



The wood-decaying fungal diversity unveiled by morphology and phylogeny in Ailaoshan Mountain, Yunnan, China

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Published: 2020-07-02

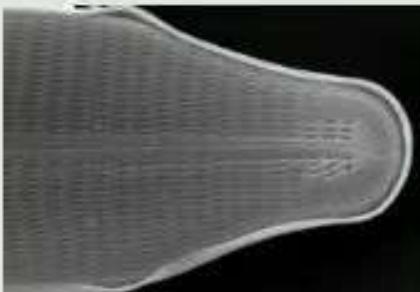
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***Dryopteris microlepioides*, a new synonym of *Trichoneuron microlepioides* (Drypteridaceae)**

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The wood-decaying fungal diversity unveiled by morphology and phylogeny in Ailaoshan Mountain, Yunnan, China

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Abstract

Seven field surveys were carried out in the Ailaoshan area of Yunnan Province, China, from 2016 to 2021, in which 2,814 specimens of wood-decaying fungal species were collected and identified based on morphology and phylogenetic analyses. One hundred and three wood-decaying species were identified, belonging to 64 genera, 29 families, and nine orders. Polyporales is the most abundant order in this area, accounting for 55.34% of all species, while Polyporaceae is the most abundant family, accounting for 18.45% of all species discovered in this area. The wood-decaying fungal checklist is provided according to the latest fungi classification system. Of these species, 11 are edible and therapeutic, four are forest pathogens, eight are threatened, and nine have just been reported from Ailaoshan Mountain. These species comprise 10.68%, 3.88%, 7.77%, and 8.74% of all species, respectively, while 71 species, or 68.93%, have unclear functional relationships. The sequences of the Internal Transcribed Spacer (ITS) gene region of the studied specimens were generated, and the phylogenetic analyses were performed with the maximum likelihood, maximum parsimony, and Bayesian inference methods. This study enriches the diversity of wood-decaying fungi in the Ailaoshan area. Also, it provides a theoretical basis for the future protection and utilization of wood-decaying fungal resources in this area.

Key words: fungal resources, molecular systematics, subtropical zone, taxonomy, wood-associated fungi

Introduction

Wood-decaying fungi belonging to the Agaricomycetes (Basidiomycota) grow on living wood, fallen wood, decayed wood, and forest land (Larsson 2007; Krah *et al.* 2018; Wu *et al.* 2020; Dai *et al.* 2021a). They secrete various enzymes to degrade lignin, cellulose, and hemicellulose in wood and play a very key role in the degradation and reduction of material circulation and energy flow in forest ecosystems (Wei & Dai 2004, Dai & Zhuang 2010; Purhonen *et al.* 2020; Hobbie *et al.* 2021). Wood-decaying fungi are important members of the forest ecosystem (Yang 2016; Guan *et al.* 2020a, Luo *et al.* 2021; Qu *et al.* 2022; Dong *et al.* 2023; Zhao *et al.* 2023; Yang *et al.* 2024). Among wood-decaying fungi, corticioid fungi, poroid fungi, and hydnoid fungi are the three main groups (Dai 2012a, 2012b; Liu *et al.* 2023).

Wood-decaying fungi have rich diversity worldwide and play an important role in the ecosystem (Guo & Chen 2021). The species diversity, taxonomy, and phylogeny of the wood-decaying fungi have been intensively studied in recent years, and the number of taxa has dramatically increased (Dai *et al.* 2014; Zhao & Wu 2017; Chen & Zhao 2020; Guan *et al.* 2020a, 2020b, 2021a, 2021b; Luo *et al.* 2019, 2021, 2022a, 2022b; He *et al.* 2021; He & Zhao 2022; Yang *et al.* 2024). Many species of wood-decaying fungi have edible and medicinal values, while others contain toxic metabolites (Dai *et al.* 2015; Baldrian 2018). Recognition of species diversity, taxonomy, and importance will aid in the conservation of wood-decaying fungi worldwide (Krah *et al.* 2018).

Yunnan Province has abundant climate types, abundant precipitation, long wet season, and obvious north-south and vertical differences, in which the unique geographical conditions and climate environment have bred extremely rich wood rot fungi resources (Wang & Cai 2023). Systematic surveys of wood-decaying fungi are being carried out

in most parts of Yunnan Province, including Wuliangshan, Ailaoshan, Zixishan, Gaoligongshan and Mopanshan areas, and mycologists have found that the wood-decaying fungi resources in these areas are extremely abundant (Dai 2011; Guo *et al.* 2013; Dai *et al.* 2014, 2015a; Shen *et al.* 2018; Shen *et al.* 2022; Chen & Zhao 2020; Guan *et al.* 2023; He *et al.* 2021, 2022; Xu *et al.* 2020; Luo *et al.* 2021; Qu *et al.* 2022; Dong *et al.* 2023; Duan *et al.* 2023; Yuan *et al.* 2023; Yang *et al.* 2023a, 2023b). However, the knowledge of wood-decaying fungi still needs to be improved in Yunnan.

Ailaoshan, a natural wonder, is located in the center of Yunnan Province, China, near the intersection of the Hengduan Mountains region and the Yunnan-Guizhou Plateau. Encompassing a vast area of 67936 hm², it extends in a northwest-southeast direction, with a length of approximately 102 km (Lu *et al.* 2018). It is the southern extension of Yunling Mountain and the watershed between Yuanjiang and the Amo River, with an east-west width of 4–20 km, an altitude range of 800–3157 m, and a vertical height difference of 2357 m (Li *et al.* 2021). Its forest coverage rate is remarkable, standing at a majestic 85.1%. Ailaoshan's primary forest types include mixed warm coniferous forests, deciduous broad-leaved forests, and evergreen broad-leaved forests. These forests, thriving in their unique geographic position, climatic conditions, and vegetation types, have fostered an abundance of rich forest decay fungi, a sight that never fails to amaze visitors to this natural wonder.

The study conducted seven field expeditions in the Ailaoshan area between 2016 and 2021. Its goals were to recognize species diversity, understand the importance of wood-decaying fungal species in this area, and provide scientific understanding for utilizing and conserving this fungal resource.

Materials and methods

Sample collection and herbarium specimen preparation

The fresh fruiting bodies of basidiomycetous macrofungi growing on trees of stumps, trunks, and branches were collected in the Ailaoshan area from 2016 to 2021. At least three basidiomata were required, and the smallest fruiting structure had to include the hymenophore. The samples were photographed *in situ* using a Canon 80D camera, and their fresh macroscopic details were recorded. The samples were transported to a field station where the fruiting bodies were dried on an electric food dryer (Fsfruit) at 45°C for 48 hours (Hu *et al.* 2022). After the specimen was dried, it was sealed in an envelope and a zip-lock plastic bag and labeled. The dried specimens were deposited in the herbarium of Southwest Forestry University (SWFC), Kunming, Yunnan Province, China.

Morphological studies

The macromorphological descriptions were based on field notes and photos captured in the field and lab. Colour terms followed Petersen (1996). The micromorphological data were obtained from the dried specimens, and sections were separately prepared in Cotton Blue, Melzer's reagent, and 5% potassium hydroxide and observed under a Nikon Eclipse E100 light microscope following Zhao & Wu (2017). Based on morphological and molecular data, the identification was carried out with reference to previous publications (Chen *et al.* 2020; Liu *et al.* 2020; Dai *et al.* 2021; Luo *et al.* 2021; Westphalen *et al.* 2021; Phukhamsakda *et al.* 2022; Zhao *et al.* 2023).

Molecular procedures and phylogenetic analysis

CTAB rapid plant genome extraction kit-DN14 (Aidlab Biotechnologies Co., Ltd., Beijing, China) was used to obtain genomic DNA from dried specimens according to the manufacturer's instructions. ITS region was amplified with primer pair ITS5 and ITS4 (White *et al.* 1990). The PCR procedure for ITS was as follows: initial denaturation at 95 °C for 3 min, followed by 35 cycles at 94 °C for 40 s, 58 °C for 45 s, and 72 °C for 1 min, and a final extension of 72 °C for 10 min. The PCR products were purified using a QIAquick PCR purification kit (Qiagen Inc., Valencia, CA, USA) and directly sequenced at Kunming Tsingke Biological Technology Limited Company, Kunming Yunnan Province, P.R. China. All newly generated sequences were deposited at GenBank (Table 1).

The sequences were aligned in MAFFT version 7 using the G-INS-i strategy (Katoh *et al.* 2019). The alignment was adjusted manually using AliView version 1.27 (Larsson 2014). A sequence from the type material of *Exobasidium vaccinii* (Fuckel) Woronin acquired from GenBank was utilized as an outgroup to root the ITS phylogenetic tree (Figure 1).

Maximum parsimony analysis was applied to the ITS dataset sequences. Approaches to phylogenetic analysis followed Zhao & Wu (2017) and the tree construction procedure was performed in PAUP* version 4.0b10 (Swofford 2002). All of the characters were equally weighted and gaps were treated as missing data. Trees were inferred using

the heuristic search option with TBR branch swapping and 1000 random sequence additions. Max-trees were set to 5000, branches of zero length were collapsed, and all parsimonious trees were saved. Clade robustness was assessed using a bootstrap (BT) analysis with 1000 replicates (Felsenstein 1985). Descriptive tree statistics tree length (TL), the consistency index (CI), the retention index (RI), the rescaled consistency index (RC), and the homoplasy index (HI) were calculated for each maximum parsimonious tree (MPT) generated. Sequences were also analyzed using maximum likelihood (ML) with RAxML-HPC2 through the Cipres Science Gateway (Miller *et al.* 2012). Branch support (BS) for ML analysis was determined by 1000 bootstrap replicates.

MrModeltest 2.3 (Nylander 2004) was used to determine the best-fit evolution model for each data set for Bayesian inference (BI). Bayesian inference was calculated with MrBayes3.1.2 with a general time reversible (GTR+I+G) model of DNA substitution and a gamma distribution rate variation across sites (Ronquist & Huelsenbeck 2003). Four Markov chains were run for 2 runs from random starting trees for 7 million generations (Figure 1) and trees were sampled every 100 generations. The first one-fourth generations were discarded as burn-ins. A majority rule consensus tree of all remaining trees was calculated. A majority rule consensus tree of all remaining trees was calculated. Branches were considered as significantly supported if they received a maximum likelihood bootstrap (BS) of $\geq 70\%$, a maximum parsimony bootstrap (BT) of $\geq 50\%$, or Bayesian posterior probabilities (BPP) of ≥ 0.95 .

TABLE 1. Names, sample numbers, references, and corresponding GenBank accession numbers of the sequences used in this study.

Species name	Sample no.	GenBank accession no.	References
ITS			
<i>Abundisporus quercicola</i>	CLZhao 4895	MK268806	Present study
<i>Abundisporus quercicola</i>	Dai 3084	KC415907	Zhao & Cui (2013a)
<i>Adustoporia sinuosa</i>	CLZhao 4818	MK268816	Present study
<i>Adustoporia sinuosa</i>	Vlasak 0509_17	KT711021	Spirin <i>et al.</i> (2015b)
<i>Aleurodiscus cerussatus</i>	NH11910	AF506399	Larsson & Larsson (2003)
<i>Aleurodiscus cerussatus</i>	CLZhao 4102	MK268808	Present study
<i>Aleurodiscus isabellinus</i>	CLZhao 3918	MK404311	Present study
<i>Aleurodiscus isabellinus</i>	He 5294	MH109053	Tian <i>et al.</i> (2018)
<i>Aleurodiscus tropicus</i>	CLZhao 4039	MH114607	Present study
<i>Aleurodiscus tropicus</i>	He3830	KX553875	Dai & He (2017)
<i>Alloexidiopsis yunnanensis</i>	CLZhao 9200	MT215571	Guan <i>et al.</i> (2020a)
<i>Alloexidiopsis yunnanensis</i>	CLZhao 9132	MT215566	Guan <i>et al.</i> (2020a)
<i>Bjerkandera adusta</i>	CLZhao 2761	MK268852	Present study
<i>Bjerkandera adusta</i>	935	ON391775	Pristas <i>et al.</i> (2022)
<i>Brunneoporus malicola</i>	CLZhao 3832	MH114612	Present study
<i>Brunneoporus malicola</i>	Vlasak 0404/23-J	KU866274	Spirin <i>et al.</i> (2016)
<i>Byssomerulius corium</i>	CLZhao 3999	MH114629	Present study
<i>Byssomerulius corium</i>	FP-107055	KP135008	Floudas & Hibbett (2015)
<i>Cabalodontia albofibrillosa</i>	CLZhao 8722	MZ713669	Present study
<i>Cabalodontia albofibrillosa</i>	SWFC 006394	MK894083	Unpublished
<i>Cerrena albocinnamomea</i>	CLZhao 3952	MH114615	Present study
<i>Cerrena albocinnamomea</i>	Dai12892	KC485522	Yuan (2014)
<i>Cerrena zonata</i>	CLZhao 5320	ON377090	Present study
<i>Cerrena zonata</i>	HKAS122586	ON794386	Wang <i>et al.</i> (2022)
<i>Coltricia weii</i>	CLZhao 4773	OM891745	Present study
<i>Coltricia weii</i>	Dai 13422	KX364797	Bian & Dai (2017)
<i>Crustodontia rhododendri</i>	CLZhao 8498	MK404480	Zhao <i>et al.</i> (2023)
<i>Crustodontia rhododendri</i>	CLZhao 6168	MW732400	Zhao <i>et al.</i> (2023)
<i>Crustodontia tongxiniana</i>	CLZhao 5175	MW732429	Present study

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TABLE 1. (Continued)

Species name	Sample no.	GenBank accession no.	References
		ITS	
<i>Crustodontia tongxiniana</i>	CLZhao 5217	MT020778	Huang & Zhao (2020)
<i>Crustomyces subabruptus</i>	CLZhao 4176	MK268878	Present study
<i>Crustomyces subabruptus</i>	CLZhao 5214	OR285305	Present study
<i>Cubamyces lactineus</i>	CLZhao 4811	MK269099	Present study
<i>Cubamyces lactineus</i>	A80FB1	OQ558859	Hong <i>et al.</i> (2023)
<i>Cylindrobasidium evolvens</i>	CLZhao 5051	MK268881	Present study
<i>Cylindrobasidium evolvens</i>	PDD:79912	KT201654	Qin & Yang (2016)
<i>Dacryobolus montanus</i>	CLZhao 5692	MK268883	Present study
<i>Dacryobolus montanus</i>	He 6314	ON417157	Liu <i>et al.</i> (2022)
<i>Daedaleopsis confragosa</i>	CLZhao 4813	MK268892	Present study
<i>Daedaleopsis confragosa</i>	MOGU 155-19	OM530258	Cartabia <i>et al.</i> (2021)
<i>Dentipellis fragilis</i>	CLZhao 3874	MH114643	Present study
<i>Dentipellis fragilis</i>	NH6569	AF506387	Larsson & Larsson (2003)
<i>Earliella scabrosa</i>	CLZhao 3989	MH114644	Present study
<i>Earliella scabrosa</i>	biocode08-110	MZ996936	Osmundson <i>et al.</i> (2022)
<i>Elaphroporia ailaoshanensis</i>	CLZhao 595	MG231568	Wu <i>et al.</i> (2018)
<i>Elaphroporia ailaoshanensis</i>	CLZhao 598	MG231823	Wu <i>et al.</i> (2018)
<i>Exobasidium vaccinii</i>	CBS:183.56	MH857572	Vu <i>et al.</i> (2019)
<i>Fragiliporia fragilis</i>	Dai 13559	KJ734261	Zhao <i>et al.</i> (2015b)
<i>Fragiliporia fragilis</i>	Yuan 5516	KJ734263	Zhao <i>et al.</i> (2015b)
<i>Fuscoporia gilva</i>	CLZhao 6155	MK795135	Present study
<i>Fuscoporia gilva</i>	OAB0087	ON876017	Olou <i>et al.</i> (2023)
<i>Fuscoporia pulviniformis</i>	CLZhao 8327	ON332074	Present study
<i>Fuscoporia pulviniformis</i>	Dai 17247	MH050748	Chen & Dai (2019)
<i>Fuscoporia torulosa</i>	CLZhao 2762	MK343537	Present study
<i>Fuscoporia torulosa</i>	Dai 15518	MN816732	Chen <i>et al.</i> (2020)
<i>Ganoderma lingzhi</i>	CLZhao 4770	MK268933	Present study
<i>Ganoderma lingzhi</i>	Dai 12374	JQ781867	Cao <i>et al.</i> (2012)
<i>Heterobasidion orientale</i>	CLZhao 3868	MH114692	Present study
<i>Heterobasidion orientale</i>	MSM 0099	MH233931	Saba <i>et al.</i> (2018)
<i>Hydnophanerochaete odontoidea</i>	CLZhao 8245	MK404433	Present study
<i>Hydnophanerochaete odontoidea</i>	Wu 9310-8	MF399408	Wu <i>et al.</i> (2018)
<i>Hydnoporia corrugata</i>	CLZhao 5711	MK268964	Present study
<i>Hydnoporia corrugata</i>	He839	JQ279607	Unpublished
<i>Hymenochaete anomala</i>	CLZhao 8200	MK404350	Present study
<i>Hymenochaete anomala</i>	He135	JQ279567	He & Dai (2012)
<i>Hymenochaete cinnamomea</i>	CLZhao 5006	MK268963	Present study
<i>Hymenochaete cinnamomea</i>	HHB-11978-Sp	OQ539565	Yu <i>et al.</i> (2023)
<i>Hymenochaete innexa</i>	CLZhao 4846	MK268967	Present study
<i>Hymenochaete innexa</i>	He446	JQ279585	He & Dai (2012)
<i>Hymenochaete microcycla</i>	CLZhao 2811	MK404358	Present study
<i>Hymenochaete microcycla</i>	CLZhao 4150	OM959417	Present study
<i>Hymenochaete rheicolor</i>	CLZhao 4829	MK269000	Present study

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TABLE 1. (Continued)

Species name	Sample no.	GenBank accession no.	References
			ITS
<i>Hymenochaete rheicolor</i>	He503	JQ279530	He & Dai (2012)
<i>Hymenochaete rubiginosa</i>	CLZhao 5745	MK269006	Present study
<i>Hymenochaete rubiginosa</i>	He1049	JQ716407	He & Li (2013)
<i>Hymenochaete separabilis</i>	CLZhao 5684	MK269009	Present study
<i>Hymenochaete separabilis</i>	He267	JQ279573	He & Dai (2012)
<i>Hymenochaete sphaericola</i>	CLZhao 3881	MH114715	Present study
<i>Hymenochaete sphaericola</i>	He413	JQ279600	He & Dai (2012)
<i>Hymenochaete vaginata</i>	CLZhao 3945	MH114717	Present study
<i>Hymenochaete vaginata</i>	He 2599	KU975484	Unpublished
<i>Hymenochaete villosa</i>	CLZhao 5444	ON332079	Present study
<i>Hymenochaete villosa</i>	Cui8139	JQ279527	He & Dai (2012)
<i>Hymenochaete xerantica</i>	CLZhao 8397	OM891750	Present study
<i>Hymenochaete xerantica</i>	CLZhao 8638	OM891755	Present study
<i>Hymenochaetopsis rigidula</i>	CLZhao 5661	MK269016	Present study
<i>Hymenochaetopsis rigidula</i>	He379	JQ279613	He & Dai 2012
<i>Hyphoderma microporoides</i>	CL Zhao 8695	MW917170	Guan & Chao (2021a)
<i>Hyphoderma microporoides</i>	CLZhao 6857	MW917169	Guan & Chao (2021a)
<i>Hyphoderma moniliforme</i>	CLZhao 5936	MK795144	Present study
<i>Hyphoderma moniliforme</i>	Wu 0211-46	KC928284	Yurchenko & Wu (2015)
<i>Hyphodontia mollis</i>	CLZhao 5763	MK268888	Present study
<i>Hyphodontia mollis</i>	Wu 0808-32	JX175043	Yurchenko & Wu (2014)
<i>Hyphodontia tropica</i>	CLZhao 3920	MH114772	Present study
<i>Hyphodontia tropica</i>	ICMP 13837	AF145587	Paulus <i>et al.</i> (2000)
<i>Irpex lacteus</i>	CLZhao 3829	MH114794	Present study
<i>Irpex lacteus</i>	LE-BIN 4341	OM033738	Kotlova <i>et al.</i> (2022)
<i>Junghuhnia nitida</i>	CLZhao 4903	MK269091	Present study
<i>Junghuhnia nitida</i>	MT 33/12	KY174989	Westphalen <i>et al.</i> (2021)
<i>Laetiporus ailaoshanensis</i>	CLZhao 3913	OM891737	Present study
<i>Laetiporus ailaoshanensis</i>	Dai 15629	KY886714	Song & Cui (2017)
<i>Lentinus brumalis</i>	CLZhao 4898	MK269243	Present study
<i>Lentinus brumalis</i>	LSPQ-NSM-117	KU761245	Dufresne <i>et al.</i> (2017)
<i>Lenzites betulinus</i>	CLZhao 3825	MH114801	Present study
<i>Lenzites betulinus</i>	IUM5468	KU350750	Im <i>et al.</i> (2016)
<i>Lyomyces bambusinus</i>	CLZhao 4831	MN945968	Chen & Zhao (2020)
<i>Lyomyces bambusinus</i>	CLZhao 3675	MN945969	Chen & Zhao (2020)
<i>Lyomyces cremeus</i>	CLZhao 8295	MN945972	Chen & Zhao (2020)
<i>Lyomyces cremeus</i>	CLZhao 2812	MN945973	Chen & Zhao (2020)
<i>Lyomyces macrosporus</i>	CLZhao 8605	OM959497	Present study
<i>Lyomyces macrosporus</i>	CLZhao 3951	MN945976	Chen & Zhao (2020)
<i>Megasporoporiella pseudocavernulosa</i>	CLZhao 2803	MK404418	Present study
<i>Megasporoporiella pseudocavernulosa</i>	Dai 19379	MW694882	Wang <i>et al.</i> (2021)
<i>Merulius tomentopileatus</i>	CLZhao 5833	MT020761	Present study
<i>Merulius tomentopileatus</i>	TNM:F30815	MZ637039	Chen <i>et al.</i> (2021)

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TABLE 1. (Continued)

Species name	Sample no.	GenBank accession no.	References
		ITS	
<i>Microporus vernicipes</i>	KUC11046	KJ714006	Jang <i>et al.</i> (2015)
<i>Microporus vernicipes</i>	CLZhao 5510	ON319073	Present study
<i>Microporus xanthopus</i>	CLZhao 5498	ON319077	Present study
<i>Microporus xanthopus</i>	OAB0075	ON876040	Olou <i>et al.</i> (2023)
<i>Mutatoderma mutatum</i>	CLZhao 5287	OR285306	Present study
<i>Mutatoderma mutatum</i>	CBS:290.36	MH855802	Vu <i>et al.</i> (2019)
<i>Nigroporus vinosus</i>	CLZhao 3139	MZ713665	Present study
<i>Nigroporus vinosus</i>	PW17-221	MK589284	Thamvithayakorn <i>et al.</i> (2019)
<i>Peniophora cinerea</i>	CLZhao 5716	MK269148	Present study
<i>Peniophora cinerea</i>	V1M4F82	KT692548	Comby <i>et al.</i> (2016)
<i>Peniophora incarnata</i>	CLZhao 6016	MK795172	Present study
<i>Peniophora incarnata</i>	AF112	OQ450439	Unpublished
<i>Peniophorella praetermissa</i>	CLZhao 3919	OM985740	Present study
<i>Peniophorella praetermissa</i>	TMI 20754 (TMI)	DQ647476	Hallenberg <i>et al.</i> (2007)
<i>Perenniporia luteola</i>	CLZhao 5761	MK269153	Present study
<i>Perenniporia luteola</i>	Harkonen 1308b	JX141457	Zhao & Cui (2013c)
<i>Phaeophlebiopsis peniophoroides</i>	CLZhao 5166	MK269160	Present study
<i>Phaeophlebiopsis peniophoroides</i>	FP-150577	KP135417	Floudas & Hibbett (2015)
<i>Phanerochaete sordida</i>	CLZhao 4835	MK269184	Present study
<i>Phanerochaete sordida</i>	HHB-9899-sp	AY219382	De Koker <i>et al.</i> (2003)
<i>Phanerochaete velutina</i>	CLZhao 8156	MK404438	Present study
<i>Phanerochaete velutina</i>	CBS:137.75	MH860903	Vu <i>et al.</i> (2019)
<i>Phellinus adamantinus</i>	CLZhao 2820	MK404439	Present study
<i>Phellinus adamantinus</i>	Dai 17592	MF860791	Zhou <i>et al.</i> (2021)
<i>Phlebia ailaoshanensis</i>	CLZhao 3882	MH784919	Shen <i>et al.</i> (2018)
<i>Phlebia ailaoshanensis</i>	CLZhao 3904	MH784922	Shen <i>et al.</i> (2018)
<i>Phlebia radiata</i>	CLZhao 4882	MK404484	Present study
<i>Phlebia radiata</i>	JLL-15608-sp	AY219366	De Koker <i>et al.</i> (2003)
<i>Phlebicolorata rosea</i>	Dai 13573	KJ698635	Zhao <i>et al.</i> (2015a)
<i>Phlebicolorata rosea</i>	Dai 13584	KJ698636	Zhao <i>et al.</i> (2015a)
<i>Phlebiopsis crassa</i>	CLZhao 3943	MH114864	Present study
<i>Phlebiopsis crassa</i>	TNM:F30336	MZ637049	Chen <i>et al.</i> (2021)
<i>Phlebiopsis gigantea</i>	CLZhao 3965	MH114868	Present study
<i>Phlebiopsis gigantea</i>	CLZhao 8163	MK404489	Present study
<i>Phlebiopsis yunnanensis</i>	CLZhao 3958	MH744140	Present study
<i>Phlebiopsis yunnanensis</i>	CLZhao 3990	MH744141	Zhao <i>et al.</i> (2019)
<i>Picipes badius</i>	CLZhao 4949	ON319080	Present study
<i>Picipes badius</i>	Cui10853	KU189780	Zhou <i>et al.</i> (2016)
<i>Podoscypha yunnanensis</i>	CLZhao 3963	MK298400	Present study
<i>Podoscypha yunnanensis</i>	CLZhao 4035	MK298403	Wu <i>et al.</i> (2018)
<i>Punctularia bambusicola</i>	CLZhao 9098	MW559983	Present study
<i>Punctularia bambusicola</i>	CLZhao 4133	MW559982	Guan <i>et al.</i> (2021b)
<i>Pycnoporus sanguineus</i>	CLZhao 4807	MK269258	Present study

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TABLE 1. (Continued)

Species name	Sample no.	GenBank accession no.	References
		ITS	
<i>Pycnoporus sanguineus</i>	KA12-1267	KR673511	Kim <i>et al.</i> (2015)
<i>Sistotrema brinkmannii</i>	CLZhao 5221	MK269275	Present study
<i>Sistotrema brinkmannii</i>	FP-100507-Sp	OQ539595	Yu <i>et al.</i> (2023)
<i>Sistotremastrum guttuliferum</i>	CLZhao 5531	MK343645	Present study
<i>Sistotremastrum guttuliferum</i>	MA:Fungi 82105	JX310445	Telleria <i>et al.</i> (2013)
<i>Steccherinum aurantilaetum</i>	CLZhao 3807	MH114797	Present study
<i>Steccherinum aurantilaetum</i>	CLZhao 3969	MH114616	Present study
<i>Steccherinum bourdotii</i>	CLZhao 8150	MK404501	Present study
<i>Steccherinum bourdotii</i>	MT10/19	MT849312	Westphalen <i>et al.</i> (2021)
<i>Steccherinum fimbriatum</i>	CLZhao 8399	MK404503	Present study
<i>Steccherinum fimbriatum</i>	HR97926	MT849299	Westphalen <i>et al.</i> (2018)
<i>Steccherinum ochraceum</i>	CLZhao 3902	MH114886	Present study
<i>Steccherinum ochraceum</i>	KHL11902 (GB)	JQ031130	Sjökvist <i>et al.</i> (2012)
<i>Steccherinum xanthum</i>	CLZhao 5024	MW204587	Present study
<i>Steccherinum xanthum</i>	CLZhao 9138	MZ713697	Present study
<i>Stereum hirsutum</i>	CLZhao 3912	MH114889	Present study
<i>Stereum hirsutum</i>	NH7960	AF506479	Larsson <i>et al.</i> (2004)
<i>Stereum sanguinolentum</i>	CLZhao 5054	MK269301	Present study
<i>Stereum sanguinolentum</i>	CBS:116.71	MH860027	Vu <i>et al.</i> (2019)
<i>Terana coerulea</i>	CLZhao 5793	MK269227	Present study
<i>Terana coerulea</i>	CBS:163.56	MH857560	Vu <i>et al.</i> (2019)
<i>Theleporus rimosus</i>	CLZhao 5548	MK343667	Present study
<i>Theleporus rimosus</i>	Yuan 6873	KP342529	Yuan (2015)
<i>Trametes hirsuta</i>	CLZhao 4029	MH114902	Present study
<i>Trametes hirsuta</i>	LE 231641	HQ435869	Malysheva & Zmitrovich (2011)
<i>Trametes versicolor</i>	CLZhao 4857	ON319086	Present study
<i>Trametes versicolor</i>	Cui6915	JQ314354	Li & Cui (2013)
<i>Truncospora ochroleuca</i>	CLZhao 5733	MK268887	Present study
<i>Truncospora ochroleuca</i>	JV0610/7B	KJ410698	Spirin <i>et al.</i> (2015a)
<i>Xenasmatella ailaoshanensis</i>	CLZhao 4839	MN487106	Present study
<i>Xenasmatella ailaoshanensis</i>	CLZhao 3895	MN487105	Huang <i>et al.</i> (2019)
<i>Xylodon flaviporus</i>	CLZhao 8339	OM891748	Present study
<i>Xylodon flaviporus</i>	KA17-0796	MK920119	Kwon <i>et al.</i> (2019)
<i>Xylodon gossypinus</i>	CLZhao 8375	MZ663804	Present study
<i>Xylodon gossypinus</i>	CLZhao 4465	MZ663803	Luo <i>et al.</i> (2021)
<i>Xylodon heterocystidiatus</i>	CLZhao 4827	MK269242	Present study
<i>Xylodon heterocystidiatus</i>	CLZhao 15557	MW742678	Dong <i>et al.</i> (2023)
<i>Xylodon macrosporus</i>	CLZhao 8787	MZ663808	Present study
<i>Xylodon macrosporus</i>	CLZhao 2379	MZ663805	Luo <i>et al.</i> (2021)
<i>Xylodon montanus</i>	CLZhao 8118	OL619259	Qu <i>et al.</i> (2021)
<i>Xylodon montanus</i>	CLZhao 8179	OL619260	Qu <i>et al.</i> (2021)
<i>Xylodon nesporii</i>	CLZhao 3988	MH114741	Present study
<i>Xylodon nesporii</i>	CLZhao 5713	MK269035	Present study

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TABLE 1. (Continued)

Species name	Sample no.	GenBank accession no.	References
		ITS	
<i>Xylodon rhizomorphus</i>	CLZhao 8294	OM891747	Present study
<i>Xylodon rhizomorphus</i>	Dai 12389	KF917546	Zhao <i>et al.</i> (2014)
<i>Xylodon taiwanianus</i>	CLZhao 8319	MK404393	Present study
<i>Xylodon taiwanianus</i>	CBS:125875	MH864080	Vu <i>et al.</i> (2019)
<i>Yuchengia narymica</i>	CLZhao 3898	MH114926	Present study
<i>Yuchengia narymica</i>	Dai 6998	JN048775	Zhao <i>et al.</i> (2013b)

Results

Phylogenetic analyses

The ITS dataset (Figure 1) included sequences from 197 fungal specimens representing 99 species. The dataset had an aligned length of 1317 characters, of which 416 characters were constant, 143 parsimony-uninformative, and 758 parsimony-informative. The maximum parsimony analysis yielded 1 equally parsimonious tree (TL = 11693, CI = 0.1745, HI = 0.8388, RI = 0.6026, RC = 0.1052). The best-fit model for ITS alignment estimated and applied in the Bayesian was GTR+I+G, lset nst = 6, rates = invgamma; prset statefreqpr = dirichlet (1,1,1,1). The Bayesian and ML analyses showed a similar topology to that of the MP analysis with split frequencies = 0.015088 (BI), and the effective sample size (ESS) across the two runs is double the average ESS (avg ESS) = 250.5.

The phylogeny (Figure 1) inferred from ITS sequences demonstrated that 2814 specimens of wood-decaying fungi belonging to 103 taxa and all of them nested into twenty-eight families: Adustoporiaceae, Auriculariaceae, Bondarzewiaceae, Dacryobolaceae, Fomitopsidaceae, Fragiliporiaceae, Ganodermataceae, Grammotheleaceae, Hericiaceae, Hydnaceae, Hymenochaetaceae, Hyphodermataceae, Irpicaceae, Laetiporaceae, Meruliaceae, Peniophoraceae, Phaeophlebiopsis, Phanerochaetaceae, Physalacriaceae, Podoscyphaceae, Polyporaceae, Punctulariaceae, Rickenellaceae, Schizophoraceae, Sistotremastraceae, Steccherinaceae, Stereaceae and Xenasmataceae, belonging to nine orders: Agaricales, Auriculariales, Cantharellales, Corticiales, Hymenochaetales, Polyporales, Russulales, Sistotrematales and Xenasmatales of Agaricomycetes.

Checklist

An alphabetical list (according to genus name) of corticioid fungal identified in these investigations is given below. The authors of scientific names are according to the second edition of Authors of Fungal Names (<http://www.indexfungorum.org/AuthorsOfFungalNames.html>). Substrate and collecting data are provided after the name of each species.

1. ***Abundisporus quercicola*** Y.C. Dai, Annales Botanici Fennici 39 (3): 171 (2003). White rot in a broad-leaved forest. Ailaoshan National Nature Reserve, Zhenyuan County, Puer, Yunnan Province, China, on a trunk of angiosperm, 12 January 2018, CLZhao 4955, CLZhao 4895; Jinshan Primitive Forest Park, Xinping County, Yuxi, Yunnan Province, China, on a trunk of angiosperm, 2 January 2019, CLZhao 9166.

2. ***Adustoporia sinuosa*** (Fr.) Audet, Mushrooms nomenclatural novelties 11: 1 (2017). Brown rot in a broad-leaved forest. Ailaoshan National Nature Reserve, Heping Town, Zhenyuan County, Puer, Yunnan Province, China, on a fallen trunk of angiosperm, 11 January 2018, CLZhao 4818.

3. ***Aleurodiscus cerussatus*** (Bres.) Höhn. & Litsch., Sitzungsberichte der Kaiserlichen Akademie der Wissenschaften Math.-naturw. Klasse Abt. I 116: 760, 807 (1907). White rot in a broad-leaved forest. Ailaoshan National Nature Reserve, Jingdong County, Puer, Yunnan Province, China, on a trunk of angiosperm, 5 October 2017, CLZhao 4102.

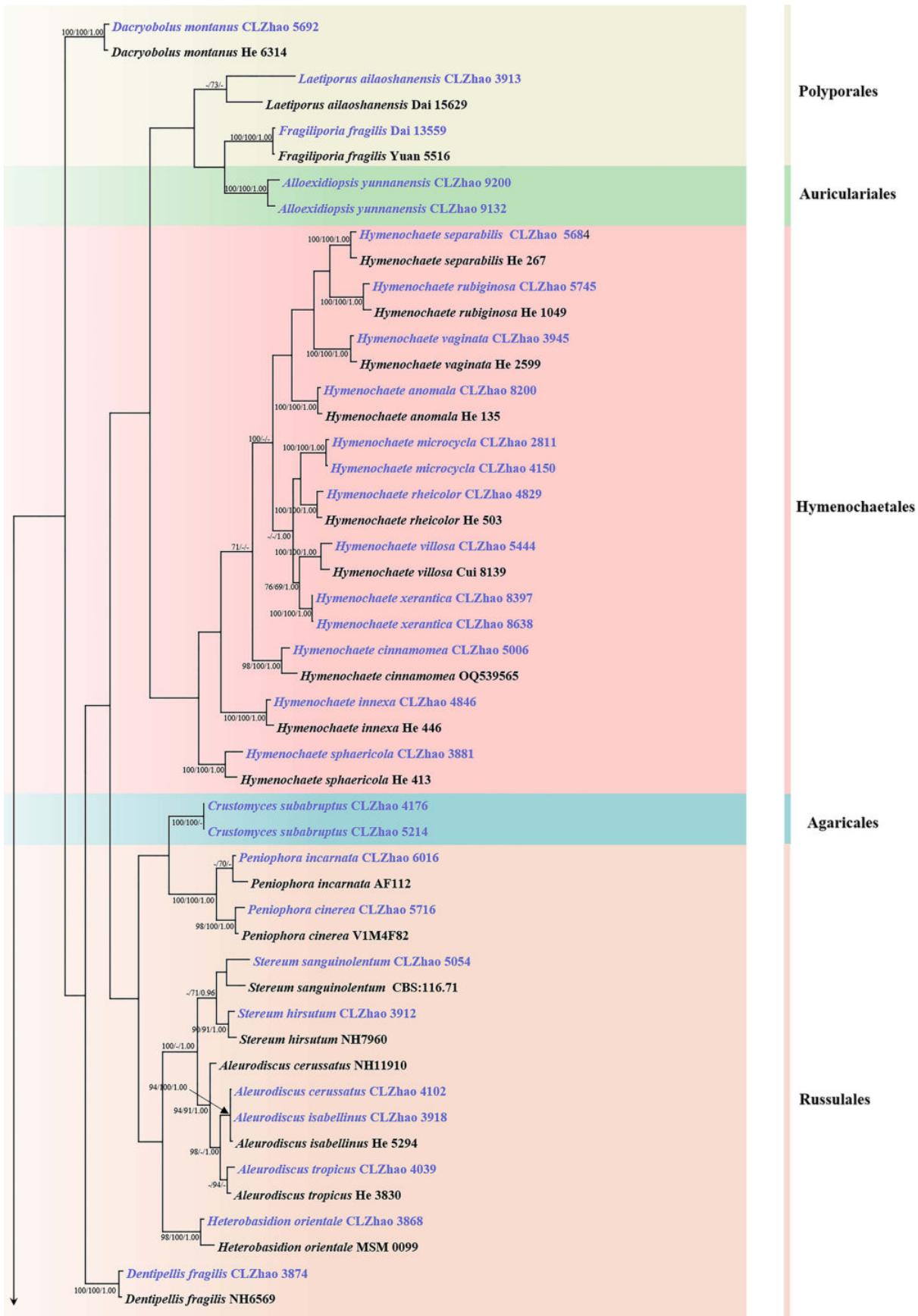


FIGURE 1. Maximum parsimony strict consensus tree illustrating the phylogeny of 103 species in Agaricomycetes based on ITS sequences. Branches are labelled with a maximum likelihood boot-strap >70%, a parsimony bootstrap >50%, and Bayesian posterior probabilities >0.97, respectively. The sequences of collections labelled in black are downloaded from GenBank, while those in purple are generated in this study.

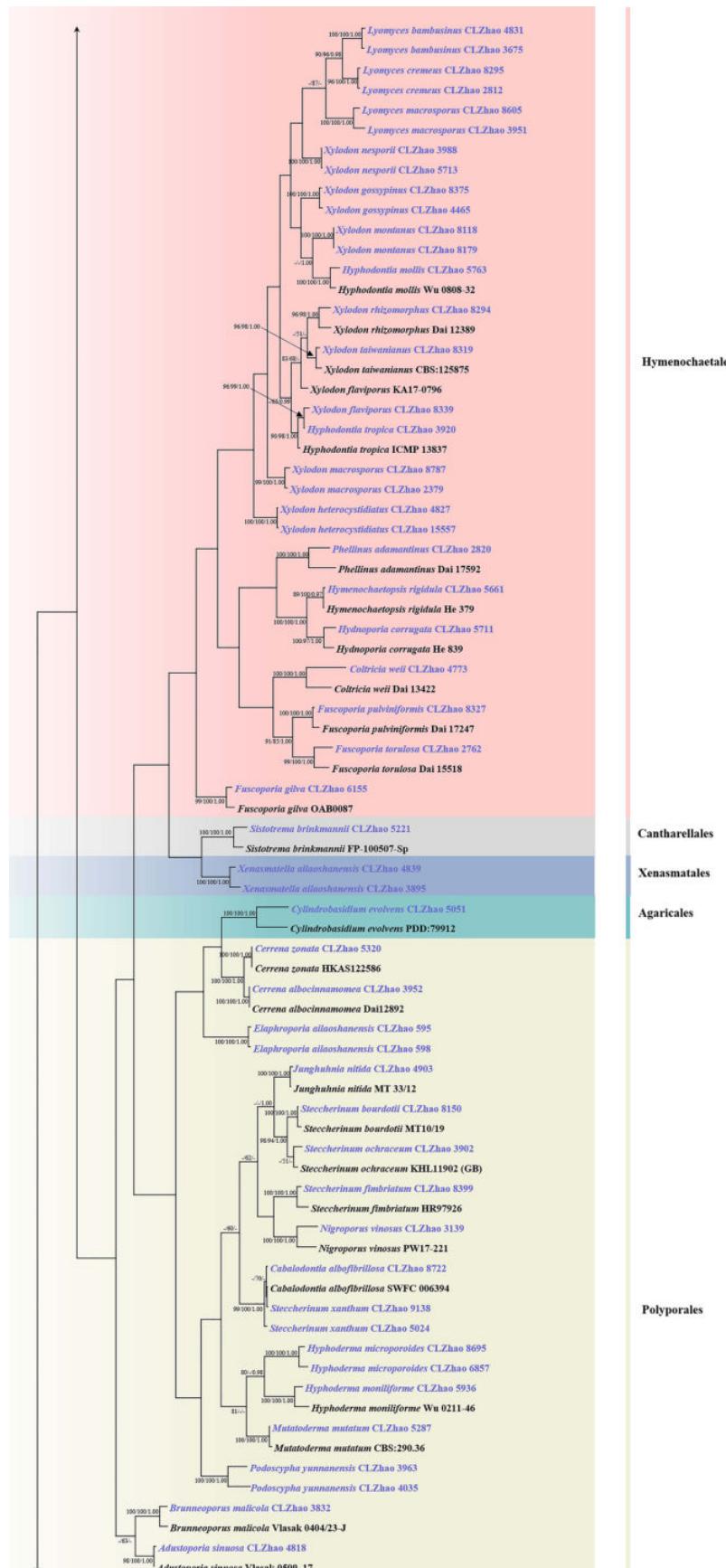


FIGURE 1. Cont.

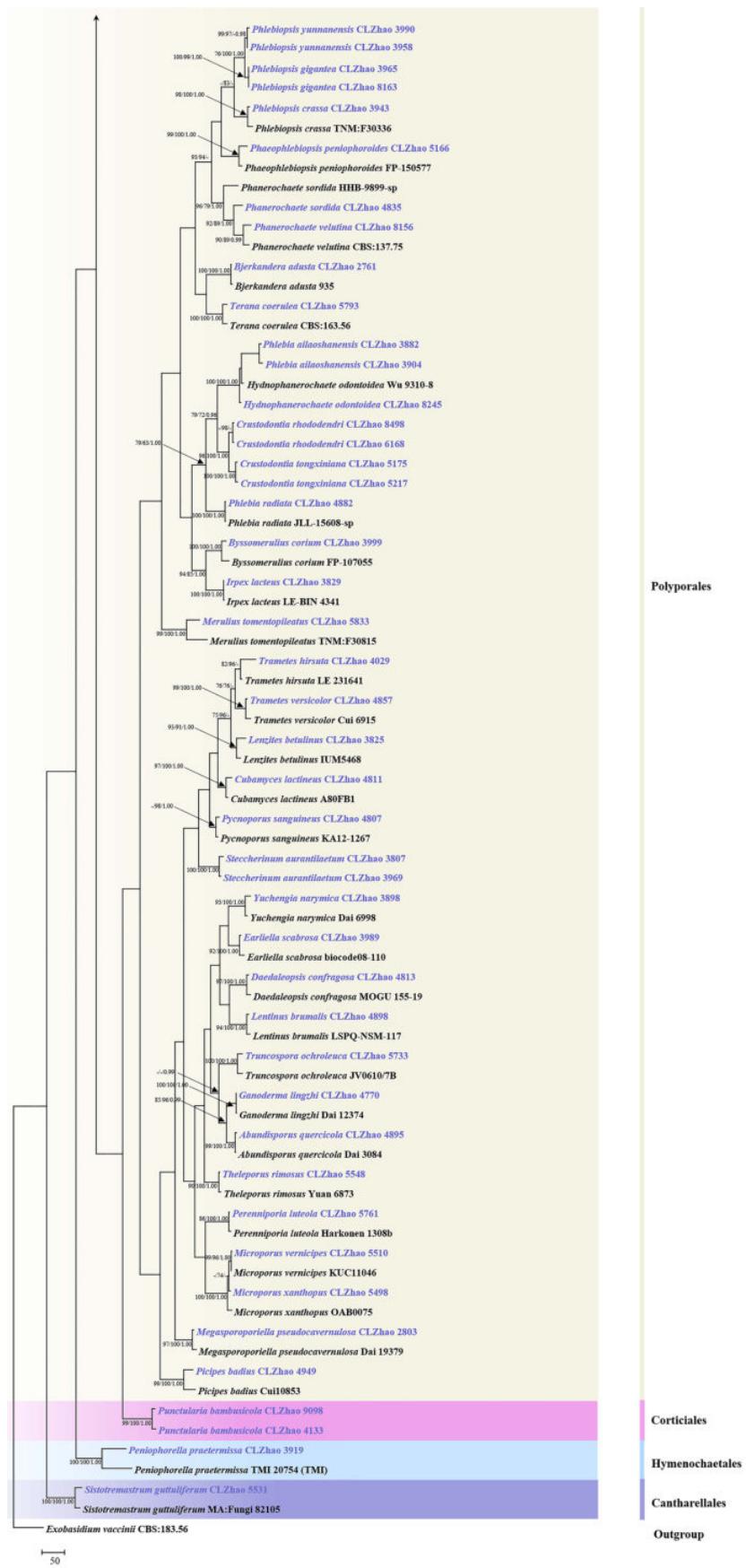


FIGURE 1. Cont.

4. *Aleurodiscus isabellinus* S.H. He & Y.C. Dai, in Tian, Ghobad-Nejhad, He & Dai, MycoKeys 37: 100 (2018). White rot in a broad-leaved forest. Ailaoshan National Nature Reserve, Puer, Yunnan Province, China, on a fallen branch of angiosperm, 4 October 2017, CLZhao 3918; Tea horse ancient road scenic spot, Xinpingshui County, Yuxi, Yunnan Province, China, on a fallen trunk of angiosperm, 13 January 2018, CLZhao 5176; CLZhao 5199; CLZhao 5405; Ailaoshan National Nature Reserve, Liangzi Village, Heping Town, Zhenyuan County, Puer, Yunnan Province, China, on a fallen trunk of angiosperm, 14 January 2018, CLZhao 5625.

5. *Aleurodiscus tropicus* L.D. Dai & S.H. He, in Dai, Wu, Nakasone, Burdsall & He, Mycoscience 58(3): 215 (2017). White rot in a broad-leaved forest. Ailaoshan National Nature Reserve, Jingdong County, Puer, Yunnan Province, China, on a dead Bamboo, 4 October 2017, CLZhao 4039.

6. *Alloexidiopsis yunnanensis* (C.L. Zhao) L.W. Zhou & S.L. Liu, Frontiers in Microbiology 13 (no. 894641): 9 (2022). White rot in a broad-leaved forest. Jinshan Forest Park, Xinpingshui County, Yuxi, Yunnan Province, China, on a fallen trunk of angiosperm, 2 January 2019, CLZhao 9200; Ailaoshan National Nature Reserve, Jingdong County, Puer, Yunnan Province, China, on a fallen trunk of angiosperm, 4 October 2017, CLZhao 4023.

7. *Bjerkandera adusta* (Willd.) P. Karst., Medd. Soc. Fauna Flora Fenn. 5: 38 (1879). White rot in a mixed coniferous broad-leaved forest. Ailaoshan Scenic Spot, Xinpingshui County, Yuxi, Yunnan Province, China, on a trunk or a stump of angiosperm, on the fallen branch of *Pinus*, 21 August 2017, CLZhao 2761; white rot in a broad-leaved forest. Ailaoshan National Nature Reserve, Puer, Yunnan Province, China, on a trunk of angiosperm, 4 October 2017, CLZhao 3799, CLZhao 3891, CLZhao 3935; Jinshan Primitive Forest Park, Zhenyuan County, Puer, Yunnan Province, China, on a trunk of angiosperm, 12 January 2018, CLZhao 4925; on a stump of angiosperm, 14 January 2018, CLZhao 5453, CLZhao 5455, CLZhao 5458, CLZhao 5471; Jinshan Primeval Forest, Puer, Yunnan Province, China, on a trunk of angiosperm, 2 January 2019, CLZhao 9207.

8. *Brunneoporus malicola* (Berk. & M.A. Curtis) Audet, Mushrooms nomenclatural novelties 2: 1 (2017). Brown rot in a broad-leaved forest. Ailaoshan, Taizhong Town, Jingdong County, Puer, Yunnan Province, China, on a fallen trunk of angiosperm, 4 October 2017, CLZhao 3832.

9. *Byssomerulius corium* (Pers.) Parmasto, Eesti NSV Tead. Akad. Toim., Biol. seer 16(4): 383 (1967). White rot in a broad-leaved forest. Ailaoshan National Nature Reserve, Taizhong Town, Jingdong County, Puer, Yunnan Province, China, on a fallen trunk of angiosperm, 4 October 2017, CLZhao 3999.

10. *Cabalodontia albofibrillosa* (Hjortstam & Ryvarden) Westphalen, in Westphalen, Motato-Vásquez, Tomšovský & Gugliotta, Mycologia: 10.1080/00275514.2021.1894536, 5 (2021). White rot in a broad-leaved forest. Ailaoshan National Nature Reserve, Puer, Yunnan Province, China, on a trunk of angiosperm, 25 August 2018, CLZhao 8722.

11. *Cerrena albocinnamomea* (Y.C. Dai & Niemelä) H.S. Yuan, Mycological Progress 13(2): 362 (2013). White rot in a broad-leaved forest. Ailaoshan National Nature Reserve, Puer, Yunnan Province, China, on a trunk of angiosperm, 4 October 2017, CLZhao 3952; Jinshan Primitive Forest Park, Zhenyuan County, Puer, Yunnan Province, China, on a trunk of angiosperm, 12 January 2018, CLZhao 5022, CLZhao 5029, CLZhao 5046; Tea horse ancient road scenic spot, Xinpingshui County, Yuxi, Yunnan Province, China, on a trunk of angiosperm, 13 January 2018, CLZhao 5268, CLZhao 5270, CLZhao 5304; Jinshan Primeval Forest, Puer, Yunnan Province, China, on a trunk of angiosperm, 2 January 2019, CLZhao 9146.

12. *Cerrena zonata* (Berk.) H.S. Yuan, Mycological Progress 13(2): 363 (2013). White rot in a broad-leaved forest. Ailaoshan Scenic Area, Xinpingshui County, Yuxi, Yunnan Province, China, on a trunk or a stump of angiosperm, 21 August 2017, CLZhao 2751; Tea horse ancient road scenic spot, Xinpingshui County, Yuxi, Yunnan Province, China, on a living tree of angiosperm, 13 January 2018, CLZhao 5320; Ailaoshan National Nature Reserve, Liangzi Village, Heping Town, Zhenyuan County, Puer, Yunnan Province, China, on a stump of angiosperm, 14 January 2018, CLZhao 5518, CLZhao 5539.

13. *Coltricia weii* Y.C. Dai, Sydowia 62 (1): 16 (2010). White rot in a broad-leaved forest. Ailaoshan National Nature Reserve, Jingdong County, Puer, Yunnan Province, China, on the ground, 6 October 2017, CLZhao 4773.

14. *Crustodontia rhododendri* C.L. Zhao, J. Fungi 9 (3, no. 320): 13 (2023). White rot in a broad-leaved forest. Damoshan, Puer, Zhenyuan County, Yunnan Province, China, on a fallen branch of *Rhododendron simii*, 15 January 2018, CLZhao 6168; Ailaoshan Ecological Station, Xuiba, Yunnan Province, China, on a fallen branch of the angiosperm, 23 August 2018, CLZhao 8413; 24 August 2018, CLZhao 8498, CLZhao 8645; on a dead tree of angiosperm, 24 August 2018, CLZhao 8620; Ailaoshan National Nature Reserve, Zhenyuan County, Puer, Yunnan Province, China, on a fallen branch of the angiosperm, 14 January 2018, CLZhao 5614, CLZhao 5623, CLZhao 5628, CLZhao 5680; 15 January 2018, CLZhao 5821, CLZhao 5841; on a stump of angiosperm, 15 January 2018, CLZhao 5873.

15. *Crustodontia tongxiniana* (C.L. Zhao) C.C. Chen & Sheng H. Wu, in Chen, Chen & Wu, Fungal Diversity 111: 421 (2021). White rot in a broad-leaved forest. Tea Horse Ancient Road Scenic Spot, Xinping County, Yuxi, Yunnan Province, China, on a trunk of angiosperm, 13 January 2018, CLZhao 5175; 21 August 2018, CLZhao 8168.
16. *Crustomyces subabruptus* (Bourdot & Galzin) Jülich, Persoonia 10 (1): 140 (1978). White rot in a broad-leaved forest. Wuliangshan, Jingdong County, Puer, Yunnan Province, China, on a trunk of angiosperm, 5 October 2017, CLZhao 4176; Ailaoshan National Nature Reserve, Jingdong County, Puer, Yunnan Province, China, on a trunk of angiosperm, 13 January 2018, CLZhao 5214.
17. *Cubamyces lactineus* (Berk.) Lücking, Willdenowia 50 (3): 396 (2020). White rot in a broad-leaved forest. Ailaoshan National Nature Reserve, Heping Town, Zhenyuan County, Puer, Yunnan Province, China, on a trunk of angiosperm, 11 January 2018, CLZhao 4811, CLZhao 4823.
18. *Cylindrobasidium evolvens* (Fr.) Jülich, Persoonia 8 (1): 72 (1974). White rot in a broad-leaved forest. Ailaoshan National Nature Reserve, Jingdong County, Puer, Yunnan Province, China, on a trunk of angiosperm, 12 January 2018, CLZhao 5051.
19. *Dacryobolus montanus* X.Z. Wan & H.S. Yuan, Phytotaxa 265 (2): 107 (2016). Brown rot in a broad-leaved forest. Liangzi Village, Heping Town, Zhenyuan County, Puer, Yunnan Province, China, on a fallen trunk of angiosperm, 14 January 2018, CLZhao 5692; Ailaoshan National Nature Reserve, Taizhong Town, Jingdong County, Puer, Yunnan Province, China, on a trunk of angiosperm, 23 August 2018, CLZhao 8360.
20. *Daedaleopsis confragosa* (Bolton) J. Schröt., in Cohn, Krypt.-Fl. Schlesien (Breslau) 3.1(25–32): 492 (1888). White rot in a broad-leaved forest. Ailaoshan National Nature Reserve, Heping Town, Zhenyuan County, Puer, Yunnan Province, China, on a fallen trunk of angiosperm, 11 January 2018, CLZhao 4813, CLZhao 4820, CLZhao 4828, CLZhao 4836.
21. *Dentipellis fragilis* (Pers.) Donk, Persoonia 2(2): 233 (1962). White rot in a broad-leaved forest. Ailaoshan National Nature Reserve, Puer, Yunnan Province, China, on a trunk of angiosperm, 4 October 2017, CLZhao 3874; Ailaoshan Ecological Station, Puer, Yunnan Province, China, on a trunk of angiosperm, 24 August 2018, CLZhao 8609.
22. *Earliella scabrosa* (Pers.) Gilb. & Ryvarden, Mycotaxon 22(2): 364 (1985). White rot in a broad-leaved forest. Ailaoshan National Nature Reserve, Taizhong Township, Jingdong County, Puer, Yunnan Province, China, on a trunk of angiosperm, 4 October 2017, CLZhao 3989, CLZhao 4008.
23. *Elaphroporia ailaoshanensis* Z.Q. Wu & C.L. Zhao, in Wu, Xu, Shen, Liu, Luo & Zhao, MycoKeys 29: 89 (2018). White rot in a broad-leaved forest. Ailaoshan National Nature Reserve, Jingdong County, Puer, Yunnan Province, China, on a trunk of angiosperm, 12 October 2016, CLZhao 595, CLZhao 596, CLZhao 597, CLZhao 598.
24. *Fragiliporia fragilis* Y.C. Dai, B.K. Cui & C.L. Zhao, in Zhao, Cui, Song & Dai, Fungal Diversity 70: 115–126. White rot in a broad-leaved forest. Ailaoshan National Nature Reserve, Jingdong County, Puer, Yunnan Province, China, on a fallen trunk of angiosperm, 15 October 2013, Dai 13559, Dai 13561 (BJFC015021, BJFC015023, BJFC).
25. *Fuscoporia gilva* (Schwein.) T. Wagner & M. Fisch., Mycologia 94 (6): 1013 (2002). White rot in a broad-leaved forest. Damoshan, Heping Town, Zhenyuan County, Puer, Yunnan Province, China, on a dead tree of angiosperm, 16 January 2018, CLZhao 6155; Ailaoshan Ecological Station, Puer, Yunnan Province, China, on a trunk of angiosperm, 25 August 2018, CLZhao 8740; Heping Town, Zhenyuan County, Puer, Yunnan Province, China, on a stump of angiosperm, 1 January 2019, CLZhao 9096.
26. *Fuscoporia pulviniformis* Tchotet, M.P.A. Coetzee, Rajchenb. & Jol. Roux, Mycologia 112 (4): 734 (2020). White rot in a broad-leaved forest. Ailaoshan Ecological Station, Puer, Yunnan Province, China, on a fallen trunk of angiosperm, 23 August 2018, CLZhao 8327.
27. *Fuscoporia torulosa* (Pers.) T. Wagner & M. Fisch., Mycological Research 105 (7): 780 (2001). White rot in a broad-leaved forest. Ailaoshan Scenic Spot, Xinping County, Yuxi, Yunnan Province, China, on a trunk of angiosperm, 21 August 2017, CLZhao 2762; Jinshan Primitive Forest Park, Zhenyuan County, Puer, Yunnan Province, China, on a trunk of angiosperm, 12 January 2018, CLZhao 5017; Tea horse ancient road scenic spot, Xinping County, Yuxi, Yunnan Province, China, on a trunk of angiosperm, 13 January 2018, CLZhao 5324, CLZhao 5325; Ailaoshan Ecological Station, Puer, Yunnan Province, China, on a trunk of angiosperm, 23 August 2018, CLZhao 8318.
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Discussion

This study conducted seven field investigations on Ailaoshan National Nature Reserve and collected wood-decaying fungal samples from different forest types. One hundred and three ITS sequences were newly generated from 103 specimens, each representing one of the species. These species belong to one class, nine orders, 29 families, and 64 genera within Basidiomycota. There were 57 species of Polyporales, accounting for 55.34% of the total species, indicating that Polyporales was the dominant group in this area; there were 30 species of Hymenochaetales, accounting for 29.13%, which were subdominant groups in the region; nine species belong to Russulales; two species belong to Agaricales; the other five species belong to Auriculariales, Cantharellales, Corticiales, Sistotrematales, and Xenasmatales (Table 2, Figure 2). Photos of wood-decaying fungi *in situ* are presented for selected species (Figure 3).

There are 11 species of wood-decaying fungi with edible and medicinal fungi were found in the study: *Abundisporus quercicola*, *Bjerkandera adusta*, *Earliella scabrosa*, *Ganoderma lingzhi*, *Irpex lacteus*, *Lenzites betulinus*, *Pycnoporus sanguineus*, *Pyrrhoderma adamantinum*, *Stereum hirsutum*, *S. sanguinolentum* and *Trametes versicolor*, accounted for 10.68% of the total species (Dai & Yang 2008; Wu *et al.* 2019a). Four of the wood-decaying fungi we recorded are forest pathogens: *Abundisporus quercicola*, *Bjerkandera adusta*, *Daedaleopsis confragosa*, and *Stereum sanguinolentum*, accounted for 3.88% of the total species (Dai 2012a). Due to environmental pollution, climate change, habitat loss and fragmentation, and over-exploitation of resources, macrofungi's diversity is seriously threatened (Li *et al.* 2020; Yao *et al.* 2020; Wei *et al.* 2020). In our study, there are eight wood-decaying fungi we recorded are threatened species: *Hypoderma moniliforme*, *Hypodontia mollis*, *Peniophora incarnata*, *Perenniporia luteola*, *Picipes badius*, *Xylodon flaviporus*, *X. heterocystidiatus*, and *X. taiwanianus*, accounted for 7.77% of the total of the species (Yao *et al.* 2020). According to the previous studies combined with field observations, six species (5.83% of the total), *Amyloporia sinuosa*, *Brunneoporus malicola*, *Ceriporiopsis rosea*, *Dacryobolus montanus*, *Laetiporus ailaoshanensis* and *Punctularia bambusicola* can cause a brown-rot; the remaining 97 species (94.17% of the total) cause a white-rot (Dai 2011; Dai 2012a; Fukasawa *et al.* 2020; He & Zhao 2021). Therefore, a comprehensive

understanding of the threat status of wood-decaying fungi can better propose targeted conservation strategies in future studies, which is of great significance for strengthening the biodiversity conservation of macrofungi. Yunnan Province has the most abundant macrofungi diversity. Wood-decaying fungi have been extensively studied, and their members increased rapidly (Zhao *et al.* 2023; Deng *et al.* 2024; Yang *et al.* 2024). *Crustodontia rhododendri*, *Elaphroporia ailaooshanensis*, *Hyphoderma microporoides*, *Phlebia ailaooshanensis*, *Phlebiopsis yunnanensis*, *Podoscypha yunnanensis*, *Steccherinum xanthum*, *Xylodon gossypinus*, and *X. macrosporus*, accounted for 8.74% of the total species, were newly published in recent years from Ailaoshan area (Zhao *et al.* 2018, 2023; Wu *et al.* 2018; Guan *et al.* 2021a, 2021b; Shen *et al.* 2018; Wu *et al.* 2019b; Luo *et al.* 2021; Zhou *et al.* 2021).

TABLE 2. The taxonomic position of 103 corticioid fungal basidiomycetous species in the Ailaoshan Mountains.

Class	Order	Family	Number of genera	Number of species	
Agaricomycetes	Agaricales	Cystostereaceae	1	1	
		Physalacriaceae	1	1	
	Auriculariales	Auriculariaceae	1	1	
		Cantharellales	Hydnaceae	1	1
		Corticiales	Punctulariaceae	1	1
	Hymenochaetales	Hymenochaetaceae	6	18	
		Rickenellaceae	1	1	
	Polyporales	Schizoporaceae	2	11	
		Adustoporiaceae	1	1	
		Dacryobolaceae	1	1	
		Fomitopsidaceae	1	1	
		Fragiliporiaceae	1	1	
		Ganodermataceae	1	1	
		Grammotheleaceae	1	1	
		Hyphodermataceae	2	4	
		Irpicaceae	2	4	
		Laetiporaceae	1	1	
		Meruliaceae	8	10	
		Phaeophlebiopsis	1	1	
		Phanerochaetaceae	4	7	
	Russulales	Podoscyphaceae	1	1	
		Polyporaceae	16	19	
		Steccherinaceae	2	6	
		Bondarzewiaceae	1	1	
		Hericiaceae	1	1	
		Peniophoraceae	1	2	
		Stereaceae	2	5	
	Sistotrematales	Sistotremastraceae	1	1	
		Xenasmataceae	1	1	

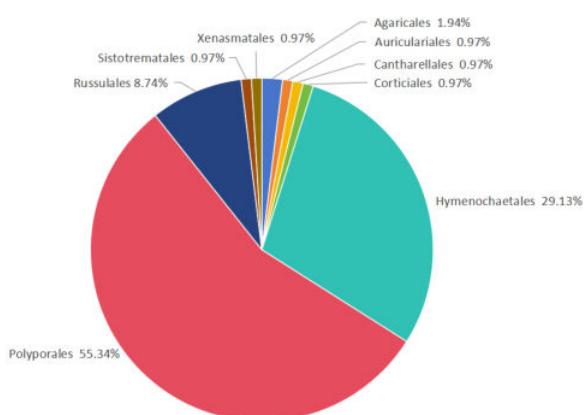


FIGURE 2. Taxonomic composition of 103 corticioid fungal species at the order level in the Ailaoshan Mountains.



FIGURE 3. Fruiting bodies in situ of (A) *Abundisporus quercicola* (CLZhao 4895) (B) *Alloexidiopsis yunnanensis* (CLZhao 9200) (C) *Coltricia weii* (CLZhao 4773) (D) *Daedaleopsis confragosa* (CLZhao 4813) (E) *Fuscoporia pulviniformis* (CLZhao 8327) (F) *Hymenochaete rheicolor* (CLZhao 4829) (G) *Hymenochaete xerantica* (CLZhao 8397) (H) *Laetiporus ailaoshanensis* (CLZhao 3913) (I) *Lenzites betulinus* (CLZhao 3825) (J) *Lyomyces macrosporus* (CLZhao 8605) (K) *Megasporoporiella pseudocavernulosa* (CLZhao 2803) (L) *Microporus vernicipes* (CLZhao 5510) in the Ailaoshan Mountains. Bars: (A), (B), (E) = 2 cm; (C), (F), (G), (H), (I), (J), (K), (L) = 1 cm; (D) = 3 cm.

Recently, some notable explorations have begun to pay attention to the diversity of wood-decaying fungi in Yunnan Province (Wang & Cai 2023). Ninety white-rot fungi and five brown-rot fungi were reported in the Wuliangshan area, China; 49 white-rot fungi and three brown-rot fungi were reported in Haikou Forestry Park, China; 99 white-rot fungi and five brown-rot fungi were reported in Wenshan area, China; 72 white-rot fungi and 24 brown-rot fungi were reported in Laojunshan Mountains, China (Dai & Cui 2012; He *et al.* 2021; He & Zhao 2022; Dong *et al.* 2023). In the current study, 103 wood-decaying fungal species were collected from the Ailaoshan area, Yunnan Province, China, in which six species cause brown rot, and the remaining 97 can cause white rot. In comparison, those in the Wuliangshan area are 5.36%, in the Haikou Forestry Park 5.77%, and in the Wenshan area 4.81%, which indicates that the proportions of brown-rot fungi in the four areas seem similar (He *et al.* 2021; He & Zhao 2022; Dong *et al.* 2023). However, the proportion of brown-rot fungi to wood-decaying fungi in the Laojunshan Mountains is 25%, which is greatly higher than in the Ailaoshan area (Dai & Cui 2012). In addition, there were 11 forest pathogens reported in the Gaoligong Mountains, which accounted for 8.59% of the total wood-decaying fungi (Dai *et al.* 2014), while there are four forest pathogens in the Ailaoshan area account for 3.88%.

Wood-decaying fungi a vital group in the forest ecosystem (Dai 2012a; Zhao *et al.* 2023; Deng *et al.* 2024; Yang *et al.* 2024), contribute significantly to material cycling. They decompose cellulose, semi-cellulose, and lignin of wood into nutrition that can be easily absorbed by themselves and other organisms (Wei 2021; Dai *et al.* 2021a). Given the importance of deadwood decomposition in nutrient cycling, soil formation, and ecosystem carbon budget, it has received increasing attention from ecologists, pathologists, and forest managers (Tedesco *et al.* 2014; Hyde *et al.* 2019; Ji *et al.* 2022; Liu *et al.* 2023). The functional traits of wood-decaying fungi can reflect the adaptation of species to environmental conditions and help to understand the mechanisms underlying the aggregation of fungal communities in different environments (Tedesco *et al.* 2014; Dai *et al.* 2021b; Wijayawardene *et al.* 2022). Since wood-decaying fungi have multiple functions in forests, it is necessary to conduct systematic surveys of wood-decaying fungi and understand their distribution in forest communities, which provides insights into nutrient cycling and biodiversity conservation (Dai *et al.* 2021a; Wei 2021; Wang & Cai 2023).

Due to the unique preservation of forest communities in the Ailaoshan area, specimen collection in certain regions poses a challenge. As a result, the diversity of wood-decaying fungi in this area remains a mystery. This paper is the first in a series of studies dedicated to understanding the wood-decaying fungi in this area, a crucial step in revealing the abundance of these species. However, the underlying fungal diversity in the Ailaoshan area is still largely unpredictable, sparking a need for a more intensive investigation to complement future biodiversity research.

The conclusion of this study is summarized as follows: seven field surveys were carried out in the Ailaoshan area of Yunnan Province, China, from 2016 to 2021, in which 2,814 specimens of wood-decaying fungal species were collected. One hundred and three species of wood rot fungi were identified, belonging to 64 genera, 29 families, and nine orders. According to the latest classification system of fungi, the checklist of these wood-decaying fungal species is provided. This study not only enriched the species diversity of wood-decaying fungi in this area but also unveiled a fascinating world of biodiversity. It also provided a theoretical basis for the protection and utilization of wood-decaying fungal resources in this area in the future, inspiring and motivating the scientific community and professionals in the field of mycology and biodiversity conservation to further explore and utilize these resources.

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