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Diversity of wood-decaying fungi in Zixishan area (Hengduan Mountains), Yunnan Province, China

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Abstract

Six field surveys were carried out in Zixishan area, Yunnan Province, China during 2016–2021, and 1407 specimens of wood-decaying fungi were collected. The paper summarizes the obtained results on the wood-decaying fungi of this area, consisting of 74 species belonging to 49 genera, 24 families and 7 orders. Polyporales is the dominant order (51.35% of the total species), and *Hyphoderma*, and *Peniophorella* are the dominant genera (Each accounted for 6.76% of the total) in this area. Their hosts and substrates were also identified and a checklist of wood-decaying fungi is provided. The taxa were identified by morphology and molecular evidence. The sequences of the Internal Transcribed Spacer (ITS) gene region of the studied specimens were generated and the phylogenetic analyses were performed. Five new species were earlier described in Zixishan area viz. *Hyphoderma fissuratum* C.L. Zhao & X. Ma (2021: 37), *H. microporoides* C.L. Zhao & Q.X. Guan (2021: 9), *H. tenuissimum* C.L. Zhao & Q.X. Guan (2021: 153), *Hyphodermella zixishanensis* C.L. Zhao (2021: 4), and *Phanerochaete pruinosa* C.L. Zhao & D.Q. Wang (2021: 8). This work aimed to provide an updated checklist of wood-decaying fungi in Zixishan area, Yunnan Province, China, as well as to enrich the knowledge of the fungal diversity in China and worldwide.

Key words: Basidiomycota, Biological resources, Diversity, Molecular systematics

Introduction

Fungi are a diverse, monophyletic group of eukaryotes that show immense ecological and economic impacts on ecosystems (James *et al.* 2020). Approximately 155,000 species of fungi have been described (Dai *et al.* 2021, Wang *et al.* 2021a, Wijayawardene *et al.* 2022) out of the predicted number of fungi 2.2–3.8 million species of fungi (Blackwell 2011, Taylor *et al.* 2014, Hibbett 2016, Hawksworth & Lücking 2017). The diversity of flora of seed plants in Yunnan Province is higher than in other areas in China. The number of discovered new fungal taxa was about 2000 in this Province from 2000 to 2022 and the endemic species of woody plants are rich, supplying good substrates for wood-decaying fungi (Dai 2003, Dai *et al.* 2021, Zhao *et al.* 2023). The wood-decaying fungi can be used for industrial, medicinal, and edible uses, which comprise mostly Basidiomycetes and Ascomycetes, (Russell & Paterson 2006, Dai 2012, Dai *et al.* 2015, 2021, Vinay *et al.* 2015, Wu *et al.* 2019, 2020a, M'Barek *et al.* 2020, Runnel *et al.* 2021, Luo *et al.* 2022, Cai *et al.* 2023, Yang *et al.* 2023, Zhao *et al.* 2023), and the wood-decaying fungi display a considerable ability to degrade different environmental contaminants on their extensive organic compound degradation abilities (James *et al.* 2020).

Zixishan area in Yunnan Province is located at the junction of the Jinsha River System (Longchuan River) and Honghe River system (Lishe River) in the central region of the Yunnan Plateau. The climate is subtropical

plateau monsoon climate and under such climate conditions, a subtropical semi-humid evergreen broad-leaved forest ecosystem has been formed. The dry and wet seasons are distinct, and the rainfall is abundant. The mountain streams continue to meander and linger in the valleys (Wang 2016). Zixishan area is typically zonal primitive vegetation in the middle Plateau region of Yunnan Province due to its special geographical climate and abundant rain, with rich species of vegetation and vertical distribution. The forest coverage rate is as high as 96%, in which it has more than 1500 species of plants, including 712 species of seed plants and ferns belonging to 401 genera and 146 families, with 13 wild and cultivated rare and endangered plants. It is the largest forest park in Yunnan Province, enjoying the reputation of "Central Yunnan Emerald", "Natural Oxygen Bar", "Natural Large Garden" and "Natural Botanical Garden" (Feng *et al.* 2019, Wu *et al.* 2020b).

The wood-decaying fungi are mostly reported in northwest Yunnan Province, China, and some polypore and corticioid fungi have been reported in southeast Yunnan Province (Xie 1992, Chen 1994, Guo *et al.* 2013, Zhang *et al.* 2012, Dai *et al.* 2014, Chen *et al.* 2020a, Wang & Zhao 2021a, Luo *et al.* 2022, Zhao *et al.* 2023). According to modern taxonomy, wood-decaying fungi mainly belong to 10 orders in Agaricomycetes viz. Agaricales, Auriculariales, Cantharellales, Corticiales, Gloeophyllales, Hymenochaetales, Polyporales, Russulales, Thelephorales and Trechisporales (Dai 2012, Wu *et al.* 2020a, Dai *et al.* 2015, 2021, Zhao *et al.* 2023). Therefore, the current wood-decaying fungi catalogue includes the poroid and corticioid species. Some remarkable explorations of wood-decaying fungi have been made in 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.* 2020a, Gu & Zhao 2021, Luo *et al.* 2021, 2022, Qu *et al.* 2022, Luo *et al.* 2022, Cai *et al.* 2023, Yang *et al.* 2023, Zhao *et al.* 2023), and five new species were described in Zixishan area viz. *Hyphoderma fissuratum* C.L. Zhao & X. Ma (2021: 37), *H. microporoides* C.L. Zhao & Q.X. Guan (2021: 9), *H. tenuissimum* C.L. Zhao & Q.X. Guan (2021: 153), *Hyphodermella zixishanensis* C.L. Zhao (2021: 4), and *Phanerochaete pruinosa* C.L. Zhao & D.Q. Wang (2021: 8) (Chen *et al.* 2020a, Wang *et al.* 2020b, Guan & Zhao 2021, Luo *et al.* 2021, Zong *et al.* 2021, Luo *et al.* 2022). In the present study, six field surveys were carried out in Zixishan area, combined with morphological characteristics and molecular evidence, and the present study identified 74 species from all specimens.

Materials and methods

Sample collection and herbarium specimen preparation

The fresh fruiting bodies of basidiomycetous macrofungi growing on angiosperm stumps, trunks and branches were collected within 1×1 km² 3 times every year in Zixishan area of Yunnan Province from 2016–2021. The samples were photographed in situ and their macroscopic details were recorded. Photograph were taken by a Jianeng 80D camera. All the photos were focus-stacked and merged using Helicon Focus software. Macroscopic details were recorded and transported to a field station where the fruit bodies were dried on an electronic food dryer (Fruit, Foshan, China) at 45 °C for 48 hours. Once dried, the specimens were sealed in an envelope, added to zip-lock plastic bags 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. The color terms are from that of Petersen (1996). The micromorphological data were obtained from the dried specimens and observed under a light microscope following Zhao *et al.* (2023). 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 ratio between the specimens studied, n (a/b) = number of spores (a) measured from given number (b) of specimens.

Molecular procedures and phylogenetic analysis

CTAB rapid plant genome extraction kit-DN14 (Aidlab Biotechnologies Co., Ltd, Beijing) was used to extract 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, California, 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).

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

Species name	Sample no.	GenBank Accession No. ITS	References
<i>Aleurodiscus isabellinus</i>	CLZhao 21151	OM955789	Present study
<i>A. isabellinus</i>	He 5294	MH109053	Tian <i>et al.</i> (2018)
<i>A. mirabilis</i>	CLZhao 6781	OM955790	Present study
<i>A. mirabilis</i>	He 3730	KX306878	Dai & He (2017)
<i>Antrodia xantha</i>	CLZhao 6685	OM955795	Present study
<i>A. xantha</i>	Dai 12984	MG787578	Unpublished
<i>Butyrea japonica</i>	CLZhao 7218	OM955796	Present study
<i>B. japonica</i>	SFC20170823-29	MN973797	Lee <i>et al.</i> (2020)
<i>Byssomerulius corium</i>	CLZhao 6910	OM955797	Present study
<i>B. corium</i>	Wu 1207-55	MZ636932	Chen <i>et al.</i> (2021)
<i>Ceriporia nanlingensis</i>	CLZhao 7208	OM955803	Present study
<i>C. nanlingensis</i>	Dai8173	JX623942	Jia <i>et al.</i> (2014)
<i>C. pseudocystidiata</i>	CLZhao 7682	OM955808	Present study
<i>C. pseudocystidiata</i>	Cui6878	JX623943	Jia <i>et al.</i> (2014)
<i>Ceriporiopsis semisupina</i>	CLZhao 7426	OM955809	Present study
<i>Ce. semisupina</i>	Chen 3327	MZ636937	Chen <i>et al.</i> (2021)
<i>Cerrena zonata</i>	CLZhao 7676	OM955819	Present study
<i>Cer. zonata</i>	Dai7821	KC485529	Yuan (2014)
<i>Coltricia crassa</i>	CLZhao 7157	OM955820	Present study
<i>C. crassa</i>	Dai 15163	KU360679	Bian & Dai (2015)
<i>Crepatura ellipsospora</i>	CLZhao 6851	OM955821	Present study
<i>C. ellipsospora</i>	CLZhao 697	MK343695	Ma & Zhao (2019)
<i>Crustodontia chrysocreas</i>	CLZhao 21107	OM955826	Present study
<i>C. chrysocreas</i>	CBS 125889	MH864087	Vu <i>et al.</i> (2019)
<i>Crustomyces subabruptus</i>	CLZhao 21086	OM955828	Present study
<i>Cr. subabruptus</i>	K(M):249975	MZ159685	Unpublished
<i>Cyanosporus submicroporus</i>	CLZhao 6920	OM955827	Present study
<i>C. submicroporus</i>	Cui 18156	MW182186	Liu <i>et al.</i> (2022)
<i>Dentipellicula leptodon</i>	CLZhao 6818	OM955830	Present study
<i>D. leptodon</i>	CBS 125879	MH864083	Vu <i>et al.</i> (2019)
<i>Diplomitoporus flavescens</i>	CLZhao 7009	OM955844	Present study
<i>D. flavescens</i>	IBL66	MZ410695	Unpublished
<i>Fomitopsis pinicola</i>	CLZhao 7716	OM955845	Present study
<i>F. pinicola</i>	Cui 10312	KR605781	Han <i>et al.</i> (2016)
<i>Fuscoporia chinensis</i>	CLZhao 21152	OM955848	Present study
<i>F. chinensis</i>	Dai 15713	MN816721	Chen <i>et al.</i> (2020)
<i>Gloeocystidiellum porosum</i>	CLZhao 6984	OM955849	Present study
<i>G. porosum</i>	CBS 189.56	MH857576	Vu <i>et al.</i> (2019)
<i>Heterobasidion insulare</i>	CLZhao 6829	OM955850	Present study
<i>H. insulare</i>	Dai 13933	MT146489	Yuan <i>et al.</i> (2021)
<i>Hydnophanerochaete odontoidea</i>	CLZhao 6785	OM955750	Present study
<i>H. odontoidea</i>	CLZhao 4036	MH784927	Shen <i>et al.</i> (2018)
<i>Hydnoporia corrugata</i>	CLZhao 7171	OM955854	Present study
<i>Hy. corrugata</i>	HHB 19233	MW740292	Unpublished
<i>Hy. yasudae</i>	CLZhao 21214	OM955855	Present study

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TABLE 1. (Continued)

Species name	Sample no.	GenBank Accession No. ITS	References
<i>Hy. yasudae</i>	Miettinen X2653	MK514597	Miettinen <i>et al.</i> (2019)
<i>Hymenochaete cruenta</i>	CLZhao 21195	OM955856	Present study
<i>H. cruenta</i>	He 766	JQ279595	He & Dai (2012)
<i>H. minor</i>	CLZhao 7197	OM955857	Present study
<i>H. minor</i>	He 933	JQ279555	He & Dai (2012)
<i>H. rheicolor</i>	CLZhao 6801	OM955858	Present study
<i>H. rheicolor</i>	Cui 8317	JQ279529	He & Dai (2012)
<i>H. xerantica</i>	CLZhao 7141	OM955861	Present study
<i>H. xerantica</i>	Cui 9209	JQ279519	He & Dai (2012)
<i>Hyphoderma cremeoalbum</i>	CLZhao 17007	OM955862	Present study
<i>H. cremeoalbum</i>	NH 11538	DQ677492	Larsson (2007)
<i>H. crystallinum</i>	CLZhao 15841	MW917165	Present study
<i>H. crystallinum</i>	CLZhao 18459	MW917166	Guan & Zhao (2021a)
<i>H. fissuratum</i>	CLZhao 6731	MT791331	Present study
<i>H. fissuratum</i>	CLZhao 6726	MT791330	Ma <i>et al.</i> (2021)
<i>H. floccosum</i>	CLZhao 17215	MW301687	Present study
<i>H. floccosum</i>	CLZhao 17129	MW301683	Guan & Zhao (2021a)
<i>H. membranacea</i>	CLZhao 5844	MW917167	Present study
<i>H. membranacea</i>	CLZhao 6971	MW917168	Guan & Zhao (2021a)
<i>H. microporoides</i>	CLZhao 8695	MW917170	Present study
<i>H. microporoides</i>	CLZhao 6857	MW917169	Guan & Zhao (2021b)
<i>H. moniliforme</i>	CLZhao 21162	OM955863	Present study
<i>H. moniliforme</i>	Wu 0211-46	KC928284	Yurchenko & Wu (2015)
<i>H. mopanshanense</i>	CLZhao 6498	MT791329	Present study
<i>H. mopanshanense</i>	CLZhao 6493	MT791328	Ma <i>et al.</i> (2021)
<i>H. sinense</i>	CLZhao 7963	MW301679	Present study
<i>H. sinense</i>	CLZhao 7981	MW301680	Guan & Zhao (2021b)
<i>H. tenuissimum</i>	CLZhao 16210	MW443050	Present study
<i>H. tenuissimum</i>	CLZhao 7003	MW443048	Guan & Zhao (2021b)
<i>H. transiens</i>	CLZhao 1667	MT955166	Present study
<i>H. transiens</i>	NH 12304	DQ677504	Larsson (2007)
<i>Hyphodermella zixishanensis</i>	CLZhao 7412	MZ305282	Present study
<i>Hy. zixishanensis</i>	CLZhao 7124	MZ305276	Wang <i>et al.</i> (2021b)
<i>Hy. aurantiaca</i>	CLZhao 10521	MW209029	Present study
<i>Hy. aurantiaca</i>	CLZhao 10500	MW209025	Wang & Zhao (2021a)
<i>Hyphodontia tropica</i>	CLZhao 6714	OM955867	Present study
<i>Hyp. tropica</i>	CLZhao 6716	OM955868	Present study
<i>Leptoporus mollis</i>	CLZhao 7427	OM955917	Present study
<i>L. mollis</i>	Dai 21062	MW377302	Liu <i>et al.</i> (2023)
<i>Lyomyces cremeus</i>	CLZhao 7281	OM955918	Present study
<i>L. cremeus</i>	CLZhao 7244	OM955921	Present study
<i>L. cremeus</i>	CLZhao 7285	OM955919	Present study
<i>L. cremeus</i>	CLZhao 2812	MN945973	Zhao & Cui (2013)
<i>L. cremeus</i>	CLZhao 7294	OM955920	Present study
<i>L. cremeus</i>	CLZhao 4138	MN945974	Zhao & Cui (2013)
<i>L. crustosus</i>	CLZhao 6897	OM955922	Present study
<i>L. crustosus</i>	CLZhao 7274	OM955923	Present study
<i>L. orientalis</i>	CLZhao 7132	OM955926	Present study
<i>L. orientalis</i>	KAS-GEL 3376	DQ340325	Yurchenko <i>et al.</i> (2017)
<i>L. vietnamensis</i>	CLZhao 7100	OM955927	Present study

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TABLE 1. (Continued)

Species name	Sample no.	GenBank Accession No. ITS	References
<i>L. vietnamensis</i>	TNM F9073	JX175044	Yurchenko & Wu (2015)
<i>Megasporia major</i>	CLZhao 7064	OM955928	Present study
<i>M. major</i>	GC 1407-21	KY688205	Chen <i>et al.</i> (2018)
<i>Peniophora versiformis</i>	CLZhao 7051	OM955931	Present study
<i>P. versiformis</i>	CBS 361.54	MH857362	Vu <i>et al.</i> (2019)
<i>Peniophorella fissurata</i>	CLZhao 7290	OM955718	Present study
<i>Pe. fissurata</i>	CLZhao 9421	MN864260	Guan <i>et al.</i> (2020)
<i>Pe. praetermissa</i>	CLZhao 21158	OM955719	Present study
<i>Pe. praetermissa</i>	NH 7827	DQ647460	Hallenberg <i>et al.</i> (2007)
<i>Pe. pubera</i>	CLZhao 7509	OM955722	Present study
<i>Pe. pubera</i>	NH 10512	DQ647505	Hallenberg <i>et al.</i> (2007)
<i>Pe. rude</i>	CLZhao 7142	OM955723	Present study
<i>Pe. rude</i>	Wu 0104-3	DQ647495	Hallenberg <i>et al.</i> (2007)
<i>Pe. subpraetermissa</i>	CLZhao 6882	OM955728	Present study
<i>Pe. subpraetermissa</i>	Wu 950627	DQ647493	Hallenberg <i>et al.</i> (2007)
<i>Phanerochaete conrescens</i>	CLZhao 7002	OM955732	Present study
<i>P. conrescens</i>	He 4657	MT235662	Unpublished
<i>P. pruinosa</i>	CLZhao 7713	MZ435347	Present study
<i>P. pruinosa</i>	CLZhao 7712	MZ435346	Wang & Zhao (2021b)
<i>P. rhizomorpha</i>	CLZhao 10470	MZ435348	Present study
<i>P. rhizomorpha</i>	CLZhao 10477	MZ435349	Wang & Zhao (2021b)
<i>P. sordida</i>	CLZhao 7486	OM955733	Present study
<i>P. sordida</i>	He 5400	MT235676	Unpublished
<i>Phlebia acerina</i>	CLZhao 7664	OM955744	Present study
<i>P. acerina</i>	HHB 11146	KP135372	Floudas & Hibbett (2015)
<i>Phlebiopsis crassa</i>	CLZhao 7130	OM955764	Present study
<i>Ph. crassa</i>	FP 102496	AY219341	De Koker <i>et al.</i> (2003)
<i>Ph. yunnanensis</i>	CLZhao 7367	OM955788	Present study
<i>Ph. yunnanensis</i>	CLZhao 3900	MH744141	Zhao <i>et al.</i> (2019)
<i>Porodaedalea chinensis</i>	CLZhao 7487	OM955768	Present study
<i>P. chinensis</i>	Dai 16864	KX852282	Dai <i>et al.</i> (2017)
<i>Postia caesia</i>	CLZhao 6904	OM955769	Present study
<i>Po. caesia</i>	K(M) 31967	AY599567	Yao <i>et al.</i> (2005)
<i>Scytinostroma phaeosarcum</i>	CLZhao 21302	OM955775	Present study
<i>S. phaeosarcum</i>	CBS 728.81	MH861463	Vu <i>et al.</i> (2019)
<i>Skeletocutis nivea</i>	CLZhao 7034	OM955776	Present study
<i>S. nivea</i>	FD-5	KP135331	Floudas & Hibbett (2015)
<i>S. pseudo-odora</i>	CLZhao 6938	OM955777	Present study
<i>S. pseudo-odora</i>	Dai 16527	KY245961	Fan <i>et al.</i> (2017)
<i>Steccherinum nitidum</i>	CLZhao 7198	MZ713646	Present study
<i>S. nitidum</i>	KHL 11903	JN710560	Miettinen <i>et al.</i> (2012)
<i>Stereum hirsutum</i>	CLZhao 7420	OM955779	Present study
<i>St. hirsutum</i>	CBS 108532	MH862810	Vu <i>et al.</i> (2019)
<i>St. sanguinolentum</i>	CLZhao 6856	OM955780	Present study
<i>S. sanguinolentum</i>	CLZhao 7581	OM955786	Present study
<i>Tyromyces kmetii</i>	CLZhao 7305	OM955787	Present study
<i>T. kmetii</i>	Dai 12403	KF698747	Unpublished

Sequencher 4.6 (GeneCodes, Ann Arbor, MI, USA) 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 an outgroup to root tree He *et al.* (2022) in ITS analysis (Fig. 1).

Maximum parsimony analysis was applied to the ITS sequence dataset. Approaches to phylogenetic analysis followed Zhao & Wu (2017) and the tree construction procedure was performed in PAUP* version 4.0b10 (Swofford 2002). All 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 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 2003). Four Markov chains were run for 2 runs from random starting trees for 9.8 million thousand generations (Fig. 1) and trees were sampled every 100 generations. The first one-fourth of the 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 .

Results

Molecular

The ITS dataset (Fig. 1) included sequences from 142 fungal specimens representing 59 species. The dataset had an aligned length of 1163 characters, of which 383 characters were constant, 115 parsimony-uninformative, and 665 parsimony-informative. The maximum parsimony analysis yielded 30 equally parsimonious trees (TL = 8531, CI = 0.2003, HI = 0.7997, RI = 0.6236, RC = 0.1249). 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 = 0.006466 (BI), and the effective sample size (ESS) across the two runs is double the average ESS (avg ESS) = 290.

Species diversity and floristic composition

A total of 74 species were identified in all collected specimens, distributed in seven orders, 24 families and 49 genera (Table 2). Of these 74 species listed, 38 species belong to order Polyporales, accounting for 51.35%, which indicated that Polyporales is the dominant group in this area, and 21 species belong to the order Hymenochaetales, accounting for 28.38% indicated that Hymenochaetales are the subdominant group in this area; six species belong to the Russulales; two species belong to Trechisporales; one species belongs to the Auriculariales; one species belongs to the Agaricales; and one species belongs to the Gloeophyllales. The Polyporales is the dominant order (51.35% of the total species) *Hyphoderma* and *Peniophorella* are the dominant genera (Each accounted for 6.76% of the total) in this area.

Ecological habit analysis

The largest number of the woody macrofungal species was found on the trunk, with 46 species, followed by 41 species on the branches, eight species on the stump and one species on the ground. The number of endemic species in trunks, branches and stumps was 27, 22 and three, respectively, accounting for 36.49 %, 29.73% and 4.10% of the total woody macrofungi species. The endemic species of woody macrofungi were the most abundant on the trunk (Fig. 2).

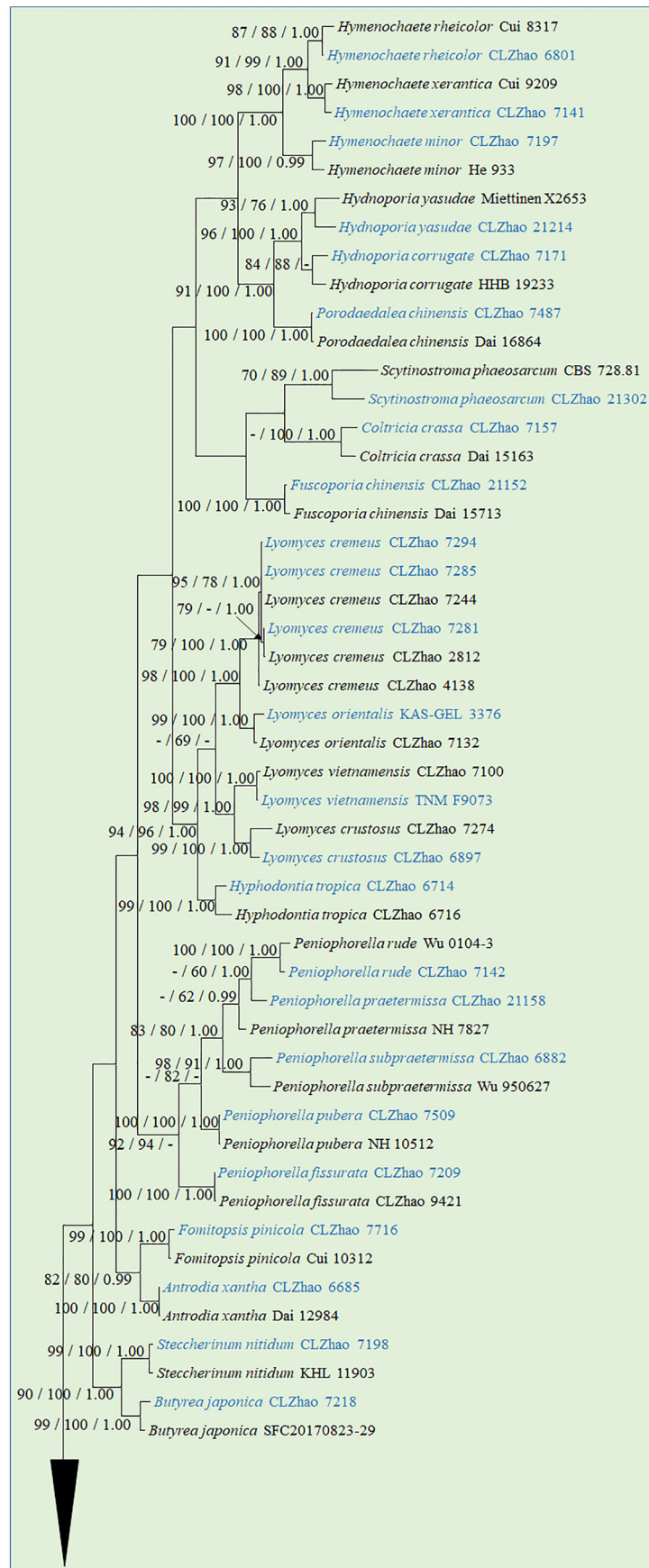


FIGURE 1. Maximum parsimony strict consensus tree illustrating the phylogeny of 68 species in Agaricomycetes based on ITS sequences. Branches are labelled with a maximum likelihood boot-strap $\geq 70\%$, a parsimony bootstrap $\geq 50\%$ and Bayesian posterior probabilities ≥ 0.97 , respectively. The sequences of collections labelled in black are downloaded from GenBank, while those in blue are generated in this study.

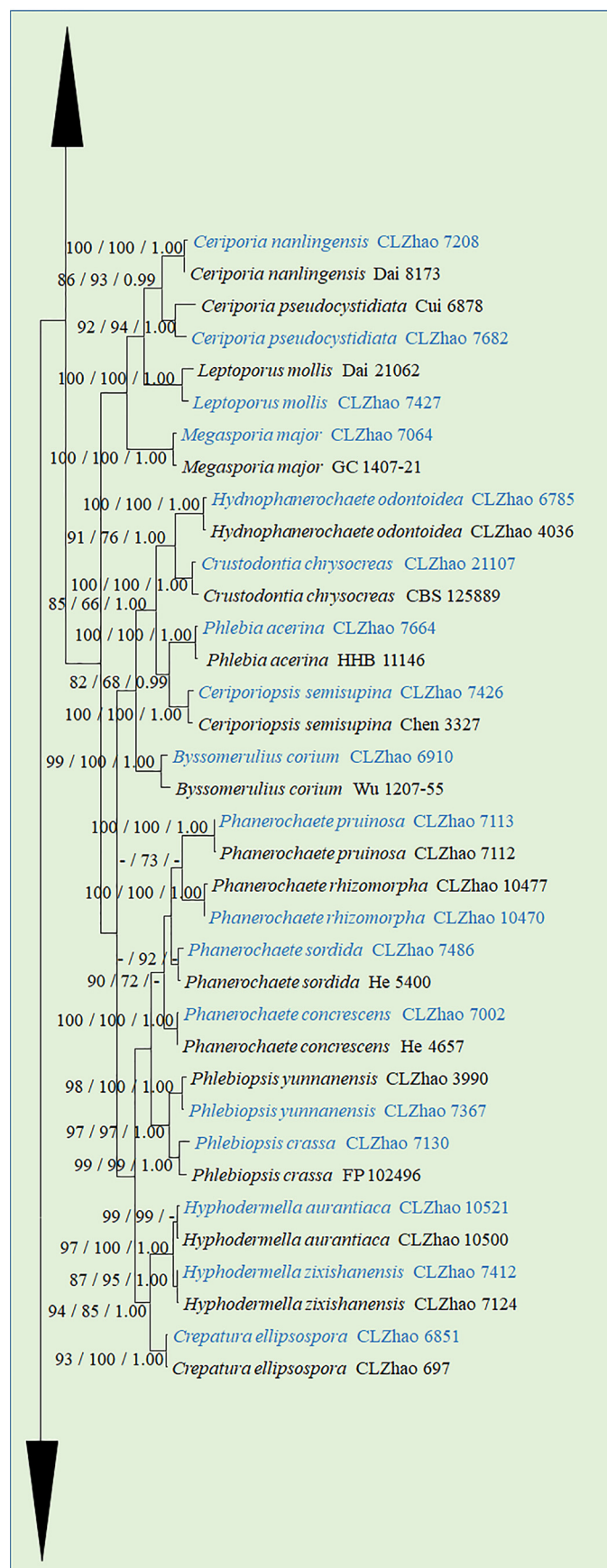


FIGURE 1. Continued.

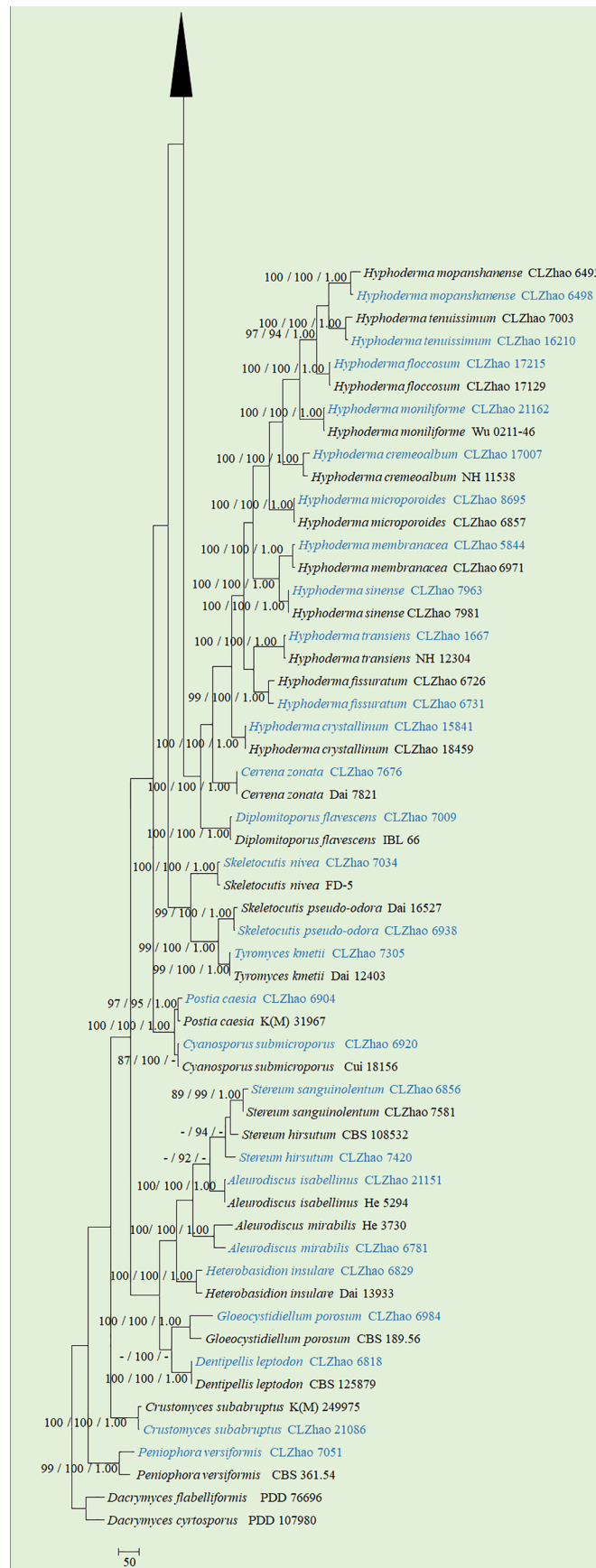


FIGURE 1. Continued.

TABLE 2. Number of wood-inhabiting poroid and corticioid species in the most orders, families, and genera in the study area and proportion accounting for total species number.

Order	Family	Spp.	%	Family	Genera	Spp	%	Genera	Species	%
Agaricales	1	1	1.35	Radulomycetaceae	1	1	1.35	<i>Radulomyces</i>	1	1.35
Auriculariales	1	1	1.35	Auriculariaceae	1	1	1.35	<i>Auricularia</i>	1	1.35
Gloeophyllales	1	1	1.35	Gloeophyllaceae	1	1	1.35	<i>Gloeophyllum</i>	1	1.35
Hymenochaetales	3	21	28.38	Hymenochaetaceae	5	9	12.16	<i>Coltricia</i>	1	1.35
								<i>Fuscoporia</i>	1	1.35
								<i>Hymenochaete</i>	4	5.41
								<i>Hydnoporia</i>	2	2.70
								<i>Tubulicrinis</i>	1	1.35
				Rickenellaceae	2	6	8.11	<i>Peniophorella</i>	5	6.76
								<i>Schizocorticium</i>	1	1.35
				Schizoporaceae	3	6	8.11	<i>Hyphodontia</i>	1	1.35
								<i>Lyomyces</i>	4	5.41
								<i>Xylodon</i>	1	1.35
Polyporales	11	38	51.35	Cerrenaceae	1	1	1.35	<i>Cerrena</i>	1	1.35
				Cystostereaceae	1	1	1.35	<i>Crustomyces</i>	1	1.35
				Dacryobolaceae	1	1	1.35	<i>Postia</i>	1	1.35
				Fomitopsidaceae	2	2	2.70	<i>Antrodia</i>	1	1.35
								<i>Fomitopsis</i>	1	1.35
				Hyphodermataceae	1	5	6.76	<i>Hyphoderma</i>	5	6.76
				Irpicaceae	5	6	8.11	<i>Byssomerulius</i>	1	1.35
								<i>Ceriporia</i>	2	2.70
								<i>Gloeoporus</i>	1	1.35
				Incrustoporiaceae				<i>Irpex</i>	1	1.35
								<i>Leptoporus</i>	1	1.35
				Meruliaceae	2	3	4.05	<i>Skeletocutis</i>	2	2.70
								<i>Tyromyces</i>	1	1.35
					6	6	8.11	<i>Ceriporiopsis</i>	1	1.35
								<i>Crustodontia</i>	1	1.35
								<i>Phlebia</i>	1	1.35
								<i>Hydnophanerochaete</i>	1	1.35
				Phanerochaetaceae	5	9	12.16	<i>Bjerkandera</i>	1	1.35
								<i>Crepatura</i>	1	1.35
								<i>Hyphodermella</i>	1	1.35
								<i>Phanerochaete</i>	4	5.41
								<i>Phlebiopsis</i>	2	2.70
				Polyporaceae	4	4	5.41	<i>Cyanosporus</i>	1	1.35
								<i>Diplomitoporus</i>	1	1.35
								<i>Megasporia</i>	1	1.35
								<i>Microporus</i>	1	1.35
				Steccherinaceae	2	2	2.70	<i>Butyrea</i>	1	1.35
								<i>Steccherinum</i>	1	1.35
Russulales	6	10	13.51	Bondarzewiaceae	1	1	1.35	<i>Heterobasidion</i>	1	1.35
				Gloeocystidiellaceae	1	1	1.35	<i>Gloeocystidiellum</i>	1	1.35
				Hericiaceae	1	1	1.35	<i>Dentipellicula</i>	1	1.35
				Lachnocladiaceae	2	3	4.05	<i>Peniophora</i>	2	2.70
				Peniophoraceae				<i>Scytinostroma</i>	1	1.35
				Stereaceae	2	4	5.41	<i>Aleurodiscus</i>	2	2.70
								<i>Stereum</i>	2	2.70
Tremellales	1	2	2.70	Tremellaceae	1	2	2.70	<i>Tremella</i>	2	2.70
7 orders			100	24 families			100	49 genera	74 species	100

Geographical component analysis of the family

The geographical composition of families can be divided into two broad categories, with 17 worldwide widespread families viz. Auriculariaceae, Bondarzewiaceae, Cerrenaceae, Fomitopsidaceae, Gloeophyllaceae, Hymenochaetaceae, Hyphodermataceae, Incrustoporiaceae, Irpicaceae, Meruliaceae, Peniophoraceae, Phanerochaetaceae, Polyporaceae, Schizoporaceae, Steccherinaceae, Stereaceae, and Tremellaceae. It comprises three Northern temperate distribution families viz. Dacryobolaceae, Hericiaceae and Radulomycetaceae. The geographical components of the macrofungi in Zixishan area, were mainly the world's widespread family, accounting for 70.83% of the total number of families.

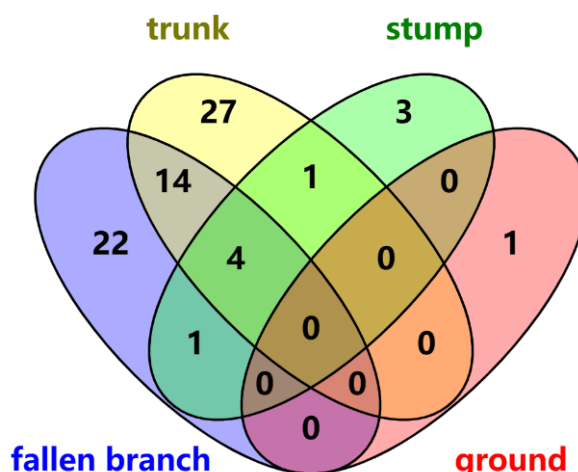


FIGURE 2. Venn diagram of species number of wood-decaying fungi in four parasitic positions.

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 collection data are provided after the name of each species. The hosts are listed alphabetically, and within the same host tree, they are arranged in the following order: living tree, dead standing tree, trunk, fallen branch and stump. The collectors and collection numbers are also listed alphabetically (Dai 2011, 2012).

Agaricales Underw.

Radulomycetaceae Leal-Dutra, Dentinger & G.W. Griff.

Radulomyces M.P. Christ. (1)

Auriculariales J. Schröt.

Auriculariaceae Fr.

Auricularia Bull. (1)

Gloeophyllales Thorn

Gloeophyllaceae Jülich

Gloeophyllum P. Karst. (1)

Hymenochaetales Oberw.

Hymenochaetaceae Donk

Coltricia Gray (1)

Fuscoporia Murrill (1)

Hydnoporia Murrill (2)

Hydnochaete Bres. (4)

Tubulicrinis Donk (1)

Rickenellaceae Vizzini

Peniophorella P. Karst. (5)

Schizocorticium Sheng H. Wu (1)

Schizoporaceae Jülich

Hyphodontia J. Erikss. (1)

Lyomyces P. Karst. (4)

Xylodon (Pers.) Gray (1)

Polyporales Gäum.

Cerrenaceae Miettinen, Justo & Hibbett

Cerrena Gray (1)

Cystostereaceae Jülich

Crustomyces Jülich (1)

Dacrybolaceae Jülich

Postia Fr. (1)

Fomitopsidaceae Jülich

Antrodia P. Karst. (1)

Fomitopsis P. Karst. (1)

Hyphodermataceae Jülich

Hyphoderma Fr. (5)

Incrustoporiaceae Jülich

Skeletocutis Kotl. & Pouzar (2)

Tyromyces P. Karst. (1)

Irpicaceae Spirin & Zmitr.

Byssomerulius Parmasto (1)

Ceriporia Donk (2)

Irpex Fr. (1)

Leptoporus Quél. (1)

Gloeoporus Mont. (1)

Meruliaceae Rea

Ceriporiopsis Domański (1)

Crustodontia Hjortstam & Ryvarden (1)

Hydnophanerochaete Sheng H. Wu & C.C. Chen (1)

Phlebia Fr. (1)

Phanerochaetaceae Jülich

Bjerkandera P. Karst. (1)

Crepatura C.L. Zhao (1)

Hyphodermella J. Erikss. & Ryvarden (1)

Phanerochaete P. Karst. (4)

Phlebiopsis Jülich (2)

Polyporaceae Fr. ex Corda

Cyanosporus McGinty (1)

Diplomitoporus Domański (1)

Megasporia B.K. Cui, Y.C. Dai & Hai J. Li (1)

Microporus P. Beauv. (1)

Steccherinaceae Parmasto

Butyrea Miettinen (1)

Steccherinum Gray (1)

Russulales genera incertae sedis

Bondarzewiaceae Kotl. & Pouzar

Heterobasidion Bref. (1)

Stereaceae Pilát

Gloeocystidiellum Donk (1)

Hericiaceae Donk

Dentipellicula Y.C. Dai & L.W. Zhou (1)

Peniophoraceae Lotsy

Peniophora Cooke (2)

Scytinostroma Donk (1)

Stereaceae Pilát

Aleurodiscus Rabenh. ex J. Schröt. (2)

Stereum Hill ex Pers. (2)

Tremellomycetes Doweld

Tremellaceae Fr.

Tremella Pers. (2)

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

Specimen examined: ZiDing Temple, Zixishan National Forest Park, Chuxiong, Yunnan Province, China, the fallen branch of *Pinus*, 2 July 2021, CLZhao 21151 (SWFC) (GenBank: ITS-OM955789).

Aleurodiscus mirabilis (Berk. & M.A. Curtis) Höhn., *Sber. Akad. Wiss. Wien, Math. -naturw. Kl., Abt. 1* 118: 818 (1909)

Specimens examined: Zixishan National Forest Park, Chuxiong, Yunnan Province, China, the fallen branch of angiosperm, 30 June 2018, CLZhao 6781, CLZhao 6790, CLZhao 12629 (SWFC) (GenBank: ITS-OM955790).

Antrodia xantha (Fr.) Ryvarden, *Norwegian Journal of Botany* 20 (1): 8 (1973)

Specimens examined: Zixishan National Forest Park, Chuxiong, Yunnan Province, China, the stump of *Pinus yunnanensis*, 25 July 2018, CLZhao 6667, CLZhao 6681, CLZhao 6685 (SWFC) (GenBank: ITS-OM955795).

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

Specimen examined: Zixishan National Forest Park, Chuxiong, Yunnan Province, China, the trunk of *Quercus*, 2 July 2018, CLZhao 7565 (SWFC).

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

Specimens examined: Zixishan National Forest Park, Chuxiong, Yunnan Province, China, the trunk of angiosperm, 2 July 2021, CLZhao 21134; the fallen branch of angiosperm, CLZhao 21147; 3 July 2021, CLZhao 21234; the fallen branch of angiosperm, 3 July 2021, CLZhao 21222 (SWFC).

Butyrea japonica (Núñez & Ryvarden) Miettinen & Ryvarden, *Annales Botanici Fennici* 53: 161 (2016)

Specimen examined: Zixishan National Forest Park, Chuxiong, Yunnan Province, China, the trunk of angiosperm, 1 July 2018, CLZhao 7218 (SWFC) (GenBank: ITS-OM955796).

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

Specimens examined: Xianren Valley, Zixishan National Forest Park, Chuxiong, Yunnan Province, China, the trunk of angiosperm, 30 June 2018, CLZhao 12623; the fallen branch of angiosperm, 30 June 2018, CLZhao 6910; the fallen branch of angiosperm, 2 July 2018, CLZhao 7538, CLZhao 7546 (SWFC) (GenBank: ITS-OM955797).

Cerrena zonata (Berk.) H.S. Yuan, *Mycological Progress* 13 (2): 363 (2013)

Specimens examined: Zixishan National Forest Park, Chuxiong, Yunnan Province, China, the trunk of angiosperm, 1 July 2018, CLZhao 7067, CLZhao 7167; the stump of angiosperm, 2 July 2018, CLZhao 7446, CLZhao 7579, CLZhao 7607; 17 August 2018, CLZhao 7676 (SWFC) (GenBank: ITS-OM955819).

Ceriporia nanlingensis B.K. Cui & B.S. Jia, *Mycotaxon* 116: 458 (2011)

Specimens examined: Zijinshan Forest farm, Xianren Valley, Zixishan National Forest Park, Chuxiong, Yunnan Province, China, the trunk of angiosperm, 30 June 2018, CLZhao 6889; Zijinshan Forest farm, Zixishan National Forest Park, Chuxiong, Yunnan Province, the trunk of angiosperm, 1 July 2018, CLZhao 6974; the fallen branch of angiosperm, 1 July 2018, CLZhao 7103; the trunk of angiosperm, 2 July 2018, CLZhao 7208, the trunk of angiosperm, 2 July 2018, CLZhao 7416, Baotouwang, Wanghai Villa, Zixishan National Forest Park, Chuxiong, Yunnan Province, CLZhao 7490, CLZhao 7512, the fallen branch of angiosperm, 2 July 2018, CLZhao 7539, the trunk of angiosperm, 2 July 2018, CLZhao 7625 (SWFC) (GenBank: ITS-OM955803).

Ceriporia pseudocystidiata B.S. Jia & Y.C. Dai, *Mycological Progress* 13 (1): 86 (2013)

Specimen examined: Xianren Valley, Zixishan National Forest Park, Chuxiong, Yunnan Province, China, the trunk of *Pinus*, 17 August 2018, CLZhao 7682 (SWFC) (GenBank: ITS-OM955808).

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

Specimens examined: Zijinshan Forest farm, Zixishan National Forest Park, Chuxiong, Yunnan Province, China, the trunk of angiosperm, 1 July 2018, CLZhao 7106; Baotouwang, Zixishan National Forest Park, Chuxiong, Yunnan Province, the trunk of angiosperm, 2 July 2018, CLZhao 7426; Zixishan National Forest Park, Chuxiong, Yunnan Province, the trunk of angiosperm, 1 August 2018, CLZhao 7719, CLZhao 7711 (SWFC) (GenBank: ITS-OM955809).

Coltricia crassa Y.C. Dai, *Fungal Diversity* 45: 140 (2010)

Specimens examined: Zijinshan Forest farm, Zixishan National Forest Park, Chuxiong, Yunnan Province, China, the

ground, 1 July 2018, CLZhao 7157, CLZhao 7174; Wanghai Villa, Zixishan National Forest Park, Chuxiong, Yunnan Province, the ground, 2 July 2018, CLZhao 7304; Zixishan National Forest Park, Chuxiong, Yunnan Province, the ground, 17 August 2018, CLZhao 7717 (SWFC) (GenBank: ITS-OM955820).

Crepatura ellipsospora C.L. Zhao, Mycological Progress 18 (6): 791 (2019)

Specimens examined: Xianren Valley, Zixishan National Forest Park, Chuxiong, Yunnan Province, China, the fallen branch of angiosperm, 30 June 2018, CLZhao 6851; Zijinshan Forest farm, Zixishan National Forest Park, Chuxiong, Yunnan Province, the fallen branch of angiosperm, 1 July 2018, CLZhao 7035, CLZhao 7194, CLZhao 7249;; Baotouwang, Zixishan National Forest Park, Chuxiong, Yunnan Province, the trunk of *Camellia japonica* L., 2 July 2018, CLZhao 7366 (SWFC) (GenBank: ITS-OM955821).

Crustodontia chrysocreas (Berk. & M.A. Curtis) Hjortstam & Ryvarden, Syn. Fung. (Oslo) 20: 36 (2005)

Specimen examined: Xianren Valley, Zixishan National Forest Park, Chuxiong, Yunnan Province, China, the trunk of angiosperm, 1 July 2021, CLZhao 21107 (SWFC) (GenBank: ITS-OM955826).

Crustomyces subabruptus (Bourdote & Galzin) Jülich, Persoonia 10 (1): 140 (1978)

Specimens examined: Zixishan National Forest Park, Chuxiong, Yunnan Province, China, the fallen branch of angiosperm, 1 July 2021, CLZhao 21086; 2 July 2021, CLZhao 21168, CLZhao 21169 (SWFC) (GenBank: ITS-OM955828).

Cyanosporus submicroporus B.K. Cui & Shun Liu, Frontiers in Microbiology 12 (no. 631166): 12 (2021)

Specimen examined: Zixishan National Forest Park, Chuxiong, Yunnan Province, China, the fallen branch of angiosperm, 1 July 2018, CLZhao 6920 (SWFC) (GenBank: ITS-OM955827).

Dentipellicula leptodon (Mont.) Y.C. Dai & L.W. Zhou, Mycologia 105 (3) : 641 (2013)

Specimens examined: Zixishan National Forest Park, Chuxiong, Yunnan Province, China, the trunk of angiosperm, 30 June 2018, CLZhao 6818, CLZhao 6834; 1 July 2018, CLZhao 7039, CLZhao 7099, CLZhao 7250, CLZhao 7252; 2 July 2018, CLZhao 7362, CLZhao 7591; 17 August 2018, CLZhao 7704; the trunk of *Camellia japonica* L., 1 July 2018, CLZhao 7069, CLZhao 7137; the trunk of *Quercus*, 1 July 2018, CLZhao 7122; the trunk of *Pinus*, CLZhao 7564 (SWFC) (GenBank: ITS-OM955830).

Diplomitoporus flavescens (Bres.) Domański, Acta Societatis Botanicorum Poloniae 39: 191 (1970)

Specimen examined: Zixishan National Forest Park, Chuxiong, Yunnan Province, China, the trunk of *Pinus*, 1 July 2018, CLZhao 7009 (SWFC) (GenBank: ITS-OM955844).

Fomitopsis pinicola (Sw.) P. Karst., Meddelanden af Societas pro Fauna et Flora Fennica 6: 9 (1881)

Specimens examined: Zixishan National Forest Park, Chuxiong, Yunnan Province, China, the stump of *Pinus*, 2 July 2018, CLZhao 7489; 1 August 2018, CLZhao 7727, CLZhao 7732; 17 August 2018, CLZhao 7716; 3 May 2019, CLZhao 12607, CLZhao 12608; Wanghai Villa, Zixishan National Forest Park, Chuxiong, Yunnan Province, 3 July 2021, CLZhao 21225 (SWFC) (GenBank: ITS-OM955845).

Fuscoporia chinensis Q. Chen, F. Wu & Y.C. Dai, Mycosphere 11 (1): 1491 (2020)

Specimen examined: Xiangshuijing Waterfall, Zixishan National Forest Park, Chuxiong, Yunnan Province, China, the trunk of angiosperm, 2 July 2021, CLZhao 21152 (SWFC) (GenBank: ITS-OM955848).

Gloeoporus taxicola (Pers.) Gilb. & Ryvarden, Mycotaxon 22 (2): 364 (1985)

Specimen examined: Wanghai Villa, Zixishan National Forest Park, Chuxiong, Yunnan Province, China, the trunk of angiosperm, 2 July 2018, CLZhao 7501 (SWFC).

Gloeophyllum sepiarium (Wulfen) P. Karst., Bidrag till Kännedom av Finlands Natur och Folk 37: 79 (1882)

Specimen examined: Zixishan National Forest Park, Chuxiong, Yunnan Province, China, the angiosperm dead tree, 2 July 2018, CLZhao 7519 (SWFC).

Gloeocystidiellum porosum (Berk. & M.A. Curtis) Donk, Meddel. Nedl. Mycol. Ver. 18-20: 156 (1931)

Specimen examined: Zixishan National Forest Park, Chuxiong, Yunnan Province, China, the fallen branch of angiosperm, 1 July 2018, CLZhao 6984 (SWFC) (GenBank: ITS-OM955849).

Heterobasidium insulare (Murrill) Ryvarden, Norw. J. Bot. 19: 237 (1972)

Specimens examined: Zixishan National Forest Park, Chuxiong, Yunnan Province, China, the trunk of *Pinus*, 30 June 2018, CLZhao 6829; the stump of *Pinus*, 30 June 2018, CLZhao 6870; 2 July 2018, CLZhao 7027, CLZhao 7312 (SWFC) (GenBank: ITS-OM955850).

Hydnoporia corrugata (Fr.) K.H. Larss. & Spirin, Fungal Systematics and Evolution 4: 88 (2019)

Specimens examined: Zixishan National Forest Park, Chuxiong, Yunnan Province, China, the fallen branch of angiosperm, 1 July 2018, CLZhao 7171, CLZhao 7173, CLZhao 7232; 2 July 2018, CLZhao 7520; Xiangguo Garden, Zixishan National Forest Park, Chuxiong, Yunnan Province, the fallen branch of angiosperm, 3 July 2021, CLZhao 21289 (SWFC) (GenBank: ITS-OM955854).

- Hydnoporia yasudae*** (Imazeki) Spirin & Miettinen, Fungal Systematics and Evolution 4: 94 (2019)
Specimen examined: Wanghai Villa, Zixishan National Forest Park, Chuxiong, Yunnan Province, China, the fallen branch of angiosperm, 3 July 2021, CLZhao 21214 (SWFC) (GenBank: ITS-OM955855).
- Hydnophanerochaete odontoidea*** (Sheng H. Wu) Sheng H. Wu & C.C. Chen, MycoKeys 39: 86 (2018)
Specimens examined: Zijinshan Forest farm, Zixishan National Forest Park, Chuxiong, Yunnan Province, China, the fallen branch of angiosperm, 26 June 2018, CLZhao 6732, CLZhao 6735; 26 June 2018, CLZhao 6741, CLZhao 6743; 1 July 2018, CLZhao 7231; the stump of angiosperm, 26 June 2018, CLZhao 6738; the trunk of angiosperm, 30 June 2018, CLZhao 6785, CLZhao 6899, CLZhao 6900; 1 July 2018, CLZhao 6987 (SWFC) (GenBank: ITS-OM955750).
- Hymenochaete cruenta*** (Pers.) Donk, Persoonia 1 (1): 51 (1959)
Specimens examined: Baotouwang, Zixishan National Forest Park, Chuxiong, Yunnan Province, China, the trunk of *Camellia japonica* L., 2 July 2018, CLZhao 7307; Wanghai Villa, Zixishan National Forest Park, Chuxiong, Yunnan Province, the fallen branch of angiosperm, 3 July 2021, CLZhao 21195 (SWFC) (GenBank: ITS-OM955856).
- Hymenochaete minor*** S.H. He & Y.C. Dai, Fungal Diversity 56: 84 (2012)
Specimen examined: Zixishan National Forest Park, Chuxiong, Yunnan Province, China, the fallen branch of angiosperm, 1 July 2018, CLZhao 7197 (SWFC) (GenBank: ITS-OM955857).
- Hymenochaete rheicolor*** (Mont.) Lév., Annales des Sciences Naturelles Botanique 5: 151 (1846)
Specimens examined: Xianren Valley, Zixishan National Forest Park, Chuxiong, Yunnan Province, China, the fallen branch of angiosperm, 30 June 2018, CLZhao 6801; the trunk of angiosperm, 30 June 2018, CLZhao 6883; Zijinshan Forest farm, Zixishan National Forest Park, Chuxiong, Yunnan Province, the fallen branch of angiosperm, 1 July 2018, CLZhao 7090; Baotouwang, Zixishan National Forest Park, Chuxiong, Yunnan Province, the fallen branch of angiosperm, 2 July 2018, CLZhao 7505; Zixishan National Forest Park, Chuxiong, Yunnan Province, the fallen branch of angiosperm, 31 June 2018, CLZhao 8835 (SWFC) (GenBank: ITS-OM955858).
- Hymenochaete xerantica*** (Berk.) S.H. He & Y.C. Dai, Fungal Diversity 56: 90 (2012)
Specimen examined: Zijinshan Forest farm, Zixishan National Forest Park, Chuxiong, Yunnan Province, China, the trunk of angiosperm, 1 July 2018, CLZhao 7141 (SWFC) (GenBank: ITS-OM955861).
- Hyphoderma chuxiongense*** C.L. Zhao & Q.X. Guan sp.
Specimen examined: Zixishan National Forest Park, Chuxiong, Yunnan Province, China, the fallen branch of angiosperm, 1 July 2018, CLZhao 7083 (SWFC).
- Hyphoderma fissuratum*** C.L. Zhao & X. Ma, Mycoscience 62: 37 (2021)
Specimens examined: Zixishan National Forest Park, Chuxiong, Yunnan Province, China, the stump of angiosperm, 26 June 2018, CLZhao 6726, CLZhao 6731 (SWFC) (GenBank: ITS-MT791331).
- Hyphoderma microporoides*** C.L. Zhao & Q.X. Guan, Journal of Fungi 7 (4, no. 308): 9 (2021)
Specimen examined: Zixishan National Forest Park, Chuxiong, Yunnan Province, China, the trunk of fallen angiosperm, 30 June 2018, CLZhao 6857 (SWFC) (GenBank: ITS-MW917169).
- Hyphoderma moniliforme*** (P.H.B. Talbot) Manjón, G. Moreno & Hjortstam, Mycotaxon 33: 261
Specimens examined: Zixishan National Forest Park, Chuxiong, Yunnan Province, China, the stump of *Pinus*, 30 June 2018, CLZhao 6871; the fallen branch of angiosperm, 1 July 2021, CLZhao 21091; 2 July 2021, CLZhao 21162; 3 July 2021, CLZhao 21193 (SWFC) (GenBank: ITS-OM955863).
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Irpex lacteus (Fr.) Fr., Elenchus Fungorum 1: 145 (1828)

Specimens examined: Zixishan National Forest Park, Chuxiong, Yunnan Province, China, the trunk of angiosperm, 1 July 2021, CLZhao 21090; the fallen branch of angiosperm, 2 July 2021, CLZhao 21136; the fallen branch of angiosperm, 3 July 2021, CLZhao 21190; CLZhao 21253 (SWFC).

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Discussion

In the 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 (2008), 1589 genera and over 30,000 species were included in Basidiomycota (Kirk *et al.* 2008; Dai *et al.* 2015) and many taxa were recorded all over the world every year, which observably increase the fungal diversity (Dai *et al.* 2015, Cui *et al.* 2019, Ayesha *et al.* 2020, Himani & Krishnappa 2020, Blanco-Dios 2021, Boonyuen 2021, Kumar & Singh 2021, Zong *et al.* 2021, Luo *et al.* 2022, Wijayawardene *et al.* 2022, Cai *et al.* 2023, Yang *et al.* 2023, Zhao *et al.* 2023). Most new fungal species were discovered in southern China (Wu *et al.* 2020), while Yunnan is the most important source of new discoveries accounting for 1/4 of the total in China (Dai *et al.* 2021). However, the diversity of wood-decaying fungi in Zixishan area has not been found. The present work is the first report of a series of studies devoted to wood-decaying fungi in this area and contributes to revealing the abundance of wood-decaying species. According to the previous studies (Dai 2011, 2012, Dai *et al.* 2015, 2021, He & Zhao 2022) combined with field observations, the Wuliangshan area reported 90 white-rot fungi and five brown-rot fungi and Haikou Forestry Park reported 46 white-rot fungi and three brown-rot fungi, and Huangshan Mountains reported 73 white-rot fungi and 12 brown-rot fungi, and Great Xingan Mountains reported 93 white-rot fungi and 33 brown-rot fungi. In the present study, a total of 1,407 specimens belonging to 74 wood-decaying poroid and corticioid species were collected from Zixishan area, including 63 white rot species (85.14% of the total) and the remaining 11 brown-rot species (14.86% of the total). In contrast, the proportion of brown-rot fungi in Zixishan area is similar to that in Huangshan Mountains, which is 14.12% (Cui & Jia 2011), and it is higher than Wuliangshan area and Haikou Forestry compared to 5.26% and 6.12% (He *et al.* 2021, He & Zhao 2022), but it is lower than Great Xingan Mountains compared to 26.19% (Cui & Yu 2011).

In forest ecosystems, wood-inhabiting poroid and corticioid fungal function as wood decomposers release matter and energy to the ecological system (Cui *et al.* 2006, Wei 2010, Gafforov *et al.* 2020, Dai *et al.* 2021). Combined nLSU, SSU, 5.8s, *rpb1*, *rpb2*, and *tefl* phylogenetic analyses in the subphyla Agaricomycotina, Pucciniomycotina and Ustilaginomycotina, showed that 1928 currently used genera names are distributed in 241 families, 68 orders, 18 classes and four subphyla. In the present study, 74 species were nested in 50 genera, 24 families and eight orders based on ITS dataset, which is similar to the topology of a previous study (He *et al.* 2019). In the present study, sequences of ITS gene regions of the studied samples were generated, which illustrate that all collected fungal specimens from Zixishan area belonging to Agaricomycetes distribute into Agaricales, Auriculariales, Corticiales, Hymenochaetales, Gloeophyllales, Polyporales, Russulales and Trechisporales. The phylogenetic analyses of all studied samples showed that the individual taxon clusters closely with downloaded reliable sequences from previous studies with good statistical support (Fig. 1).

Eighty pathogenic wood-decaying fungi mainly belong to the families Ganodermataceae, Climacodontaceae, Corticiaceae, Hericiaceae, Hymenochataceae, Polyporaceae, and Schizophyllaceae of Basidiomycota were reported by Dai *et al.* (2000). Out of 240 fungi collected in Hainan area (China), 199 were polypores, and 41 were corticioid and others were wood-inhabiting fungi (Ma *et al.* 2022). A total of 1819 species belonging to 509 genera were reported in China, which were divided into 10 groups, including 196 larger Ascomycetes, 21 jelly fungi, 47 coral fungi, 637 polyporoid, hydneous and thelephoroid fungi, 11 cantharelloid fungi, 653 agarics, 130 boletes, 75 gasteroid fungi, 16 larger pathogenic fungi on crops, and 33 larger Myxomycetes (Li *et al.* 2015). The macrofungi included 310 species, located in three phyla, eight classes, 24 orders, 66 families, and 152 genera in Saihanwula National Nature Reserve of Inner Mongolia, China (Liu & Li 2019). The fungal diversity of wood-decaying fungi in Wuliangshan area (Yunnan Province) revealed 95 species, belonging to Auriculariales, Boletales, Cantharellales, Corticiales, Gloeophyllales, Hymenochaetales, Polyporales, Russulales and Trechisporales of Basidiomycota (He & Zhao 2022). These results indicate that the tropical and subtropical areas have enriched fungal diversity, which pushes our research regarding the richness of the wood-decaying fungi in China.

Based on the dramatic changes in higher-level taxonomy in the last twenty years, the tripling of the fungal phyla from four to 12 has occurred, and the biodiversity of many hidden and microscopic fungi was undersampled, and the current research indicated that perhaps less than 5% of the estimated species have been formally described (Blackwell 2011, Hawksworth & Lücking 2017, Dai *et al.* 2021). This work aims to enrich the fungal diversity worldwide, which will support the rational utilization and effective protection of fungal resources and provides a scientific basis for the prevention and control of forest diseases in Zixishan area.

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