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研究论文



蓝小菇

Mycena galericulata (Scop.) Gray
属于担子菌门Basidiomycota，
蘑菇纲Agaricomycetes，蘑菇目
Agaricales，小菇科Mycenaceae。
湖南师范大学陈作红教授2022年
7月29日摄于湖南省八大公山国
家级自然保护区。

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Mycena galericulata (Scop.) Gray
Basidiomycota, Agaricomycetes, Agaricales, Mycenaceae. Courtesy of Prof. CHEN Zuohong, Hunan Normal University, taken from Badagongshan National Nature Reserve, Hunan, 29 July 2022.

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云南省文山地区木腐菌真菌资源多样性研究

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摘要: 本研究于 2017–2021 年在云南省文山地区进行了 5 次实地调查, 共采集木腐真菌标本 2 923 号。采用经典分类学方法开展了该地区采集标本的准确鉴定, 并编制了木腐真菌完整名录。采用最大似然法、最大简约法和贝叶斯推理法对研究标本的 ITS nrRNA 基因序列构建系统发育树, 剖析分类单元的聚类关系及物种间的系统发育关系。研究结果揭示该地区共报道木腐真菌 104 种, 隶属于 5 目 18 科 55 属。其中多孔菌目为优势目(占总数的 51.92%), 多孔菌科为优势科(占总数的 24.04%), 木齿菌属为优势属(占总数的 12.50%)。

关键词: 担子菌门; 生物资源; 多样性; 分子系统学; 文山地区

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Diversity of wood-decaying fungi in Wenshan Area, Yunnan Province, China

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Abstract: Five field surveys were carried out in Wenshan area, Yunnan Province, China during 2017–2021, and 2 923 specimens of wood-decaying fungi were collected. A checklist of wood-decaying fungi with their hosts and substrates is given. The taxa were identified in the light of their morphology and molecular evidence. The sequences of ITS nrRNA gene region of the studied specimens were generated and the phylogenetic analyses were performed with the maximum likelihood, maximum parsimony and Bayesian inference methods. The paper summarizes the obtained results of investigation on the wood-decaying fungi of this area,

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consisting of 104 species belonging to 55 genera, 18 families and 5 orders. Polyporales is the dominant order (51.92% of the total orders found in this area), and Polyporaceae is the dominant family (24.04% of the total) and *Xylodon* is the dominant genus (12.50% of the total).

Keywords: Basidiomycota; biological resources; diversity; molecular systematics; Wenshan

INTRODUCTION

Fungi are a diverse, monophyletic group of eukaryotes and these organisms show immense ecological and economic impacts for playing an important role in the ecosystems as diverse as soil, trees, hidden layers within their substrate (James *et al.* 2020). Approximately 150 thousand species of fungi have been described (Dai *et al.* 2021; Wang & Zhao 2021), but the potential biodiversity of the group is likely to be 2.2–3.8 millions of species (Blackwell 2011; Taylor *et al.* 2014; Hibbett 2016; Hawksworth & Lücking 2017). The diversity for flora of seed plants in Yunnan Province is higher than that in other areas of China. The number of discovered new fungal species totalled 1 345 from this province from 2000 to 2020. Endemic woody plants are rich in Yunnan, supplying rich and varied substrates for wood-decaying fungi. Wood-decaying fungi with industrial, medicinal, edible and economic value, comprise most basidiomycetes and ascomycetes growing on various kinds of living trees, dead and fallen trunk, fallen branch and stump (Russell & Paterson 2006; Dai 2012a; Dai *et al.* 2015, 2021; Vinay *et al.* 2015; Wu *et al.* 2019, 2020; M'Barek *et al.* 2020; Runnel *et al.* 2021; Luo *et al.* 2022), displaying a considerable ability to degrade plant remains and different environmental contaminants through their extensive organic compound degradation abilities (James *et al.* 2020).

The Wenshan area is located in the southeast part of Yunnan Province, including Laojunshan National Nature Reserve and Xiaoqiaogou National Nature Reserve and their surrounding areas (Yang *et al.* 2008). The geographical location is between 103°48'–104°52' E and 23°16'–22°29' N with the altitude of 1 200–2 991 m; the average annual precipitation is more than 1 500 mm (Yang *et al.* 2008; Li *et al.* 2021). The plant resources are rich, with 187 families, 946 genera and 3 085

species of seed plants (Yang *et al.* 2008). The vegetation types varied with elevation differences (Yang *et al.* 2008; Li *et al.* 2021). The Wenshan area has five main types of well-preserved vegetation namely the mid-mountain wet, semi-wet evergreen broad-leaved forest, monsoon evergreen broad-leaved forest, mossy evergreen broad-leaved forest and mossy dwarf forest (Yang *et al.* 2008), which are precondition of the fungal diversity of this area.

Most of wood-decaying fungi are reported in northwest Yunnan, and some polypore and the corticioid fungi have been reported in the southeast of the Yunnan Province (Xie 1992; Chen 1994; Zhang *et al.* 2012; Guo *et al.* 2013; Dai *et al.* 2014; Chen *et al.* 2020; Wang & Zhao 2021). According to the modern taxonomy, wood-decaying fungi mainly belong to ten orders of Agaricomycetes, *viz.*, Agaricales, Auriculariales, Cantharellales, Corticiales, Gloeophyllales, Hymenochaetales, Polyporales, Russulales, Thelephorales and Trechisporales (Dai 2012a; Dai *et al.* 2015, 2021; Wu *et al.* 2020). The current wood-decaying fungal catalogues include the poroid and corticioid hymenophores. In the present study, five field trips were carried out in Wenshan area, and 104 species were identified. This work aims at providing an updated checklist of wood-decaying fungi in Wenshan, as well as enriching the knowledge of the fungal diversity of China.

1 MATERIALS AND METHODS

1.1 Sample collection and herbarium specimen preparation

The fresh fruiting bodies of basidiomycetous macrofungi growing on angiosperm stumps, trunks and branches were collected in 5 sampling points (approximately the four corners of the square and centre) within 1×1 km² for 2–3 times every year in Wenshan area from 2017–2021. Three basidiomata

at least are required and each individual is up to 3 cm long, 2 cm wide, in which the smallest fruiting structure has to include the hymenophore. The samples were photographed *in situ* and its fresh macroscopic details were recorded. Photographs were recorded by a Jianeng 80D camera. All the photos were focus stacked and merged using Helicon Focus software. The samples were transported to a field station where the fruit bodies were dried on an electronic food dryer (Fruit) at 45 °C for 48 hours. Then the dried specimens were sealed in an envelope and zip-lock plastic bags and labeled. The dried specimens were deposited in the herbarium of Southwest Forestry University (SWFC), Kunming, Yunnan Province, China.

1.2 Morphological studies

The macromorphological descriptions were based on field notes. The color terms are from those of Petersen (1996). The micromorphological data were obtained from the dried specimens and observed under a light microscope following Dai (2012a). The following abbreviations were used for the micro-characteristics' description: KOH, 5% potassium hydroxide; CB, Cotton Blue; CB-, acyanophilous; CB+, cyanophilous; IKI, Melzer's reagent; IKI-, both inamyloid and indextrinoid; L, mean spore length (arithmetic average of 30 spores); W, mean spore width (arithmetic average of 30 spores); Q, variation in the L/W ratios between the specimens studied; n (a/b), number of spores (a) measured from given number (b) of specimens.

1.3 Molecular procedures and phylogenetic analysis

CTAB rapid plant genome extraction kit-DN14 (Aidlab Biotechnologies Co., Ltd) 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.) and

directly sequenced at Kunming Tsingke Biological Technology Limited Company. All of the newly generated sequences were deposited at GenBank (Table 1).

Sequencher 4.6 (GeneCodes) was used to edit the DNA sequence. Sequences were aligned in MAFFT 7 (<http://mafft.cbrc.jp/alignment/server/>) using the "G-INS-i" strategy and manually adjusted in BioEdit (Hall 1999). Sequences from type materials of *Dacrymyces flabelliformis* Burds. & Laursen and *D. cyrtosporus* Shirouzu acquired from GenBank were utilized as another outgroup to root tree following James *et al.* (2020) in the ITS analysis (Fig. 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 1 000 random sequence additions. Max-trees were set to 5 000, branches of zero length were collapsed and all parsimonious trees were saved. Clade robustness was assessed using a bootstrap (BT) analysis with 1 000 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 1 000 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 9.8 million thousand

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

Species name	Specimen No.	GenBank accession No.	References
		ITS	
<i>Abundisporus fuscopurpureus</i>	CLZhao 10707	MW742669	Present study
<i>Abundisporus fuscopurpureus</i>	Cui 8638	JN048771	Zhao <i>et al.</i> 2013
<i>Auricularia cornea</i>	CLZhao 10992	MW742652	Present study
<i>Auricularia cornea</i>	TFB 3470	JX065149	Looney <i>et al.</i> 2013
<i>Auricularia delicata</i>	CLZhao 11076	MW742674	Present study
<i>Auricularia delicata</i>	CNSBLitz 0098	JX065171	Looney <i>et al.</i> 2013
<i>Auricularia villosula</i>	CLZhao 11296	MW742676	Present study
<i>Auricularia villosula</i>	MFLU 162127	KX621163	Bandara <i>et al.</i> 2017
<i>Bjerkandera adusta</i>	CLZhao 10719	MW742575	Present study
<i>Bjerkandera adusta</i>	CX-9	KY706088	Bouacem <i>et al.</i> 2017
<i>Brevicellicium olivascens</i>	CLZhao 16223	MW582728	Present study
<i>Brevicellicium olivascens</i>	KHL 8571	JN649327	Sjökvist <i>et al.</i> 2012
<i>Byssomerulius corium</i>	CLZhao 11247	MW742584	Present study
<i>Byssomerulius corium</i>	FCUG 2701	MZ636931	Chen <i>et al.</i> 2021
<i>Cerioporus mollis</i>	CLZhao 12084	MW582729	Present study
<i>Cerioporus mollis</i>	WD794	AB587623	Sotome <i>et al.</i> 2011
<i>Cerioporus scutellatus</i>	CLZhao 12114	MW582730	Present study
<i>Cerioporus scutellatus</i>	WD 2272	LC412118	Sotome <i>et al.</i> 2019
<i>Ceriporiopsis semisupina</i>	CLZhao 17017	MW582738	Present study
<i>Ceriporiopsis semisupina</i>	Cui 11146	KU509525	Zhao 2012
<i>Climacodon pulcherrimus</i>	CLZhao 11238	MW742592	Present study
<i>Climacodon pulcherrimus</i>	CBS 130.40	MH856063	Vu <i>et al.</i> 2019
<i>Coriolopsis sanguinaria</i>	CLZhao 10773	MW742555	Present study
<i>Coriolopsis sanguinaria</i>	Cui 14507	MK192428	Ji <i>et al.</i> 2019
<i>Dacryobolus montanus</i>	CLZhao 16336	MW582749	Present study
<i>Dacryobolus montanus</i>	Yuan 5758	KC344412	Yuan <i>et al.</i> 2016
<i>Dacrymyces cyrtosporus</i>	PDD 107980	NR148190	He & Zhao 2022
<i>Dacrymyces flabelliformis</i>	PDD 76696	NR_166790	He & Zhao 2022
<i>Daedaleopsis confragosa</i>	CLZhao 17302	MW582750	Present study
<i>Daedaleopsis confragosa</i>	MOGU 148-19	OM422749	Cartabia <i>et al.</i> 2021
<i>Datronia mollis</i>	CLZhao 10927	MW742552	Present study
<i>Datronia mollis</i>	Dai 11253	JX559258	Li <i>et al.</i> 2014
<i>Datronia stereoides</i>	CLZhao 11227	MW742548	Present study
<i>Datronia stereoides</i>	Cui 8132	JX559270	Li <i>et al.</i> 2014
<i>Dentocorticium bicolor</i>	CLZhao 17117	MW582751	Present study
<i>Dentocorticium bicolor</i>	He 2757	MF626355	Liu <i>et al.</i> 2018
<i>Dentocorticium ussuricum</i>	CLZhao 16063	MW582752	Present study
<i>Dentocorticium ussuricum</i>	He 3322	MF626360	Liu <i>et al.</i> 2018
<i>Efibia yunnanensis</i>	CLZhao 11641	MT611529	Present study
<i>Efibia yunnanensis</i>	Wu 880515-1	MZ636977	Chen <i>et al.</i> 2021
<i>Foraminispora yunnanensis</i>	CLZhao 15955	MW582753	Present study
<i>Foraminispora yunnanensis</i>	Cui 7974	KJ531653	Li & Yuan 2015
<i>Fulvoderma australe</i>	CLZhao 10680	MW742566	Present study
<i>Fulvoderma australe</i>	Dai 11671	MF860771	Zhou <i>et al.</i> 2018
<i>Fuscoporia subferrea</i>	CLZhao 10733	MW742564	Present study
<i>Fuscoporia subferrea</i>	Dai 16327	KX961098	Chen & Yuan 2017

(to be continued)

(Table 1 continued)

Species name	Specimen No.	GenBank accession No.	References
		ITS	
<i>Fuscoporia torulosa</i>	CLZhao 12061	MW582757	Present study
<i>Fuscoporia torulosa</i>	JV 1405/2	KX961106	Chen & Yuan 2017
<i>Ganoderma gibbosum</i>	CLZhao 11324	MW742521	Present study
<i>Ganoderma gibbosum</i>	KUT 0805	AB733121	Sun <i>et al.</i> 2020
<i>Ganoderma lingzhi</i>	CLZhao 16116	MW582758	Present study
<i>Ganoderma lingzhi</i>	Dai 12574	KJ143908	Zhou <i>et al.</i> 2014
<i>Gloeodontia yunnanensis</i>	CLZhao 10504	MN908252	Present study
<i>Gloeodontia yunnanensis</i>	CLZhao 11058	MN908253	Present study
<i>Hydnochaete tabacinoides</i>	CLZhao 10804	MW742562	Present study
<i>Hydnochaete tabacinoides</i>	Cui 10428	JQ279604	He & Dai 2012
<i>Hymenochaete innexa</i>	CLZhao 12082	MW582760	Present study
<i>Hymenochaete innexa</i>	He 555	JQ279584	He & Dai 2012
<i>Hymenochaete minor</i>	CLZhao 11986	MW582761	Present study
<i>Hymenochaete minor</i>	He 936	JQ279556	He & Dai 2012
<i>Hymenochaete muroiana</i>	CLZhao 12080	MW582762	Present study
<i>Hymenochaete muroiana</i>	He 172	JQ279541	He & Dai 2012
<i>Hymenochaete porioides</i>	CLZhao 10685	MW742520	Present study
<i>Hymenochaete porioides</i>	Cui 8057	JQ279518	He & Dai 2012
<i>Hymenochaete rheicolor</i>	CLZhao 11186	MW742560	Present study
<i>Hymenochaete rheicolor</i>	Cui 8317	JQ279529	He & Dai 2012
<i>Hymenochaete separabilis</i>	CLZhao 11996	MW582764	Present study
<i>Hymenochaete separabilis</i>	He 267	JQ279573	He & Dai 2012
<i>Hyphoderma moniliforme</i>	CLZhao 17280	MW582765	Present study
<i>Hyphoderma moniliforme</i>	TNM F14735	KC928282	Yurchenko & Wu 2015
<i>Hyphoderma nudicephalum</i>	CLZhao 16801	MW582767	Present study
<i>Hyphoderma nudicephalum</i>	Wu 9508225	AJ534268	Nilsson <i>et al.</i> 2003
<i>Hyphoderma subsetigerum</i>	CLZhao 16499	MW582770	Present study
<i>Hyphoderma subsetigerum</i>	WU 9508-155	AJ534275	Nilsson <i>et al.</i> 2003
<i>Hyphodontia pallidula</i>	CLZhao 11983	MW582771	Present study
<i>Hyphodontia pallidula</i>	SFC 20180601-01	MK992821	Lupala <i>et al.</i> 2019
<i>Hyphodontia subglobosa</i>	CLZhao 16499	MW582770	Present study
<i>Hyphodontia subglobosa</i>	Wu 890805-2	KY081798	Riebesehl & Langer 2017
<i>Hyphodontia tropica</i>	CLZhao 10834	MW742641	Present study
<i>Hyphodontia tropica</i>	CU8-G6-ITS4_M11.ab1	MN752433	Alshammari & Stephenson 2018
<i>Irpea lacteus</i>	CLZhao 10931	MW742570	Present study
<i>Irpea lacteus</i>	CD 2	FJ744594	Xu <i>et al.</i> 2009
<i>Laxitextum bicolor</i>	CLZhao 10765	MW742677	Present study
<i>Laxitextum bicolor</i>	CBS 412.34	MH855587	Vu <i>et al.</i> 2019
<i>Lopharia mirabilis</i>	CLZhao 11167	MW742515	Present study
<i>Lopharia mirabilis</i>	Dai 13722	MF626346	Liu <i>et al.</i> 2018
<i>Lyomyces crustosus</i>	CLZhao 12151	MW578312	Present study
<i>Lyomyces crustosus</i>	UC 2022841	KP814310	Chen & Zhao 2020
<i>Lyomyces microfasciculatus</i>	CLZhao 16872	MW578325	Present study
<i>Lyomyces microfasciculatus</i>	TNM F 24757	JN129976	Chen & Zhao 2020
<i>Lyomyces orientalis</i>	CLZhao 16242	MW578331	Present study
<i>Lyomyces orientalis</i>	KAS-GEL 3376	DQ340325	Chen & Zhao 2020

(to be continued)

(Table 1 continued)

Species name	Specimen No.	GenBank accession No.	References
		ITS	
<i>Lyomyces wuliangshanensis</i>	CLZhao 16183	MW578337	Present study
<i>Lyomyces wuliangshanensis</i>	CLZhao 4475	MN945983	Chen & Zhao 2020
<i>Megasporoporiella subcavernulosa</i>	CLZhao 12005	MW582734	Present study
<i>Megasporoporiella subcavernulosa</i>	Dai 12423	JQ780384	Li & Cui 2013
<i>Microporus vernicipes</i>	CLZhao 10632	MW742522	Present study
<i>Microporus vernicipes</i>	KUC 11046	KJ714006	Jang <i>et al.</i> 2016
<i>Microporus xanthopus</i>	CLZhao 10946	MW742529	Present study
<i>Microporus xanthopus</i>	KA 038	MK975984	Nguyen <i>et al.</i> 2019
<i>Neodatronia gaoligongensis</i>	CLZhao 16765	MW578338	Present study
<i>Neodatronia gaoligongensis</i>	Cui 8055	JX559269	Li <i>et al.</i> 2014
<i>Peniophora cinerea</i>	CLZhao 11292	MW742675	Present study
<i>Peniophora cinerea</i>	CBS 261.37	MH855905	Vu <i>et al.</i> 2019
<i>Peniophorella fissurata</i>	CLZhao 11412	MN864261	Present study
<i>Peniophorella fissurata</i>	CLZhao 9421	MN864260	Guan <i>et al.</i> 2020
<i>Peniophorella praetermissa</i>	CLZhao 16977	MW578339	Present study
<i>Peniophorella praetermissa</i>	NH 9815	DQ647454	Guan <i>et al.</i> 2020
<i>Peniophorella rude</i>	CLZhao 11231	MW742666	Present study
<i>Peniophorella rude</i>	Wu 9307-39	DQ647499	Guan <i>et al.</i> 2020
<i>Perenniporiopsis minutissima</i>	CLZhao 16380	MW578342	Present study
<i>Perenniporiopsis minutissima</i>	Dai 11643	HQ876602	Zhao & Cui 2012
<i>Perenniporiopsis concrescens</i>	CLZhao 10805	MW742583	Present study
<i>Perenniporiopsis concrescens</i>	Spirin 6111	KP994352	Volobuev <i>et al.</i> 2015
<i>Perenniporiopsis sordida</i>	CLZhao 17153	MW578356	Present study
<i>Perenniporiopsis sordida</i>	FD-241	KP135136	Floudas & Hibbett 2015
<i>Phellinus gilvus</i>	CLZhao 12135	MW581164	Present study
<i>Phellinus gilvus</i>	MQN016	AB811862	Bang <i>et al.</i> 2014
<i>Phlebia acerina</i>	CLZhao 16763	MW581168	Present study
<i>Phlebia acerina</i>	FD-301	KP135378	Justo <i>et al.</i> 2017
<i>Phlebia ailaoshanensis</i>	CLZhao 16987	MW581175	Present study
<i>Phlebia ailaoshanensis</i>	CLZhao 4036	MH784927	Shen <i>et al.</i> 2018
<i>Phlebiopsis crassa</i>	CLZhao 10755	MW742613	Present study
<i>Phlebiopsis crassa</i>	KKN-86	KP135394	Floudas & Hibbett 2015
<i>Postia caesia</i>	CLZhao 16937	MW581197	Present study
<i>Postia caesia</i>	K(M) 31967	AY599567	Yao <i>et al.</i> 2005
<i>Postia glauca</i>	CLZhao 10833	MW742586	Present study
<i>Postia glauca</i>	X1339	MG137079	Miettinen <i>et al.</i> 2018
<i>Pyrrhoderma adamantium</i>	CLZhao 11306	MW742519	Present study
<i>Pyrrhoderma adamantium</i>	Dai 17593	MF860792	Zhou <i>et al.</i> 2018
<i>Scytinostroma yunnanense</i>	CLZhao 10758	MT611445	Present study
<i>Scytinostroma yunnanense</i>	CLZhao 10802	MT611446	Present study
<i>Skeletocutis diluta</i>	CLZhao 11968	MW581199	Present study
<i>Skeletocutis diluta</i>	JV 061016K	JF692197	Vlasák <i>et al.</i> 2012
<i>Skeletocutis kuehneri</i>	CLZhao 11198	MW742653	Present study
<i>Skeletocutis kuehneri</i>	X 3324	MF685361	Miettinen & Niemelä 2018
<i>Steccherinum ochraceum</i>	CLZhao 16289	MW581200	Present study
<i>Steccherinum ochraceum</i>	KHL 11902	JN710590	Dong <i>et al.</i> 2022

(to be continued)

(Table 1 continued)

Species name	Specimen No.	GenBank accession No.	References
		ITS	
<i>Trametes gibbosa</i>	CLZhao 11089	MW742546	Present study
<i>Trametes gibbosa</i>	L-11664-sp	JN164943	Justo <i>et al.</i> 2017
<i>Trametes versicolor</i>	CLZhao 10760	MW742530	Present study
<i>Trametes versicolor</i>	FP-135156-sp	JN164919	Justo <i>et al.</i> 2017
<i>Trechispora nivea</i>	CLZhao 16478	MW581205	Present study
<i>Trechispora nivea</i>	EP.20-A1683	MT458536	Polemis <i>et al.</i> 2020
<i>Trichaptum biforme</i>	CLZhao 10652	MW742514	Present study
<i>Trichaptum biforme</i>	CBS 842.95	MH862562	Vu <i>et al.</i> 2019
<i>Xenasmatella tenuis</i>	CLZhao 11258	MT832959	Present study
<i>Xenasmatella tenuis</i>	CLZhao 4528	MT832960	Zhao & Cui 2013
<i>Xylodon bubalinus</i>	CLZhao 16006	MW581207	Present study
<i>Xylodon bubalinus</i>	Cui 6834	KY290981	Wang & Chen 2017
<i>Xylodon flavipora</i>	CLZhao 10988	MW742632	Present study
<i>Xylodon flavipora</i>	CFMR:DLL 2011-134	KJ140637	Brazee <i>et al.</i> 2014
<i>Xylodon heterocystidiatus</i>	CLZhao 15557	MW742678	Present study
<i>Xylodon heterocystidiatus</i>	Wu 9209-27	JX175045	Chen <i>et al.</i> 2017
<i>Xylodon kunmingensis</i>	CLZhao 17170	MW566128	Present study
<i>Xylodon kunmingensis</i>	CLZhao 3019	MK404532	Shi <i>et al.</i> 2019
<i>Xylodon nespori</i>	CLZhao 16090	MW566132	Present study
<i>Xylodon nespori</i>	Nordon 030915	DQ873622	Larsson <i>et al.</i> 2006
<i>Xylodon niemelaei</i>	CLZhao 16357	MW566133	Present study
<i>Xylodon niemelaei</i>	GC 1508-146	KX857798	Chen <i>et al.</i> 2017
<i>Xylodon reticulatus</i>	CLZhao 17077	MW566135	Present study
<i>Xylodon reticulatus</i>	GC 1512-1	KX857808	Chen <i>et al.</i> 2017
<i>Xylodon serpentiformis</i>	CLZhao 16115	MW566142	Present study
<i>Xylodon serpentiformis</i>	TUB-FO 40675	MH880228	Riebesehl <i>et al.</i> 2019
<i>Xylodon subtropicus</i>	CLZhao 16523	MW566144	Present study
<i>Xylodon subtropicus</i>	Wu 1508-2	KX857806	Chen <i>et al.</i> 2017
<i>Xylodon taiwanianus</i>	CLZhao 15928	MW566145	Present study
<i>Xylodon taiwanianus</i>	CBS 125875	MH864080	Vu <i>et al.</i> 2019

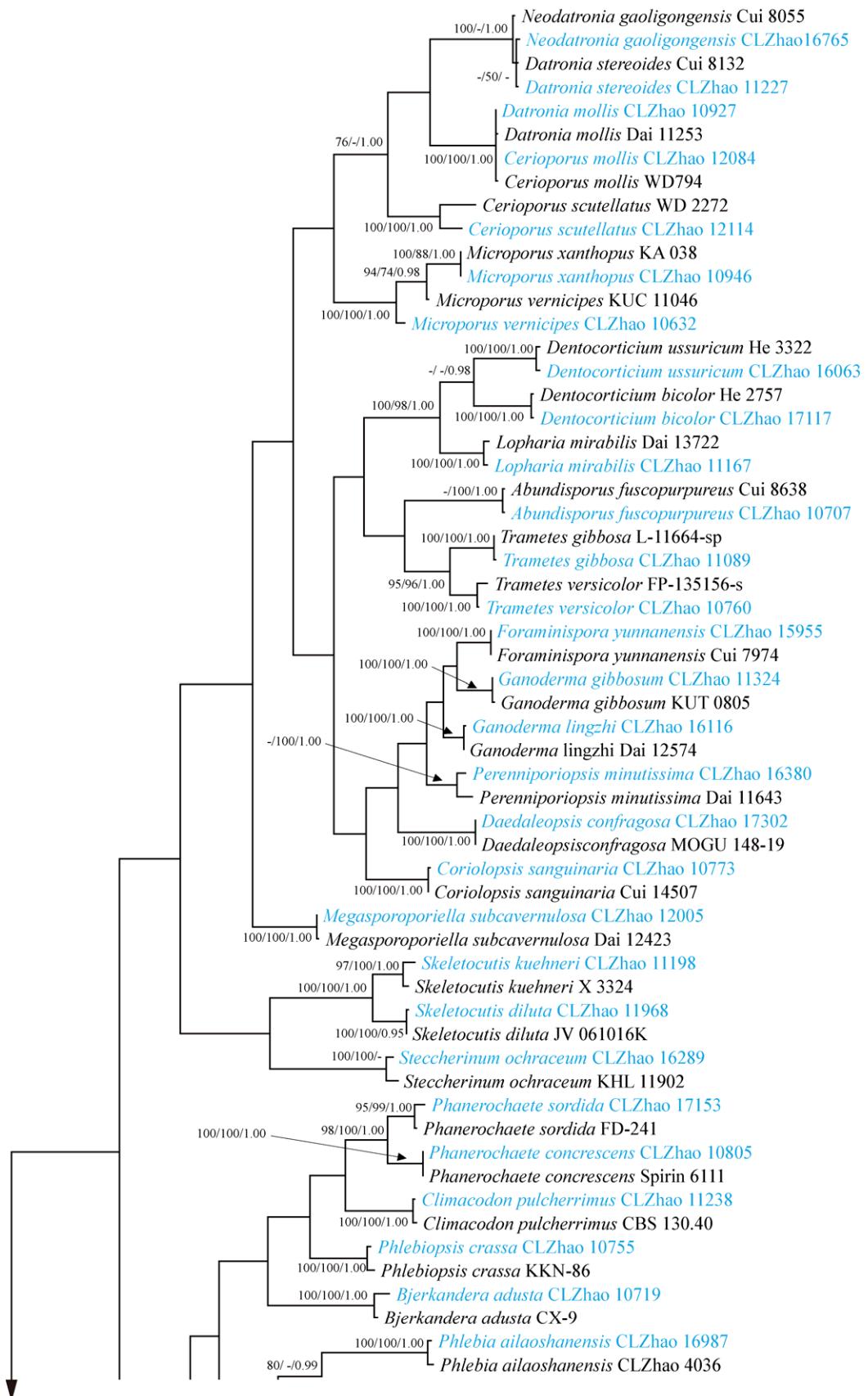
generations (Fig. 1) and trees were sampled every 100 generations. The first one-fourth generations were discarded as burn-ins. A majority rule consensus tree of all remaining trees was calculated. A majority rule consensus tree of all remaining trees was calculated. Branches were considered as significantly supported if they received a maximum likelihood bootstrap (BS) of >70%, a maximum parsimony bootstrap (BT) of >50%, or Bayesian posterior probabilities (BPP) of >0.95.

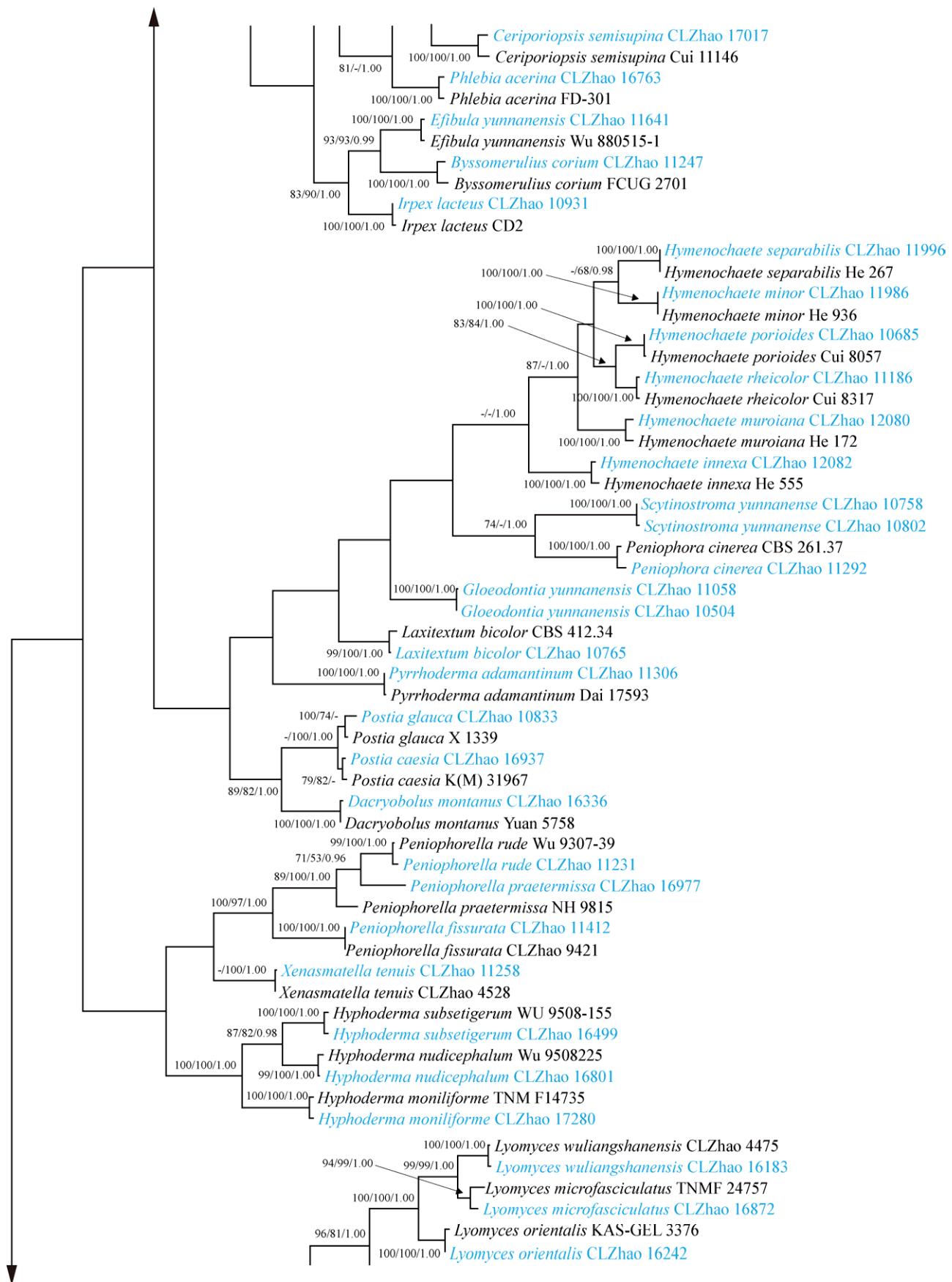
2 RESULTS

2.1 Molecular Phylogeny

The ITS dataset (Fig. 1) included sequences

from 168 fungal specimens representing 85 species. The dataset had an aligned length of 1 100 characters, of which 329 characters were constant, 60 parsimony-uninformative, and 711 parsimony-informative. The maximum parsimony analysis yielded 30 equally parsimonious tree (TL=7 253, CI=0.232 2, HI=0.767 8, RI=0.716 1, RC=0.166 3). 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=0.008 988 (BI), and the effective sample size (ESS) across the two runs is the double of the average ESS (avg ESS)=247.





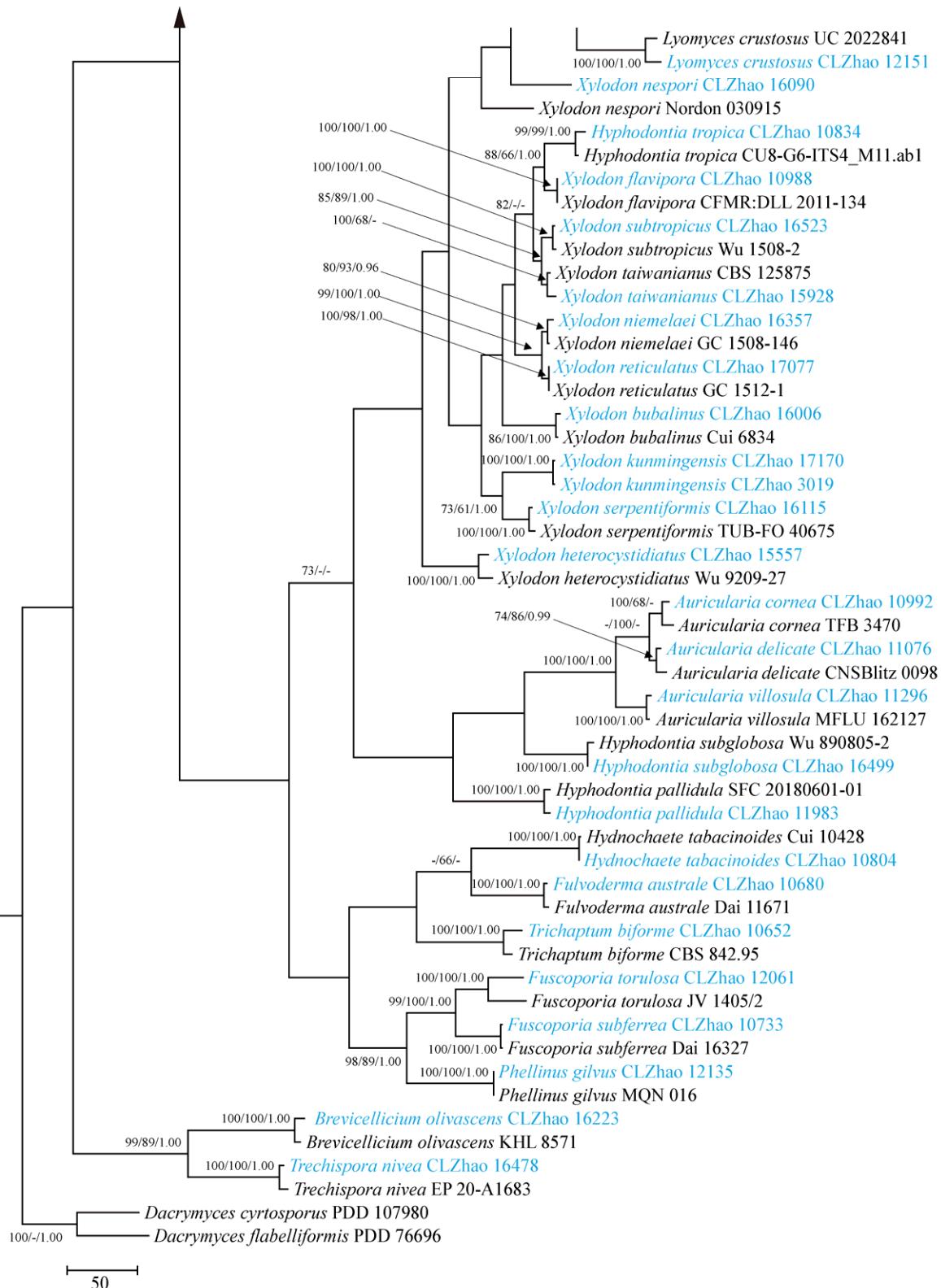


Fig. 1 Maximum parsimony strict consensus tree illustrating the phylogeny of 85 species in Agaricomycetes based on ITS sequences. Branches are labelled with a maximum likelihood boot-strap >70%, a parsimony bootstrap >50% and Bayesian posterior probabilities >0.97, respectively. The sequences of collections labelled in black are downloaded from GenBank, while those in blue are generated in this study.

2.2 Checklist

An alphabetical list (according to genus name) of wood-decaying fungi 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.htm>, accessed on 21 April 2022). Substrate and collecting data are provided after the name of each species. The hosts are listed alphabetically, and within the same host tree, they are arranged by following order: living tree, dead standing tree, trunk, fallen branch and stump. The collectors and collection numbers are listed alphabetically as well (Dai 2011, 2012a).

Abundisporus fuscopurpureus (Pers.) Ryvarden, Belg. Jl Bot. 131(2): 154 (1999)

Specimens examined: the stump of angiosperm, 14 January 2019, CLZhao 10707, 10783 (SWFC).

Aleurodiscus isabellinus S.H. He & Y.C. Dai, in Tian, Ghobad-Nejhad, He & Dai, MycoKeys 37: 100 (2018)

Specimens examined: the fallen branch of angiosperm, 7 July 2019, CLZhao 15559, 15599 (SWFC).

Antrodiella zonata (Berk.) Ryvarden, Boletín de la Sociedad Argentina de Botánica 28: 228 (1992)

Specimens examined: the trunk of angiosperm, 14 January 2019, CLZhao 10744; 15 January 2019, CLZhao 10891, 10901, 10907, 10925, 10970, 10998, 11039, 11064, 11081, 11131; 23 January 2019, CLZhao 12003, 12010, 12059; the fallen branch of angiosperm, 23 January 2019, CLZhao 12012, 25 July 2019, CLZhao 16127; 26 July 2019, CLZhao 16425, 16442; the stump of angiosperm, 14 January 2019, CLZhao 10701, 25 July 2019, CLZhao 16219; the stump of *Pinus yunnanensis* Franch., 28 July 2019, CLZhao 17137 (SWFC).

Auricularia cornea Ehrenb., in Nees von Esenbeck (ed.), Horae Phys. Berol.: 91 (1820)

Specimens examined: the trunk of angiosperm, 15 January 2019, CLZhao 10922 (SWFC).

Auricularia delicata (Mont. ex Fr.) Henn., Bot. Jb.

17: 492 (1893)

Specimens examined: the trunk of angiosperm, 15 January 2019, CLZhao 10897, 10972, 11001, 11076 (SWFC).

Auricularia villosula Malysheva, in Malysheva & Bulakh, Nov. sist. Niz. Rast. 48: 174 (2014)

Specimens examined: the fallen branch of angiosperm, 16 January 2019, CLZhao 11296 (SWFC).

Bjerkandera adusta (Willd.) P. Karst., Meddelanden af Societas pro Fauna et Flora Fennica 5: 38 (1879)

Specimens examined: the trunk of angiosperm, 14 January 2019, CLZhao 10634, 10719, 10747, 10825; 15 January 2019, CLZhao 10893, 10914, 10942; 23 January 2019, CLZhao 12046; the fallen branch of angiosperm, 14 January 2019, CLZhao 10826; 23 January 2019, CLZhao 12013; 26 July 2019, CLZhao 16340, 16551; the dead branch of angiosperm, 23 January 2019, CLZhao 11997, 12054, 12057, 12064, 12100, 12122, 12142, 12149, 12154; the stump of angiosperm, 15 January 2019, CLZhao 10917; 28 July 2019, CLZhao 17266 (SWFC).

Bjerkandera atroalba (Rick) Westph. & Tomšovský, Mycol. Progr. 14(no. 100): 3 (2015)

Specimens examined: the trunk of angiosperm, 15 January 2019, CLZhao 10954, 10968 (SWFC).

Brevicellicium olivascens (Bres.) K.H. Larss. & Hjortstam, Mycotaxon 7(1): 119 (1978)

Specimens examined: the fallen branch of angiosperm, 25 July 2019, CLZhao 16223 (SWFC).

Byssomerulius corium (Pers.) Parmasto, Eesti NSV Tead. Akad. Toim., Biol. Seer 16(4): 383 (1967)

Specimens examined: the fallen branch of angiosperm, 16 January 2019, CLZhao 11247, 11302 (SWFC).

Cerioporus mollis (Sommerf.) Zmitr. & Kovalenko, International Journal of Medicinal Mushrooms 18(1): 33 (2016)

Specimens examined: the trunk of angiosperm, 23 January 2019, CLZhao 12084 (SWFC).

Cerioporus scutellatus (Schwein.) Zmitr., Folia Cryptogamica Petropolitana 6: 47 (2018)

Specimens examined: the fallen branch of angiosperm, 23 January 2019, CLZhao 12114 (SWFC).

Ceriporiopsis semisupina C.L. Zhao, B.K. Cui & Y.C. Dai, Phytotaxa 164: 23 (2014)

Specimens examined: the stump of *Pinus yunnanensis* Franch., 28 July 2019, CLZhao 17148, 17161, 17168; the stump of *Picea asperata* Mast., 28 July 2019, CLZhao 17017, 17209 (SWFC).

Climacodon pulcherrimus (Berk. & M.A. Curtis) Nikol., Flora Plantarum Cryptogamarum URSS 6, Fungi 6 (Fungi, 2): 194 (1961)

Specimens examined: the trunk of angiosperm, 14 January 2019, CLZhao 10621, 11190, 11202, 11233, 11238 (SWFC).

Coriolopsis sanguinaria (Klotzsch) Teng, Chung-kuo Ti Chen-chun, [Fungi of China]: 760 (1963)

Specimens examined: the trunk of angiosperm, 14 January 2019, CLZhao 10646, 10672, 10773; 7 July 2019, CLZhao 15594 (SWFC).

Dacryobolus karstenii (Bres.) Oberw. ex Parmasto, Consp. System. Corticiac. (Tartu): 98 (1968)

Specimens examined: the fallen branch of angiosperm, 14 January 2019, CLZhao 10828 (SWFC).

Dacryobolus montanus X.Z. Wan & H.S. Yuan, Phytotaxa 265(2): 107 (2016)

Specimens examined: the fallen branch of angiosperm, 26 July 2019, CLZhao 16336 (SWFC).

Daedaleopsis confragosa (Bolton) J. Schröt., in Cohn, Krypt.-Fl. Schlesien (Breslau) 3.1(25–32): 492 (1888)

Specimens examined: the stump of angiosperm, 28 July 2019, CLZhao 17302 (SWFC).

Datronia mollis (Sommerf.) Donk, Persoonia 4(3): 338 (1966)

Specimens examined: the trunk of angiosperm, 14 January 2019, CLZhao 10927

(SWFC).

Datronia stereoides (Fr.) Ryvarden, Blyttia 25: 168 (1967)

Specimens examined: the fallen branch of angiosperm, 16 January 2019, CLZhao 11196, 11227, 11256, 11266, 11318 (SWFC).

Dentocorticium bicolor (P.H.B. Talbot) Nakasone & S.H. He, MycoKeys 32: 42 (2018)

Specimens examined: the fallen branch of angiosperm, 24 July 2019, CLZhao 16061; 28 July 2019, CLZhao 17117 (SWFC).

Dentocorticium ussuricum (Parmasto) M.J. Larsen & Gilb., Norwegian Journal of Botany 21: 226 (1974)

Specimens examined: the fallen branch of angiosperm, 24 July 2019, CLZhao 16063 (SWFC).

Earliella scabrosa Gilb. & Ryvarden, Mycotaxon 22(2): 364 (1985)

Specimens examined: the stump of angiosperm, 7 July 2019, CLZhao 15645, 15646, 15648, 15650, 15652, 15654 (SWFC).

Efibula yunnanensis C.L. Zhao, in Ma, Shi & Zhao, Phytotaxa 451: 242 (2020)

Specimens examined: the fallen branch of angiosperm, 19 January 2019, CLZhao 11641, 11637 (SWFC).

Fibodontia alba Yurchenko & Sheng H. Wu, Mycoscience 55: 339 (2014)

Specimens examined: the fallen branch of angiosperm, 27 July 2019, CLZhao 16776; 28 July 2019, CLZhao 17032 (SWFC).

Foraminispora yunnanensis (J.D. Zhao & X.Q. Zhang) Y.F. Sun & B.K. Cui, Persoonia 44: 220 (2020)

Specimens examined: the ground, 23 July 2019, CLZhao 15955 (SWFC).

Fulvoderma australe L.W. Zhou & Y.C. Dai, Mycologia 110(5): 876 (2018)

Specimens examined: the trunk of angiosperm, 14 January 2019, CLZhao 10680, 10703, 10722, 10800, 10815 (SWFC).

Fuscoporia subferrea Q. Chen & Yuan Yuan, Mycosphere 8(6): 1241 (2017)

Specimens examined: the trunk of angiosperm, 28 July 2019, CLZhao 17086; the

fallen branch of angiosperm, 14 January 2019, CLZhao 10733, 10798; 28 July 2019, CLZhao 16961, 17010, 17024, 17219 (SWFC).

Fuscoporia torulosa (Pers.) T. Wagner & M. Fisch., Mycological Research 105(7): 780 (2001)

Specimens examined: the stump of angiosperm, 23 January 2019, CLZhao 12061 (SWFC).

Ganoderma australe (Fr.) Pat., Bulletin de la Société Mycologique de France 5: 71 (1889)

Specimens examined: the living tree of *Cinnamomum bodinieri* Levl., 25 July 2019, CLZhao 16132; the stump of *Phoebe zhennan*, 24 July 2019, CLZhao 15997; the stump of *Cinnamomum bodinieri* Levl., 25 July 2019, CLZhao 16073 (SWFC).

Ganoderma gibbosum (Blume & T. Nees) Pat., Annales du Jardin Botanique de Buitenzorg Suppl. 1: 114 (1897)

Specimens examined: the stump of angiosperm, 16 January 2019, CLZhao 11324 (SWFC).

Ganoderma lingzhi S.H. Wu, Y. Cao & Y.C. Dai, Fungal Diversity 56(1): 54 (2012)

Specimens examined: the stump of *Cerasus* Mill., 25 July 2019, CLZhao 16116 (SWFC).

Gloeodontia yunnanensis C.L. Zhao, in Chen, Shi, Wu & Zhao, Phytotaxa 432(2): 115 (2020)

Specimens examined: the stump of angiosperm, 15 January 2019, CLZhao 11058 (SWFC).

Heteroradulum niveum J.J. Li & C.L. Zhao, in Li, Zhao & Liu, Diversity 14(1, no. 40): 5 (2022)

Specimens examined: the trunk of angiosperm, 26 July 2019, CLZhao 16483; the fallen branch of angiosperm, 16 January 2019, CLZhao 11204, 11210; 25 July 2019, CLZhao 16260, 16280; 26 July 2019, CLZhao 16398, 16424, 16432, 16472 (SWFC).

Hydnochaete tabacinoides (Yasuda) Imazeki, Bull. Tokyo Sci. Mus. 6: 103 (1943)

Specimens examined: the fallen branch of angiosperm, 14 January 2019, CLZhao 10804, 10823 (SWFC).

Hymenochaete innexa G. Cunn., Transactions and Proceedings of the Royal Society of New Zealand 85(1): 47 (1957)

Specimens examined: the trunk of angiosperm, 23 January 2019, CLZhao 12082; the dead angiosperm tree, 23 January 2019, CLZhao 12017 (SWFC).

Hymenochaete minor S.H. He & Y.C. Dai, Fungal Diversity 56: 84 (2012)

Specimens examined: the dead angiosperm tree, 23 January 2019, CLZhao 11986 (SWFC).

Hymenochaete muroiana I. Hino & Katum., Icones fungorum bambusicolorum Japonicorum: 237 (1961)

Specimens examined: the dead bamboo, 23 January 2019, CLZhao 12080 (SWFC).

Hymenochaete porioides T. Wagner & M. Fisch., Mycol. Progr. 1(1): 101 (2002)

Specimens examined: the fallen branch of angiosperm, 9 January 2019, CLZhao 10176, 10232, 10242; 10 January 2019, CLZhao 10386 (SWFC).

Hymenochaete rheicolor (Mont.) Lév., Annls Sci. Nat., Bot., sér. 3 5: 151 (1846)

Specimens examined: the trunk of angiosperm, 14 January 2019, CLZhao 10799, 10817, 10839, 10849; 15 January 2019, CLZhao 10884, 10895; 16 January 2019, CLZhao 11186, 11216 (SWFC).

Hymenochaete separabilis J.C. Léger, Bulletin de la Société Mycologique de France 97(1): 7 (1981)

Specimens examined: the fallen branch of angiosperm, 23 January 2019, CLZhao 11996 (SWFC).

Hypoderma floccosum C.L. Zhao & Q.X. Guan, Mycosistema 40(3): 454 (2021)

Specimens examined: fallen branch of angiosperm, 26 July 2019, CLZhao 16492; 28 July 2019, CLZhao 17065, 17079, 17129, 17215, 17296 (SWFC).

Hypoderma moniliforme (P.H.B. Talbot) Manjón, G. Moreno & Hjortstam, Mycotaxon 33: 261 (1988)

Specimens examined: the fallen branch of angiosperm, 28 July 2019, CLZhao 17280 (SWFC).

Hypoderma nudicephalum Gilb. & M. Blackw., Mycotaxon 33: 378 (1988)

Specimens examined: the trunk of angiosperm, 26 July 2019, CLZhao 16468; the

fallen branch of angiosperm, 27 July 2019, CLZhao 16801, 16896; the dead bamboo, 15 January 2019, CLZhao 11249 (SWFC).

Hypoderma subsetigerum Sheng H. Wu, *Mycologia* 89(1): 136 (1997)

Specimens examined: the fallen branch of angiosperm, 25 July 2019, CLZhao 16201, 16206; 26 July 2019, CLZhao 16499; 28 July 2019, CLZhao 16934, 16955, 17232, 17319 (SWFC).

Hypodontia pallidula (Bres.) J. Erikss., *Symbolae Botanicae Upsalienses* 16(1): 104 (1958)

Specimens examined: the trunk of angiosperm, 22 January 2019, CLZhao 11983 (SWFC).

Hypodontia subglobosa Sheng H. Wu, *Acta Botanica Fennica* 142: 106 (1990)

Specimens examined: the fallen branch of angiosperm, 27 July 2019, CLZhao 16789, 16794, 16845 (SWFC).

Hypodontia tropica Sheng H. Wu, *Mycotaxon* 76: 62 (2000)

Specimens examined: the trunk of angiosperm, 14 January 2019, CLZhao 10664, 10706, 10746, 10761, 10768, 10784, 10797, 10834, 10843; 15 January 2019, CLZhao 10900, 11129; 23 January 2019, CLZhao 11991, 12115; 25 July 2019, CLZhao 16245; 26 July 2019, CLZhao 16429, 16485; 28 July 2019, CLZhao 16990; the fallen branch of angiosperm, 14 January 2019, CLZhao 10654, 10661, 10837; 15 January 2019, CLZhao 11135, 11140, 11144, 11147; 16 January 2019, CLZhao 11225; 23 January 2019, CLZhao 12006, 12009, 12069, 12118; 24 July 2019, CLZhao 16051; 26 July 2019, CLZhao 16285, 16459, 16490, 16505, 16520; 28 July 2019, CLZhao 17180; the dead angiosperm tree, 23 January 2019, CLZhao 12040; the fallen branch of *Camellia japonica* L., 23 January 2019, CLZhao 15949; the stump of angiosperm, 14 January 2019, CLZhao 10810; 16 January 2019, CLZhao 11226; 25 July 2019, CLZhao 16229 (SWFC).

Irpex lacteus (Fr.) Fr., *Elenchus Fungorum* 1: 145 (1828)

Specimens examined: the trunk of angiosperm, 23 January 2019, CLZhao 12048; the fallen branch of angiosperm, 15 January 2019, CLZhao 10931, 11017, 11027; 16 January 2019,

CLZhao 11319; 22 January 2019, CLZhao 11953, 11969; 28 July 2019, CLZhao 17036; the fallen branch of *Picea asperata* Mast., 26 July 2019, CLZhao 16313; the stump of angiosperm, 25 July 2019, CLZhao 16213 (SWFC).

Laxitextum bicolor (Pers.) Lentz, U.S. Dept. Agric. Monogr. 24: 19 (1956)

Specimens examined: the trunk of angiosperm, 14 January 2019, CLZhao 10765 (SWFC).

Lenzites betulinus (L.) Fr., *Epicrisis Systematis Mycologici*: 405 (1838)

Specimens examined: the stump of angiosperm, 27 July 2019, CLZhao 16848 (SWFC).

Lopharia mirabilis (Berk. & Broome) Pat., *Bull. Soc. mycol. Fr.* 11(1): 14 (1895)

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Specimens examined: the fallen branch of *Camellia japonica* L., 23 July 2019, CLZhao 15979; the fallen branch of angiosperm, 26 July 2019, CLZhao 16523 (SWFC).

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3 DISCUSSION

In kingdom of fungi, two phyla Ascomycota and Basidiomycota cover around 97% of all fungal species (Willis 2018). According to the Ainsworth & Bisby's Dictionary of Fungi (Kirk *et al.* 2008), 1 589 genera and over 30 000 species were included in Basidiomycota (Dai *et al.* 2015) and many taxa were continuously recorded all over the world (Dai *et al.* 2015; Cui *et al.* 2019; Ayesha *et al.* 2020; Himani & Krishnappa 2020; Blanco-Dios 2021; Boonyuen *et al.* 2021; Kumar & Singh 2021; Zong *et al.* 2021a; Luo *et al.* 2022). Most new species were discovered from southern China (Wu *et al.* 2020), while Yunnan is the most important source of new species, sharing about 1/4 of total new species discovered in China (Dai *et al.* 2021). However, the diversity of wood-decaying fungi in Wenshan area is yet imperfectly investigated. The present paper is the first report of a series of studies on wood-decaying fungi in this area. In China, according to the previous studies (Dai 2011, 2012a; Dai *et al.* 2015, 2021; He & Zhao 2022) combined with field observations, 99 white-rot fungi and 5 brown-rot fungi were reported in the Wuliangshan area; 46 white-rot fungi and 3 brown-rot fungi were reported in Haikou Forestry Park; 73 white-rot fungi and 12 brown-rot fungi were reported in Huangshan Mountains; 93 white-rot fungi and 33 brown-rot fungi were reported in Great Xingan Mountains. In the present study, 2 923 specimens belonging to 104 wood-decaying poroid and corticioid species were collected from Wenshan area, including 5 brown rot species (4.81% of the total), *Dacryobolus karstenii*, *D. montanus*, *Lyomyces crustosus*, *Postia caesia* and *Trichaptum abietinum*, and 99 white rot species (95.19% of the total). Brown-rot fungi in Wenshan area account for 4.81% of the total wood-decaying fungi, while those in Haikou Forestry 6.12%, indicating that the

proportion of brown-rot fungi in the two areas seems similar (He *et al.* 2021; He & Zhao 2022). However, the proportion of brown-rot fungi to wood-decaying fungi in Huangshan Mountains and Great Xingan Mountains is 14.12%, 26.19%, respectively (Cui & Jia 2011; Cui & Yu 2011).

Some remarkable explorations of wood-decaying fungi have been made from Yunnan Province (Yuan & Dai 2008; Wu *et al.* 2017, 2021, 2022; Zhao & Wu 2017; Shen *et al.* 2018; Wu *et al.* 2018; Liu *et al.* 2019; Luo *et al.* 2019; Xu *et al.* 2019; Chen & Zhao 2020; Huang *et al.* 2020; Wang *et al.* 2020b; Gu & Zhao 2021; Luo *et al.* 2021, 2022; Qu *et al.* 2022), and nine new species, *Efibula yunnanensis*, *Gloeodontia yunnanensis*, *Heteroradulum niveum*, *Hyphoderma floccosum*, *Scytinostroma yunnanense*, *Xenasmatella tenuis*, *Xylodon grandineus*, *Xylodon sinensis* and *Xylodon wenshanensis*, were found from Wenshan area (Chen *et al.* 2020; Ma *et al.* 2020; Wang *et al.* 2020a; Guan & Zhao 2021; Luo *et al.* 2021, 2022; Zong *et al.* 2021b; Li *et al.* 2022). In the present paper 104 species obtained are distributed in 55 genera, 18 families, and 5 orders (Table 2). Of these 54 species belong to Polyporales, accounting for 51.92% of total species, indicating that Polyporales is the dominant group in this area; 38 species belong to Hymenochaetales, accounting for 36.54%, indicating that Hymenochaetales are the subdominant group in this area; 6 species belong to Russulales; 4 species belong to Auriculariales; 2 species belong to Trechisporales. Biogeographically, 75 species are rare and endemic (less than 5 specimens, Dai 2003, 2012a; Dai *et al.* 2010a), and 45 species are Eurasian. Fungal diversity in Wenshan area is still unpredictable and more intensive investigations are needed.

Wood-inhabiting poroid and corticioid fungi acting as wood decomposers release matter and energy to the ecological system in the forest ecosystems (Cui *et al.* 2006; Wei 2010; Gafforov *et al.* 2020; Dai *et al.* 2021). Previous studies have proved that *Auricularia cornea*, *A. delicate* and *A. villosula* are edible (Dai *et al.* 2010b; Wu & Dai 2015; Dai & Yang 2018; Wu *et al.* 2021), and

Antrodiella zonata, *Auricularia delicata*, *Bjerkandera adusta*, *Irpex lacteus*, *Lenzites betulina*, *Pycnoporus sanguineus*, *Pyrrhoderma adamantinum*, *Trametes gibbosa*, *T. hirsute*, *T. versicolor*, *Trichaptum abietinum* and *T. biforme* are medicinal (Dai & Yang 2008; Wu *et al.* 2019). In which *Auricularia delicata* is simultaneously edible and medicinal (Dai & Yang 2008; Dai *et al.* 2010b). *Antrodiella zonata*, *Bjerkandera adusta* and *Ganoderma australe* were regarded as forest pathogens (Dai 2012b). All these species were reported in Wenshan area.

Previous research of the molecular systematics on the larger scale for the subphyla Agaricomycotina, Pucciniomycotina and Ustilaginomycotina combined with nLSU, SSU, 5.8S, rpb1, rpb2, and tef1 datasets (He *et al.* 2019) showed that 1 928 currently used genera names were distributed in 241 families, 68 orders, and 18 classes. In the present study, 104 species nested in 55 genera, 18 families, 5 orders based on ITS dataset are consistent with the previous studied topology (He *et al.* 2019). All collected fungal specimens from Wenshan area belonging to Agaricomycetes distribute over Auriculariales, Hymenochaetales, Polyporales, Russulales and Trechisporales. Phylogenetic analyses of all studied samples show that the individual taxon clusters closely with downloaded reliable sequence from previous studies with a supported rate (Fig. 1).

Comprehensive collection and researches of wood-decaying fungi in China have been carried out, and eighty pathogenic wood-decaying fungi mainly belonging to the families Ganodermataceae, Climacodontaceae, Corticiaceae, Hericiaceae, Hymenochataceae, Polyporaceae, Schizophyllaceae of Basidiomycota were reported (Dai *et al.* 2000). The investigation of wood-inhabiting fungi from Hainan area has yielded 240 species including 199 species of polypores, and 41 corticoid and other wood-inhabiting fungi (Ma *et al.* 2022). 1 819 species of wood-inhabiting fungi belonging to 509 genera were reported in China, which divided into 10 groups, including 196 species of larger ascomycetes, 21 jelly fungi, 47 coral fungi, 637 polyporoid, hydnaceous and thelephoroid fungi, 11

Table 2 Number of wood-inhabiting poroid and corticioid species in the main orders, families, and genera in the studied area and the proportion to total number of species

Order	Family	Genus	spp.	Proportion (%)	Genus	spp.	Proportion (%)
Auriculariales	Auriculariaceae	2	4	3.85	<i>Auricularia</i>	3	2.88
					<i>Heteroradulum</i>	1	0.96
	Subtotal	2	4	3.85			
Hymenochaetales	Hymenochaetaceae	6	12	11.54	<i>Fuscoporia</i>	2	1.92
					<i>Hymenochaete</i>	6	5.77
					Other genera (4)	4	3.85
		1	3	2.88	<i>Hyphodontia</i>	3	2.88
	Rickenellaceae	1	3	2.88	<i>Peniophorella</i>	3	2.88
	Schizoporaceae	3	18	17.31	<i>Fibodontia</i>	1	0.96
					<i>Lyomyces</i>	4	3.85
					<i>Xylodon</i>	13	12.50
		1	2	1.92	<i>Trichaptum</i>	2	1.92
		12	38	36.54			
Polyporales	Dacryobolaceae	2	4	3.85	<i>Dacryobolus</i>	2	1.92
					<i>Postia</i>	2	1.92
	Hyphodermataceae	1	4	3.85	<i>Hyphoderma</i>	4	3.85
	Incrustoporiaceae	1	3	2.88	<i>Skeletocutis</i>	3	2.88
	Irpicaceae	3	3	2.88	<i>Byssomerulus</i>	1	0.96
					<i>Efibula</i>	1	0.96
					<i>Irpex</i>	1	0.96
		4	7	6.73	<i>Phlebia</i>	4	3.85
					<i>Climacodon</i>	1	0.96
					Other genera (2)	2	1.92
Russulales	Phanerochaetaceae	3	6	5.77	<i>Phanerochaete</i>	3	2.88
					<i>Bjerkandera</i>	2	1.92
					<i>Phlebiopsis</i>	1	0.96
	Polyporaceae	17	25	24.04	<i>Ganoderma</i>	3	2.88
					<i>Trametes</i>	3	2.88
					Other genera (15)	19	18.27
		2	2	1.92	<i>Antrodiaella</i>	1	0.96
					<i>Steccherinum</i>	1	0.96
		33	54	51.92			
Trechisporales	Hericiaceae	1	1	0.96	<i>Laxitextum</i>	1	0.96
	Peniophoraceae	2	2	1.92	<i>Peniophora</i>	1	0.96
					<i>Scytonostroma</i>	1	0.96
					<i>Aleurodiscus</i>	1	0.96
	Stereaceae	1	1	0.96	<i>Xenasmatella</i>	1	0.96
	Xenasmataceae	1	1	0.96	<i>Gloeodontia</i>	1	0.96
	Incertae sedis	1	1	0.96			
Total	Subtotal	6	6	5.77			
	Hydnodontaceae	2	2	1.92	<i>Brevicellicium</i>	1	0.96
	Subtotal	2	2	1.92	<i>Trechispora</i>	1	0.96
Total	18	55	104	100	55	104	100

cantharelloid fungi, 653 agarics, 130 boletes, 75 gasteroid fungi, 16 larger pathogenic fungi, and 33 larger Myxomycetes (Li *et al.* 2015). 310 species belonging to 3 phyla, 8 class, 24 order, 66 family, 153 genera were reported in Saihanwula National Nature Reserve of Inner Mongolia, China (Liu & Li 2019). The wood-decaying fungi found in Wuliangshan area of Yunnan Province include 95 species belonging to Auriculariales, Boletales, Cantharellales, Corticiales, Gloeophyllales, Hymenochaetales, Polyporales, Russulales and Trechisporales of Basidiomycota (He & Zhao 2022). These reports indicate that the tropical and subtropical areas are rich in fungal diversity, and it goes without saying that the richness of the wood-decaying fungi is affirmative.

Dramatic changes in higher-level taxonomy in the last twenty years has added fungal phyla from 4 to 12 and the biodiversity of many hidden and microscopic species is undersampled, and the current researches indicate that perhaps less than 5% of the estimate two to four million species have been formally described (Blackwell 2011; Hawksworth & Lücking 2017; Dai *et al.* 2021). Enrichment of the knowledge of the fungal diversity worldwide for supporting the rational utilization and effective protection of fungal resources and providing scientific basis for the prevention and control of forest diseases is still a heavy task.

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