnan Province, China. The fresh basidiomata were photographed after collecting from the field and the macro-morphological characters were recorded in detail before drying in an oven at around 45ºC.

A 20% KOH solution was used on fresh pileus and stipe surfaces, lamella, and context for chemical reaction. Observation of the basidiomata was performed under ultraviolet light at a wave length of 360 nm. The specimens are housed in the Fungarium, Institute of Microbiology, Chinese Academy of Sciences (also as Herbarium Mycologicum Academiae Sinicae, HMAS). Description of the micro-morphological characters was based on dried collections. Thin sections were prepared by hand with a razor blade. The sections of dried basidiomata were mounted in 5% KOH solution. Basidiospores, basidia, tramal hyphae, context, and cutis of pileus and stipe were measured using an ocular micrometer. At least 30 basidiospores and 20 basidia of each mature collection were measured.

DNA extraction, amplification and sequencing

Genomic DNA was extracted from dried specimens using standard protocol (Rogers & Bendich,1994). The DNA extracts were used as templates for PCR. Amplification reactions were performed to obtain sequences of nuclear ribosomal internal transcribed spacer region (ITS) using primer pairs ITS5/ITS4 (White et al.,1990). The amplification was carried out under the following conditions: initial denaturation for 3 min at 95 °C, followed by 30 cycles, at 95 °C for 30 s, at 55 °C for 45 s, at 72 °C for 60 s, and a final elongation step at 72 °C for 10 min.

Phylogenetic analysis

The newly generated ITS sequences were submitted to GenBank. The ITS sequences for the phylogenetic analyses were selected based on results of BLASTn (>94% identity) in GenBank. Two species, *C. veronicae* (KC017355) and *C. veronicoides* (GQ890324), were chosen as outgroup. Seventy-three sequences (table 1) were aligned and edited with BioEdit 7.2.2 (Hall,1999). Bayesian Inference (BI) and Maximum Likelihood (ML) methods were implemented to analyses in this study. MrModeltest 2.3 was used to calculate the best model for BI analysis (Nylander et al., 2008). The BI analysis was performed with MrBayes 3.2.6 (Ronquist & Huelsenbeck, 2003), and the ML analysis was conducted in MEGA X (Kumar et al., 2018). The matrix contained 75 ITS sequences with 681 nucleotide sites is available from TreeBASE under S30908 (http://purl.org/phylo/treebase/phylows/study/TB2:S30908).

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 Index Fungorum from where they will be made available to the Global Names Index. The unique Index Fungorum number can be resolved and the associated information viewed through any standard web browser by appending the Index Fungorum number contained in this publication to the prefix " https://www.indexfungorum.org/Names/NamesRecord.asp?RecordID=". The online version of this work is archived and available from the following digital repositories: PeerJ, PubMed Central SCIE, and CLOCKSS.

Results

Molecular phylogeny

The ITS matrix for phylogenetic analyses included 73 sequences, representing 15 species. The resulting alignments were deposited at TreeBASE (http://www.treebase.org; submission ID xxx; accessed on xx November 2023). The BI and ML trees showed similar topologies, and the ML tree was selected as the representative phylogeny (Figure 1). According to the phylogenetic tree, the independences of *Cortinarius hengduanensis* and *C. yadingensis* were well-surppoted. *Cortinarius hengduanensis* has a close relationship with *C. flavifolius* Peck, *C. yadingensis* nests in a clade of sect. *Leprocybe* and clusters together with *C. contoneus*, *C. hughesiae* Ammirati, Matheny, Liimat. & Niskanen, *C. selinolens* Bidaud & Bellanger and *C. subcotoneus* Bidaud.

Taxonomy

Cortinarius hengduanensis P. Hong, K. Wang, Z. Du, M.L. Xie, D. Liu & T.Z. Wei, sp. nov. Figure 2.

Index Fungorum: IF901373.

Holotype:—CHINA, Yunnan, Shangri-La County, Haba Mountains Nature Reserve, alt. 3000 m, in mixed forest with *Pinus densata* Mast. and *Quercus aquifolioides* Rehder et E. H. Wilson, 16 Aug. 2008, T.-Z. Wei, X.-Q. Zhang & F.-Q. Yu 194, HMAS 250455 (GenBank ID: KX513581).

Etymology:—"hengduan", Chinese, referring Hengduan Mountains of Southwest China, the locality of the type collection.

Diagnosis:—*Cortinarius hengduanensis* has olive tinged basidiomata, squamulose pileus, and small subglobose to broadly ellipsoid basidiospores (5.5–7.5 × 5–6.5 μm). ITS sequences of the new species (GenBank ID: KX513581–KX513583, OR538887 and OR538888) ~~and~~ deviate from that of *C. flavifolius* by at least 28 substitutions and indel positions. In mixed forest with *Pinus yunnanensis* Franch., *P. densata* and *Quercus aquifolioides*.

Description:—*Pileus* 4.5–12.5 cm diam., hemispherical at first, later becoming convex to applanate, with a shallow and obtuse umbo at center when mature, margin sometimes uplifted or undulate; surface non-viscid, uneven, tomentose, persistently covered with small olive-brown to dark olive-brown squamules in all stages; margin radially striate; olive-green with brownish tint at first, then brownish olive, olive-brown to dull brown with paler margin, sometimes darker at center. *Lamellae* adnate to emarginate, 3–8 mm wide; close to moderately crowded, with lamellulae, olive to grayish green when young, brown with olive tint to rust-brown when mature, margin paler. *Stipe* 5.5–12 × 0.7–2.6 cm, cylindrical or base enlarged and up to 3 cm in diam.; surface rough, completely covered with universal veil at first, then longitudinally fibrillose above and with conspicuous finally with annular girdles below; olivaceous yellow, tinged rust-brown from basidiospores; at first solid, then soft to hollow. *Context* up to 8 mm thick at pileus center, whitish to pale when dry, olive-gray when moist, fleshy, soft; odor indistinct, taste mild. *Partial veil* arachnoid, greenish to olive, then becoming rust brown from mature basidiospores. *Universal veil* distinct and persistent, fibrillose, covering whole basidiomata at first, then forming fibrils and squamules on pileus and fibrils, strips or girdles on stipe surface; pale with olive tint at first, brownish with olive tint to olive-brown when mature. *Basidiospore deposit* rust brown. *Chemical reaction with 20% KOH* dark reddish brown on pileus and lamella, brown on stipe and reddish brown on context. *Fluorescence reaction under ultraviolet light* distinctly bright yellow on lamellae, and weaker on surfaces of pileus and stipe.

Basidiospores (5.2–) 5.5–7 (–7.5) × (4.8–) 5–6 (–6.5) µm, Q= (1.08–) 1.1–1.2 (–1.23) (av.=1.15); subglobose to broadly ellipsoid, yellowish brown, moderately to distinctly verrucose. *Basidia* 28–35 × 8–10 µm, clavate, thin-walled, mostly subhyaline, with four sterigmata. *Lamella edges* heterogeneous, with sterile cells, 20–30 × 6–9 µm, clavate, subhyaline, thin-walled. *Pleurocystidia* absent. Subhymenial layer up to 10 µm thick, of narrow and branched hyphae, hyaline, thin-walled, 2–4 µm diam. *Hymenophoral trama* regular, 80–100 µm wide, of hyaline and thin-walled hyphae, 5–20 µm diam. *Pileipellis* simplex, of subcylindrical hyaline, 9–15 µm diam., brownish to yellowish brown. Hyphae of the cortina 3–6 µm diam., subhyaline to yellowish, thin-walled. *Clamp connections* present.

Additional Specimens Examined: CHINA, Yunnan, Songming County, Aziying Town, alt. 2000 m, in mixed forest with *Pinus yunnanensis* Franch. and *Quercus aquifolioides*, 5 Aug. 2005, T.-Z. Wei & F.-Q. Yu Gm1082, HMAS 145537 (GenBank ID: KX513582); Deqin County, Baima Mountains, alt. 3100 m, in mixed forest with *P. densata* and *Q. aquifolioides*, 19 Aug. 2008, T.-Z. Wei, X.-Q. Zhang & F.-Q. Yu 258, HMAS 250509 (GenBank ID: KX513583); **Xizang**, Nyingchi County, Bayi Town, 29°38′02.58″N, 94°23′44.72″E, alt. 3360 m, in mixed forest with *P. densata* and *Q. aquifolioides*, 14 Sept. 2014, T.-Z. Wei, J.-Y. Zhuang, X.-Y. Liu & H. Huang 5281, HMAS 270305 (GenBank ID: OR538888); Lulang Town, alt. 3481 m, 22 Sept. 2014, W-L Lu & Q-M Wang, 3017, HMAS 272520 (GenBank ID: OR538887).

Notes: *Cortinarius hengduanensis* is characterized by its distinct olive tinged basidiomata, fibrilloso-squamulose pileus and subglobose to broadly ellipsoid basidiospores (5.2–7.5 × 4.8–6.5 µm). The new taxon is close to *C. flavifolius*, the latter also has fibrillose to squamulose pileus and subglobose basidiospores (Ammirati et al.,2021). ~~However, differs from *C. hengduanensis*,~~ *C. flavifolius* does not have any olive or greenish tint, and its basidiospores are

6.7–8.9 × 4.8–5.9 µm (Ammirati et al.,2021) ~~and~~ larger than ~~that~~ of *C. hengduanensis*.

Cortinarius yadingensis P. Hong, K. Wang, Z. Du, M.L. Xie, D. Liu & T.Z. Wei, sp. nov.

Figure 3.

Index Fungorum: IF901374.

Holotype:—CHINA, Sichuan, Daocheng County, Yading Scenic Spot, alt. 4034 m, in mixed forest of *Abies* sp., *Larix potaninii* Batalin, *Picea* sp. and *Q. aquifolioides*, 18 Aug. 2016, T-Z Wei, L-H Sun, Z-X Wu & R-C Zhang, 7168, HMAS 254819 (GenBank ID: OR538892).

Etymology:—“yading”, Chinese, referring Yading Scenic Spot of Sichuan Province, China, the locality of the type collection.

Diagnosis:—*Cortinarius yadingensis* has distinct brown squamules on ~~whole~~ basidiomata surface and subglobose to broadly ellipsoid basidiospores (6.5–9 × 6.3–7.6 µm). Differs from ~~its~~ related species by its non-olive tinged basidiomata. ITS sequences of the new species (GenBank ID: OR538889–OR538893) are distinct from other members of sect. *Leprocybe* and deviating from them by at least 11 substitutions and indel positions. In mixed forest with *Abies* sp., *Larix potaninii*, *Picea* sp. and *Q. aquifolioides*.

Description:—*Pileus* 2–6 cm diam., hemispherical at first, later becoming convex to applanate, mostly with a shallow and obtuse umbo at center when mature, margin decurrent to straight, sometimes split when mature; surface pale brown, grayish brown to rust brown, densely with brown to dark brown fibrillose squamules, non-viscid, radially striate, silky and shining. *Lamellae* emarginato-adnate, up to 5 mm wide; brownish when young, rust-brown when mature; moderately crowded, with lamellulae, margin paler. *Stipe* 3.5–8 × 0.5–1 cm, subcylindrical, with base up to 1.5 cm in diam.; surface brownish to pale brown, densely with brown to dark brown fibrillose squamules, with annular zone from partial veil, non-viscid, longitudinally striate; at first solid then soft to hollow. *Context* up to 5 mm thick at pileus center, pale brown to grayish brown, fleshy, soft; odor indistinct, smell mild. *Partial veil* arachnoid, grayish when young, form rust brown ring from basidiospores when mature. *Universal veil* persistently distinct, form fibrillose brown to dark brown squamules ~~at~~ surface of basidiomata. Basidiospore deposit rust brown. *Chemical reaction with 20% KOH* dark brown to blackish brown on pileus, lamella and stipe surface, and reddish brown at context. *Fluorescence reaction under ultraviolet* light bright yellow on lamellae, and weaker on surfaces of pileus and stipe.

Basidiospores (6.5–) 7–8.5 (–9) × (6.3–) 6.5–7.2 (–7.6) µm, Q= (1.03–) 1.08–1.2 (–1.24) (av.=1.16); subglobose, yellow-brown, distinctly verrucose. *Basidia* 28–35 × 8–10 µm, clavate, thin-walled, mostly subhyaline, with four sterigmata. *Lamella edges* heterogeneous, with sterile ~~cells~~ 20–30 × 6–9 µm, clavate, subhyaline, thin-walled. *Pleurocystidia* absent. *Subhymenial layer* up to 10 µm thick, of narrow and branched hyphae, hyaline, thin-walled, 2–4 µm diam. Hymenophoral trama regular, 80–100 µm wide, of hyaline and thin-walled hyphae, 5–20 µm diam. *Pileipellis* simplex, of subcylindrical hyaline, 9–15 µm diam., brownish to yellowish brown. *Hyphae of the cortina* 3–6 µm diam., subhyaline to yellowish, thin-walled. *Clamp connections* present.

Additional Specimens Examined: CHINA, Sichuan, Litang County, side of road to Daocheng County, alt. 3937 m, in conifer forest with *Abies* sp. and *Picea* sp., 17 Aug. 2016, T-Z Wei, L-H Sun, Z-X Wu & R-C zhang, 7117, HMAS 254811 (GenBank ID: OR538889); Daocheng County, Yading Scenic Spot, alt. 4034 m, in mixed forest of *Abies* sp., *Larix potaninii*, *Picea* sp. and *Q. aquifolioides*, 18 Aug. 2016, T-Z Wei, L-H Sun, Z-X Wu & R-C Zhang, 7169, HMAS 254820 (GenBank ID: OR538893); 7123, HMAS 280697 (GenBank ID: OR538890); 7127, HMAS 280698 (GenBank ID: 254819).

Notes: *Cortinarius yadingensis* is characterized by its grayish brown to brown pileus and stipe with distinct squamules, and subglobose to ellipsoid basidiospores (6.5–9 × 6.3–7.6 µm) ~~with distinct warts.~~ The species is phylogenetically close to four species of sect. *Leprocybe*, *C. cotoneus* (Breitenbach & Kränzlin 2000, Soop,2018), *C. hughesiae* Ammirati, Matheny, Liimat. & Niskanen (Ammirati et al.,2021), *C. selinolens* Bidaud & Bellanger (Bidaud et al.,2021) and *C. subcotoneus* (Bidaud et al.,2005). Compared with *C. yadingensis*, all the four related species have similar finely tomentose to squamulose pileus and strongly verrucose basidiospores. ~~However, differs from~~ *C. yadingensis*, all the related species have olive tinged basidiomata. Phylogenetically, *C. yadingensis* can be distinguished from its sister species by at least 11 substitutions and indels in ITS.

Discussion

According to Bidaud et al. (2021), Ammirati et al. (2021) and Liimatainen et al. (2022), subgen. *Leprocybe* was re-defined as *Cortinarius* species with small- to medium-sized (occasionally large-sized) basidiomata, obvious fluorescent reaction, tomentose to squamulose pileus and subglobose basidiospores, and all these unique characters can be found in both ~~of~~ *C. hengduanensis* and *C. yadingensis*. *Cortinarius hengduanensis* has olive ~~appearance,~~ which was also found in most of species in sect. *Fuscotomentosi*, sect. *Leprocybe*, sect. *Melanoti*, sect. *Squamiveneti* and sect. *Veneti* (Bidaud et al.,2021;Ammirati et al.,2021). *Cortinarius yadingensis* does not has any olive tint, its pileus and stipe surfaces are covered by densely dark brown fibrillose squamules, which are found in few *Leprocybe* species lacking olive ~~tint~~, such as *C. pescolanensis* (Picillo & Marchionni,2016), but phylogenetic analysis of the present research does not support close relationship between *C. yadingensis* and *C. pescolanensis*.

Acknowlegements

Support from National Key Basic Research Special Foundation of China (2013FY110400), National Key Research and Development Program of China (2017YFD0300104), National Natural Science Foundation of China (No. 31270072), the Special Funds for the Young Scholars of Taxonomy of the Chinese Academy of Sciences (No. ZSBR-001).

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Table 1(on next page)

ITS sequences of subgen. Leprocybe used in phylogenetic analysis.

Note: * means from this study.

Table 1. ITS sequences of subgen. *Leprocybe* used in phylogenetic analysis.

Name	Voucher	Locality	GenBank ID	References
Cortinarius clandestinus	B. Dentinger 325	USA	MW009208	Ammirati et al. 2021
C. clandestinus	SMI200A	Canada	FJ039583	Harrower et al. 2011
C. clandestinus	SAT03-137-02	USA	FJ717552	Harrower et al. 2011
C. clandestinus	SMI24	Canada	FJ157136	Harrower et al. 2011
C. clandestinus	JFA 10285	USA	MW009201	Ammirati et al. 2021
C. clandestinus	T. Niskanen 11-454	USA	MW009204	Ammirati et al. 2021
C. clandestinus	JFA 13263	USA	MW009203	Ammirati et al. 2021
C. clandestinus	JFA 8986	USA	MW009202	Ammirati et al. 2021
C. clandestinus	M. Moser 1995-165a	USA	MW009206	Ammirati et al. 2021
C. cotoneus	PML 5260	France	MW010117	Bidaud et al. 2021
C. cotoneus	PML 5429	France	MW010116	Bidaud et al. 2021
C. cotoneus	CFP1032	Sweden	MW009216	Ammirati et al. 2021
C. flavifolius	TENN:068695 (epitype)	USA	MW009217	Ammirati et al. 2021
C. flavifolius	256	USA	MW009238	Ammirati et al. 2021
C. flavifolius	T. Niskanen 14-227	USA	MW009218	Ammirati et al. 2021
C. fuscoflavidus	JFA 11644	USA	MW009221	Ammirati et al. 2021
C. fuscoflavidus	T. Niskanen 09-158	USA	MW009222	Ammirati et al. 2021
C. fuscoflavidus	DBB41055	USA	MW009223	Ammirati et al. 2021
C. hengduanensis	HMAS250455 (holotype)	China	KX513581	*
C. hengduanensis	HMAS145537	China	KX513582	*
C. hengduanensis	HMAS250509	China	KX513583	*
C. hengduanensis	HMAS272520	China	OR538887	*
C. hengduanensis	HMAS270305	China	OR538888	*
C. hughesiae	JFA 13086	USA	MW009224	Ammirati et al. 2021
C. hughesiae	TENN:068689	USA	MW009225	Ammirati et al. 2021
C. leproleptopus	R. Henry 8409	France	MW009226	Ammirati et al. 2021
C. leproleptopus	ST40	Italy	MW010181	Bidaud et al. 2021
C. leproleptopus	AB 08-10-395	France	MW010171	Bidaud et al. 2021
C. leproleptopus	AB 08-10-320	France	MW010166	Bidaud et al. 2021
C. leproleptopus	AB 08-09-215	France	MW010165	Bidaud et al. 2021
C. leproleptopus	AB 08-09-199	France	MW010164	Bidaud et al. 2021
C. leproleptopus	GE01-049	France	MW010150	Bidaud et al. 2021
C. leproleptopus	PML 5420	France	MW010133	Bidaud et al. 2021
C. leproleptopus	FR2312003	France	MW010065	Bidaud et al. 2021
C. leproleptopus	GS9	Germany	MW010100	Bidaud et al. 2021
C. leproleptopus	GS8	Germany	MW010099	Bidaud et al. 2021
C. leproleptopus	GS4	Germany	MW010095	Bidaud et al. 2021
C. leproleptopus	GS1	Germany	MW010092	Bidaud et al. 2021
C. lutescens	f1781	USA	MW009228	Ammirati et al. 2021
C. lutescens	H:7000893	Canada	MW009229	Ammirati et al. 2021
C. pescolanensis	MCVE 29054 (holotype)	Italy	NR_153070	Picillo & Marchionni 2016
C. pescolanensis	BP13/291	Italy	KX010945	Picillo & Marchionni 2016
C. pescolanensis	JB-8114/13	Spain	KY657256	Ballara et al. 2017
C. pescolanensis	JMB2013092404	France	MW010107	Bidaud et al. 2021
C. pescolanensis	PML 3262	France	MW010129	Bidaud et al. 2021
C. pescolanensis	PAM02082506	France	MW010186	Bidaud et al. 2021
C. pescolanensis	JMB2013092503	France	MW010109	Bidaud et al. 2021
C. pescolanensis	PML 5449	France	MW010140	Bidaud et al. 2021
C. pescolanensis	PML 5426	France	MW010135	Bidaud et al. 2021
C. pescolanensis	PML 5448	France	MW010139	Bidaud et al. 2021
C. selinolens	MPU1116858	France	MW010172	Bidaud et al. 2021
C. *selinolens*	FR2013185	Tunisia	MW010072	Bidaud et al. 2021
C. subcotoneus	PML 2143 (holotype)	France	MW010122	Bidaud et al. 2021
C. subcotoneus	AB 08-10-331	France	MW010167	Bidaud et al. 2021
C. subcotoneus	AB 08-10-387	France	MW010168	Bidaud et al. 2021
C. subcotoneus	AB 08-10-394	France	MW010170	Bidaud et al. 2021
C. subcotoneus	GS7	Germany	MW010098	Bidaud et al. 2021
C. subcotoneus	GS15	Germany	MW010106	Bidaud et al. 2021
C. veneto-occidentalis	T. Niskanen 11-051	USA	MW009243	Ammirati et al. 2021
C. veneto-occidentalis	T. Niskanen 11-053	USA	MW009246	Ammirati et al. 2021
C. veneto-occidentalis	T. Niskanen 11-281	Canada	MW009248	Ammirati et al. 2021
C. veneto-occidentalis	T. Niskanen 11-258	USA	MW009245	Ammirati et al. 2021

C. veneto-occidentalis	T. Niskanen 11-106	USA	MW009244	Ammirati et al. 2021
C. venetus	CFP112	Sweden	MW009250	Ammirati et al. 2021
C. venetus	PC:245	France	MW009252	Ammirati et al. 2021
C. venetus	AB 12-09-62	France	MW010178	Bidaud et al. 2021
C. venetus	GH20100927	Germany	MW010090	Bidaud et al. 2021
C. venetus	GS13	Germany	MW010104	Bidaud et al. 2021
C. yadingensis	HMAS254811	China	OR538889	*
C. yadingensis	HMAS280697	China	OR538890	*
C. yadingensis	HMAS280698	China	OR538891	*
C. yadingensis	HMAS254819 (holotype)	China	OR538892	*
C. yadingensis	HMAS254820	China	OR538893	*
C. veronicae	PDD68468 (holotype)	New Zealand	KC017355	Bidaud et al. 2021
C. veronicoides	MEL2120747	Australia	GQ890324	Danks et al. 2010

Note: * means from this study.

1

Figure 1

ML phylogram inferred from the ITS dataset of *Cortinarius* species.

The ML bootstrap values (ML)≥50% and Bayesian posterior probabilities (BPP)≥0.95 are shown on the branches (BPP/ML). New species are marked in black bold font.

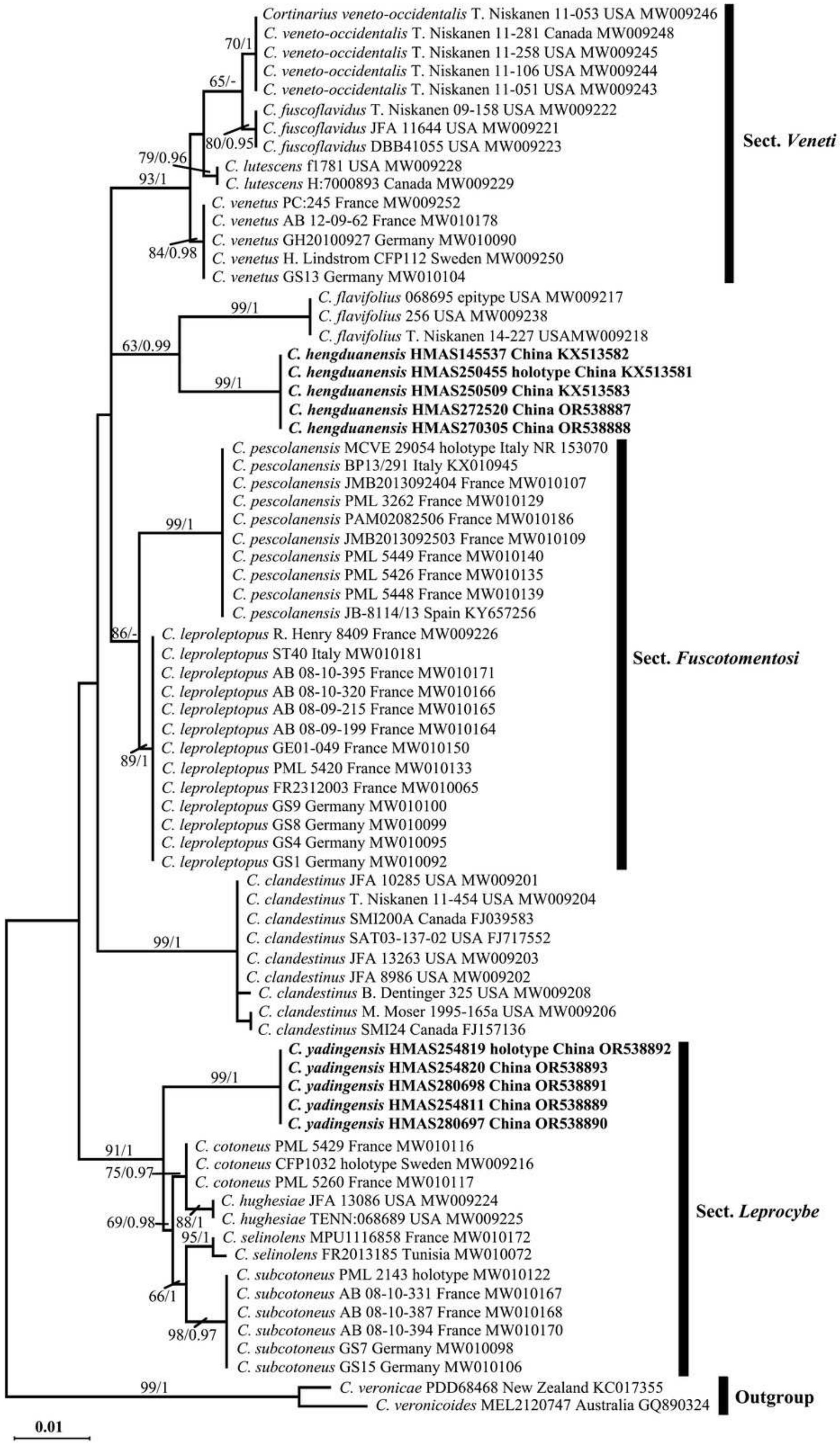
Cortinarius veneto-occidentalis T. Niskanen 11-053 USA MW009246
C. veneto-occidentalis T. Niskanen 11-281 Canada MW009248
70/1
C. veneto-occidentalis T. Niskanen 11-258 USA MW009245
65/-
C. veneto-occidentalis T. Niskanen 11-106 USA MW009244
C. veneto-occidentalis T. Niskanen 11-051 USA MW009243
C. fuscoflavidus T. Niskanen 09-158 USA MW009222
C. fuscoflavidus JFA 11644 USA MW009221
80/0.95
C. fuscoflavidus DBB41055 USA MW009223
79/0.96
C. lutescens f1781 USA MW009228
93/1
C. lutescens H:7000893 Canada MW009229
C. venetus PC:245 France MW009252
C. venetus AB 12-09-62 France MW010178
C. venetus GH20100927 Germany MW010090
84/0.98
C. venetus H. Lindstrom CFP112 Sweden MW009250
C. venetus GS13 Germany MW010104
Sect. Veneti
99/1
C. flavifolius 068695 epitype USA MW009217
C. flavifolius 256 USA MW009238
63/0.99
C. flavifolius T. Niskanen 14-227 USAMW009218
C. hengduanensis HMAS145537 China KX513582
C. hengduanensis HMAS250455 holotype China KX513581
99/1
C. hengduanensis HMAS250509 China KX513583
C. hengduanensis HMAS272520 China OR538887
C. hengduanensis HMAS270305 China OR538888
C. pescolanensis MCVE 29054 holotype Italy NR 153070
C. pescolanensis BP13/291 Italy KX010945
C. pescolanensis JMB2013092404 France MW010107
C. pescolanensis PML 3262 France MW010129
99/1
C. pescolanensis PAM02082506 France MW010186
C. pescolanensis JMB2013092503 France MW010109
C. pescolanensis PML 5449 France MW010140
C. pescolanensis PML 5426 France MW010135
C. pescolanensis PML 5448 France MW010139
C. pescolanensis JB-8114/13 Spain KY657256
86/-
C. leproleptopus R. Henry 8409 France MW009226
C. leproleptopus ST40 Italy MW010181
C. leproleptopus AB 08-10-395 France MW010171
C. leproleptopus AB 08-10-320 France MW010166
C. leproleptopus AB 08-09-215 France MW010165
C. leproleptopus AB 08-09-199 France MW010164
C. leproleptopus GE01-049 France MW010150
89/1
C. leproleptopus PML 5420 France MW010133
C. leproleptopus FR2312003 France MW010065
C. leproleptopus GS9 Germany MW010100
C. leproleptopus GS8 Germany MW010099
C. leproleptopus GS4 Germany MW010095
C. leproleptopus GS1 Germany MW010092
Sect. Fuscotomentosi
C. clandestinus JFA 10285 USA MW009201
C. clandestinus T. Niskanen 11-454 USA MW009204
C. clandestinus SMI200A Canada FJ039583
99/1
C. clandestinus SAT03-137-02 USA FJ717552
C. clandestinus JFA 13263 USA MW009203
C. clandestinus JFA 8986 USA MW009202
C. clandestinus B. Dentinger 325 USA MW009208
C. clandestinus M. Moser 1995-165a USA MW009206
C. clandestinus SMI24 Canada FJ157136
C. yadingensis HMAS254819 holotype China OR538892
99/1
C. yadingensis HMAS254820 China OR538893
C. yadingensis HMAS280698 China OR538891
C. yadingensis HMAS254811 China OR538889
C. yadingensis HMAS280697 China OR538890
91/1
C. cotoneus PML 5429 France MW010116
75/0.97
C. cotoneus CFP1032 holotype Sweden MW009216
C. cotoneus PML 5260 France MW010117
C. hughesiae JFA 13086 USA MW009224
69/0.98
88/1
C. hughesiae TENN:068689 USA MW009225
95/1
C. selinolens MPU1116858 France MW010172
C. selinolens FR2013185 Tunisia MW010072
C. subcotoneus PML 2143 holotype MW010122
66/1
C. subcotoneus AB 08-10-331 France MW010167
C. subcotoneus AB 08-10-387 France MW010168
98/0.97
C. subcotoneus AB 08-10-394 France MW010170
C. subcotoneus GS7 Germany MW010098
C. subcotoneus GS15 Germany MW010106
Sect. Leprocybe
99/1
C. veronicae PDD68468 New Zealand KC017355
C. veronicoides MEL2120747 Australia GQ890324
Outgroup
0.01

Figure 2

Cortinarius hengduanensis.

A-B. HMAS 250455 (holotype). A. Basidiomata (scale bar=5 cm); B. basidiospores (scale bar=10 μm). C-D. HMAS 250509. C. Basidiomata (scale bar=5 cm); D. basidiospores (scale bar=10 μm).

Figure 3

Cortinarius yadingensis.

A-B. HMAS 254819 (holotype). A. Basidiomata (scale bar=3 cm); B. basidiospores (scale bar=10 µm). C-D. HMAS 254811. C. Basidiomata (scale bar=2 cm); D. basidiospores (scale bar=10 µm).