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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

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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 km^2 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 (Fsfruit, 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.	References
		ITS	
Aleurodiscus isabellinus	CLZhao 21151	OM955789	Present study
A. isabellinus	He 5294	MH109053	Tian *et al.* (2018)
A. mirabilis	CLZhao 6781	OM955790	Present study
A. mirabilis	He 3730	KX306878	Dai & He (2017)
Antrodia xantha	CLZhao 6685	OM955795	Present study
A. xantha	Dai 12984	MG787578	Unpublished
Butyrea japonica	CLZhao 7218	OM955796	Present study
B. japonica	SFC20170823-29	MN973797	Lee *et al.* (2020)
Byssomerulius corium	CLZhao 6910	OM955797	Present study
B. corium	Wu 1207-55	MZ636932	Chen *et al.* (2021)
Ceriporia nanlingensis	CLZhao 7208	OM955803	Present study
C. nanlingensis	Dai8173	JX623942	Jia *et al.* (2014)
C. pseudocystidiata	CLZhao 7682	OM955808	Present study
C. pseudocystidiata	Cui6878	JX623943	Jia *et al.* (2014)
Ceriporiopsis semisupina	CLZhao 7426	OM955809	Present study
Ce. semisupina	Chen 3327	MZ636937	Chen *et al.* (2021)
Cerrena zonata	CLZhao 7676	OM955819	Present study
Cer. zonata	Dai7821	KC485529	Yuan (2014)
Coltricia crassa	CLZhao 7157	OM955820	Present study
C. crassa	Dai 15163	KU360679	Bian & Dai (2015)
Crepatura ellipsospora	CLZhao 6851	OM955821	Present study
C. ellipsospora	CLZhao 697	MK343695	Ma & Zhao (2019)
Crustodontia chrysocreas	CLZhao 21107	OM955826	Present study
C. chrysocreas	CBS 125889	MH864087	Vu *et al.* (2019)
Crustomyces subabruptus	CLZhao 21086	OM955828	Present study
Cr. subabruptus	K(M):249975	MZ159685	Unpublished
Cyanosporus submicroporus	CLZhao 6920	OM955827	Present study
C. submicroporus	Cui 18156	MW182186	Liu *et al.* (2022)
Dentipellicula leptodon	CLZhao 6818	OM955830	Present study
D. leptodon	CBS 125879	MH864083	Vu *et al.* (2019)
Diplomitoporus flavescens	CLZhao 7009	OM955844	Present study
D. flavescens	IBL66	MZ410695	Unpublished
Fomitopsis pinicola	CLZhao 7716	OM955845	Present study
F. pinicola	Cui 10312	KR605781	Han *et al.* (2016)
Fuscoporia chinensis	CLZhao 21152	OM955848	Present study
F. chinensis	Dai 15713	MN816721	Chen *et al.* (2020)
Gloeocystidiellum porosum	CLZhao 6984	OM955849	Present study
G. porosum	CBS 189.56	MH857576	Vu *et al.* (2019)
Heterobasidion insulare	CLZhao 6829	OM955850	Present study
H. insulare	Dai 13933	MT146489	Yuan *et al.* (2021)
Hydnophanerochaete odontoidea	CLZhao 6785	OM955750	Present study
H. odontoidea	CLZhao 4036	MH784927	Shen *et al.* (2018)
Hydnoporia corrugata	CLZhao 7171	OM955854	Present study
Hy. corrugata	HHB 19233	MW740292	Unpublished
Hy. yasudae	CLZhao 21214	OM955855	Present study

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TABLE 1. (Continued)

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

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TABLE 1. (Continued)

Species name	Sample no.	GenBank Accession No. ITS	References
L. vietnamensis	TNM F9073	JX175044	Yurchenko & Wu (2015)
Megasporia major	CLZhao 7064	OM955928	Present study
M. major	GC 1407-21	KY688205	Chen *et al.* (2018)
Peniophora versiformis	CLZhao 7051	OM955931	Present study
P. versiformis	CBS 361.54	MH857362	Vu *et al.* (2019)
Peniophorella fissurata	CLZhao 7290	OM955718	Present study
Pe. fissurata	CLZhao 9421	MN864260	Guan *et al.* (2020)
Pe. praetermissa	CLZhao 21158	OM955719	Present study
Pe. praetermissa	NH 7827	DQ647460	Hallenberg *et al.* (2007)
Pe. pubera	CLZhao 7509	OM955722	Present study
Pe. pubera	NH 10512	DQ647505	Hallenberg *et al.* (2007)
Pe. rude	CLZhao 7142	OM955723	Present study
Pe. rude	Wu 0104-3	DQ647495	Hallenberg *et al.* (2007)
Pe. subpraetermissa	CLZhao 6882	OM955728	Present study
Pe. subpraetermissa	Wu 950627	DQ647493	Hallenberg *et al.* (2007)
Phanerochaete concrescens	CLZhao 7002	OM955732	Present study
P. concrescens	He 4657	MT235662	Unpublished
P. pruinosa	CLZhao 7713	MZ435347	Present study
P. pruinosa	CLZhao 7712	MZ435346	Wang & Zhao (2021b)
P. rhizomorpha	CLZhao 10470	MZ435348	Present study
P. rhizomorpha	CLZhao 10477	MZ435349	Wang & Zhao (2021b)
P. sordida	CLZhao 7486	OM955733	Present study
P. sordida	He 5400	MT235676	Unpublished
Phlebia acerina	CLZhao 7664	OM955744	Present study
P. acerina	HHB 11146	KP135372	Floudas & Hibbett (2015)
Phlebiopsis crassa	CLZhao 7130	OM955764	Present study
Ph. crassa	FP 102496	AY219341	De Koker *et al.* (2003)
Ph. yunnanensis	CLZhao 7367	OM955788	Present study
Ph. yunnanensis	CLZhao 3900	MH744141	Zhao *et al.* (2019)
Porodaedalea chinensis	CLZhao 7487	OM955768	Present study
P. chinensis	Dai 16864	KX852282	Dai *et al.* (2017)
Postia caesia	CLZhao 6904	OM955769	Present study
Po. caesia	K(M) 31967	AY599567	Yao *et al.* (2005)
Scytinostroma phaeosarcum	CLZhao 21302	OM955775	Present study
S. phaeosarcum	CBS 728.81	MH861463	Vu *et al.* (2019)
Skeletocutis nivea	CLZhao 7034	OM955776	Present study
S. nivea	FD-5	KP135331	Floudas & Hibbett (2015)
S. pseudo-odora	CLZhao 6938	OM955777	Present study
S. pseudo-odora	Dai 16527	KY245961	Fan *et al.* (2017)
Steccherinum nitidum	CLZhao 7198	MZ713646	Present study
S. nitidum	KHL 11903	JN710560	Miettinen *et al.* (2012)
Stereum hirsutum	CLZhao 7420	OM955779	Present study
St. hirsutum	CBS 108532	MH862810	Vu *et al.* (2019)
St. sanguinolentum	CLZhao 6856	OM955780	Present study
S. sanguinolentum	CLZhao 7581	OM955786	Present study
Tyromyces kmetii	CLZhao 7305	OM955787	Present study
T. kmetii	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 ≥ 70%, a maximum parsimony bootstrap (BT) of ≥ 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).

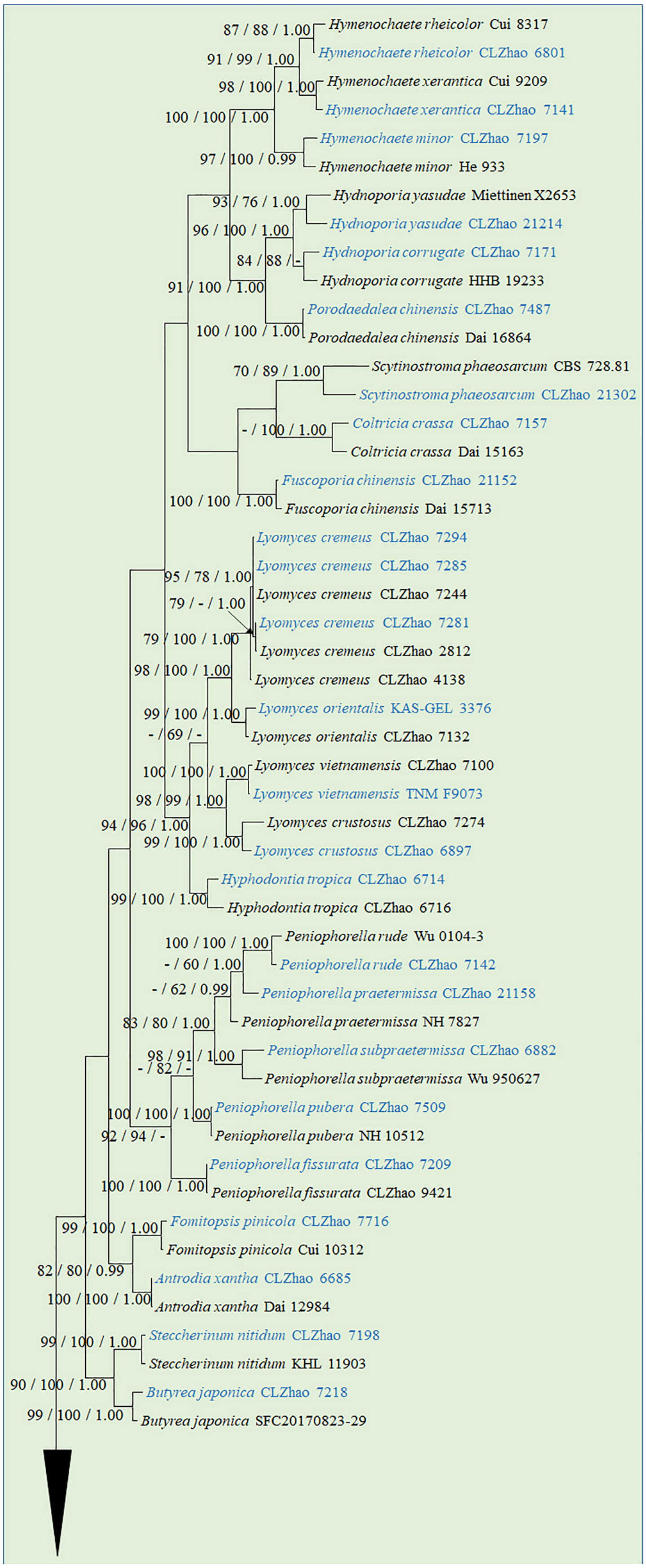

FIGURE 1. Maximum parsimony strict consensus tree illustrating the phylogeny of 68 species in Agaricomycetes based on ITS sequences. Branches are labelled with a maximum likelihood boot-strap ≥ 70%, a parsimony bootstrap ≥ 50% and Bayesian posterior probabilities ≥ 0.97, respectively. The sequences of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

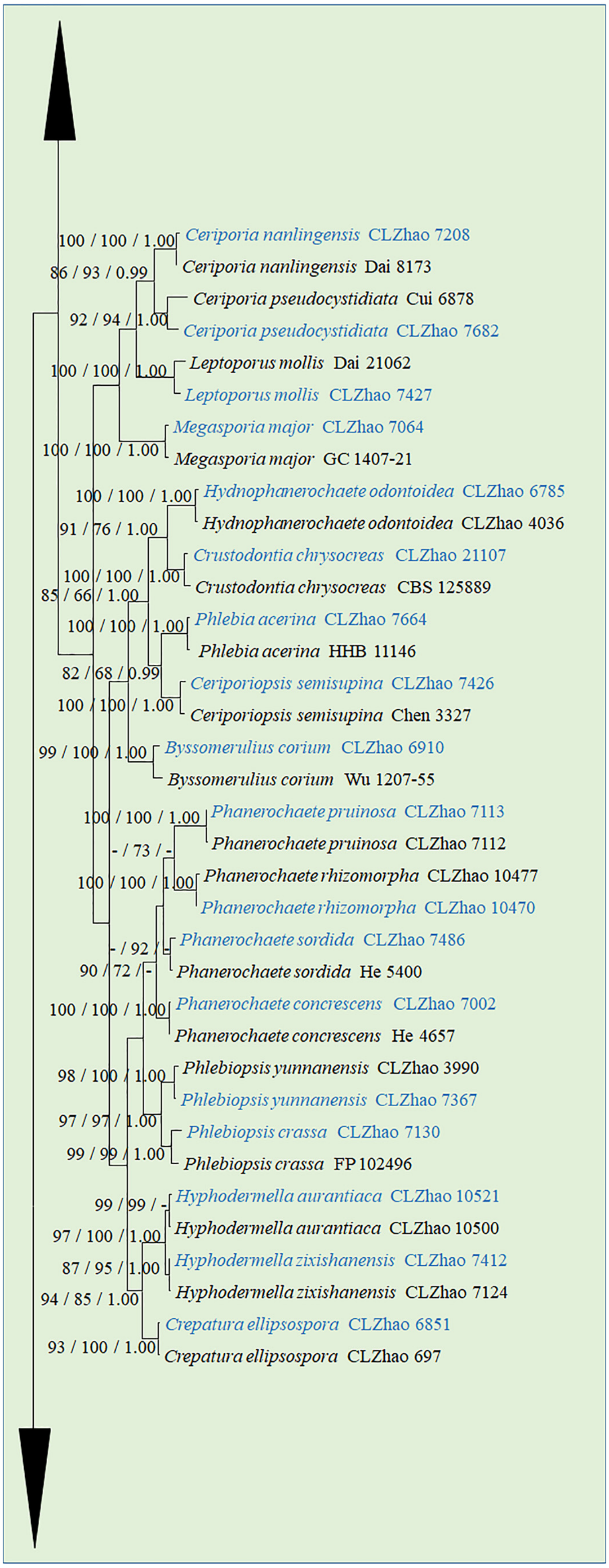

FIGURE 1. Continued.

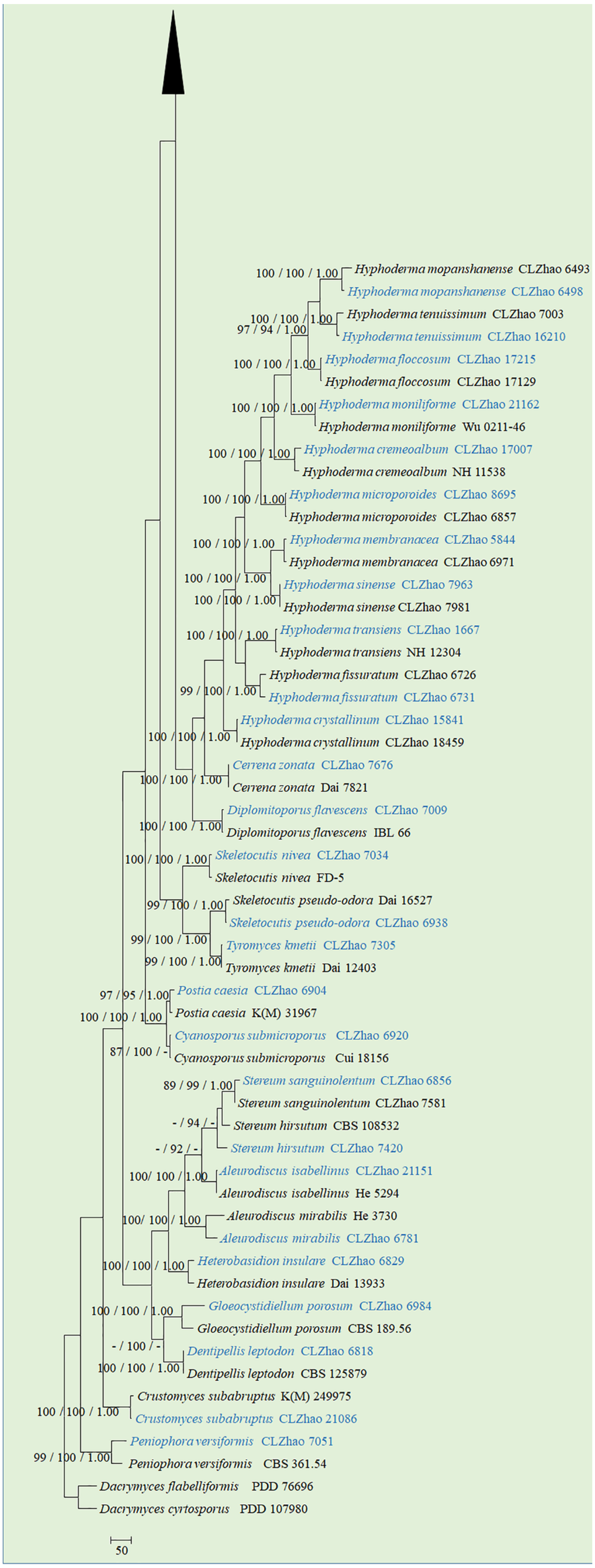

FIGURE 1. Continued.

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

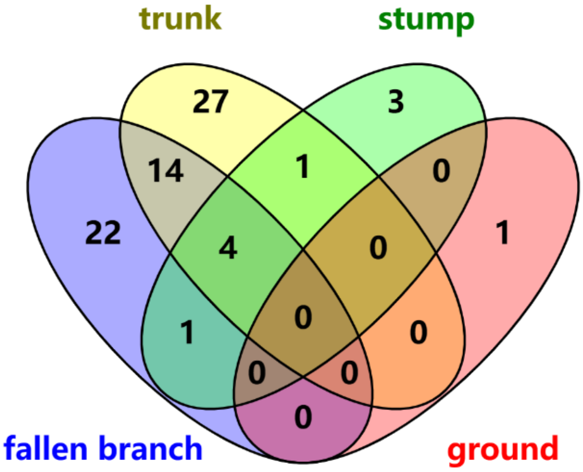

FIGURE 2. Venn diagram of species number of wood-decaying fungi in four parasitic positions.

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)
Dacryobolaceae 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 yunnanensisi*, 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, CLZhao7416, Baotouwang, Wanghai Villa, Zixishan National Forest Park, Chuxiong, Yunnan Province, CLZhao 7490, CLZhao 7512, the fallen branch of angiosperm, 2 July 2018, CLZhao7539, the trunk of angiosperm, 2 July 2018, CLZhao7625 (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 (Bourdot & 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, Medded. 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).

Heterobasidion insulare (Murrill) Ryvarden, Norw. Jl 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).

Hyphoderma tenuissimum C.L. Zhao & Q.X. Guan, MycoKeys 83: 153 (2021)

Specimens examined: Zixishan National Forest Park, Chuxiong, Yunnan Province, China, the fallen branch of angiosperm, 1 July 2021, CLZhao 6930, CLZhao 7003, CLZhao 7221; 1 July 2021, CLZhao 21291 (SWFC) (GenBank: ITS-MW443050).

Hyphodermella zixishanensis C.L. Zhao, Nordic Journal of Botany 39 (8): e03329, 4 (2021)

Specimens examined: Zixishan National Forest Park, Chuxiong, Yunnan Province, China, the fallen branch of angiosperm, 1 July 2018, CLZhao 7204, CLZhao 7206, CLZhao 7124, CLZhao 7129, CLZhao 7159, CLZhao 7228; 2 July 2018 CLZhao 7412, CLZhao 7433, CLZhao 7535 (SWFC) (GenBank: ITS-MZ305282).

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

Specimens examined: Ziding temple, Zixishan National Forest Park, Chuxiong, Yunnan Province, China, the fallen branch of angiosperm, 25 June 2018, CLZhao 6714, CLZhao 6716; Zijinshan Forest farm, Zixishan National Forest Park, Chuxiong, Yunnan Province, the trunk of angiosperm, 26 June 2018, CLZhao 6730; the stump of angiosperm, 26 June 2018, CLZhao 6736; Xianren Valley, Zixishan National Forest Park, Chuxiong, Yunnan Province, the fallen branch of angiosperm, 30 June 2018, CLZhao 6779; 1 July 2018, CLZhao 6953, CLZhao 6968, CLZhao 6996, CLZhao 7042, CLZhao 7114, CLZhao 7181, CLZhao 7186, CLZhao 7189, CLZhao 7212;

the trunk of angiosperm, 30 June 2018, CLZhao 6799, 30 June 2018, CLZhao 6825, CLZhao 6842, CLZhao 6844, CLZhao 6853, CLZhao 6867, CLZhao 6875, CLZhao 6884, CLZhao 6885, CLZhao 6886, CLZhao 6891, CLZhao 6894, CLZhao 6902; 1 July 2018, CLZhao 6943, CLZhao 6945, CLZhao 7013, CLZhao 7017, CLZhao 7097, CLZhao 7153; the fallen branch of *Quercus*, 1 July 2018, CLZhao 7073, CLZhao 7149; the trunk of *Camellia japonica*, 1 July 2018, CLZhao 6914, CLZhao 7077, CLZhao 7138; the trunk of *Pinus*, 1 July 2018, CLZhao 7000; Baotouwang, Zixishan National Forest Park, Chuxiong, Yunnan Province, the fallen branch of angiosperm, 2 July 2018, CLZhao 7325; the trunk of angiosperm, 2 July 2018, CLZhao 7360, CLZhao 7434, CLZhao 7442, CLZhao 7452, CLZhao 7456, CLZhao 7459, CLZhao 7498; the trunk of *Quercus*, 2 July 2018, CLZhao 7344; the trunk of *Pinus*, 2 July 2018, CLZhao 7407; the stump of angiosperm, 2 July 2018, CLZhao 7431, CLZhao 7470, CLZhao 7475, CLZhao 7478, CLZhao 7526, CLZhao 7556, CLZhao 7628, CLZhao 7660; the stump of *Pinus yunnanensis*, 2 July 2018, CLZhao 7444; the living tree of *Pinus*, 2 July 2018, CLZhao 7465 (SWFC) (GenBank: ITS-OM955867).

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).

Leptoporus mollis (Pers.) Quél., Enchiridion Fungorum in Europa media et praesertim in Gallia Vigentium: 176 (1886)

Specimen examined: Baotouwang, Wanghai Villa, Zixishan National Forest Park, Chuxiong, Yunnan Province, China, the fallen branch of angiosperm, 2 July 2018, CLZhao 7427 (SWFC) (GenBank: ITS-OM955917).

Lyomyces cremeus C.L. Zhao, in Chen & Zhao, MycoKeys 65: 101–118 (2020)

Specimens examined: Zixishan National Forest Park, Chuxiong, Yunnan Province, China, the trunk of angiosperm, 1 July 2018, CLZhao 7244, CLZhao 7281, CLZhao 7285, CLZhao 7294 (SWFC) (GenBank: ITS-OM955918).

Lyomyces crustosus (Pers.) P. Karst., Revue Mycologique Toulouse 3 (9): 23 (1881)

Specimens examined: Zixishan National Forest Park, Chuxiong, Yunnan Province, China, the trunk of angiosperm, 30 June 2018, CLZhao 6897; the fallen branch of angiosperm, 1 July 2018, CLZhao 7274 (SWFC) (GenBank: ITS-OM955922).

Lyomyces orientalis Riebesehl, Yurchenko & Langer, Mycological Progress 16 (9): 874 (2017)

Specimen examined: Zixishan National Forest Park, Chuxiong, Yunnan Province, China, the trunk of angiosperm, 1 July 2018, CLZhao 7132 (SWFC) (GenBank: ITS-OM955926).

Lyomyces vietnamensis (Yurchenko & Sheng H. Wu) Riebesehl & Langer, Mycological Progress 16 (6): 651 (2017)

Specimen examined: Zixishan National Forest Park, Chuxiong, Yunnan Province, China, the fallen branch of angiosperm, 1 July 2018, CLZhao 7100 (SWFC) (GenBank: ITS-OM955927).

Megasporia major (G.Y. Zheng & Z.S. Bi) B.K. Cui & Hai J. Li, Mycologia 105 (2): 375 (2013)

Specimen examined: Zixishan National Forest Park, Chuxiong, Yunnan Province, China, the fallen branch of angiosperm, 1 July 2018, CLZhao 7064 (SWFC) (GenBank: ITS-OM955928).

Microporus affinis (Blume & T. Nees) Kuntze, Revisio generum plantarum 3 (2): 494 (1898)

Specimen examined: Zixishan National Forest Park, Chuxiong, Yunnan Province, China, the trunk of angiosperm, 30 June 2018, CLZhao 6888 (SWFC).

Peniophora lycii (Pers.) Höhn. & Litsch., Sber. Akad. Wiss. Wien, Math.-naturw. Kl., Abt. 1 116: 747 (1907)

Specimen examined: Zixishan National Forest Park, Chuxiong, Yunnan Province, China, the trunk of angiosperm, 2 July 2018, CLZhao 7342 (SWFC).

Peniophora versiformis (Berk. & M.A. Curtis) Bourdot & Galzin, Hyménomyc. de France (Sceaux): 327 (1928) [1927]

Specimen examined: Zixishan National Forest Park, Chuxiong, Yunnan Province, China, the fallen branch of angiosperm, 1 July 2018, CLZhao 7051(SWFC) (GenBank: ITS-OM955931).

Peniophorella fissurata C.L. Zhao, Mycological Progress 19 (4): 400 (2020)

Specimen examined: Zixishan National Forest Park, Chuxiong, Yunnan Province, China, the fallen branch of angiosperm, 1 July 2018, CLZhao 7290 (SWFC) (GenBank: ITS-OM955718).

Peniophorella praetermissa (P. Karst.) K.H. Larss., Mycological Research 111 (2): 192 (2007)

Specimens examined:Xiangshuijing Waterfall, Zixishan National Forest Park, Chuxiong, Yunnan Province, China, the fallen branch of angiosperm, 2 July 2021, CLZhao 21144; 2 July 2021, CLZhao 21158 (SWFC) (GenBank: ITS-OM955719).

Peniophorella pubera (Fr.) P. Karst., Bidrag till Kännedom av Finlands Natur och Folk 48: 427 (1889)

Specimens examined: Wanghai Villa, Zixishan National Forest Park, Chuxiong, Yunnan Province,China, the trunk of angiosperm, 2 July 2018, CLZhao 7500; 2 July 2018, CLZhao 7509 (SWFC) (GenBank: ITS-OM955722).

Peniophorella rude K.H. Larss., Mycological Research 111 (2): 192 (2007)

Specimens examined: Zixishan National Forest Park, Chuxiong, Yunnan Province,China, the trunk of angiosperm, 1 July 2018, CLZhao 7142; the fallen branch of *Pinus*, 1 July 2018, CLZhao 7300; the trunk of *Quercus*, 2 July 2018, CLZhao 7309; the trunk of angiosperm, 2 July 2018, CLZhao 7311; the trunk of *Camellia japonica* L., 2 July 2018, CLZhao 7336 (SWFC) (GenBank: ITS-OM955723).

Peniophorella subpraetermissa (Sheng H. Wu) K.H. Larss., Mycological Research 111 (2): 192 (2007)

Specimens examined: Zixishan National Forest Park, Chuxiong, Yunnan Province,China, the trunk of angiosperm, 30 June 2018, CLZhao 6882; 30 June 2018, CLZhao 6893 (SWFC) (GenBank: ITS-OM955728).

Phanerochaete angustocystidiata Sheng H. Wu, Botanical Bulletin of the Academia Sinica (Taipei) 41: 166 (2000)

Specimens examined: Xianren Valley, Zixishan National Forest Park, Chuxiong, Yunnan Province, China, the fallen branch of angiosperm, 30 June 2018, CLZhao 6847, CLZhao 6901 (SWFC).

Phanerochaete concrescens Spirin & Volobuev, in Volobuev, Okun, Ordynets & Spirin, Mycol. Progr. 14 (no. 80): 7 (2015)

Specimens examined: Zijinshan Forest farm, Xianren Valley, Zixishan National Forest Park, Chuxiong, Yunnan Province, China, the trunk of angiosperm, 1 July 2018, CLZhao 7002, CLZhao 7107, CLZhao 7201; Baotouwang, Zixishan National Forest Park, Chuxiong, Yunnan Province, the fallen branch of angiosperm, 2 July 2018, CLZhao 7534;Xiangguo Garden, Zixishan National Forest Park, Chuxiong, Yunnan Province, 3 July 2018, CLZhao 21290, CLZhao 21295, CLZhao 21297 (SWFC) (GenBank: ITS-OM955732).

Phanerochaete pruinosa C.L. Zhao & D.Q. Wang, Journal of Fungi 7 (12, no. 1063): 8 (2021)

Specimens examined: Zixishan National Forest Park, Chuxiong, Yunnan Province, China, the fallen branch of angiosperm, 1 July 2018, CLZhao 7112, CLZhao 7113 (SWFC) (GenBank: ITS-MZ435347).

Phanerochaete sordida (P. Karst.) J. Erikss. & Ryvarden, Cortic. N. Eur. (Oslo) 5: 1023 (1978)

Specimens examined: Baotouwang, Zixishan National Forest Park, Chuxiong, Yunnan Province, China, the fallen branch of angiosperm, 2 July 2018, CLZhao 7486; Wanghai Villa, Zixishan National Forest Park, Chuxiong, Yunnan Province, the fallen branch of angiosperm, 1 July 2021, CLZhao 21081, CLZhao 21105 (SWFC) (GenBank: ITS-OM955733).

Phlebia acerina **Peck**, Ann. Rep. N.Y. St. Mus. 42: 123 (1889)

Specimens examined: Ziding Temple, Zixishan National Forest Park, Chuxiong, Yunnan Province, China, the trunk of *Pinu*s, 25 June 2018, CLZhao 6673; the fallen branch of angiosperm, 25 June 2018, CLZhao 6737; 1 July 2018, CLZhao 6934, CLZhao 6947; 1 July 2018, CLZhao 7182, CLZhao 7226; the stump of angiosperm, 25 June 2018, CLZhao 6748; the trunk of angiosperm, 25 June 2018, CLZhao 6827, CLZhao 6848, CLZhao 6878; 1 July 2018, CLZhao 6916, CLZhao 7008, CLZhao 7047, CLZhao 7056, CLZhao 7085, CLZhao 7087, CLZhao 7095, CLZhao 7109, CLZhao 7115, CLZhao 7175, CLZhao 7257; the fallen branch of *Camellia japonica* L., 1 July 2018, CLZhao 6929; the trunk of *Camellia japonica* L., 1 July 2018, CLZhao 7144, CLZhao 7151; Baotouwang, Zixishan National Forest Park, Chuxiong, Yunnan Province, the fallen branch of angiosperm, 2 July 2018, CLZhao 7326; the trunk of *Camellia japonica* L., 2 July 2018, CLZhao 7379; the trunk of *Quercus*, 2 July 2018, CLZhao 7382, CLZhao 7664; Zixishan National Forest Park, Chuxiong, Yunnan Province, the stump of angiosperm, 17 Aguest 2018, CLZhao 7710 (SWFC) (GenBank: ITS-OM955744).

Phlebiopsis crassa (Lév.) Floudas & Hibbett, Fungal Biology 119 (7): 710 (2015)

Specimens examined: Zijinshan Forest farm, Zixishan National Forest Park, Chuxiong, Yunnan Province, China, the fallen branch of angiosperm, 1 July 2018, CLZhao 7130; Wanghai Villa, Zixishan National Forest Park, Chuxiong, Yunnan Province, the trunk of *Camellia japonica* L., 2 July 2018, CLZhao 7338; the trunk of angiosperm, 2 July 2018, CLZhao 7352, CLZhao 7634, CLZhao 7646 (SWFC) (GenBank: ITS-OM955764).

Phlebiopsis yunnanensis C.L. Zhao, Nova Hedwigia 108 (1-2): 273 (2018)

Specimen examined: Baotouwang, Wanghai Villa, Zixishan National Forest Park, Chuxiong, Yunnan Province, China, the trunk of angiosperm, 2 July 2018, CLZhao 7367 (SWFC) (GenBank: ITS-OM955788).

Postia caesia (Schrad.) P. Karst., Revue Mycologique Toulouse 3 (9): 17 (1881)

Specimens examined: Zixishan National Forest Park, Chuxiong, Yunnan Province, China, the trunk of angiosperm, 30 June 2018, CLZhao 6904; the trunk of *Pinus;* 1 August 2018, CLZhao 7735 (SWFC) (GenBank: ITS-OM955769).

Radulomyces zixishanensis C.L. Zhao sp.

Specimen examined: Zixishan National Forest Park, Chuxiong, Yunnan Province, China, the trunk of angiosperm, 2 July 2021, CLZhao 21127 (SWFC).

Schizocorticium parvisporum Sheng H. Wu & C.L. Wei, Mycological Progress 20 (6): 777 (2021)

Specimens examined: Baotouwang, Wanghai Villa, Zixishan National Forest Park, Chuxiong, Yunnan Province, China, the trunk of angiosperm, 2 July 2018, CLZhao 7363; Baotouwang, Wanghai Villa, Xiangshuijing Waterfall, Zixishan National Forest Park, Chuxiong, Yunnan Province, the fallen branch of angiosperm, 2 July 2021, CLZhao 21161 (SWFC).

Scytinostroma phaeosarcum Boidin & Lanq., Kew Bull. 31(3): 623 (1976)

Specimens examined: Zixishan National Forest Park, Chuxiong, Yunnan Province, China, the fallen branch of angiosperm, 1 July 2018, CLZhao 7199; Ziding Temple, Zixishan National Forest Park, Chuxiong, Yunnan Province, 2 July 2021, CLZhao 21172; Forest Deyun Monument, Zixishan National Forest Park, Chuxiong, Yunnan Province, China, CLZhao 21238;Forest Deyun Monument, Zixishan National Forest Park, Chuxiong, Yunnan Province, China, the fallen branch of *Pinus*, 3 July 2021, CLZhao 21302 (SWFC) (GenBank: ITS-OM955775).

Skeletocutis nivea (Jungh.) Jean Keller, Persoonia 10 (3): 353 (1979)

Specimen examined: Zixishan National Forest Park, Chuxiong, Yunnan Province, China, the trunk of angiosperm, 1 July 2018, CLZhao 7034 (SWFC) (GenBank: ITS-OM955776).

Skeletocutis pseudo-odora L.F. Fan & Jing Si, Mycosphere 8 (6): 1254 (2017)

Specimens examined: Zixishan National Forest Park, Chuxiong, Yunnan Province, China, the fallen branch of *Pinus*, 1 July 2018, CLZhao 6938; the fallen branch of angiosperm, 1 July 2018, CLZhao 7258 (SWFC) (GenBank: ITS-OM955777).

Steccherinum nitidum (Pers.) Vesterh., in Knudsen & Hansen, Nordic Jl Bot. 16(2): 216 (1996).

Specimens examined: Zixishan National Forest Park, Chuxiong, Yunnan Province, China, the fallen branch of angiosperm, 1 July 2018, CLZhao 7198, CLZhao 7446 (SWFC) (GenBank: ITS-MZ713646).

Stereum hirsutum (Willd.) Pers., Observ. mycol. (Lipsiae) 2: 90 (1800) [1799]

Specimen examined: Zixishan National Forest Park, Chuxiong, Yunnan Province, China, the trunk of angiosperm, 2 July 2018, CLZhao 7420 (SWFC) (GenBank: ITS-OM955779).

Stereum sanguinolentum (Alb. & Schwein.) Fr., Epicr. syst. mycol. (Upsaliae): 549 (1838)

Specimens examined: Zixishan National Forest Park, Chuxiong, Yunnan Province, China, the fallen branch of angiosperm, 30 June 2018, CLZhao 6856, CLZhao 6926; 1 July 2018, CLZhao 7123; 2 July 2018, CLZhao 7531, CLZhao 7581; the angiosperm dead tree , 2 July 2018, CLZhao 7536; the trunk of *Pinus*, 2 July 2018, CLZhao 7575; the trunk of angiosperm, 2 July 2018, CLZhao 7479 (SWFC) (GenBank: ITS-OM955780).

Trametes hirsuta **(Wulfen) Lloyd, Mycol. Writ. 7(Letter 73): 1319 (1924)**

Specimen examined: Zixishan National Forest Park, Chuxiong, Yunnan Province, China, the trunk of angiosperm, 3 July 2021, CLZhao 21464 (SWFC).

Tremella fuciformis Berk., Hooker's Journal of Botany and Kew Garden Miscellany 8: 277 (1856)

Specimen examined: Zixishan National Forest Park, Chuxiong, Yunnan Province, China, the trunk of angiosperm, 31 June 2018, CLZhao 8838 (SWFC).

Tubulicrinis yunnanensis C.L. Zhao, Mycoscience 61 (4): 187 (2020)

Specimens examined: Zixishan National Forest Park, Chuxiong, Yunnan Province, China, the fallen branch of angiosperm, 3 July 2021, CLZhao 21271; the fallen branch of angiosperm, 3 July 2021, CLZhao 21279 (SWFC).

Tyromyces kmetii (Bres.) Bondartsev & Singer, Annales Mycologici 39 (1): 52 (1941)

Specimen examined: Zixishan National Forest Park, Chuxiong, Yunnan Province, China, the trunk of *Pinus*, 2 July 2018, CLZhao 7305 (SWFC) (GenBank: ITS-OM955787).

Xylodon spathulatus (Schrad.) Kuntze, Revisio generum plantarum 3 (2): 541 (1898)

Specimens examined: Zijinshan Forest farm, Zixishan National Forest Park, Chuxiong, Yunnan Province, China, the trunk of angiosperm, 30 July 2018, CLZhao 6873; Wanghai Villa, Zixishan National Forest Park, Chuxiong, Yunnan Province, the fallen branch of angiosperm, 2 July 2018, CLZhao 7549 (SWFC).

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 *tef1* 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, Russulalesand 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 corticoid 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, hydnaceous 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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References

Ayesha, P., Maham, A., Ariza, A. & Husnain, H. (2020) "*Ganoderma lucidum* sensu lato" – a sacred mushroom for immortality. *Studies in Fungi* 5: 508–516.
https://doi.org/10.5943/sif/5/1/31

Blackwell, M. (2011) The Fungi: 1, 2, 3 ... 5.1 million species? *American Journal of Botany* 98: 426–438.
https://doi.org/10.3732/ajb.1000298

Bian, L.S. & Dai, Y.C. (2015) *Coltriciella globosa* and *C. pseudodependens* spp. nov. (Hymenochaetales) from southern China based on morphological and molecular characters. *Mycoscience* 56 (2): 190–197.
https://doi.org/10.1016/j.myc.2014.06.001

Blanco-Dios, J.B. (2021) Notes on the genus *Entoloma* s.l. in the Northwest of the Iberian Peninsula (XI): a new species in subgenus *Entoloma*. *Studies in Fungi* 6: 64–70.
https://doi.org/10.5943/sif/6/1/2

Boonyuen, N., Chuaseeharonnachai, C., Nuankaew, S., Kwantong, P., Pornputtapong, N.S., Suwannarach, N., Jones, E.B.G. & Somrithipol, S. (2021) Novelties in Fuscosporellaceae (Fuscosporellales): two new *Parafuscosporella* from Thailand revealed by morphology and phylogenetic analyses. *Diversity* 13: 1–14.
https://doi.org/10.3390/d13110517

Chen, J.B. (1994) Two new species of *Hypogymnia*. *Mycosystema* 13: 107–110.

Cui, B.K. & Jia, B.S. (2011) Wood–rotting fungi in eastern China 7. Polypores from Huangshan Mountain, Anhui Province. *Mycosystema* 30: 529–535.

Cai, J., Zou, L., Wu, X. & Zhao, C.L. (2023) *Physisporinus yunnanensis* sp. nov. (Polyporales, Basidiomycota) from Southern China. *Phytotaxa* 579: 98–106.
https://doi.org/10.11646/phytotaxa.579.2.3

Chen, C.C., Chen, C.Y. & Wu, S.H. (2021) Species diversity, taxonomy and multi–gene phylogeny of phlebioid clade (Phanerochaetaceae, Irpicaceae, Meruliaceae) of Polyporales. *Fungal Diversity* 111: 337–442.
https://doi.org/10.1007/s13225-021-00490-w

Cui, B.K., Wei, Y.L. & Dai, Y.C. (2006) Polypores from Zijin Mountain, Jiangsu Province. *Mycosystema* 25: 9–14.
https://doi.org/10.3969/j.issn.1672-6472.2006.01.003

Cui, B.K. & Yu, C.J. (2011) Fungal flora and population structure of polypores in the Great Xingan Mountains. *Acta Ecological Sinica* 31: 3700–3709.

Chen, Q., Du, P., Vlasak, J., Wu, F. & Dai, Y.C. (2020a) Global diversity and phylogeny of *Fuscoporia* (Hymenochaetales, Basidiomycota). *Mycosphere* 11: 1477–1513.
https://doi.org/10.5943/mycosphere/11/1/10

Chen, C.C., Wu, S.H. & Chen, C.Y. (2018) Four species of polyporoid fungi newly recorded from Taiwan. *Mycotaxon* 133: 45–54.
https://doi.org/10.5248/133.45
https://doi.org/10.5248/133.45

Chen, J.Z. & Zhao, C.L. (2020) Morphological and molecular identification of four new resupinate species of *Lyomyces* (Hymenochaetales) from southern China. *MycoKeys* 65: 101–118.
https://doi.org/10.3897/mycokeys.65.48660

Chen, L., Shi, Z.J., Wu, C.H. & Zhao, C.L. (2020b) *Gloeodontia yunnanensis* sp. nov. (Russulales, Basidiomycota) from China, evidenced by morphological characters and phylogenetic analyses. *Phytotaxa* 432: 111–118.
https://doi.org/10.11646/phytotaxa.432.2.1

De Koker, T.H., Nakasone, K.K., Haarhof, J., Burdsall Jr, H.H. & Janse, B.J.H. (2003) Phylogenetic relationships of the genus *Phanerochaete* inferred from the internal transcribed spacer region. *Mycological Research* 107 (9): 1032–1040. https://doi.org/10.1017/s095375620300827x

Dai, Y.C., Qin, G.F. & Xu, M.Q. (2000) The Forest pathogens of root and butt rot on northeast China. *Forest Research* 13: 15–22.

Dai, Y.C. (2003) Rare and threatened polypores in the ecosystem of Changbaishan Nature Reserve of Northeastern China. *Chinese Journal of Applied Ecology* 14: 1015–1018.

Dai, Y.C. (2012) Polypore diversity in China with an annotated checklist of Chinese polypores. *Mycoscience* 53: 49–80. https://doi.org/10.1007/s10267-011-0134-3

Dai, Y.C., Cui, B.K., He, S.H. & Schigel, D. (2014) Wood-decaying fungi in eastern Himalayas 4. Species from Gaoligong Mountains, Yunnan Province, China. *Mycosystema* 33: 611–620. https://doi.org/10.13346/j.mycosystema.130299

Dai, Y.C., Cui, B.K., Si, J., He, S.H., Hyde, K.D., Yuan, H.S., Liu, X.Y. & Zhou, L.W. (2015) Dynamics of the worldwide number of fungi with emphasis on fungal diversity in China. *Mycological Progress* 14: 1–9. https://doi.org/10.1007/s11557-015-1084-5

Dai, S., Vlasák, J., Tomšovský, M. & Wu, F. (2017) *Porodaedalea chinensis* (*Hymenochaetaceae*, Basidiomycota) – a new polypore from China. *Mycosphere* 8: 986–993. https://doi.org/10.5943/mycosphere/8/6/2

Dai, Y.C. & He, S.H. (2017) A new species and a new combination of *Aleurodiscus* s.l. (Russulales, Basidiomycota). *mycosphere* 8: 908–916. https://doi.org/10.5943/mycosphere/8/7/7

Dai, Y.C., Yang, Z.L., Cui, B.K., Wu, G., Yuan, H.S., Zhou, L.W., He, S.H., Ge, Z.W., Wu, F., Wei, Y.L., Yuan, Y. & Si, J. (2021) Diversity and systematics of the important macrofungi in Chinese forests. *Mycosystema* 40: 770–805. https://doi.org/10.13346/j.mycosystema.210036

Felsenstein, J. (1985) Confidence intervals on phylogenetics: an approach using bootstrap. *Evolution* 39: 783–791. https://doi.org/10.2307/2408678

Feng, J., Zhao, H.W., He, Y.H., Dong, Y.X., Luo, Z.P. & Xiong, Z.P. (2019) Investigation on pests and diseases of *Pinus huashan* seed orchard in Zixishan farm, Chuxiong City. *Forest Investigation and Planning* 44: 56–60.

Floudas, D. & Hibbett, D.S. (2015) Revisiting the taxonomy of *Phanerochaete* (Polyporales, Basidiomycota) using a four gene dataset and extensive ITS sampling. *Fungal Biology* 119 8: 679–719. https://doi.org/10.1016/j.funbio.2015.04.003

Fan, L.F., Ji, X.H. & Si, J. (2017) A new species in the *Skeletocutis subincarnata* complex (Polyporales, Basidiomycota) from southwestern China. *Mycosphere* 8: 1253–1260. https://doi.org/10.5943/mycosphere/8/6/10

Gafforov, Y., Ordynets, A., Langer, E., Yarasheva, M., de Mello, G.A., Schigel, D., Pecoraro, L., Zhou, Y., Cai, L. & Zhou, L.W. (2020) Species diversity with comprehensive annotations of wood–inhabiting poroid and corticioid fungi in Uzbekistan. *Frontiers in Microbiology* 11: 1–36. https://doi.org/10.3389/fmicb.2020.598321

Guan, Q.X. & Zhao, C.L. (2021a) Two new corticioid species, *Hyphoderma sinense* and *H. floccosum* (Hyphodermataceae, Polyporales), from southern China. *Mycosystema* 40: 447–461. https://doi.org/10.13346/j.mycosystema.200382

Guan, Q.X., Zhao, T.J. & Zhao, C.L. (2020) Morphological characters and phylogenetic analyses reveal two new species of *Peniophorella* from southern China. *Mycological Progress* 19: 397–404. https://doi.org/10.1007/s11557-020-01568-6

Gu, Z.R. & Zhao, C.L. (2021) The hidden wood-decaying fungal diversity: *Rhizochaete* from East Asia. *Diversity* 3: 1–12. https://doi.org/10.3390/d13100503

Guan, Q.X. & Zhao, C.L. (2021b) Taxonomy and Phylogeny of the Wood–Inhabiting Fungal Genus *Hyphoderma* with Descriptions of Three New Species from East Asia. *Journal of Fungi* 7: 308. https://doi.org/10.3390/jof7040308

Guo, L., Li, Z.Y., Lu, C.X., He, S.H. & Chen, S.Z. (2013) *Exobasidium* and *Septobasidium* of Gaoligong and Nu Mountains in Yunnan Province. *Mycosystema* 32: 207–212.

Hall, T.A. (1999) Bioedit: a user–friendly biological sequence alignment editor and analysis program for Windows 95/98/NT. *Nucleic Acids Symposium Series* 41: 95–98.

Hawksworth, D.L. & Lücking, R. (2017) Fungal diversity revisited: 2.2 to 3.8 million species. *Microbiology Spectrum* 5 (4): FUNK-0052-2016.

https://doi.org/10.1128/microbiolspec.FUNK-0052-2016

He, M.Q., Zhao, R.L., Hyde, K.D., Begerow, D., Kemler, M., Yurkov, A., McKenzie, E.H.C., Raspe, O., Kakishima, M., Sa´nchez–Ramı´rez, S., Vellinga, E.C., Halling, R., Papp, V., Zmitrovich, I.V., Buyck, B., Ertz, D., Wijayawardene, N.N., Cui, B.K., Schoutteten, N., Liu, X.Z., Li, T.H.,Yao, Y.J., Zhu, X.Y., Liu, A.Q., Li, G.J., Zhang, M.Z., Ling, Z.L., Cao, B., Antonı´n, V., Boekhout, T., Silva, B.D.B., Crop, E.D., Decock, C., Dima, B.l., Dutta, A.K., Fell, J.W., Geml, J., Ghobad–Nejhad, M., Giachini, A.J., Gibertoni, T.B., Gorjo´n, S.P., Haelewaters, D., He, S.H., Hodkinson, B.P., Horak, E., Hoshino, T., Justo, A., Lim, Y.W., Jr., N.M., Mesˇic´, A., Moncalvo, J.M., Mueller, G.M., Nagy, L.G., Nilsson, R.H., Noordeloos, M., Nuytinck, J., Orihara, T., Ratchadawan, C., Rajchenberg, M., Silva–Filho, A.G.S., Sulzbacher, M.A., Tkalcˇec, Z., Valenzuela, R., Verbeken, A., Vizzini, A., Wartchow, F., Wei, T.Z., Weiß, M., Zhao, C.L. & Kirk, P.M. (2019) Notes, outline and divergence times of Basidiomycota. *Fungal Diversity* 99: 105–367.
https://doi.org/10.1007/s13225-019-00435-4

He, X., Chen, J.Z. & Zhao, C.L. (2021) Diversity of wood–decaying fungi in Haikou Forestry Farm, Yunnan Province, P.R. China. *Studies in Fungi* 6: 365–377.
https://doi.org/10.5943/sif/6/1/27

He, S.H. & Dai, Y.C. (2012) Taxonomy and phylogeny of *Hymenochaete* and allied genera of Hymenochaetaceae (Basidiomycota) in China. *Fungal Diversity* 56: 77–93.
https://doi.org/10.1007/s13225-012-0174-9

Hallenberg, N., Nilsson, R.H., Antonelli, A., Wu, S.H., Maekawa, N. & Norden, B. (2007) The *Peniophorella praetermissa* species complex (Basidiomycota). *Mycological Research* 111: 1366–1376.
https://doi.org/10.1016/j.mycres.2007.10.001

He, X. & Zhao, C.L. (2022) Diversity of wood-decaying fungi in Wuliangshan area, Yunnan Province, P.R. China. *Diversity* 14: 1–29.
https://doi.org/10.3390/d14020131

Hibbett, D. (2016) The invisible dimension of fungal diversity. *Science* 351: 1150–1151.
https://doi.org/10.1126/science.aae0380

Han, M.L., Chen, Y..Y., Shen, L.L., Song, J., Vlasák, J., Dai, Y.C. & Cui, B.K. (2016) Taxonomy and phylogeny of the brown-rot fungi: *Fomitopsis* and its related genera. *Fungal Diversity* 80: 343–373.
https://doi.org/10.1007/s13225-016-0364-y

Himani, S. & Krishnappa, M. (2020) *Xylaria oxyacanthae* (Xylariaceae), a new record on *Diospyros melanoxylon* from India. *Studies in Fungi* 5: 485–490.
https://doi.org/10.5943/sif/5/1/29

Huang, R.X., Luo, K.Y. & Zhao, C.L. (2020) *Phlebia nigrodontea* sp. nov. in Meruliaceae (Polyporales) with a black hymenial surface. *Phytotaxa* 458: 195–206.
https://doi.org/10.11646/phytotaxa.458.3.2

James, T.Y., Stajich, J.E., Hittinger, C.T. & Rokas, A. (2020) Toward a fully resolved fungal tree of life. *Annual Review of Microbiology* 74: 291–313.
https://doi.org/10.1146/annurev-micro-022020-051835

Jia, B.S., Zhou, L.W., Cui, B..K., Rivoire, B. & Dai, Y.C. (2014) Taxonomy and phylogeny of *Ceriporia* (Polyporales, Basidiomycota) with an emphasis of Chinese collections. *Mycological Progress* 13: 81–93.
https://doi.org/10.1007/s11557-013-0895-5

Kirk, P.M., Cannon, P.F., Minter, D.W. & Stalpers, J.A. (2008) *Ainsworth & Bisby's Dictionary of the Fungi, 10th edn.* CAB International, Wallingford.
https://doi.org/10.1016/j.mycres.2009.07.003

Kumar, S. & Singh, R. (2021) Global diversity and distribution of distoseptosporic micromycete *Corynespora* Güssow (Corynesporascaceae): an updated checklist with current status. *Studies in Fungi* 6: 1–63.
https://doi.org/10.5943/sif/6/1/1

Li, Y., Li, T.H., Yang, Z.L., Bau, T. & Dai, Y.C. (2015) *Atlas of chinese macrofungal resources.* Central China Farmer's Publishing House: Zhengzhou. pp. 1–1351.

Lee, H., Park, M.S., Park, J.H., Park, K.H., Lim, Y.W., Park, K.H., Yoo, S., Lee, J.W., Kim, N.K., Lee, J.S., Park, J.Y., Kim, C., Kim, J.J. & Lim, Y.W. (2020) Seventeen Unrecorded Species from Gayasan National Park in Korea. *Mycobiology* 48 (3): 184–194.
https://doi.org/10.1080/12298093.2020.1765719

Liu, S., Shen, L.L., Wang, Y., Xu, T.M., Gates, G. & Cui, B.K. (2022) Species Diversity and Molecular Phylogeny of *Cyanosporus* (Polyporales, Basidiomycota). *MycoKeys* 86: 19–46.
https://doi.org/10.3897/mycokeys.86.78305

Larsson, K.H. (2007) Molecular phylogeny of *Hyphoderma* and the reinstatement of *Peniophorella*. *Mycological Research* 111 (2): 186–195.

https://doi.org/10.1016/j.mycres.2006.10.002

Liu, S., Chen, Y.Y., Sun, Y.F., He, X.L., Song, C.G., Si, J., Liu, D.M., Gates, G. & Cui, B.K. (2023) Systematic classification and phylogenetic relationships of the brown–rot fungi within the Polyporales. *Fungal Diversity* 118: 1–94. https://doi.org/10.1007/s13225-022-00511-2

Liu, T.Z. & Li, G.L. (2019) *Atlas of macrofungi in Saihanwula national nature reserve of Inner Mongolia.* Inner Mongolia Science and Technology Press: Chifeng. pp. 1–341

Liu, X.F., Shen, S. & Zhao, C.L. (2019) Morphological and molecular identification of a new species of *Eichleriella* (Auriculariales, Basidiomycota) in China. *Phytotaxa* 404 (6): 245–254. https://doi.org/10.11646/phytotaxa.404.6.3

Luo, K.Y., Chen, Z.Y. & Zhao, C.L. (2022) Phylogenetic and taxonomic analyses of three new wood–inhabiting fungi of *Xylodon* (Basidiomycota) in a forest ecological system. *Journal of Fungi* 8: 1–18. https://doi.org/10.3390/jof8040405

Luo, K.Y., Ma, X. & Zhao, C.L. (2019) *Neofavolus yunnanensis* sp. nov. (Polyporales, Basidiomycota) from China: evidence from morphology and DNA sequence data. *Phytotaxa* 408: 109–116. https://doi.org/10.11646/phytotaxa.408.2.3

Luo, X., Chen, Y.H. & Zhao, C.L. (2021) *Lyomyces fissuratus* and *L. fumosus* (Schizoporaceae, Hymenochaetales), new species from southern China. *Annales Botanici Fennici* 58: 219–230. https://doi.org/10.5735/085.058.0404

Ma, H.X., Si, J., Dai, Y.C., Zhu, A.H., Cui, B.K., Fan, Y.G., Yuan, Y. & He, S.H. (2022) Diversity of wood–inhabiting macrofungi in Hainan Province, South China. *Mycosystema* 41: 695–712. https://doi.org/10.13346/j.mycosystema.210424

Ma, X. & Zhao, C.L. (2019) *Crepatura ellipsospora* gen. et sp. nov. in Phanerochaetaceae (Polyporales, Basidiomycota) bearing a tuberculate hymenial surface. *Mycological Progress* 18: 785–793. https://doi.org/10.1007/s11557-019-01488-0

Miettinen, O., Spirin, V. & Larsson, K.H. (2019) *Hydnoporia*, an older name for *Pseudochaete* and *Hymenochaetopsis*, and typification of the genus *Hymenochaete* (Hymenochaetales, Basidiomycota). *Fungal Systematics and Evolution* 2: 77–96. https://doi.org/10.3114/fuse.2019.04.07

Ma, X., Huang, R.X., Zhang, Y & Zhao, C.L. (2021) *Hyphoderma fissuratum* and *H. mopanshanense* spp. nov. (Polyporales) from southern China. *Mycoscience* 62: 36–41. https://doi.org/mycosci.2020.08.004

Miettinen, O., Larsson, E., Sjokvist, E. & Larsson, K.H. (2012) Comprehensive taxon sampling reveals unaccounted diversity and morphological plasticity in a group of dimitic polypores (Polyporales, Basidiomycota). *Cladistics* 28: 251–270. https://doi.org/10.1111/j.1096-0031.2011.00380.x

M'Barek, H.N., Arif, S. & Hajjaj, H. (2020) Consolidated bioethanol production from olive mill waste: wood–decay fungi from central Morocco as promising decomposition and fermentation biocatalysts. *Biotechnology Reports* 28: e00541. https://doi.org/10.1016/j.btre.2020.e00541

Miller, M.A., Pfeiffer, W. & Schwartz, T. (2012) The CIPRES science gateway: enabling high–impact science for phylogenetics researchers with limited resources. *Association For Computing Machinery* 39: 1–8. https://doi.org/10.1145/2335755.2335836

Nylander, J.A.A. (2004) *MrModeltest v2.* Program distributed by the author; Evolutionary Biology Centre, Uppsala University: Uppsala Sweden. pp. 1–3.

Petersen, J.H. (1996) *Farvekort. The Danish mycological society's colour–chart.* Foreningen til Svampekundskabens Fremme: Paris, France. pp. 1–6.

Qu, M.H., Wang, D.Q. & Zhao, C.L. (2022) A phylogenetic and taxonomic study on *Xylodon* (Hymenochaetales): focusing on three new *Xylodon* species from southern China. *Journal of Fungi* 8: 1–18. https://doi.org/10.3390/jof8010035

Ronquist, F. & Huelsenbeck, J.P. (2003) MrBayes 3: Bayesian phylogenetic inference under mixed models. *Bioinformatics* 19: 1572–1574. https://doi.org/10.1093/bioinformatics/btg180

Runnel, K., Miettinen, O. & Lohmus, A. (2021) Polypore fungi as a flagship group to indicate changes in biodiversity – a test case from Estonia. *IMA Fungus* 12: 1–31. https://doi.org/10.1186/s43008-020-00050-y

Russell, R. & Paterson, M. (2006) *Ganoderma* – a therapeutic fungal biofactory. *Phytochemistry* 67: 1985–2001. https://doi.org/10.1002/chin.200650268

Swofford, D.L. (2002) *PAUP*: phylogenetic analysis using parsimony (*and other methods).* Version 4.0b10. *Massachusetts* Sinauer Associates.
https://doi.org/10.1111/j.0014-3820.2002.tb00191.x

Shen, S., Ma, X., Xu, T.M. & Zhao, C.L. (2018) *Phlebia ailaoshanensis* sp. nov. (Polyporales, Basidiomycota) evidenced by morphological characters and phylogenetic analyses. *Phytotaxa* 373 (3): 184–196.
https://doi.org/10.11646/phytotaxa.373.3.2

Taylor, D.L., Hollingsworth, T.N. & Mcfarland, J.W. (2014) A first comprehensive census of fung in soil reveals bothhyperdiversity and fine–scale niche partitioning. *Ecological Monographs* 84: 3–20.
https://doi.org/10.1890/12-1693.1

Tian, Y., Ghobad–Nejhad, M., He, S.H. & Dai, Y.C. (2018) Three new species of *Aleurodiscus* s.l. (Russulales, Basidiomycota) from southern China. *MycoKeys* 37: 93–107.
https://doi.org/10.3897/mycokeys.37.25901

Vinay, D.S., Ryan, E.P., Pawelec, G., Talib, W.H., Stagg, J., Elkord, E., Lichtor, T., Decker, W.K., Whelan, R.L., Shantha Kumara, H.M.C., Signori, E., Honoki, K., Georgakilas, A.G., Amin, A., Helferich, W.G., Boosani, C.S., Guha, G., Ciriolo, M.R., Chen, S., Mohammed, S.I., Azmi, A.S., Keith, W.N., Bilsland, A., Bhakta, D., Halicka, D., Fujii, H., Aquilano, K., Ashraf, S.S., Nowsheen, S., Yang, X., Choi, B.K. & Kwon, B.S. (2015) Immune evasion in cancer: Mechanistic basis and therapeutic strategies. *Seminars in Cancer Biology* 35: S185–S198.
https://doi.org/10.1016/j.semcancer.2015.03.004

Vu, D., Groenewald, M., de Vries, M., Gehrmann, T., Stielow, B., Eberhardt, U., Al–Hatmi, A., Groenewald, J.Z., Cardinali, G., Houbraken, J., Boekhout, T., Crous, P.W., Robert, V. & Verkley, G.J.M. (2019) Large-scale generation and analysis of filamentous fungal DNA barcodes boosts coverage for kingdom fungi and reveals thresholds for fungal species and higher taxon delimitation. *Studies in Mycology* 92: 135–154.
https://doi.org/10.1016/j.simyco.2018.05.001

Wang, D.Q. & Zhao, C.L. (2021a) Morphological and Phylogenetic Evidence for Recognition of Two New Species of *Phanerochaete* from East Asia. *Journal of Fungi* 7: 1063.
https://doi.org/10.3390/jof7121063

Wang, H., He, X. & Zhao, C.L. (2020a) *Scytinostroma yunnanense* sp. nov. (Russulales, Basidiomycota) evidenced by morphological characteristics and phylogenetic analyses in China. *Phytotaxa* 451 (2): 145–153.
https://doi.org/10.11646/phytotaxa.451.2.4

Wijayawardene, N.N., Hyde, K.D., Dai, D.Q., Sánchez-García, M., Goto, B.T., Saxena, R.K., Erdoğdu, M., Selçuk, F., Rajeshkumar, K.C., Aptroot, A., Błaszkowski, J., Boonyuen, N., da Silva, G., de Souza, F.A., Dong, W., Ertz, D., Haelewaters, D., Jones, E.B.G., Karunarathna, S.C., Kirk, P.M., Kukwa, M., Kumla, J., Leontyev, D.V., Lumbsch, H.T., Maharachchikumbura, S.S.N., Marguno, F., Martínez-Rodríguez, P., Mešić, A., Monteiro, J.S., Oehl, F., Pawłowska, J., Pem, D., Pfliegler, W.P., Phillips, A.J.L., Pošta, A., He, M.Q., Li, J.X., Raza, M., Sruthi, O.P., Suetrong, S., Suwannarach, N., Tedersoo, L., Thiyagaraja, V., Tibpromma, S., Tkalčec, Z., Tokarev, Y.S., Wanasinghe, D.N., Wijesundara, D.S.A., Wimalaseana, S.D.M.K., Madrid, H., Zhang, G.Q., Gao, Y., Sánchez-Castro, I., Tang, L.Z., Stadler, M., Yurkov, A. & Thines, M. (2022) Outline of Fungi and fungus-like taxa – 2021. *Mycosphere* 13: 53–453.
https://doi.org/10.5943/mycosphere/13/1/2

Wang, R.Z., Yuan, Z.Y., Han, C.Z. & Zhao, C.L. (2020b) Morphological and molecular identification of a new species of *Cinereomyces* (Polyporales, Basidiomycota) in southern China. *Phytotaxa* 459 (1): 51–60.
https://doi.org/10.11646/phytotaxa.459.1.5

Wei, Y.L. (2010) Species diversity, fungal flora and distribution characters of polypores in Changbai Mountains, China. *Chinese Journal of Applied Ecology* 22: 2711–2717.

Wu, M.P., Zhan, L.J., Li, P.Y. & Tao, Y. (2020a) Evaluation of forest recreation value of Zixishan in Chuxiong. *Cooperative Economy and Science and Technology* 18: 44–47.

Wang, X.T. (2016) Zixishan: "natural garden" in central Yunnan. *Green Vision* 5: 59–62.

Wang, H., Gu, Z.R. & Zhao, C.L. (2021a) *Hyphodermella zixishanensis* (Polyporales, Basidiomycota), a new species with reddish hymenial surface. *Nordic Journal of Botany* 39: e03329.
https://doi.org/10.1111/njb.03329

Wang, H. & Zhao, C.L. (2021b) *Hyphodermella aurantiaca* sp. nova (Polyporales, Basidiomycota) as Evidenced by Morphological Characters and Phylogenetic Analyses. *Annales Botanici Fennici* 58: 61–168.
https://doi.org/10.5735/085.058.0110

White, T.J., Bruns, T., Lee, S. & Taylor, J. (1990) Amplification and direct sequencing of fungal ribosomal RNA genes for phylogenetics. *PCR Protocols: A Guide to Methods and Applications* 18: 315–322.

https://doi.org/10.1016/b978-0-12-372180-8.50042-1

Willis, K.J. (2018) *State of the World's Fungi 2018: Report.* Royal Botanic Gardens Kew, pp. 1–88.

Wang, Y., Liu, S., Ji, X., Sun, Y.F., Song, C.G., Liu, D.M. & Cui, B.K. (2021b) Diversity and floristic composition of porous bacteria in the southern section of Hengduan Mountain. *Bacteria Acta Physica Sinica* 40: 2599–2619.

Wu, F., Tohtirjap, A., Fan, L.F., Zhou, L.W., Alvarenga, R.L.M., Gibertoni, T.B. & Dai, Y.C. (2021) Global diversity and updated phylogeny of *Auricularia* (Auriculariales, Basidiomycota). *Journal of Fungi* 7: 933. https://doi.org/10.3390/jof7110933

Wu, F., Yuan, H.S., Zhou, L.W., Yuan, Y., Cui, B.K. & Dai, Y.C. (2020b) Polypore diversity in South China. *Mycosystema* 39: 653–682. https://doi.org/10.13346/j.mycosystema.200087

Wu, F., Zhou, L.W., Vlasák, J. & Dai, Y.C. (2022) Global diversity and systematics of Hymenochaetaceae with poroid hymenophore. *Fungal Diversity* 113: 1–192. https://doi.org/10.1007/s13225-021-00496-4

Wu, F., Zhou, L.W., Yang, Z.L., Bau, T., Li, T.H. & Dai, Y.C. (2019) Resource diversity of Chinese macrofungi: edible, medicinal and poisonous species. *Fungal Diversity* 98: 1–76. https://doi.org/10.1007/s13225-019-00432-7

Wu, Z.Q., Shen, S., Luo, K.Y., Wang, Z.H. & Zhao, C.L. (2017) Morphological and molecular identification of a new species of *Atraporiella* (Polyporales, Basidiomycota) in China. *Phytotaxa* 332: 31–40. https://doi.org/10.11646/phytotaxa.332.1.3

Wu, Z.Q., Xu, T.M., Shen, S., Liu, X.F., Luo, K.Y. & Zhao, C.L. (2018) *Elaphroporia ailaoshanensis* gen. et sp nov in Polyporales (Basidiomycota). *MycoKey*s 29: 81–95. https://doi.org/10.3897/mycokeys.29.22086

Xie, D.Z. (1992) A new species of *Phyllactinia*. *Mycosystema* 11: 96–98.

Xu, T.M., Liu, X.F., Chen, Y.H. & Zhao, C.L. (2019) *Rhomboidia wuliangshanensis* gen. et sp. nov. from southwestern China. *Mycotaxon* 134: 649–662. https://doi.org/10.5248/134.649

Yuan, H.S. (2014) Molecular phylogenetic evaluation of *Antrodiella* and morphologically allied genera in China. *Mycological Progress* 13: 353–364. https://doi.org/10.1007/s11557-013-0921-7

Yuan, Y., Chen, J.J., Korhonen, K., Martin, F. & Dai, Y.C. (2021) An updated global species diversity and phylogeny in the forest pathogenic genus *Heterobasidion* (Basidiomycota, Russulales). *Frontiers in Microbiology* 11: 596393. https://doi.org/10.3389/fmicb.2020.596393

Yurchenko, E. & Wu, S.H. (2015) *Hyphoderma moniliforme* and *H. nemorale* (Basidiomycota) newly recorded from China. *mycosphere* 6: 113–121. https://doi.org/10.5943/mycosphere/6/1/11

Yurchenko, E., Riebesehl, J. & Langer, E. (2017) Clarification of *Lyomyces sambuci* complex with the descriptions of four new species. *Mycological Progress* 16: 865–876. https://doi.org/10.1007/s11557-017-1321-1

Yao, Y.J., Pegler, D.N. & Chase, M.W. (2005) Molecular variation in the *Postia caesia* complex. *FEMS Microbiology Letters* 242: 109–116. https://doi.org/10.1016/j.femsle.2004.10.046

Yuan, H.S. & Dai, Y.C. (2008) Polypores from northern and central Yunnan Province, Southwestern China. *Sydowia* 60: 147–159.

Yang, Y., Li, R., Liu, C.M. & Zhao, C.L. (2023) Morphological and molecular identification for two new species of woodinhabiting macrofungi (Basidiomycota) from Yunnan-Guizhou Plateau, China. *Phytotaxa* 591: 1–18. https://doi.org/10.11646/phytotaxa.591.1.1

Zhao, C.L. & Wu, Z.Q. (2017) *Ceriporiopsis kunmingensis* sp. nov. (Polyporales, Basidiomycota) evidenced by morphological characters and phylogenetic analysis. *Mycological Progress* 16: 93–100. https://doi.org/10.1007/s11557-016-1259-8

Zhang, Y., Zhou, D.Q., Ou, X.K. & Zhou, T.X. (2012) New records and distribution of macrofungi in Laojun Mountain, northwest Yunnan, China. *Mycosystema* 31: 196–212.

Zong, T.K., Liu, C.M., Wu, J.R. & Zhao, C.L. (2021) *Trechispora daweishanensis* and *T. xantha* spp. nov. (Hydnodontaceae, Trechisporales) found in Yunnan Province of China. *Phytotaxa* 479: 147–159. https://doi.org/10.11646/phytotaxa.479.2.1

Zhao, C.L. & Cui, B.K. (2013) Morphological and molecular identification of four new resupinate species of *Perenniporia* (Polyporales) from southern China. *Mycologia* 105: 945–58.

https://doi.org/10.3852/12-201

Zhao, C.L., Liu, X.F. & Ma, X. (2019) *Phlebiopsis yunnanensis* sp. nov. (Polyporales, Basidiomycota) evidenced by morphological characters and phylogenetic analysis. *Nova Hedwigia* 108: 265–279.
https://doi.org/10.1127/nova_hedwigia/2018/0508

Zhao, C.L., Qu, M.H., Huang, R.X. & Karunarathna, S.C. (2023) Multi-Gene Phylogeny and Taxonomy of the Wood-Rotting Fungal Genus *Phlebia sensu lato* (Polyporales, Basidiomycota). *Journal of Fungi* 9 (3): 1–41.
https://doi.org/10.3390/jof9030320