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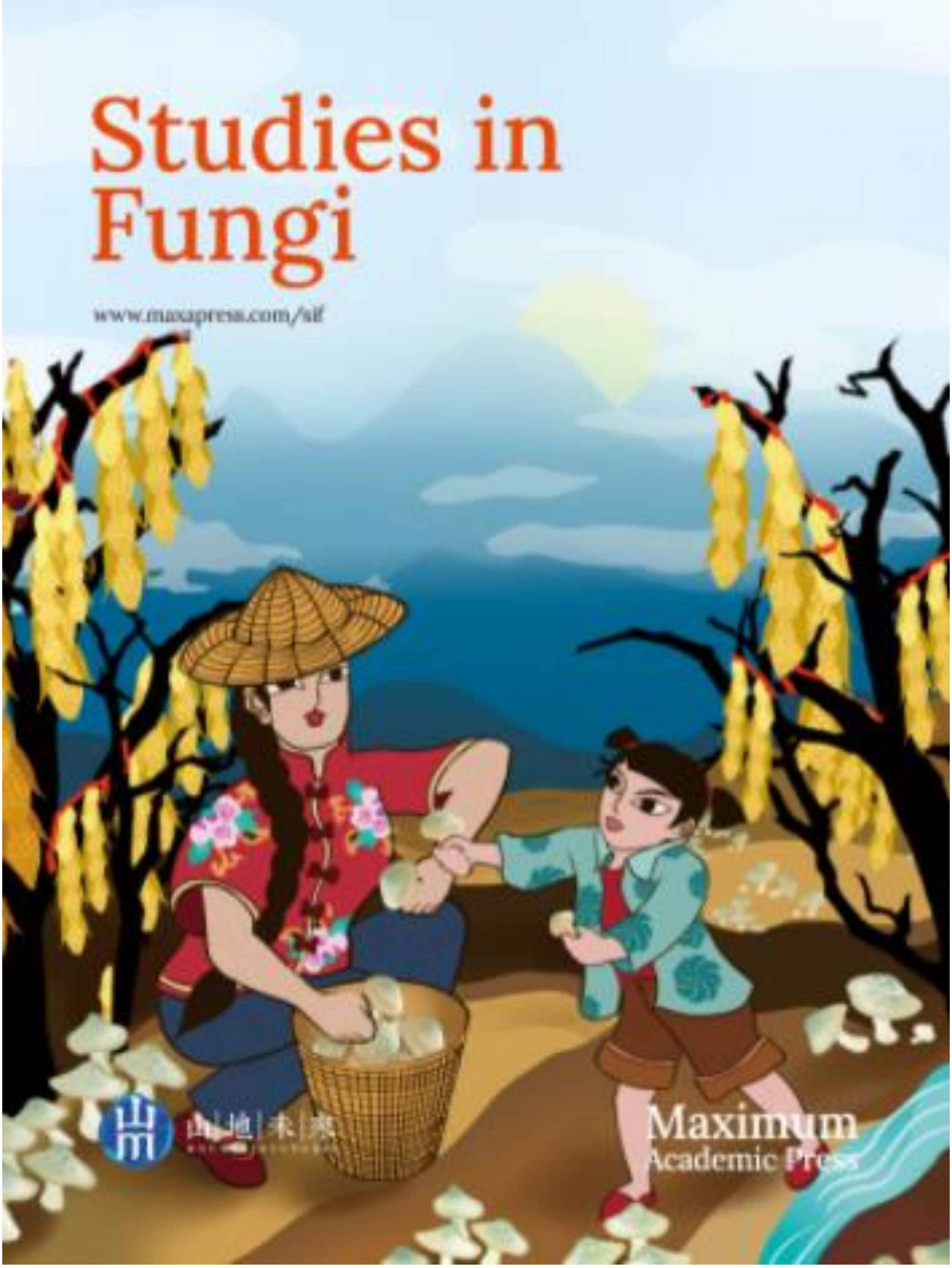

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Article

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Diversity of wood – decaying fungi in Haikou Forestry Farm, Yunnan Province, P.R. China

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Abstract

Nine field trips carried out in Haikou Forestry Farm, Yunnan Province, P.R. China resulted in 681 specimens of wood-decaying fungi. The present paper summarizes 52 species collected that are distributed in 37 genera, 16 families, 6 orders including their hosts and substrates. A checklist of wood-decaying fungi in Haikou Forestry Farm is also given. Phylogenetic analysis of ITS nrRNA gene region was performed for all the collected samples with maximum likelihood, maximum parsimony and Bayesian inference methods. The phylogenetic tree showed that fifty-two species nested in sixteen families belonging to six orders in Agaricomycetes.

Keywords – Basidiomycota – biological resources – diversity – Haikou Forestry Farm – mycota

Introduction

The diversity for flora of seed plants in Yunnan Province, P.R. China is observably high, and the endemic species of woody plants are rich, in which both supply good substrates for wood-decaying fungi. Wood-decaying fungi are kind of large basidiomycetes that grow on various kinds of wood, such as the living trees, dead standing trees, fallen trunk, fallen branch and stump (Dai 2012a), which can be used for industrial value, medicinal value, edible value and economic value (Russell & Paterson 2006, Dai et al. 2015, Vinay et al. 2015, M'Barek et al. 2020, Wu et al. 2020, Runnel et al. 2021).

Haikou Forestry Farm is located in Haikou Town, Kunming, belonging to the Jinsha River system and the geographical location is between 102°28'-102°38' E and 24°4'-24°56' N, with the altitude of 1800-2400 m (Xu et al. 2015, Zhang et al. 2017). It has a subtropical monsoon climate and the native tree species with mostly subtropical evergreen broadleaf trees (Xiong & Zhou 2019). The main vegetation includes warm coniferous forest (*Pinus yunnanensis* Franch., *P. armandii* Franch. and *Keteleeria evelyniana* Mast.), deciduous broad-leaved forest (*Alnus nepalensis* D. Don), and semi-humid evergreen broad-leaved forest (*Lithocarpus dealbatus* (J. D. Hooker et Thomson ex Miquel) Rehder and *Castanopsis delavayi* Franch.).

However, the previously documented wood-decaying fungi are mostly in northwest Yunnan Province, China, and few polypore and corticioid fungi have been reported in here so far. According to the modern taxonomy (Dai 2012a), wood-decaying fungi mainly belong to ten orders of Agaricomycetes, viz., Agaricales, Auriculariales, Cantharellales, Corticiales, Gloeophyllales, Hymenochaetales, Polyporales, Russulales, Thelephorales and Trechisporales. Therefore, the current wood-decaying fungi catalogues include poroid and corticioid hymenophore. In the present study, nine field trips were carried out in different areas of Haikou Forestry Farm, and about 681 specimens were collected, in which 52 species belonging to 37 genera, 16 families, 6 orders, which

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were identified from these materials. This paper is going to summarize the distribution of wood-decaying fungi and enrich the fungal diversity in this area.

Materials & Methods

Morphological studies

The studied specimens are deposited at the herbarium of Southwest Forestry University (SWFC), Kunming, Yunnan Province, P.R. China. Macromorphological descriptions were based on field notes. Colour terms are from Petersen (1996). Micromorphological data were obtained from the dried specimens, and observed under a light microscope following Dai (2012a). The following abbreviations were used for the micro characteristics description: KOH = 5% potassium hydroxide, CB = Cotton Blue, CB– = acyanophilous, CB+ = cyanophilous, IKI = Melzer's reagent, IKI– = both inamyloid and indextrinoid, L = mean spore length (arithmetic average of all spores), W = mean spore width (arithmetic average of all spores), Q = variation in the L/W ratios between the specimens studied, n (a/b) = number of spores (a) measured from given number (b) of specimens.

Molecular procedures and phylogenetic analysis

CTAB rapid plant genome extraction kit-DN14 (Aidlab Biotechnologies Co., Ltd, Beijing) was used to obtain genomic DNA from dried specimens, according to the manufacturer's instructions that a small piece of dried fungal specimen (about 30 mg) was ground to powder with liquid nitrogen. The powder was transferred to a 1.5 mL centrifuge tube, suspended in 0.4 mL of lysis buffer, and incubated in a 65°C water bath for 60 min. After that, 0.4 mL phenol-chloroform (24:1) was added to each tube and the suspension was shaken vigorously. After centrifugation at 13,000 rpm for 5 min, 0.3 mL supernatant was transferred to a new tube and mixed with 0.45 mL binding buffer. The mixture was then transferred to an adsorbing column (AC) for centrifugation at 13,000 rpm for 0.5 min. Then, 0.5 mL inhibitor removal fluid was added in AC for a centrifugation at 12,000 rpm for 0.5 min. After washing twice with 0.5 mL washing buffer, the AC was transferred to a clean centrifuge tube, and 100 mL elution buffer was added to the middle of adsorbed film to elute the genome DNA. 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 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).

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 of *Tremella flava* Chee J. Chen and *T. mesenterica* Retz. obtained from GenBank was used as an outgroup to root tree following He et al. (2019) in ITS analysis (Fig. 1).

Maximum parsimony analysis was applied to the ITS dataset sequences. Approaches to phylogenetic analysis followed Zhao & Wu (2017) and the tree construction procedure was performed in PAUP* version 4.0b10 (Swofford 2002). All characters were equally weighted and gaps were treated as missing data. Trees were inferred using the heuristic search option with TBR branch swapping and 1000 random sequence additions. Max-trees were set to 5000, branches of zero length were collapsed and all parsimonious trees were saved. Clade robustness was assessed using a bootstrap (BT) analysis with 1,000 replicates (Felsenstein 1985). Descriptive tree statistics tree length (TL), consistency index (CI), retention index (RI), rescaled consistency index (RC), and 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 (www.phylo.org; Miller et al. 2009). Branch support (BS) for ML analysis was determined by 1000 bootstrap replicates.

Table 1 Names, sample numbers and corresponding GenBank accession numbers of ITS sequences used in this study

Species name	Sample no.	GenBank accession no.	References
Acanthofungus rimosus	Wu 9601-1	MF043521	He et al. (2019)
Acanthophysellum cerussatum	He 2208	KX306874	He et al. (2019)
Aleurobotrys botryosus	He 2712	KX306877	He et al. (2019)
Antrodia tanakae	CLZhao 720	MG231457	This study
Armillaria aotearoa	NZFS 2425	NR151846	Hood & Ramsfield 2016
Auricularia angiospermarum	BJFC 017274	NR151847	Wu et al. 2015
Auricularia villosula	CLZhao 1296	MG231464	This study
Bankera fuligineoalba	REB-285	JN135196	He et al. (2019)
Boletinellus merulioides	2630a	KM248952	He et al. (2019)
Bondarzewia berkeleyi	Dai 12759	KJ583202	He et al. (2019)
Boreostereum radiatum	RLG-9717-Sp	HM536085	Garcia-Sandoval et al. 2011
Brunneoporus malicola	CLZhao 1530	MG231451	This study
Candelabrochaete langloisii	FP-110343	KY948793	He et al. (2019)
Ceraceomyces serpens	HHB-15692-Sp	KP135031	He et al. (2019)
Cinereomyces lindbladii	CBS 290.71	MH860129	Vu et al. 2019
Cinereomyces lindbladii	CLZhao 1523	MG231489	This study
Coniolepiota spongodes	ECV-2010a	HM488756	He et al. (2019)
Coprinellus curtus	SZMC-NL-2339	FM878016	He et al. (2019)
Coprinus comatus	AFTOL-ID 626	AY854066	He et al. (2019)
Coriolopsis polyzona	Cui 11040	KR605824	He et al. (2019)
Crepatura ellipsospora	CLZhao 697	MK343695	Ma & Zhao 2019
Cyclomyces lamellatus	Cui 7629	JQ279603	He et al. (2019)
Cylindrobasidium laeve	CLZhao 767	MG231497	This study
Daedalea quercina	FFUI-4	MN596945	Direct Submission
Daedaleopsis confragosa	CLZhao 1481	MG231506	This study
Efibula americana	FP-102165	KP135016	He et al. (2019)
Eichleriella alliciens	HHB 7194	KX262120	He et al. (2019)
Exidiopsis effusa	OM 19136	KX262145	He et al. (2019)
Flammulina velutipes	AFTOL-ID 558	AY854073	He et al. (2019)
Fomitiporia mediterranea	AFTOL-ID 688	AY854080	He et al. (2019)
Funalia gallica	CLZhao 1306	MG231491	This study
Funalia trogii	CLZhao 1557	MG231874	This study
Gloeophyllum sepiarium	CLZhao 732	MG231532	This study
Gloeophyllum trabeum	1320	HM536094	He et al. (2019)
Gloeoporus taxicola	CLZhao 1441	MG231549	This study
Grifola frondosa	AFTOL-ID 701	AY854084	He et al. (2019)
Gymnopus confluens	ZRL 20151148	LT716054	He et al. (2019)
Heliocybe sulcata	IBUG 9930	HM536095	He et al. (2019)
Heterobasidion annosum	06129/6	KJ583211	He et al. (2019)
Heterobasidion insulare	CLZhao 2899	MK268944	This study
Heterobasidion orientale	CLZhao 696	MG231561	This study
Hymenochaetopsis yasudae	CLZhao 1422	MG231607	This study
Hymenopellis radicata	AFTOL-ID 561	DQ241780	He et al. (2019)
Hyphoderma macaronesicum	TFC Mic 15939	NR119817	Schoch et al. 2014
Hyphoderma setigerum	CBS 421.72	MH860512	Vu et al. 2019
Hyphoderma transiens	CLZhao 1365	MK404378	This study
Hyphoderma variolosum	CBS 735.91	MH862321	Vu et al. 2019
Hyphodermella rosae	FP-150552	KP134978	He et al. (2019)
Inocutis dryophilus	DLL 2012-001	KU139186	He et al. (2019)
Irpex lacteus	CLZhao 1258	MG231709	This study
Junghuhnia crustacea	X 262	JN710553	Miettinen et al. 2012
Lacrymaria lacrymabunda	CBS 211.31	MH855192	He et al. (2019)
Laurilia sulcata	CBS 365.49	MH856552	Vu et al. 2019
Lenzitopsis daii	Yuan 2959	JN169799	He et al. (2019)

Table 1 Continued.

Species name	Sample no.	GenBank accession no.	References
Lycoperdon ericaeum	ZRL 20151498	LT716030	He et al. (2019)
Macrolepiota dolichaula	xml 2013058	LT716021	He et al. (2019)
Megalocystidium luridum	CBS 106.71	MH860024	Vu et al. 2019
Megasporoporiella subcavernulosa	CLZhao 1438	MG231737	This study
Melanogaster rivularis	S 190	HQ714731	He et al. (2019)
Meripilus giganteus	FP-135344	KP135307	He et al. (2019)
Meruliopsis albostramineus	HHB-10729	KP135051	He et al. (2019)
Microporus xanthopus	CLZhao 1285	MG231749	This study
Nigroporus vinosus	KA17-0261	MN294801	Direct Submission
Oligoporus farinosus	CIEFAP 91	JX090117	Pildain & Rajchenberg 2013
Omphalotus olearius	AFTOL-ID 1718	DQ494681	He et al. (2019)
Perenniporia hainaniana	Cui 6364	JQ861743	He et al. (2019)
Phaeophlebiopsis caribbeana	HHB-6990	KP135415	He et al. (2019)
Phanerochaete concrescens	CLZhao 1430	MG231768	This study
Phanerochaete sordida	CLZhao 1459	MG231774	This study
Phellinus ellipsoideus	Cui 4270	JQ837948	He et al. (2019)
Phlebiopsis crassa	CLZhao 786	MG231791	This study
Phylloporus pelletieri	Pp 1	DQ534566	He et al. (2019)
Pisolithus tinctorius	AWW 219	EU718114	He et al. (2019)
Polyozellus multiplex	AFTOL-ID 677	DQ411528	He et al. (2019)
Polyporus arcularius	CLZhao 1338	MG231798	This study
Porphyrellus porphyrosporus	MB 97-023	DQ534563	He et al. (2019)
Postia lactea	Cui 9319	KX900894	Direct Submission
Psathyrella candolleana	ZRL 20151400	LT716063	He et al. (2019)
Pseudochaete subrigidula	He 1157	JQ716403	He et al. (2019)
Pycnoporus sanguineus	ZRL 2015009	LT716078	He et al. (2019)
Rhizochaete americana	FP-102188	KP135409	He et al. (2019)
Rhizomarasmius oreinus	AQUI 6763	NR132910	Moreau et al. 2015
Rhodocollybia maculata	AFTOL-ID 540	DQ404383	He et al. (2019)
Rhodotus asperior	HKAS 56754	KC179737	He et al. (2019)
Rigidoporus undatus	Miettinen 13591	KY948731	He et al. (2019)
Sarcodon joeides	REB-270	KC571772	He et al. (2019)
Schizophyllum commune	CLZhao 1528	MG231811	This study
Schizophyllum leprieurii	ROBLEDO 1313	KM098065	Direct Submission
Scleroderma areolatum	AWW 211	EU718115	He et al. (2019)
Sparsitubus nelumbiformis	Cui 8497	KX880631	He et al. (2019)
Steccherinum bourdotii	CLZhao 1347	MG231820	This study
Steccherinum ochraceum	CLZhao 2897	MK269280	This study
Stereum hirsutum	CLZhao 1411	MG231830	This study
Stereum rugosum	CLZhao 1310	MG231836	This study
Stereum sanguinolentum	CLZhao 668	MG231838	This study
Trametes hirsuta	CLZhao 1544	MG231868	This study
Trametopsis cervina	TJV 93 216T	JN165020	He et al. (2019)
Tremella flava	CBS 8471	KY105681	He et al. (2019)
Tremella mesenterica	CBS 6973	NR155937	He et al. (2019)
Trulla dentipora	AS 2288	KY970064	Direct Submission
Veluticeps fimbriata	L-10628-Sp	HM536100	He et al. (2019)
Xylobolus frustulatus	He 2231	KU881905	He et al. (2019)

MrModeltest 2.3 (Nylander 2004) was used to determine the best-fit evolution model for each data set for Bayesian inference (BI). Bayesian inference was calculated with MrBayes3.1.2 with a general time reversible (GTR+I+G) model of DNA substitution and a gamma distribution rate variation across sites (Ronquist & Huelsenbeck 2003). Four Markov chains were run for 2 runs

from random starting trees for 1500 thousand generations (Fig. 1), and trees were sampled every 100 generations. The first one-fourth generations were discarded as burn-in. 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 maximum likelihood bootstrap (BS) >70%, maximum parsimony bootstrap (BT) >50%, or Bayesian posterior probabilities (BPP) >0.95.

Results

Molecular phylogeny

The ITS dataset (Fig. 1) included sequences from 102 fungal specimens representing 101 species. The dataset had an aligned length of 1389 characters, of which 308 characters were constant, 283 parsimony-uninformative, and 798 parsimony-informative. Maximum parsimony analysis yielded 1 equally parsimonious tree (TL = 8644, CI = 0.2678, HI = 0.7322, RI = 0.4535, RC = 0.1215). 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). Bayesian resulted in a similar topology with an average standard deviation of split frequencies = 0.029534 (BI), and the effective sample size (ESS) across the two runs is the double of the average ESS (avg ESS) = 354.

The phylogeny (Fig. 1) inferred from ITS sequences demonstrated that fifty-two species nested in sixteen families, Auriculariaceae, Bondarzewiaceae, Dacryobolaceae, Fomitopsidaceae, Gelatoporiaceae, Gloeophyllaceae, Hymenochaetaceae, Hyphodermataceae, Irpicaceae, Phanerochaetaceae, Physalacriaceae, Polyporaceae, Schizophyllaceae, Schizoporaceae, Steccherinaceae and Stereaceae, belonging to six orders Agaricales, Auriculariales, Gloeophyllales, Hymenochaetales, Polyporales, Russulales in Agaricomycetes.

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

1. ***Antrodia tanakae*** (Murrill) Spirin & Miettinen, on the fallen branch of *Acacia dealbata* Link, CLZhao 720; on the stump of *Acacia dealbata*, CLZhao 1536
2. ***Auricularia villosula*** Malysheva, on the fallen branch of *Alnus nepalensis*, CLZhao 1428; on the trunk of *Juglans regia* L., CLZhao 743; on the trunk of *Quercus*, CLZhao 1296; on the fallen branch of *Quercus*, CLZhao 1340
3. ***Basidioradulum crustosum*** (Pers.) Zmitr., Malysheva & Spirin, on the fallen angiosperm branch, CLZhao 3028
4. ***Bjerkandera adusta*** (Willd.) P. Karst, on the stump of *Pinus yunnanensis*, CLZhao 1555; on the dead tree of *Quercus*, CLZhao 1275
5. ***Brunneoporus malicola*** (Berk. & M.A. Curtis) Audet, on the stump of *Acacia dealbata*, CLZhao 1524; on the trunk of *Quercus acutissima* Carr., CLZhao 1530
6. ***Byssomerulius corium*** (Pers.) Parmasto, on the fallen angiosperm branch, CLZhao 1560; on the fallen branch of *Pinus yunnanensis*, CLZhao 734, CLZhao 781; on the fallen branch of *Quercus*, CLZhao 693, CLZhao 1266, CLZhao 1274, CLZhao 1313; on the stump of *Quercus*, CLZhao 1341
7. ***Cinereomyces lindbladii*** (Berk.) Jülich, on the trunk of *Pinus yunnanensis*, CLZhao 1523
8. ***Crepatura ellipsospora*** C.L. Zhao, on the trunk of *Alnus*, CLZhao 697; on the fallen branch of *Quercus*, CLZhao 868, CLZhao 1260, CLZhao 1265

9. ***Cylindrobasidium laeve*** (Pers.) Chamuris, on the dead bamboo, CLZhao 756, CLZhao 767
10. ***Daedaleopsis confragosa*** (Bolton) J. Schröt, on the trunk of *Alnus nepalensis*, CLZhao 1481
11. ***Funalia gallica*** (Fr.) Bondartsev & Singer, on the trunk of *Alnus nepalensis*, CLZhao 1309; on the fallen branch of *Alnus nepalensis*, CLZhao 1306
12. ***Funalia trogii*** Berk., on the trunk of *Alnus nepalensis*, CLZhao 1540; on the angiosperm trunk, CLZhao 741, CLZhao 3009, CLZhao 1557; on the fallen angiosperm branch CLZhao 1552
13. ***Fuscoporia torulosa*** (Pers.) T. Wagner & M. Fisch, on the fallen branch of *Quercus*, CLZhao 1305
14. ***Gloeophyllum sepiarium*** (Wulfen) P. Karst, on the trunk of *Pinus yunnanensis*, CLZhao 732, CLZhao 764; on the fallen branch of *Pinus yunnanensis*, CLZhao 774, CLZhao 904; on the stump of *Pinus yunnanensis*, CLZhao 731, CLZhao 784
15. ***Gloeoporus dichrous*** (Fr.) Bres., on the fallen branch of *Alnus nepalensis*, CLZhao 1471
16. ***Gloeoporus taxicola*** (Pers.) Gilb. & Ryvarden, on the trunk of *Pinus armandii*, CLZhao 1441
17. ***Heterobasidion insulare*** (Murrill) Ryvarden, on the stump of *Pinus yunnanensis*, CLZhao 2899
18. ***Heterobasidion orientale*** Tokuda, T. Hatt. & Y.C. Dai, trunk of *Pinus yunnanensis*, CLZhao 696
19. ***Hymenochaete adusta*** (Lév.) Har. & Pat., J. Bot, on the trunk of *Alnus*, CLZhao 700
20. ***Hymenochaete rheicolor*** (Mont.) Lév., on the trunk of *Alnus*, CLZhao 672, CLZhao 679; on the fallen branch of *Quercus*, CLZhao 666, CLZhao 671, CLZhao 682
21. ***Hymenochaete villosa*** (Lév.) Bres., on the trunk of *Quercus acutissima*, CLZhao 1533
22. ***Hymenochaetopsis corrugata*** (Fr.) S.H. He & Jiao Yang, on the fallen angiosperm branch, CLZhao 2893
23. ***Hymenochaetopsis yasudae*** (Imazeki) S.H. He & Jiao Yang, on the fallen branch of *Alnus nepalensis*, CLZhao 1422, CLZhao 1445; on the living tree of *Pinus armandii*, CLZhao 1475; on the fallen branch of *Pinus armandii*, CLZhao 1486, CLZhao 1495, CLZhao 1549
24. ***Hyphoderma transiens*** (Bres.) Parmasto, on the fallen angiosperm branch, CLZhao 1493; on the trunk of *Populus yunnanensis* Dode, CLZhao 1365
25. ***Hyphodontia tropica*** Sheng H. Wu, on the fallen angiosperm branch, CLZhao 2898, CLZhao 2901
26. ***Irpex lacteus*** (Fr.) Fr., on the trunk of *Acacia dealbata*, CLZhao 1258
27. ***Lopharia cinerascens*** (Schwein.) G. Cunn., on the fallen branch of *Alnus nepalensis*, CLZhao 1499
28. ***Megasporoporiella subcavernulosa*** (Y.C. Dai & Sheng H. Wu) B.K. Cui, on the fallen branch of *Alnus nepalensis*, CLZhao 1438, CLZhao 1466; on the stump of *Alnus nepalensis*, CLZhao 1412; on the fallen angiosperm branch, CLZhao 2966, CLZhao 2984, CLZhao 3016; on the stump of *Cupressus funebris* Endl., CLZhao 1444, CLZhao 1491
29. ***Microporus xanthopus*** (Fr.) Kuntze, on the fallen branch of *Alnus nepalensis*, CLZhao 1503; on the fallen angiosperm branch, CLZhao 3012; on the trunk of *Quercus*, CLZhao 1253, CLZhao 1285; on the fallen branch of *Quercus*, CLZhao 1268, CLZhao 1304; on the stump of *Quercus*, CLZhao 1343
30. ***Phanerochaete concrescens*** Spirin & Volobuev, on the fallen branch of *Alnus nepalensis*, CLZhao 1541, CLZhao 1545; on the fallen angiosperm branch, CLZhao 2929, CLZhao 2931, CLZhao 2939, CLZhao 2940, CLZhao 2945, CLZhao 2946, CLZhao 2949; on the trunk of *Pinus yunnanensis*, CLZhao 2916
31. ***Phanerochaete sordida*** (P. Karst.) J. Erikss. & Ryvarden, on the trunk of *Alnus*, CLZhao 698; on the fallen branch of *Alnus nepalensis*, CLZhao 1459, CLZhao 1541, CLZhao 1545; on the angiosperm trunk, CLZhao 1461; on the fallen angiosperm branch, CLZhao 2929, CLZhao 2931, CLZhao 2939, CLZhao 2940, CLZhao 2945, CLZhao 2946, CLZhao 2949, CLZhao 4738, CLZhao 4746, CLZhao 4754; on the fallen branch of *Pinus armandii*, CLZhao 1515; on the trunk of *Pinus yunnanensis*, CLZhao 2916
32. ***Phellinus gilvus*** (Schwein.) Pat., on the fallen branch of *Alnus nepalensis*, CLZhao 1334

33. ***Phlebiopsis crassa*** (Lév.) Floudas & Hibbett, on the angiosperm trunk, CLZhao 786; on the fallen branch of *Coriaria nepalensis* Wall., CLZhao 1295, CLZhao 1308; on the trunk of *Pinus yunnanensis*, CLZhao 724; on the trunk of *Quercus*, CLZhao 1269, CLZhao 1314; on the fallen branch of *Quercus acutissima*, CLZhao 1532

34. ***Polyporus arcularius*** (Batsch) Fr. on the stump of *Coriaria nepalensis*, CLZhao 1338; on the fallen branch of *Quercus*, CLZhao 1316

35. ***Postia hibernica*** (Berk. Broome) Jülich, on the fallen angiosperm branch, CLZhao 2903; on the fallen branch of *Pinus yunnanensis*, CLZhao 2909

36. ***Pulcherricium coeruleum*** (Lam.) Parmasto, on the fallen branch of *Alnus nepalensis*, CLZhao 1434; on the fallen angiosperm branch, CLZhao 3003, CLZhao 3020

37. ***Schizophyllum commune*** Fr., on the trunk of *Acacia dealbata*, CLZhao 1527; on the fallen branch of *Acacia dealbata*, CLZhao 1528, CLZhao 1529; on the trunk of *Alnus nepalensis*, CLZhao 1537; on the stump of *Alnus nepalensis*, CLZhao 1562; on the stump of *Eucalyptus robusta*, CLZhao 1561

38. ***Steccherinum bourdotii*** Saliba & A. David, on the fallen branch of *Alnus nepalensis*, CLZhao 1472; on the fallen branch of *Pinus armandii*, CLZhao 1347

39. ***Steccherinum ochraceum*** (Pers. ex J.F. Gmel.) Gray, on the fallen angiosperm branch, CLZhao 2897, CLZhao 2968

40. ***Stereum gausapatum*** (Fr.) Fr., on the trunk of *Alder*, 11 January 2017, CLZhao 668, CLZhao 669, CLZhao 673, CLZhao 677, CLZhao 683, CLZhao 694, CLZhao 707; on the dead tree of *Quercus*, 22 April 2017, CLZhao 1259, CLZhao 1270, CLZhao 1290, CLZhao 1300, CLZhao 1318, CLZhao 1320

41. ***Stereum hirsutum*** (Willd.) Pers., on the fallen branch of *Alnus nepalensis*, CLZhao 1404, CLZhao 1405, CLZhao 1427, CLZhao 1455, CLZhao 1457, CLZhao 1465, CLZhao 1469, CLZhao 1470, CLZhao 1479, CLZhao 1482, CLZhao 1489, CLZhao 1498; on the fallen angiosperm branch, CLZhao 740; on fallen branch of *Coriaria nepalensis*, CLZhao 1559; on fallen branch of *Pinus yunnanensis*, CLZhao 2906; on the fallen branch of *Quercus*, CLZhao 1291

42. ***Stereum rugosum*** Pers., on the trunk of *Quercus*, CLZhao 1310

43. ***Stereum sanguinolentum*** (Alb. & Schwein.) Fr., on the trunk of *Alnus*, CLZhao 673; on the stump of *Pinus yunnanensis*, CLZhao 669

44. ***Trametes hirsuta*** (Wulfen) Lloyd, on the fallen branch of *Alnus nepalensis*, CLZhao 1544; on the angiosperm trunk, CLZhao 1344; on the trunk of *Pinus yunnanensis*, CLZhao 739

45. ***Trametes strumosa*** (Fr.) Zmitr., on the angiosperm trunk, CLZhao 718

46. ***Trametes versicolor*** (L.) Lloyd, on the trunk of *Alnus nepalensis*, CLZhao 1539, CLZhao 1546; on the fallen branch of *Alnus nepalensis*, CLZhao 1431; on the stump of *Alnus nepalensis*, CLZhao 1510; on the angiosperm trunk, CLZhao 748, CLZhao 1293, CLZhao 1477; on the trunk of *Cupressus funebris*, CLZhao 1509; on the trunk of *Quercus*, CLZhao 1330; on the fallen branch of *Quercus*, CLZhao 686, CLZhao 714, CLZhao 1302, CLZhao 1307

47. ***Trametopsis cervina*** (Schwein.) Tomšovský, on the trunk of *Alnus nepalensis*, CLZhao 1246; on the fallen branch of *Quercus*, CLZhao 1315

48. ***Trichaptum abietinum*** (Dicks.) Ryvarden, on the angiosperm stump, CLZhao 719, CLZhao 723, CLZhao 736, CLZhao 777, CLZhao 3004; on the trunk of *Pinus yunnanensis*, CLZhao 730

49. ***Tubulicrinis xantha*** C.L. Zhao, on the fallen branch of *Pinus yunnanensis*, CLZhao 2868, CLZhao 2869, CLZhao 2883

50. ***Xylodon kunmingensis*** L. W. Zhou & C.L. Zhao, on the fallen angiosperm branch, CLZhao 3010, CLZhao 3019; on the stump of angiosperm, CLZhao 755; on the fallen branch of *Pinus yunnanensis*, CLZhao 752

51. ***Xylodon nespori*** (Bres.) Hjortstam & Ryvarden, on the trunk of *Cupressus funebris*, CLZhao 1492

52. ***Xylodon rimosissimus*** (Peck) Hjortstam & Ryvarden, on the fallen branch of *Pinus armandii*, CLZhao 1487

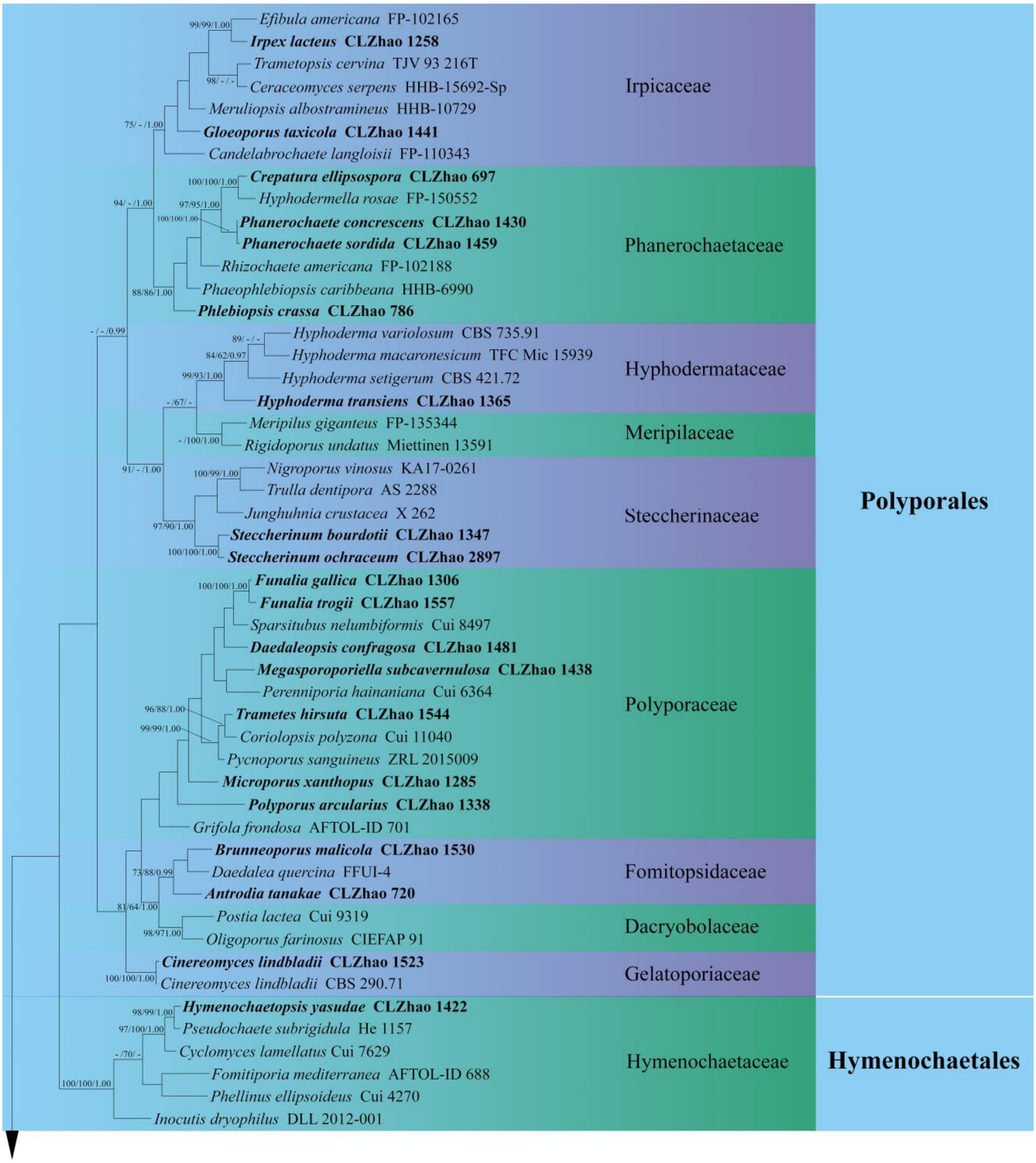

Fig. 1 – Maximum parsimony strict consensus tree illustrating the phylogeny of 52 species with related taxa in Agaricomycetes based on ITS sequences. Branches are labelled with maximum likelihood bootstrap equal to or greater than 70%, parsimony bootstrap equal to or greater than 50% and Bayesian posterior probabilities equal to or greater than 0.97, respectively. The taxa from the present study are indicated in black bold.

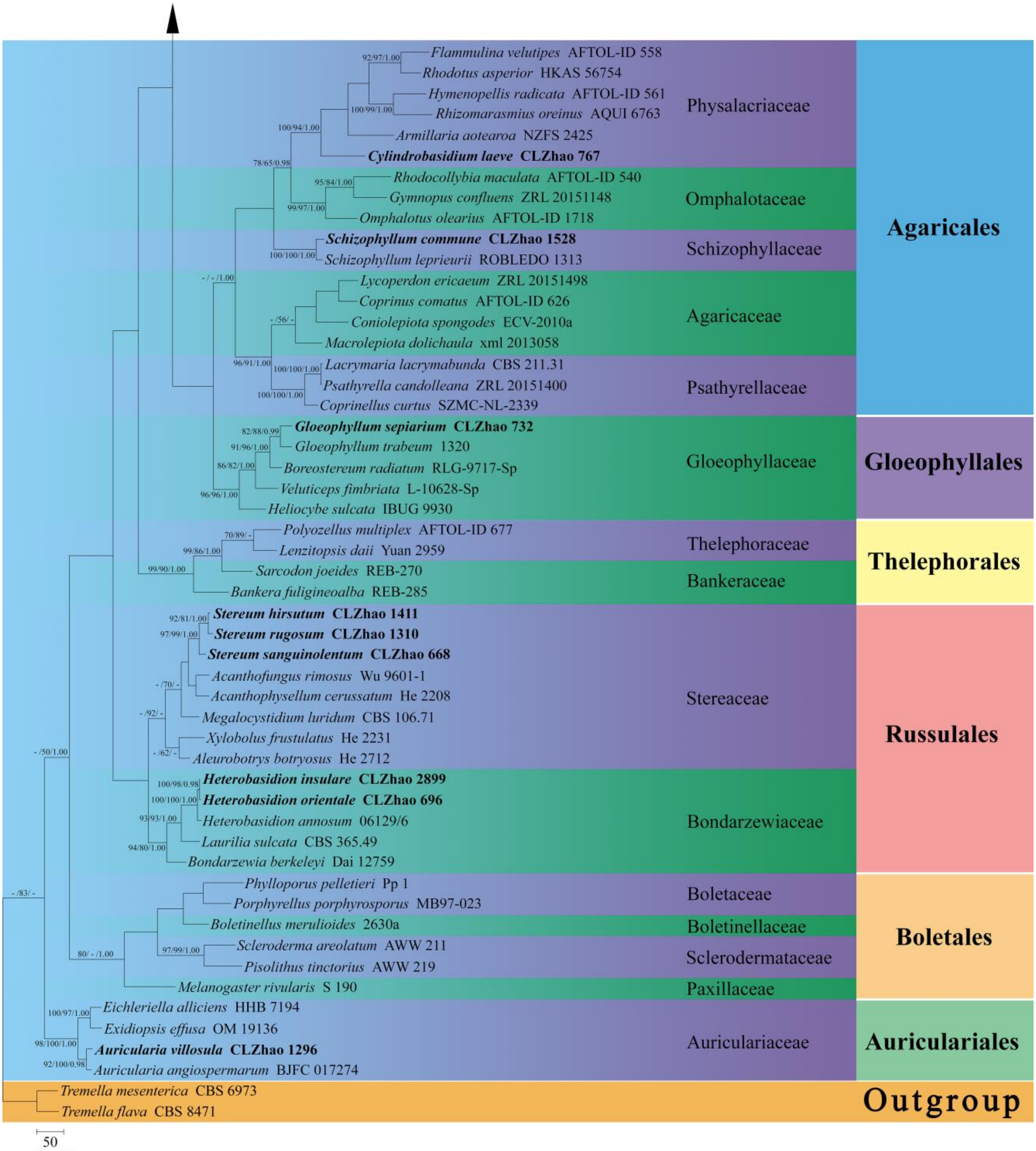

Fig. 1 – Continued.

Discussion

In the kingdom Fungi, the phyla Ascomycota and Basidiomycota cover around 97% of all fungal species (Willis 2018). According to the latest version of Ainsworth & Bisby's Dictionary of the Fungi (Kirk et al. 2008), there are 1589 genera and more than 30 thousand species of Basidiomycota, which comprise nearly 32% of all described fungal taxa (Dai et al. 2015), and more and more taxa were recorded worldwide every year, which observably increase the fungal diversity (Sarma & Hyde 2018, Yafetto 2018, Freitas-Neto et al. 2019, Hipol et al. 2019, Ayesha et al. 2020, De Leon AM et al. 2020, Huang et al. 2020, Himani & Krishnappa 2020, Blanco-Dios 2021, Kumar et al. 2021, Wang & Zhao 2021, Zong et al. 2021).

Although some notable explorations of wood-decaying fungi have been made from Yunnan Province (Cui & Dai 2012, Wu et al. 2017, 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. 2020, Wu et al. 2021, Zong et al. 2021), only three new species were found from Haikou Forestry Farm (Ma & Zhao 2019, Shi et al. 2019, He et al. 2020). Species in the present list are mostly new to the studied area. The 681 specimens belong to 52 species, which are distributed in 37 genera, 16 families, 6 orders, in which 11 are pathogenic (Dai 2012b), and 28 are medicinal (Dai & Yang 2008), and a few are edible (Dai et al. 2010). Among them, 28 species belong to order Polyporales and 14 species belong to order Hymenochaetales and 6 species belong to order Russulales, and 2 species belong to order Agaricales and 1 species belong to order Auriculariales and 1 species belong to order Gloeophyllales.

The molecular phylogenetic analyses with combined nLSU, SSU, 5.8s, rpb1, rpb2, and tef1 datasets for the subphyla Agaricomycotina, Pucciniomycotina and Ustilaginomycotina revealed that 1928 currently used genera names are distributed in 241 families, 68 orders, 18 classes and four subphyla (He et al. 2019). In the present study, 52 species nested in 37 genera, 16 families, 6 orders based on ITS dataset, which is similar to the topology of the phylogenetic analyses in He et al. (2019).

This work will comprehensively improve the understanding of the diversity of wood-decaying fungi in this area, which is conducive to the rational utilization and effective protection of fungal resources, and provides scientific basis for the prevention and control of forest diseases in this farm.

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