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Exploring the Relationships between Macrofungi Diversity and Major Environmental Factors in Wunvfeng National Forest Park in Northeast China

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Abstract: In this paper, we analyze the macrofungi communities of five forest types in Wunvfeng National Forest Park (Jilin, China) by collecting fruiting bodies from 2019–2021. Each forest type had three repeats and covered the main habitats of macrofungi. In addition, we evaluate selected environmental variables and macrofungi communities to relate species composition to potential environmental factors. We collected 1235 specimens belonging to 283 species, 116 genera, and 62 families. We found that *Amanitaceae*, *Boletaceae*, *Russulaceae*, and *Tricholomataceae* were the most diverse family; further, *Amanita*, *Cortinarius*, *Lactarius*, *Russula*, and *Tricholoma* were the dominant genera in the area. The macrofungi diversity showed increasing trends from *Pinus koraiensis* Siebold et Zuccarini forests to *Quercus mongolica* Fischer ex Ledebour forests. The cumulative species richness was as follows: *Q. mongolica* forest A > broadleaf mixed forest B > *Q. mongolica*, *P. koraiensis* mix forest D (*Q. mongolica* was the dominant species) > *Q. mongolica* and *P. koraiensis* mix forest C (*P. koraiensis* was the dominant species) > *P. koraiensis* forest (E). Ectomycorrhizal fungi were the dominant functional group; they were mainly in forest type A and were influenced by soil moisture content and *Q. mongolica* content ($p < 0.05$). The wood-rotting fungus showed richer species diversity than other forest types in broadleaf forests A and B. Overall, we concluded that most fungal communities preferred forest types with a relatively high *Q. mongolica* content. Therefore, the deliberate protection of *Q. mongolica* forests proves to be a better strategy for maintaining fungal diversity in Wunvfeng National Forest Park.

Keywords: community composition; conservation; edaphic variables; forest type; macrofungal species richness

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1. Introduction

Fungal communities are essential for forest ecosystems and have many functions [1,2]. Ectomycorrhizal fungi (EM) participate in the soil nutrient cycle of forest ecosystems and promote the host plant's absorption of nutrients, such as nitrogen, phosphorus, and water, thereby maintaining the above-ground primary productivity of the forest ecosystem [3]. Saprotrophic fungi can degrade wood components (i.e., lignin, cellulose, and hemicellulose [4]), and they are considered essential wood-decay-promoting organisms. These functions indicate a crucial role in maintaining the forest ecosystem's stability [5].

Many biotic and abiotic factors can affect the diversity and composition of fungal communities [6,7]. The composition of EM is strongly influenced by the soil's nitrogen content [8,9], pH [10], temperature and moisture [11,12], the species composition of the host trees [13,14], and by the seasons [15]. Fungal communities living on the wood are closely dependent upon environmental factors, such as the amount, diameter, and stage of wood decomposition [16], wood chemistry [17], age [18], and tree species [19]. Factors influencing terricolous saprotrophic communities include litter quantity and pH [20], soil

P content [21,22], plant species [23,24], and temperature [25]. The processes of natural or human-induced change in the vegetation composition of forests are also important drivers of fungal diversity [26–28], as they are associated with significant changes in litter and soil quality in the long term [29–31].

Our study sites are all within the Wunvfeng National Forest Park in the southeastern mountainous region of the Jilin Province, China. The reserve was established in 1992 and is part of the Changbai Mountain system. The original vegetation included *Quercus mongolica* Fischer ex Ledebour forests and mixed broadleaf forests, which changed when *Pinus koraiensis* Siebold et Zuccarini was planted in the 1980s [32]. Currently, the vegetation composition includes a *P. koraiensis* forest, and *P. koraiensis*–*Q. mongolica* mixed forests provide a unique opportunity to investigate the fungal communities of different forest types under the same climatic conditions. Usually, *Pinus* species are dependent upon macrofungi in symbiotic associations, which are essential for their growth and survival [33] because symbiotic associations facilitate the trees' uptake of water and nutrients [34,35]. Some specific fungal species may be found in relatively stable *Pinus* forests. Thus, understanding the distribution characteristics of fungal communities in planted and native forests can provide better strategies for fungal diversity conservation, especially for the deliberate conservation of forest types that host a more significant number of fungal species. In this context, we conducted a three-year survey of macrofungi in different vegetation types in Wunvfeng National Forest Park. We study the relationship between selected environmental factors and community composition. We aim to investigate whether fungal communities differ among the five forest types and whether native forests dominated by *Q. mongolica* are potentially associated with fungal communities.

2. Materials and Methods

2.1. Study Area Description

Our study site, Wunvfeng National Forest Park, covers an area of 6867 hm^2 [36] and is situated in Ji'an City in the extreme southeast part of the Jilin Province, Northeast China (126°2′21″–126°17′57″ E, 41°11′37″–41°21′40″ N). The area is characterized by a temperate continental monsoon climate with a mean annual precipitation of 950 mm with peaks from June–August and a mean annual air temperature of 6.5 °C [36]. The forest cover is 95%, and the dominant tree species is *Q. mongolica*. *P. koraiensis* was planted as a non-native tree species in 1980. At present, it has formed stable forest communities. Dark-brown soil [37] is the most frequent soil type. The fundamental geomorphological units belong to the Changbai Mountains, ranging in altitude from 500–1500 m [38].

2.2. Fruiting Body Sampling

We designated five following forest types: A, B, C, D, and E. Three 50 m × 50 m sampling plots with at least 500 m distance between them were located within each forest type (pictures of each forest type are provided in Figure 1).

Quercus mongolica site (A): Old-growth *Q. mongolica* forests with the original habitat, and no fallen or standing deadwood has been removed. There are 275 *Q. mongolica* with a coverage rate of 96.15%.

Broad-leaved forest site (B): Mixed broadleaved forest (uneven-aged), with *Q. mongolica*, *Tilia amurensis* Rupr., *Fraxinus mandshurica* Rupr., *Acer palmatum* Thunb., *Juglans regia* L., close to nature managed. There are 158 *Q. mongolica* with a coverage rate of 48.46%.

Pinus koraiensis and *Quercus mongolica* mixed sites (C): 30–50-year-old *P. koraiensis* forest, close to nature managed, and naturally grown *Q. mongolica*. *P. koraiensis* was artificially grown and is the dominant species. There are 42 *Q. mongolica* with a coverage rate of 18.03%.

Quercus mongolica and *Pinus koraiensis* mixed sites (D): 30–60-year-old *Q. mongolica* forests, close to nature managed, and artificially grown *P. koraiensis*. *Q. mongolica* is the dominant species. There are 183 *Q. mongolica* with a coverage rate of 74.69%.

Figure 1. Sampling plot distribution and forest types in Wunvfeng National Forest Park. Note: Sampling plot distribution (**A**); Plots A1, A2, A3 = *Q. mongolica forest* (**B**); Plots B1, B2, B3 = Broad-leaved forest (**C**); Plots C1, C2, C3 = *P. koraiensis* and *Q. mongolica* mixed forest (*P. koraiensis* is the dominant species (**D**)); Plots D1, D2, D3 = *P. koraiensis* and *Q. mongolica* mixed forest, (*Q. mongolica* is the dominant species (**E**)); Plots E1, E2, E3 = *P. koraiensis* forest (**F**).

Pinus. koraiensis sites (E): Single species; 40-year-old *P. koraiensis* forests planted in 1980, close to nature managed, no fallen trees removed. There are zero *Q. mongolica* with a coverage rate of 0%.

We collected samples 20–25 times per month from June to October 2019–2021. We randomly acquired macrofungi from each plot. We photographed the specimens in the field using a Canon EOS 800D digital camera and recorded fresh morphological characteristics and ecological characteristics (Figure 2). We selected the context or stipe tissue (1–2 g) of the same specimen when it was fresh and stored it in a sealed bag with silica gel for DNA extraction; we dried them in an oven (45–50 °C) and placed them in specimen boxes. We then took a morphotype of each specimen to the laboratory and used it for morphological species identification.

2.3. Soil Sampling, Analysis and Environmental Data Collection

We collected soil samples four times per month during July–September 2020. After cleaning and removing plant material and debris from the surface, we collected individual soil samples from the center and 4 corners in 15 plots using an auger (5 cm radius, 5 cm depth). We mixed the soil samples from the same plots well and placed them in sealed bags. After removing impurities, we enclosed the fresh samples (20 g) from each clod in an aluminum box. We dried the samples to a constant weight in an oven at 105 °C to measure water content (SWC); we used natural air-dried composite samples (200 g) for each plot to analyze for pH, organic matter (SOM), available phosphorus (P), effective nitrogen (N), and available potassium (K) using the method described by Xing et al. [39]. Finally, we averaged the data from three plots of the five fore for subsequent analysis.

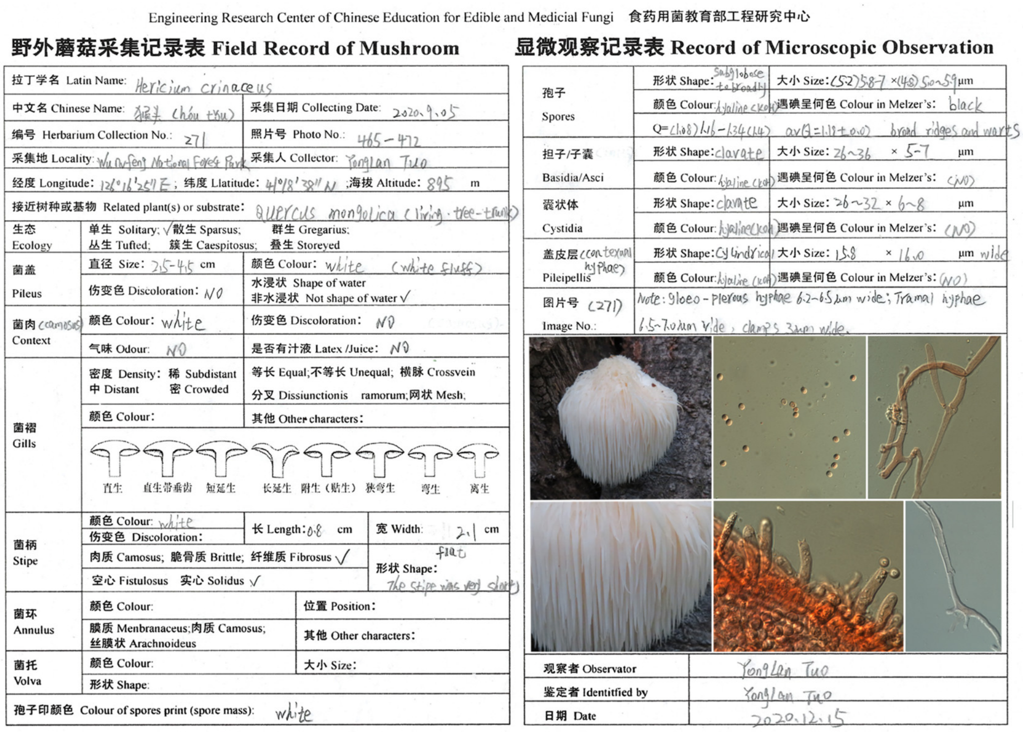

Figure 2. Field record of mushrooms and microscopic characteristic observation.

We obtained the temperature and relative humidity of the air and soil temperature from July–September 2020 from meteorological monitoring sites in the forest park. The tested results for the soil are included in Table 1.

Table 1. *Quercus mongolica content and selected environmental variables properties in five forest types.*

Environment Parameters	Forest				
	A	B	C	D	E
N (mg/kg)	68.2 ^{a}	56.59 ^{b}	44.07 ^{c}	46.65 ^{c}	47.94 ^{c}
P (mg/kg)	20.99 ^{b}	24.37 ^{a}	18.33 ^{b}	14.99 ^{c}	20.49 ^{b}
K (mg/kg)	408.9 ^{a}	372.73 ^{ab}	325.44 ^{b}	267.35 ^{c}	264.69 ^{c}
SOM (g/kg)	37.1 ^{a}	16.76 ^{c}	25.03 ^{b}	39.69 ^{a}	28.64 ^{b}
Soil pH	5.48 ^{c}	5.96 ^{a}	5.69 ^{b}	5.34 ^{c}	5.75 ^{b}
Temp1 (°C)	24 ^{a}	21.48 ^{b}	22.12 ^{b}	22.07 ^{b}	22.07 ^{b}
Temp2 (°C)	19.1 ^{a}	18.93 ^{a}	20.14 ^{a}	19.99 ^{a}	19.34 ^{a}
SWC (g/20 g)	6 ^{a}	5.2 ^{a}	3.8 ^{b}	5.6 ^{a}	4.8 ^{ab}
RH	0.82 ^{a}	0.83 ^{a}	0.83 ^{a}	0.83 ^{a}	0.86 ^{a}
QM	275 ^{a}	179 ^{b}	42 ^{c}	183 ^{b}	0 ^{d}

Note: Abbreviations: N = soil effective nitrogen; P = soil available phosphorus; K = soil available potassium; SOM = soil organic matter; pH = soil pH; Temp1 = soil temperature; Temp2 = air temperature; SWC = soil water content; RH = air relative humidity; QM = Number of *Q. mongolica*; Different lowercase letters indicate significantly different QM and environment parameter values among five forest type ($p < 0.05$).

2.4. Species Identification

We identified the macrofungi using morphological observations methods. We used molecular methods for the species that were morphologically difficult to identify. We measured different microscopic structures of taxonomic importance (e.g., spores, basidia, cystidia) [40]. We examined the morphological features of the fruiting bodies using appropriate monographs, including by Li et al. [41] and Liu et al. [42], to identify each macrofungi specimens. The specimens are currently housed in the Herbarium of Mycology of Jilin Agricultural University (HMJAU), Changchun, China.

Molecular identification involved sequencing the internal transcribed spacer (ITS). For this, we extracted the DNA of the macrofungi using a NuClean Plant Genomic DNA Kit (Cowin Biosciences, Taizhou, China), following the manufacturer's instructions. We conducted final elutions in a total volume of 50 µL. We showed a polymerase chain reaction (PCR) with the primer pairs ITS-1F and ITS-4 [43]; finally, we sequenced the PCR products using the Sanger method. We conducted the PCR in 25 µL reactions consisting of 2 µL genomic DNA, 0.5 µL Taq, and one µL upstream and downstream primers, respectively. We used 14.5 µL ddH$_2$O, five µL 5 × PCR buffer, and 1 µL dNTP in the PCR reactions that we ran under the following conditions: 95 °C for 3 min, followed by 35 cycles of 94 °C for 40 s, 55 °C for 45 s, 72 °C for 1.5 min, and a final extension step at 72 °C for 6 min before storage at 4 °C We purified the PCR products and sequenced them at Sangon Biotech Co., Ltd. (Shanghai, China). We performed molecular identification via BLAST comparisons. Species with >98% sequence similarity were also identified with morphological characteristics. GenBank accession numbers obtained are provided in Appendix B.

We identified ecological functions (ectomycorrhizal fungi; soil saprotroph; wood-decaying fungi; litter saprotroph; dung saprotroph; endophyte-insect pathogen) at the genera level using a FUNGuild (available online: http://www.funguild.org (accessed on 18 November 2021) search; these can be found in Appendix B. We classified macrofungi into eight types (agarics; large ascomycetes; boletes; polyporoid fungi; coral fungi; gasteoid fungi; jelly fungi; hydnaceous fungi, and cantharelloid fungi) according to the method of Li et al. [41]. The fungal nomenclature follows the Index Fungorum (available online: http://www.indexfungorum.org (accessed on 15 November 2021)). Setting scientific names at all taxonomic ranks in italics facilitates quick recognition in scientific papers [44].

2.5. Statistical Analysis

We used three alpha diversity indices to analyze the community composition of the macrofungi. The Menhinick richness index (R) reflected the species richness of the community. The Shannon index (D) reflected the diversity of the community species. Pielou's evenness index (E) reflected the distribution of the number of individuals in each species. The diversity index formulae were as follows:

$$\mathrm{R} = \mathrm{S}/\sqrt{N} \tag{1}$$

$$\mathrm{D} = -\sum P_i \ln (P_i) \tag{2}$$

$$\mathrm{E} = \mathrm{H}'/\mathrm{lnS};\ \mathrm{H}' = -\sum P_i \ln (P_i) \tag{3}$$

where P_i is the proportion of species i to the total number of individuals of all species in the plot; ln is the natural logarithm; S is the total number of species in the plot; and N is the total number of individuals observed in the plot.

We analyzed the relationships between ectomycorrhizal fungi communities and selected variables using the canonical correlation analysis (CCA) from Canoco 5.0 [45]. We first used detrended correspondence analysis (DCA) to determine the appropriate model for direct gradient analysis. The results indicated that a unimodal model (gradient lengths > 3 standard units) would best fit our study data; we utilized CCA. Furthermore, we tested explanatory variables using the Monte Carlo permutation test provided by Canoco 5.0 software (with 999 randomizations). The species data matrix for the CCA analysis was based on the presence–absence data of ectomycorrhizal fungi species in each forest type (three-year accumulation of the five forest types).

We used Origin 9.0 software to construct species stacked histograms at the genera level [46] to compare community compositions of the macrofungi species in the five forests and provide the relative proportion of macrofungi species richness (data include the number of species at the genera level in each forest type). Additionally, we generated pie charts, Venn diagrams, and species accumulation curves using Hiplot (available online: https://hiplot.com.cn/basic/venn (accessed on 20 October 2021)). The pie chart data were derived from the number of macrofungi types. The Venn diagram data included the species in each forest type. The accumulation curve data consisted of the cumulative number of species per collection.

3. Results

3.1. Species Richness

We collected 1235 specimens from 5 forest types, 940 (76.11%) of which we identified at the species level, and we classified these into 283 fungal species. We identified 244 species based on morphology and 39 species using morphology and molecular methods (Appendix B). The unidentified sporocarps were not part of our further analysis. We classified the macrofungi species into 116 genera, 62 families, 18 orders, and 2 phyla. Basidiomycota was the dominant phylum, divided into 12 orders, 50 families, 102 genera, and 265 species. Ascomycota was divided into 6 orders, 12 families, 14 genera, and 18 species. The *Russulaceae* was the most diverse family with 36 different species, followed by *Tricholomataceae* (21 species), *Boletaceae* (19 species), and *Amanitaceae* (16 species). Together, these accounted for 32.51% of the total collected species. The most abundant genera were *Amanita, Cortinarius, Lactarius,* and *Russula*. The *Agaricales* were the most prevalent order in the five forest types (59.36%). In terms of the trophic groups, most of the species were ectomycorrhizal fungi (47%), followed by wood-decaying fungi (20.14%) and soil saprotrophs (18.37%).

3.2. Macrofungal Types

The most significant genera of *Agarics* accounted for 69.26% of the identified species, followed by boletes, larger ascomytetes, and polyporoid fungi, accounting for 9.89%, 6.36%, and 6.01% of the identified species, respectively. In contrast, hydnaceous and cantharelloid fungi were less abundant, accounting for 1.06% and 0.71%, respectively (see Figure 3). For more detailed information, see Appendix B. For images of some species, see Appendix A.

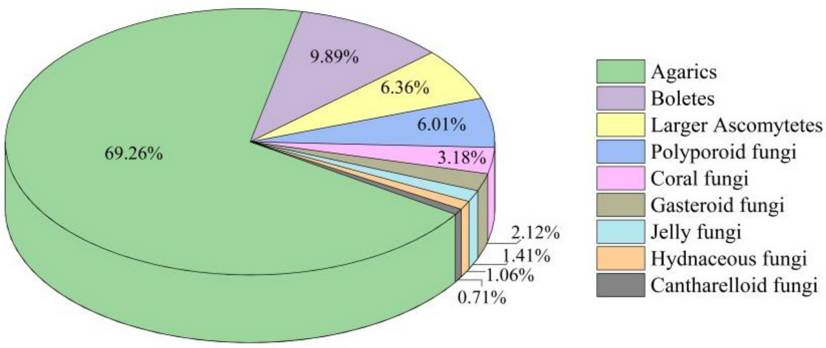

Figure 3. The proportion of different macrofungal types.

3.3. Analysis of Dominant Families and Genera

Among the identified species, there were 9 dominant families (number of species ≥10 species) of macrofungi (Table 2). The *Russulaceae* was the most diverse family. In addition, 53 families contained less than 10 species, accounting for 85.48% of the families and 48.06% of the identified species (Appendix B).

Table 2. Dominant families (≥10 species) of macrofungi in Wunvfeng National Forest Park.

Family	Number of Species	Percentage (%)
Russulaceae	36	12.72%
Tricholomataceae	21	7.42%
Boletaceae	19	6.71%
Amanitaceae	16	5.65%
Cortinariaceae	14	4.95%
Hygrophoraceae	11	3.89%
Agaricaceae	10	3.53%
Hymenochaetaceae	10	3.53%
Meruliaceae	10	3.53%
Total	147	51.94%

Among the identified species, there were 15 dominant genera (number of species ≥ 5 species) of macrofungi (Table 3). The *Amanita*, *Lactarius*, and *Russula* were the most diverse genera. In addition, 34 genera contained 2–4 species, accounting for 29.31% of the genera and 29.68% of the identified species; 67 of the genera contained only 1 species, accounting for 57.76% of the genera and 23.67% of the identified species (Appendix B).

Table 3. Dominant genera (≥5 species) of macrofungi in Wunvfeng National Forest Park.

Genera	Number of Species	Percentage (%)
Lactarius	18	6.36%
Amanita	16	5.65%
Russula	16	5.65%
Cortinarius	12	4.24%
Tricholoma	9	3.18%
Mycena	8	2.83%
Suillus	7	2.47%
Entoloma	7	2.47%
Agaricus	6	2.12%
Gymnopus	6	2.12%
Hygrocybe	6	2.12%
Pluteus	6	2.12%
Clitocybe	5	1.77%
Marasmius	5	1.77%
Ramaria	5	1.77%
total	132	46.64%

3.4. Forest Type and Species Composition

The community of macrofungi was different among the five forest types (Figure 4). The species richness increased from E (18 species, 6.36%) < C (35 species, 12.37%) < D (49 species, 17.31%) < B (86 species, 30.39%) < A (142 species, 50.18%). The *Lactarius* (13 species), *Amanita* (12 species), *Coprinellus* (10 species), and *Russula* (7 species) were the most species-rich genera in forest type A. The *Russula* (6 species) and *Gymnopilus* (4 species) were the most species-rich genera in forest type B. The *Gymnopus* (4 species) and *Suillus* (4 species) were the most species-rich genera in forest type C. The *Russula* (8 species), *Amanita* (7 species), and *Mycena* (4 species) were the most species-rich genera in forest type D. Finally, the *Gymnopus* (2 species), *Helvella* (2 species), and *Hydnellum* (2 species) were the relatively abundant genera in forest type E. More detailed information is shown in Appendix B.

3.5. Cumulative Abundance of Macrofungi in Five Forest Types

The accumulation curves for the species identified in the five forests show a steady increase with more samplings (Figure 5). We reached saturation of macrofungi richness after 150 surveys. The species accumulation curves of A (*Q. mongolica* forest) and B (broad-leaved forest) showed relatively steep upward slopes and produced higher macrofungi abundance values than the other forests. Nevertheless, forest type A (*Q. mongolica* forest) obtained the highest macrofungi diversity values.

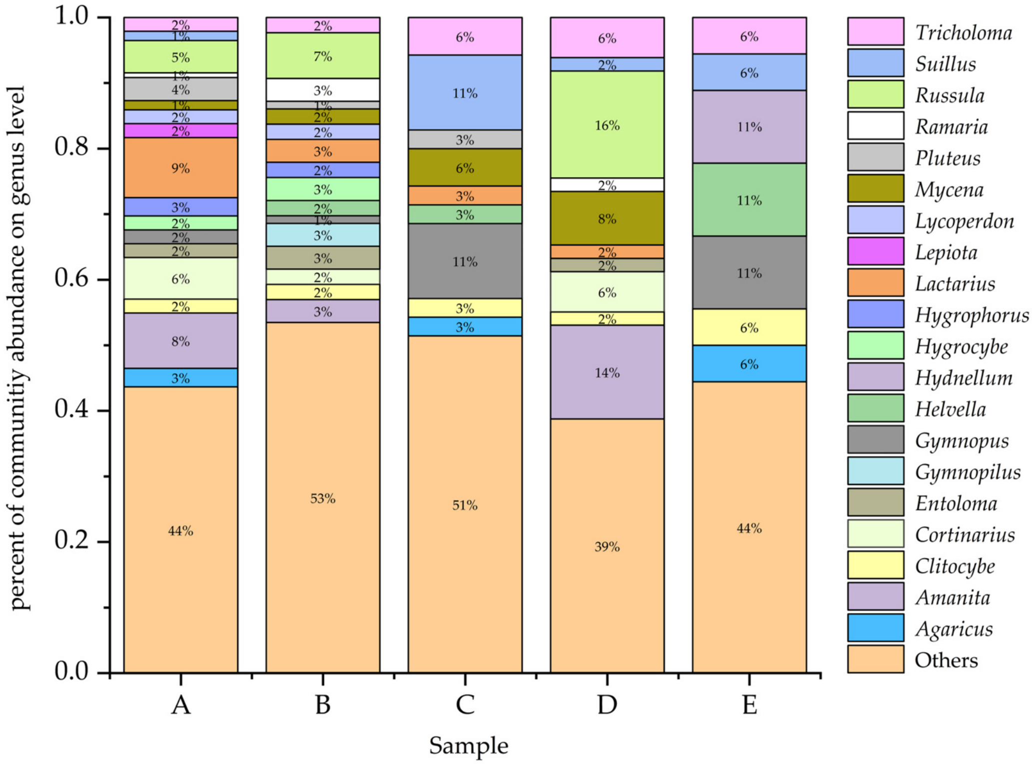

Figure 4. The relative proportions of macrofungi taxa at the genera level in five forest types. (**A**): *Q. mongolica* forest; (**B**): Broad-leaved forest; (**C**): *P. koraiensis* and *Q. mongolica* mixed forest with *P. koraiensis* being the dominant species; (**D**): *P. koraiensis* and *Q. mongolica* mixed forest with *Q. mongolica* being the dominant species; (**E**): *Pinus koraiensis* forest.

Two genera (*Clitocybe* and *Tricholoma*) were shared in five forest types, but no species were shared. The unique species (found only in 1 forest) increased from E < C < D < B < A and consisted of 13, 22, 31, 50, and 104 fungal species, respectively (Figure 6). Forest type A shared 27 species with B, 7 species with C, 11 species with D, and 2 species with E. Forest type B shared six species with C, eleven species with D, and three species with E. Forest type C shared three species with D and three species with E. The *Gymnopus densilamellatus* Antonín, Ryoo & Ka, and *Suillus grevillei* (Klotzsch) Singer only appeared in E and C. The *S. luteus* (L.) Roussel only appeared in D and C; *Helvella crispa* (Scop.) Fr. only appeared in B and E. The *Amanita oberwinklerana* Zhu L. Yang & Yoshim., *Amanita orsonii* Ash. Kumar & T.N. Lakh., *Amanita virosa* Bertill., *Boletus edulis* Bull., *Phellinus pomaceus* (Pers.) Maire, *Russula paludosa* Britzelm., and *Tricholoma sejunctum* (Sowerby) Quél., only appeared in A and D. The *Agaricus moelleri* Wasser, *Gymnopus dryophilus* (Bull.) Murrill, *Pluteus leoninus* (Schaeff.) P. Kumm., and *Rhodocollybia butyracea* (Bull.) Lennox only appeared in A and C.

The species richness increased from E < C < D < B < A (Table 4). Broad-leaved forests A and B, with the highest richness indices of 7.4023 and 5.4832, respectively, accounted for 80.57% of the total species. Among them, 142 species were found in forest type A, accounting for 50.18% of the total species. This indicates that the broadleaf forest was the main habitat of macrofungi in the area, especially regarding the *Q. mongolica* forest. Mixed forests C and D, with richness indices of 2.8296 and 4.6509, contained 84 species, accounting for 29.68% of the total species. However, we found that the species abundance was higher in forest type D (49 species) than in forest type C (35 species), indicating that macrofungal species are associated with *Q. mongolica*. In *P. koraiensis* forest E, with the smallest species richness index of 2.286, we only found 18 species, accounting for 6.36% of the total species. This indicates that *P. koraiensis* forests can only provide habitats for a few fungal species.

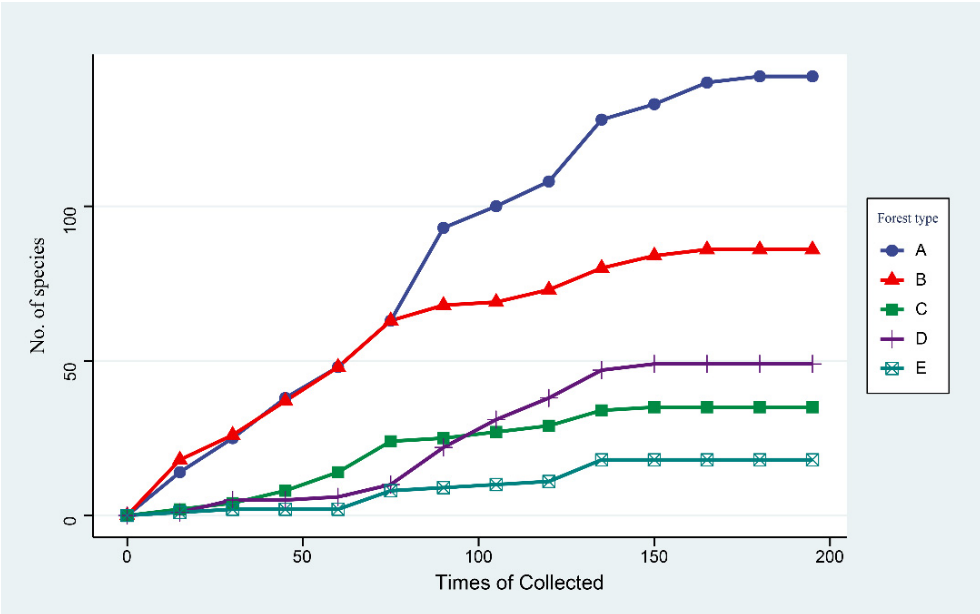

Figure 5. Sample-based rarefaction curves (n = 195 observations per forest type within 3 years). (**A**): *Q. mongolica* forest; (**B**): broad-leaved forest; (**C**): *P. koraiensis* and *Q. mongolica* mixed forest with *P. koraiensis* being the dominant species; (**D**): *P. koraiensis* and *Q. mongolica* mixed forest with *Q. mongolica* being the dominant species; (**E**): *P. koraiensis* forest.

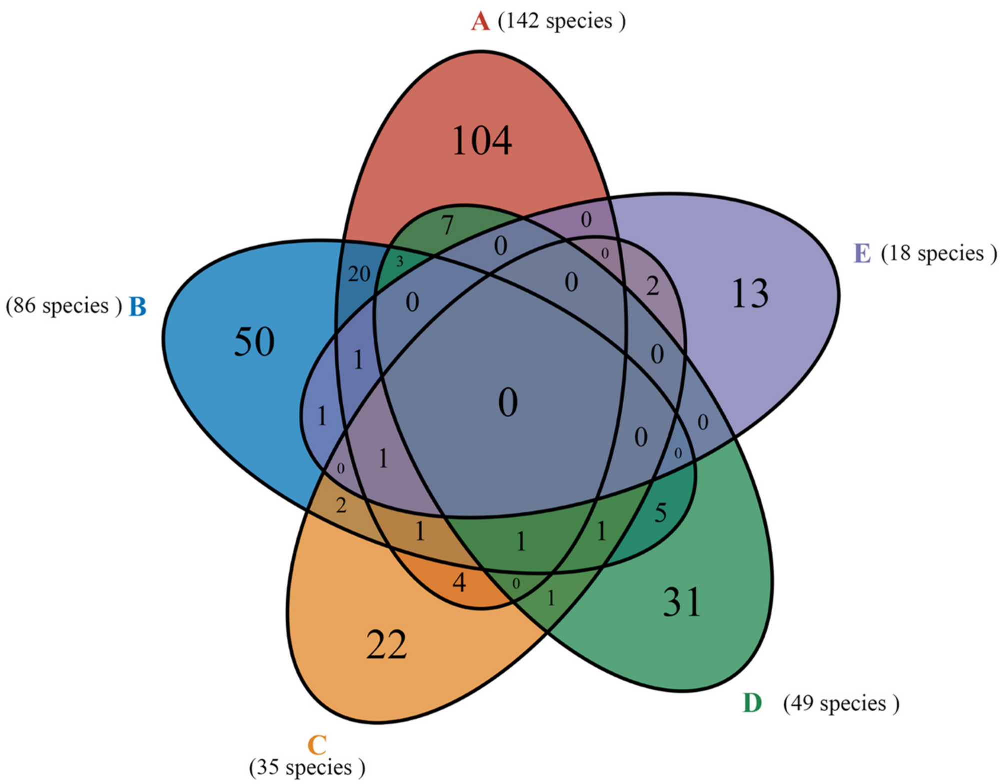

Figure 6. A Venn diagram of 283 fungal species shows shared and unique fungi for the five forest types. The numbers in parentheses are the values of all observed fungi in each forest type studied (cumulative species richness).

Table 4. Diversity indices of macrofungi in five forest types.

Forest Type	Number of Species	Number of Collections	Richness Index	Diversity Index	Evenness Index
			R	D	E
A	142	368	7.4023	4.7296	0.9543
B	86	246	5.4832	4.207	0.9445
C	35	153	2.8296	3.2048	0.9014
D	49	111	4.6509	3.7074	0.9526
E	18	62	2.286	2.6146	0.9046

Note: Abbreviations: A = *Q. mongolica* forest; B = Broad-leaved forest; C = *P, koraiensis* and *Q. mongolica* mixed forest, with *P. koraiensis* as the dominant species; D = *P. koraiensis* and *Q. mongolica* mixed forest, with *Q. mongolica* as the dominant species; E = *P. koraiensis* forest. The number of collections is the cumulative number of fruiting bodies per species.

3.6. Functional Diversity of Macrofungal Communities

The main functional groups were ectomycorrhizal fungi (EM), wood-decaying fungi (WS), and soil saprotroph (SS). The EM (133 species, 47.0%), WS (57 species, 20.14%), SS (52 species, 18.37%), and LS (38 species, 13.43%) increased from coniferous forest (E) < mixed coniferous forest (C, D) < broadleaf forest (A, B). EM fungi were most abundant in forest type A (Table 5). The highest content of EM fungi was *Amanita*, *Cortinarius*, *Lactarius,* and *Russula*. The most common WS were *Pleurotus* and *Polyporus*. The highest occurrence of SS was *Agaricus*, *Entoloma,* and *Hygrocybe*. The LS, *Clitocybe*, *Gymnopus*, *Mycena,* and *Pluteus*, showed the highest occurrence.

Table 5. Cumulative species richness of functional groups in five forest types.

Forest Type	Trophic Groups					
	EM (133)	WS (57)	SS (52)	LS (38)	EI (2)	DS (1)
A	71	26	25	20	1	0
B	27	28	18	11	0	1
C	13	3	9	10	0	0
D	36	5	2	6	0	0
E	10	2	2	4	0	0

Note: Abbreviations: EM = Ectomycorrhizal fungi; WS = Wood-decaying fungi; SS = Soil saprotroph; LS = Litter saprotroph; EI = Endophyte-insect pathogen; DS = Dung saprotroph. Values shown are the cumulative number of macrofungal functional groups in each forest type.

3.7. CCA Analysis of Macrofungal Communities and Selected Environmental Factors

We performed a canonical correspondence analysis (CCA) for the 130 ectomycorrhizal fungi (EM) species recorded in the 5 forest types. The variables included *Q. mongolica* content, effective soil nitrogen, soil available phosphorus, soil available potassium, soil organic matter, soil pH, soil temperature, air temperature, soil water content, effective soil nitrogen, and air relative humidity. The CCA results show that all samples were roughly separated into five groups according to their corresponding locations. Eigenvalue axis 1 (0.8963) is higher than axis 2 (0.7955), with a cumulative contribution of 28.8% and 25.57%, respectively. Of all the variables, the *Q. mongolica* content and soil moisture content were the most significant factors influencing the EM fungi. Many EM fungi (e.g., *Amanita*, *Cortinarius*, *Lactarius*) positively correlate with *Q. mongolica* and soil water (Figure 7).

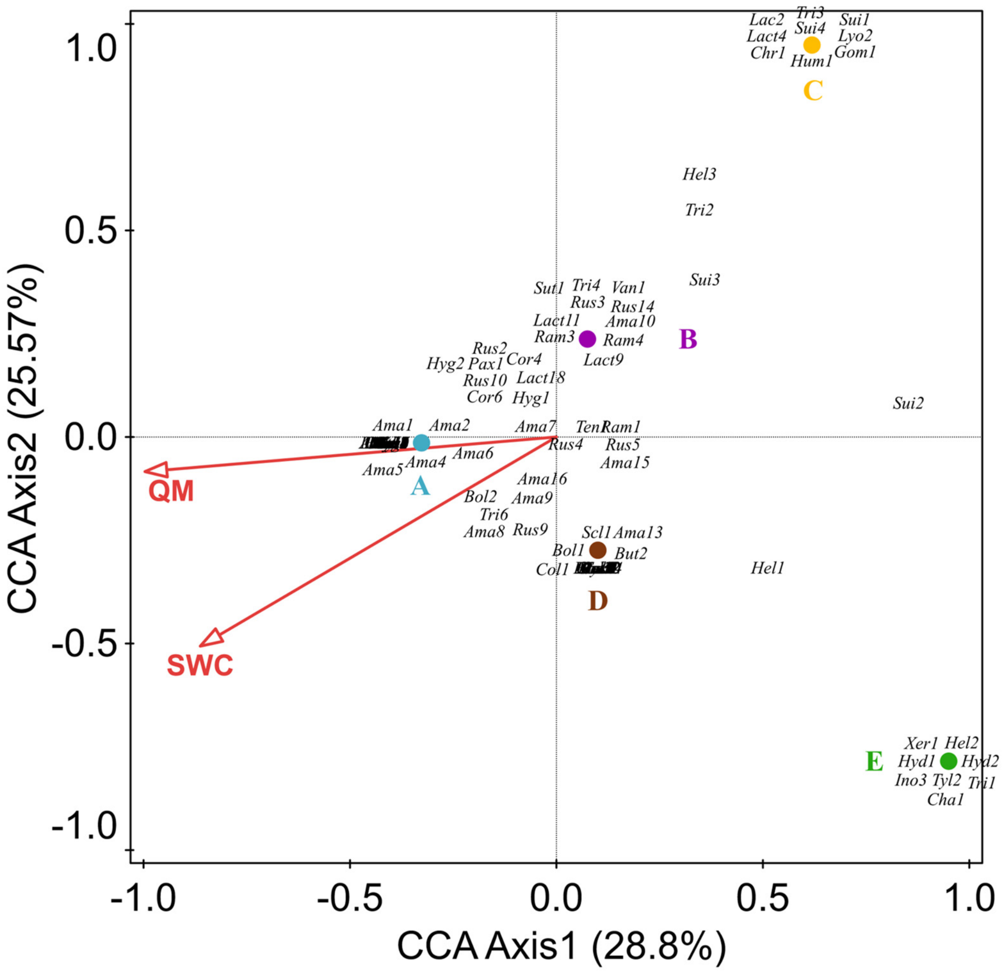

Figure 7. Canonical correspondence analysis (CCA) of selected variables and the ectomycorrhizal fungi species (dominant group). All displayed variables passed the most significant test ($p < 0.05$); QM: the number of *Q. mongolica*; SWC: soil water content; (**A**): *Q. mongolica* forest; (**B**): Broad–leaved forest; (**C**): *P. koraiensis* and *Q. mongolica* mixed forest with *P. koraiensis* being the dominant species; (**D**): *P. koraiensis* and *Q. mongolica* mixed forest with *Q. mongolica* being the dominant species; (**E**): *P. koraiensis* forest. Letters are composed of the first three–letter abbreviations of the scientific name of the species and a number, and the corresponding names are provided in Appendix C. Some species' labels are overlapping. See Appendix C.

4. Discussion

This study is the first systematic survey of macrofungal diversity in Wunvfeng National Forest Park, Ji'an, China. We divided the forests into five main types: *Q. mongolica* forests (A), mixed broad-leaved forests (B), artificial *P. koraiensis* forests (E), and mixed forests (C, D). This enabled us to analyze the composition of macrofungi according to the relative content change of *Q. mongolica* in different forest types. The results show differences in species richness and diversity among forest types with different relative contents of *Q. mongolica*. The species richness increases with the relative content of *Q. mongolica*. Forest types with a high cover of *Q. mongolica* may provide a stable environment for the growth of macrofungi [47]. More importantly, *Quercus* is the main host plant of EM fungi [48], such as *Lactarius* [49,50], *Amanita* [51], *Russula* [52], and *Cortinarius* [53]. Our results reveal that the EM fungi are mainly distributed in the *Q. mongolica* forest. Most EM fungi had a significant positive correlation with *Q. mongolica* content (Figure 7), especially *Amanita*, *Cortinarius*, and *Lactarius*. In addition, we found that 11 species are shared in forest types A and D (e.g., *Amanita ibotengutake* T. Oda, C. Tanaka & Tsuda, *Amanita oberwinklerana* Zhu L. Yang & Yoshim, *Amanita orsonii* Ash. Kumar & T.N. Lakh., and *Amanita virosa* Bertill).

However, they are not found in the *P. koraiensis* forest. These species may be associated with *Q. mongolica* (Figure 7, Ama7, Ama8, Ama9, Ama16), because the macrofungal communities change accordingly with the forest's succession [54]. Therefore, these macrofungi shared in forest types D and A are likely to be in the early stages that develop from spore banks present in the soil [55].

The species richness of *P. koraiensis* forests is the lowest in our study. We only found 18 species. Theoretically, species richness may be similar between *Q. mongolica* and *P. koraiensis* forests because the EM fungi in temperate forests are significantly associated with *Quercus* and *Pinus* [56]. However, we only observed ten species of EM fungi in *P. koraiensis* forest (E) (e.g., *Hydnellum aurantiacum* (Batsch) P. Karst., *Hydnellum peckii* Banker, and *Tricholoma matsutake* (S. Ito & S. Imai) Singer). Our results differ from those of Gao [57], who found more EM fungi in *P. koraiensis* forests (aged < 150 years). On the one hand, EM fungi may need more time to form a stable symbiosis with the host plants [58]; on the other hand, the exotic trees have difficulty developing long-lasting symbiotic relationships with local EM fungi [59].

In our study, wood-dwelling fungi (57 species) are also a critical taxon that is mainly distributed in the *Q. mongolica* and mixed broad-leaved forests and grows on larger diameter *Q. mongolica* fallen wood (e.g., *Armillaria gallica* Marxm. & Romagn. and *Neolentinus cyathiformis* (Schaeff.) Della Magg. & Trassin). The wood-dwelling macrofungi may be related to forest type, as they tend to favor specific forest types under similar climatic conditions. In general, these combinations are determined by fungi closely related to the dominant tree, mainly because their enzymes have adapted to wood with different chemical and physical properties [60]. Another reason may be that large logs that provide a larger surface area have a greater chance of being colonized by fungal spores and mycelium than small logs. Species that produce large fruiting bodies also require more space [61]. Furthermore, we only found a few fallen trees in the *Q. mongolica* and mixed broadleaved forests; we found no fallen trees in the *P. koraiensis* forest, which is another factor that might affect fungal assemblage. The amount of deadwood also affects the macrofungal assemblage, which previous authors highlighted as the most crucial microhabitat in the forest [62,63]. The diversity of woody macrofungi strongly depends on the presence and amount of deadwood [64,65].

Saprophytic soil fungi (52 species) rely mainly on the decomposition of soil organic matter for nutrients, and they tend to prefer specific forest types under similar climatic conditions. Generally, the deciduous leaves of broad-leaved trees are more conducive to soil organic matter accumulation than coniferous forests [66]. The forest types with high soil organic matter have more opportunities to be colonized by fungal spores and mycelium [67]. Moreover, we only found thicker deciduous leaves in the *Q. mongolica* and mixed broad-leaved forests, affecting the grass rot fungal assemblage because litter saprotroph fungi strongly depend on deciduous leaves' presence and volume [68].

The composition of fungi is also influenced and constrained by soil environmental variables [69,70]. These include soil moisture [71], soil pH [72], soil nutrients [73] and soil total C [74]. We analyzed the correlation between the main functional groups (ectomycorrhizal fungi) and selected environmental factors. The results showed that most ectomycorrhizal fungi are closely related to soil water content, especially *Amanita*, *Cortinarius*, *Lactarius*, and *Russula* (Figure 7). This result suggests that specific fungal communities respond to soil parameters differently [75–77]. Previous studies have shown that soil moisture is one factor that regulates the composition of the ectomycorrhizal fungi community [78–81]. Hydraulic lift contributes to maintaining EM fungi roots' integrity and viability of extraradical hyphae [82]; further, EM fungi take up water and organic and inorganic nutrients from the soil via the extraradical hyphae and translocate these to colonized tree roots, receiving carbohydrates from the host in return [83]. This may be an important reason why most ectomycorrhizal fungi prefer forest types with relatively high soil water content.

This study with three years of species data is a small contribution that allows us to understand the distribution of fungal species in forest types with the different covers of *Q. mongolica*. The Wunvfeng National Forest Park has a strict protection policy for animals and plants, including soil protection. Thus, our soil data (with permission) are from July to September 2020 only. Nevertheless, our results illuminate the potential links between community composition and environmental factors because the July–September 2020 species data include almost all our species.

5. Conclusions

The *Q. mongolica* forests we analyzed are rich in macrofungal species. Although our data are based on only three years of sampling, we conclude that, as *Q. mongolica* increases in the forest, the abundance and diversity of macrofungal taxa also increase. We also observed that most EM species favored forest types with high *Q. mongolica* content (e.g., *Amanita*, *Cortinarius*, *Lactarius*, and *Russula*), indicating that some EM fungal communities are closely associated with *Q. mongolica*. We call for further studies to support this claim. In addition, we have only found *Tricholoma matsutake* (S. Ito & S. Imai) Singer in *P. koraiensis* forests, which is classified as an endangered species and considered an ectomycorrhizal fungus that is closely associated with *Pinus* trees. Therefore, according to our research, maintaining *P. koraiensis* forests is beneficial for conserving endangered species. However, deliberate conservation of *Q. mongolica* forests would be more useful for maintaining the diversity of macrofungal communities. Whether *P. koraiensis* affects other fungal species will need to be monitored over 3–5 years.

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Data Availability Statement: Not applicable.

Conflicts of Interest: The authors state no conflict of interest.

Appendix A. Photos of Some Species

Larger Ascomycetes.

Figure A1. (**A**) *Leotia lubrica*; (**B**) *Helvella elastica*; (**C**) *Sowerbyella rhenana*; (**D**) *Spathularia flavida*; (**E**) *Ophiocordyceps nutans*; (**F**) *Xylaria hypoxylon*; Bars: 1 cm.

Coral fungi.

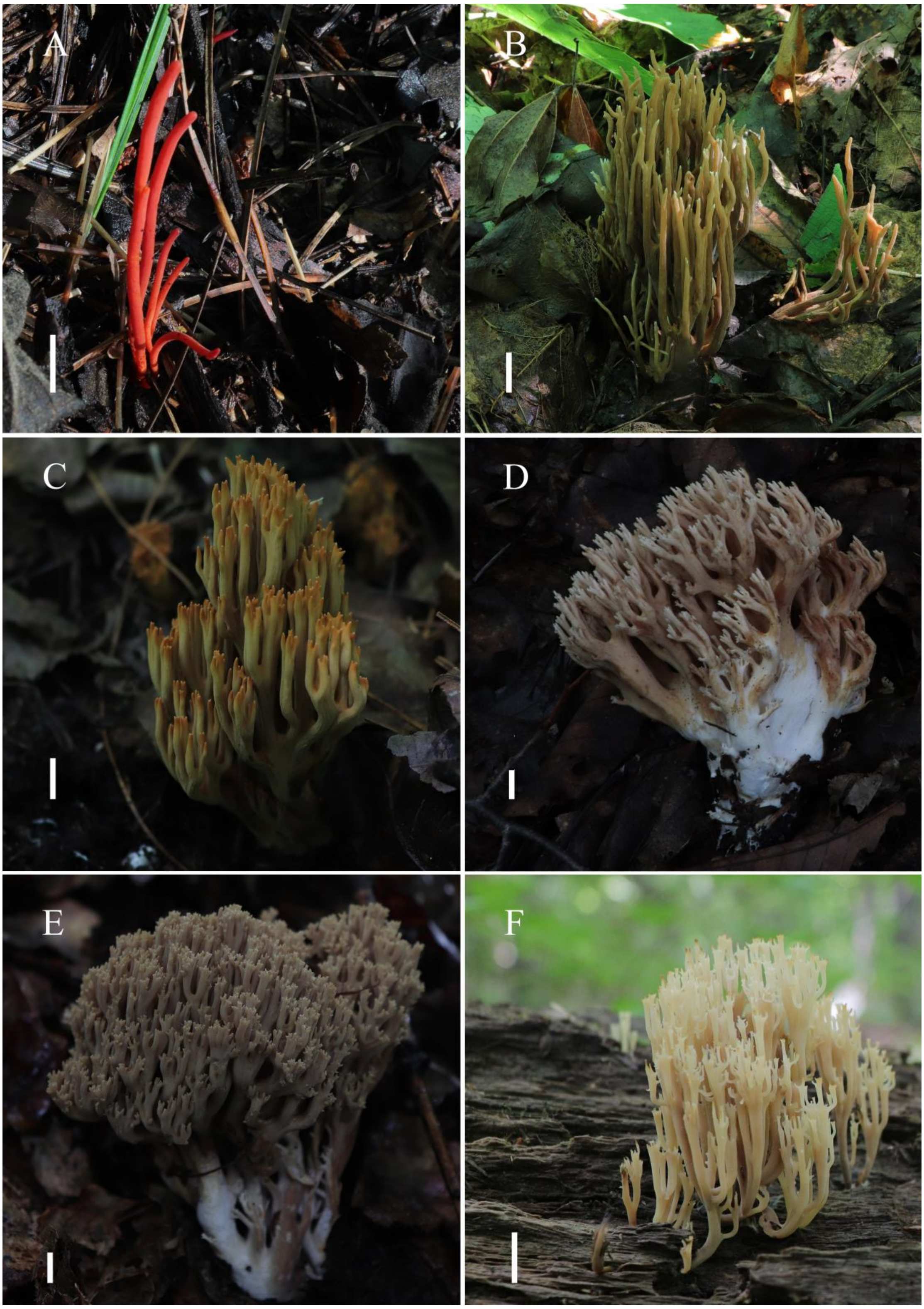

Figure A2. (**A**) *Clavulinopsis sulcata*; (**B**) *Ramaria stricta*; (**C**) *R. cokeri*; (**D**) *R. sanguinipes*; (**E**) *R. fennica*; (**F**) *Artomyces pyxidatus*; Bars: 1 cm.

Agarics.

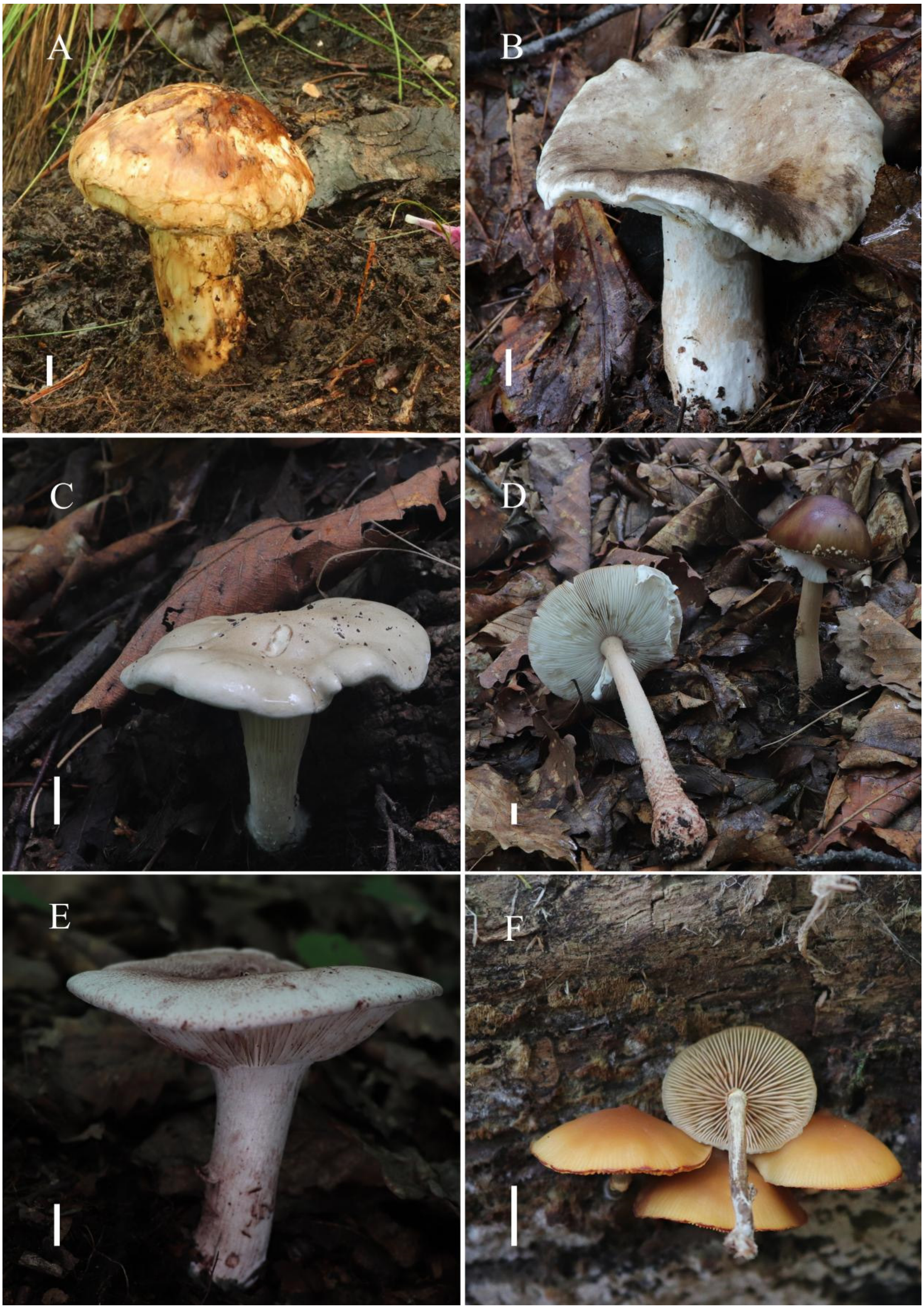

Figure A3. (**A**) *Tricholoma matsutake*; (**B**) *Russula furcata*; (**C**) *Clitocybe fasciculata*; (**D**) *Amanita orsonii*; (**E**) *Hygrophorus russula*; (**F**) *Galerina marginata*; Bars: 1 cm.

Boletes.

Figure A4. (**A**) *Pulveroboletus macrosporus*; (**B**) *Tylopilus felleus*; (**C**) *Boletus edulis*; (**D**) *Chalciporus piperatus*; (**E**) *Butyriboletus roseoflavus*; (**F**) *Suillus grevillei*; Bars: 1 cm.

Polyporoid fungi.

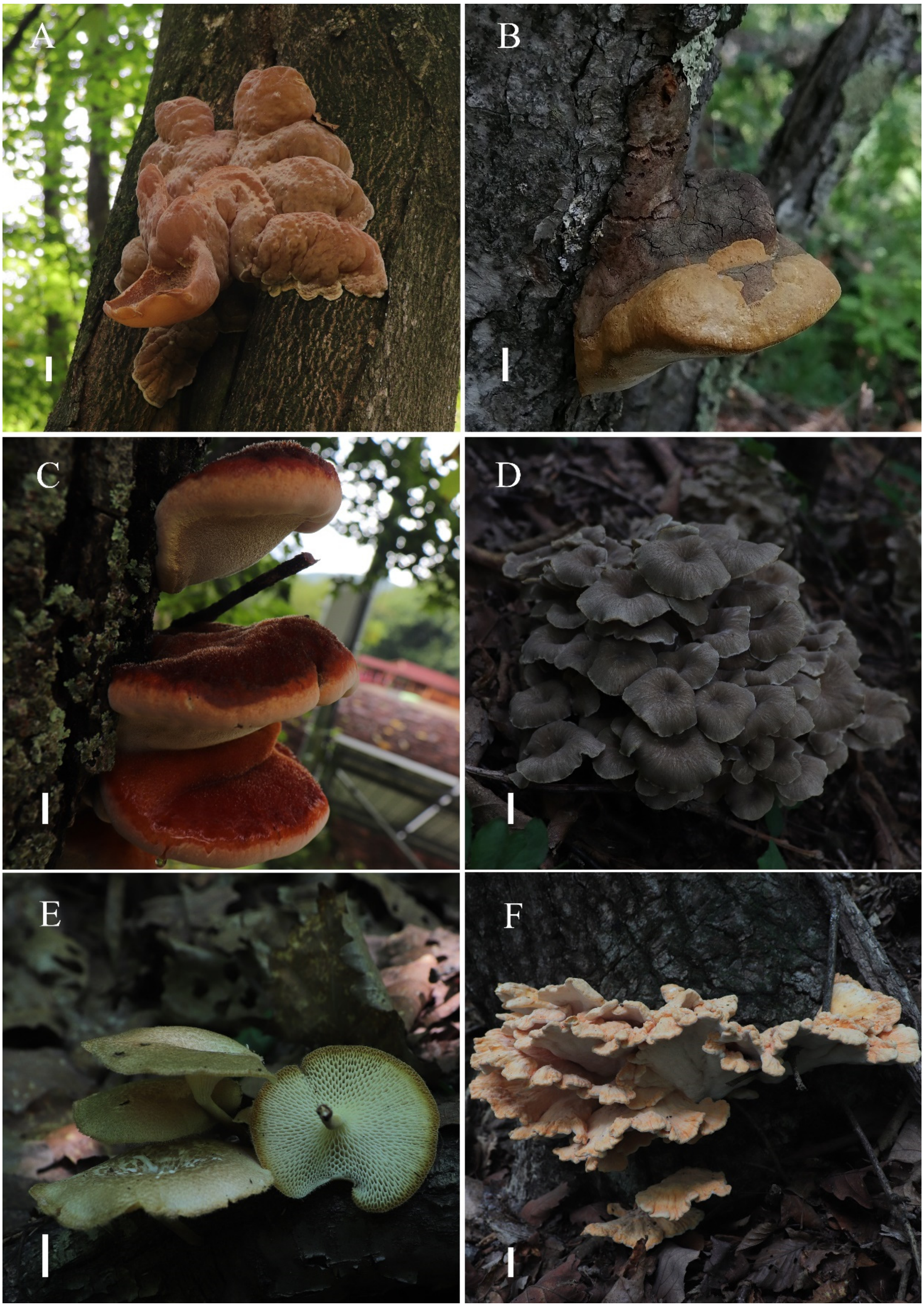

Figure A5. (**A**) *Gloeostereum incarnatum*; (**B**) *Phellinus pomaceus*; (**C**) *Inonotus hispidus*; (**D**) *Polyporus umbellatus*; (**E**) *Lentinus arcularius*; (**F**) *Laetiporus sulphureus*; Bars: 1 cm.

Jelly fungi and *Hydnaceous fungi*.

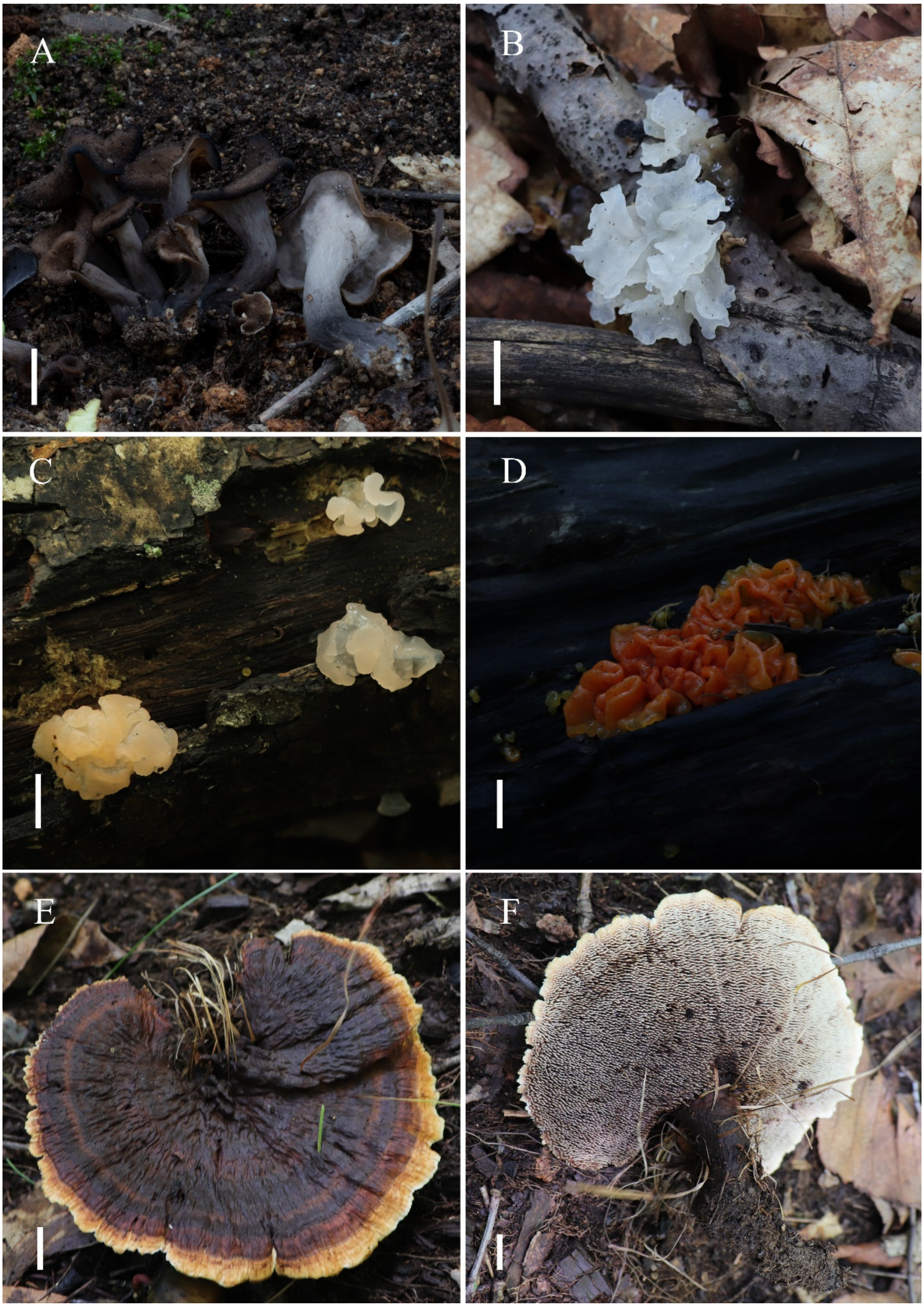

Figure A6. (**A**) *Craterellus cornucopioides*; (**B**) *Tremella fuciformis*; (**C**) *Dacrymyces yunnanensis*; (**D**) *D. chrysospermus*; (**E**,**F**) *Hydnellum aurantiacum*; Bars: 1 cm.

Appendix B. Macrofungi were collected in five forest types of Wunvfeng National Forest Park

Species	Family	Genera	A	B	C	D	E	F	N	ML	Categories	SN	GenBank Number
Agaricus arvensis Schaeff.	*Agaricaceae*	*Agaricus*	√						4	SS	Agarics	HMJAU60588	
Agaricus dulcidulus Schulzer	*Agaricaceae*	*Agaricus*	√						2	SS	Agarics	HMJAU60589	
Agaricus moelleri Wasser	*Agaricaceae*	*Agaricus*	√		√				3	SS	Agarics	HMJAU60590	
Agaricus placomyces Peck	*Agaricaceae*	*Agaricus*					√		1	SS	Agarics	HMJAU60591	
Agaricus semotus Fr.	*Agaricaceae*	*Agaricus*						√	2	SS	Agarics	HMJAU60592	
Agaricus subrufescens Peck	*Agaricaceae*	*Agaricus*	√						1	SS	Agarics	HMJAU60593	
Agrocybe arvalis (Fr.) Singer	*Strophariaceae*	*Agrocybe*		√					3	SS	Agarics	HMJAU60594	
Agrocybe erebia (Fr.) Kühner ex Singe	*Strophariaceae*	*Agrocybe*						√	2	SS	Agarics	HMJAU60595	
Agrocybe praecox (Pers.) Fayod	*Strophariaceae*	*Agrocybe*	√	√	√				6	SS	Agarics	HMJAU60596	
Amanita altipes Zhu L. Yang, M. Weiss & Oberw.	*Amanitaceae*	*Amanita*	√						1	EM	Agarics	HMJAU60597	
Amanita chepangiana Tulloss & Bhandary	*Amanitaceae*	*Amanita*	√						1	EM	Agarics	HMJAU60598	
Amanita excelsa (Fr.) Bertill.	*Amanitaceae*	*Amanita*				√			1	EM	Agarics	HMJAU60599	
Amanita flavipes S. Imai	*Amanitaceae*	*Amanita*	√						2	EM	Agarics	HMJAU60600	
Amanita fuliginea Hongo	*Amanitaceae*	*Amanita*	√						2	EM	Agarics	HMJAU60601	
Amanita hemibapha (Berk. & Broome) Sacc.	*Amanitaceae*	*Amanita*	√						2	EM	Agarics	HMJAU60602	
Amanita ibotengutake T. Oda, C. Tanaka & Tsuda	*Amanitaceae*	*Amanita*	√	√		√			6	EM	Agarics	HMJAU60603	
Amanita oberwinklerana Zhu L. Yang & Yoshim.	*Amanitaceae*	*Amanita*	√			√			3	EM	Agarics	HMJAU60604	
Amanita orsonii Ash. Kumar & T.N. Lakh.	*Amanitaceae*	*Amanita*	√			√			5	EM	Agarics	HMJAU60605	
Amanita pallidocarnea (Höhn.) Boedijn	*Amanitaceae*	*Amanita*		√					2	EM	Agarics	HMJAU60606	
Amanita pallidorosea P. Zhang & Zhu L. Yang	*Amanitaceae*	*Amanita*	√						2	EM	Agarics	HMJAU60607	
Amanita rimosa P. Zhang & Zhu L.	*Amanitaceae*	*Amanita*	√						1	EM	Agarics	HMJAU60608	
Amanita rubescens Pers.	*Amanitaceae*	*Amanita*				√			2	EM	Agarics	HMJAU60609	
Amanita subglobosa Zhu L. Yang	*Amanitaceae*	*Amanita*	√						1	EM	Agarics	HMJAU60610	
Amanita vaginata (Bull.) Lam.	*Amanitaceae*	*Amanita*		√		√			3	EM	Agarics	HMJAU60611	

Species	Family	Genera	A	B	C	D	E	F	N	ML	Categories	SN	GenBank Number
Amanita virosa Secr.	*Amanitaceae*	*Amanita*	√			√			4	EM	Agarics	HMJAU60612	
Ampulloclitocybe clavipes (Pers.) Redhead, Lutzoni, Moncalvo & Vilgalys	*Hygrophoraceae*	*Ampulloclitocybe*	√						4	LS	Agarics	HMJAU60613	
Armillaria gallica Marxm. & Romagn.	*Physalacriaceae*	*Armillaria*	√	√		√			15	WS	Agarics	HMJAU60614	OL891486
Armillaria mellea (Vahl) P. Kumm.	*Physalacriaceae*	*Armillaria*	√						1	WS	Agarics	HMJAU60615	
Artomyces pyxidatus (Pers.) Jülich	*Auriscalpiaceae*	*Artomyces*	√	√					7	WS	Coral fungi	HMJAU60616	
Bjerkandera adusta (Willd.) P. Karst.	*Phanerochaetaceae*	*Bjerkandera*		√					1	WS	Polyporoid fungi	HMJAU60617	
Boletus aereus Bull.	*Boletaceae*	*Boletus*				√			2	EM	Boletes	HMJAU60618	
Boletus edulis Bull.	*Boletaceae*	*Boletus*	√			√			4	EM	Boletes	HMJAU60619	
Bothia castanella (Peck) Halling, T.J. Baroni & Manfr. Binder	*Boletaceae*	*Bothia*	√						2	EM	Boletes	HMJAU60620	
Bulgaria inquinans (Pers.) Fr.	*Phacidiaceae*	*Bulgaria*	√						1	WS	Larger Ascomytetes	HMJAU60621	
Butyriboletus regius D. Arora & J.L. Frank	*Boletaceae*	*Butyriboletus*	√						2	EM	Boletes	HMJAU60622	OL891490
Butyriboletus roseoflavus (Hai B. Li & Hai L. Wei) D. Arora & J.L. Frank	*Boletaceae*	*Butyriboletus*				√			3	EM	Boletes	HMJAU60623	OL891497
Calocybe persicolor (Fr.) Singer	*Lyophyllaceae*	*Calocybe*			√				3	SS	Agarics	HMJAU60624	
Chalciporus piperatus (Bull.) Bataille	*Boletaceae*	*Chalciporus*					√		1	EM	Boletes	HMJAU60625	
Chroogomphus helveticus (Singer) M.M. Moser	*Gomphidiaceae*	*Chroogomphus*			√				4	EM	Agarics	HMJAU60626	OL891485
Clavaria fragilis Holmsk.	*Clavariaceae*	*Clavaria*			√				1	SS	Coral fungi	HMJAU60627	
Clavulinopsis corniculata (Schaeff.) Corner	*Clavariaceae*	*Clavulinopsis*	√						1	SS	Coral fungi	HMJAU60628	
Clavulinopsis sulcata Overeem	*Clavariaceae*	*Clavulinopsis*					√		10	SS	Coral fungi	HMJAU60629	

Species	Family	Genera	A	B	C	D	E	F	N	ML	Categories	SN	GenBank Number
Clitocybe fasciculata H.E. Bigelow & A.H. Sm.	*Tricholomataceae*	*Clitocybe*	√	√	√	√			2	LS	Agarics	HMJAU60630	
Clitocybe geotropa (Bull.) Quél.	*Tricholomataceae*	*Clitocybe*						√	1	LS	Agarics	HMJAU60631	
Clitocybe gibba (Pers.) P. Kumm.	*Tricholomataceae*	*Clitocybe*						√	4	LS	Agarics	HMJAU60632	
Clitocybe odora (Bull.) P. Kumm.	*Tricholomataceae*	*Clitocybe*	√						1	LS	Agarics	HMJAU60633	
Clitocybe subditopoda Peck	*Tricholomataceae*	*Clitocybe*	√	√			√		10	LS	Agarics	HMJAU60634	
Coltricia crassa Y.C. Dai	*Hymenochaetaceae*	*Coltricia*				√			2	EM	Polyporoid fungi	HMJAU60635	
Coltricia strigosipes Corner	*Hymenochaetaceae*	*Coltricia*	√						1	EM	Polyporoid fungi	HMJAU60636	
Coprinellus disseminatus (Pers.) J.E. Lange	*Psathyrellaceae*	*Coprinellus*		√					8	SS	Agarics	HMJAU60637	
Coprinellus radians (Desm.) Vilgalys, Hopple & Jacq. Johnson	*Psathyrellaceae*	*Coprinellus*	√						5	SS	Agarics	HMJAU60638	
Coprinus comatus (O.F. Müll.) Pers.	*Agaricaceae*	*Coprinus*		√					1	DS	Agarics	HMJAU60639	
Cordyceps militaris Cordyceps militaris (L.) *Fr.*	*Cordycipitaceae*	*Cordyceps*						√	3	EI	Larger Ascomytetes	HMJAU60640	
Cortinarius anomalus (Fr.) Fr.	*Cortinariaceae*	*Cortinarius*				√			2	EM	Agarics	HMJAU60641	OL891464
Cortinarius armillatus (Fr.) Fr.	*Cortinariaceae*	*Cortinarius*	√						4	EM	Agarics	HMJAU60642	OL891465
Cortinarius balaustinus Fr.	*Cortinariaceae*	*Cortinarius*	√						3	EM	Agarics	HMJAU60643	
Cortinarius bivelus (Fr.) Fr.	*Cortinariaceae*	*Cortinarius*	√	√					5	EM	Agarics	HMJAU60644	OL891467
Cortinarius caperatus (Pers.) Fr.	*Cortinariaceae*	*Cortinarius*	√						1	EM	Agarics	HMJAU60645	OL891466
Cortinarius cotoneus Fr.	*Cortinariaceae*	*Cortinarius*	√	√					3	EM	Agarics	HMJAU60646	OL891468
Cortinarius ectypus J. Favre	*Cortinariaceae*	*Cortinarius*	√						2	EM	Agarics	HMJAU60647	
Cortinarius flammeouraceus Niskanen, Kytov., Liimat., Ammirati & Dima	*Cortinariaceae*	*Cortinarius*	√						4	EM	Agarics	HMJAU60648	OL891470
Cortinarius hesleri Ammirati, Niskanen, Liimat. & Matheny	*Cortinariaceae*	*Cortinarius*	√						1	EM	Agarics	HMJAU60649	

Species	Family	Genera	A	B	C	D	E	F	N	ML	Categories	SN	GenBank Number
Cortinarius pholideus (Lilj.) Fr.	*Cortinariaceae*	*Cortinarius*				√			3	EM	Agarics	HMJAU60650	OL891469
Cortinarius sanguineus (Wulfen) Gray	*Cortinariaceae*	*Cortinarius*				√			2	EM	Agarics	HMJAU60651	
Cortinarius subbalaustinus Rob. Henry	*Cortinariaceae*	*Cortinarius*	√						1	EM	Agarics	HMJAU60652	
Cortinarius torvus (Fr.) Fr.	*Cortinariaceae*	*Cortinarius*	√						1	EM	Agarics	HMJAU60653	
Cotylidia diaphana (Cooke) Lentz	*Rickenellaceae*	*Cotylidia*			√				4	SS	Jelly fungi	HMJAU60654	
Craterellus cornucopioides (L.) Pers.	*Hydnaceae*	*Craterellus*	√						1	EM	Cantharelloid	HMJAU60655	
Crepidotus applanatus (Pers.) P. Kumm.	*Crepidotaceae*	*Crepidotus*				√			1	WS	Agarics	HMJAU60656	
Crepidotus malachius Sacc.	*Crepidotaceae*	*Crepidotus*		√					5	WS	Agarics	HMJAU60657	
Cyclocybe erebia (Fr.) Vizzini & Matheny	*Tubariaceae*	*Cyclocybe*	√						2	SS	Agarics	HMJAU60658	
Cystoderma granulosum (Batsch) Fayod	*Agaricaceae*	*Cystoderma*	√						4	SS	Agarics	HMJAU60659	
Dacrymyces chrysospermus Berk. & M.A. Curtis	*Dacrymycetaceae*	*Dacrymyces*	√						3	WS	Jelly fungi	HMJAU60660	
Dacrymyces yunnanensis B. Liu & L. Fan	*Dacrymycetaceae*	*Dacrymyces*	√	√					6	WS	Jelly fungi	HMJAU60661	
Daldinia concentrica (Bolton) Ces. & De Not.	*Hypoxylaceae*	*Daldinia*		√					5	WS	Larger Ascomytetes	HMJAU60662	
Elmerina cladophora (Berk.) Bres.	*Auriculariaceae*	*Elmerina*	√	√					3	WS	Polyporoid fungi	HMJAU60663	
Elmerina hispida (Imazeki) Y.C. Dai & L.W. Zhou	*Auriculariaceae*	*Elmerina*				√			1	WS	Polyporoid fungi	HMJAU60664	
Entoloma abortivum (Berk. & M.A. Curtis) Donk	*Entolomataceae*	*Entoloma*		√					2	SS	Agarics	HMJAU60665	
Entoloma alboumbonatum Hesler	*Entolomataceae*	*Entoloma*				√			2	SS	Agarics	HMJAU60666	
Entoloma caespitosum W.M. Zhang	*Entolomataceae*	*Entoloma*		√					5	SS	Agarics	HMJAU60667	
Entoloma clypeatum (L.) P. Kumm.	*Entolomataceae*	*Entoloma*	√						4	SS	Agarics	HMJAU60668	
Entoloma holoconiotum (Largent & Thiers) Noordel. & Co-David	*Entolomataceae*	*Entoloma*		√					4	SS	Agarics	HMJAU60669	
Entoloma mediterraneense Noordel. & Hauskn.	*Entolomataceae*	*Entoloma*	√						1	SS	Agarics	HMJAU60670	
Entoloma rhodopolium (Fr.) P. Kumm.	*Entolomataceae*	*Entoloma*	√						2	SS	Agarics	HMJAU60671	

Species	Family	Genera	A	B	C	D	E	F	N	ML	Categories	SN	GenBank Number
Entonaema liquescens Möller	*Hypoxylaceae*	*Entonaema*		√					3	WS	Larger Ascomytetes	HMJAU60672	
Favolus squamosus (Huds.) A. Ames	*Polyporaceae*	*Favolus*	√						1	WS	Polyporoid fungi	HMJAU60673	
Flammulaster erinaceellus (Peck) Watling	*Tubariaceae*	*Flammulaster*		√					6	WS	Agarics	HMJAU60674	
Galerina helvoliceps (Berk. & M.A. Curtis) Singe	*Hymenogastraceae*	*Galerina*	√						4	WS	Agarics	HMJAU60675	
Galerina marginata (Batsch) Kühner	*Hymenogastraceae*	*Galerina*		√					4	WS	Agarics	HMJAU60676	
Geastrum triplex Jungh.	*Geastraceae*	*Geastrum*	√						1	LS	Gasteroid fungi	HMJAU60677	
Gerhardtia borealis (Fr.) Contu & A. Ortega	*Lyophyllaceae*	*Gerhardtia*				√			3	SS	Agarics	HMJAU60678	
Gerronema nemorale Har. Takah.	*Marasmiaceae*	*Gerronema*	√						1	WS	Agarics	HMJAU60679	
Gloeostereum incarnatum S. Ito & S. Imai	*Cyphellaceae*	*Gloeostereum*		√					4	WS	Polyporoid fungi	HMJAU60680	
Gomphidius maculatus (Scop.) Fr.	*Gomphidiaceae*	*Gomphidius*			√				2	EM	Cantharelloid	HMJAU60681	
Gymnopilus junonius (Fr.) P.D. Orton	*Hymenogastraceae*	*Gymnopilus*		√					3	WS	Agarics	HMJAU60682	
Gymnopilus penetrans (Fr.) Murrill	*Hymenogastraceae*	*Gymnopilus*		√					2	WS	Agarics	HMJAU60683	
Gymnopilus suberis (Maire) Singer	*Hymenogastraceae*	*Gymnopilus*		√					6	WS	Agarics	HMJAU60684	
Gymnopus alnicola J.L. Mata & Halling	*Omphalotaceae*	*Gymnopus*			√				4	LS	Agarics	HMJAU60685	
Gymnopus confluens (Pers.) Antonín, Halling & Noordel.	*Omphalotaceae*	*Gymnopus*			√		√		14	LS	Agarics	HMJAU60686	OL884222
Gymnopus densilamellatus Antonín, Ryoo & Ka	*Omphalotaceae*	*Gymnopus*	√	√	√		√		25	LS	Agarics	HMJAU60687	OL884223
Gymnopus dryophilus (Bull.) Murrill	*Omphalotaceae*	*Gymnopus*	√		√				30	LS	Agarics	HMJAU60688	OL891463
Gymnopus gibbosus (Corner) A.W. Wilson, Desjardin & E. Horak	*Omphalotaceae*	*Gymnopus*					√		7	LS	Agarics	HMJAU60689	OL884224
Gymnopus loiseleurietorum (M.M. Moser, Gerhold & Tobies) Antonín & Noordel.	*Omphalotaceae*	*Gymnopus*	√						7	LS	Agarics	HMJAU60690	

Species	Family	Genera	A	B	C	D	E	F	N	ML	Categories	SN	GenBank Number
Harrya chromapes (Frost) Halling, Nuhn, Osmundson & Manfr.	*Boletaceae*	*Harrya*	√						1	EM	Boletes	HMJAU60691	OL891492
Hebeloma birrus (Fr.) Gillet	*Hymenogastraceae*	*Hebeloma*	√						6	EM	Agarics	HMJAU60692	OL891483
Heliocybe sulcata (Berk.) Redhead & Ginns	*Gloeophyllaceae*	*Heliocybe*	√						2	WS	Agarics	HMJAU60693	
Helvella crispa (Scop.) Fr.	*Hydnaceae*	*Helvella*		√			√		2	EM	Larger Ascomytetes	HMJAU60694	
Helvella elastica Bull.	*Helvellaceae*	*Helvella*					√		1	EM	Larger Ascomytetes	HMJAU60695	
Helvella macropus (Pers.) P. Karst.	*Helvellaceae*	*Helvella*		√	√				3	EM	Larger Ascomytetes	HMJAU60696	
Hemistropharia albocrenulata (Peck) Jacobsson & E. Larss.	*Tubariaceae*	*Hemistropharia*		√					1	SS	Agarics	HMJAU60697	
Hericium erinaceus (Bull.) Pers.	*Hericiaceae*	*Hericium*		√					1	WS	Hydnaceous fungi	HMJAU60698	
Humaria hemisphaerica (F.H. Wigg.) Fuckel	*Pyronemataceae*	*Humaria*			√				1	EM	Larger Ascomytetes	HMJAU60699	
Hydnellum aurantiacum (Batsch) P. Karst.	*Bankeraceae*	*Hydnellum*					√		2	EM	Hydnaceous fungi	HMJAU60700	OL891471
Hydnellum peckii Banker	*Bankeraceae*	*Hydnellum*					√		2	EM	Hydnaceous fungi	HMJAU60701	OL891487
Hygrocybe cantharellus (Schwein.) Murrill	*Hygrophoraceae*	*Hygrocybe*	√						5	SS	Agarics	HMJAU60702	
Hygrocybe chlorophana (Fr.) Wünsche	*Hygrophoraceae*	*Hygrocybe*		√					5	SS	Agarics	HMJAU60703	
Hygrocybe coccinea (Schaeff.) P. Kumm.	*Hygrophoraceae*	*Hygrocybe*	√						4	SS	Agarics	HMJAU60704	
Hygrocybe coccineocrenata.D. Orton) M.M. Moser	*Hygrophoraceae*	*Hygrocybe*		√					5	SS	Agarics	HMJAU60705	
Hygrocybe miniata (Fr.) P. Kumm.	*Hygrophoraceae*	*Hygrocybe*	√						4	SS	Agarics	HMJAU60706	
Hygrocybe reidii Kühner	*Hygrophoraceae*	*Hygrocybe*		√					1	SS	Agarics	HMJAU60707	
Hygrophoropsis aurantiaca (Wulfen) Maire	*Hygrophoropsidaceae*	*Hygrophoropsis*	√	√					7	LS	Agarics	HMJAU60708	OL891484

Species	Family	Genera	A	B	C	D	E	F	N	ML	Categories	SN	GenBank Number
Hygrophorus conicus (Schaeff.) Fr.	*Hygrophoraceae*	*Hygrophorus*	√	√					6	EM	Agarics	HMJAU60709	
Hygrophorus nemoreus (Pers.) Fr.	*Hygrophoraceae*	*Hygrophorus*	√	√					9	EM	Agarics	HMJAU60710	
Hygrophorus pudorinus (Fr.) Fr.	*Hygrophoraceae*	*Hygrophorus*	√						1	EM	Agarics	HMJAU60711	
Hygrophorus russula (Schaeff. ex Fr.) Kauffman	*Hygrophoraceae*	*Hygrophorus*	√						2	EM	Agarics	HMJAU60712	
Hypholoma capnoides (Fr.) P. Kumm.	*Strophariaceae*	*Hypholoma*					√		2	WS	Agarics	HMJAU60713	
Hypholoma sublateritium (Fr.) Quél.	*Strophariaceae*	*Hypholoma*	√						4	WS	Agarics	HMJAU60714	
Infundibulicybe geotropa (Bull.) Harmaja	*Tricholomataceae*	*Infundibulicybe*		√					2	SS	Agarics	HMJAU60715	
Infundibulicybe gibba (Pers.) Harmaja	*Tricholomataceae*	*Infundibulicybe*	√						2	SS	Agarics	HMJAU60716	
Inocybe assimilata Britzelm.	*Inocybaceae*	*Inocybe*	√						2	EM	Agarics	HMJAU60717	
Inocybe asterospora Quél.	*Inocybaceae*	*Inocybe*	√						1	EM	Agarics	HMJAU60718	
Inocybe suaveolens D.E. Stuntz	*Inocybaceae*	*Inocybe*					√		2	EM	Agarics	HMJAU60719	OL891472
Inonotus hispidus (Bull.) P. Karst.	*Hymenochaetaceae*	*Inonotus*		√					3	WS	Polyporoid fungi	HMJAU60720	
Laccaria amethystina Cooke	*Hydnangiaceae*	*Laccaria*				√			4	EM	Agarics	HMJAU60721	
Laccaria laccata (Scop.) Cooke	*Hydnangiaceae*	*Laccaria*			√				4	EM	Agarics	HMJAU60722	
Lactarius albidocinereus X.H. Wang, S.F. Shi & T. Bau	*Russulaceae*	*Lactarius*				√			2	EM	Agarics	HMJAU60723	OL891473
Lactarius brunneoviolascens Bon	*Russulaceae*	*Lactarius*	√						1	EM	Agarics	HMJAU60724	
Lactarius conglutinatus X.H. Wang	*Russulaceae*	*Lactarius*	√						6	EM	Agarics	HMJAU60725	
Lactarius deterrimus Gröger	*Russulaceae*	*Lactarius*			√				5	EM	Agarics	HMJAU60726	
Lactarius flavidus Boud.	*Russulaceae*	*Lactarius*	√						1	EM	Agarics	HMJAU60727	
Lactarius glyciosmus (Fr.) Fr.	*Russulaceae*	*Lactarius*	√						1	EM	Agarics	HMJAU60728	
Lactarius hirtipes J.Z. Ying	*Russulaceae*	*Lactarius*	√						3	EM	Agarics	HMJAU60729	
Lactarius lilacinus Fr.	*Russulaceae*	*Lactarius*	√						3	EM	Agarics	HMJAU60730	
Lactarius pallidus Pers.	*Russulaceae*	*Lactarius*		√					2	EM	Agarics	HMJAU60731	

Species	Family	Genera	A	B	C	D	E	F	N	ML	Categories	SN	GenBank Number
Lactarius piperatus (L.) Pers.	*Russulaceae*	*Lactarius*	√						1	EM	Agarics	HMJAU60732	
Lactarius proximellus Beardslee & Burl.	*Russulaceae*	*Lactarius*		√					1	EM	Agarics	HMJAU60733	
Lactarius pubescens Fr.	*Russulaceae*	*Lactarius*	√						1	EM	Agarics	HMJAU60734	
Lactarius subvellereus Peck	*Russulaceae*	*Lactarius*	√						2	EM	Agarics	HMJAU60735	
Lactarius torminosus (Schaeff.) Pers.	*Russulaceae*	*Lactarius*				√			2	EM	Agarics	HMJAU60736	
Lactarius trivialis (Fr.) Fr.	*Russulaceae*	*Lactarius*	√						1	EM	Agarics	HMJAU60737	OL891474
Lactarius vietus (Fr.) Fr.	*Russulaceae*	*Lactarius*	√						2	EM	Agarics	HMJAU60738	
Lactarius volemus (Fr.) Fr.	*Russulaceae*	*Lactarius*	√						3	EM	Agarics	HMJAU60739	
Lactarius zonarius (Bull.) Fr.	*Russulaceae*	*Lactarius*	√	√					2	EM	Agarics	HMJAU60740	
Lactifluus bertillonii (Neuhoff ex Z. Schaef.) Verbeken	*Russulaceae*	*Lactifluus*	√						1	EM	Agarics	HMJAU60741	OL891489
Lactifluus pilosus (Verbeken, H.T. Le & Lumyong) Verbeken	*Russulaceae*	*Lactifluus*	√						1	EM	Agarics	HMJAU60742	
Laetiporus sulphureus (Bull.) Murrill	*Laetiporaceae*	*Laetiporus*	√	√					2	WS	Polyporoid fungi	HMJAU60743	
Leccinum aurantiacum (Bull.) Gray	*Boletaceae*	*Leccinum*	√						2	EM	Boletes	HMJAU60744	
Leccinum scabrum (Bull.) Gray	*Boletaceae*	*Leccinum*				√			1	EM	Boletes	HMJAU60745	
Leccinum versipelle (Fr. & Hök) Snell	*Boletaceae*	*Leccinum*	√						1	EM	Boletes	HMJAU60746	
Lentinellus ursinus (Fr.) Kühner	*Auriscalpiaceae*	*Lentinellus*	√						6	WS	Agarics	HMJAU60747	
Lentinus edodes (Berk.) Singer	*Omphalotaceae*	*Lentinus*	√						2	WS	Agarics	HMJAU60748	
Lentinus sajor-caju (Fr.) Fr.	*Polyporaceae*	*Lentinus*		√					6	WS	Agarics	HMJAU60749	OL891475
Leotia lubrica (Scop.) Pers.	*Leotiaceae*	*Leotia*	√						4	SS	Larger Ascomytetes	HMJAU60750	
Lepiota castanea Quél.	*Agaricaceae*	*Lepiota*	√						5	LS	Agarics	HMJAU60751	
Lepiota cristata (Bolton) P. Kumm.	*Agaricaceae*	*Lepiota*	√						4	LS	Agarics	HMJAU60752	
Lepista nuda (Bull.) Cooke	*Tricholomataceae*	*Lepista*	√	√					9	SS	Agarics	HMJAU60753	

Species	Family	Genera	A	B	C	D	E	F	N	ML	Categories	SN	GenBank Number
Lepista personata (Fr.) Cooke	*Tricholomataceae*	*Lepista*		√					1	SS	Agarics	HMJAU60754	
Leucocybe connata (Schumach.) Vizzini, P. Alvarado, G. Moreno & Consiglio	*Lyophyllaceae*	*Leucocybe*	√						3	EM	Agarics	HMJAU60755	
Lycoperdon mammiforme Pers.	*Lycoperdaceae*	*Lycoperdon*	√						8	SS	Agarics	HMJAU60756	
Lycoperdon perlatum Pers.	*Lycoperdaceae*	*Lycoperdon*	√	√					5	SS	Gasteroid fungi	HMJAU60757	
Lycoperdon umbrinum Pers.	*Lycoperdaceae*	*Lycoperdon*		√					3	SS	Gasteroid fungi	HMJAU60758	
Lyophyllum decastes (Fr.) Singer	*Lyophyllaceae*	*Lyophyllum*	√						3	EM	Agarics	HMJAU60759	
Lyophyllum infumatum (Bres.) Kühner	*Lyophyllaceae*	*Lyophyllum*			√				1	EM	Agarics	HMJAU60760	OL891476
Macrocystidia cucumis (Pers.) Joss.	*Macrocystidiaceae*	*Macrocystidia*		√					2	SS	Agarics	HMJAU60761	
Marasmius confertus Berk. & Broome	*Marasmiaceae*	*Marasmius*	√						2	LS	Agarics	HMJAU60762	
Marasmius maximus Hongo	*Marasmiaceae*	*Marasmius*	√	√					8	LS	Agarics	HMJAU60763	
Marasmius nigrodiscus (Peck) Halling	*Marasmiaceae*	*Marasmius*			√				2	LS	Agarics	HMJAU60764	
Marasmius occultatiformis Antonín, Ryoo & H.D. Shin	*Marasmiaceae*	*Marasmius*				√			4	LS	Agarics	HMJAU60765	
Marasmius siccus (Schwein.) Fr.	*Marasmiaceae*	*Marasmius*		√					1	LS	Agarics	HMJAU60766	
Megacollybia clitocyboidea R.H. Petersen, Takehashi & Nagas.	*Megacollybia*	*Megacollybia*	√	√					4	WS	Agarics	HMJAU60767	
Melanoleuca cognata (Huds.) Fr.	*Tricholomataceae*	*Melanoleuca*			√				1	SS	Agarics	HMJAU60768	
Mucidula brunneomarginata Lj.N. Vassiljeva) R.H. Petersen	*Physalacriaceae*	*Mucidula*		√					2	WS	Agarics	HMJAU60769	
Mutinus caninus (Huds.) Fr.	*Phallaceae*	*Mutinus*			√				4	LS	Gasteroid fungi	HMJAU60770	
Mycena galericulata (Scop.) Gray	*Mycenaceae*	*Mycena*				√			5	LS	Agarics	HMJAU60771	
Mycena haematopus (Pers.) P. Kumm.	*Mycenaceae*	*Mycena*			√				3	LS	Agarics	HMJAU60772	
Mycena pelianthina (Fr.) Quél.	*Mycenaceae*	*Mycena*						√	1	LS	Agarics	HMJAU60773	

Species	Family	Genera	A	B	C	D	E	F	N	ML	Categories	SN	GenBank Number
Mycena polygramma (Bull.) Gray	*Mycenaceae*	*Mycena*				√			2	LS	Agarics	HMJAU60774	
Mycena pura (Pers.) P. Kumm.	*Mycenaceae*	*Mycena*		√	√	√			4	LS	Agarics	HMJAU60775	
Mycena roseocandida (Peck) Sacc.	*Mycenaceae*	*Mycena*	√						1	LS	Agarics	HMJAU60776	
Mycena sanguinolenta (Alb. & Schwein.) P. Kumm.	*Mycenaceae*	*Mycena*	√						8	LS	Agarics	HMJAU60777	
Mycena stylobates (Pers.) P. Kumm.	*Mycenaceae*	*Mycena*		√		√			12	LS	Agarics	HMJAU60778	
Neolentinus cyathiformis (Schaeff.) Della Magg. & Trassin.	*Gloeophyllaceae*	*Neolentinus*	√	√					15	WS	Agarics	HMJAU60779	OL891477
Omphalina pyxidata (Bull.) Quél.	*Tricholomataceae*	*Omphalina*		√					3	LS	Agarics	HMJAU60780	
Ophiocordyceps nutans (Pat.) G.H. Sung, J.M. Sung, Hywel-Jones & Spatafora	*Ophiocordycipitaceae*	*Ophiocordyceps*		√					1	EI	Larger Ascomytetes	HMJAU60781	
Oudemansiella mucida (Schrad.) Höhn.	*Physalacriaceae*	*Oudemansiella*	√						4	WS	Agarics	HMJAU60782	
Paxillus involutus (Batsch) Fr.	*Paxillaceae*	*Paxillus*	√	√					2	EM	Agarics	HMJAU60783	
Paxillus orientalis Gelardi, Vizzini, E. Horak & G. Wu	*Paxillaceae*	*Paxillus*	√						1	EM	Agarics	HMJAU60784	
Peziza domiciliana Cooke	*Pezizaceae*	*Peziza*	√						3	SS	Larger Ascomytetes	HMJAU60785	
Phallus tenuissimus T.H. Li, W.Q. Deng & B. Liu	*Phallaceae*	*Phallus*		√					2	LS	Gasteroid fungi	HMJAU60786	
Phellinus pomaceus (Pers.) Maire	*Hymenochaetaceae*	*Phellinus*	√			√			2	WS	Polyporoid fungi	HMJAU60787	
Pholiota aurivella (Batsch) P. Kumm.	*Strophariaceae*	*Pholiota*	√						4	WS	Agarics	HMJAU60788	
Pholiota squarrosoides (Peck) Sacc.	*Strophariaceae*	*Pholiota*						√	3	WS	Agarics	HMJAU60789	
Phylloporus yunnanensis N.K. Zeng, Zhu L. Yang & L.P. Tang	*Boletaceae*	*Phylloporus*	√						2	EM	Boletes	HMJAU60790	
Phyllotopsis nidulans (Pers.) Singer	*Phyllotopsidaceae*	*Phyllotopsis*			√				7	WS	Agarics	HMJAU60791	

Species	Family	Genera	A	B	C	D	E	F	N	ML	Categories	SN	GenBank Number
Piptoporus soloniensis (Dubois) Pilát	*Fomitopsidaceae*	*Piptoporus*						√	2	WS	Polyporoid fungi	HMJAU60792	OL891488
Pleurotus citrinopileatus Singer	*Pleurotaceae*	*Pleurotus*		√					4	WS	Agarics	HMJAU60793	
Pleurotus ostreatus (Jacq.) P. Kumm.	*Pleurotaceae*	*Pleurotus*	√	√					8	WS	Agarics	HMJAU60794	OL891478
Pleurotus pulmonarius (Fr.) Quél.	*Pleurotaceae*	*Pleurotus*	√						2	WS	Agarics	HMJAU60795	
Pluteus atromarginatus (Konrad) Kühner	*Pluteaceae*	*Pluteus*		√					2	LS	Agarics	HMJAU60796	
Pluteus cervinus (Schaeff.) P. Kumm.	*Pluteaceae*	*Pluteus*	√						1	LS	Agarics	HMJAU60797	
Pluteus hispidulus (Fr.) Gillet	*Pluteaceae*	*Pluteus*	√						1	LS	Agarics	HMJAU60798	
Pluteus leoninus (Schaeff.) P. Kumm	*Pluteaceae*	*Pluteus*	√		√				1	LS	Agarics	HMJAU60799	
Pluteus phlebophorus (Ditmar) P. Kumm.	*Pluteaceae*	*Pluteus*	√						2	LS	Agarics	HMJAU60800	
Pluteus pouzarianus Singer	*Pluteaceae*	*Pluteus*	√						2	LS	Agarics	HMJAU60801	
Podoscypha nitidula (Berk.) Pat.	*Podoscyphaceae*	*Podoscypha*		√					3	WS	Polyporoid fungi	HMJAU60802	
Polyporus arcularius (Batsch) Fr.	*Polyporaceae*	*Polyporus*		√					10	WS	Polyporoid fungi	HMJAU60803	
Polyporus submelanopus H.J. Xue & L.W. Zhou	*Polyporaceae*	*Polyporus*		√					1	WS	Polyporoid fungi	HMJAU60804	
Polyporus umbellatus (Pers.) Fr.	*Polyporaceae*	*Polyporus*	√						4	SS	Polyporoid fungi	HMJAU60805	
Psathyrella delineata (Peck) A.H. Sm.	*Psathyrellaceae*	*Psathyrella*				√			1	WS	Agarics	HMJAU60806	
Psathyrella typhae (Kalchbr.) A. Pearson & Dennis	*Psathyrellaceae*	*Psathyrella*					√		4	WS	Agarics	HMJAU60807	
Pseudolaccaria fellea (Peck) Vizzini, Matheny & Consiglio & M. Marchetti	*Callistosporiaceae*	*Pseudolaccaria*			√				3	WS	Agarics	HMJAU60808	
Pseudoplectania nigrella (Pers.) Fuckel	*Sarcosomataceae*	*Pseudoplectania*			√				5	SS	Larger Ascomytetes	HMJAU60809	
Pulveroboletus macrosporus G. Wu & Zhu L. Yang	*Boletaceae*	*Pulveroboletus*				√			1	EM	Boletes	HMJAU60810	

Species	Family	Genera	A	B	C	D	E	F	N	ML	Categories	SN	GenBank Number
Ramaria cokeri R.H. Petersen	*Gomphaceae*	*Ramaria*		√		√			2	EM	Coral fungi	HMJAU60811	
Ramaria fennica (P. Karst.) Ricken	*Gomphaceae*	*Ramaria*						√	1	EM	Coral fungi	HMJAU60812	
Ramaria marrii Scates	*Gomphaceae*	*Ramaria*	√						2	EM	Coral fungi	HMJAU60813	
Ramaria sanguinipes R.H. Petersen & M. Zang	*Gomphaceae*	*Ramaria*		√					2	EM	Coral fungi	HMJAU60814	
Ramaria stricta (Pers.) Quél.	*Gomphaceae*	*Ramaria*		√					3	EM	Coral fungi	HMJAU60815	
Rhodocollybia butyracea (Bull.) Lennox	*Omphalotaceae*	*Rhodocollybia*	√		√				12	SS	Agarics	HMJAU60816	
Russula aeruginea Lindblad ex Fr.	*Russulaceae*	*Russula*				√			3	EM	Agarics	HMJAU60817	
Russula amoena Quél.	*Russulaceae*	*Russula*	√	√					2	EM	Agarics	HMJAU60818	
Russula cyanoxantha (Schaeff.) Fr.	*Russulaceae*	*Russula*		√					1	EM	Agarics	HMJAU60819	
Russula emetica (Schaeff.) Pers.	*Russulaceae*	*Russula*	√	√		√			18	EM	Agarics	HMJAU60820	
Russula foetens Pers.	*Russulaceae*	*Russula*		√		√			3	EM	Agarics	HMJAU60821	
Russula furcata Pers.	*Russulaceae*	*Russula*				√			3	EM	Agarics	HMJAU60822	
Russula grata Britzelm.	*Russulaceae*	*Russula*	√						2	EM	Agarics	HMJAU60823	
Russula lakhanpalii A. Ghosh, K. Das & R.P. Bhatt	*Russulaceae*	*Russula*				√			2	EM	Agarics	HMJAU60824	OL891479
Russula paludosa Britzelm.	*Russulaceae*	*Russula*	√			√			6	EM	Agarics	HMJAU60825	
Russula risigallina (Batsch) Sacc.	*Russulaceae*	*Russula*						√	3	EM	Agarics	HMJAU60826	
Russula rosea Pers.	*Russulaceae*	*Russula*	√	√					4	EM	Agarics	HMJAU60827	
Russula senecis S. Imai	*Russulaceae*	*Russula*				√			6	EM	Agarics	HMJAU60828	
Russula sororia (Fr.) Romell	*Russulaceae*	*Russula*				√			3	EM	Agarics	HMJAU60829	
Russula veternosa Fr.	*Russulaceae*	*Russula*	√						2	EM	Agarics	HMJAU60830	
Russula vinosa Lindblad	*Russulaceae*	*Russula*		√					2	EM	Agarics	HMJAU60831	
Russula virescens (Schaeff.) Fr.	*Russulaceae*	*Russula*	√						1	EM	Agarics	HMJAU60832	

Species	Family	Genera	A	B	C	D	E	F	N	ML	Categories	SN	GenBank Number
Sarcodontia spumea (Sowerby) Spirin	*Meruliaceae*	*Sarcodontia*		√					3	WS	Polyporoid fungi	HMJAU60833	
Schizophyllum commune Fr.	*Schizophyllaceae*	*Schizophyllum*	√						4	WS	Agarics	HMJAU60834	
Scleroderma areolatum Ehrenb.	*Sclerodermataceae*	*Scleroderma*				√			4	EM	Gasteroid fungi	HMJAU60835	
Sowerbyella rhenana (Fuckel) J. Moravec	*Pyronemataceae*	*Sowerbyella*				√			5	EM	Larger Ascomytetes	HMJAU60836	
Spathularia flavida Pers.	*Cudoniaceae*	*Spathularia*			√				4	SS	Larger Ascomytetes	HMJAU60837	
Stropharia rugosoannulata Farl. ex Murrill	*Tubariaceae*	*Stropharia*		√					3	SS	Agarics	HMJAU60838	
Suillus americanus (Peck) Snell	*Suillaceae*	*Suillus*			√				1	EM	Boletes	HMJAU60839	
Suillus granulatus (L.) Roussel	*Suillaceae*	*Suillus*						√	1	EM	Boletes	HMJAU60840	
Suillus grevillei (Klotzsch) Singer	*Suillaceae*	*Suillus*			√		√		10	EM	Boletes	HMJAU60841	OL891494
Suillus luteus (L.) Roussel	*Suillaceae*	*Suillus*			√	√			4	EM	Boletes	HMJAU60842	OL891496
Suillus placidus (Bonord.) Singer	*Suillaceae*	*Suillus*			√				3	EM	Boletes	HMJAU60843	OL884444
Suillus subaureus (Peck) Snell	*Suillaceae*	*Suillus*	√						5	EM	Boletes	HMJAU60844	OL891495
Suillus tomentosus Singer, Snell & E.A. Dick	*Suillaceae*	*Suillus*	√						3	EM	Boletes	HMJAU60845	
Sutorius brunneissimus (W.F. Chiu) G. Wu & Zhu L. Yang	*Boletaceae*	*Sutorius*		√					1	EM	Boletes	HMJAU60846	
Tengioboletus glutinosus G. Wu & Zhu L. Yang	*Boletaceae*	*Tengioboletus*		√		√			5	EM	Boletes	HMJAU60847	
Tremella Fuciformis Berk.	*Tremellaceae*	*Tremella*	√						3	WS	Jelly fungi	HMJAU60848	
Trichoderma rhododendri (Jaklitsch) Jaklitsch & Voglmayr	*Hypocreaceae*	*Trichoderma*			√				3	WS	Larger Ascomytetes	HMJAU60849	
Tricholoma matsutake (S. Ito & S. Imai) Singer	*Tricholomataceae*	*Tricholoma*					√		4	EM	Agarics	HMJAU60850	
Tricholoma psammopus (Kalchbr.) Quél.	*Tricholomataceae*	*Tricholoma*		√	√				5	EM	Agarics	HMJAU60851	OL891480
Tricholoma saponaceum (Fr.) P. Kumm.	*Tricholomataceae*	*Tricholoma*			√				2	EM	Agarics	HMJAU60852	
Tricholoma sejunctum (Sowerby) Quél.	*Sarcoscyphaceae*	*Tricholoma*		√					4	EM	Agarics	HMJAU60853	OL891481

Species	Family	Genera	A	B	C	D	E	F	N	ML	Categories	SN	GenBank Number
Tricholoma stans (Fr.) Sacc.	*Tricholomataceae*	*Tricholoma*				√			2	EM	Agarics	HMJAU60854	
Tricholoma subacutum Peck	*Tricholomataceae*	*Tricholoma*	√			√			2	EM	Agarics	HMJAU60855	
Tricholoma ustale (Fr.) P. Kumm.	*Tricholomataceae*	*Tricholoma*				√			1	EM	Agarics	HMJAU60856	OL891482
Tricholoma ustaloides Romagn.	*Tricholomataceae*	*Tricholoma*	√						1	EM	Agarics	HMJAU60857	
Tricholomopsis rutilans (Schaeff.) Singer	*Tricholomataceae*	*Tricholomopsis*						√	2	SS	Agarics	HMJAU60858	
Tylopilus eximius (Peck) Singer	*Boletaceae*	*Tylopilus*				√			1	EM	Boletes	HMJAU60859	OL891491
Tylopilus felleus (Bull.) P. Karst.	*Boletaceae*	*Tylopilus*					√		1	EM	Boletes	HMJAU60860	
Tylopilus virens (W.F. Chiu) Hongo	*Boletaceae*	*Tylopilus*	√						2	EM	Boletes	HMJAU60861	OL891493
Tyromyces lacteus (Fr.) Murrill	*Incrustoporiaceae*	*Tyromyces*	√						1	WS	Polyporoid fungi	HMJAU60862	
Vanrija pseudolonga (M. Takash., Sugita, Shinoda & Nakase) Weiß	*Cryptococcaceae*	*Vanrija*		√					1	EM	Boletes	HMJAU60863	
Volvopluteus michiganensis (A.H. Sm.) Justo & Minnis	*Pluteaceae*	*Volvopluteus*	√						1	SS	Boletes	HMJAU60864	
Wynnea gigantea Berk. & M.A. Curtis	*Wynneaceae*	*Wynnea*	√	√					5	SS	Larger Ascomytetes	HMJAU60865	
Xerocomus ferrugineus (Schaeff.) Alessio	*Boletaceae*	*Xerocomus*					√		1	EM	Boletes	HMJAU60866	
Xerocomus magniporus M. Zang & R.H. Petersen	*Boletaceae*	*Xerocomus*	√						1	EM	Boletes	HMJAU60867	
Xeromphalina campanella (Batsch) Kühner & Maire	*Mycenaceae*	*Xeromphalina*						√	1	WS	Agarics	HMJAU60868	
Xylaria hypoxylon (L.) Grev.	*Xylariaceae*	*Xylaria*		√					4	WS	Larger Ascomytetes	HMJAU60869	
Xylaria polymorpha (Pers.) Grev.	*Xylariaceae*	*Xylaria*	√						1	WS	Larger Ascomytetes	HMJAU60870	

Note: Abbreviations: A = *Q. mongolica* forest; B = Broad-leaved forest; C = *P. koraiensis* and *Q. mongolica* mixed forest, with *P. koraiensis* as the dominant species; D = *P. koraiensis* and *Q. mongolica* mixed forest, with *Q. mongolica* as the dominant species; E = *P. koraiensis* forest; F = random collection; N = Number of fruiting bodies; ML = Mode of Life; SN = Specimen Number; EM = ectomycorrhizal; SS = soil saprotroph; WS = wood saprotroph; LS = litter saprotroph; DS = dung saprotroph; EI = endophyte-insect pathogen.

Appendix C. Species Scientific Names and Corresponding Abbreviations

Species	Acronyms	Species	Acronyms	Species	Acronyms	Species	Acronyms	Species	Acronyms
Amanita altipes	Ama1	*Cortinarius armillatus*	Cor2 (A)	*Inocybe assimilata*	Ino1 (A)	*Leccinum scabrum*	Lec2 (D)	*Russula vinosa*	Ru14
Amanita chepangiana	Ama2	*Cortinarius balaustinus*	Cor3 (A)	*Inocybe asterospora*	Ino2 (A)	*Leccinum versipelle*	Lec3 (A)	*Russula virescens*	Ru15 (A)
Amanita excelsa	Ama3 (D)	*Cortinarius bivelus*	Cor4	*Inocybe suaveolens*	Ino3	*Leucocybe connata*	Leu1 (A)	*Scleroderma areolatum*	Scl1
Amanita flavipes	Ama4	*Cortinarius caperatus*	Cor5 (A)	*Laccaria amethystina*	Lac1 (D)	*Lyophyllum decastes*	Lyo1 (A)	*Sowerbyella rhenana*	Sow1 (D)
Amanita fuliginea	Ama5	*Cortinarius cotoneus*	Cor6	*Laccaria laccata*	Lac2	*Lyophyllum infumatum*	Lyo2	*Suillus americanus*	Sui1
Amanita hemibapha	Ama6	*Cortinarius ectypus*	Cor7 (A)	*Lactarius albidocinereus*	Lact1 (D)	*Paxillus involutus*	Pax1	*Suillus grevillei*	Sui2
Amanita ibotengutake	Ama7	*Cortinarius flammeouraceus*	Cor8 (A)	*Lactarius brunneoviolascens*	Lact2 (A)	*Paxillus orientalis*	Pax2 (A)	*Suillus luteus*	Sui3
Amanita oberwinklerana	Ama8	*Cortinarius hesleri*	Cor9 (A)	*Lactarius conglutinatus*	Lact3 (A)	*Phylloporus yunnanensis*	Phy1 (A)	*Suillus placidus*	Sui4
Amanita orsonii	Ama9	*Cortinarius pholideus*	Cor10 (D)	*Lactarius deterrimus*	Lact4	*Pulveroboletus macrosporus*	Pul1 (D)	*Suillus subaureus*	Sui5 (A)
Amanita pallidocarnea	Ama10	*Cortinarius sanguineus*	Cor11 (D)	*Lactarius flavidus*	Lact5 (A)	*Ramaria cokeri*	Ram 1	*Suillus tomentosus*	Sui6 (A)
Amanita pallidorosea	Ama11 (A)	*Cortinarius subbalaustinus*	Cor12 (A)	*Lactarius glyciosmus*	Lact6 (A)	*Ramaria marrii*	Ram2 (A)	*Sutorius brunneissimus*	Sut1
Amanita rimosa	Ama12 (A)	*Cortinarius torvus*	Cor13 (A)	*Lactarius hirtipes*	Lact7 (A)	*Ramaria sanguinipes*	Ram 3	*Tengioboletus glutinosus*	Ten1
Amanita rubescens	Ama13	*Craterellus cornucopioides*	Cra1(A)	*Lactarius lilacinus*	Lact8 (A)	*Ramaria stricta*	Ram 4	*Tricholoma matsutake*	Tri1
Amanita subglobosa	Ama14 (A)	*Gomphidius maculatus*	Gom1	*Lactarius pallidus*	Lact9	*Russula aeruginea*	Rus1 (D)	*Tricholoma psammopus*	Tri2

Species	Acronyms	Species	Acronyms	Species	Acronyms	Species	Acronyms	Species	Acronyms
Amanita vaginata	Ama15	*Harrya chromapes*	Har1 (A)	*Lactarius piperatus*	Lact10 (A)	*Russula amoena*	Rus2	*Tricholoma saponaceum*	Tri3
Amanita virosa	Ama16	*Hebeloma birrus*	Heb1 (A)	*Lactarius proximellus*	Lact11	*Russula cyanoxantha*	Rus3	*Tricholoma sejunctum*	Tri4
Boletus aereus	Bol1	*Helvella crispa*	Hel1	*Lactarius pubescens*	Lact12 (A)	*Russula emetica*	Rus4	*Tricholoma stans*	Tri5 (D)
Boletus edulis	Bol2	*Helvella elastica*	Hel2	*Lactarius subvellereus*	Lact13 (A)	*Russula foetens*	Rus5	*Tricholoma subacutum*	Tri6
Bothia castanella	Bot1 (A)	*Helvella macropus*	Hel3	*Lactarius torminosus*	Lact14 (D)	*Russula furcata*	Rus6 (D)	*Tricholoma ustale*	Tri7 (D)
Butyriboletus regius	But1 (A)	*Humaria hemisphaerica*	Hum1	*Lactarius trivialis*	Lact15 (A)	*Russula grata*	Rus7(A)	*Tricholoma ustaloides*	Tri8 (A)
Butyriboletus roseoflavu	But2	*Hydnellum aurantiacum*	Hyd1	*Lactarius vietus*	Lact16 (A)	*Russula lakhanpalii*	Rus8 (D)	*Tylopilus eximius*	Tyl1 (D)
Chalciporus piperatus	Cha1	*Hydnellum peckii*	Hyd2	*Lactarius volemus*	Lact17 (A)	*Russula paludosa*	Rus9	*Tylopilus felleus*	Tyl2
Chroogomphus helveticus	Chr1	*Hygrophorus conicus*	Hyg1	*Lactarius zonarius*	Lact18	*Russula rosea*	Rus10	*Tylopilus virens*	Tyl3 (A)
Coltricia crassa	Col1	*Hygrophorus nemoreus*	Hyg2	*Lactifluus bertillonii*	Lacti1 (A)	*Russula senecis*	Rus11 (D)	*Vanrija pseudolonga*	Van1
Coltricia strigosipes	Col2 (A)	*Hygrophorus pudorinus*	Hyg3 (A)	*Lactifluus pilosus*	Lacti2 (A)	*Russula sororia*	Rus12 (D)	*Xerocomus ferrugineus*	Xer1
Cortinarius anomalus	Cor1 (D)	*Hygrophorus russula*	Hyg4 (A)	*Leccinum aurantiacum*	Lec1 (A)	*Russula veternosa*	Rus13 (A)	*Xerocomus magniporus*	Xer2 (A)

Note: Abbreviations: Overlapping species labels are marked and noted in parentheses. A = *Q. mongolica* forest; D = *P. koraiensis* and *Q. mongolica* mixed forest, with *Q. mongolica* as the dominant species.

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