

RESEARCH ARTICLE



Morphological characters and molecular data reveal ten new forest macrofungi species from Hebei Province, North China

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ABSTRACT

China has a complex and diverse forest ecological environment, which breeds abundant forest macrofungi, including some edible, medicinal, and poisonous species. During the investigations of macrofungi in the Saihanba National Nature Reserve, North China, we collected abundant specimens of Agaricales and Polyporales within the Agaricomycetes. Based on the morphological characters and molecular evidence of DNA sequences including the internal transcribed spacer (ITS) regions, the large subunit of nuclear ribosomal RNA gene (nLSU), the small subunit of mitochondrial rRNA gene (mtSSU), the small subunit of nuclear ribosomal RNA gene (nuSSU), the largest subunit of RNA polymerase II (RPB1), the second largest subunit of RNA polymerase II gene (RPB2), the β -tubulin gene (TUB), and the translation elongation factor 1- α gene (TEF1), this study identifies ten species of Agaricales and Polyporales new to science, viz. *Cyanosporus subpopuli*, *Gelatinofungus betulina*, *Lycoperdon pseudoperlatum*, *Macrocyttidia hebeiensis*, *Mycena subbrunnea*, *M. subpura*, *M. variispora*, *M. violacea-ardesiaca*, *Picipes griseus*, and *Pleuroflammula hebeiensis*. Detailed morphological descriptions, fruiting bodies, and microscopic structure diagrams of these ten novel species are provided.

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1. Introduction

China has complex climatic zones and forest types that provide a suitable sufficient ecological environment for the growth of macrofungi. Recently, many novel species of macrofungi have been found in China, especially in the Southwest and Northeast regions, but few new species have been found in North China (Cui et al. 2019; Li et al. 2020; Cao et al. 2021; Dai et al. 2021; Liu et al. 2021a, 2021b, 2022b, 2022c, 2023a, 2023b; Ji et al. 2022; Sun et al. 2022; Tuo et al. 2022; Wang et al. 2022; Wu et al. 2022; He et al. 2023). Saihanba National Nature Reserve (42°21'–42°31' N, 116°53'–117°31' E) is located in Weichang County, Hebei Province, North China, at the junction of the Inner Mongolian Plateau and Northern Hebei mountainous areas. It has a low latitude and is a transition zone from warm temperate to temperate, one of the richest areas in the forest-grass interspersed zone with diverse vegetation types (Erdős et al. 2018), providing a rich substrate for macrofungi. During the investigations of macrofungi in the Saihanba National Nature Reserve, we collected some specimens of Agaricales

Underw. and Polyporales Gäum. within the Agaricomycetes, which cannot be identified as known species.

Members of Agaricales are important components of macrofungi (Bánki et al. 2022). Agaricales is a diverse order that includes gilled and some non-gilled fungi, among which many species possess medicinal and edible value or toxicity, thus receiving extensive attention (Wu et al. 2019). Regarding the classification system of Agaricales, it was mainly based on morphology in earlier days and then combined with anatomical features (Singer 1986). With the advancement of technology, molecular phylogenetic techniques have been used for the systematic study of the members in Agaricales (Moncalvo et al. 2002; Lodge et al. 2014; Zhao et al. 2017). Correspondingly, the classification system of Agaricales has been constantly changing: Kirk et al. (2008) confirmed Agaricales contains 13,233 species, belonging to 33 families and 413 genera; He et al. (2019) identified a total of 17,291 species belonging to 38 families, 508 genera; recent studies

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summarised over 40,000 species in Agaricales, belonging to 8 suborders, 46 families, and 482 genera (Kalichman et al. 2020; Mou and Bau 2021; Bánki et al. 2022). Wang et al. (2023b) updated the phylogenetic and taxonomic relationships of Agaricales based on 555 single-copy orthologous genes and proposed the 10-suborders classification system of Agaricales, including 2 new suborders.

Most species of Polyporales grow on various types of wood, which play a vital role in material circulation and energy flow in forest ecosystems. In addition, some members of Polyporales are edible fungi, medicinal fungi, or forest pathogens. In Kirk et al. (2008), Polyporales contains approximately 1,800 species, 216 genera, and 13 families; and in He et al. (2019), Polyporales includes approximately 2,500 species, 285 genera, and 18 families. In recent years, several phylogenetic studies have focused on the Polyporales and many new taxa of Polyporales have been discovered (Chen et al. 2021; Liu et al. 2023a, 2023b; Wang et al. 2023a).

Preliminary morphological observations indicate unidentified specimens of Agaricales belong to *Lycoperdon* Pers. and *Pleuroflammula* Singer in the suborder Agaricineae Aime, Dentinger & Gaya, *Macrocyttidia* Joss. in the suborder Tricholomatineae Aime, Dentinger & Gaya, *Mycena* sect. *Calodontes* (Fr. ex Berk.) Quél. in the Mycenaceae clade, respectively (Dentinger et al. 2016; Olariaga et al. 2020; Wang et al. 2023b; Vizzini et al. 2024). Among them, *Lycoperdon* was established earlier, with *L. perlatum* Pers. as type species (Persoon 1796), and some species have medicinal and edible value (Wu et al. 2019). Species of *Lycoperdon* possess subglobose to pyriforme basidiospores (Cortez et al. 2013; Yuan et al. 2020). Phylogenetic studies revealed *Lycoperdon* belongs to Lycoperdaceae F. Berchtold & J. Presl, with about 55 species including several new species described in recent years (Cortez et al. 2013; Kim et al. 2016; He et al. 2019; Yuan et al. 2020; Krakhmalnyi et al. 2023). *Pleuroflammula* was established by Singer and Smith (1946), with *P. dussii* (Pat.) Singer as the type species. Recent studies have shown that *Pleuroflammula* belongs to Crepidotaceae (S. Imai) Singer (Matheny et al. 2006; Petersen et al. 2010; Gierczyk and Kubiński 2019; Crous et al. 2021). So far, there are approximately 20 known species of *Pleuroflammula*, most of which have been found in USA and Southern Hemisphere countries (Horak 1978, 2018; Crous et al. 2021). *Macrocyttidia* was established

by Jossierand (1933) with *M. cucumis* (Pers.) Joss. as the type species. Although Kühner (1979) established Macrocyttidiaceae to accommodate *Macrocyttidia*, the family-level status of *Macrocyttidia* is still controversial (Moncalvo et al. 2002). Recent studies have revealed that *Macrocyttidia* is related to the families of Tricholomatineae, and Vizzini et al. (2024) proved that the *Macrocyttidia* belonged to Macrocyttidiaceae. *Mycena* (Pers.) Roussel is a larger genus in Agaricales (about 600 species), belonging to Mycenaceae Overeem and typified by *M. galericulata* (Scop.) Gray (He et al. 2019). Mycologists mainly accept the infrageneric classification proposed by Maas Geesteranus, which divides *Mycena* into related sections based on morphological features (Robich 2016; Cooper et al. 2018). Currently, approximately 40 species from 18 sections of *Mycena* are luminescent fungi (Oliveira et al. 2021; Cortés-Pérez et al. 2023).

Preliminary morphological observations indicate that unidentified specimens of Polyporales belong to *Cyanosporus* McGinty in the antrodia clade, *Gelatinofungus* Sheng H. Wu, C.C. Chen & C.L. Wei in the phlebioid clade, and *Picipes* Zmitr. & Kovalenko in the core polyporoid clade, respectively (Cui et al. 2019; Chen et al. 2021; Liu et al. 2023a). Among them, *Cyanosporus* was established by McGinty (1909) with *Polyporus caesius* (Schr.) Fr. as the type species. But *Postia caesia* (Schr.) P. Karst. were regularly used instead of *Cyanosporus caesius* (Schr.) McGinty in some studies (Donk 1960; Lowe 1975). Subsequently, many species of the *Postia caesia* complex were discovered (David 1980; Miettinen et al. 2018). In recent years, phylogenetic studies proved that *Cyanosporus* contains *Postia caesia* complex, and many new *Cyanosporus* species were described (Shen et al. 2019; Liu et al. 2021a, 2022b). Liu et al. (2023a) placed this genus in the new family Postiaceae B.K. Cui, Shun Liu & Y.C. Dai. *Gelatinofungus* was proposed by Chen et al. (2021), is a monophyletic genus which contains *G. brunneus* Sheng H. Wu, C.C. Chen & C.L. Wei and belongs to Phanerochaetaceae Jülich of the phlebioid clade. *Picipes* was typified by *P. badius* (Pers.) Zmitr. & Kovalenko, was proposed by Zmitrovich and Kovalenko (2016) based on the combined datasets of ITS, nLSU, and TEF1. Zhou et al. (2016) confirmed that species in *Melanopus* group distribute into the *Picipes* clade and the *Squamosus* clade, and described 4 new species and proposed nine new combinations of *Picipes*. Ji et al. (2022) carried out the analyses of

morphology, phylogenies, and divergence times of *Polyporus* P. Micheli ex Adans. and related genera, and described seven new species of *Picipes*.

To elucidate the accurate phylogenetic position of these unidentified specimens, we selected appropriate gene fragments based on relevant phylogenetic studies (Yuan et al. 2020; Chen et al. 2021; Ji et al. 2022; Kumar et al. 2022; Liu et al. 2022a, 2022b; Vizzini et al. 2024), including the eight DNA fragments (ITS, nLSU, mtSSU, nuSSU, RPB1, RPB2, TBB1, TEF1), to conduct phylogenetic studies on the respective genera.

2. Materials and methods

2.1. Morphological studies

The specimens used in this study are deposited at the Museum of Biology Peking University (MBPU). The methods of morphological study and microstructure drawing, and the abbreviations used in this paper follow Liu et al. (2023a) and Wang et al. (2023b).

2.2. DNA extraction, amplification, and sequencing

DNA extraction and the polymerase chain reaction (PCR) procedures used in this study following Sun et al. (2022) and Liu et al. (2023a). The primer pairs ITS5/ITS4, LR0R/LR7, MS1/MS2, NS1/NS4, Mp-f1/Mp-r1, bRPB2-6F/bRPB2-7 R, Bt-1a/Bt-1b, and EF1-983F/EF1-1567 R were used to amplify the ITS, nLSU, mtSSU, nuSSU, RPB1, RPB2, TBB1, and TEF1 regions, respectively (White et al. 1990; Glass and Donaldson 1995; Matheny 2005; Rehner and Buckley 2005; Harder et al. 2013). The PCR cycling schedule for ITS, nLSU, mtSSU, nuSSU, RPB1, RPB2, TBB1, and TEF1 used in this study following Cui et al. (2019) and Liu et al. (2023a) with some modifications, the annealing temperatures of ITS, nLSU, mtSSU, nuSSU, RPB1, RPB2, TBB1, and TEF1 were 54–55 °C, 50 °C, 53–55 °C, 51 °C, 55–57 °C, 56–57 °C, 53 °C, and 54–57 °C, respectively. The PCR products obtained from the experiment were purified and sequenced with the same primers at the Beijing Genomics Institute (BGI), China. All newly generated sequences in this study were submitted to GenBank (Table 1).

2.3. Phylogenetic analyses

Additional sequences used in the phylogenetic analyses were obtained from GenBank (Table 1).

Firstly, all sequences need to be aligned in MAFFT 7 (Kato and Standley 2013), then manually adjusted in BioEdit (Hall 1999), and finally spliced in Mesquite (Maddison and Maddison 2017). Unclear nucleotides and missing sequences are defined as “N”.

The phylogenetic analyses used in this study followed the approach of Cui et al. (2019) and Liu et al. (2023a). This study analysed five datasets by using Maximum Parsimony (MP), Maximum Likelihood (ML), and Bayesian Inference (BI) methods. Evaluate the congruences of eight gene sequences (ITS, nLSU, mtSSU, nuSSU, RPB1, RPB2, TBB1, and TEF1) by using the length difference (ILD) test implemented in PAUP * 4.0b10 under heuristic search and 1,000 homogeneity replicates (Farris et al. 1994; Swofford 2002). *Antrodia serpens* (Fr.) Donk and *A. tanakae* (Murrill) Spirin & Miettinen were selected as the outgroups for the phylogenetic analyses of *Cyanosporus* (Liu et al. 2022a); *Bjerkandera adusta* (Willd.) P. Karst. and *B. carnegieae* (D.V. Baxter) Robledo, Nakasone & B. Ortiz were selected as the outgroups for the phylogenetic analyses of *Gelatinofungus* (Chen et al. 2021); *Mycenastrum corium* (Guers.) Desv. was selected as an outgroup for the phylogenetic analyses of *Lycoperdon* (Yuan et al. 2020); *Agaricus bisporus* (J.E. Lange) Imbach, *Apioperdon pyriforme* (Schaeff.) Vizzini, *Crepidotus cf. applanatus*, and *Inocybe myriadophylla* Vauras & E. Larss. were used as outgroups for the phylogenetic analyses of *Macrocyttidia* (Vizzini et al. 2024); members of *Mycena* sect. *Supinae* Konrad & Maubl. were selected as the outgroups for the phylogenetic analyses of *Mycena* sect. *Calodontes* (Osmundson et al. 2013; Liu et al. 2022c); *Trametes conchifer* (Schwein.) Pilát and *T. polyzona* (Pers.) Justo were selected as the outgroups for the phylogenetic analyses of *Picipes* (Ji et al. 2022); *Inocybe phaeoleuca* Kühner and *I. subpaleacea* Kühner were used as outgroups for the phylogenetic analyses of *Pleuroflammula* following Kumar et al. (2022). Branches that received bootstrap supports were considered as significantly supported with maximum parsimony (MP), maximum likelihood (ML), and Bayesian posterior probabilities (BPP) greater than 75% (MP and ML), and 0.95 (BPP), respectively. The obtained phylogenetic trees were visualised in FigTree v.1.4.4 (<http://tree.bio.ed.ac.uk/software/figtree/>).

Table 1. A list of species, specimens, and GenBank accession number of sequences used in this study.

Species name	Sample no.	Locality	ITS	nLSU	GenBank accessions						
					mtSSU	nuSSU	RPB1	RPB2	TBB1	TEF1	
<i>Agaricus bisporus</i>	AFTOL ID 448	USA	DQ404388	AY635775	-	AY787216	-	-	-	GU187673	
<i>Alboeifbula bambusicola</i>	Chen 2304	China	MZ636926	MZ637091	-	-	MZ748355	OK135980	-	MZ913590	
<i>Alboeifbula bambusicola</i>	Wu 1209-26	China	MZ636927	MZ637092	-	-	-	-	-	-	
<i>Alboeifbula gracilis</i>	Wu 0606-83	China	MZ636928	MZ637093	-	-	-	OK135981	-	-	
<i>Alboeifbula gracilis</i>	Wu 1809-106	China	MZ636929	MZ637094	-	-	MZ748356	OK135982	-	MZ913591	
<i>Alboeifbula gracilis</i>	Wu 1809-152	China	MZ636930	MZ637095	-	-	MZ748357	OK135982	-	-	
<i>Amaropostia hainanensis</i>	Cui 13739	China	KX900909	KX900979	KX901053	KX901123	KX901171	KX901223	-	-	
<i>Amaropostia stiptica</i>	Cui 10043	China	KX900906	KX900976	KX901046	KX901119	KX901167	KX901219	-	-	
<i>Amylocystis lapponica</i>	HHB-13400	USA	KC585237	KC585059	-	-	-	-	-	-	
<i>Amylocystis lapponica</i>	OKM-4418	USA	KC585238	KC585060	-	-	-	-	-	-	
<i>Antrrodia serpens</i>	Dai 7465	Luxembourg	KR605813	KR605752	KR606013	KR605913	-	KR610832	-	KR610742	
<i>Antrrodia tanakae</i>	Cui 9743	China	KR605814	KR605753	KR606014	KR605914	-	KR610833	-	KR610743	
<i>Apioperdon pyriforme</i>	AFTOL ID 480	USA	AY854075	AF287873	-	AF026619	AY860523	AY218495	-	AY883426	
<i>Asproinocybe sinensis</i>	HMJAU 59026	China	OK377048	OK377051	-	OK377040	OK625398	OK625401	-	OK625331	
<i>Attractosporocybe inornata</i>	HKAS 105578	China	MZ714587	MZ714592	-	KJ681075	MZ681888	MZ681898	-	MZ681877	
<i>Bjerkandera adusta</i>	HHB-12826-Sp	USA	KP134983	KP135198	-	-	KP134784	KP134913	-	KT305938	
<i>Bjerkandera carnegieae</i>	RLG-7277-T	USA	KY948792	KY948854	-	-	KY948935	OL405700	-	OL405699	
<i>Bonomycetes sinopicus</i>	Fungi 3689	Spain	MG696619	MG696627	-	MG696623	-	MG702595	-	MG702592	
<i>Bovista cretacea</i>	Jeppson 5702	Norway	DQ112610	DQ112610	-	-	-	-	-	-	
<i>Bovista paludosa</i>	Jeppson 4301	Norway	DQ112609	DQ112609	-	-	-	-	-	-	
<i>Calciopsis guttulata</i>	Cui 10018	China	KF727432	KJ684978	KX901065	KX901138	KX901181	KX901236	-	KX901276	
<i>Calciopsis guttulata</i>	Cui 10028	China	KF727433	KJ684979	KX901066	KX901139	KX901182	KX901237	-	KX901277	
<i>Callistosporium graminicolor</i>	AFTOL-ID 978	USA	DQ484065	AY745702	-	AY752974	GU187493	-	-	GU187761	
<i>Calvatia candida</i>	Jeppson 3514	Hungary	DQ112624	DQ112624	-	-	-	-	-	-	
<i>Catathelasma ventricosum</i>	DAOM 225247	USA	MN017537	MN017477	-	-	-	-	-	-	
<i>Clitocybe dealbata</i>	IE-B5G HC95.cp3	Switzerland	AF357061	AF223175	-	MN017585	KP255480	MN018851	-	MN026906	
<i>Clitocybe ditopa</i>	AMB 19311	Spain	OR863426	OR863496	-	DQ825431	DQ825414	DQ825407	-	EF421080	
<i>Clitocybe nebularis</i>	AFTOL ID 1495	Switzerland	AF357063	DQ457658	-	OR863563	-	OR828253	-	OR828314	
<i>Clitocybe subulitopoda</i>	AFTOL ID 533	USA	DQ202269	AY691889	-	DQ437681	DQ825415	EF421011	-	EF421081	
<i>Clitopaxillus alexandri</i>	TO AV 45634	Spain	MG321345	MG321393	-	AY771608	DQ447892	AY780942	-	DQ408150	
<i>Collybia tuberosa</i>	AFTOL-ID 557	USA	AY854072	AY639884	-	MG321329	-	MG334546	-	MG334537	
<i>Cremonoderma unicum</i>	Wu 1707-94	China	MZ636939	MZ637102	-	AY771606	AY857982	AY787219	-	AY881025	
<i>Cremonoderma unicum</i>	Wu 1707-100	China	MZ636938	MZ637101	-	-	MZ748358	OK135987	-	MZ913705	
<i>Crepatura ellipsozona</i>	CLZhao 1260	China	MK343693	MK343697	-	-	-	-	-	-	
<i>Crepatura ellipsozona</i>	CLZhao 1265	China	MK343692	MK343696	-	-	-	-	-	-	
<i>Crepatura ellipsozona</i>	CLZhao 697	China	MK343695	MK343699	-	-	-	-	-	-	
<i>Crepatura ellipsozona</i>	CLZhao 868	China	MK343694	MK343698	-	-	-	-	-	-	
<i>Crepidotus alabamensis</i>	TBGT 15610	India	MK459545	MK459543	-	-	-	-	-	-	

(Continued)

Table 1. (Continued).

Species name	Sample no.	Locality	ITS	GenBank accessions						
				nLSU	mtSSU	nuSSU	RPB1	RPB2	TBB1	TEF1
<i>Crepidotus alabamensis</i>	MUOB 277157	USA	OL142283	–	–	–	–	–	–	–
<i>Crepidotus asiaticus</i>	TJB 9995	Thailand	MF077337	MF077336	–	–	–	–	–	–
<i>Crepidotus asiaticus</i>	TJB 10018	Thailand	MF077339	MF077338	–	–	–	–	–	–
<i>Crepidotus asiaticus</i>	FFAAS 0336	China	MW580871	–	–	–	–	–	–	–
<i>Crepidotus fraxinicola</i>	iNaturalist 35038176	USA	ON033053	–	–	–	–	–	–	–
<i>Crepidotus fraxinicola</i>	MycMap 5922	USA	MN906146	–	–	–	–	–	–	–
<i>Crepidotus fraxinicola</i>	MycMap 6297	USA	MK560109	–	–	–	–	–	–	–
<i>Crepidotus mollis</i>	Ubc f 16579	Canada	FJ627025	–	–	–	–	–	–	–
<i>Crepidotus mollis</i>	iNAT 67832314	USA	MW676780	–	–	–	–	–	–	–
<i>Crepidotus mollis</i>	Robich 6723	Spain	JF907959	–	–	–	–	–	–	–
<i>Crepidotus tortus</i>	TBGT 17194	India	MK462161	–	–	–	–	–	–	–
<i>Crepidotus cf. applanatus</i>	WTUPBM717	USA	DQ202273	AY380406	–	AY705951	AY333303	AY333311	–	DQ028581
<i>Cyanosporus alni</i>	Petr Vampola 12.10.1995	Slovakia	MG137026	–	–	–	–	–	–	–
<i>Cyanosporus alni</i>	Cui 7185	China	KX900879	KX900949	KX901017	KX901092	KX901155	KX901202	–	KX901254
<i>Cyanosporus alni</i>	Dai 14845	Poland	KX900880	KX900950	KX901018	KX901093	KX901156	KX901203	–	KX901255
<i>Cyanosporus arbuti</i>	Viacheslav Spirin 8327	USA	MG137039	–	–	–	–	–	–	MG137132
<i>Cyanosporus auricomus</i>	Cui 13518	China	KX900887	KX900957	KX901025	KX901100	–	KX901209	–	–
<i>Cyanosporus auricomus</i>	Tuomo Niemelä 8310	Finland	MG137040	–	–	–	–	–	–	–
<i>Cyanosporus bifarius</i>	Cui 17534	China	OL423598	OL423608	OL437195	OL423620	OL444985	OL446999	–	OL444994
<i>Cyanosporus bifarius</i>	Cui 16277	China	OL423599	OL423609	OL437196	OL423621	OL444986	OL447000	–	OL444995
<i>Cyanosporus bubalinus</i>	Cui 16976	China	MW182172	MW182225	MW182208	MW182189	MW191547	MW191563	–	MW191530
<i>Cyanosporus bubalinus</i>	Cui 16985	China	MW182173	MW182226	MW182209	MW182190	MW191548	MW191564	–	MW191531
<i>Cyanosporus caesiosimulans</i>	Viacheslav Spirin 4199	Russia	MG137061	–	–	–	–	–	–	MG137140
<i>Cyanosporus caesiosimulans</i>	Otto Miettinen 16976	USA	MG137054	–	–	–	–	–	–	MG137137
<i>Cyanosporus caesius</i>	Gerhard Schuster 51	Germany	MG137045	–	–	–	–	–	–	–
<i>Cyanosporus caesius</i>	Cui 18630	France	OL423600	OL423610	OL437197	OL423622	–	–	–	OL444996
<i>Cyanosporus coeruleivirens</i>	Otto Miettinen 12214	Indonesia	MG137063	–	–	–	–	–	–	–
<i>Cyanosporus coeruleivirens</i>	Dai 19220	China	MW182174	MW182227	MW182210	MW182191	MW191549	–	–	MW191532
<i>Cyanosporus comatus</i>	Otto Miettinen 147551	USA	MG137066	–	–	–	–	–	–	–
<i>Cyanosporus cyanescens</i>	Otto Miettinen 13602	Finland	MG137067	–	–	–	–	–	–	MG137142
<i>Cyanosporus cyanescens</i>	Otto Miettinen 159192	Spain	MG137071	–	–	–	–	–	–	MG137144
<i>Cyanosporus flavus</i>	Cui 18547	China	MW448564	MW448561	–	MW448557	MW452596	MW452599	–	MW452601
<i>Cyanosporus flavus</i>	Cui 18562	China	MW448565	MW448562	–	MW448558	MW452597	MW452600	–	MW452602
<i>Cyanosporus fusiformis</i>	Cui 10775	China	KX900868	KX900938	KX901006	KX901081	–	KX901191	–	KX901245
<i>Cyanosporus fusiformis</i>	Dai 15036	China	KX900867	KX900937	KX901005	KX901080	–	KX901190	–	KX901244
<i>Cyanosporus glaucus</i>	Viacheslav Spirin 5317	Russia	MG137078	–	–	–	–	–	–	–
<i>Cyanosporus glaucus</i>	Viacheslav Spirin 6580	Russia	MG137081	–	–	–	–	–	–	MG137145
<i>Cyanosporus gossypinus</i>	Bernard Rivoire 6658	France	–	–	–	–	–	–	–	MG137146

(Continued)

Table 1. (Continued).

Species name	Sample no.	Locality	GenBank accessions									
			ITS	nLSU	mtSSU	nuSSU	RPB1	RPB2	TBB1	TEF1		
<i>Cyanosporus hirsutus</i>	Cui 17083	China	MW182179	MW182233	MW182214	MW182197	MW191554	MW191568	–	MW191538		
<i>Cyanosporus hirsutus</i>	Cui 17343	China	OL423601	OL423611	OL437198	OL423623	OL444987	OL447001	–	OL444997		
<i>Cyanosporus livens</i>	Viacheslav Spirin 8728	USA	MG137090	–	–	–	–	–	–	MG137150		
<i>Cyanosporus livens</i>	Otto Miettinen 17177	USA	MG137082	–	–	–	–	–	–	MG137147		
<i>Cyanosporus luteocaezia</i>	Bernard Rivoire 2605	France	MG137091	–	–	–	–	–	–	–		
<i>Cyanosporus magnus</i>	Dai 21105	China	OL423603	OL423613	OL437200	OL423625	OL444989	OL447003	–	OL444999		
<i>Cyanosporus magnus</i>	Otto Miettinen 10634	China	KC595944	KC595944	–	–	–	–	–	MG137151		
<i>Cyanosporus mediterraneocaezsius</i>	LY BR 4274	France	KX900886	–	KX901024	KX901099	–	–	–	–		
<i>Cyanosporus microporus</i>	Cui 11014	China	KX900878	KX900948	KX901016	KX901091	–	KX901201	–	–		
<i>Cyanosporus microporus</i>	Dai 11717	China	KX900877	KX900947	KX901015	KX901090	–	KX901200	–	–		
<i>Cyanosporus nothofagicicola</i>	Cui 16697	Australia	MW182181	MW182235	MW182216	MW182199	MW191556	MW191570	–	MW191540		
<i>Cyanosporus nothofagicicola</i>	Dai 18765	Australia	MW182182	MW182236	MW182217	MW182200	MW191557	–	–	MW191541		
<i>Cyanosporus piceicola</i>	Cui 10626	China	KX900862	KX900932	KX901001	KX901075	–	KX901185	–	–		
<i>Cyanosporus piceicola</i>	Cui 12158	China	KX900866	KX900936	KX901004	KX901079	KX901153	KX901189	–	KX901243		
<i>Cyanosporus populi</i>	Otto Miettinen 17043	USA	MG137092	–	–	–	–	–	–	MG137153		
<i>Cyanosporus populi</i>	Cui 17557	China	OL423605	OL423615	OL437202	OL423627	OL444991	OL447005	–	OL445001		
<i>Cyanosporus rigidus</i>	Cui 17032	China	OL423606	OL423617	OL437204	OL423629	OL444993	–	–	OL445003		
<i>Cyanosporus simulans</i>	Otto Miettinen 20422	Finland	MG137110	–	–	–	–	–	–	MG137160		
<i>Cyanosporus simulans</i>	Tuomo Niemelä 8846	Finland	MG137103	–	–	–	–	–	–	–		
<i>Cyanosporus subcaezsius</i>	Josef Vlasák 0110/24	Czech Republic	MG137117	–	–	–	–	–	–	MG137164		
<i>Cyanosporus subcaezsius</i>	Alix David 652	France	MG137116	–	–	–	–	–	–	–		
<i>Cyanosporus subhirsutus</i>	Cui 11330	China	KX900873	KX900943	KX901011	KX901086	–	KX901196	–	KX901250		
<i>Cyanosporus subhirsutus</i>	Dai 14892	China	KX900871	KX900941	KX901009	KX901084	–	KX901194	–	KX901248		
<i>Cyanosporus submicroporus</i>	Cui 16306	China	MW182184	MW182239	MW182220	MW182203	MW191560	MW191573	–	MW191544		
<i>Cyanosporus submicroporus</i>	Cui 18156	China	MW182186	MW182241	MW182222	MW182205	–	MW191574	–	–		
<i>Cyanosporus subpopuli</i>	Liu 382	China	PP956594	PP956602	PP949487	–	–	–	–	PP962219		
<i>Cyanosporus subpopuli</i>	Liu 394	China	PP956595	PP956603	PP949488	–	–	–	–	PP962220		
<i>Cyanosporus subpopuli</i>	Liu 395	China	PP956596	PP956604	PP949489	–	–	–	–	PP962221		
<i>Cyanosporus subungulatus</i>	Cui 18046	China	MW448566	MW448563	MW448560	MW448559	MW452598	–	–	MW452603		
<i>Cyanosporus subungulatus</i>	Zhao 10833	China	MW742586	OL423616	OL437203	OL423628	OL444992	–	–	OL445002		
<i>Cyanosporus subviridis</i>	Viacheslav Spirin 8774a	USA	MG137120	–	–	–	–	–	–	MG137166		
<i>Cyanosporus subviridis</i>	Reijo Penttilä 14376	Finland	–	–	–	–	–	–	–	MG137165		
<i>Cyanosporus tenuicortexus</i>	Cui 16280	China	OL423607	OL423618	OL437205	OL423630	–	–	–	OL445004		
<i>Cyanosporus tenuicortexus</i>	Zhao 813	China	MG231802	OL423619	OL437206	OL423631	–	–	–	OL445005		
<i>Cyanosporus tenuis</i>	Cui 10788	China	KX900885	KX900955	KX901023	KX901098	KX901161	KX901208	–	–		
<i>Cyanosporus tenuis</i>	Dai 12974	China	KX900884	KX900954	KX901022	KX901097	KX901160	KX901207	–	KX901258		
<i>Cyanosporus tricolor</i>	Cui 12233	China	KX900876	KX900946	KX901014	KX901089	–	KX901199	–	KX901253		
<i>Cyanosporus tricolor</i>	Cui 10790	China	KX900875	KX900945	KX901013	KX901088	–	KX901198	–	KX901252		

(Continued)

Table 1. (Continued).

Species name	Sample no.	Locality	ITS	nLSU	GenBank accessions						TBB1	TEF1
					mtSSU	nuSSU	RPB1	RPB2				
<i>Cyanosporus unguilatus</i>	Cui 10778	China	KX900870	KX900940	KX901008	KX901083	–	KX901193	–	KX901247		
<i>Cyanosporus unguilatus</i>	Dai 12897	China	KX900869	KX900939	KX901007	KX901082	KX901154	KX901192	–	KX901246		
<i>Cyanosporus yanae</i>	Heikki Kotiranta 27606	Russia	MG137122	–	–	–	–	–	–	MG137168		
<i>Cyanosporus yanae</i>	Heikki Kotiranta 27454	Russia	MG137121	–	–	–	–	–	–	MG137167		
<i>Cystidiopostia hibernica</i>	Cui 2658	China	KX900905	KX900975	KX901045	KX901118	–	KX901218	–	–		
<i>Cystidiopostia inocybe</i>	LY BR 3703	France	KX900903	KX900973	KX901044	KX901116	–	–	–	KX901267		
<i>Cystidiopostia pileata</i>	Cui 10034	China	KX900908	KX900956	KX901050	KX901122	KX901170	KX901222	–	KX901269		
<i>Datronia mollis</i>	RLG 6304	USA	JN165002	JN164791	–	–	JN164818	JN164872	–	JN164901		
<i>Datronia stereoides</i>	Holonen	Finland	KC415179	KC415196	–	–	–	–	–	–		
<i>Datroniella scutellata</i>	RLG 9584 T	USA	JN165004	JN164792	–	–	JN164817	JN164873	–	JN164902		
<i>Datroniella tropica</i>	Dai 13147	China	KC415181	KC415189	–	–	–	KC477838	–	–		
<i>Echinochaete brachypora</i>	TFMF 24996	Japan	AB462321	AB462309	–	–	–	–	–	–		
<i>Echinochaete ruficeps</i>	TFMF 15716	Japan	AB462310	AB368065	–	–	–	AB368123	–	–		
<i>Echinochaete russiceps</i>	TFMF 24250	Japan	AB462313	AB462301	–	–	–	–	–	–		
<i>Entoloma prunuloides</i>	AFTOL ID 523	USA	DQ206983	AY700180	–	AY665784	DQ447898	DQ385883	–	DQ457633		
<i>Entoloma undatum</i>	HKAS 115925	China	MZ855875	MZ853561	–	–	MZ852812	MZ852824	–	–		
<i>Favolus acervatus</i>	Cui 11053	China	KU189774	KU189805	KU189956	KU189835	KU189889	KU189994	KU189864	KU189920		
<i>Favolus emerici</i>	Cui 10926	China	KU189776	KU189807	–	KU189837	KU189890	KU189995	KU189866	KU189922		
<i>Favolus niveus</i>	Cui 11129	China	KX548955	KX548981	KX549019	KX549002	KX549067	KX549074	KX549035	KX549045		
<i>Fayodia bisphaerigera</i>	OW 24119	Norway	OR863429	OR863499	–	–	–	OR828256	–	OR828317		
<i>Fuscopostia duplicata</i>	Dai 13411	China	KF699125	KJ684976	KR606027	KR605928	KX901174	KR610845	–	KR610756		
<i>Fuscopostia fragilis</i>	JV 0610-8	Czech	JF950573	–	–	–	–	–	–	–		
<i>Fuscopostia leucomallia</i>	Cui 9599	China	KF699123	KJ684983	KX901056	KX901129	KX901176	KX901228	–	KX901272		
<i>Gamundia striatula</i>	JL 4518	Norway	OR863431	OR863501	–	OR863566	–	OR828258	–	OR828319		
<i>Gelatinofungus betulina</i>	Liu 473	China	PP956597	PP956605	–	–	–	–	–	PP962222		
<i>Gelatinofungus betulina</i>	Liu 105	China	PP956598	PP956606	–	–	–	–	–	PP962223		
<i>Gelatinofungus brunneus</i>	GC 1703-31	China	LC387339	LC387344	–	–	LC387347	LC387367	–	LC387385		
<i>Gelatinofungus brunneus</i>	Wu 1207-162	China	MZ636978	MZ637139	–	–	MZ748366	OK136005	–	MZ913615		
<i>Gelatinofungus brunneus</i>	Wu 1207-163	China	MZ636979	MZ637140	–	–	MZ748367	OK136006	–	MZ913616		
<i>Gelatinofungus</i> sp.	RLG-10795-Sp	USA	KY948785	KY948857	–	–	KY948937	OK136007	–	MZ913619		
<i>Harmajaesa harperi</i>	LIP 0401361	Spain	MG321366	MG321399	–	MG321333	–	MG334549	–	MG334541		
<i>Hertzogia martiorum</i>	AMB 18863	Italy	OR863441	OR863510	–	OR863574	–	OR828265	–	OR828323		
<i>Hexagonia glabra</i>	Dai 10691	China	JX569733	JX569750	–	–	–	KF274649	–	–		
<i>Hexagonia tenuis</i>	Cui 8468	China	JX559277	JX559302	–	–	–	JX559311	–	–		
<i>Hyphodermella corrugata</i>	MA-Fungi 24238	Portugal	FN600378	JN939586	–	–	–	–	–	–		
<i>Hyphodermella corrugata</i>	MA-Fungi 5527	Morocco	FN600372	JN939597	–	–	–	–	–	–		
<i>Hyphodermella poroides</i>	Dai 10848	China	KX008368	KX011853	–	–	–	–	–	–		
<i>Hyphodermella poroides</i>	Dai 12045	China	KX008367	KX011852	–	–	–	–	–	–		

(Continued)

(Continued)

Table 1. (Continued).

Species name	Sample no.	Locality	ITS	nLSU	mtSSU	GenBank accessions				
						nuSSU	RPB1	RPB2	TBB1	TEF1
<i>Hyphodermella rosae</i>	FP- 150552	USA	KP134978	KP135223	-	-	-	-	-	-
<i>Hyphodermella rosae</i>	GC 1604-113	China	MZ636986	MZ637147	-	-	-	-	-	-
<i>Hyphodermella rosae</i>	GC 1608-2	Japan	MZ636987	MZ637148	-	-	MZ748411	OK135983	-	MZ913592
<i>Hypsizygus ulmarius</i>	DUKE JM	USA	EF421105	AF042584	-	-	EF421030	EF420996	-	EF421062
<i>Infundibulicibe geotropa</i>	AMB 18861	Italy	OR863450	OR863518	-	OR863577	-	OR828268	-	-
<i>Infundibulicibe gibba</i>	AFTOL ID 1508	USA	DQ490635	DQ457682	-	DQ115780	DQ447913	DQ472727	-	GU187759
<i>Inocybe myriadophylla</i>	AFTOL-ID 482	Finland	DQ221106	AY700196	-	AY657016	DQ447916	AY803751	-	DQ435791
<i>Inocybe phaeoleuca</i>	EL 29708	Hungary	KJ399958	-	-	-	-	-	-	-
<i>Inocybe subpaleacea</i>	JV 29282	Finland	KJ849311	KJ849311	-	-	-	-	-	-
<i>Jahnoporus brachiatus</i>	X3232	Russia	KU165781	-	-	-	-	-	-	-
<i>Jahnoporus hirtus</i>	Spinosa 10 X 2014	USA	KU165784	-	-	-	KY949044	-	-	-
<i>Jahnoporus oreinus</i>	X3241	Russia	KU165785	-	-	-	-	-	-	-
<i>Langemannia gigantea</i>	Jeppson 3566	Sweden	DQ112623	DQ112623	-	-	-	-	-	-
<i>Lentinus arcularius</i>	Cui 11398	China	KU189766	KU189797	KU189947	KU189826	KU189884	KU189980	-	KU189911
<i>Lentinus brumalis</i>	Cui 10750	China	KU189765	KU189796	-	KU189825	KU189883	KU189979	KU189857	KU189910
<i>Lentinus substrictus</i>	Wei 1582	China	KU189767	KU189798	KU189948	KU189827	-	KU189981	KU189858	KU189912
<i>Lepista glaucocana</i>	AMB 18862	Italy	OR863452	OR863520	-	OR863579	-	-	-	-
<i>Lepista Irina</i>	AFTOL ID 815	USA	DQ221109	DQ234538	-	AY705948	DQ447919	DQ385885	-	DQ028591
<i>Lepista ricekii</i>	AMB 18864	Italy	OR863453	OR863521	-	OR863580	-	OR828270	-	-
<i>Lepista saeva</i>	TENN 066100	USA	KJ137270	KJ417193	-	KJ417159	-	KJ424376	-	-
<i>Leucocybe candicans</i>	AFTOL ID 541	USA	DQ202268	AY645055	-	AY771609	DQ447891	DQ385881	-	DQ408149
<i>Lycoperdon altimontanum</i>	Dobremez 710910	Sweden	DQ112589	DQ112589	-	-	-	-	-	-
<i>Lycoperdon altimontanum</i>	MJ 4270	Sweden	DQ112588	DQ112588	-	-	-	-	-	-
<i>Lycoperdon cf. niveum</i>	MJ 4068	Sweden	DQ112571	DQ112571	-	-	-	-	-	-
<i>Lycoperdon cretaceum</i>	MJ 4105	Sweden	DQ112597	DQ112597	-	-	-	-	-	-
<i>Lycoperdon cretaceum</i>	Jeppson 4302	Norway	DQ112598	DQ112598	-	-	-	-	-	-
<i>Lycoperdon curtisii</i>	HIP1	USA	HQ235043	-	-	-	-	-	-	-
<i>Lycoperdon curtisii</i>	VPK 1	Pakistan	MK414502	-	-	-	-	-	-	-
<i>Lycoperdon curtisii</i>	NCP 9	USA	HQ235045	-	-	-	-	-	-	-
<i>Lycoperdon curtisii</i>	NCP 49	USA	HQ235048	-	-	-	-	-	-	-
<i>Lycoperdon decipiens</i>	Jeppson 7715	Sweden	DQ112583	DQ112583	-	-	-	-	-	-
<i>Lycoperdon decipiens</i>	MJ 4330	Sweden	DQ112582	DQ112582	-	-	-	-	-	-
<i>Lycoperdon demoulinii</i>	UFRN Fungos 2554	Brazil	KU958309	KU958310	-	-	-	-	-	-
<i>Lycoperdon demoulinii</i>	UFRN Fungos 655	Brazil	KU958307	KU958308	-	-	-	-	-	-
<i>Lycoperdon dermoxanthum</i>	Jeppson 4568	Sweden	DQ112579	DQ112579	-	-	-	-	-	-
<i>Lycoperdon dermoxanthum</i>	WEW 051	USA	OM203536	-	-	-	-	-	-	-
<i>Lycoperdon ericaeum</i>	Jeppson 4866	Sweden	DQ112606	DQ112606	-	-	-	-	-	-
<i>Lycoperdon ericaeum</i>	Jeppson 5395	Sweden	DQ112605	DQ112605	-	-	-	-	-	-

(Continued)

Table 1. (Continued).

Species name	Sample no.	Locality	ITS	GenBank accessions					TEF1
				nLSU	mtSSU	nuSSU	RPB1	RPB2	TBB1
<i>Lycoperdon excipuliforme</i>	Jeppson 6467	Sweden	DQ112590	DQ112590	-	-	-	-	-
<i>Lycoperdon excipuliforme</i>	Mushroom 469025	USA	OM397395	OM397395	-	-	-	-	-
<i>Lycoperdon frigidum</i>	Lange 191	Svalbard	DQ112559	DQ112559	-	-	-	-	-
<i>Lycoperdon frigidum</i>	MJ 484	Sweden	DQ112568	-	-	-	-	-	-
<i>Lycoperdon intermedium</i>	STB 091	USA	EU833667	-	-	-	-	-	-
<i>Lycoperdon lahorensae</i>	VPK 6	Pakistan	MK414506	-	-	-	-	-	-
<i>Lycoperdon lahorensae</i>	NYG 8	Pakistan	KC844917	-	-	-	-	-	-
<i>Lycoperdon lahorensae</i>	NYG 7	Pakistan	KC844918	-	-	-	-	-	-
<i>Lycoperdon lambinonii</i>	Jeppson 5245	Norway	DQ112576	DQ112576	-	-	-	-	-
<i>Lycoperdon lambinonii</i>	Demolin 4622	Sweden	DQ112575	DQ112575	-	-	-	-	-
<i>Lycoperdon lividum</i>	Jeppson 4005	Sweden	DQ112600	DQ112600	-	-	-	-	-
<i>Lycoperdon mammiforme</i>	MJ 4841	Sweden	DQ112567	DQ112567	-	-	-	-	-
<i>Lycoperdon mammiforme</i>	DA 42	Germany	AJ237621	-	-	-	-	-	-
<i>Lycoperdon marginatum</i>	Parker 750822	Sweden	DQ112632	-	-	-	-	-	-
<i>Lycoperdon marginatum</i>	iNat 59167384	USA	MW031164	-	-	-	-	-	-
<i>Lycoperdon marginatum</i>	iNat 58324716	USA	ON129309	-	-	-	-	-	-
<i>Lycoperdon marginatum</i>	MO 430514	USA	ON256799	-	-	-	-	-	-
<i>Lycoperdon molle</i>	STB 098 A	USA	EU833662	-	-	-	-	-	-
<i>Lycoperdon molle</i>	NSK 1017218	Russia	OP725695	-	-	-	-	-	-
<i>Lycoperdon molle</i>	HBAU 15544	China	MZ145083	-	-	-	-	-	-
<i>Lycoperdon muscorum</i>	Jeppson 7717	Sweden	DQ112604	DQ112604	-	-	-	-	-
<i>Lycoperdon muscorum</i>	Martin 2673	Spain	JN572904	-	-	-	-	-	-
<i>Lycoperdon muscorum</i>	Jeppson 9017	Sweden	JN572905	JN572905	-	-	-	-	-
<i>Lycoperdon nigrescens</i>	TNS F 70022	Japan	KU507384	KU507396	-	-	-	-	-
<i>Lycoperdon nigrescens</i>	Kasuya B602	Japan	OQ025262	OQ025246	-	-	-	-	-
<i>Lycoperdon nigrescens</i>	TNS F 70025	Japan	KU507387	KU507399	-	-	-	-	-
<i>Lycoperdon nigrescens</i>	TNS F 70024	Japan	KU507386	KU507398	-	-	-	-	-
<i>Lycoperdon norvegicum</i>	MJ 5453	Sweden	DQ112631	DQ112631	-	-	-	-	-
<i>Lycoperdon norvegicum</i>	Infungi 3	Kazakhstan	ON704897	-	-	-	-	-	-
<i>Lycoperdon perlatum</i>	MJ 4684	Sweden	DQ112630	DQ112630	-	-	-	-	-
<i>Lycoperdon perlatum</i>	HAI G 69	Israel	OR594101	-	-	-	-	-	-
<i>Lycoperdon perlatum</i>	MO 506660	USA	OR336196	-	-	-	-	-	-
<i>Lycoperdon perlatum</i>	SL 2038	Singapore	OR354962	-	-	-	-	-	-
<i>Lycoperdon perlatum</i>	NSK 1017331	Russia	OR242700	-	-	-	-	-	-
<i>Lycoperdon perlatum</i>	Liu 2	China	PP037937	PP025318	-	-	-	-	-
<i>Lycoperdon perlatum</i>	Liu 329	China	PP037940	PP025319	-	-	-	-	-
<i>Lycoperdon perlatum</i>	Liu 364	China	PP037941	PP025320	-	-	-	-	-
<i>Lycoperdon perlatum</i>	Liu 386	China	PP037942	PP025321	-	-	-	-	-

(Continued)



Table 1. (Continued).

Species name	Sample no.	Locality	ITS	nLSU	mtSSU	nuSSU	GenBank accessions			
							RPB1	RPB2	TBB1	TEF1
<i>Lycoperdon pratense</i>	MJ 4864	Sweden	DQ112554	DQ112554	–	–	–	–	–	–
<i>Lycoperdon pratense</i>	VPK 2a	Pakistan	MK414499	–	–	–	–	–	–	–
<i>Lycoperdon pratense</i>	MP 9	Canada	KY706181	KY706181	–	–	–	–	–	–
<i>Lycoperdon pratense</i>	VPK 9	Pakistan	MK414501	–	–	–	–	–	–	–
<i>Lycoperdon pseudocurtisii</i>	VPK 3a	Pakistan	MK414503	–	–	–	–	–	–	–
<i>Lycoperdon pseudocurtisii</i>	VPK 3b	Pakistan	MK414504	–	–	–	–	–	–	–
<i>Lycoperdon pseudocurtisii</i>	VPK 3c	Pakistan	MK414505	–	–	–	–	–	–	–
<i>Lycoperdon pseudoperlatum</i>	Liu 22	China	PP037938	–	–	–	–	–	–	–
<i>Lycoperdon pseudoperlatum</i>	Liu 193	China	PP037939	–	–	–	–	–	–	–
<i>Lycoperdon pyriforme</i>	Jeppson 4849	Sweden	DQ112558	DQ112558	–	–	–	–	–	–
<i>Lycoperdon pyriforme</i>	LPOL	USA	AJ237618	–	–	–	–	–	–	–
<i>Lycoperdon pyriforme</i>	LPNE	Nepal	AJ237619	–	–	–	–	–	–	–
<i>Lycoperdon radiculatum</i>	Parker 970911	USA	DQ112608	DQ112608	–	–	–	–	–	–
<i>Lycoperdon radiculatum</i>	CM 073	Algeria	KY996490	–	–	–	–	–	–	–
<i>Lycoperdon rupicola</i>	Jeppson 4304	Norway	DQ112580	DQ112580	–	–	–	–	–	–
<i>Lycoperdon rupicola</i>	Vetter 407	Sweden	DQ112581	DQ112581	–	–	–	–	–	–
<i>Lycoperdon rupicola</i>	Jeppson 7007	Sweden	JN572902	JN572902	–	–	–	–	–	–
<i>Lycoperdon rupicola</i>	JLF 2009 59	Norway	JN572901	JN572901	–	–	–	–	–	–
<i>Lycoperdon rupicola</i>	Carlsson 96144	Sweden	JN572903	JN572903	–	–	–	–	–	–
<i>Lycoperdon subcretaceum</i>	Jeppson 9032	Norway	JN572908	JN572908	–	–	–	–	–	–
<i>Lycoperdon subumbrinum</i>	Jeppson 6377	Sweden	DQ112602	DQ112602	–	–	–	–	–	–
<i>Lycoperdon subumbrinum</i>	Jeppson 6394	Sweden	DQ112601	DQ112601	–	–	–	–	–	–
<i>Lycoperdon subumbrinum</i>	Örstadius 148-03	Sweden	DQ112603	DQ112603	–	–	–	–	–	–
<i>Lycoperdon subumbrinum</i>	Jeppson 8096	Sweden	JN572906	JN572906	–	–	–	–	–	–
<i>Lycoperdon subumbrinum</i>	Jeppson 7524	Slovakia	JN572907	JN572907	–	–	–	–	–	–
<i>Lycoperdon umbrinum</i>	Jeppson 4556	Sweden	DQ112591	DQ112591	–	–	–	–	–	–
<i>Lycoperdon umbrinum</i>	MJ 4556a	Sweden	DQ112593	DQ112593	–	–	–	–	–	–
<i>Lycoperdon umbrinum</i>	MJ 4559	Sweden	DQ112592	DQ112592	–	–	–	–	–	–
<i>Lycoperdon utiforme</i>	Jeppson 5388	Sweden	DQ112607	DQ112607	–	–	–	–	–	–
<i>Lycoperdon utiforme</i>	MGW 541	USA	EU833659	–	–	–	–	–	–	–
<i>Lyophyllum semitale</i>	HC 8513	Switzerland	AF357049	AF042581	–	–	EF421036	EF421002	–	EF421068
<i>Lyophyllum turcicum</i>	GB:0065321	Norway	OR863458	OR863525	–	OR863583	–	OR828273	–	OR828328
<i>Macrocystidia aff. cucumis</i>	JK 184	USA	ON478249	–	–	–	–	–	–	–
<i>Macrocystidia cucumis</i>	JX 129473345	Finland	OR863460	OR863527	–	OR863585	–	OR828275	–	OR828330
<i>Macrocystidia hebeiensis</i>	Liu 67	China	PP956599	PP956607	–	–	–	–	–	PP962224
<i>Macrocystidia hebeiensis</i>	Liu 25	China	PP956600	PP956608	–	–	–	–	–	PP962225
<i>Macrocystidia reducta</i>	PDD 95703	New Zealand	JQ694109	–	–	–	–	–	–	–
<i>Macrocystidia sp.</i>	Kekki 3956	Finland	OR863459	OR863526	–	OR863584	–	OR828274	–	OR828329

(Continued)



Table 1. (Continued).

Species name	Sample no.	Locality	ITS	nLSU	mtSSU	nuSSU	GenBank accessions			
							RPB1	RPB2	TBB1	TEF1
<i>Microporus affinis</i>	Cui 7714	China	JX569739	JX569746	–	–	–	KF274661	–	–
<i>Microporus flabelliformis</i>	Dai 11574	China	JX569740	JX569747	–	–	–	KF274662	–	–
<i>Microporus vernicipes</i>	KUC 20130711–23	South Korea	KJ668503	KJ668355	–	–	–	–	–	–
<i>Microporus xanthopus</i>	Cui 8284	China	JX290074	JX290071	–	–	–	JX559313	–	–
<i>Musumecia betlachensis</i>	TO HG 2284	France	JF926520	JF926521	–	KJ681069	–	KJ681060	–	KJ681082
<i>Mycena aff. pura1</i>	TL 9433	Ecuador	FN394622	–	–	–	KF723688	–	–	KF723642
<i>Mycena aff. pura1</i>	TL 9450	Ecuador	KJ144653	–	–	–	KF723689	–	–	KF723643
<i>Mycena aff. pura2</i>	TL 8052	Ecuador	FN394623	–	–	–	KF723687	–	–	KF723641
<i>Mycena aff. pura2</i>	TL 9678	Ecuador	FN394621	–	–	–	KF723690	–	–	KF723644
<i>Mycena arcangeliana</i>	252 b	Italy	JF908401	–	–	–	–	–	–	–
<i>Mycena arcangeliana</i>	252 f	Italy	JF908402	–	–	–	–	–	–	–
<i>Mycena brunnea</i>	CBH 187	Denmark	FN394564	–	–	–	KF723678	–	–	KF723632
<i>Mycena brunnea</i>	CBH 386	Denmark	FN394565	–	–	–	KF723679	–	–	KF723633
<i>Mycena brunneoviolacea</i>	BAP 594	USA	MH414546	–	–	–	–	–	–	–
<i>Mycena cahaya</i>	ACL 134	Malaysia	KF537248	–	–	–	–	–	–	–
<i>Mycena cf. pura I</i>	CBH 039	Denmark	FN394588	–	–	–	KF723680	–	–	KF723634
<i>Mycena cf. pura II</i>	CBH 105	Denmark	FN394581	–	–	–	KF723671	–	–	KF723625
<i>Mycena cf. pura II</i>	CBH 169	Denmark	FN394579	–	–	–	KF723672	–	–	KF723626
<i>Mycena cf. pura II</i>	CBH 404	Denmark	FN394566	–	–	–	KF723674	–	–	KF723628
<i>Mycena cf. pura III</i>	CBH 019	Denmark	FN394605	–	–	–	KF723675	–	–	KF723629
<i>Mycena cf. pura III</i>	CBH 022	Denmark	FN394574	–	–	–	KF723676	–	–	KF723630
<i>Mycena cf. pura III</i>	KK	Slovakia	FN394606	–	–	–	KF723677	–	–	KF723631
<i>Mycena cf. pura IV</i>	CBH 410	Denmark	FN394595	–	–	–	KF723667	–	–	KF723621
<i>Mycena cf. pura IV</i>	JV 06979	Denmark	FN394585	–	–	–	KF723668	–	–	KF723622
<i>Mycena cf. pura IV</i>	TL 4571	Denmark	FN394583	–	–	–	KF723669	–	–	KF723623
<i>Mycena cf. pura IX</i>	CBH 166	Denmark	FN394607	–	–	–	KF723701	–	–	KF723655
<i>Mycena cf. pura IX</i>	CBH 358	Denmark	FN394608	–	–	–	KF723702	–	–	KF723656
<i>Mycena cf. pura IX</i>	CBH 367	Denmark	KF913022	–	–	–	KF723703	–	–	KF723657
<i>Mycena cf. pura IX</i>	CBH 371	Denmark	KF913023	–	–	–	KF723704	–	–	KF723658
<i>Mycena cf. pura VI</i>	BAP 132	USA	FN394561	–	–	–	KF723660	–	–	KF723614
<i>Mycena cf. pura VII</i>	IS1011200	USA	FN394611	–	–	–	–	–	–	–
<i>Mycena cf. pura VIII</i>	CBH 216	Denmark	FN394598	–	–	–	KF723662	–	–	KF723616
<i>Mycena cf. pura VIII</i>	CBH 402	Denmark	FN394599	–	–	–	KF723663	–	–	KF723617
<i>Mycena cf. pura VIII</i>	BAP 165 A	USA	FN394563	–	–	–	KF723698	–	–	KF723652
<i>Mycena cf. pura X</i>	CBH 400	Denmark	FN394617	–	–	–	KF723699	–	–	KF723653
<i>Mycena diosma</i>	LK 1191/2000	Germany	FN394619	–	–	–	KF723700	–	–	KF723654
<i>Mycena diosma</i>	10315	Austria	FN394560	–	–	–	KF723694	–	–	KF723648
<i>Mycena lammiensis</i>	TUR 165927	Finland	FN394552	–	–	–	KF723697	–	–	KF723651

(Continued)

Table 1. (Continued).

GenBank accessions										
Species name	Sample no.	Locality	ITS	nLSU	mtSSU	nuSSU	RPB1	RPB2	TB81	TEF1
<i>Mycena luceata</i>	ACP 2116	Mexico	OR233614	-	-	-	OR233746	-	-	OR233755
<i>Mycena luceata</i>	ACP 2126	Mexico	OR233613	-	-	-	OR233745	-	-	OR233754
<i>Mycena luciferina</i>	ACP 2114	Mexico	OR233612	-	-	-	OR233744	-	-	-
<i>Mycena lucisnieblae</i>	ACP 2140	Mexico	OR233610	-	-	-	OR233742	-	-	OR233752
<i>Mycena lucisnieblae</i>	ACP 2139	Mexico	OR233611	-	-	-	OR233743	-	-	OR233753
<i>Mycena lucisnieblae</i>	ACP 2149	Mexico	OR233609	-	-	-	OR233741	-	-	OR233751
<i>Mycena luteovariegata</i>	CBH 226	Denmark	FN394604	-	-	-	KF723664	-	-	KF723618
<i>Mycena luteovariegata</i>	TL 5614	Denmark	FN394602	-	-	-	KF723666	-	-	KF723620
<i>Mycena luteovariegata</i>	DB 2005/152	Denmark	FN394603	-	-	-	-	-	-	-
<i>Mycena luxmanantlanensis</i>	ACP 2160	Mexico	OR233603	-	-	-	OR233737	-	-	OR233747
<i>Mycena luxmanantlanensis</i>	ACP 2159	Mexico	OR233604	-	-	-	OR233738	-	-	OR233748
<i>Mycena meligena</i>	39	Italy	JF908423	-	-	-	-	-	-	-
<i>Mycena meligena</i>	39d	Italy	JF908429	-	-	-	-	-	-	-
<i>Mycena pearsoniana</i>	JV 06890	Denmark	FN394612	-	-	-	KF723692	-	-	KF723646
<i>Mycena pearsoniana</i>	CBH 068	Germany	FN394614	-	-	-	KF723691	-	-	KF723645
<i>Mycena pearsoniana</i>	LK 880/2002	Germany	FN394613	-	-	-	KF723693	-	-	KF723647
<i>Mycena pearsoniana</i>	FCME 25817	USA	JN182198	-	-	-	-	-	-	-
<i>Mycena pelianthina</i>	CBH 015	Denmark	FN394549	-	-	-	KF723695	-	-	KF723649
<i>Mycena pelianthina</i>	CBH 016	Denmark	FN394547	-	-	-	KF723696	-	-	KF723650
<i>Mycena polycystidiata</i>	FFAAS 0417	China	ON427731	-	-	-	ON468456	-	-	ON468469
<i>Mycena polycystidiata</i>	FFAAS 0421	China	ON427733	-	-	-	ON468458	-	-	ON468471
<i>Mycena polycystidiata</i>	Liu 494	China	PP037955	-	-	-	-	-	-	-
<i>Mycena pseudocorticola</i>	124 a	Italy	JF908386	-	-	-	-	-	-	-
<i>Mycena pura</i>	TENN 65043	USA	JN182202	-	-	-	-	-	-	-
<i>Mycena pura</i>	HMJAU 43121	China	MK309793	-	-	-	-	-	-	-
<i>Mycena rosea</i>	TL 12409	Denmark	FN394557	-	-	-	KF723685	-	-	KF723639
<i>Mycena rosea</i>	CBH 097	Denmark	FN394556	-	-	-	KF723681	-	-	KF723635
<i>Mycena rosea</i>	CBH 409	Germany	FN394551	-	-	-	KF723683	-	-	KF723637
<i>Mycena rubobrunnea</i>	FFAAS 0415	China	ON427729	-	-	-	ON468454	-	-	ON468467
<i>Mycena rubobrunnea</i>	FFAAS 0414	China	ON427728	-	-	-	ON468453	-	-	ON468466
<i>Mycena rubobrunnea</i>	FFAAS 0416	China	ON427730	-	-	-	ON468455	-	-	ON468468
<i>Mycena seminau</i>	ACL 308	Malaysia	KF537252	-	-	-	-	-	-	-
<i>Mycena seminau</i>	ACL 136	Malaysia	KF537250	-	-	-	-	-	-	-
<i>Mycena shengshanensis</i>	FFAAS 0425	China	ON427740	-	-	-	ON468465	-	-	ON468478
<i>Mycena shengshanensis</i>	FFAAS 0424	China	ON427739	-	-	-	ON468464	-	-	ON468477
<i>Mycena sinar</i>	ACL 092	Malaysia	KF537247	-	-	-	-	-	-	-
<i>Mycena sinar</i>	ACL 135	Malaysia	KF537249	-	-	-	-	-	-	-
<i>Mycena sinar</i> var. <i>tangkaisinar</i>	ACL 307	Malaysia	KF537251	-	-	-	-	-	-	-

(Continued)

(Continued)

Table 1. (Continued).

Species name	Sample no.	Locality	ITS	nLSU	mtSSU	GenBank accessions				
						nuSSU	RPB1	RPB2	TB81	TEF1
<i>Mycena sophiae</i>	ACP 2157	Mexico	OR233606	–	–	–	OR233739	–	–	OR233749
<i>Mycena sophiae</i>	ACP 2161	Mexico	OR233605	–	–	–	–	–	–	OR233757
<i>Mycena subbrunnea</i>	Liu 59	China	PP037944	–	–	–	PP034075	–	–	PP034078
<i>Mycena subbrunnea</i>	Liu 265	China	PP037946	–	–	–	PP034076	–	–	PP034079
<i>Mycena subbrunnea</i>	Liu 313	China	PP037947	–	–	–	–	–	–	PP034080
<i>Mycena subbrunnea</i>	Liu 315	China	PP037948	–	–	–	–	–	–	PP034081
<i>Mycena subbrunnea</i>	Liu 453	China	PP037951	–	–	–	PP034077	–	–	PP034082
<i>Mycena subpura</i>	Liu 10	China	PP037943	–	–	–	–	–	–	PP034083
<i>Mycena subpura</i>	Liu 489	China	PP037954	–	–	–	–	–	–	PP034084
<i>Mycena subulata</i>	FFAAS 0420	China	ON427736	–	–	–	ON468461	–	–	ON468474
<i>Mycena subulata</i>	FFAAS 0426	China	ON427738	–	–	–	ON468463	–	–	ON468476
<i>Mycena subulata</i>	FFAAS 0419	China	ON427735	–	–	–	ON468460	–	–	ON468473
<i>Mycena subulata</i>	FFAAS 0423	China	ON427737	–	–	–	ON468462	–	–	ON468475
<i>Mycena supina</i>	128 a	Italy	JF908388	–	–	–	–	–	–	–
<i>Mycena variispora</i>	Liu 129	China	PP037945	–	–	–	–	–	–	PP034085
<i>Mycena variispora</i>	Liu 369	China	PP037949	–	–	–	–	–	–	PP034086
<i>Mycena variispora</i>	Liu 370	China	PP037950	–	–	–	–	–	–	PP034087
<i>Mycena violacea-ardesiaca</i>	Liu 475	China	PP037952	–	–	–	–	–	–	PP034088
<i>Mycena violacea-ardesiaca</i>	Liu 477	China	PP037953	–	–	–	–	–	–	PP034089
<i>Mycena yuezhui</i>	FFAAS 0344	China	MW581490	–	–	–	MW868166	–	–	MW882249
<i>Mycena yuezhui</i>	FFAAS 0347	China	MW581493	–	–	–	MW868167	–	–	MW882252
<i>Mycenastrum corium</i>	MJ 5467	Sweden	DQ112628	–	–	–	–	–	–	–
<i>Mycenastrum corium</i>	STB 113	USA	EU833666	–	–	–	–	–	–	–
<i>Mycobonia flava</i>	CuTENN 10256	Costa Rica	AY513570	AJ487934	–	–	–	–	–	–
<i>Mycobonia flava</i>	TENN 59088	Argentina	AY513571	AJ487933	–	–	–	–	–	–
<i>Neodatronia gaoligongensis</i>	Cui 8055	China	JX559269	JX559286	–	–	–	JX559317	–	–
<i>Neodatronia sinensis</i>	Dai 11921	China	JX559272	JX559283	–	–	–	JX559320	–	–
<i>Neofavolus alveolaris</i>	Cui 9900	China	KX548974	KX548996	KX549030	KX549014	KX549072	KX549078	KX549040	KX549060
<i>Neofavolus alveolaris</i>	Dai 11290	China	KU189768	KU189799	KU189949	KU189828	KU189885	KU189982	KU189859	KU189913
<i>Neofavolus mikawai</i>	Cui 11152	China	KU189773	KU189804	KU189955	KU189834	KU189888	KU189986	KU189863	KU189919
<i>Neofavolus mikawai</i>	Dai 12361	China	KX548975	KX548997	KX549031	KX549015	–	KX549079	KX549041	KX549061
<i>Neofavolus squamatus</i>	Cui 12175	China	KX900070	KX900184	KX900250	KX900295	–	KX900317	KX899942	KX900370
<i>Nolanea sericea</i>	VHA503/02	USA	DQ367430	DQ367423	–	DQ367421	DQ825424	DQ367435	–	DQ367428
<i>Notholepista fistulosa</i>	HKAS 115934	China	OK104077	OK104059	–	–	OK105132	OK105137	–	OK105127
<i>Notholepista fistulosa</i>	HMJU 288	China	MZ435890	MZ435886	–	MZ435871	MZ441382	MZ441374	–	MZ441378
<i>Notholepista fistulosa</i>	HMJU 592	China	MZ435891	MZ435887	–	MZ435872	MZ441383	MZ441375	–	MZ441379
<i>Notholepista subzonalis</i>	GB 0087013	Sweden	KP453695	KJ417208	–	KJ417167	–	KJ424385	–	–
<i>Odontoefibula orientalis</i>	GC 1703-76	China	LC379004	LC379156	–	–	LC379161	LC387360	–	LC387379

(Continued)



Table 1. (Continued).

Species name	Sample no.	Locality	ITS	nLSU	mtSSU	GenBank accessions				
						nuSSU	RPB1	RPB2	TBB1	TEF1
<i>Odontofibula orientalis</i>	Wu 0805-59	China	LC363488	LC363493	–	–	–	–	–	
<i>Odontofibula orientalis</i>	Wu 0910-57	China	LC363490	LC363495	–	–	LC363501	LC387362	LC387381	
<i>Oligoporus rennyi</i>	TN-6645	Finland	KC595929	KC595929	–	–	–	–	–	
<i>Oligoporus sericeomollis</i>	Cui 9870	China	KX900920	KX900990	KX901068	KX901141	KX901184	–	–	
<i>Omphalina pyxidata</i>	AMB 19294	Italy	OR863467	OR863534	–	OR863591	–	OR828282	–	
<i>Omphalina pyxidata</i>	AMB 19295	Italy	OR863468	OR863535	–	OR863592	–	OR828283	–	
<i>Osteina obducta</i>	Cui 10074	China	KX900924	KX900994	KX901071	KX901144	–	KX901240	–	
<i>Osteina undosa</i>	Dai 7105	China	KX900921	KX900991	KX901069	KX901142	–	KX901238	–	
<i>Oxychaete cervinogilva</i>	Dmitry Schigel 5216	Australia	KX752596	KX752596	–	–	KX752626	–	–	
<i>Oxychaete cervinogilva</i>	GC 1501-16	China	MZ422783	MZ637173	–	–	–	–	MZ913613	
<i>Paralepista flaccida</i>	KUN-HKAS 115937	China	MZ855885	MZ853571	–	–	MZ857194	MZ681894	MZ857193	
<i>Paralepista flaccida</i>	TO AV20140410	Italy	OR863469	OR863536	–	–	–	OR828284	OR828336	
<i>Paralepistopsis amoenolens</i>	AMB:18867	Italy	OR863470	OR863537	–	–	–	OR828285	OR828337	
<i>Phaeophlebiopsis caribbeana</i>	FD-442	USA	KP135416	–	–	–	–	–	–	
<i>Phaeophlebiopsis caribbeana</i>	HHB-6990	USA	KP135415	KP135243	–	–	KP134810	KP134931	MZ913643	
<i>Phaeophlebiopsis himalayensis</i>	Chen 3143	China	MZ637013	MZ637174	–	–	MZ748359	OK135992	MZ913633	
<i>Phaeophlebiopsis himalayensis</i>	FP-150577	USA	KP135417	KP135273	–	–	–	–	–	
<i>Phaeophlebiopsis ravenelii</i>	CBS 411.50	France	MH856691	MH868208	–	–	–	–	–	
<i>Phaeophlebiopsis ravenelii</i>	FCUG 2126	Spain	MZ637015	GQ470675	–	–	–	–	–	
<i>Phaeophlebiopsis ravenelii</i>	C 61963	Ecuador	AY571056	AY571019	–	–	MZ748361	OK135993	MZ913634	
<i>Phaeosolenia platensis</i>	C 61839	Ecuador	AY571055	AY571018	–	–	–	–	–	
<i>Phanerina mellea</i>	WEI 17-224	China	LC387333	LC387340	–	–	LC387345	LC387363	LC387382	
<i>Phanerina mellea</i>	Wu 1010-34	China	MZ422784	MZ637176	–	–	–	–	–	
<i>Phanerochaete aculeata</i>	Wu 1809-278	China	MZ422786	MZ637178	–	–	–	–	–	
<i>Phanerochaete aculeata</i>	Wu 880701-2	China	MZ422787	GQ470636	–	–	MZ748380	OK136008	MZ913593	
<i>Phanerochaete albida</i>	GC 1407-14	China	MZ422788	MZ637179	–	–	MZ748384	OK136013	MZ913704	
<i>Phanerochaete albida</i>	WEI 18-365	China	MZ422789	MZ637180	–	–	–	–	–	
<i>Phanerochaete alpina</i>	Wu 1308-61	China	MZ422790	MZ637182	–	–	MZ748394	OK136022	MZ913598	
<i>Phanerochaete alpina</i>	Wu 1308-77	China	MZ422791	MZ637183	–	–	–	–	–	
<i>Phanerochaete livescens</i>	GC 1612-11	China	MZ422819	MZ637204	–	–	MZ748383	OK136012	MZ913597	
<i>Phanerochaete livescens</i>	Wu 1307-41	China	MZ422820	MZ637205	–	–	–	–	–	
<i>Phanerochaete rhizomorpha</i>	Wu 0910-61	China	MZ422826	MZ637210	–	–	–	–	–	
<i>Phanerochaete rhizomorpha</i>	Wu 1707-112	China	MZ422827	MZ637211	–	–	–	–	–	
<i>Phanerochaete sordida</i>	GC 1708-162	China	MZ422828	MZ637212	–	–	MZ748391	OK136019	MZ913636	
<i>Phanerochaete sordida</i>	Wu 1109-55	China	MZ422829	MZ637213	–	–	MZ748388	OK136016	MZ913637	
<i>Phanerochaete velutina</i>	GC 1604-56	China	MZ422844	MZ637224	–	–	MZ748389	OK136017	MZ913638	
<i>Phanerochaete velutina</i>	Spirin 3949	Russia	KU893879	–	–	–	MZ748386	OK136015	MZ913642	
<i>Phlebiopsis alba</i>	GC 1508-110	China	MZ637042	MZ637246	–	–	MZ748368	OK135994	MZ913620	

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(Continued)



Table 1. (Continued).

Species name	Sample no.	Locality	ITS	nLSU	GenBank accessions					
					mtSSU	nuSSU	RPB1	RPB2	TBB1	TEF1
<i>Phlebiopsis alba</i>	GC 1708-20	China	MZ637043	MZ637247	-	-	-	-	-	-
<i>Phlebiopsis brunneocystidiata</i>	Chen 1143	China	MZ637048	MZ637249	-	-	-	-	-	-
<i>Phlebiopsis brunneocystidiata</i>	Chen 666	China	MT561707	GQ470640	-	-	-	-	-	-
<i>Phlebiopsis gigantea</i>	FCUG 1417	Norway	MZ637051	AF141634	-	-	MZ748372	OK135998	-	MZ913625
<i>Phlebiopsis gigantea</i>	FP-70857-Sp	USA	KP135390	KP135272	-	-	MZ748370	OK135996	-	MZ913623
<i>Phlebiopsis odontoides</i>	GC 1708-181	China	MZ637054	MZ637255	-	-	MZ748371	OK135997	-	MZ913624
<i>Phlebiopsis odontoides</i>	GC 1708-182	China	MZ637055	MZ637256	-	-	-	-	-	-
<i>Phlebiopsis yunnanensis</i>	CLZhao 3958	China	MH744140	MH744142	-	-	-	-	-	-
<i>Phlebiopsis yunnanensis</i>	GC 1708-169	China	MZ637060	MZ637260	-	-	-	-	-	-
<i>Phlebiopsis yushanica</i>	Chen 2302	China	MZ637046	-	-	-	-	-	-	-
<i>Phlebiopsis yushanica</i>	Chen 2358	China	MZ637047	MZ637261	-	-	MZ748377	OK136003	-	MZ913644
<i>Picipes allaoshanensis</i>	Cui 12578	China	KX900067	KX900182	-	KX900293	-	KX900315	-	KX900368
<i>Picipes allaoshanensis</i>	Cui 12585	China	KX900068	KX900183	KX900248	KX900294	-	KX900316	-	KX900369
<i>Picipes americanus</i>	JV 0509-149	USA	KC572002	KC572041	-	-	-	-	-	-
<i>Picipes americanus</i>	JV 0809-104	USA	KC572003	KC572042	-	-	-	-	-	-
<i>Picipes annularius</i>	Cui 10123	China	KX900060	KX900176	-	KX900286	-	-	-	KX900363
<i>Picipes atratus</i>	Cui 11289	China	KX900043	KX900159	-	KX900271	KX900384	KX900307	KX899935	-
<i>Picipes atratus</i>	Dai 13375	China	KX900042	KX900158	KX900227	KX900270	KX900383	-	-	-
<i>Picipes auriculatus</i>	Cui 13616	China	KX900063	KX900179	KX900245	KX900289	-	-	-	-
<i>Picipes auriculatus</i>	Yuan 4221	China	KX900064	KX900180	KX900246	KX900290	-	-	-	KX900366
<i>Picipes austroandinus</i>	MR10472	Argentina	AF516568	-	-	-	-	-	-	-
<i>Picipes austroandinus</i>	MR10701	Argentina	AF516569	-	-	-	-	-	-	-
<i>Picipes badius</i>	Cui 10853	China	KU189780	KU189811	KX900198	KU189844	KU189894	KU189894	KU189871	KU189929
<i>Picipes badius</i>	Cui 11136	China	KU189781	KU189812	KU189964	KU189845	KU189895	KU189990	KU189872	KU189930
<i>Picipes baishanzuensis</i>	Cui 11395	China	KU189763	KU189794	KU189946	KU189824	-	KU189978	KU189856	KU189908
<i>Picipes baishanzuensis</i>	Dai 13418	China	KU189762	KU189793	KU189945	KU189823	KU189882	KU189977	KU189855	KU189907
<i>Picipes brevistipitatus</i>	Cui 11345	China	KX900074	KX900188	KX900237	KX900280	-	-	-	KX905085
<i>Picipes brevistipitatus</i>	Cui 13652	China	KX900075	KX900189	KX900238	KX900281	-	-	-	KX905086
<i>Picipes cf. dictyopus</i>	Cui 11109	China	KX900025	KX900145	KX900220	KX900267	KX900380	KX900303	KX899934	KX900347
<i>Picipes cf. dictyopus</i>	Cui 11092	China	KX900026	KX900146	KX900221	KX900268	KX900381	KX900304	-	KX900348
<i>Picipes conferticola</i>	Cui 9950	China	KU189783	KU189814	KU189968	KU189848	KU189897	KU189993	KU189875	KU189934
<i>Picipes conferticola</i>	Dai 11114	China	JX473244	KC572061	KU189969	KU189849	-	-	-	KU189935
<i>Picipes dictyopus</i>	TENN 59385	Belize	AF516561	AJ487945	-	-	-	-	-	-
<i>Picipes fraxinicola</i>	Dai 2494	China	KC572023	KC572062	KU189966	-	-	-	-	KU189932
<i>Picipes fraxinicola</i>	Wei 6025	China	KC572024	KC572063	-	-	-	-	-	-
<i>Picipes fraxinicola</i>	Liu 137	China	PP956601	PP956609	PP949490	-	-	-	-	PP962226
<i>Picipes melanopus</i>	H 6003449	Finland	JQ964422	KC572064	-	-	-	-	-	-
<i>Picipes melanopus</i>	MJ 372-93	Czech	KC572026	KC572065	-	-	-	-	-	-

(Continued)

Table 1. (Continued).

Species name	Sample no.	Locality	ITS	nLSU	mtSSU	nuSSU	GenBank accessions			
							RPB1	RPB2	TB81	TEF1
<i>Picipes nigromarginatus</i>	Cui 8113	China	KX900062	KX900178	KX900244	KX900288	–	–	–	KX900365
<i>Picipes pumilus</i>	Cui 5464	China	KX851628	KX851682	KX851710	KX851735	KX851753	KX851765	KX851581	KX851785
<i>Picipes pumilus</i>	Dai 6705	China	KX851630	KX851684	KX851711	KX851737	–	–	–	KX851787
<i>Picipes rhizophilus</i>	Dai 11599	China	KC572028	KC572067	KU189967	KU189847	KU189896	KU189992	KU189874	KU189933
<i>Picipes rhizophilus</i>	Dai 16082	China	KX851634	KX851687	KX851713	KX851738	–	–	–	KX851788
<i>Picipes subdictyopus</i>	Cui 11220	China	KX900057	KX900173	KX900240	KX900283	KX900390	KX900314	–	KX900360
<i>Picipes subdictyopus</i>	Cui 12539	China	KX900058	KX900174	KX900241	KX900284	–	–	–	KX900361
<i>Picipes submelanopus</i>	Dai 13294	China	KU189770	KU189801	KU189951	KU189830	KU189886	KU189984	KU189860	KU189915
<i>Picipes submelanopus</i>	Dai 13296	China	KU189771	KU189802	KU189952	KU189831	–	–	KU189861	KU189916
<i>Picipes subtipicus</i>	Cui 2662	China	KU189759	KU189791	KU189943	KU189821	–	–	–	KU189905
<i>Picipes subtipicus</i>	Li 1928	China	KU189758	KU189790	KU189942	KU189820	KU189881	KU189976	KU189854	KU189904
<i>Picipes subtubaeformis</i>	Cui 10793	China	KU189753	KU189785	KU189938	KU189816	KU189877	KU189973	KU189851	KU189900
<i>Picipes subtubaeformis</i>	Dai 11870	China	KU189752	KU189784	KU189937	KU189815	KU189876	KU189972	KU189850	KU189899
<i>Picipes taibaiensis</i>	Dai 5741	China	JX489169	KC572071	–	–	–	–	–	–
<i>Picipes taibaiensis</i>	Dai 5746	China	KX196783	KX196784	KX196786	KX196787	–	–	–	KX196785
<i>Picipes tibeticus</i>	Cui 12215	China	KU189755	KU189787	KU189940	KU189818	KU189879	KU189975	KU189853	KU189902
<i>Picipes tibeticus</i>	Cui 12225	China	KU189756	KU189788	KU189941	KU189819	KU189880	–	–	KU189903
<i>Picipes tubaeformis</i>	Niemela 6855	Finland	KC572036	KC572073	–	–	–	–	–	–
<i>Picipes tubaeformis</i>	JV 0309-1	USA	KC572034	KC572072	–	–	–	–	–	–
<i>Picipes ulleungus</i>	Cui 12410	China	KX900022	KX900142	KX900217	KX900266	–	KX900302	KX899932	KX900344
<i>Picipes virgatus</i>	CuiTENN 11219	Argentina	AF516581	AJ488122	–	–	–	–	–	–
<i>Picipes virgatus</i>	CuiTENN 11406	Argentina	AF516582	AJ488123	–	–	–	–	–	–
<i>Picipes wuyishanensis</i>	Dai 7409	China	KX900061	KX900177	KX900243	KX900287	–	–	–	KX900364
<i>Pleuroflammula cf. tuberculosa</i>	Mushroom 327183	USA	MT371761	–	–	–	–	–	–	–
<i>Pleuroflammula croceosanguinea</i>	TFB 8631	Argentina	KY559341	–	–	–	–	–	–	–
<i>Pleuroflammula flammia</i>	iNAT 103385419	USA	OM403095	–	–	–	–	–	–	–
<i>Pleuroflammula flammia</i>	AFTOL ID 1381	USA	DQ494685	–	–	–	–	–	–	–
<i>Pleuroflammula flammia</i>	Mushroom 320434	USA	MZ962681	–	–	–	–	–	–	–
<i>Pleuroflammula flammia</i>	Liu 33	China	PP037963	PP025329	–	–	–	–	–	–
<i>Pleuroflammula hebeiensis</i>	Liu 41	China	PP037964	PP025330	–	–	–	–	–	–
<i>Pleuroflammula hebeiensis</i>	Russell 15950297	USA	OP476999	–	–	–	–	–	–	–
<i>Pleuroflammula multifolia</i>	Russell 128633338	USA	OP549230	–	–	–	–	–	–	–
<i>Pleuroflammula multifolia</i>	Russell 57375215	USA	ON059274	–	–	–	–	–	–	–
<i>Pleuroflammula multifolia</i>	Russell 92052546	USA	OM972317	–	–	–	–	–	–	–
<i>Pleuroflammula multifolia</i>	Russell 130285590	USA	OP643340	–	–	–	–	–	–	–
<i>Pleuroflammula pannonica</i>	SNMM 3413	Slovakia	MW726639	MW726637	–	–	–	–	–	–
<i>Pleuroflammula pannonica</i>	SNMM 333	Slovakia	MW726640	MW726638	–	–	–	–	–	–
<i>Pleuroflammula pannonica</i>	CA 01	USA	OQ540552	–	–	–	–	–	–	–

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(Continued)



Table 1. (Continued).

Species name	Sample no.	Locality	ITS	nLSU	mtSSU	GenBank accessions				
						nuSSU	RPB1	RPB2	TBB1	TEF1
<i>Pleuroflammula praestans</i>	ZRL 2015066	China	LT1716043	–	–	–	–	–	–	–
<i>Pleuroflammula praestans</i>	Tian	China	JF961350	–	–	–	–	–	–	–
<i>Pleuroflammula</i> sp.	EJT 2011	China	JF961354	–	–	–	–	–	–	–
<i>Pleuroflammula subsulphurea</i>	NBMF 00959	Canada	MN206909	–	–	–	–	–	–	–
<i>Pleuroflammula subsulphurea</i>	MICH 139881	USA	OM985869	–	–	–	–	–	–	–
<i>Pleuroflammula subsulphurea</i>	ITS2 OTU 79	Canada	MW424597	–	–	–	–	–	–	–
<i>Pleuroflammula subsulphurea</i>	MUOB 366306	USA	OK376743	–	–	–	–	–	–	–
<i>Pleuroflammula tuberculosa</i>	Tian	China	JF961346	–	–	–	–	–	–	–
<i>Pleuroflammula tuberculosa</i>	PAM 02072903	France	HQ832452	HQ832465	–	–	–	–	–	–
<i>Pleuroflammula tuberculosa</i>	EJT 2011b	China	JF961362	–	–	–	–	–	–	–
<i>Pogonoloma spinulosum</i>	KM107286	United Kingdom	KP453705	KJ417238	–	KU058571	KU139037	KJ424401	–	–
<i>Polyporus auratus</i>	Dai 13665	China	KX900056	KX900172	KX900239	KX900282	–	KX900313	–	KX900359
<i>Polyporus cuticulatus</i>	Dai 13141	China	KX851613	KX851667	KX851701	KX851727	KX851749	–	KX851576	KX851776
<i>Porostereum fulvum</i>	LY:18491	France	MG649452	MG649454	–	–	–	–	–	–
<i>Porostereum spadiceum</i>	WHC 1498	China	MZ637063	MZ637262	–	–	MZ748444	–	–	MZ913696
<i>Porostereum spadiceum</i>	Wu 0707-8	China	MZ637064	–	–	–	–	–	–	–
<i>Porostereum spadiceum</i>	Wu 9508-139	China	MZ637062	MZ637263	–	–	MZ748445	OK136067	–	MZ913697
<i>Postia hirsuta</i>	Cui 11237	China	KJ684970	KJ684984	KX901038	KX901113	–	–	–	KX901266
<i>Postia lactea</i>	Cui 12141	China	KX900892	KX900962	KX901029	KX901104	KX901163	KX901211	–	KX901260
<i>Postia ochraceoalba</i>	Cui 10802	China	KM107903	KM107908	KX901041	KX901115	–	KX901216	–	–
<i>Postia sublawei</i>	Cui 9597	China	KX900900	KX900970	KX901037	KX901112	–	–	–	KX901265
<i>Postia tephroleuca</i>	Dai 12610	Finland	KX900897	KX900967	KX901034	KX901109	KX901166	KX901214	–	KX901263
<i>Pseudoclitocybe cyathiformis</i>	AFTOL ID 1998	USA	GU187553	EF551313	–	GU187659	DQ067939	GU187815	–	GU187742
<i>Pseudoclitopilus rhodoleucus</i>	GB 0110967	Sweden	KP453696	KJ417218	–	KU058577	KU139046	KJ424393	–	–
<i>Pseudoclitopilus rhodoleucus</i>	KUN HKAS 105563	China	MZ714588	MZ714594	–	–	MZ681889	MZ681899	–	MZ681878
<i>Pseudofavolus cucullatus</i>	Dai 13584A	China	KX900071	KX900185	KX900251	–	–	–	–	KX900371
<i>Pseudofavolus cucullatus</i>	WD 2157	Japan	AB587637	AB368114	–	–	–	AB368170	–	–
<i>Pseudolaccaria pachyphylla</i>	GB:0066637	Sweden	KU058504	KU058542	–	KU058579	KU139048	KU139006	–	–
<i>Pseudoomphalina kalchbrenneri</i>	GB 0066625	Sweden	KU058503	KU058541	–	KU058578	KU139047	KU139005	–	–
<i>Pseudoomphalina umbrinopur-purascens</i>	LS S20181215-2	Spain	MK424270	MK424271	–	OR863598	–	OR828292	–	–
<i>Quasiphebria densa</i>	HHB-12357	USA	MZ637065	MZ637264	–	–	MZ748408	–	–	MZ913628
<i>Quasiphebria densa</i>	WEI 17-057	China	MZ637066	MZ637265	–	–	MZ748410	OK135986	–	MZ913630
<i>Quasiphebria densa</i>	Wu 9304-33	China	MZ637067	MZ637266	–	–	MZ748409	–	–	MZ913629
<i>Rhizochaete borneensis</i>	WEI 16-426	China	MZ637070	MZ637270	–	–	–	–	–	–
<i>Rhizochaete brunnea</i>	MR11455	Argentina	AY219389	AY219389	–	–	–	–	–	–
<i>Rhizochaete chinensis</i>	Wu 0910-45	China	LC387335	MF110294	–	–	LC387348	LC387370	–	LC270925
<i>Rhizochaete chinensis</i>	Wu 0910-59	China	MZ637071	MZ637271	–	–	–	–	–	–
<i>Rhizochaete fouquieriae</i>	KKN-121	USA	AY219390	GU187608	–	–	MZ748362	OK135988	–	MZ913708

(Continued)

(Continued)

Table 1. (Continued).

Species name	Sample no.	Locality	ITS	nLSU	mtSSU	GenBank accessions				
						nuSSU	RPB1	RPB2	TBB1	TEF1
<i>Rhizochaete lutea</i>	Wu 880417-5	China	MZ637072	GQ470651	-	-	MZ748365	OK135989	-	-
<i>Rhizochaete sulphurina</i>	HHB-5604	USA	KY273031	GU187610	-	-	MZ748363	OK135991	-	MZ913707
<i>Rhizochaete sulphurina</i>	Wu 0409-227	China	MZ637075	-	-	-	-	-	-	-
<i>Rhizocybe alba</i>	KUN HKAS 55110	China	MZ675560	MZ675571	-	-	MZ681882	MZ681893	-	MZ681871
<i>Ripartites odorus</i>	FDI Rita 08-12-2018	Italy	MN595290	MN595290	-	OR863599	-	-	-	OR828346
<i>Ripartites odorus</i>	T Clements 248705	USA	MK559718	OR863544	-	-	-	OR828294	-	OR828345
<i>Ripartites tricholoma</i>	Kekki 1910	Finland	OR863479	OR863546	-	OR863601	-	OR828297	-	OR828348
<i>Ripartites tricholoma</i>	KUN HKAS 77956	China	MZ675562	MZ675573	-	-	MZ681884	-	-	MZ681873
<i>Roseograndinia jilinensis</i>	Wu 1307-132	China	MZ637076	MZ637274	-	-	MZ748412	OK135984	-	MZ913631
<i>Roseograndinia jilinensis</i>	Wu 1307-137	China	MZ637077	MZ637275	-	-	MZ748413	OK135985	-	MZ913632
<i>Roseograndinia minispora</i>	WEI 18-508	China	MZ637078	MZ637276	-	-	-	-	-	-
<i>Roseograndinia minispora</i>	WEI 18-511	China	MZ637079	MZ637277	-	-	-	-	-	-
<i>Simocybe cf. ragazziana</i>	KM 195255	United Kingdom	MZ159526	-	-	-	-	-	-	-
<i>Simocybe rhabbarina</i>	Poli 4583 15	Italy	KT934412	KT934415	-	-	-	-	-	-
<i>Simocybe sumptuosa</i>	GC 08205	Italy	KT715798	KT715799	-	-	-	-	-	-
<i>Simocybe sumptuosa</i>	RA 7181	USA	MK217451	-	-	-	-	-	-	-
<i>Singerocybe umbilicata</i>	KUN HKAS 105572	China	MZ714585	MZ714591	-	-	MZ681886	MZ681896	-	MZ681875
<i>Terana caerulea</i>	FP-104073	USA	KP134980	KP135276	-	-	KP134865	KP134960	-	-
<i>Terana caerulea</i>	GC 1507-2	China	MZ637090	MZ637287	-	-	MZ748414	OK136037	-	MZ913654
<i>Trametes conchifer</i>	FP 106793	USA	JN164924	JN164797	-	-	JN164823	JN164849	-	JN164887
<i>Trametes polyzona</i>	Cui 11040	China	KR605824	KR605767	KR606029	KR605932	-	KR610849	-	KR610760
<i>Trichocybe puberula</i>	Ferisin 113 2016 03	Italy	OR863482	OR863549	-	OR863603	-	OR828300	-	OR828351
<i>Tricholoma viridolivaceum</i>	TENN 063670	New Zealand	JF706316	JF706317	-	JF706318	KU139072	JF706319	-	-
<i>Tricholomella constricta</i>	HC 84/75	Switzerland	AF357036	AF223188	-	DQ825434	DQ825422	DQ825412	-	-
<i>Tricholosporum goniospermum</i>	AR 122	Italy	KU559848	MW367864	-	KU559865	-	KU559863	-	-
<i>Tricholosporum guangxiense</i>	HMJAU 59028	China	OK377047	OK377056	-	OK377043	-	OK625403	-	OK625333

Newly generated sequences are shown in black bold.

3. Results

3.1. Phylogeny

To better clarify the phylogenetic position of the unknown species, we chose appropriate gene fragments and performed phylogenetic analyses for each genus to which the unknown species belongs, respectively (including *Cyanosporus*, *Gelatinofungus*, *Lycoperdon*, *Macrocyttidia*, *Mycena*, *Picipes*, and *Pleuroflammula*). In this study, phylogenetic analyses included 1,881 sequences derived from eight gene fragments (ITS, nLSU, mtSSU, nuSSU, RPB1, RPB2, TBB1, and TEF1), representing 558 fungal samples from 298 species. The best-fit evolutionary models were selected for Bayesian analyses by using MrModeltest 2 v.2.3. In this study, the model for each region of each gene fragment used for phylogenetic analysis was GTR + I + G, with equal frequency of nucleotides. In the phylogenetic analyses of this study, the topology generated by ML analysis is similar to Bayesian analysis and MP analysis, and only the ML topology is shown.

The combined dataset of ITS + nLSU + mtSSU + nuSSU + RPB1 + RPB2 + TEF1 gene fragments is used to infer the phylogeny of *Cyanosporus* (Figure 1), which includes sequences from 94 fungal samples representing 60 species. The aligned dataset includes a total of 5,630 characters with gaps, of which 329 characters are variable and parsimony-uninformative, 3,829 characters are constant, and the remaining 1,472 characters are parsimony-informative. 42 equally parsimonious trees were generated in the MP analysis (TL = 5,674, CI = 0.481, RI = 0.727, RC = 0.35, HI = 0.519).

The combined dataset of ITS + nLSU + RPB1 + RPB2 + TEF1 gene fragments is used to infer the phylogeny of *Gelatinofungus* (Figure 2), which includes sequences from 86 fungal samples representing 42 species. The aligned dataset includes a total of 5,215 characters with gaps, of which 354 characters are variable and parsimony-uninformative, 3,007 characters are constant, and the remaining 1,854 characters are parsimony-informative. 31 equally parsimonious trees were generated in the MP analysis (TL = 11,951, CI = 0.325, RI = 0.59, RC = 0.192, HI = 0.675).

The combined dataset of ITS + nLSU gene fragments is used to infer the phylogeny of *Lycoperdon* (Figure 3), which includes sequences from 91 fungal

samples representing 36 species. The aligned dataset includes a total of 1,532 characters with gaps, of which 87 characters are variable and parsimony-uninformative, 1,193 characters are constant, and the remaining 252 characters are parsimony-informative. 12 equally parsimonious trees were generated in the MP analysis (TL = 796, CI = 0.553, RI = 0.815, RC = 0.451, HI = 0.447).

The combined dataset of ITS + nLSU + nuSSU + RPB1 + RPB2 + TEF1 gene fragments is used to infer the phylogeny of *Macrocyttidia* (Figure 4), which includes sequences from 66 fungal samples representing 57 species. The aligned dataset includes a total of 5,490 characters with gaps, of which 372 characters are variable and parsimony-uninformative, 3,245 characters are constant, and the remaining 1,873 characters are parsimony-informative. 26 equally parsimonious trees were generated in the MP analysis (TL = 17,579, CI = 0.239, RI = 0.327, RC = 0.089, HI = 0.761).

The combined dataset of ITS + RPB1 + TEF1 gene fragments is used to infer the phylogeny of *Mycena* (Figure 5), which includes sequences from 92 fungal samples representing 33 species. The aligned dataset includes a total of 1,498 characters with gaps, of which 54 characters are variable and parsimony-uninformative, 1,025 characters are constant, and the remaining 419 characters are parsimony-informative. 22 equally parsimonious trees were generated in the MP analysis (TL = 1,236, CI = 0.510, RI = 0.819, RC = 0.417, HI = 0.490).

The combined dataset of ITS + nLSU + mtSSU + nuSSU + RPB1 + RPB2 + TBB1 + TEF1 gene fragments is used to infer the phylogeny of *Picipes* (Figure 6), which includes sequences from 84 fungal samples representing 58 species. The aligned dataset includes a total of 6,893 characters with gaps, of which 333 characters are variable and parsimony-uninformative, 4,461 characters are constant, and the remaining 2,099 characters are parsimony-informative. 29 equally parsimonious trees were generated in the MP analysis (TL = 10,950, CI = 0.383, RI = 0.667, RC = 0.255, HI = 0.617).

The combined dataset of ITS + nLSU gene fragments is used to infer the phylogeny of *Pleuroflammula* (Figure 7), which includes sequences from 45 fungal samples representing 20 species. The aligned dataset includes a

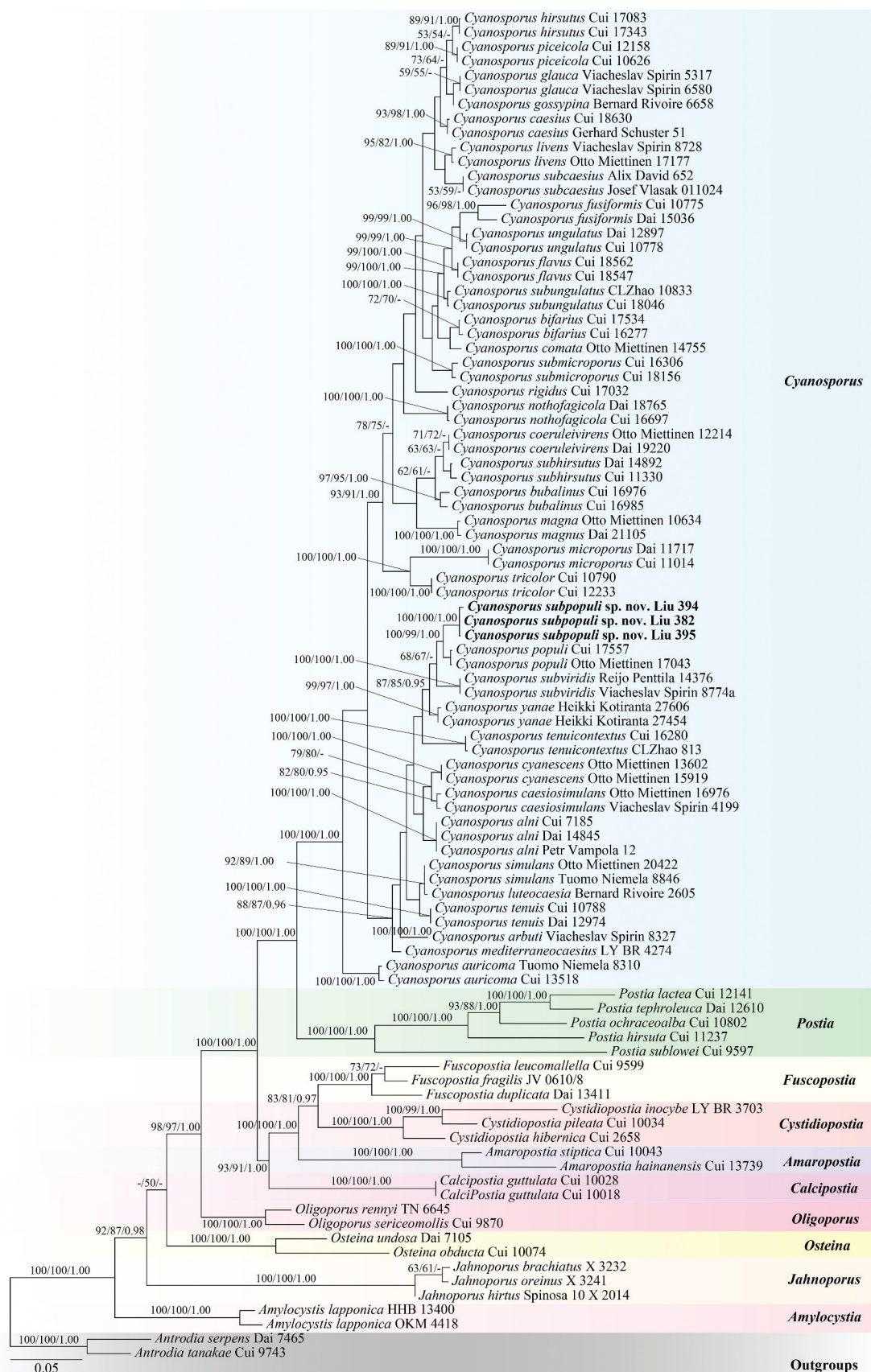


Figure 1. Maximum likelihood tree illustrating the phylogeny of *Cyanosporus* based on the combined sequence dataset of ITS + nLSU + mtSSU + nuSSU + RPB1 + RPB2 + TEF1. Branches are labelled with parsimony bootstrap proportions higher than 50%, maximum likelihood bootstrap higher than 50%, and Bayesian posterior probabilities more than 0.90 respectively. Bold names = New species.

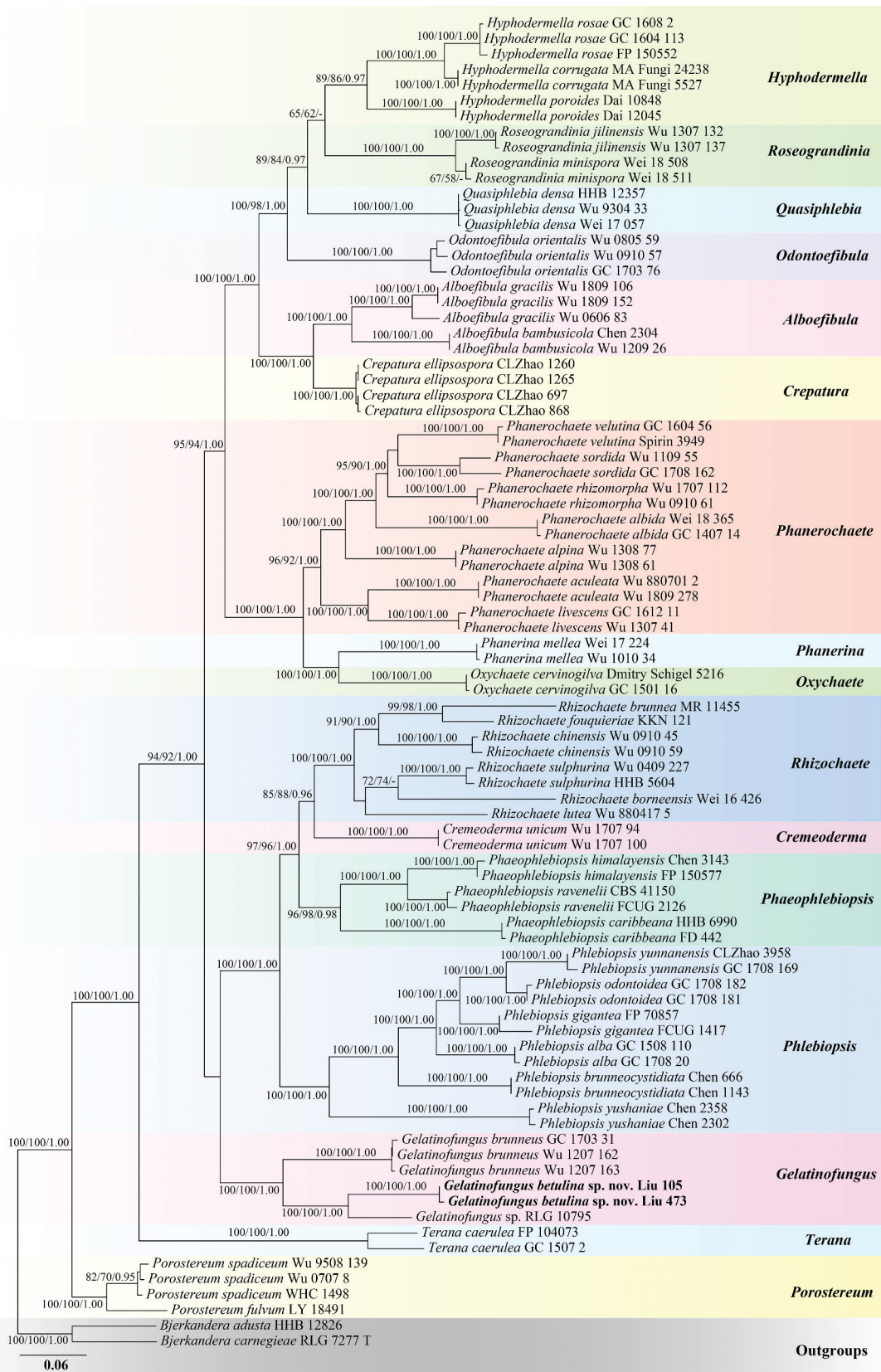


Figure 2. Maximum likelihood tree illustrating the phylogeny of *Gelatinofungus* based on the combined sequence dataset of ITS + nLSU + RPB1 + RPB2 + TEF1. Branches are labelled with parsimony bootstrap proportions higher than 50%, maximum likelihood bootstrap higher than 50%, and Bayesian posterior probabilities more than 0.90 respectively. Bold names = New species.

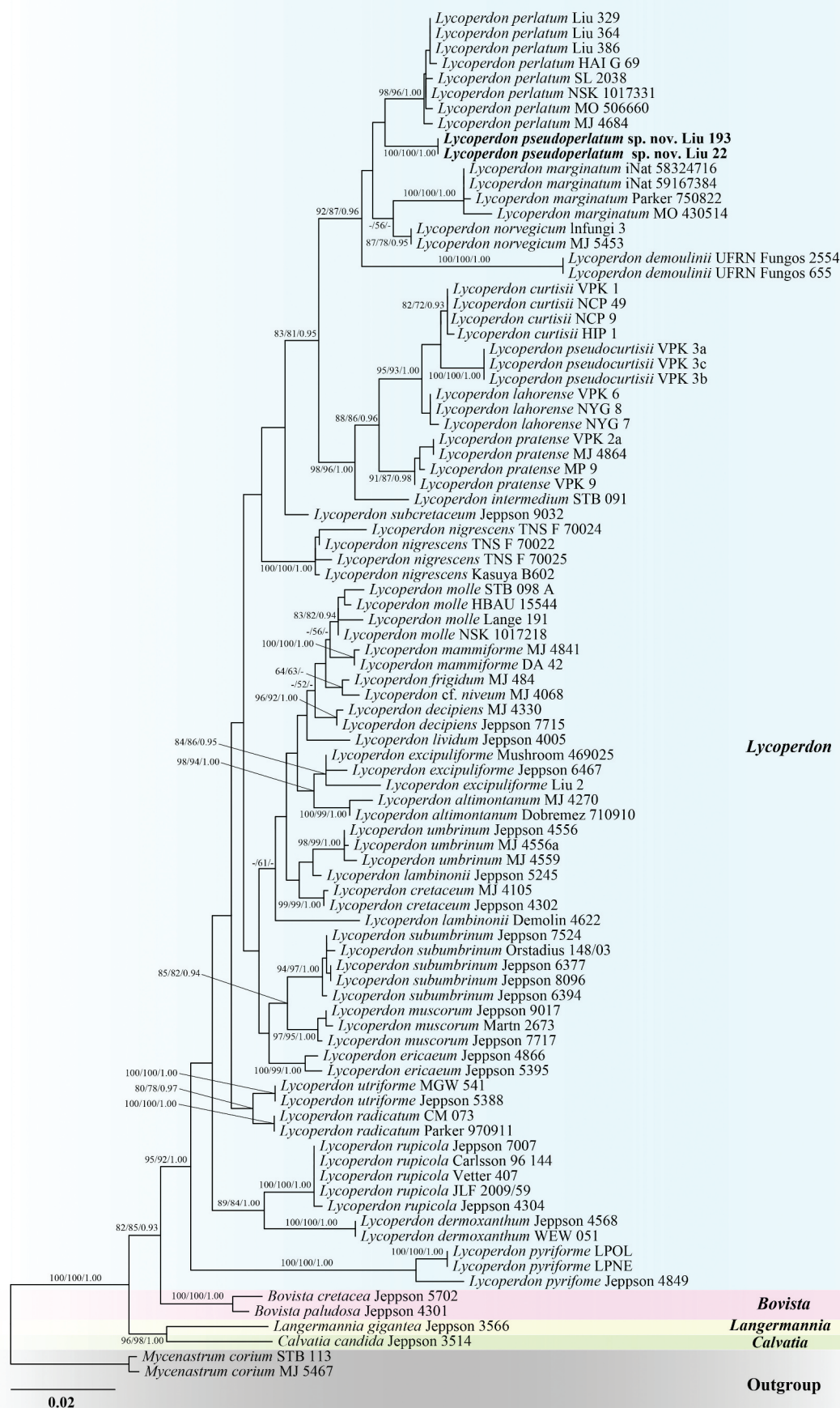


Figure 3. Maximum likelihood tree illustrating the phylogeny of *Lycoperdon* based on the combined sequence dataset of ITS + nLSU. Branches are labelled with parsimony bootstrap proportions higher than 50%, maximum likelihood bootstrap higher than 50%, and Bayesian posterior probabilities more than 0.90 respectively. Bold names = New species.

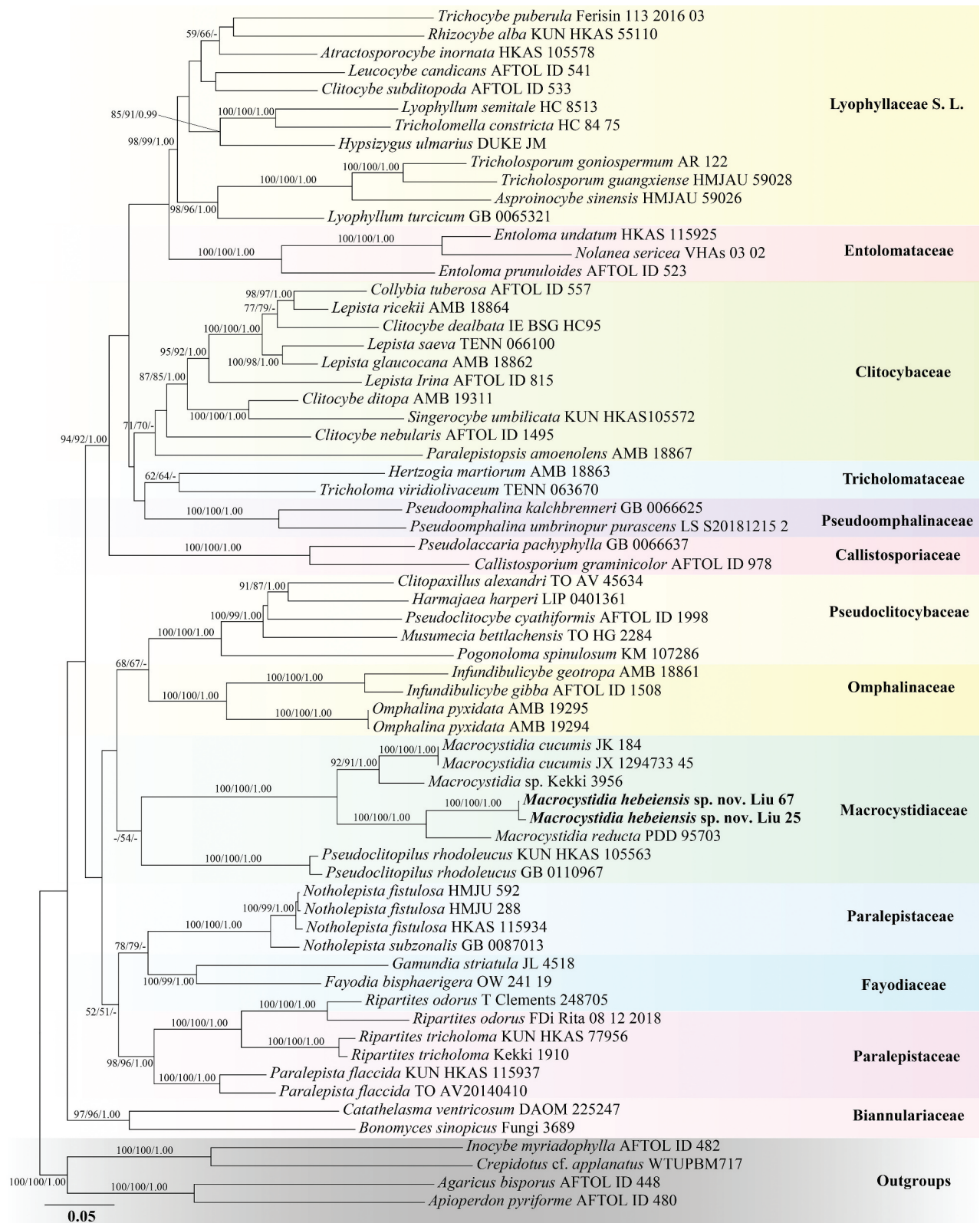


Figure 4. Maximum likelihood tree illustrating the phylogeny of *Macrocytidia* based on the combined sequence dataset of ITS + nLSU + nuSSU + RPB1 + RPB2 + TEF1. Branches are labelled with parsimony bootstrap proportions higher than 50%, maximum likelihood bootstrap higher than 50%, and Bayesian posterior probabilities more than 0.90 respectively. Bold names = New species.

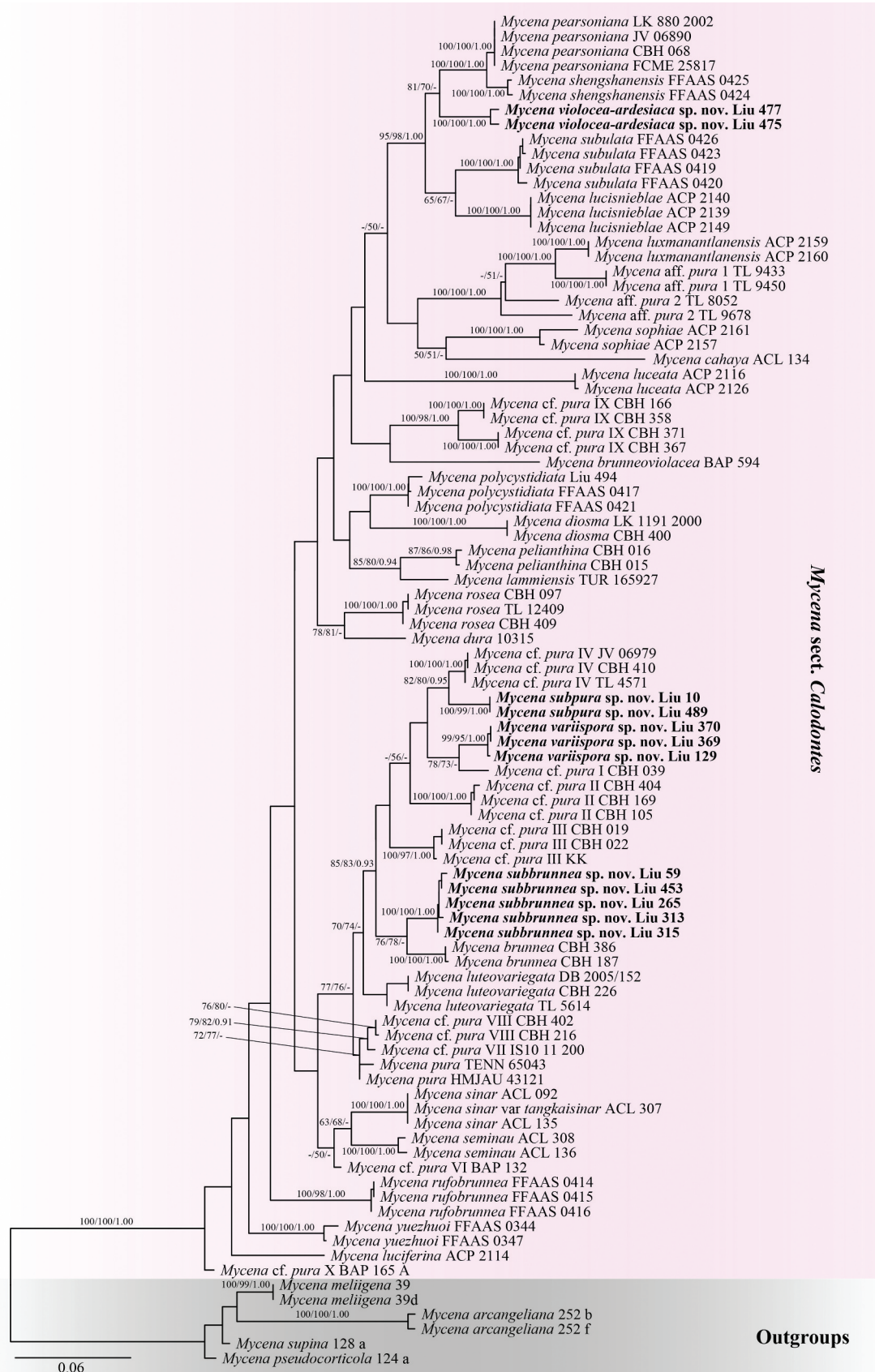


Figure 5. Maximum likelihood tree illustrating the phylogeny of *Mycena* sect. *Calodontes* based on the combined sequence dataset of ITS + RPB1 + TEF1. Branches are labelled with parsimony bootstrap proportions higher than 50%, maximum likelihood bootstrap higher than 50%, and Bayesian posterior probabilities more than 0.90 respectively. Bold names = New species.

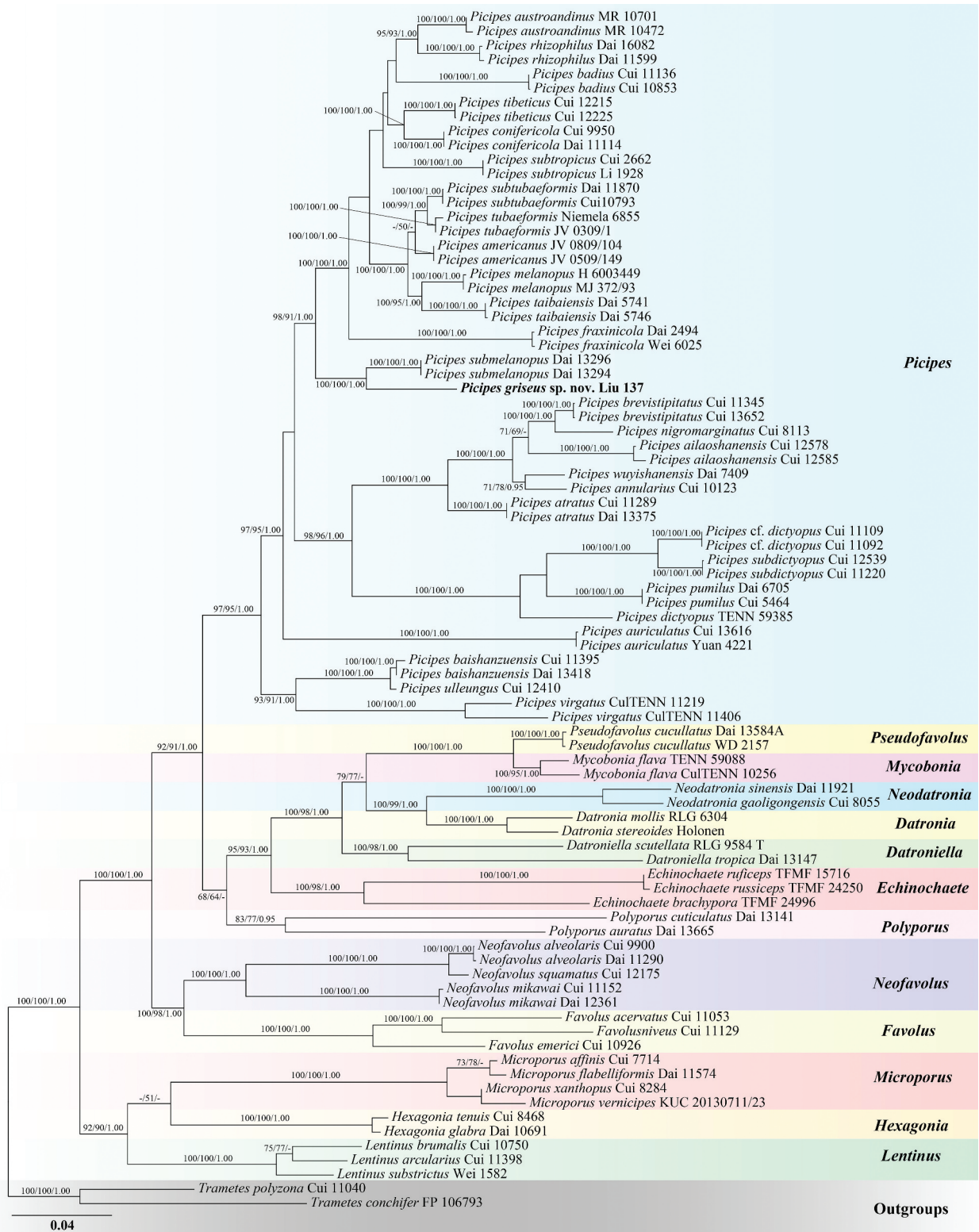


Figure 6. Maximum likelihood tree illustrating the phylogeny of *Picipes* based on the combined sequence dataset of ITS + nLSU + mtSSU + nuSSU + RPB1 + RPB2 + TBB1 + TEF1. Branches are labelled with parsimony bootstrap proportions higher than 50%, maximum likelihood bootstrap higher than 50%, and Bayesian posterior probabilities more than 0.90 respectively. Bold names = New species.

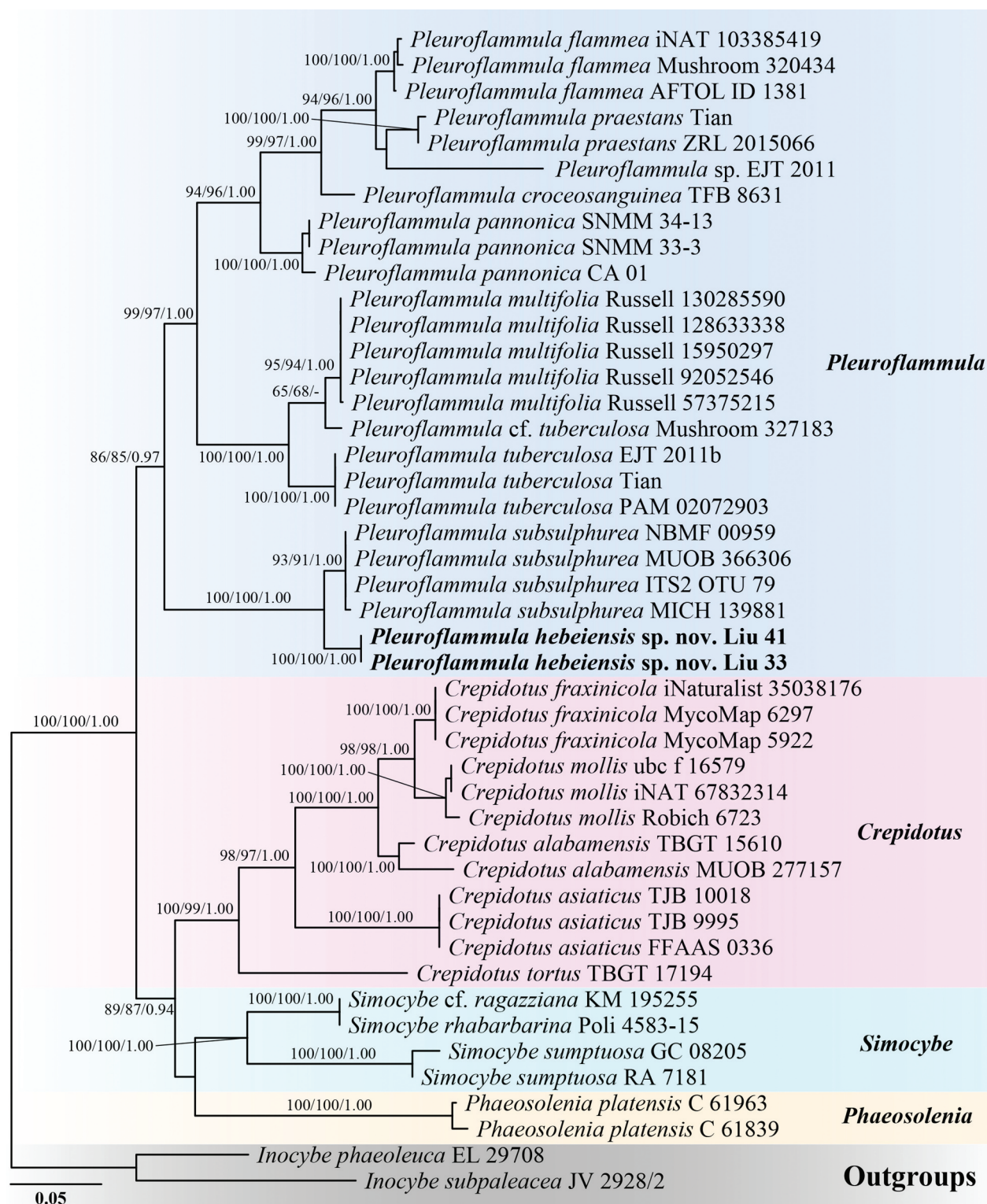


Figure 7. Maximum likelihood tree illustrating the phylogeny of *Pleuroflammula* based on the combined sequence dataset of ITS + nLSU. Branches are labelled with parsimony bootstrap proportions higher than 50%, maximum likelihood bootstrap higher than 50%, and Bayesian posterior probabilities more than 0.90 respectively. Bold names = New species.

total of 1,542 characters with gaps, of which 81 characters are variable and parsimony-uninformative, 1,028 characters are constant, and the remaining 433 characters are parsimony-informative. Eight equally parsimonious trees were generated in the MP analysis (TL = 1,523, CI = 0.557, RI = 0.824, RC = 0.459, HI = 0.443).

3.2. Taxonomy

Cyanosporus subpopuli Shun Liu & Biao Zhu, sp. nov.
Figures 8, 9

MycoBank: MB 854463.

Etymology: The epithet, *subpopuli*, refers to the new species being morphologically similar to *Cyanosporus populi* (Miettinen) B.K. Cui & Shun Liu.

Diagnosis: This species differs from other species by its solitary or imbricate basidiomata with white to cream colour when fresh, allantoid basidiospores ($4.6\text{--}5.4 \times 1\text{--}1.5 \mu\text{m}$), and growing on *Picea*.

Type: China. Hebei Province, Chengde City, Weichang County, Saihanba National Forest Park, on the stump of *Picea*, 28 August 2023, Liu 394 (MBPU).

Basidiomata annual, pileate, solitary or imbricate, soft and corky, becoming corky to fragile when dry. Pileus semicircular to flabelliform, projecting up to 2.2 cm, 4.5 cm wide, and 1.1 cm thick. Pileal surface white to cream when fresh, becoming pale mouse-grey when dry, glabrous; margin acute to slightly obtuse. Pore surface white to cream when fresh, becoming pinkish-buff to buff-yellow when dry; sterile margin narrow to almost lacking; pores angular, 5–7 per mm; dissepiments thin, lacerate. Context white to cream, soft corky, up to 3 mm thick. Tubes pale mouse-grey to ash-grey, fragile, up to 8 mm long.

Hyphal system monomitic; generative hyphae with clamp connections, IKI–, CB–; hyphae unchanged in KOH. Generative hyphae in context hyaline, thin- to thick-walled, $2.8\text{--}5.5 \mu\text{m}$ in diam. Generative hyphae in tubes hyaline, thin- to thick-walled, $2.2\text{--}3.5 \mu\text{m}$ in diam.

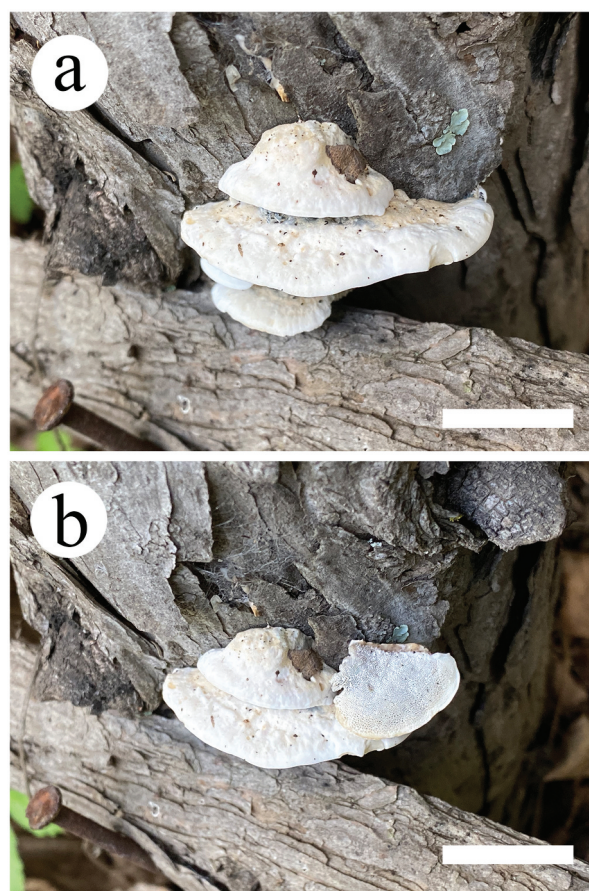


Figure 8. Basidiomata of *Cyanosporus subpopuli* (Liu 394). Bars: a, b = 2 cm.

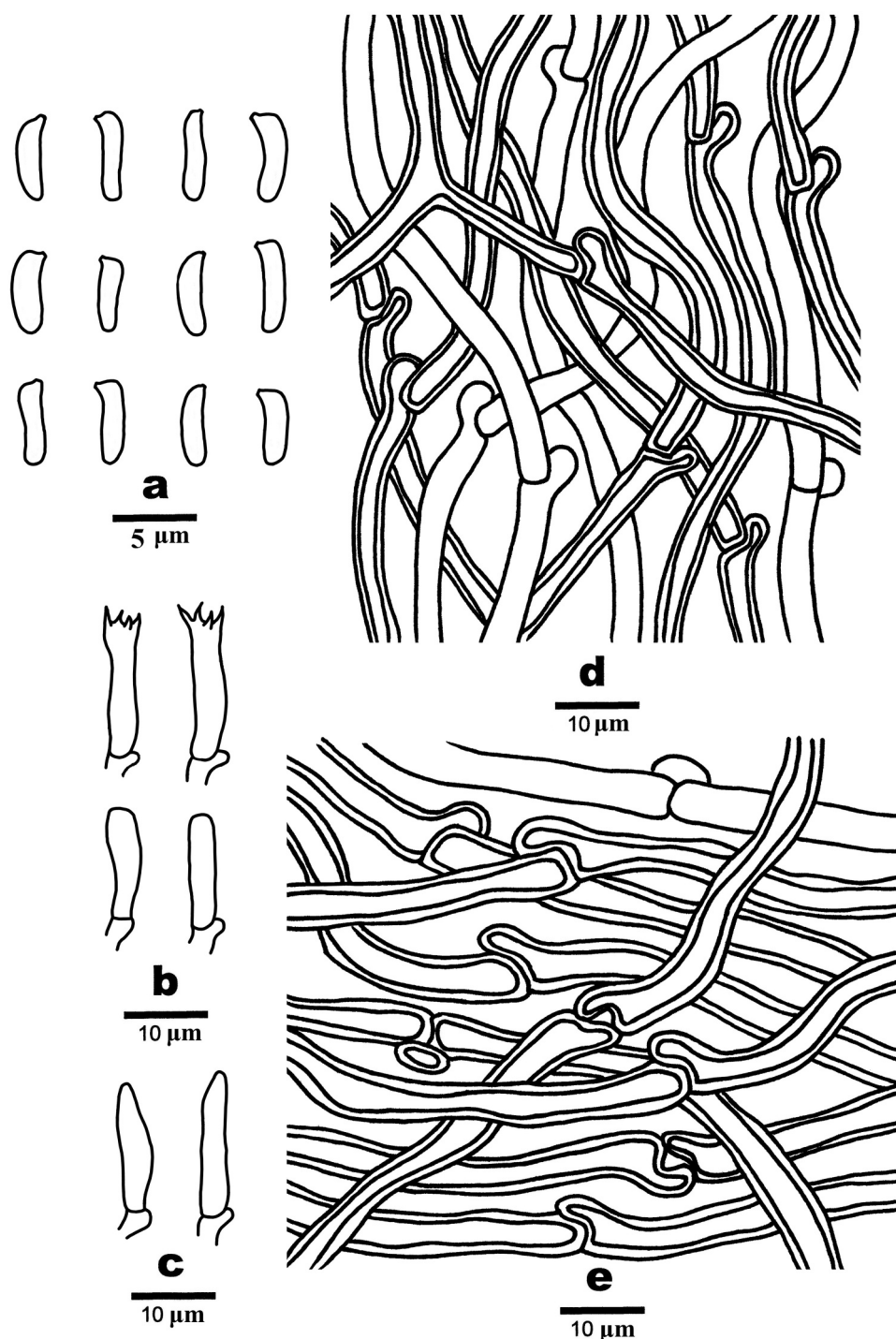


Figure 9. Microscopic structures of *Cyanosporus subpopuli* (drawn from the holotype). (a) Basidiospores. (b) Basidia and basidioles. (c) Cystidioles. (d) Hyphae from trama. (e) Hyphae from context. Bars: a = 5 µm; b–e = 10 µm.

Cystidia absent; cystidioles present, $14.3\text{--}19.2 \times 2.8\text{--}4.5$ µm. Basidia clavate, bearing four sterigmata and a basal clamp connection, $18.2\text{--}22.7 \times 3.7\text{--}4.3$ µm; basidioles dominant, in shape similar to basidia, but smaller. Basidiospores allantoid, slightly curved, hyaline, thin- to slightly thick-walled, smooth, IKI–, CB–, $(4.4\text{--})4.6\text{--}5.4 \times 1\text{--}1.5$

$(\text{--}1.6)$ µm, $L = 4.94$ µm, $W = 1.25$ µm, $Q = 3.57\text{--}4.6$ ($n = 60/2$).

Habitat: Saprophyte on stump or fallen trunk of *Picea*.

Additional specimens examined: China. Hebei Province, Chengde City, Weichang County, Saihanba

National Forest Park, on fallen trunk of *Picea*, 28 August 2023, Liu 382 (MBPU); on stump of *Picea*, 28 August 2023, Liu 395 (MBPU).

Gelatinofungus betulina Shun Liu & Biao Zhu, sp. nov. [Figures 10, 11](#)

MycoBank: MB 854464.

Etymology: The epithet, *betulina*, refers to the species grows on *Betula* species.

Diagnosis: This species differs from *Gelatinofungus brunneus* by its effused-reflexed to pileate or resupinate basidiomata, cream to buff-yellow pileal surface when fresh, becoming cinnamon-buff to clay-buff when dry, and narrower basidiospores ($5.7\text{--}6.4 \times 2.6\text{--}3.2 \mu\text{m}$).

Type: China. Hebei Province, Chengde City, Weichang County, Saihanba National Forest Park, on fallen branches of *Betula*, 29 August 2023, Liu 473 (MBPU).

Basidiomata annual, resupinate to effused-reflexed or pileate, corky when fresh, becoming corky to fragile

upon drying. Pileus semicircular to flabelliform, projecting up to 2 cm, 2.5 cm wide, and 0.9 mm thick at the base. Pileal surface cream to buff-yellow when fresh, becoming cinnamon-buff to clay-buff when dry, glabrous; margin acute to slightly obtuse. Hymenophore surface white to cream when fresh, becoming pinkish-buff to buff-yellow when dry.

Hyphal system monomitic; generative hyphae with clamp connections. Subiculum fairly uniform, with compact texture. Hymenial layer thickening, subhymenium clearly differentiated from subiculum, with compact texture, $65\text{--}220 \mu\text{m}$ thick; hyphae vertical, difficult to discern, colourless, $2\text{--}3.2 \mu\text{m}$ diam., with thin to up to $0.5 \mu\text{m}$ diam. thick walls. Brownish oily materials scattered throughout the sections. Hyphidia $10\text{--}30 \times 1.5\text{--}4.5 \mu\text{m}$, cylindrical with obtuse or acute apices, thin-walled, homogenous. Basidia clavate, bearing four sterigmata and a basal clamp connection, $16.5\text{--}29.5 \times 4\text{--}6.5 \mu\text{m}$. Cystidia and cystidioles lacking. Basidiospores oblong-ellipsoid, hyaline,

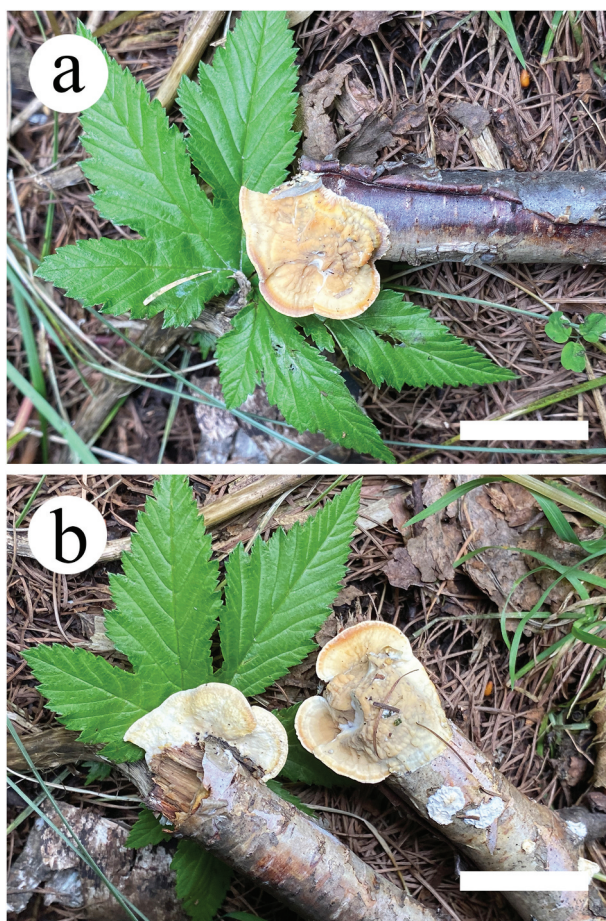


Figure 10. Basidiomata of *Gelatinofungus betulina* (Liu 473). Bars: a, b = 2 cm.

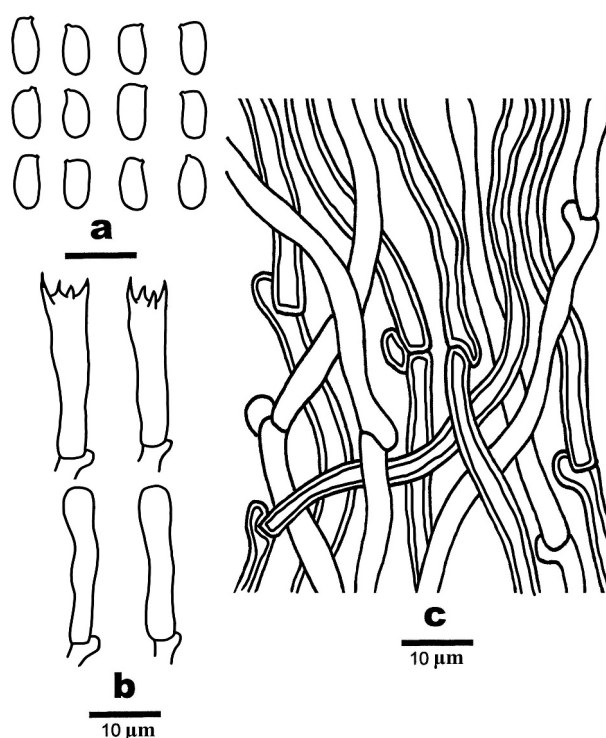


Figure 11. Microscopic structures of *Gelatinofungus betulina* (drawn from the holotype). (a) Basidiospores. (b) Basidia and basidioles. (c) Hyphae from subiculum. Bars: a–c = 10 µm.

thin-walled, smooth, IKI–, CB–, (5.5–)5.7–6.4 × 2.6–3.2 µm, L = 6 µm, W = 2.94 µm, Q = 1.88–2.21 ($n = 60/2$).

Habitat: Saprophyte on fallen branches of *Betula*.

Additional specimen examined: China. Hebei Province, Chengde City, Weichang County, Saihanba National Forest Park, on fallen branches of *Betula*, 5 August 2023, Liu 105 (MBPU).

Lycoperdon pseudoperlatum Shun Liu & Biao Zhu, sp. nov. [Figures 12, 13](#)

Mycobank: MB 854465.

Etymology: The epithet, *pseudoperlatum*, refers to the species similar to *Lycoperdon perlatum* Pers.

Diagnosis: This species can be distinguished from other *Lycoperdon* species by its fibrillose-squamulose, white to pinkish buff basidiomata, cream to greyish brown exoperidium, and asperulate, globose to olivaceous basidiospores (2.7–3.5 µm diam.).

Type: China. Hebei Province, Chengde City, Weichang County, Saihanba National Forest Park, on the ground of *Betula* dominated forests, 7 August 2023, Liu 193 (MBPU).

Basidiomata solitary, pyriform, subglobose or almost pestle-shaped, 1.5–3.2 cm in diam., 2.4–4.8 cm in height, fibrillose-squamulose, white to pinkish buff; margin concolorous with pileus surface. White and

branched rhizomorphs attached to the substratum, covered with particles of soil. Exoperidium consisting of 0.5–2 mm long, slightly fragile, cream to greyish brown, conical thorns surrounded by a row of persistent circular warts; the pattern on pseudo-stipe is not very obvious or distinct. Endoperidium papery, buff-yellow. Gleba cream then pinkish buff with well-developed pseudocolumella. Diaphragm distinct. Subgleba well-developed, alveolate, cream to buff.

Basidiospores asperulate, olivaceous to globose, 2.7–3.5 µm diam. Eucapillitium absent. Paracapillitium abundant, septate, hyaline to pale olivaceous, cytoplasmic richness in hyphae, attached with some amorphous material, 2.5–5.5 µm diam., thick-walled, with attenuate tips, branched. Exoperidium composed of hyaline to pale olivaceous, subglobose to globose, thin-walled hyphal sphaerocysts. Endoperidium composed of tightly interwoven, hyaline to pale olivaceous, aseptate, thick-walled, up to 4 µm diam., branched hyphae.

Habitat: Saprophytic on fallen leaves in coniferous forest.

Additional specimen examined: China. Hebei Province, Chengde City, Weichang County, Saihanba National Forest Park, on the ground of *Betula* dominated forests, 4 August 2023, Liu 22 (MBPU).

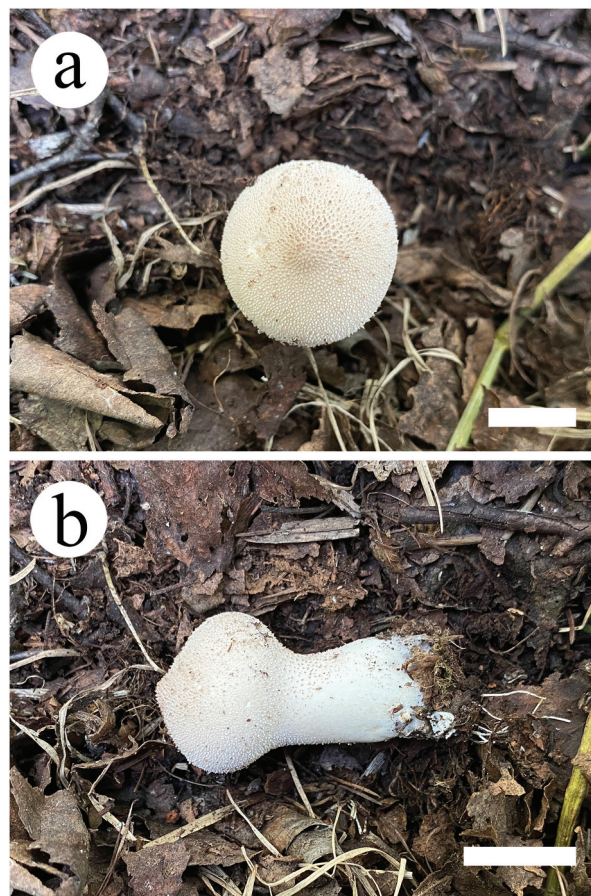


Figure 12. Basidiomata of *Lycoperdon pseudoperlatum* (Liu 193). Bars: a, b = 2 cm.

Macrocystidia hebeiensis Shun Liu & Biao Zhu, sp. nov. [Figures 14, 15](#)

MycoBank: MB 854466.

Etymology: The epithet, *hebeiensis*, refers to the species collected from Hebei Province in China.

Diagnosis: This species differs from other species by its clay-buff to fawn pileus surface, fawn to almost black stipe, and oblong-ellipsoid to ellipsoid basidiospores ($6\text{--}10 \times 3\text{--}4.2 \mu\text{m}$).

Type: China. Hebei Province, Chengde City, Weichang County, Saihanba National Forest Park, on the ground of *Larix* dominated forests, 5 August 2023, Liu 67 (MBPU).

Basidiomata solitary to gregarious. Pileus convex, hemispherical to applanate, 2–4.5 cm wide, glabrous, clay-buff to fawn; margin cream to pinkish-buff, entire, sometimes wavy. Context thin. Stipe central, cylindrical to clavate, 4–6.5 cm long and 0.3–0.6 cm wide, fawn to almost black, pruinose, covered with black tomentose at the base, hollow, fragile. Lamellae subfree, cream to pinkish-buff, close, unequal.

Basidiospores oblong-ellipsoid to ellipsoid, pale brown, thick-walled, smooth, IKI–, CB–, $6\text{--}10 \times 3\text{--}4.2 \mu\text{m}$,

$L = 8.02 \mu\text{m}$, $W = 3.72 \mu\text{m}$, $Q = 1.84\text{--}2.5$ ($n = 60/2$). Basidia clavate, thin-walled, hyaline, four sterigmata, clamped at the base, $19\text{--}32 \times 5\text{--}12 \mu\text{m}$. Pleurocystidia absent. Cheilocystidia irregularly clavate, hyaline, moderately thick-walled, $22\text{--}80 \times 15\text{--}30 \mu\text{m}$. Caulocystidia clavate or fusiform, hyaline, thin-walled, smooth, $19\text{--}40 \times 10\text{--}18 \mu\text{m}$.

Habitat: Scattered on humus and fallen leaves in *Larix* dominated forest.

Additional specimen examined: China. Hebei Province, Chengde City, Weichang County, Saihanba National Forest Park, on the ground of *Betula* dominated forests, 29 August 2023, Liu 475 (MBPU).

Mycena subbrunnea Shun Liu & Biao Zhu, sp. nov. [Figures 16, 17](#)

MycoBank: MB 854467.

Etymology: The epithet, *subbrunnea*, refers to the new species resembling *Mycena brunnea* (E. Ludw.) Olariaga, Pérez-De-Greg. & P. Arrill. in morphology and phylogeny.

Diagnosis: This species differs from other species by its cream, pinkish buff, buff-yellow to fawn pileus,

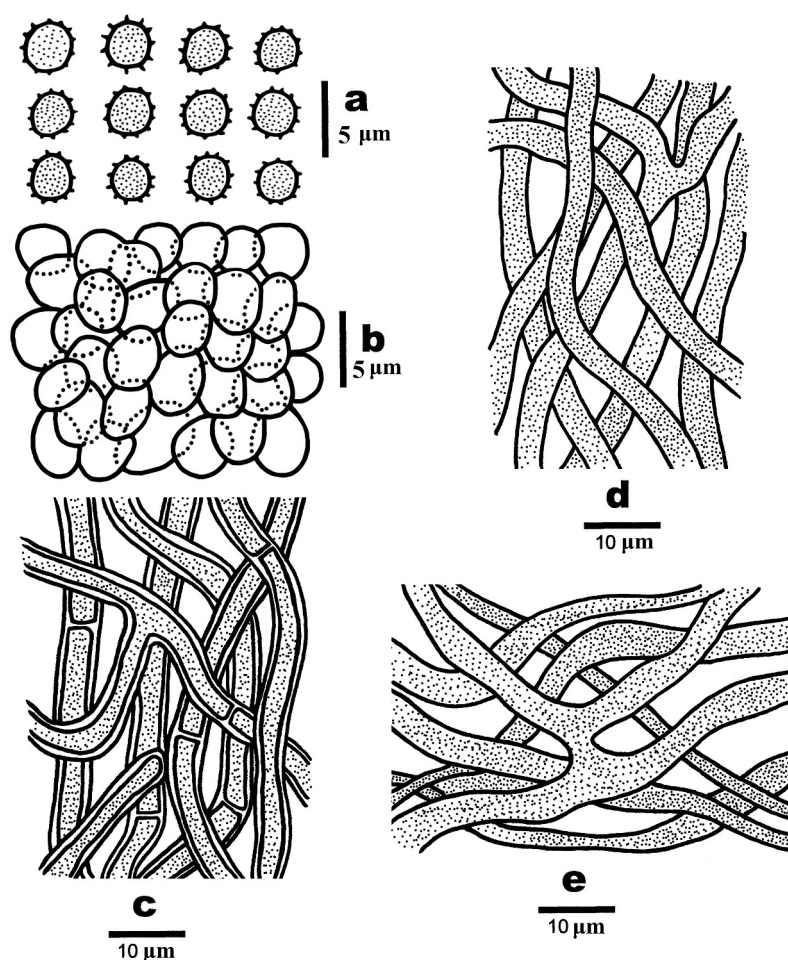


Figure 13. Microscopic structures of *Lycoperdon pseudoperlatum* (drawn from the holotype). (a) Basidiospores. (b) Exoperidial elements. (c) Paracapillitial hyphae. (d) Aseptate hyphae of subgleba. (e) Endoperidial hyphae. Bars: a, b = 5 µm; c–e = 10 µm.

white, cream to pinkish buff stipe covered with white tomentose at the base, and cylindrical basidiospores ($6.9\text{--}9 \times 3\text{--}4.1$ µm).

Type: China. Hebei Province, Chengde City, Weichang County, Saihanba National Forest Park, on the ground of *Betula* and *Larix* dominated forests, 29 August 2023, Liu 453 (MBPU).

Basidiomata solitary. Pileus convex, hemispherical to applanate, 2.2–4 cm wide, glabrous, cream, pinkish buff, buff-yellow to fawn; margin concolorous with pileus surface, entire, involute, wavy sometimes. Context thin. Stipe central, cylindrical to clavate, 4.3–9.6 cm long and 0.4–1.5 cm wide, white, cream to pinkish buff, pruinose, covered with white tomentose at the base, hollow, fragile. Lamellae adnexed to subfree, white to pinkish buff, extremely close, unequal.

Basidiospores cylindrical, hyaline, thin-walled, smooth, IKI–, CB–, ($6.7\text{--}6.9\text{--}9\text{--}9.1$) $\times$ $3\text{--}4.1\text{--}4.2$ µm,

$L = 7.82$ µm, $W = 3.31$ µm, $Q = 1.97\text{--}2.67$ ($n = 90/3$). Basidia clavate, hyaline, thin-walled, two to four sterigmata, clamped at the base, $20.2\text{--}28.3 \times 5.2\text{--}7.7$ µm. Pleurocystidia absent. Cheilocystidia clavate, hyaline, moderately thick-walled, $27\text{--}58 \times 7\text{--}17$ µm. Caulocystidia clavate or fusiform, hyaline, thick-walled, smooth, $25\text{--}63 \times 5\text{--}18$ µm. Pileipellis a cutis composed of four to five layers of cylindrical cells, $37\text{--}71 \times 4\text{--}5$ µm, smooth, thin-walled; terminal cells cylindrical to fusiform, $40\text{--}65 \times 4\text{--}17$ µm, thin-walled, hyaline; clamp connections abundant.

Habitat: Scattered on humus and fallen leaves in mixed forests of *Betula*, *Larix*, and *Pinus*.

Additional specimens examined: China. Hebei Province, Chengde City, Weichang County, Saihanba National Forest Park, on the ground of *Pinus* dominated forests, 5 August 2023, Liu 59 (MBPU); on the ground of *Betula* and *Larix* dominated forests, 27 August 2023, Liu 265 (MBPU); on the ground of

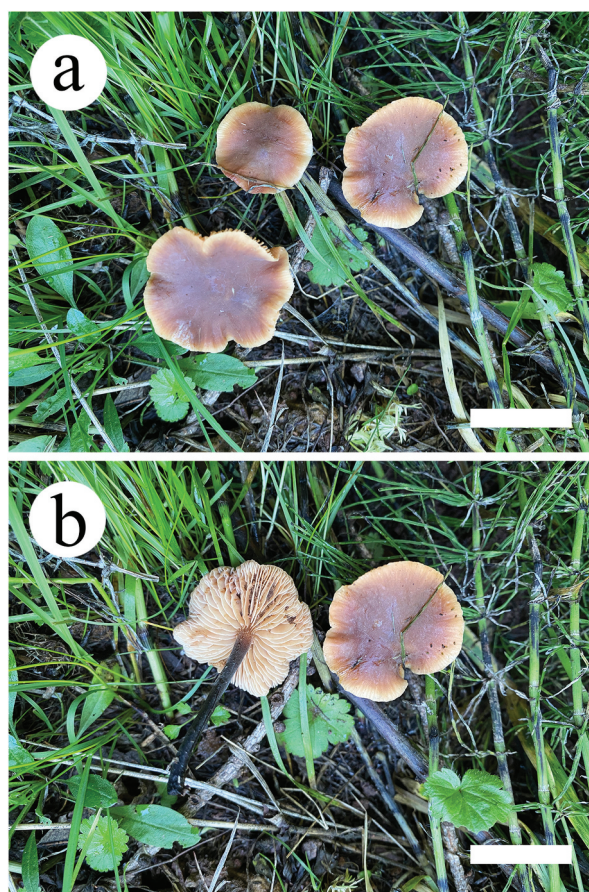


Figure 14. Basidiomata of *Macrocystidia hebeiensis* (Liu 67). Bars: a, b = 3 cm.

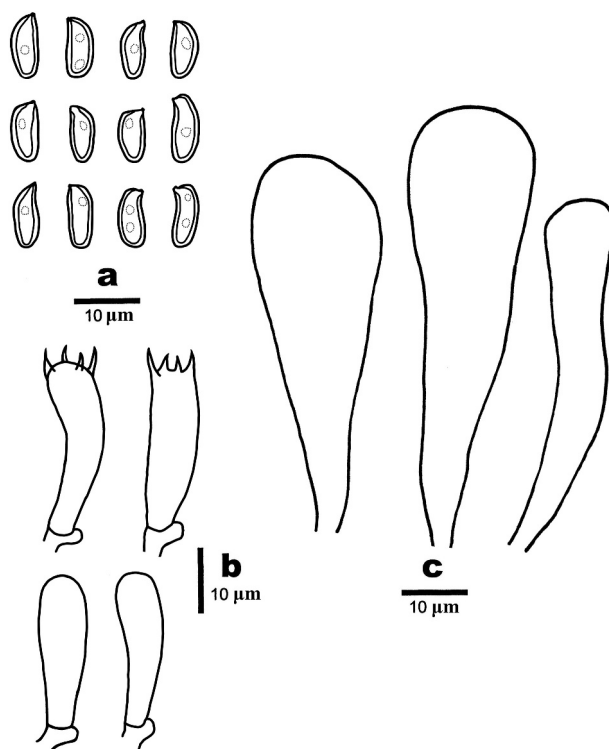


Figure 15. Microscopic structures of *Macrocystidia hebeiensis* (drawn from the holotype). (a) Basidiospores. (b) Basidia and basidioles. (c) Cheilocystidia. Bars: a–c = 10 µm.

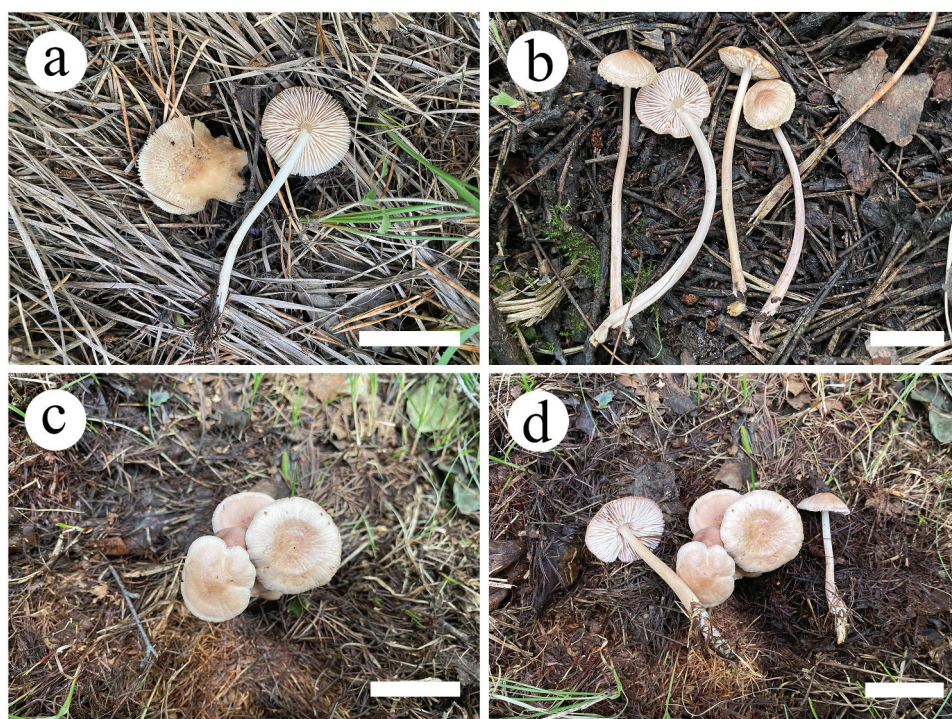


Figure 16. Basidiomata of *Mycena subbrunnea* (Liu 59, 265, 453). Bars: a–d = 4 cm.

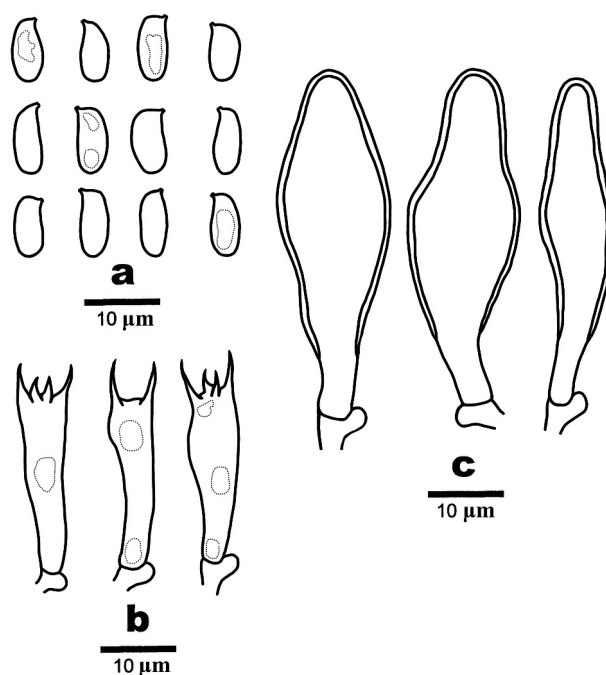


Figure 17. Microscopic structures of *Mycena subbrunnea* (drawn from the holotype). (a) Basidiospores. (b) Basidia. (c) Cheilocystidia. Bars: a–c = 10 µm.

Pinus dominated forests, 27 August 2023, Liu 313 (MBPU), Liu 315 (MBPU).

Mycena subpura Shun Liu & Biao Zhu, sp. nov.
Figures 18, 19

MycoBank: MB 854468.

Etymology: The epithet, *subpura*, refers to the new species resembling *Mycena pura* (Pers.) P. Kumm. in morphology.

Diagnosis: This species differs from other species by its pale vinaceous to fawn pileus, lilac to reddish brown stipe, pale vinaceous to livid vinaceous lamellae, and elongated ellipsoid to cylindrical basidiospores ($7\text{--}8.2 \times 3\text{--}4.1 \mu\text{m}$).

Type: China. Hebei Province, Chengde City, Weichang County, Saihanba National Forest Park, on the ground of *Betula* and *Larix* dominated forests, 29 August 2023, Liu 489 (MBPU).

Basidiomata solitary. Pileus convex, hemispherical to applanate, 1.8–3.5 cm wide, glabrous, pale vinaceous to fawn; margin concolorous with pileus surface, involute, entire, sometimes wavy. Context slightly thin. Stipe central, cylindrical to clavate, 4–6.6 cm long and 0.4–0.7 cm wide, lilac to reddish brown, pruinose, covered with greyish-white tomentose at the base, hollow, fragile. Lamellae adnexed

to subfree, pale vinaceous to livid vinaceous, extremely close, unequal.

Basidiospores elongated ellipsoid to cylindrical, hyaline, thin-walled, smooth, IKI–, CB–, $(6.8\text{--})7\text{--}8.2$ ($\text{--}8.3$) $\times 3\text{--}4.1$ ($\text{--}4.3$) μm , $L = 7.67 \mu\text{m}$, $W = 3.65 \mu\text{m}$, $Q = 1.93\text{--}2.3$ ($n = 60/2$). Basidia clavate, hyaline, thin-walled, two to four sterigmata, clamped at the base, $20.2\text{--}26.8 \times 4.2\text{--}6.5 \mu\text{m}$. Pleurocystidia absent. Cheilocystidia clavate, hyaline, moderately thick-walled, $17.4\text{--}28.6 \times 3.7\text{--}6.3 \mu\text{m}$. Caulocystidia clavate to fusiform, hyaline, thin-walled, smooth, $20\text{--}45 \times 5\text{--}13 \mu\text{m}$. Pileipellis a cutis composed of four to five layers of cylindrical cells, $44\text{--}52 \times 3\text{--}5 \mu\text{m}$, smooth, thin-walled; terminal cells cylindrical, $29\text{--}43 \times 3\text{--}12 \mu\text{m}$, thin-walled, hyaline; clamp connections abundant.

Habitat: Scattered on humus and fallen leaves in mixed forests of *Betula*, *Larix* and *Picea*.

Additional specimen examined: China. Hebei Province, Chengde City, Weichang County, Saihanba National Forest Park, on the ground of *Larix* and *Picea* dominated forests, 29 August 2023, Liu 10 (MBPU).

Mycena variispora Shun Liu & Biao Zhu, sp. nov.
Figures 20, 21

MycoBank: MB 854469.

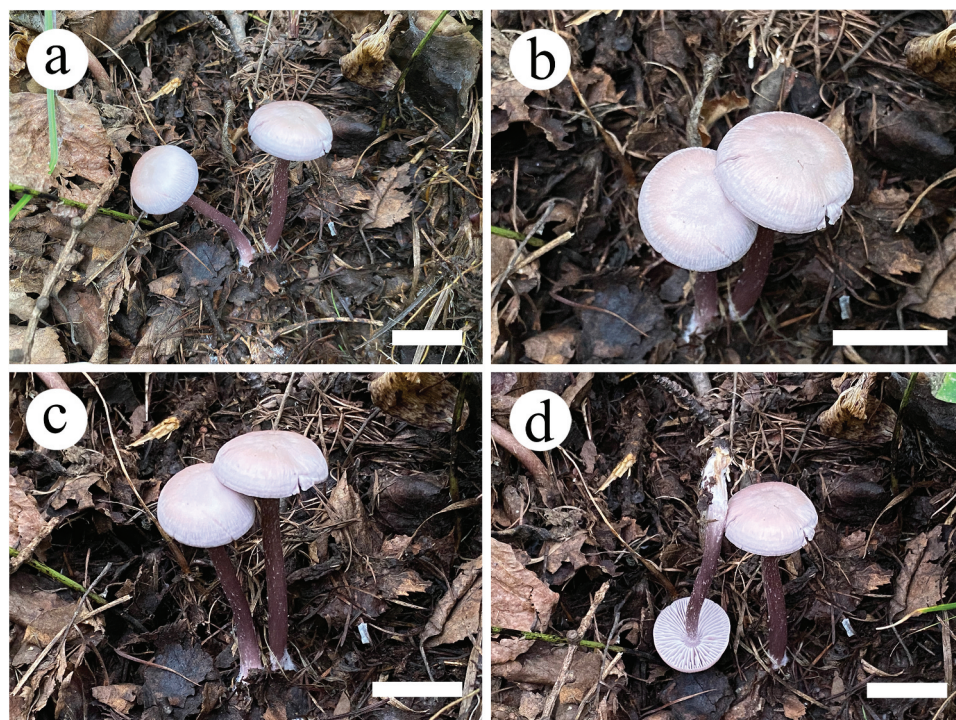


Figure 18. Basidiomata of *Mycena subpura* (Liu 489). Bars: a–d = 3 cm.

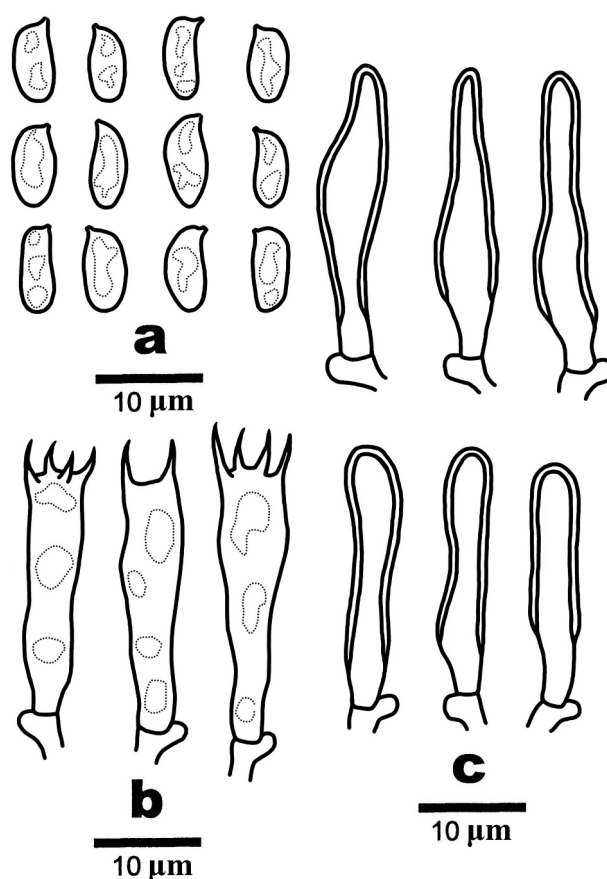


Figure 19. Microscopic structures of *Mycena subpura* (drawn from the holotype). (a) Basidiospores. (b) Basidia. (c) Cheilocystidia. Bars: a–c = 10 µm.

Etymology: The epithet, *variispora*, refers to the species having variable basidiospores.

Diagnosis: This species differs from other species by its cream, buff to lilac pileus, lilac to greyish violet stipe covered by white tomentose at the base, variable and ellipsoid to cylindrical basidiospores ($5\text{--}8.3 \times 3\text{--}4.3$ µm).

Type: China. Hebei Province, Chengde City, Weichang County, Saihanba National Forest Park, on the ground of *Betula* and *Larix* dominated forests, 28 August 2023, Liu 369.

Basidiomata solitary. Pileus convex, hemispherical to applanate, 2.2–4 cm wide, cream, glabrous, buff to lilac; margin concolorous with pileus surface, involute, entire, sometimes wavy. Context thin. Stipe central, cylindrical to clavate, 4.3–9.6 cm long and 0.4–1.5 cm wide, lilac to greyish violet, pruinose, covered with greyish-white tomentose at the base, hollow, fragile. Lamellae subfree, pale vinaceous to livid vinaceous, extremely close, unequal.

Basidiospores cylindrical to ellipsoid, hyaline, thin-walled, smooth, IKI–, CB–, $5\text{--}8.3 \times 3\text{--}4.3$ µm,

$L = 7.18$ µm, $W = 3.44$ µm, $Q = 1.43\text{--}2.44$ ($n = 90/3$). Basidia clavate, hyaline, thin-walled, four sterigmata, clamped at the base, $22.4\text{--}25.6 \times 5.4\text{--}7.5$ µm. Pleurocystidia absent. Cheilocystidia irregularly clavate, hyaline, moderately thick-walled, $39.3\text{--}58.7 \times 7.6\text{--}14.4$ µm. Caulocystidia clavate with tapered apices, hyaline, thick-walled, smooth, $27\text{--}75 \times 7\text{--}20$ µm. Pileipellis a cutis composed of three to four layers of cylindrical cells, $27\text{--}85 \times 4\text{--}7$ µm, smooth, thin-walled; terminal cells fusiform, $47\text{--}70 \times 5\text{--}20$ µm, thin-walled, hyaline; clamp connections abundant.

Habitat: Scattered on humus and fallen leaves in mixed forests of *Betula* and *Larix*.

Additional specimens examined: China. Hebei Province, Chengde City, Weichang County, Saihanba National Forest Park, on the ground of *Betula* and *Larix* dominated forests, 6 August 2023, Liu 129 (MBPU); 28 August 2023, Liu 370 (MBPU).

Mycena violacea-ardesiaca Shun Liu & Biao Zhu, sp. nov. [Figures 22, 23](#)

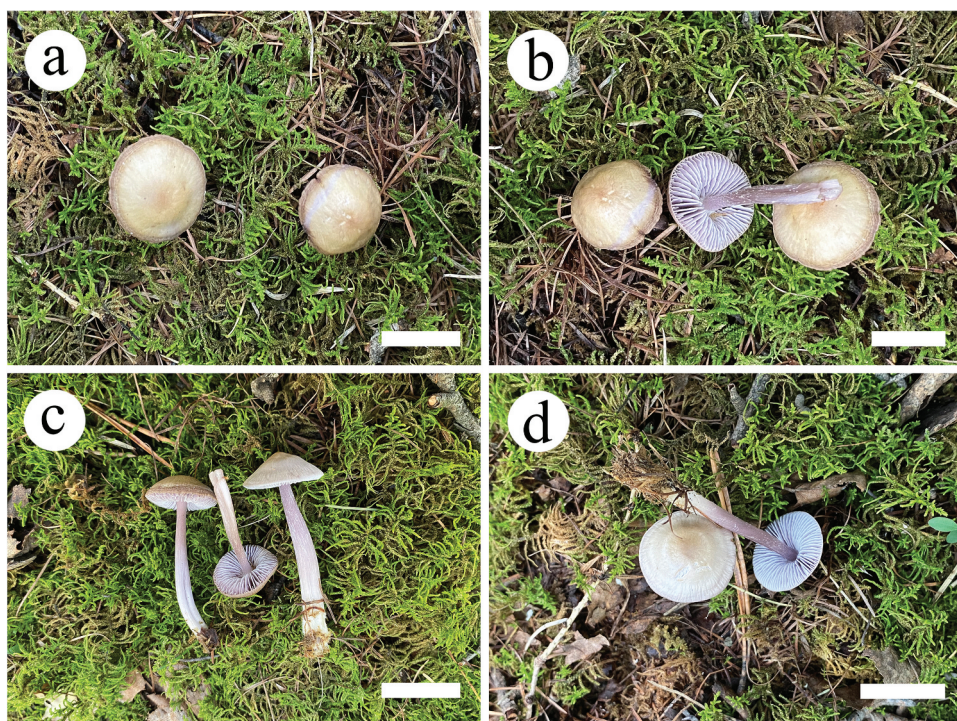


Figure 20. Basidiomata of *Mycena variispora* (holotype, Liu 369, 370). Bars: a, b = 3 cm; c, d = 4 cm.

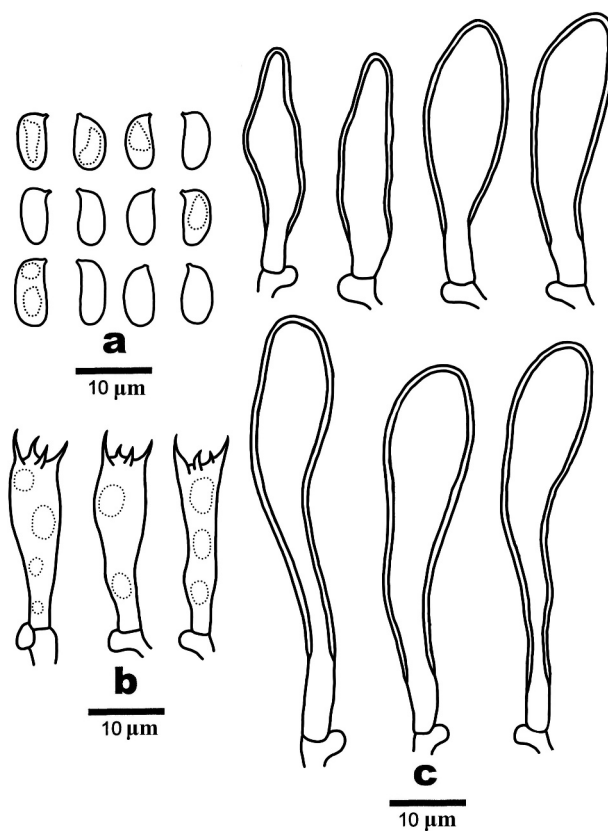


Figure 21. Microscopic structures of *Mycena variispora* (drawn from the holotype). (a) Basidiospores. (b) Basidia. (c) Cheilocystidia. Bars: a–c = 10 µm.

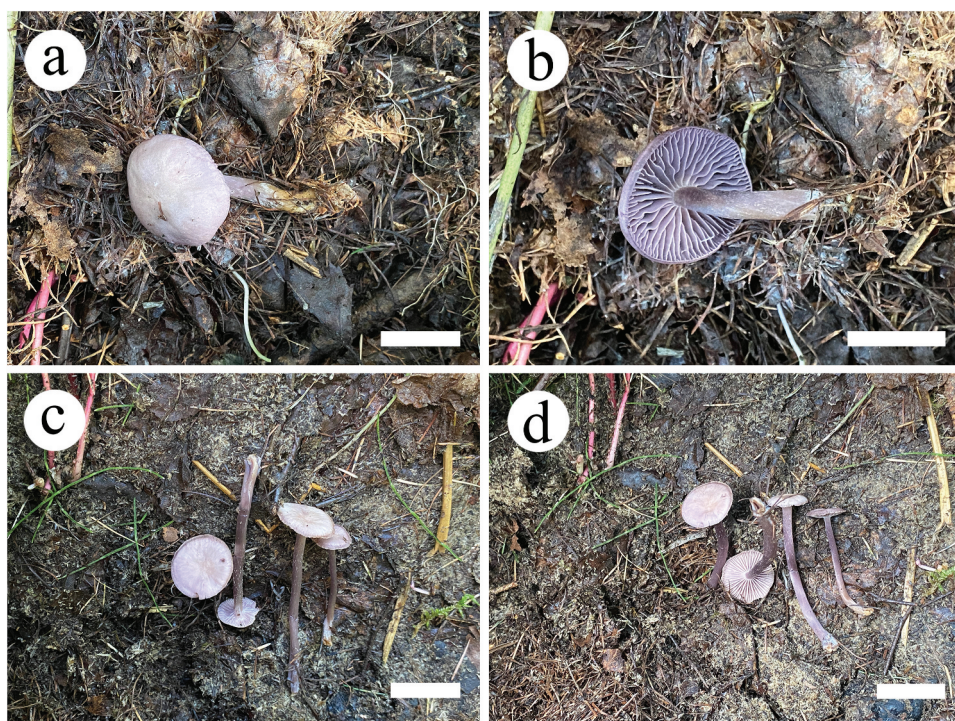


Figure 22. Basidiomata of *Mycena violacea-ardesiaca* (Liu 475, 477). Bars: a–d = 3 cm.

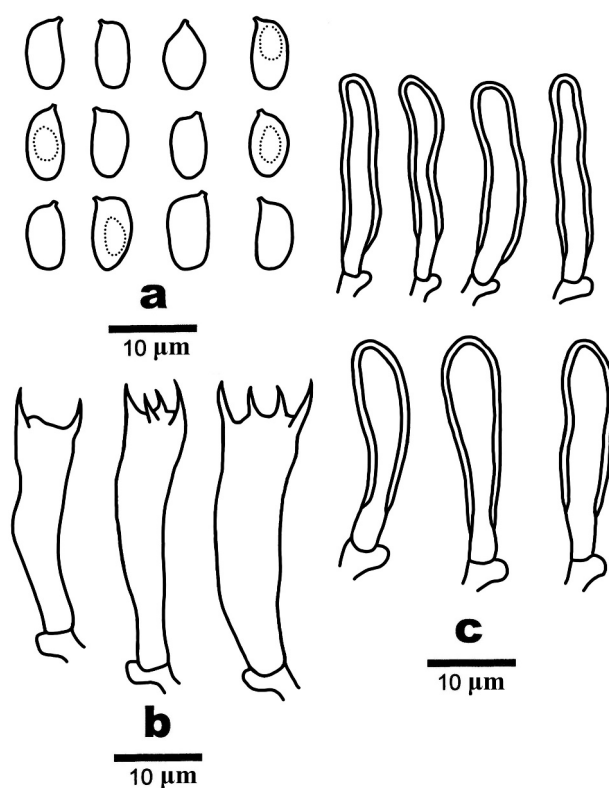


Figure 23. Microscopic structures of *Mycena violacea-ardesiaca* (drawn from the holotype). (a) Basidiospores. (b) Basidia. (c) Cheilocystidia. Bars: a–c = 10 µm.

MycoBank: MB854470.

Etymology: The epithet, *violocea-ardesiaca*, refers to the species has the violacea-ardesiaca basidiomata.

Diagnosis: This species differs from other species by its pale vinaceous to lilac pileus surface, greyish violet to fuscous stipe covered with white tomentose at the base, pale vinaceous to livid vinaceous lamellae, ellipsoid to oblong-ellipsoid basidiospores ($6.9\text{--}8 \times 3.8\text{--}5.2 \mu\text{m}$).

Type: China. Hebei Province, Chengde City, Weichang County, Saihanba National Forest Park, on the ground of *Betula* dominated forests, 29 August 2023, Liu 477 (MBPU).

Basidiomata solitary to gregarious. Pileus convex, hemispherical to applanate, 1.5–4.5 cm wide, glabrous, pale vinaceous to lilac; margin concolorous with pileus surface, involute, entire, sometimes wavy. Context thin. Stipe central, cylindrical to clavate, 4–7.2 cm long and 0.3–0.8 cm wide, greyish violet to fuscous, pruinose, covered with greyish-white tomentose at the base, hollow,

fragile. Lamellae subfree, pale vinaceous to livid vinaceous, extremely close, unequal.

Basidiospores oblong-ellipsoid to ellipsoid, hyaline, thin-walled, smooth, IKI–, CB–, $(6.7\text{--})6.9\text{--}8(8.2) \times 3.8\text{--}5.2(5.3) \mu\text{m}$, $L = 7.5 \mu\text{m}$, $W = 4.43 \mu\text{m}$, $Q = 1.46\text{--}1.86$ ($n = 60/2$). Basidia clavate, thin-walled, hyaline, two to four sterigmata, clamped at the base, $18\text{--}34 \times 4.3\text{--}9 \mu\text{m}$. Pleurocystidia absent. Cheilocystidia irregularly clavate, hyaline, moderately thick-walled, $15\text{--}32 \times 3.9\text{--}7.3 \mu\text{m}$. Caulocystidia clavate or fusiform, hyaline, thin-walled, smooth, $18\text{--}42 \times 4\text{--}12 \mu\text{m}$. Pileipellis a cutis composed of four to five layers of cylindrical cells, $47\text{--}63 \times 3\text{--}6 \mu\text{m}$, smooth, thin-walled; terminal cells cylindrical, $33\text{--}48 \times 4\text{--}16 \mu\text{m}$, thin-walled, hyaline; clamp connections abundant.

Habitat: Scattered on humus and fallen leaves in *Betula* dominated forest.

Additional specimen examined: China. Hebei Province, Chengde City, Weichang County, Saihanba National Forest Park, on the ground of *Betula* dominated forests, 29 August 2023, Liu 475 (MBPU).

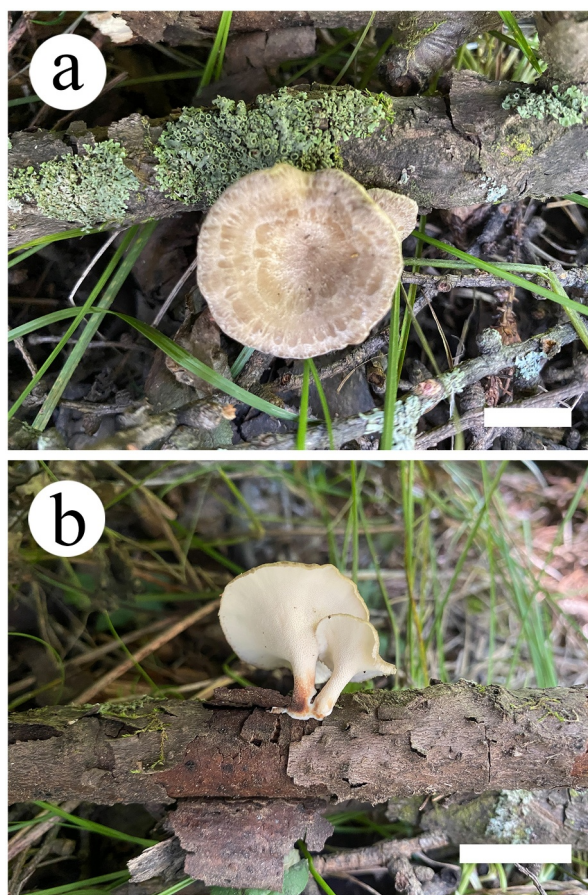


Figure 24. Basidiomata of *Picipes griseus* (Liu 137). Bars: a, b = 2 cm.

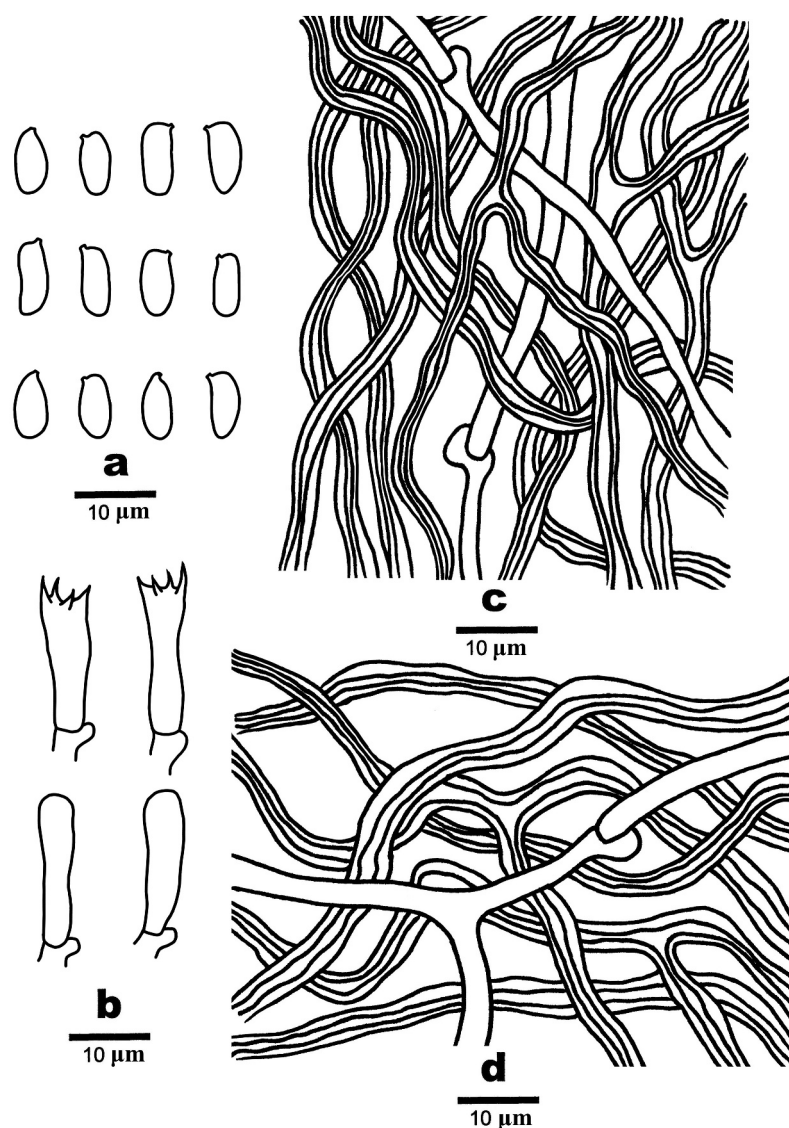


Figure 25. Microscopic structures of *Picipes griseus* (drawn from the holotype). (a) Basidiospores. (b) Basidia and basidioles. (c) Hyphae from trama. (d) Hyphae from context. Bars: a–d = 10 µm.

Picipes griseus Shun Liu & Biao Zhu, sp. nov.

Figures 24, 25

Mycobank: MB 854471.

Etymology: The epithet, *griseus*, refers to the grey pileal surface.

Diagnosis: This species differs from other species by its pale mous-grey to pinkish-buff pileal surface when fresh, becoming smoke grey when dry, subcircular pores (6–8 per mm), white to cream stipe at the upper part and fawn at the lower part when fresh, becoming cream at the upper part and greyish brown at the lower part when dry.

Type: China. Hebei Province, Chengde City, Weichang County, Saihanba National Forest Park, on fallen branches of *Prunus*, 6 August 2023, Liu 137 (MBPU).

Basidiomata annual, laterally stipitate, solitary, coriaceous when fresh, becoming hard corky when dry. Pilei semicircular, projecting up to 1.7 cm long, 2.8 cm wide, and 1 mm thick. Pileal surface pale mous-grey to pinkish-buff when fresh, becoming smoke grey when dry, glabrous, zonate, with radially aligned stripes; margin black, straight. Pore surface cream when fresh, becoming cream to pinkish-buff when dry; pores subcircular, 6–8 per mm. Context buff, woody hard when dry, up to 2 mm thick. Tubes clay brown, hard corky when dry, 1.5 mm thick. Stipe white to cream at the upper part and fawn at the lower part when fresh, becoming cream at the upper part and greyish brown at the lower part when dry, glabrous, up to 11 mm long and 3 mm in diam.

Hyphal system dimitic; generative hyphae bearing clamp connections; skeleto-binding hyphae IKI–, CB+; tissues unchanged in KOH. Generative hyphae in context infrequent, colourless, thin-walled, rarely branched, 1.8–4.2 µm in diam.; skeleto-binding hyphae in context dominant, colourless, thick-walled with a wide to narrow lumen, moderately branched, interwoven, 2–4.5 µm in diam. Generative hyphae in tubes frequent, usually present near hymenium, colourless, thin-walled, 1.5–3.5 µm in diam.; skeleto-binding hyphae in tubes dominant, thick-walled with a wide to narrow lumen, with dendroid branches, strongly interwoven, 1.6–3.8 µm in diam. Cystidia absent; cystidioles frequent, subulate, 12–21 × 3.2–4.5 µm. Basidia clavate, with a basal clamp connection and four sterigmata, 13.5–23.5 × 4–5.5 µm; basidioles in shape similar to basidia, but slightly smaller. Basidiospores cylindrical, colourless, thin-walled, smooth, IKI–, CB–, (6.5–)6.7–8(–8.2) × 2.5–3.3(–3.5) µm, L = 7.45 µm, W = 2.92 µm, Q = 2.56 ($n = 30/1$).

Habitat: Saprophyte on fallen branches of *Prunus*.

Pleuroflammula hebeiensis Shun Liu & Biao Zhu, sp. nov. [Figures 26, 27](#)

MycoBank: MB 854472.

Etymology: The epithet, *hebeiensis*, refers to the species collected from Hebei Province in China.

Diagnosis: This species differs from other species by its buff, cinnamon-buff to clay-buff basidiomata, honey-yellow to fawn lamellae, and ellipsoid to narrowly ellipsoid basidiospores (7–9 × 4–5.4 µm).

Type: China. Hebei Province, Chengde City, Weichang County, Saihanba National Forest Park, on fallen trunk of *Betula*, 4 August 2023, Liu 41 (MBPU).

Basidiomata solitary to subgregarious. Pileus convex, plano-convex, 1.6–5.5 cm wide, fibrillose-squamulose, buff, clay-buff to cinnamon-buff; margin concolorous with pileus surface, entire, involute, sometimes wavy. Context thin. Stipe central, cylindrical, 4.2–4.3 cm long and 0.3–0.6 cm wide, buff to clay-buff, pruinose, covered with greyish-white tomentose at the base, hollow, fragile. Lamellae subfree, honey-yellow to fawn, extremely close, unequal.

Basidiospores oblong-ellipsoid to ellipsoid, rust brown, thick-walled, smooth, IKI–, CB+, 7–9(–9.1) × 4–5.4(–5.6) µm, L = 7.96 µm, W = 4.94 µm, Q = 1.34–2 ($n = 60/2$). Basidia clavate, rust brown, thin-walled, four sterigmata, clamped at the base, 17.5–26.7 × 4.8–6.5 µm. Basidioles dominant, in shape similar to basidia, but smaller. Cheilocystidia

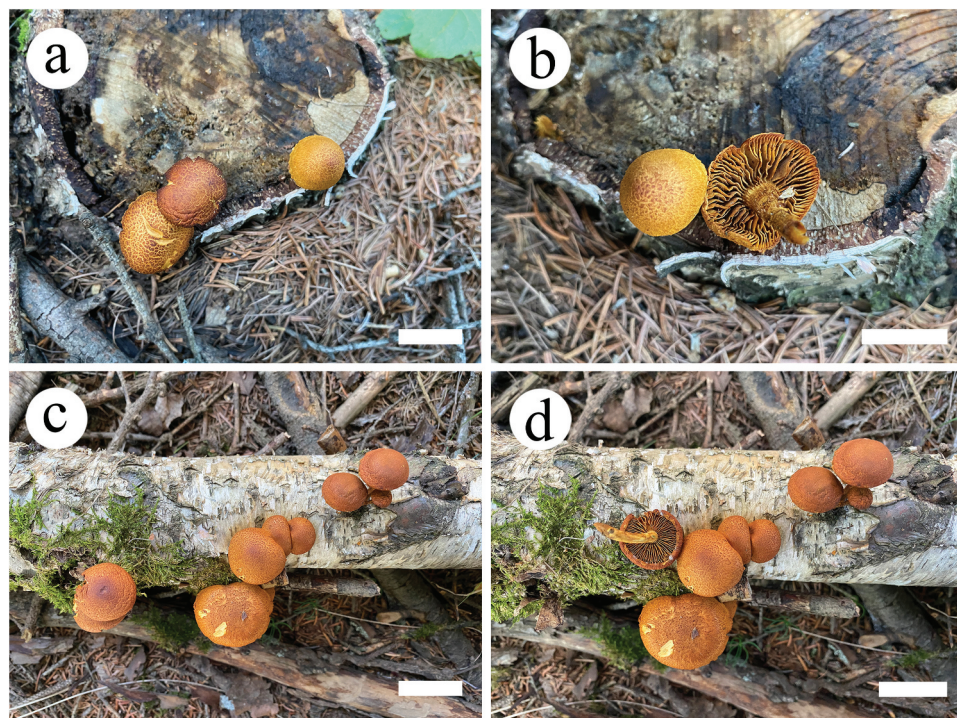


Figure 26. Basidiomata of *Pleuroflammula hebeiensis* (Liu 33, 41). Bars: a–d = 4 cm.

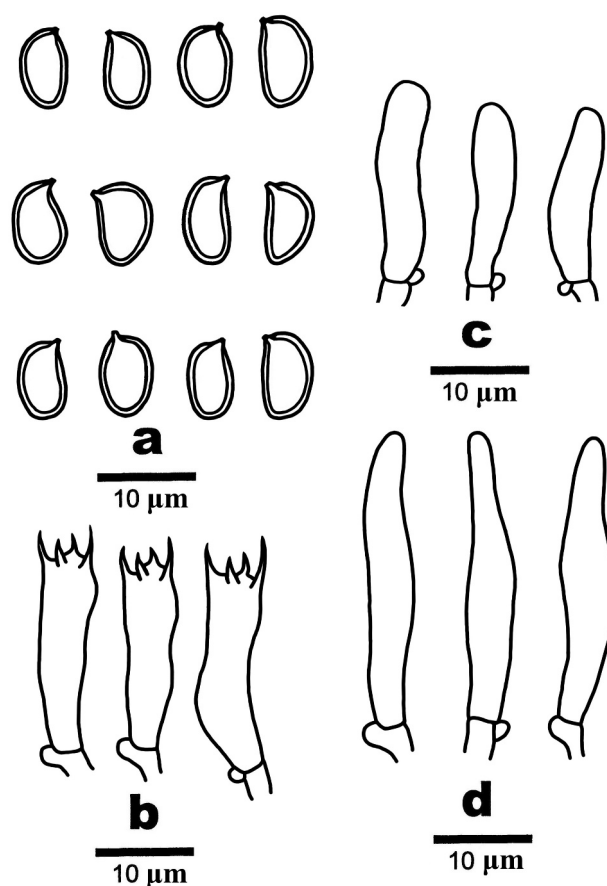


Figure 27. Microscopic structures of *Pleuroflammula hebeiensis* (drawn from the holotype). (a) Basidiospores. (b) Basidia. (c) Basidioles. (d) Cheilocystidia. Bars: a–d = 10 µm.

fusoid, hyaline, thin-walled, $21.3\text{--}45.6 \times 3.5\text{--}5.8$ µm. Pleurocystidia absent. Pileipellis a cuits, hyaline, branched, $(2.2\text{--})3\text{--}5.8(-7.3)$ µm wide; clamp connections abundant.

Habitat: Saprophytic on the fallen trunk or stump of *Betula*.

Additional specimens examined: China. Hebei Province, Chengde City, Weichang County, Saihanba National Forest Park, on stump of *Betula*, 4 August 2023, Liu 33 (MBPU); on fallen trunk of *Betula*, 7 August 2023, Liu 190 (MBPU).

4. Discussion

Macrofungal diversity is closely related to the distribution of plants, Saihanba National Forest Park is the largest artificial forest park in China, with a good growth environment for macrofungi. However, there were few studies on macrofungi in Saihanba National Forest Park in the past, and almost no new macrofungi species were discovered (Dai et al. 2021).

Through investigation of macrofungi in Saihanba National Forest Park, we clearly found that the most abundant order of macrofungi species are Agaricales and Polyporales. Combined with morphological characteristics and multi-gene fragment phylogenetic analysis, ten new species of Agaricales and Polyporales were discovered.

Species of *Cyanosporus* usually with blue-tinted basidiomata that are easily distinguishable from other genera, but are difficult to identify at the species level due to the similar morphological features. There are 35 species in this genus worldwide, of which, 21 are distributed in China (Liu et al. 2022b). In the current phylogenetic tree, *Cyanosporus subpopuli* clustered with *C. populi*, *C. subviridis* (Ryvarden & Guzmán) B.K. Cui & Shun Liu, and *C. yanae* (Miettinen & Kotir.) B.K. Cui & Shun Liu (Figure 1). However, *C. populi* differs by having effused-reflexed to pileate and thin basidiomata, shorter basidia ($10\text{--}16 \times 3.5\text{--}4.2$ µm), wider geographical distribution (holarctic, boreal to temperate) and host range (*Acer*, *Alnus*, *Betula*,

Populus, *Salix*); *C. subviridis* differs in having pale ochraceous pileus surface when fresh and ochraceous to greyish when dry, smaller basidia ($10\text{--}13 \times 3.2\text{--}4.4\ \mu\text{m}$) and basidiospores ($3.8\text{--}4.5 \times 1\text{--}1.3\ \mu\text{m}$); *C. yanae* differs in having effused-reflexed or resupinate, pale ochraceous or bluish basidiomata, and smaller basidia ($9\text{--}14 \times 3.5\text{--}4.2\ \mu\text{m}$; Miettinen et al. 2018).

Currently, *Gelatinofungus* is a monophyletic genus, with *G. brunneus* as type species (Chen et al. 2021). In phylogenetic analysis, *G. betulina* and *G. brunneus* are embedded in Phanerochaetaceae and form a high-support branch (Figure 2). Morphologically, *G. brunneus* can be distinguished from *G. betulina* by having effused basidiomata, dark purplish grey hymenial surface with brownish tints when young, becoming cinnamon to brown when old, and ellipsoid to broadly ellipsoid basidiospores ($4.7\text{--}6 \times 3.2\text{--}4\ \mu\text{m}$; Chen et al. 2021).

Lycoperdon is the type genus of Lycoperdaceae and was once placed in Lycoperdales F. Berchtold & J. Presl (Demoulin 1968). Recent studies have shown that *Lycoperdon* is embedded in Agaricales (Krakhmalnyi et al. 2023). In the current phylogenetic analyses, *Lycoperdon pseudoperlatum* is closely related to *L. perlatum* (Figure 3). Morphologically, they share pyriform substipitate basidiomata and asperulate basidiospores, but *L. perlatum* differs by having buff to snuff brown exoperidium, white or light yellow, olive-brown to grey-brown gleba, and larger basidiospores ($3.6\text{--}4.3\ \mu\text{m}$; Krakhmalnyi et al. 2023). *Lycoperdon excipuliforme* (Scop.) Pers. can also distribute in Saihanba National Forest Park, but it differs from *L. pseudoperlatum* in having larger basidiomata ($5\text{--}10\ \text{cm}$ in diam., $5\text{--}20\ \text{cm}$ in height) and basidiospores ($4.5\text{--}5.5\ \mu\text{m}$; Krakhmalnyi et al. 2023).

The classification status of *Macrocyttidia* has been controversial, and recent phylogenetic analysis shows that *Macrocyttidia* and *Pseudoclitopilus* Vizzini & Contu are embedded in Macrocyttidiaceae of the suborder Tricholomatineae. In the current phylogenetic analysis, *Macrocyttidia* and *Pseudoclitopilus* are clustered together with low support rates (Figure 4). *Macrocyttidia hebeiensis* grouped together with *M. cucumis* and *M. reducta* E. Horak & Capellano (Figure 4), but *M. cucumis* differs by having red brown to dark red brown pileus surface with yellow margin, white to buff lamellae and wider basidiospores ($8\text{--}10 \times 4\text{--}5\ \mu\text{m}$; Horak 1980); *M. reducta* differs in having ochre-brown to orange-brown pileus

surface, pale pink-brown or pale red-brown lamellae, and wider basidiospores ($7.5\text{--}10 \times 4.5\text{--}5\ \mu\text{m}$; Horak 1980).

Mycena is a species-rich and interspecies complex genus which is divided into several sections based on basidiomata colour (Na et al. 2022). *Mycena* sect. *Calodontes* forms a monophyletic branch and is embedded in *Mycena*, species in this section are characterised by pinkish, reddish to brownish pileus, and some are bioluminescent taxa (Na and Bau 2019; Liu et al. 2022c; Cortés-Pérez et al. 2023). In this study, four new species of *Mycena*, *M. subbrunnea*, *M. subpura*, *M. variispora*, and *M. violacea-ardesiaca*, were described. The phylogenetic analyses inferred from a combined DNA dataset (ITS + PRB1 + TEF1) strongly support their placement in the *Mycena* sect. *Calodontes* (Figure 5). *Mycena subbrunnea* and *M. brunnea* grouped together in the phylogenetic analyses (Figure 5). Morphologically, *M. subbrunnea* and *M. brunnea* share similar-sized basidiospores and basidia, but *M. brunnea* differs by having a predominantly brown pileus, the absence of deep purple tones, and a forest habitat (Olariaga et al. 2015). In addition, *M. subbrunnea* differs from other species of *M. pura* complex within sect. *Calodontes* by having cream, pinkish buff, buff-yellow to fawn pileus, white, cream to pinkish buff stipe, and white to pinkish buff lamellae. *Mycena violacea-ardesiaca*, *M. lucinieblae* Cortés-Pérez, Ram.-Cruz & Guzm.-Dáv., *M. pearsoniana* Dennis, *M. shengshanensis* Z.W. Liu, Y.P. Ge & Q. Na, and *M. subulata* Z.W. Liu, Y.P. Ge & Q. Na grouped together in the phylogenetic analyses (Figure 5). Morphologically, these five species share the coloured stipe, white or without dots lamellae edge; however, *M. lucinieblae* differs in having pink or purple-pink, hygrophanous pileus, pale pink to violet-white lamellae, pinkish-white to pale violet stipe, and smaller basidiospores ($5.5\text{--}7.4 \times 4\text{--}5\ \mu\text{m}$; Cortés-Pérez et al. 2023); *M. pearsoniana* differs by having vinaceous russet to vinaceous buff pileus, vinaceous buff lamellae, inamyloid and broadly ellipsoid basidiospores ($5\text{--}6.3 \times 3.5\text{--}3.8\ \mu\text{m}$; Harder et al. 2012); *M. shengshanensis* differs by having violet-brown to brown pileus at centre, white lamellae, elongated ellipsoid basidiospores ($6.1\text{--}8.1 \times 3.4\text{--}4.4\ \mu\text{m}$) and moderately thick-walled cheilocystidia (Liu et al. 2022c); *M. subulata* differs in its dull red to reddish-grey pileus slightly hygrophanous, slender fusiform cheilocystidia with distinctly long and narrow

protuberance, thick-walled caulocystidia, and elongated ellipsoid basidiospores ($6\text{--}7.3 \times 3.3\text{--}4.3 \mu\text{m}$; Liu et al. 2022c). In addition, *Mycena luxmanantlanensis* Cortés-Pérez, Ram.-Cruz & Guzm.-Dáv. share similar sized stipe and basidiospores, but *M. luxmanantlanensis* differs in having brownish-orange to orange pileus with pink tinges, and light yellow to yellowish-white stipe (Cortés-Pérez et al. 2023). Phylogenetically, *M. subpura* and *M. cf. pura* IV clustered together (Figure 5), of which *M. cf. pura* IV is distributed in Europe without specific morphological descriptions, making it impossible to compare with *M. subpura*. *Mycena pura* and *M. subpura* have similar coloured pileus, stipe, and lamellae, but *M. pura* differs from *M. subpura* by having ellipsoid to cylindrical and smaller basidiospores ($5.2\text{--}7.3 \times 2.7\text{--}3.9 \mu\text{m}$; Na 2019). *Mycena polycystidiata* and *M. shengshanensis* share similar-sized pileus and basidiospores with *M. subpura*; but *M. polycystidiata* differs from *M. subpura* by having greyish-rose and hygrophanous pileus with brownish-orange umbo, white and fragile context, white lamellae, and variable shape of pleurocystidia (Liu et al. 2022c); *M. shengshanensis* differs from *M. subpura* in having violet-brown to brown pileus at the centre, clavate and thick-walled cheilocystidia with slightly inflated apex, clavate caulocystidia with tapered apices, apex to middle thick-walled (Liu et al. 2022c). In the phylogenetic analyses, *Mycena variispora* and *M. cf. pura* I cluster together at the *M. pura* complex within sect. *Calodontes* (Figure 5). Morphologically, *M. subulate* and *M. variispora* share similar coloured pileus, but *M. subulate* differs from *M. variispora* by having white and fragile context, white lamellae, slenderly fusiform and thick-walled cheilocystidia with narrow protuberance and distinctly long, thick-walled caulocystidia, and elongated ellipsoid basidiospores ($6\text{--}7.3 \times 3.3\text{--}4.3 \mu\text{m}$; Liu et al. 2022c). *Mycena shengshanensis* and *M. variispora* have similar sized basidiospores and similar ecological habits; however, *M. shengshanensis* differs by having brown to violet-brown pileus at the centre, narrower and shorter stipe ($26\text{--}42 \times 2\text{--}4 \text{ mm}$), white lamellae, and larger basidia ($22\text{--}32 \times 6\text{--}8 \mu\text{m}$; Liu et al. 2022c); moreover, these two species have significant differences in phylogenetic trees (Figure 5).

Members of *Picipes* usually with stipitate basidiomata, dimitic hyphal system, and cylindric basidiospores (Zmitrovich and Kovalenko 2016). Currently, there are 31 species in *Picipes* (Ji et al. 2022). In the

phylogenetic tree, species of *Picipes* gather together with high statistical support (Figure 6). Phylogenetically, *P. griseus* clustered with *P. submelanopus* (H.J. Xue & L.W. Zhou) J.L. Zhou & B.K. Cui (Figure 6). Morphologically, *P. submelanopus* can be distinguished from *P. griseus* in its cinnamon-buff to pale mouse-grey pileal surface and ivory to straw-yellow pore surface when dry, larger pores (2–4 per mm), and wider basidiospores ($7.4\text{--}8.7 \times 3.3\text{--}4.3 \mu\text{m}$; Cui et al. 2019). *Picipes pumilus* (Y.C. Dai & Niemelä) J.L. Zhou & B.K. Cui and *P. tubaeformis* (P. Karst.) Zmitr. & Kovalenko share similar sized pores and basidiospores with *P. griseus*, but *P. pumilus* differs by having cream to buff pileal surface when fresh, becoming pale straw when dry, beige grey to yellowish-brown pore surface when dry and straw stipe (Cui et al. 2019); *P. tubaeformis* differs by having reddish brown to deep bay pileal surface, straw to pale brownish pore surface when dry (Zmitrovich and Kovalenko 2016). In addition, *P. pumilus* and *P. tubaeformis* are distinct from *P. griseus* in the phylogenetic analysis (Figure 6).

The classification status of *Pleuroflammula* has always been controversial and it has been placed in Inocybaceae Jülich and Strophariaceae Singer & A.H. Sm., recent studies revealed *Pleuroflammula* belongs to Crepidotaceae (Gierczyk and Kubiński 2019; Crous et al. 2021). In this study, specimens of *Pleuroflammula hebeiensis* formed a highly supported lineage and were closely related to *P. subsulphurea* (A.H. Sm. & Hesler) E. Horak (Figure 7). Morphologically, both *P. hebeiensis* and *P. subsulphurea* have convex pileus, thick-walled basidiospores and grow on angiosperm trees, but *P. subsulphurea* differs by having bright yellow to orange-yellow pileus surface, smaller basidiospores ($6.5\text{--}7.5 \times 4\text{--}4.5 \mu\text{m}$; Smith and Hesler 1968). *Pleuroflammula praestans* E. Horak is also distributed in China, but it differs from *P. hebeiensis* in having yellow to deep yellow or yellow-brown pileus, wider and ovate to ellipsoid basidiospores ($7\text{--}9.5 \times 5\text{--}6 \mu\text{m}$), and growing on the tree of Araliaceae (Horak 1978).

Although some areas of the Saihanba National Forest Park are artificial forests with relatively single stands and frequent human activities, investigations have found that Saihanba National Forest Park has a relatively rich macrofungi diversity. Biodiversity is the foundation of human survival and development. However, biodiversity is under

unprecedented threat, and currently, the issue of biodiversity has attracted wide attention from the international community. Fungi are one of the most diverse groups on Earth, Hawksworth et al. (2017) estimated that there are approximately 2.2–3.8 million fungal species worldwide by analysing data on fungal species discovery rates, fungal-to-plant ratios, and molecular sequences in environmental samples. Wu et al. (2019) derived from high-throughput sequencing techniques that there are approximately 11.7 to 13.2 million fungal species. Currently, about 150,000 fungal species have been reported and a large number of unknown fungal species remain to be discovered (He et al. 2022). Due to the short lifespan and rapid renewal of macrofungi, some of them have disappeared before being recognised. Therefore, large-scale and all-round investigation of macrofungi is still needed in the future. Some statistical models such as the maximum entropy model (MaxEnt) can be used to predict the distribution area and analyse the fitness of macrofungi to protect the fungal resources. In addition, we can explore the functional traits of macrofungi and their adaptability to the environment, which helps to reveal the distribution and adaptive strategies of macrofungi.

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