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Four New Fungal Species in Forest Ecological System from Southwestern China

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Abstract: Four new wood-inhabiting fungi were found in Southwestern China within the genera *Phanerochaete*, *Phlebiopsis*, *Asterostroma*, and *Vararia* of the families Phanerochaetaceae and Peniophoraceae, belonging to the orders Polyporales and Russulales individually. Combined with their morphological characteristics and molecular biological evidence, the present study describes them as new fungal taxa. *Asterostroma yunnanense* is characterized by the resupinate, membranaceous to pellicular basidiomata with a cream to salmon-buff hymenial surface, hyphal system dimitic bearing simple-septa, thin- to thick-walled, yellowish brown asterosetae with acute tips, and thin-walled, echinulate, amyloid, globose basidiospores. *Phanerochaete tongbiguanensis* is characterized by the resupinate basidiomata with a white to cream hymenial surface, a monomitic hyphal system with simple-septa generative hyphae, the presence of subclavate cystidia covered with a lot of crystals, and oblong ellipsoid basidiospores (6–9 × 3–4.5 µm). *Phlebiopsis fissurata* is characterized by the membranaceous, tuberculate basidiomata with a buff to slightly brown hymenial surface, a monomitic hyphal system with simple-septa, conical cystidia, and broadly ellipsoid. *Vararia yingjiangensis* is characterized by a corky basidiomata with a pinkish buff to cinnamon-buff hymenial surface, cracking, yellowish dichohyphae with slightly curved tips, subulate gloeocystidia, and thick-walled, ellipsoid basidiospores (6.5–11.5 × 5–7 µm). The phylogenetic analyses of ITS + nLSU revealed that the two new species were nested into the genera *Phanerochaete* and *Phlebiopsis* within the family Phanerochaetaceae (Polyporales), in which *Phanerochaete tongbiguanensis* was sister to *P. daliensis*; *Phlebiopsis fissurata* was grouped with *P. lamprocystidiata*. Two new species were clustered into the genera *Asterostroma* and *Vararia* within the family Peniophoraceae (Russulales), in which *Asterostroma yunnanense* was sister to *A. cervicolor*; *Vararia yingjiangensis* formed a single branch.

Keywords: Asia; macrofungi; molecular systematics; taxonomy; Yunnan province

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1. Introduction

Over the past 30 years, wood-inhabiting basidiomycetes have been extensively studied in Chinese forests, and nearly 1600 species of wood-inhabiting basidiomycetes have been found in China [1–10]. One survey showed that 86 percent of species cause white rot, and 14 percent cause brown rot [11]. Two-order Polyporales Gäum. and Russulales Kreisel ex P.M. Kirk, P.F. Cannon, and J.C. David are diverse groups of the class Agaricomycetes Doweld (Basidiomycota R.T. Moore) [12].

The genus *Asterostroma* Massee belongs to the family Peniophoraceae Lotsy (Russulales, Basidiomycota), and it is typified with *Corticium apalum* Berk & Broome. It is characterized by the resupinate, membranaceous to pellicular basidiocarps, a dimitic (asterodimitic) hyphal system, simple-septate generative hyphae, dextrinoid asterosetae, the presence of gloeocystidia, and smooth or ornamented basidiospores with or without amyloid reactions [13–16]. Based on the MycoBank database (http://www.MycoBank.org, accessed on 22 February 2024) and the Index Fungorum (http://www.indexfungorum.org, accessed on 22 February 2024), 38 specific and infraspecific names have been registered in *Asterostroma*, but the actual number of the species has reached 31, and it is still poorly studied in China [17,18]. The wood-inhabiting fungal genus *Phanerochaete* P. Karst. belonged to the family Phanerochaetaceae Jülich (Polyporales, Basidiomycota), typified by *P. alnea* (Fr.) P. Karst. [19]. it is characterized by white-rot, resupinate, and membranaceous basidiocarps; a smooth or tuberculate hymenial surface; a monomitic hyphal system; generative hyphae mostly simple-septate; the presence of smooth or encrusted cystidia; and thin-walled, non-amyloid, and acyanophilous basidiospores [20–23]. Based on the MycoBank database (http://www.MycoBank.org, accessed on 22 February 2024) and the Index Fungorum (http://www.indexfungorum.org, accessed on 22 February 2024), the genus *Phanerochaete* has 210 specific and registered names, but the actual number of species has reached 112 [23–28]. The genus *Phlebiopsis* Jülich (Phanerochaetaceae, Polyporales), typified with *P. gigantea* (Fr.) Jülich, is characterized by a combination of resupinate to effused-reflexed basidiomata with a membranaceous to subceraceous consistency when fresh, cracked when dry, a smooth to odontoid to poroid hymenophore, a monomitic hyphal system with colorless, generative hyphae with simple-septate, hyaline cystidia that are thick-walled and encrusted, usually narrowly clavate basidia, and basidiospores that are hyaline, thin-walled, smooth, cylindrical to ellipsoid, acyanophilous, and negative in Melzer's reagent [13,29]. So far, the MycoBank database (http://www.MycoBank.org, accessed on 22 February 2024) and Index Fungorum (http://www.indexfungorum.org, accessed on 22 February 2024) have registered 39 specific and infraspecific names for *Phlebiopsis*, but the actual number of the species has reached 33, and 6 species were transferred to *Phaeophlebiopsis* Floudas & Hibbett [26,30–35]. Recently, more than 150 specimens of the genus *Phlebiopsis* were collected by the mycologist from China and Southeast Asia [26,35]. The genus *Vararia* P. Karst. (Peniophoraceae, Russulales), typified by *V. investiens* (Schwein.) P. Karst., is a corticioid wood-inhabiting fungal genus with a wide distribution [13]. The genus is characterized by the resupinate basidiomata, a dimitic hyphal structure with simple-septate or clamped generative hyphae and often dextrinoid dichohyphae in Melzer's reagent, the presence of gloeocystidia, and variously shaped smooth basidiospores with or without an amyloid reaction [13,36–38]. Based on the MycoBank database (http://www.MycoBank.org, accessed on 22 February 2024) and the Index Fungorum (http://www.indexfungorum.org, accessed on 22 February 2024), there are 99 specific and infraspecific names in *Vararia* [13,39–44]. But the actual number of species has reached 76, and they occur mainly in the tropical and subtropical areas of the world [8,42–52].

Pioneering research according to the family Phanerochaetaceae Jülich (Polyporales) and Peniophoraceae Lotsy (Russulales) was just the prelude to the molecular systematics of Basidiomycota [25,53–55]. Based on the nuclear rDNA ITS1-5.8S-ITS2 (ITS), the D1–D2 domains of 28S rDNA (28S), and the RNA polymerase II largest subunit (rpb1) genes, the phylogenetic diversity revealed that the taxa of Polyporales nested in the phlebioid clade, which included the family of Phanerochaetaceae, Irpicaceae Spirin & Zmitr., and Meruliaceae Rea, in which the result showed that 54 genera were included [12,25,54–59]. Species diversity, taxonomy, and multigene phylogeny revealed that the family Phanerochaetaceae comprises four main lineages with substantial support, including the *Donkia* Pilát, *Phanerochaete*, *Phlebiopsis*, and *Bjerkandera* P. Karst. Clades, in which *Phanerochaete* s.l. was defined as a polyphyletic genus based on previous phylogeny results [25]. Revisiting the taxonomy of *Phanerochaete* (Phanerochaetaceae, Polyporales) based on RPB1, RPB2, and the ITS and LSU revealed that *Phanerochaete* was further divided into four smaller clades (*Phanerochaete sensu stricto*, *Bjerkandera*, *Hyphodermella* J. Erikss. & Ryvarden, and *Phlebiopsis*); however, only *Phanerochaete* s.s. and *Phlebiopsis* clades have been previously identified [22]. The family Peniophoraceae (Russulales) was a large and rather heterogeneous family, although it appeared monophyletic in most analyses, and it was almost totally dominated by corticioid species, and the prime exception was the clavarioid genus *Lachnocladium* Lév. [53,60]. The phylogenetic diversity displayed by the corticioid fungal species based on

5.8S and 28S nuclear rDNA revealed that the taxa of Peniophoraceae were nested in the russuloid clade, which held a considerable share of the phylogenetic framework [14–16,61]. The phylogenetic research about the major clades of mushroom-forming fungi (Homobasidiomycetes) indicate that the largest resupinate forms were divided into the polyporoid clade, russuloid clade, and hymenochaetoid clade, in which *Peniophora* Cooke was grouped with *Asterostroma* and *Scytinostroma* Donk [54]. Re-thinking the classification of corticioid fungi to clear the phylogenetic relationships inferred from 5.8S and nLSU rDNA sequences using Bayesian analysis showed that *Asterostroma*, *Gloiothele* Bres., *Peniophora*, *Scytinostroma*, and *Vararia* were clustered in the family Peniophoraceae (Russulales) [41,53].

During the investigations on wood-inhabiting fungi in Yunnan province, China, four new species were found, which could not be assigned to any described species. We present the morphological and molecular phylogenetic evidence that support the recognition of these four new species in Phanerochaetaceae and Peniophoraceae based on the internal transcribed spacer (ITS) regions and the large subunit nuclear ribosomal RNA gene (nLSU) sequences.

2. Materials and Methods

2.1. Sample Collection and Herbarium Specimen Preparation

Fresh fruiting bodies of basidiomycetous macrofungi were collected from Lincang, Dehong, Yunnan province, P.R. China. Specimens were dried in an electric food dehydrator at 40 °C and then sealed and stored in an envelope bag and deposited in the herbarium of Southwest Forestry University (SWFC), Kunming, Yunnan province, P.R. China. Macromorphological descriptions are based on field notes and photos captured in the field and lab.

2.2. Molecular Phylogeny

Macromorphological descriptions and color terminology are based on field notes and photos captured in the field or lab, and they follow those of a previous study [54]. The micromorphological data were obtained from the dried specimens based on observing them under a light microscope following a previous study [55]. The following abbreviations are used: KOH = 5% potassium hydroxide water solution, CB = Cotton Blue, CB– = acyanophilous, IKI = Melzer's reagent, IKI– = both inamyloid and indextrinoid, L = mean spore length (arithmetic average for all spores), W = mean spore width (arithmetic average for all spores), Q = variation in the L/W ratios between the specimens studied, and n = a/b (number of spores (a) measured from given number (b) of specimens).

2.3. DNA Extraction and Sequencing

According to the manufacturer's instructions, we used the CTAB rapid plant genome extraction kit-DN14 (Aidlab Biotechnologies Co., Ltd., Kunming, China) to obtain genomic DNA from dried specimens [62]. A total of 3 μL of DNA was evenly mixed with 3 μL 5 × bromophenol blue indicator and a 3 μL DNA sample to be tested, and the samples were placed on a 1.5% agarose gel plate (containing 0.5 μg/mL EB). The DNA molecular weight was labeled DL 2000 with a molecular weight of 560–23,130 bp, and the pressure was stabilized at 90 V. Electrophoresis occurred for 30 min. The nuclear ribosomal ITS region was amplified with primers ITS5 (GGA AGT AAA AGT CGT AAC AAG G) and ITS4 (TCC TCC GCT TAT TGA TAT GC) [62]. The nuclear nLSU region was amplified with primer pair LR0R (ACC CGC TGA ACT TAA GC) and LR7 (TAC TAC CAC CAA GAT CT) [62]. The basic amplification reaction system of ITS and nLSU is shown in Table 1. And the newly generated sequences were deposited in NCBI GenBank (Table 2).

Table 1. PCR reaction system and reaction conditions.

Genes	Primers	Temperature	Time	
ITS		Predegeneration 94 °C	1.5 min	35 cycles
		Denaturation 94 °C	30 s	
	Primer (10 µmol/L) (ITS 5)	Renaturation 55 °C	45 s	
	Primer (10 µmol/L) (ITS 4)	Extend 72 °C	1 min	
		Extend 72 °C	10 min	
		Save 4 °C	—	
nLSU		Predegeneration 94 °C	1.5 min	
		Denaturation 94 °C	20 s	
	Primer (10 µmol/L) (LROR)	Renaturation 48 °C	1.5 min	
	Primer (10 µmol/L) (LR 7)	Extend 72 °C	1.5 min	
		Extend 72 °C	5 min	
		Save 4 °C	—	

2.4. Phylogenetic Analyses

The sequences were aligned in MAFFT 7 (https://mafft.cbrc.jp/alignment/server/, 20 December 2023) using the "G-INS-i" strategy for the ITS and nLSU datasets and manually adjusted in BioEdit [63]. Sequences of *Gloeoporus pannocinctus* (Romell) J. Erikss. and *G. dichrous* (Fr.) Bres. Obtained from GenBank were selected as an outgroup for phylogenetic analysis of the ITS + nLSU phylogenetic tree (Figure 1) [64]. Sequences of *Confertobasidium olivaceoalbum* (Bourdot & Galzin) Jülich and *Metulodontia nive* (P. Karst.) Parmasto retrieved from GenBank were used as outgroups in the ITS + nLSU (Figure 2) analysis following a previous study [65]. The sequences of *Phaeophlebiopsis caribbeana* Floudas & Hibbett and *Phlebiopsis flavidoalba* (Cooke) Hjortstam were selected as an outgroup in the ITS analysis (Figure 3) following a previous study [64]. The sequences of *Crystallicutis serpens* (Tode) El-Gharabawy, Leal-Dutra & G.W. Griff., and *Phlebia acerina* Peck were selected as an outgroup for the phylogenetic analysis of ITS phylogenetic tree (Figure 4) [29]. The sequences of *Confertobasidium olivaceoalbum* (Bourdot & Galzin) Jülich and *Scytinostroma ochroleucum* Donk were selected as an outgroup for the phylogenetic analysis of ITS phylogenetic tree (Figure 5) [35]. The sequences of *Peniophora incarnata* (Pers.) P. Karst. and *Peniophora nuda* (Fr.) Bres. retrieved from GenBank were used as outgroups in the ITS (Figure 6) analysis following a previous study [65].

Maximum parsimony (MP), maximum likelihood (ML), and Bayesian inference (BI) analyses were applied to the combined three datasets [66]. BS (Branch Support) for ML (maximum likelihood) analysis was determined by 1000 bootstrap replicates, and bootstrap values were >70% [66]. MP (maximum parsimony) analysis was performed in PAUP* version 4.0b10, and parsimony bootstrap values were >50% [67]. BI (Bayesian inference) and clade robustness were assessed using bootstrap (BT) analysis with 1000 replicates, and Bayesian posterior probabilities were >0.95 [68,69]. All of the characters were equally weighted, and gaps were treated as missing data. Trees were inferred using the heuristic search option with TBR branch swapping and 1000 random sequence additions. Max trees were set to 5000, branches of zero length were collapsed, and all parsimonious trees were saved. Clade robustness was assessed using bootstrap (BT) analysis with 1000 replicates [68]. 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 generated. The multiple sequence alignment was also analyzed using maximum likelihood (ML) in RAxML-HPC2 through the Cipres Science Gateway [69].

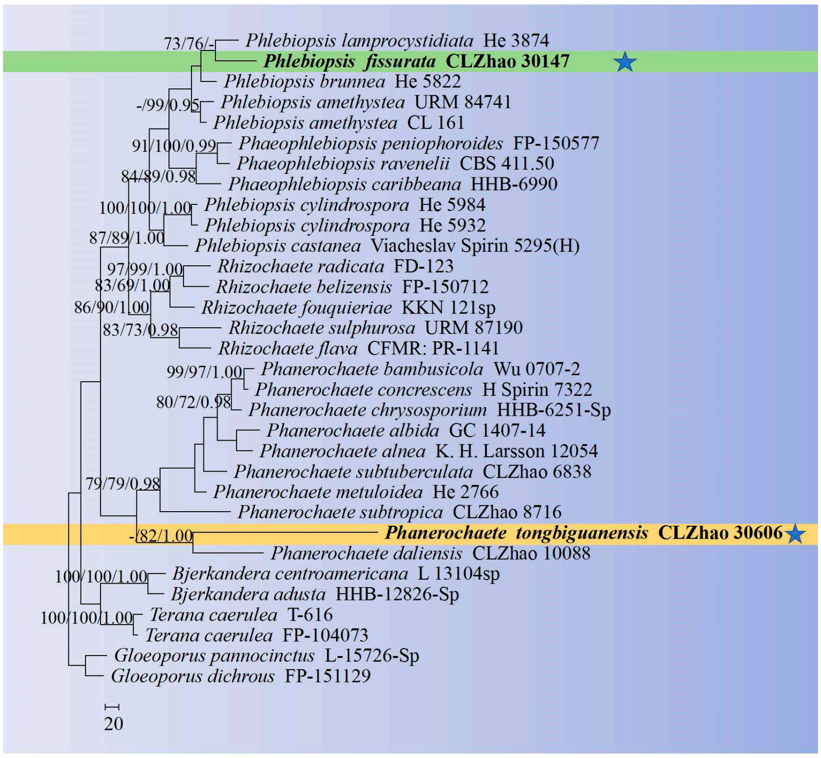

Figure 1. Maximum parsimony is a strict consensus tree illustrating the phylogeny of two new species and related genera in the family Phanerochaetaceae based on ITS + nLSU sequences. The new species are marked with asterisks.

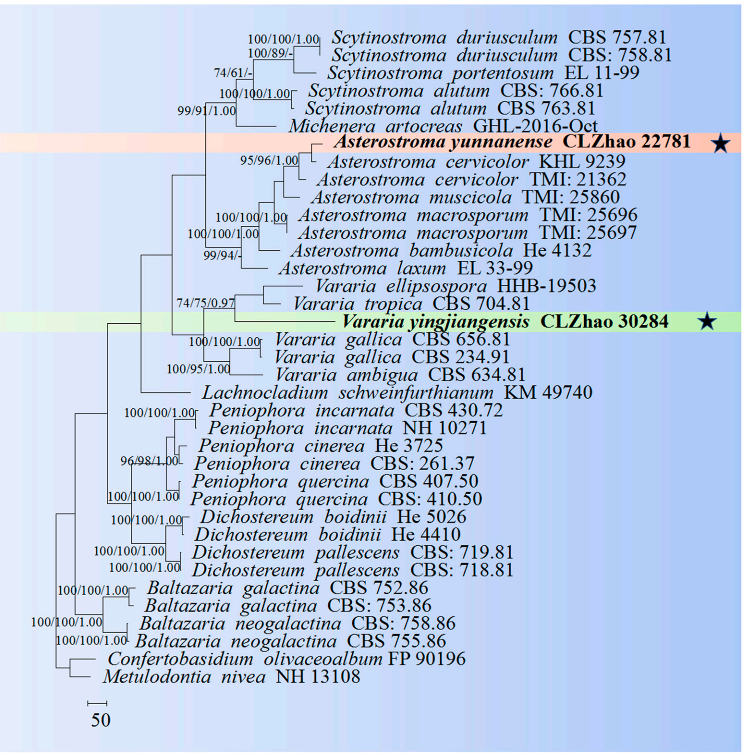

Figure 2. Maximum parsimony is a strict consensus tree illustrating the phylogeny of two new species and related genera in the family Peniophoraceae based on ITS + nLSU sequences. The new species are marked with asterisks.

Table 2. List of species, specimens, and GenBank accession numbers of sequences used in this study. The new species are in bold.

Species Name	Specimen No.	GenBank Accession No.		Country	References
		ITS	nLSU		
Asterostroma bambusicola	He4132	KY263865	KY263871	China	[42]
A. bambusicola	He4128	KY263864		China	[42]
A. cervicolor	He4020	KY263860	KY263868	China	[42]
A. cervicolor	He2314	KY263859	KY263869	China	[42]
A. cervicolor	TMI:21362	AB439560		Japan	[17]
A. cervicolor	KHL9239	AF506408	AF506408	Sweden	[41]
A. laxum	EL33-99	AF506410	AF506410	Sweden	[41]
A. macrosporum	TMI:25696	AB439544		Japan	[17]
A. macrosporum	TMI:25697	AB439545		Japan	[17]
A. medium	HFRG_EJ220212_2_FRDBI 23891920	OQ133615		United Kingdom	Unpublished
A. medium	HFRG_EJ210127_2 FRDBI 18772203	OL828779		United Kingdom	Unpublished
A. muscicola	He20121104-1	KY263862	KY263872	China	[42]
A. muscicola	He4106	KY263861	KY263873	China	[42]
A. muscicola	TMI:25860	AB439551		Japan	[17]
A. vararioides	He4140	KY263867	KY263870	China	[42]
A. vararioides	He4136	KY263866		China	[42]
A. yunnanense	**CLZhao 22781 ***	**OR048809**	**OR506285**	**China**	**Present study**
A. yunnanense	**CLZhao 22846**	**OR048810**	**OR506287**	**China**	**Present study**
A. yunnanense	**CLZhao 22786**	**OR048811**	**OR506286**	**China**	**Present study**
Baltazaria galactina	CBS 752.86	MH862034	MH873721	France	[70]
B. galactina	CBS:753.86	MH862035	MH873722	France	[70]
B. neogalactina	CBS 755.86	MH862037	MH873724	France	[70]
B. neogalactina	CBS:758.86	MH862040	MH873727	France	[70]
Bjerkandera adusta	HHB-12826-Sp	KP134983	KP135198	USA	[22]
B. centroamericana	L13104sp	KY948791	KY948855	Costa Rica	[56]
Confertobasidium olivaceoalbum	FP90196	AF511648	AF511648	Sweden	[41]
Crystallicutis serpens	HHB-15692-Sp	KP135031	KP135200	USA	[22]
Dichostereum boidinii	He4410	MH538315	MH538331	China	[70]
D. boidinii	He5026	MH538324	MH538330	China	[71]
D. pallescens	CBS:718.81	MH861456	MH873198	USA	[70]
D. pallescens	CBS:719.81	MH861457	MH873199	USA	[70]
Gloeoporus dichrous	FP-151129	KP135058		USA	[22]
G. pannocinctus	L-15726-Sp	KP135060		USA	[22]
Lachnocladium schweinfurthianum	KM49740	MH260033	MH260051	United Kingdom	[65]
Metulodontia nivea	NH13108	AF506423	AF506423	Sweden	[41]
M. artocreas	GHL-2016-Oct	MH204688	MH204692	USA	[72]
Peniophora cinerea	He3725	MK588769	MK588809	China	Unpublished
P. cinerea	CBS:261.37	MH855905	MH867412	Belgium	[70]
P. incarnata	CBS 430.72	MH860518	MH872230	Netherlands	[70]
P. incarnata	NH10271	AF506425	AF506425	Sweden	[41]
P. quercina	CBS 407.50	MH856687	MH868204	France	[70]
P. quercina	CBS:410.50	MH856690	MH868207	France	[70]
Phaeophlebiopsis caribbeana	HHB-6990	KP135415	KP135243	USA	[22]
P. peniophoroides	FP-150577	KP135417	KP135273	USA	[22]
P. ravenelii	CBS:411.50	MH856691	MH868208	France	[70]
Phanerochaete burdsallii	He 2066	MT235690	MT248177	USA	Unpublished

Table 2. *Cont.*

Species Name	Specimen No.	GenBank Accession No.		Country	References
		ITS	nLSU		
P. aculeata	Wu 1809-278	MZ422786	MZ637178	China	[25]
P. aculeata	GC 1703-117	MZ422785	MZ63717	China	[25]
P. albida	WEI 18-365	MZ422789	MZ637180	China	[25]
P. albida	GC 1407-14	MZ422788	MZ637179	China	[25]
P. allantospora	KKN-111-Sp	KP135038	KP135238	USA	[22]
P. allantospora	RLG-10478	KP135039		USA	[22]
P. alnea	K. H. Larsson 12054	KX538924		Norway	[73]
P. alnea voucher	K. H. Larsson 12054	KX538924		Norway	[73]
P. alpina	Wu 1308-61	MZ422790	MZ637182	China	[25]
P. alpina	Wu 1308-77	MZ422791	MZ637183	China	[25]
P. arizonica	RLG-10248-Sp	KP135170	KP135239	USA	[22]
P. australis	He 6013	MT235656	MT248136	China	[74]
P. australis	HHB-7105-Sp	KP135081	KP135240	USA	[22]
P. australosanguinea	MA:Fungi:91308	MH233925	MH233928	Chile	[74]
P. australosanguinea	MA:Fungi:91309	MH233926	MH233929	Chile	[74]
P. bambusicola	He 3606	MT235657	MT248137	China	[25]
P. bambusicola	Wu 0707-2	MF399404	MF399395	China	[75]
P. brunnea	He 4192	MT235658	MT248138	China	[76]
P. burdsallii	CFMR:RF9JR	KU668973		USA	[27]
P. burtii	HHB-4618-Sp	KP135117	KP135241	USA	[22]
P. burtii	FD-171	KP135116		USA	[22]
P. calotricha	Vanhanen382	KP135107		USA	[22]
P. canobrunnea	He 5726	MT235659	MT248139	Sri Lanka	[75]
P. canobrunnea	TNM:CHWC 1506-66	LC412095	LC412104	China	[76]
P. carnosa	He 5172	MT235660	MT248140	China	[76]
P. carnosa	HHB-9195	KP135129	KP135242	USA	[22]
P. chrysosporium	He 5778	MT235661	MT248141	Sri Lanka	[76]
P. chrysosporium	HHB-6251-Sp	KP135094	KP135246	USA	[22]
P. citrinosanguinea	FP-105385-Sp	KP135100	KP135234	USA	[22]
P. concrescens	He 4657	MT235662	MT248142	China	[25]
P. concrescens	H Spirin 7322	KP994380	KP994382	Russia	[77]
P. conifericola	OM8110	KP135171		Finland	[22]
P. crystallina	Chen 3823	MZ422802	MZ637188	China	[25]
P. crystallina	Chen 3576	MZ422801		China	[25]
P. cumulodentata	He 2995	MT235664	MT248144	China	[74]
P. cumulodentata	LE < RUS_:298935	KP994359	KP994386	Russia	[77]
P. cystidiata	He 4224	MT235665	MT248145	China	[76]
P. cystidiata	TNM:Wu 1708-326	LC412097	LC412100	China	[78]
P. daliensis	CLZhao F10107	OP605506	OP874696	China	[27]
P. daliensis	CLZhao F10088	OP605505	OP874695	China	[27]
P. ericina	HHB-2288	KP135167	KP135247	USA	[22]
P. ericina	He 4285	MT235666	MT248146	China	[76]
P. fusca	TNM:Wu 1409-163	LC412099	LC412106	China	[78]
P. guangdongensis	Wu 1809-348	MZ422813	MZ637199	China	[25]
P. guangdongensis	Wu 1809-319	MZ422811	MZ637197	China	[25]
P. hainanensis	He 3562	MT235692	MT248179	China	[24]
P. incarnata	He 20120728-1	MT235669	MT248149	China	[76]
P. incarnata	WEI 16-075	MF399406	MF399397	China	[75]
P. krikophora	HHB-5796	KP135164	KP135268	USA	[22]
P. laevis	He 20120917-8	MT235670	MT248150	China	[76]
P. laevis	HHB-15519	KP135149	KP135249	USA	[22]
P. leptocystidiata	He 5853	MT235685	MT248168	China	[76]
P. leptocystidiata	Dai 10468	MT235684	MT248167	China	[76]
P. livescens	He 5010	MT235671	MT248151	China	[76]
P. metuloidea	He 2766	MT235682	MT248164	China	[76]

Table 2. *Cont.*

Species Name	Specimen No.	GenBank Accession No.		Country	References
		ITS	nLSU		
P. minor	He 3988	MT235686	MT248170	China	[76]
P. parmastoi	He 4570	MT235673	MT248153	China	[76]
P. porostereoides	He1902	KX212217	KX212221	China	[42]
P. pruinosa	CLZhao 7112	MZ435346	MZ435350	China	[64]
P. pruinosa	CLZhao 7113	MZ435347	MZ435351	China	[64]
P. pseudomagnoliae	PP25	KP135091	KP135250	South Africa	[22]
P. pseudosanguinea	FD-244	KP135098	KP135251	USA	[22]
P. queletii	FP-102166-Sp	KP134995		USA	[22]
P. queletii	HHB-11463	KP134994	KP135235	USA	[22]
P. rhizomaurantiata	CLZhao 10470	MZ435348	MZ435352	China	[64]
P. rhizomaurantiata	CLZhao 10477	MZ435349	MZ435353	China	[64]
P. rhizomorpha	GC 1708-335	MZ422824	MZ637208	China	[24]
P. rhizomorpha	GC 1708-354	MZ422825	MZ637209	China	[25]
P. rhodella	FD-18	KP135187	KP135258	USA	[22]
P. robusta	Wu 1109-69	MF399409	MF399400	China	[78]
P. robusta	MG265	KP127068	KP127069	China	[23]
P. sanguineocarnosa	FD-359	KP135122	KP135245	USA	[22]
P. sinensis	He 4660	MT235688	MT248175	China	[76]
P. sinensis	GC 1809-56	MT235689	MT248176	China	[76]
P. singularis	He1873	KX212220	KX212224	China	[78]
P. spadicea	Wu 0504-15	MZ422837	MZ637219	China	[25]
P. spadicea	Wu 0504-11	MZ422836		China	[25]
P. stereoides	He 5824	MT235677	MT248158	Sri Lanka	[76]
P. stereoides	He2309	KX212219	KX212223	China	[42]
P. subcarnosa	Wu 9310-3	MZ422841	GQ470642	China	[21]
P. subcarnosa	GC 1809-90	MZ422840	MZ637222	China	[25]
P. subrosea	He 2421	MT235687	MT248174	China	[76]
P. subtropica	CLZhao F8716	OP605486	OQ195089	China	[27]
P. subtropica	CLZhao F2763	OP605518	OQ195090	China	[27]
P. subtropica	CLZhao F8716	OP605486	OQ195089	China	[27]
P. subtuberculata	CLZhao F5130	OP605484	OQ195088	China	[27]
P. subtuberculata	CLZhao F6838	OP605485	OQ195087	China	[27]
P. subtuberculata	CLZhao F6838	OP605485	OQ195087	China	[27]
P. taiwaniana	He 5269	MT235680	MT248161	Vietnam	[76]
P. taiwaniana	Wu 0112-13	MF399412	MF399403	China	[75]
P. tongbiguanensis	**CLZhao 30606 ***	**OR917875**	**OR921222**	**China**	**Present study**
P. tongbiguanensis	**CLZhao 30628**	**OR917876**		**China**	**Present study**
P. velutina	He 3079	MT235681	MT248162	China	[76]
P. velutina	H:7022032 Kotiranta 25567	KP994354	KP994387	Russia	[77]
P. yunnanensis	He 2719	MT235683	MT248166	China	[76]
Phanerodontia magnoliae	He 3321	MT235672	MT248152	China	[76]
Phlebiopsis albescens	He 5805	MT452526		China	[35]
P. amethystea	CL161	MK993644	MK993638	Brazil	[79]
P. amethystea	URM84741	MK993645	MK993639	China	[66]
P. brunnea	He 5822	MT452527	MT447451	China	[35]
P. brunneocystidiata	Chen 666	MT561707	GQ470640	China	[21]
P. castanea	Viacheslav Spirin 5295 (H)	KX752610	KX752610	Russia	[80]
P. crassa	He 3349	MT561712	MT447407	China	[35]
P. crassa	KKN-86	KP135394	KP135215	USA	[22]
P. cylindrospora	He5932	MT386403	MT447444	China	[35]
P. cylindrospora	He5984	MT386404	MT447445	China	[35]
P. lamprocystidiata	He5910	MT386383	MT386383	China	[35]
P. lamprocystidiata	He3874	MT386382	MT447418	China	[35]
P. fissurata	**CLZhao 30247**	**OR917878**	**OR921226**	**China**	**Present study**
P. fissurata	**CLZhao 30147 ***	**OR917877**	**OR921223**	**China**	**Present study**

Table 2. *Cont.*

Species Name	Specimen No.	GenBank Accession No.		Country	References
		ITS	nLSU		
P. flavidoalba	Otto Miettinen 17896 (H)	KX752607	KX752607	USA	[80]
P. flavidoalba	HHB-4617	KP135401	KP135401	USA	[22]
P. flavidoalba	FD-263	KP135402	KP135271	USA	[22]
P. friesii	He 5722	MT452528	MT447413	Sri Lanka	[35]
P. friesii	He 5817	MT452529	MT447414	Sri Lanka	[35]
P. gigantea	CBS:935.70	MH860011	MH871798	Germany	[70]
P. gigantea	FP-70857-Sp	KP135390	KP135272	USA	[22]
P. lacerata	SWFC00003692	MT180946	MT180950	China	Unpublished
P. lacerata	SWFC00003705	MT180947	MT180951	China	Unpublished
P. laxa	Wu 9311_17	MT561710	GQ470649	China	[21]
P. membranacea	He3842	MT386400		China	[35]
P. membranacea	He3849	MT386401		China	[35]
P. pilatii	He5114	MT386385		China	[35]
P. pilatii	Viacheslav Spirin 5048 (H)	KX752590	KX752590	Russia	[80]
P. sinensis	He4295	MT386395		China	[35]
P. sinensis	He4665	MT386396		China	[35]
P. yunnanensis	CLZhao 3958	MH744140	MH744142	China	[81]
P. yunnanensis	CLZhao 3990	MH744141	MH744143	China	[81]
Rhizochaete belizensis	FP-150712	KP135408	KP135280	Belize	[22]
R. flava	CFMR:PR-1141	KY273030	KY273033	Puerto Rico	[82]
R. fouquieriae	KKN121sp	KY948786	KY948858	USA	[57]
R. radicata	FD-123	KP135407	KP135279	USA	[22]
R. sulphurosa	URM87190	KT003522	KT003519	Brazil	[83]
Scytinostroma alutum	CBS:766.81	MH861486	MH873225	France	[70]
S. alutum	CBS 763.81	MH861483	MH873222	France	[70]
S. duriusculum	CBS 757.81	MH861477	MH873216	France	[70]
S. duriusculum	CBS:758.81	MH861478	MH873217	France	[70]
S. ochroleucum	TAA159869	AF506468	AF506468	Sweden	[41]
S. portentosum	EL11-99	AF506470	AF506470	Sweden	[41]
Terana caerulea	FP-104073	KP134980	KP135276	USA	[22]
T. caerulea	T-616	KP135276		USA	[22]
Vararia abortiphysa	CBS:632.81	MH861387	MH861387	Gabon	[70]
V. ambigua	CBS 634.81	MH861388	MH873137	France	[70]
V. amphithallica	CBS:687.81	MH861431	MH861431	France	[70]
V. aurantiaca	CBS:642.81	MH861394	MH861394	Gabon	[70]
V. aurantiaca	CBS:641.81	MH861393	MH861393	France	[70]
V. breviphysa	CBS:644.81	MH861396	MH861396	Gabon	[70]
V. calami	CBS:646.81	MH861398	MH861398	France	[70]
V. calami	CBS:648.81	MH861399	MH861399	France	[70]
V. callichroa	CBS:744.91	MH874000	MH874000	France	[70]
V. cinnamomea	CBS:642.84	MH873488	MH873488	Madagascar	[70]
V. cinnamomea	CBS:641.84	MH861794	MH861794	Madagascar	[70]
V. cremea	CBS:651.81	MH873147	MH873147	France	[70]
V. daweishanensis	CLZhao 17911	OP380613	OP615103	China	[43]
V. daweishanensis	CLZhao 17936	OP380614	OP380688	China	[43]
V. dussii	CBS:655.81	MH861405	MH861405	France	[70]
V. dussii	CBS:652.81	MH873148	MH873148	France	[70]
V. ellipsospora	HHB-19503	MW740328	MW740328	New Zealand	[43]
V. fragilis	CLZhao 2628	OP380611		China	[43]
V. fragilis	CLZhao 16475	OP380612	OP380687	China	[43]
V. fusispora	PDD:119539	OL709443	OL709443	New Zealand	[43]
V. gallica	CBS 234.91	MH862250	MH873932	Canada	[70]
V. gallica	CBS 656.81	MH861406	MH873152	France	[70]
V. gillesii	CBS:660.81	MH873153	MH873153	Cote d'Ivoire	[70]
V. gomezii	CBS:661.81	MH873154	MH873154	France	[70]

Table 2. *Cont.*

Species Name	Specimen No.	GenBank Accession No.		Country	References
		ITS	nLSU		
V. gracilispora	CBS:664.81	MH861412	MH861412	Gabon	[70]
V. gracilispora	CBS:663.81	MH861411		Gabon	[70]
V. insolita	CBS:668.81	MH861413	MH861413	France	[70]
V. intricata	CBS:673.81	MH861418	MH861418	France	[70]
V. investiens	FP-151122ITS	MH971976	MH971977	USA	[72]
V. malaysiana	CBS:644.84	MH873490	MH873490	Singapore	[70]
V. minispora	CBS:682.81	MH861426	MH861426	France	[70]
V. ochroleuca	CBS:465.61	MH858109	MH858109	France	[70]
V. ochroleuca	JS24400	AF506485	AF506485	Norway	[41]
V. parmastoi	CBS:879.84	MH861852	MH861852	Uzbekistan	[70]
V. pectinata	CBS:685.81	MH861429		Cote d'Ivoire	[70]
V. perplexa	CBS:695.81	MH861438	MH861438	France	[70]
V. pirispora	CBS:720.86	MH862016	MH862016	France	[70]
V. rhombospora	CBS:743.81	MH861470	MH861470	France	[70]
V. rosulenta	CBS:743.86	MH862028		France	[70]
V. rugosispora	CBS:697.81	MH861440	MH861440	Gabon	[70]
V. sigmatospora	CBS:748.91	MH874001	MH874001	Netherlands	[70]
V. sphaericospora	CBS:700.81	MH873185	MH873185	Gabon	[70]
V. sphaericospora	CBS:703.81	MH861446	MH861446	Gabon	[70]
V. trinidadensis	CBS:651.84	MH861803	MH861803	Madagascar	[70]
V. trinidadensis	CBS:650.84	MH873495	MH873495	Madagascar	[70]
V. tropica	CBS 704.81	MH861447	MH873189	France	[70]
V. vassilievae	UC2022892	KP814203	KP814203	USA	Unpublished
V. verrucosa	CBS:706.81	MH861449	MH861449	France	[70]
V. yingjiangensis	**CLZhao 30284 ***	**OR917879**	**OR921225**	**China**	**Present study**
V. yingjiangensis	**CLZhao 30392**	**OR917880**	**OR921224**	**China**	**Present study**

* Is shown in holotype.

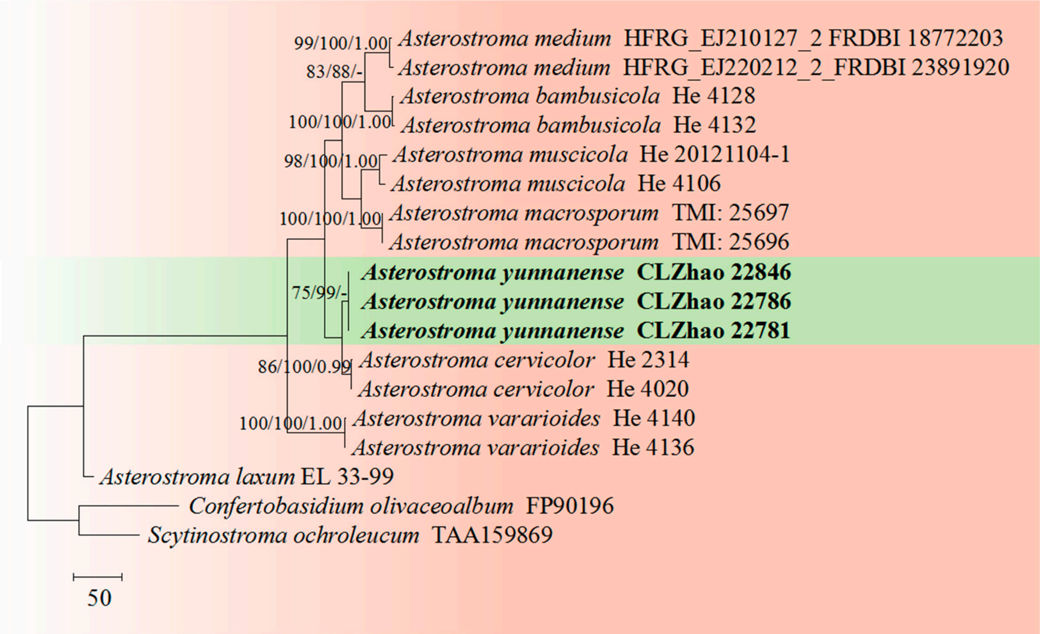

Figure 3. Maximum parsimony is a strict consensus tree illustrating the phylogeny of the new species and related species in the genus *Asterostroma* based on ITS sequences.

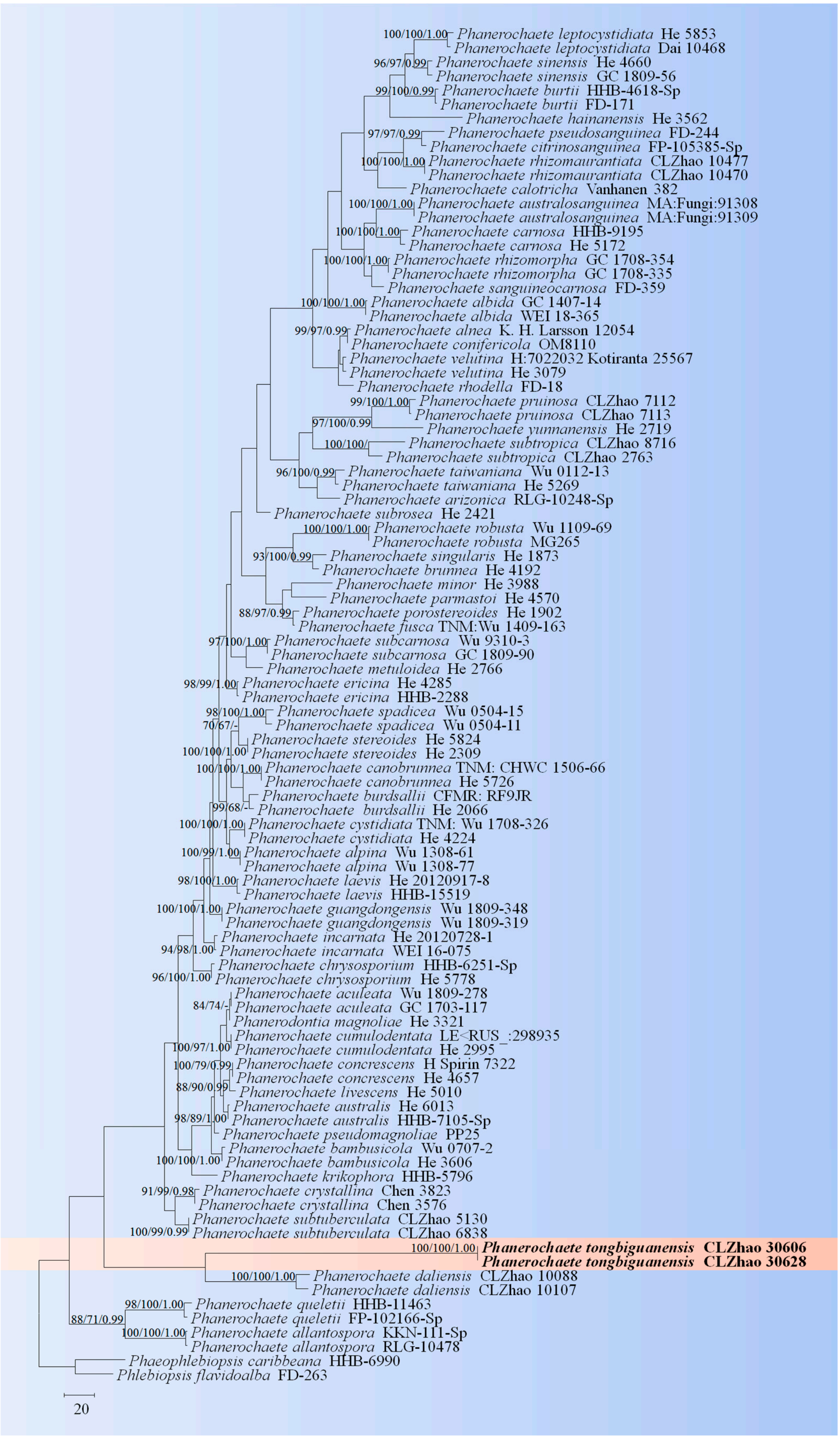

Figure 4. Maximum parsimony is a strict consensus tree illustrating the phylogeny of the new species and related species in the genus *Phanerochaete* based on ITS sequences.

Figure 5. Maximum parsimony is a strict consensus tree illustrating the phylogeny of the new species and related species in the genus *Phlebiopsis* based on ITS sequences.

The best-fit evolution model for each dataset for BI (Bayesian inference) was determined by using MrModeltest 2.3 [84]. BI was calculated with MrBayes3.1.2 with a general time reversible (GTR + I + G) model of DNA substitution and a gamma distribution rate variation rate variation across sites [85]. A total of four Markov chains were run for two runs from random starting trees for 2 million and 0.5 million generations for ITS + nLSU (Figures 1 and 2), respectively, and based on ITS for 5 million generations (Figure 3), 0.5 million generations (Figure 4), for 0.5 million generations (Figure 5), and 0.2 million generations (Figure 6), with trees and parameters sampled every 1000 generations.

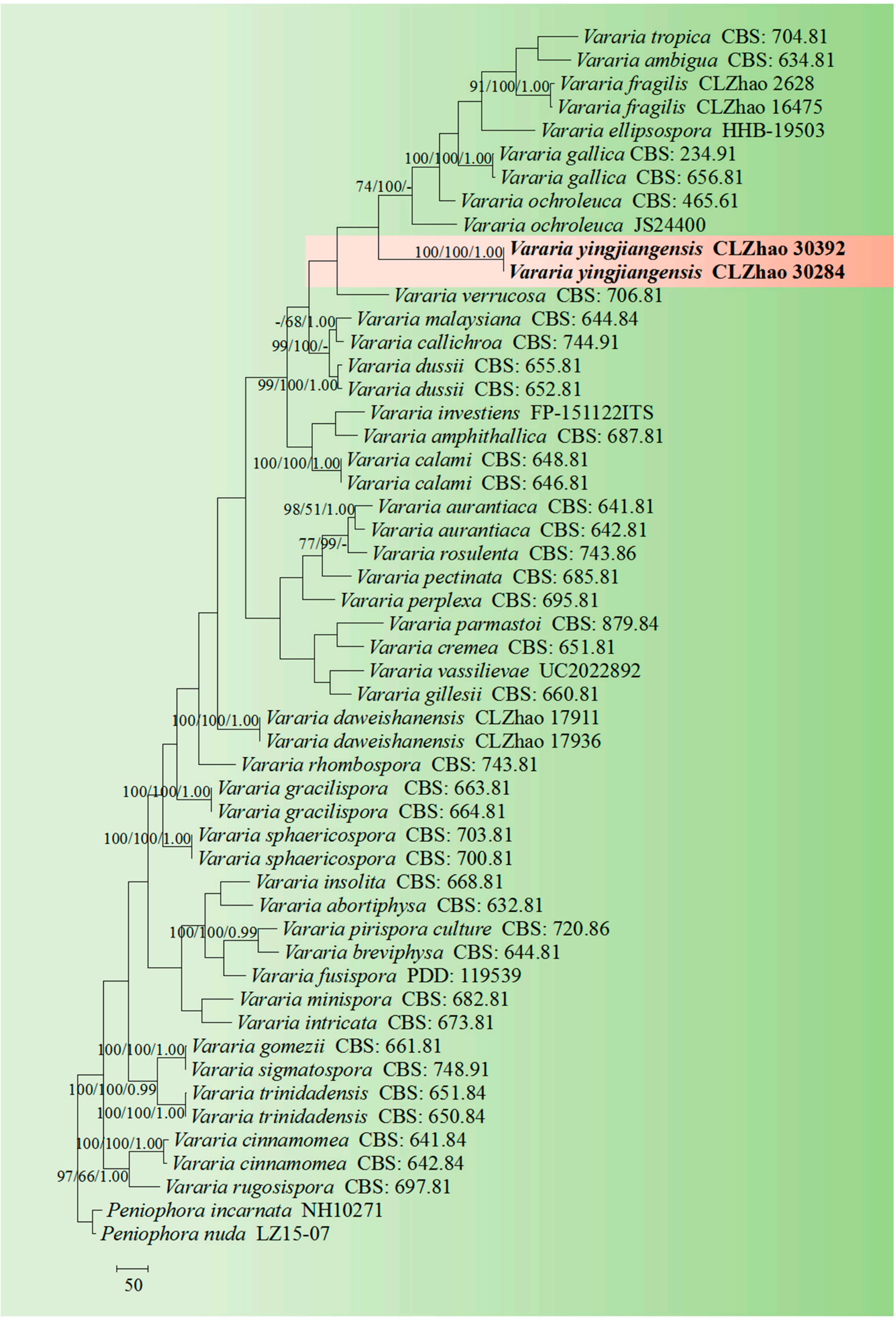

Figure 6. Maximum parsimony is a strict consensus tree illustrating the phylogeny of the new species and related species in the genus *Vararia* based on ITS sequences.

3. Results

3.1. Molecular Phylogeny

The ITS + nLSU dataset (Figure 1) included sequences from 32 fungal specimens representing 29 species. The dataset had an aligned length of 2550 characters, of which 1682 characters are constant, 424 are variable and parsimony-uninformative, and 444 are parsimony-informative. Maximum parsimony analysis yielded one equally parsimonious tree (TL = 2330, CI = 0.5408, HI = 0.4592, RI = 0.4861, RC = 0.2629). The best model for the ITS + nLSU dataset estimated and applied in the Bayesian analysis was GTR + I + G (lset nst = 6, rates = invgamma; prset statefreqpr = dirichlet (1,1,1,1). Bayesian analysis and ML analysis resulted in a similar topology to MP analysis with an average standard deviation of split frequencies = 0.008198 (BI), and the effective sample size (ESS) across the two runs is the double of the average ESS (avg ESS) = 1887. The phylogeny (Figure 1) based on the combined nLSU sequences includes six genera within the family Peniophoraceae: *Bjerkandera*, *Phaeophlebiopsis*, *Phanerochaete*, *Phlebiopsis*, *Rhizochaete* Gresl. and Nakasone & Rajchenb. and *Terana* Adans. Our current two new species were clustered into genera *Phanerochaete* and *Phlebiopsis*.

The ITS + nLSU dataset (Figure 2) included sequences from 37 fungal specimens representing 25 species. The dataset had an aligned length of 2573 characters, of which 1433 characters are constant, 383 are variable and parsimony-uninformative, and 757 are parsimony-informative. Maximum parsimony analysis yielded one equally parsimonious tree (TL = 3484, CI = 0.5347, HI = 0.4653, RI = 0.6921, RC = 0.3701). The best model for the ITS + nLSU dataset estimated and applied in the Bayesian analysis was GTR + I + G (lset nst = 6, rates = invgamma; prset statefreqpr = dirichlet (1,1,1,1). Bayesian analysis and ML analysis resulted in a similar topology to MP analysis with an average standard deviation of split frequencies = 0.005232 (BI), and the effective sample size (ESS) across the two runs is the double of the average ESS (avg ESS) = 304. The phylogeny (Figure 2) based on the combined ITS + nLSU sequences includes eight genera within the family Peniophoraceae: *Asterostroma*, *Baltazaria* Leal-Dutra, Dentinger & G.W. Griff., *Dichostereum* Pilát, *Lachnocladium*, *Michenera* Berk. & M.A. Curtis, *Peniophora*, *Scytinostroma*, and *Vararia*. Our current two new species were clustered into genera *Asterostroma* and *Vararia*.

The ITS dataset of the genus *Asterostroma* (Figure 3) included sequences from 18 fungal specimens representing 10 species. The dataset had an aligned length of 1560 characters, of which 983 characters are constant, 246 are variable and parsimony-uninformative, and 331 are parsimony-informative. Maximum parsimony analysis yielded one equally parsimonious tree (TL = 814, CI = 0.8710, HI = 0.1290, RI = 0.8930, RC = 0.7778). The best model for the ITS dataset estimated and applied in the Bayesian analysis was GTR + I + G (lset nst = 6, rates = invgamma; prset statefreqpr = dirichlet (1,1,1,1). Bayesian analysis and ML analysis resulted in a similar topology to MP analysis with an average standard deviation of split frequencies = 0.009408 (BI). The phylogenetic tree indicated that *A. yunnanense* was grouped with the close taxa *A. cervicolor* (Berk. & M.A. Curtis) Massee.

The ITS dataset of the genus *Phanerochaete* (Figure 4) included sequences from 96 fungal specimens representing 60 species. The dataset had an aligned length of 880 characters, of which 319 characters are constant, 77 are variable and parsimony-uninformative, and 484 are parsimony-informative. Maximum parsimony analysis yielded one equally parsimonious tree (TL = 2187, CI = 0.4015, HI = 0.5985, RI = 0.6231, RC = 0.2501). The best model for the ITS dataset estimated and applied in the Bayesian analysis was GTR + I + G (lset nst = 6, rates = invgamma; prset statefreqpr = dirichlet (1,1,1,1). Bayesian analysis and ML analysis resulted in a similar topology to MP analysis with an average standard deviation of split frequencies = 0.001737 (BI). The phylogenetic tree indicated that *P. tongbiguanensis* was grouped with the close taxa *P. daliensis* J. Yu & C.L. Zhao.

The ITS dataset of the genus *Phlebiopsis* (Figure 5) included sequences from 33 fungal specimens representing 20 species. The dataset had an aligned length of 665 characters, of which 392 characters are constant, 82 are variable and parsimony-uninformative, and 191 are parsimony-informative. Maximum parsimony analysis yielded six equally parsimonious trees (TL = 685, CI = 0.5650, HI = 0.4350, RI = 0.6543, RC = 0.3697). The best model for the ITS dataset estimated and applied in the Bayesian analysis was GTR + I + G (lset nst = 6, rates = invgamma; prset statefreqpr = dirichlet (1,1,1,1). Bayesian analysis and ML analysis resulted in a similar topology to MP analysis with an average standard deviation of split frequencies = 0.003384 (BI). The phylogenetic tree indicated that *P. fissurata* was grouped with the close taxa *P. lamprocystidiata* (Sheng H. Wu) Sheng H. Wu & Hallenb.

The ITS dataset of the genus *Vararia* (Figure 6) included sequences from 52 fungal specimens representing 40 species. The dataset had an aligned length of 796 characters, of which 148 characters were constant, 116 were variable and parsimony-uninformative, and 532 were parsimony-informative. Maximum parsimony analysis yielded one equally parsimonious tree (TL = 4063, CI = 0.3104, HI = 0.6896, RI = 0.4313, and RC = 0.1339). The best model for the ITS dataset estimated and applied in the Bayesian analysis was GTR + I + G. The Bayesian and ML analyses resulted in a similar topology to that of the MP analysis with split frequencies = 0.000442 (BI). The phylogram inferred from ITS sequences (Figure 6) revealed that *V. yingjiangensis* was grouped with six close taxa, namely *V. ambigua* Boidin, Lanq. & Gilles, *V. ellipsospora* G. Cunn., *V. fragilis* L. Zou & C.L. Zhao, *V. gallica* (Bourdot & Galzin) Boidin, *V. ochroleuca* (Bourdot & Galzin) Donk and *V. tropica* A.L. Welden.

3.2. Taxonomy

Asterostroma yunnanense Y.L. Deng & C.L. Zhao, sp. nov. Figures 7 and 8.

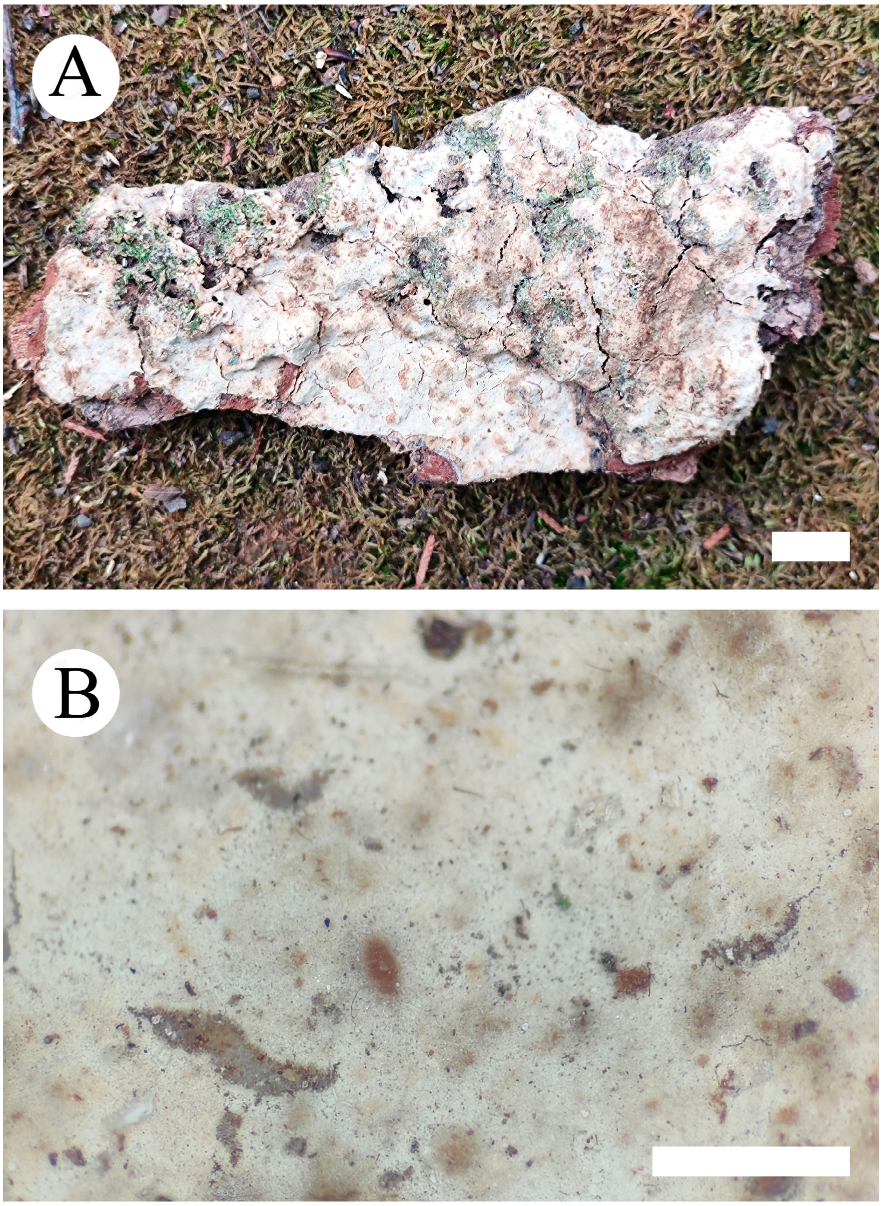

Figure 7. Basidiomata of *Asterostroma yunnanense* (holotype): the front of the basidiomata (**A**); characteristic hymenophore (**B**). Bars: (**A**) = 1 cm and (**B**) = 1 mm.

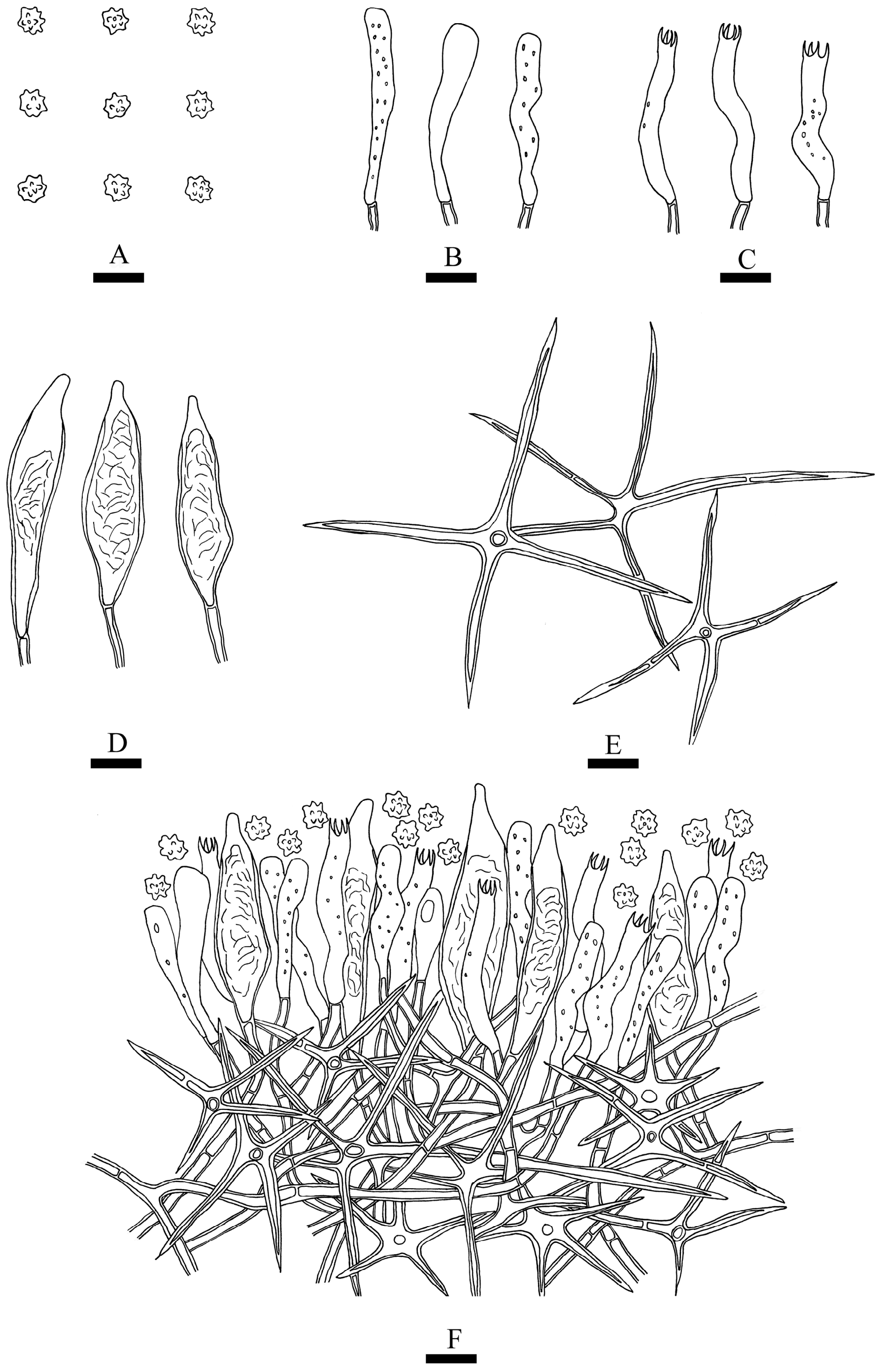

Figure 8. Microscopic structures of *Asterostroma yunnanense* (holotype): basidiospores (**A**), basidioles (**B**), basidia (**C**), gloeocystidia (**D**), asterosetae from subiculum (**E**), and a section of hymenium (**F**). Bars: (**A**–**F**) = 10 µm.

MycoBank no.: 851416

Holotype—China, Yunnan province, Lincang, Fengqing County, Yaojie Town, Xingyuan Village, 24°58′ N, 99°92′ E, altitude 1660 m asl., on the fallen branch of angiosperm, leg. C.L. Zhao, 20 July 2022, CLZhao 22781 (SWFC).

Etymology—*Yunnanense* (Lat.): referring to the locality (Yunnan province) of the type specimen.

Fruiting body—Basidiomata annual, resupinate, membranaceous to pellicular, soft, without odor and taste when fresh, up to 110 mm long, 60 mm wide, and 280 µm thick. Hymenial surface smooth, cream when fresh, cream to salmon-buff, sometimes cracked when dried. Sterile margin thinning out, becoming indistinct and concolorous with hymenophore surface, up to 1 mm.

Hyphal system—Dimitic, generative hyphae bearing simple-septa, scattered, thick-walled, colorless, 2–4 µm in diameter, IKI-, CB-, tissues unchanged in KOH. Asterosetae in subiculum are abundant, predominant, yellowish brown, thick-walled, 2–4 µm in diameter, regularly star-shaped, weakly dextrinoid, rays up to 60 µm long, with acute tips, CB-, tissues unchanged in KOH.

Hymenium—Gloeocystidia subulate, thick-walled, with a basal simple septum, 34.5–54 × 7–10 µm. Basidia cylindrical, colorless, with four sterigmata and a basal simple-septum, 31–38 × 4–5 µm.

Basidiospores—Globose, colorless, thin-walled, echinulate, amyloid, 4.5–6 × 4–5 µm, L = 5.11 µm, W = 4.33 µm, Q = 1.07–1.18 (n = 60/2).

Additional specimens examined (paratypes)—China, Yunnan province, Lincang, Fengqing County, Yaojie Town, Xingyuan Village, 24°58′ N, 99°92′ E, altitude 1660 m asl., on the trunk of angiosperm, leg. C.L. Zhao, 20 July 2022, CLZhao 22786 (SWFC); on the fallen branch of angiosperm, leg. C.L. Zhao, 20 July 2022, CLZhao 22846 (SWFC).

Phanerochaete tongbiguanensis Y.L. Deng & C.L. Zhao sp. nov. Figures 9 and 10.

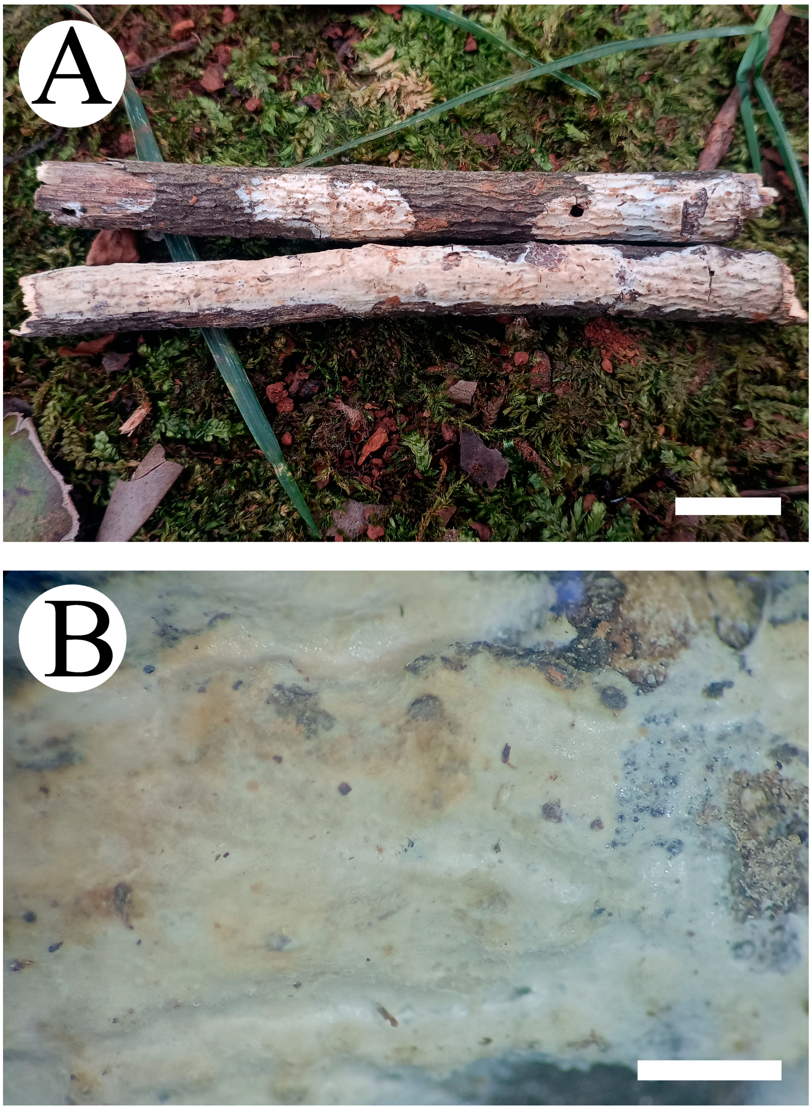

Figure 9. Basidiomata of *Phanerochaete tongbiguanensis* (holotype): the front of the basidiomata (**A**); characteristic hymenophore (**B**). Bars: (**A**) = 1 cm and (**B**) = 1 mm.

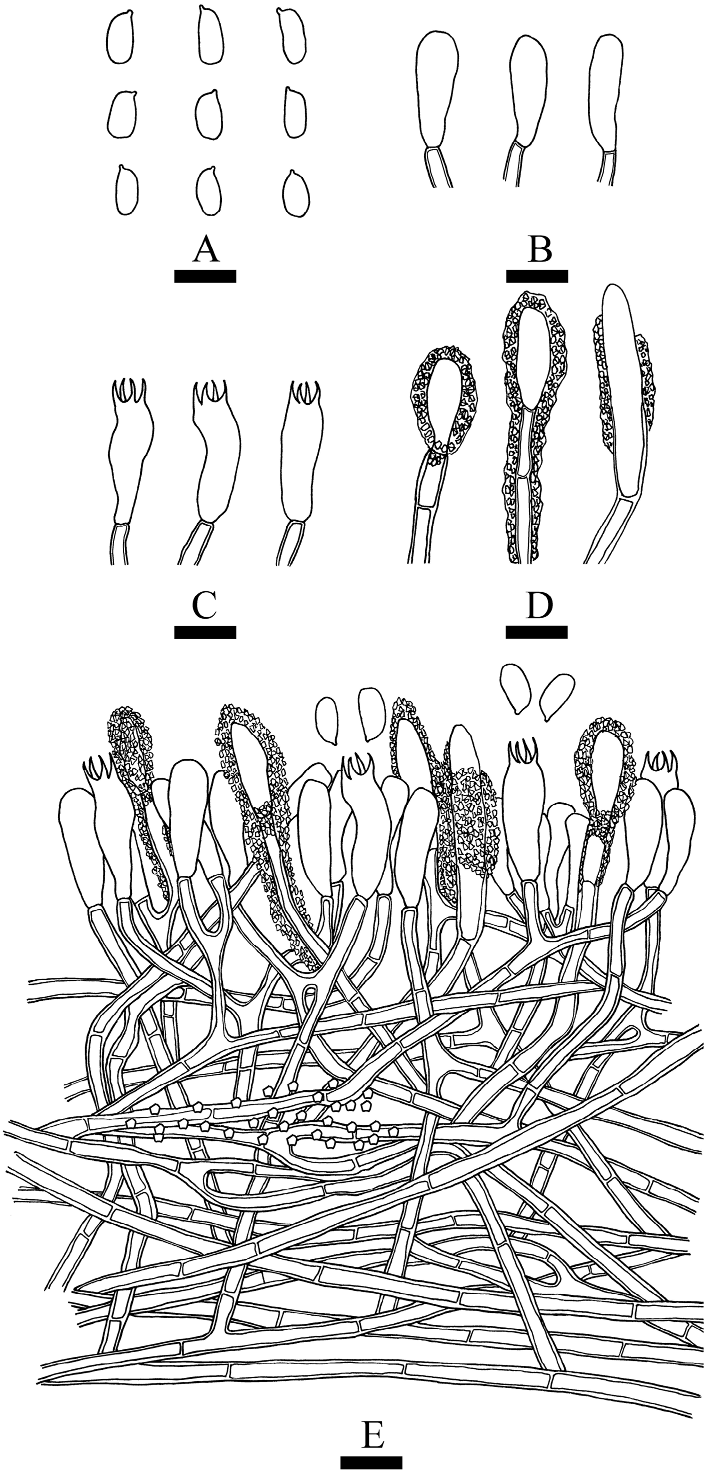

Figure 10. Microscopic structures of *Phanerochaete tongbiguanensis* (holotype): basidiospores (**A**), basidioles (**B**), basidia (**C**), cystidia (**D**), and A section of hymenium (**E**). Bars: (**A**–**E**) = 10 µm.

MycoBank no.: 851417

Holotype—China, Yunnan province, Dehong, Yingjiang County, Tongbiguan Provincial Nature Reserve, 24°71′ N, 97°94′ E, altitude 2000 m asl., on the fallen branch of angiosperm, 20 July 2023, CLZhao 30606 (SWFC).

Etymology—***Tongbiguanensis*** (Lat.): referring to the locality (Tongbiguan) of the type specimen.

Fruiting body—Basidiomata annual, resupinate, thin, adnate, leather, without odor and taste when fresh, up to 70 mm long, 10 mm wide, 70–130 µm thick. Hymenial surfaces are smooth, white to cream when fresh, to cream to slightly buff upon drying. Sterile margins are distinct, whitish, and up to 1 mm.

Hyphal system—Monomitic, generative hyphae bearing simple-septa, thick-walled, 3–4 µm in diameter, branched, colorless, IKI-, CB-; tissues unchanged in KOH; subhymenial hyphae densely covered by crystals.

Hymenium—Cystidia subclavate, colorless, covered with a lot of crystals, thick-walled, 32–41 × 6.5–11 µm. Basidia subclavate to cylindrical, with four sterigmata and a basal simple septum, 17–26 × 6–7 µm.

Basidiospores—Oblong ellipsoid, colorless, thin-walled, smooth, IKI-, CB-, 6–9 × 3–4.5 µm, L = 7.48 µm, W = 4.02 µm, Q = 1.84–1.88 (n = 60/2).

Additional specimen examined (paratype)—China, Yunnan province, Dehong, Yingjiang County, Tongbiguan Provincial Nature Reserve, 24°71′ N, 97°94′ E, altitude 2000 m asl., on the fallen branch of angiosperm, 20 July 2023, CLZhao 30628 (SWFC).

Phlebiopsis fissurata Y.L. Deng & C.L. Zhao sp. nov. Figures 11 and 12.

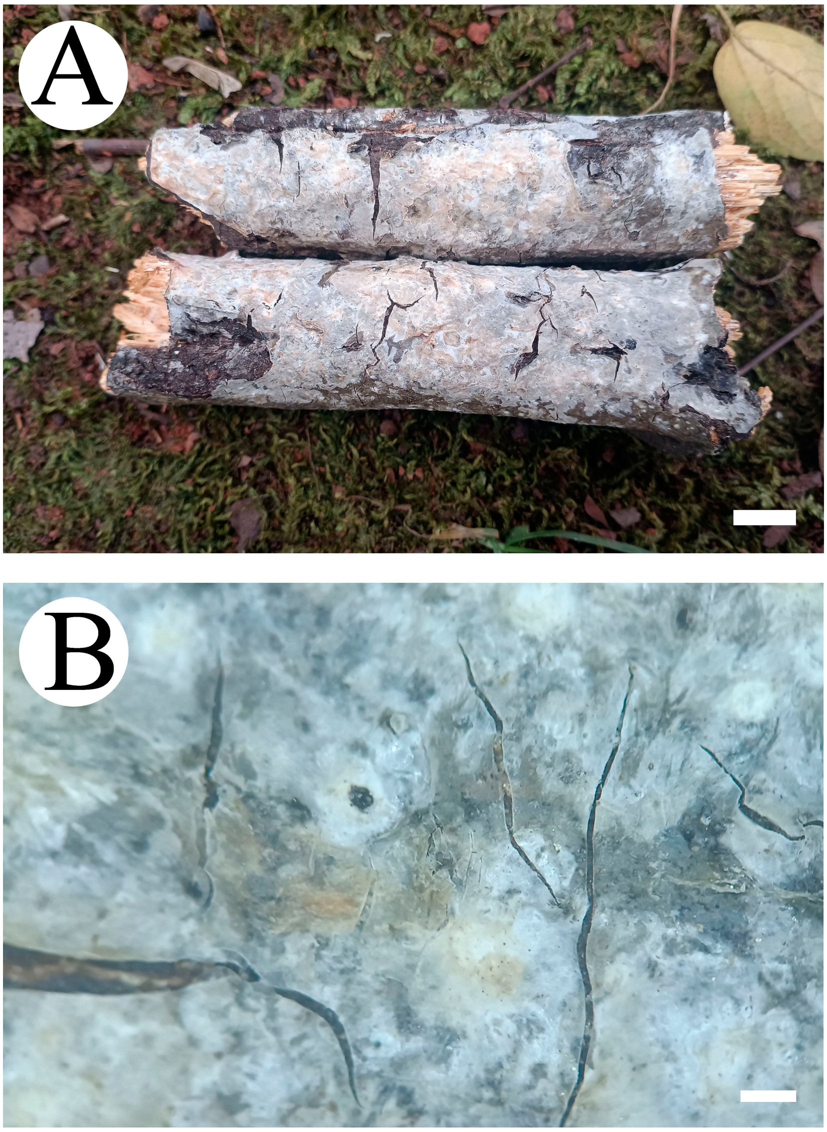

Figure 11. Basidiomata of *Phlebiopsis fissurata* (holotype): the front of the basidiomata (**A**); characteristic hymenophore (**B**). Bars: (**A**) = 1 cm and (**B**) = 1 mm.

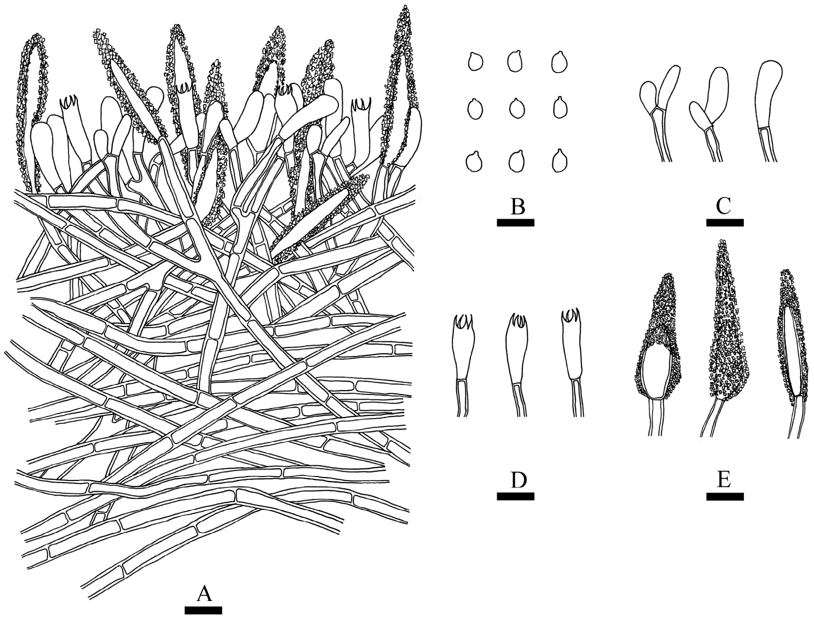

Figure 12. Microscopic structures of *Phlebiopsis fissurata* (holotype): a section of hymenium (**A**), basidiospores (**B**), basidioles (**C**), basidia (**D**), and cystidia (**E**). Bars: (**A**–**E**) = 10 µm.

MycoBank: 851421

Holotype—China, Yunnan province, Dehong, Yingjiang County, Tongbiguan Provincial Nature Reserve, 24°71′ N, 97°94′ E, altitude 2000 m asl., on the fallen branch of angiosperm, 19 July 2023, CLZhao 30147 (SWFC).

Etymology—Referring to the cracking hymenial surface.

Fruiting body—Basidiomata annual, resupinate, adnate, membranaceous, without odor and taste when fresh, up to 100 mm long, 70 mm wide, 100–210 µm thick. Hymenial surface tuberculate, white when fresh, white to buff to slightly brown upon drying, sometimes sparsely and deeply cracked with age. Sterile margins are distinct, white, and up to 2 mm.

Hyphal system—Monomitic, generative hyphae bearing simple-septa, colorless, thick-walled, branched, interwoven, 4–5 µm in diameter, IKI-, CB-; tissues unchanged in KOH.

Hymenium—Cystidia conical, colorless, covered with a lot of crystals, thick-walled, 27–48 × 6–11 µm. Basidia clavate, with four sterigmata and a basal simple septum, 16–26 × 5–7 µm.

Basidiospores—Broadly ellipsoid, thin-walled, colorless, smooth, IKI-, CB-, 4–6.5 × 3–4 µm, L = 5.03 µm, W = 3.59 µm, Q = 1.33–1.47 (n = 60/2).

Additional specimen examined (paratype)—China, Yunnan province, Dehong, Yingjiang County, Tongbiguan Provincial Nature Reserve, 24°71′ N, 97°94′ E, altitude 2000 m asl., on the fallen branch of angiosperm, 19 July 2023, CLZhao 30247 (SWFC).

Vararia yingjiangensis Y.L. Deng & C.L. Zhao sp. nov. Figures 13 and 14.

MycoBank no.: 851424

Holotype—China, Yunnan province, Dehong, Yingjiang County, Tongbiguan Provincial Nature Reserve, 24°71′ N, 94°52′ E, altitude 1500 m asl., on fallen branch of angiosperm, 19 July 2023, CLZhao 30284 (SWFC).

Etymology—***Yingjiangensis*** (Lat.): referring to the locality (Yingjiang) of the type specimen.

Fruiting body—Basidiomata annual, adnate, corky, without odor and taste when fresh, up to 80 mm long, 40 mm wide, 80–120 µm thick. Hymenial surface smooth, cream to pinkish buff when fresh, pinkish buff to cinnamon-buff when dry, cracking with age. Sterile margin thin, indistinct, slightly cream to pinkish buff, up to 2 mm.

Hyphal system—Dimitic, generative hyphae bearing simple-septa, colorless, thin- to thick-walled, occasionally branched, interwoven, 3–4 µm in diameter, IKI-, CB-, tissues unchanged in KOH. Dichohyphae yellowish, capillary, distinctly thick-walled, up to 1.4 µm in diameter and with acute tips, moderately dextrinoid in Melzer's reagent; more frequently branched.

Hymenium—Gloeocystidia two types, (i) Gloeocystidia subulate, usually with a constriction at the tip, colorless, obviously thick-walled, smooth, 25–42.5 × 5–11 µm; (ii) Gloeocystidia subulate, usually with two constrictions at the tip, colorless, obviously thick-walled, smooth, 28–35 × 6–10 µm. Basidia rare; basidioles cylindrical, dominant, thin-walled, 13–26 × 4.5–10 µm.

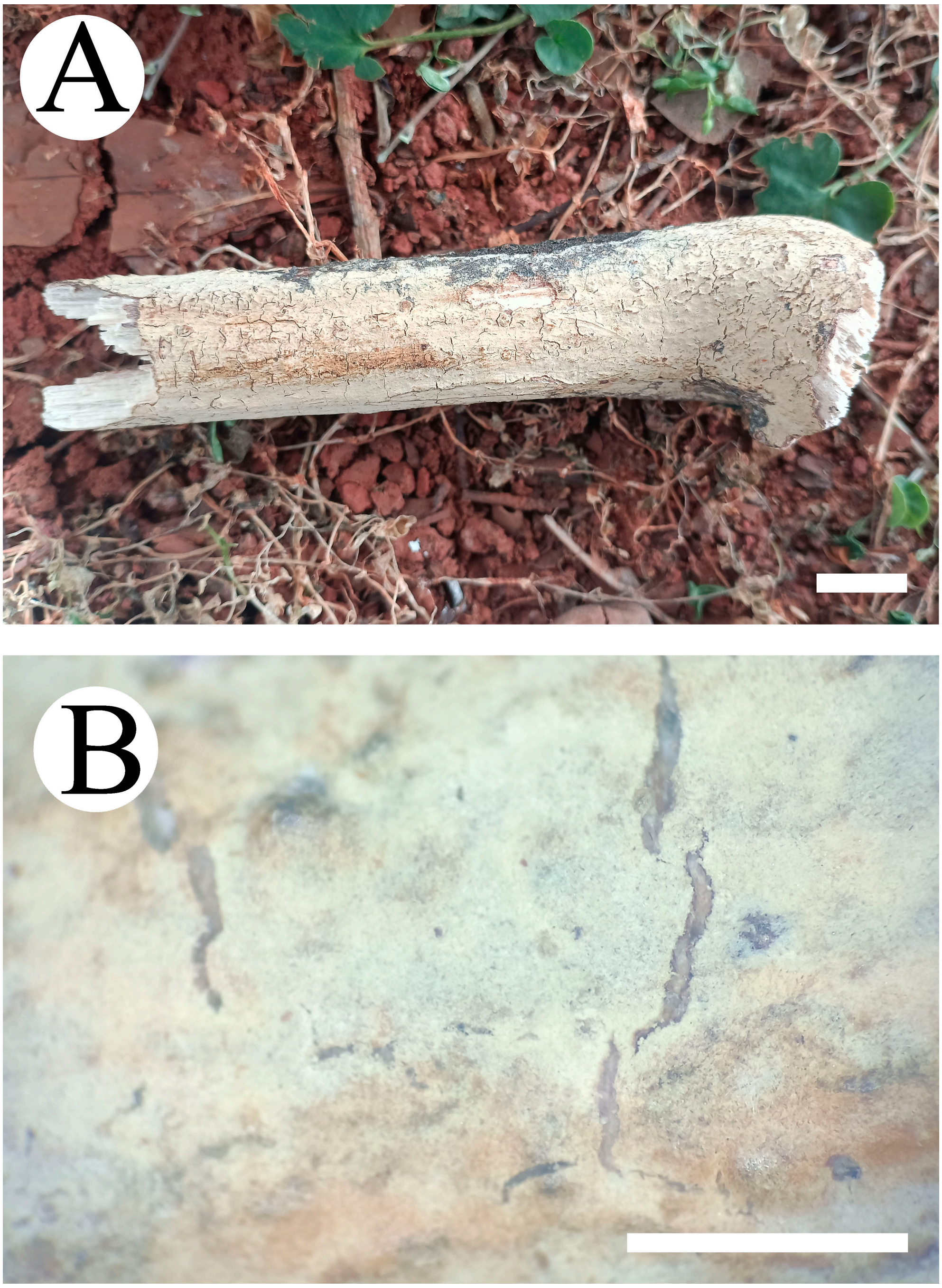

Figure 13. Basidiomata of *Vararia yingjiangensis* (holotype): the front of the basidiomata (**A**); characteristic hymenophore (**B**). Bars: (**A**) = 1 cm and (**B**) = 1 mm.

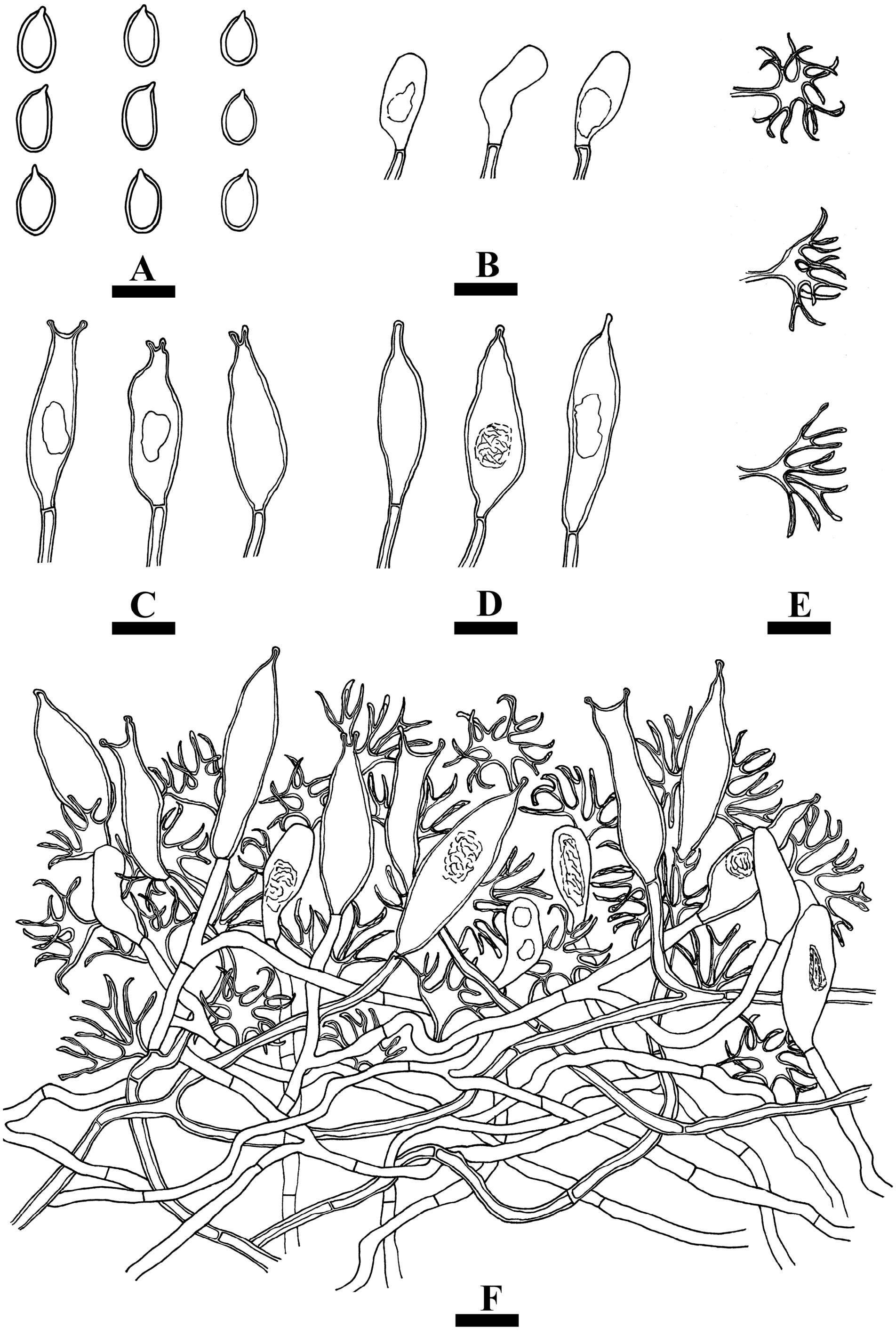

Figure 14. Microscopic structures of *Vararia yingjiangensis* (holotype): basidiospores (**A**), basidioles (**B**), gloeocystidia (**C**,**D**), dichohyphae (**E**), and a section of hymenium (**F**). Bars: (**A**–**F**) = 10 µm.

Basidiospores—Ellipsoid, slightly thick-walled, colorless, smooth, amyloid, CB-, 6.5–11.5 × 5–7 µm, L = 9.34 µm, W = 6.08 µm, Q = 1.5–1.6 (n = 60/2).

Additional specimen examined (paratype)—China, Yunnan province, Dehong, Yingjiang County, Tongbiguan Provincial Nature Reserve, 24°71′ N, 97°52′ E, altitude 1500 m asl., on fallen branch of angiosperm, 19 July 2023, CLZhao 30392 (SWFC).

4. Discussion

The family-level classification for the order Polyporales (Basidiomycota) revealed that the two taxa of *Phanerochaete daliensis* and *Phlebiopsis lamprocystidiata* nested into the family Phanerochaetaceae within the residual polyporoid clade based on the molecular systematics study amplifying the ITS, nLSU, RPB1, and RPB2 genes [21,27]. Seven genera, *Asterostroma*, *Dichostereum*, *Gloiothele*, *Peniophora*, *Scytinostroma*, *Vararia*, and *Vesiculomyces* E. Hagstr., were grouped together and clustered within the family Peniophoraceae [18]. In the present study, four new species were nested into the families Phanerochaetaceae and Peniophoraceae; from the phylogram of the ITS + nLSU data, the new species *Phanerochaete tongbiguanensis* were grouped into *Phanerochaete*, and the taxon *Phlebiopsis fissurata* was grouped into genus *Phlebiopsis* (Figure 1); the new species *Asterostroma yunnanense* was grouped into *Asterostroma*, and *Vararia yingjiangensis* was clustered into *Vararia* (Figure 2).

Based on ITS topology (Figure 3), the present study revealed that the new species *Asterostroma yunnanense* was grouped with two close taxa, *A. cervicolor* and *A. vararioides* S.L. Liu & S.H. He. However, morphologically, *A. cervicolor* is distinct from *A. yunnanense* by the thin-walled marginal hyphae (2–5 µm diameter) and thin-walled aerial hyphae 1–5 µm diameter, and smaller gloeocystidia (20–30 × 7–15 µm) [86]. The species *A. vararioides* can be distinguished by its grayish brown to dark brown hymenial surface, thin-walled generative hyphae, presence of the dichohyphidia and thin-walled, longer gloeocystidia (30–60 × 5–11 µm), larger subcylindrical to fusoid basidia (30–65 × 7–11 µm), and larger, smooth basidiospores measuring 5.5–7.5 × 5–7 µm [18].

The phylogenetic tree (Figure 4) based on the ITS data showed that the new taxon *P. tongbiguanensis* was grouped with the species *P. daliensis* and *P. subtropica* J. Yu & C.L. Zhao. However, morphologically, *P. daliensis* is distinct from *P. tongbiguanensis* by its grandinioid hymenophore, ellipsoid e to cylindrical, thick-walled, smaller basidiospores (3–6 × 1.8–3 µm) [27]. The species *P. subtropica* is distinguished from *P. tongbiguanensis* by its fusiform cystidia and smaller basidia (12–21 × 3–5 µm) and ellipsoid basidiospores measuring as 3.0–4.8 × 2.4–3.4 µm [27]. Phylogenetic tree analysis (Figure 5) revealed that the new species *P. fissurata* was grouped with the species *P. lamprocystidiata* and then closely clustered with *P. yunnanensis* C.L. Zhao and *P. gigantea* (Fr.) Jülich. However, morphologically, *P. lamprocystidiata* is distinct from *P. fissurata* by its grayish yellow hymenial surface and distinct lamprocystidia [31]. The taxon *P. yunnanensis* is distinct from *P. fissurata* by having the smaller, narrowly clavate to subcylindrical basidia (10–21 × 3.5–4.5 µm) and smaller basidiospores measuring as 3.5–4.5 × 2.5–3.5 µm. Another species *P. gigantea* can be distinguished by its greyish-white to buff basidimata, larger cystidia (50–80 × 10–15 µm), and narrowly ellipsoid, smaller basidiospores (6.5–8 × 3–3.5 µm) [13].

Based on the ITS phylogenetic analysis (Figure 6), the new species *Vararia yingjiangensis* is closely grouped with six taxa, namely *V. ambigua*, *V. ellipsospora*, *V. fragilis*, *V. gallica*, *V. ochroleuca*, and *V. tropica*. However, morphologically, *V. ochroleuca* is distinct from *V. yingjiangensis* by having the slightly thick-walled gloeocystidia, thin-walled generative hyphae, and both smaller gloeocystidia (16–34 × 4.5–7.5 µm) and basidiospores measuring as 2.6–3.8 × 2–3.2 µm [87]. The taxon *V. gallica* is distinct from *V. yingjiangensis* by having the longer basidiospores measuring as 9–12 × 3.5–5 µm [24]. The species *V. ellipsospora* is distinct from *V. yingjiangensis* by having the fimbriate basidiomata, generative hyphae with clamped connection, and flexuous to cylindrical gloeocystidia [45]. *Vararia fragilis* differs from *V. yingjiangensis* by having smaller, elliptical to ovoid gloeocystidia measuring as 5.8–16 × 3.5–7 µm. The taxon *V. ambigua* differs from *V. yingjiangensis* by its thin-walled and smaller spores measuring as 3–8 × 3–5 µm. The species *V. tropica* can be distinguished by its wider, oblong basidiospores (10–12 × 7–8 µm) [88].

Based on the phylogenetic and morphological research results, more and more new wood-inhabiting fungi are being found and reported [1,43,54,55,89–92]. In the present study, four new taxa from the subtropics are described based on morphological and molecular phylogenetic analyses, which can enrich the wood-inhabiting fungal diversity in China and the world.

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editing, C.Z. and Y.D.; visualization, C.Z.; supervision, C.Z.; project administration, C.Z.; funding acquisition, C.Z. and J.Z. All authors have read and agreed to the published version of the manuscript.

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References

1. Dai, Y.C. A revised checklist of corticioid and hydnoid fungi in China for 2010. *Mycoscience* **2011**, *52*, 69–79. [CrossRef]
2. Dai, Y.C. Pathogenic wood-decaying fungi on woody plants in China. *Mycosystema* **2012**, *31*, 493–509.
3. Sun, Y.F.; Costa-Rezende, D.H.; Xing, J.H.; Zhou, J.L.; Zhang, B.; Gibertoni, T.B.; Gates, G.; Glen, M.; Dai, Y.C.; Cui, B.K. Multigene phylogeny and taxonomy of *Amauroderma* s. lat. (*Ganodermataceae*). *Persoonia* **2019**, *44*, 206–239. [CrossRef]
4. Sun, Y.F.; Xing, J.H.; He, X.L.; Wu, D.M.; Song, C.G.; Liu, S.; Vlasák, J.; Gates, G.; Gibertoni, T.B.; Cui, B.K. Species diversity, sys-tematic revision and molecular phylogeny of *Ganodermataceae* (*Polyporales*, *Basidiomycota*) with an emphasis on Chinese collections. *Stud. Mycol.* **2022**, *101*, 287–415. [CrossRef]
5. Li, Q.S.; Wei, Y.L. Species composition and distribution characteristics of wood-decaying fungi in tropical areas of China. *Mycosystema* **2021**, *40*, 2653–2672. [CrossRef]
6. Dai, Y.C.; Fan, L.F.; Chen, J.J.; Wu, C.P.; Wu, Y.D.; Yuan, Y. Diversity of *Heterobasidion* causing root and butt rotting of conifers and proposal for entry wood quarantine aiming at *Heterobasidion* species. *Mycosystema* **2021**, *40*, 1958–1964. [CrossRef]
7. Dai, Y.C.; Liu, H.G.; Wu, F.; Si, J.; Yuan, Y.; He, S.H.; Cui, B.K.; Zhou, M.; Zhao, Q. *Resources and Diversity of Wood-Decaying Fungi in Yunnan*; Science Press: Beijing, China, 2022; p. 574.
8. 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.; et al. Diversity and systematics of the important macrofungi in Chinese forests. *Mycosystema* **2021**, *40*, 770–805. [CrossRef]
9. Liu, S.; Chen, Y.Y.; Sun, Y.F.; He, X.L.; Song, C.G.; Si, J.; Liu, D.M.; Gates, G.; Cui, B.K. Systematic classification and phylogenetic relationships of the brown rot fungi within the Polyporales. *Fungal Divers.* **2023**, *118*, 1–94. [CrossRef]
10. Liu, S.; Han, M.L.; Xu, T.M.; Wang, Y.; Wu, D.M.; Cui, B.K. Taxonomy and phylogeny of the *Fomitopsis pinicola* complex with de-scriptions of six new species from East Asia. *Front. Microbiol.* **2021**, *12*, 644979. [CrossRef]
11. Yuan, Y.; Bian, L.S.; Wu, Y.D.; Chen, J.J.; Wu, F.; Liu, H.G.; Zeng, G.Y.; Dai, Y.C. Species diversity of pathogenic wood-rotting fungi (*Agaricomycetes*, *Basidiomycota*) in China. *Mycology* **2023**, *14*, 204–226. [CrossRef] [PubMed]
12. He, M.Q.; Zhao, R.L.; Hyde, K.D.; Begerow, D.; Kemler, M.; Yurkov, A.; McKenzie, E.H.C.; Raspé, O.; Kakishima, M.; Sánchez-Ramírez, S.; et al. Notes, outline and divergence times of Basidiomycota. *Fungal Diver.* **2019**, *99*, 105–367.
13. Bernicchia, A.; Gorjón, S.P. *Fungi Europaei 12: Corticiaceae s.l.*; Edizioni Candusso: Alassio, Italy, 2011.
14. Larsson, K.H.; Larsson, E.; Kõljalg, U. High phylogenetic diversity among corticioid homobasidiomycetes. *Mycol. Res.* **2004**, *108*, 983–1002. [CrossRef]
15. Parmasto, E. *The Lachnocladiaceae of the Soviet Union. With a Key to the Boreal Species*; Institute of Zoology and Botany, Academy of Sciences of the Estonian S.S.R.: Tartu, Estonia, 1971; p. 167.
16. Hallenberg, N.; Eriksson, J. *The Lachnocladiaceae and Coniophoraceae of North Europoe*; Fungiflora: Oslo, Norway, 1985; p. 96.
17. Suhara, H.; Maekawa, N.; Ushijima, S.; Kinjo, K.; Hoshi, Y. *Asterostroma* species (*Basidiomycota*) from mangrove forests in Japan. *Mycoscience* **2010**, *51*, 75–80. [CrossRef]
18. Liu, S.L.; Tian, Y.; Nie, T.; Thawthong, A.; Hyde, K.D.; Xu, L.L.; He, S.H. Updates on East Asian *Asterostroma* (*Russulales*, *Basidiomycota*): New species and new records from Thailand and China. *Mycol. Prog.* **2017**, *16*, 667–676. [CrossRef]
19. Karsten, P. Kritisk öfversigt af Finlan's Basidsvamper (*Basidiomycetes*, *Gastero- & Hxmenomycetes*). *Bidr. Till Kännedom Finl. Nat. Och Folk.* **1889**, *48*, 1–470.
20. Wu, S.H. Six new species of *Phanerochaete* from Taiwan. *Bot. Bull. Acad. Sin.* **2000**, *41*, 165–174.
21. Wu, S.H.; Nilsson, H.R.; Chen, C.T.; Yu, S.Y.; Hallenberg, N. The white-rotting genus *Phanerochaete* is polyphyletic and distributed throughout the phleboid clade of the *Polyporales* (*Basidiomycota*). *Fungal Diver.* **2010**, *42*, 107–118. [CrossRef]
22. Floudas, D.; Hibbett, D.S. Revisiting the taxonomy of *Phanerochaete* (*Polyporales*, *Basidiomycota*) using a four gene dataset and extensive ITS sampling. *Fungal Biol.* **2015**, *119*, 679–719. [CrossRef] [PubMed]
23. Ghobad-Nejhad, M.; Liu, S.L.; Langer, E.; Dai, Y.C. Molecular and morphological evidence reveal a new non-cystidiate species belonging to the core *Phanerochaete* (*Polyporales*). *Mycol. Prog.* **2015**, *14*, 68. [CrossRef]
24. Boonmee, S.; Wanasinghe, D.N.; Calabon, M.S.; Huanraluek, N.; Chandrasiri, S.K.U.; Jones, G.E.B.; Rossi, W.; Leonardi, M.; Singh, S.K.; Rana, S.; et al. Fungal Diver. notes 1387–1511: Taxonomic and phylogenetic contributions on genera and species of fungal taxa. *Fungal Diver.* **2021**, *111*, 1–335. [CrossRef] [PubMed]

25. Chen, C.C.; Chen, C.Y.; Wu, S.H. Species diversity, taxonomy and multi-gene phylogeny of phlebioid clade (*Phanerochaetaceae*, *Irpicaceae*, *Meruliaceae*) of Polyporales. *Fungal Diver.* **2021**, *111*, 337–442. [CrossRef]
26. Li, Y.; Chen, C.C.; He, S.H. New corticioid taxa in *Phanerochaetaceae* (*Polyporales*, *Basidiomycota*) from East Asia. *Front. Microbiol.* **2023**, *14*, 1093096. [CrossRef]
27. Yu, J.; Cai, J.; Liu, H.G.; Zhao, C.L. Molecular systematics and taxonomy reveal three new taxa in *Phanerochaete* (*Phanerochaetaceae*, *Polyporales*) from the Yunnan–Guizhou plateau, East Asia. *Mycol. Prog.* **2023**, *22*, 59. [CrossRef]
28. Zhang, Q.Y.; Liu, Z.B.; Liu, H.G.; Si, J. Two new corticioid species of Phanerochaetaceae (*Polyporales*, *Basidiomycota*) from Southwest China. *Front. Cell. Infect. Microbiol.* **2023**, *13*, 1105918. [CrossRef]
29. Jülich, W. Studies in resupinate Basidiomycetes V. Some new genera and species. *Persoonia* **1978**, *10*, 137–140.
30. Dhingra, G.S. The genus *Phlebiopsis* in the Eastern Himalayas. *Nova Hedwig.* **1987**, *44*, 221–227.
31. Wu, S.H. Two new species of *Phanerochaete* from Taiwan. *Mycotaxon* **2004**, *90*, 423–429.
32. Priyanka; Dhingra, G.S.; Kaur, N. *Phlebiopsis mussooriensis* (*Agaricomycetes*), a new corticioid species from India. *Mycotaxon* **2011**, *115*, 255–258. [CrossRef]
33. Kaur, G.; Singh, A.P.; Dhingra, G.S. *Phlebiopsis punjabensis*, a new species from India. *Mycotaxon* **2015**, *130*, 907–909. [CrossRef]
34. Xu, T.M.; Zeng, Y.F.; Cheng, Y.H.; Zhao, C.L. *Phlebiopsis lacerata* sp. nov (*Polyporales*, *Basidiomycota*) from southern China. *Phytotaxa* **2020**, *440*, 268–280. [CrossRef]
35. Zhao, Y.N.; He, S.H.; Nakasone, K.K.; Wasantha, K.L.; Chen, C.C.; Liu, S.L.; Ma, H.X.; Huang, M.R. Global phylogeny and taxonomy of the wood-decaying fungal genus *Phlebiopsis* (*Polyporales*, *Basidiomycota*). *Front. Microbiol.* **2021**, *12*, 622460. [CrossRef]
36. Karsten, P.A. Kritisk Ofversigt af Finlands Basidsvampar. *Biology* **1898**, *3*, 1–36.
37. Boidin, J.; Lanquetin, P. *Vararia* subgenus *Vararia* (*Basidiomycetes*, *Lachnocladiaceae*): Étude spèciale des espèces d' Afrique intertropicale. *Bull. Soc. Mycol. Fr.* **1975**, *91*, 457–513.
38. Boidin, J. Application du concept biologique del'espèce aux Basidiomycètes. Le genre *Vararia* section *Vararia* au Gabon. *Cryptogam. Mycol.* **1980**, *1*, 265–384.
39. Boidin, J.; Lanquetin, P. Le genre *Scytinostroma* Donk (*Basidiomycetes*, *Lachnocladiaceae*). *Bibl. Mycol.* **1987**, *114*, 1–130.
40. Stalpers, J.A. The aphyllophoraceous fungi II. Keys to the species of the Hericiales. *Stud. Mycol.* **1996**, *40*, 1–183.
41. Larsson, E.; Larsson, K.H. Phylogenetic relationships of russuloid basidiomycetes with emphasis on aphyllophoralean taxa. *Mycologia* **2003**, *95*, 1037–1065. [CrossRef]
42. Liu, S.L.; He, S.H. The genus *Vararia* (*Russulales*, *Basidiomycota*) in China. Two new species and two new Chinese records. *Nord. J. Bot.* **2016**, *34*, 553–558. [CrossRef]
43. Zou, L.; Zhang, X.L.; Deng, Y.L.; Zhao, C.L. Four new wood-inhabiting fungal species of Peniophoraceae (*Russulales*, *Basidiomycota*) from the Yunnan-Guizhou Plateau, China. *J. Fungi* **2022**, *8*, 1227. [CrossRef] [PubMed]
44. Deng, Y.L.; Zhao, C.L. The molecular phylogeny and morphology revealed a new wood-rotting fungus *Vararia yunnanensis* (*Peniophoraceae*, *Russulales*) in Yunnan Province, China. *Phytotaxa* **2023**, *583*, 39–49. [CrossRef]
45. Cunningham, G.H. Thelephoraceae of New Zealand. Part IV. The genus *Vararia*. *Trans. Proc. R. Soc. N. Z.* **1955**, *82*, 973–985.
46. Gilbertson, R.L. Some species of *Vararia* from temperate North America. *Pap. Mich. Acad. Sci.* **1965**, *50*, 161–184.
47. Boidin, J. Basidiomycètes Lachnocladiaceae résupinés de la Republique Centrafricaine. *Cah. Maboké* **1967**, *5*, 23–35.
48. Pouzar, Z. Taxonomic studies in resupinate fungi I. *Česká Mykol.* **1982**, *36*, 141–145.
49. Boidin, J.; Gilles, G. Contribution à la connaissance du genre *Vararia* (*Basidiomycotina*). *Bull. Soc. Mycol.* **1999**, *115*, 115–139.
50. Duhem, B.; Buyck, B. On two new tropical *Vararia* (*Russulales*, *Basidiomycota*) with extremely small, racemose dichohyphidia. Cryptogam. *Mycology* **2012**, *33*, 427–437.
51. Sanyal, S.K.; Dhingra, G.S.; Singh, A.P. *Vararia longicystidiata* sp. nov. (*Agaricomycetes*) from India. *Mycotaxon* **2012**, *120*, 357–360. [CrossRef]
52. Nakasone, K.K. Taxonomic studies in *Chrysoderma*, *Corneromyces*, *Dendrophysellum*, *Hyphoradulum*, and *Mycobonia*. *Mycotaxon* **2015**, *130*, 369–397. [CrossRef]
53. Larsson, K.H. Re-thinking the classification of corticioid fungi. *Mycol. Res.* **2007**, *111*, 1040–1063. [CrossRef] [PubMed]
54. Luo, K.Y.; Zhao, C.L. A molecular systematics and taxonomy research on *Trechispora* (*Hydnodontaceae*, *Trechisporales*): Concentrating on three new *Trechispora* species from East Asia. *J. Fungi* **2022**, *8*, 1020. [CrossRef] [PubMed]
55. Zhao, C.L.; Qu, M.H.; Huang, R.X.; Karunarathna, S.C. Multi-gene phylogeny and taxonomy of the wood-rotting fungal genus *Phlebia* sensu lato (*Polyporales*, *Basidiomycota*). *J. Fungi* **2023**, *9*, 320. [CrossRef]
56. Binder, M.; Hibbett, D.S.; Larsson, K.H.; Larsson, E.; Langer, E.; Langer, G. The phylogenetic distribution of resupinate forms across the major clades of mushroom-forming fungi (*Homobasidiomycetes*). *Syst. Biodivers.* **2005**, *3*, 113–157. [CrossRef]
57. Binder, M.; Justo, A.; Riley, R.; Salamov, A.; Lopez-Giraldez, F.; Sjökvist, E.; Copeland, A.; Foster, B.; Sun, H.; Larsson, E.; et al. Phylogenetic and phylogenomic overview of the *Polyporales*. *Mycologia* **2013**, *105*, 350–1373. [CrossRef]
58. Justo, A.; Miettinen, O.; Floudas, D.; Ortiz-Santana, B.; Sjökvist, E.; Lindner, D.; Nakasone, K.; Niemelä, T.; Larsson, K.H.; Ryvarden, L.; et al. A revised family-level classifcation of the *Polyporales* (*Basidiomycota*). *Fungal Biol.* **2017**, *121*, 798–824. [CrossRef]
59. Haelewaters, D.; Wijayawardene, N.N.; Hyde, K.D.; Dai, D.Q.; Sánchez-García, M. Outline of Fungi and fungus-like taxa-2021. *Mycosphere* **2022**, *13*, 53–453. [CrossRef]
60. Reid, D.A. *A Monograph of the Stipitate Stereoid Fungi*; J. Cramer: Weinheim, Germany, 1965.

61. Miller, S.L.; Larsson, E.; Larsson, K.H.; Verbeken, A.; Nuytinck, J. Perspectives in the new Russulales. *Mycologia* **2006**, *98*, 960–970. [CrossRef] [PubMed]
62. White, T.J.; Bruns, T.; Lee, S.; Taylor, J. Amplification and direct sequencing of fungal ribosomal RNA genes for phylogenetics. *PCR Protoc. A Guide Methods Appl.* **1990**, *18*, 315–322. [CrossRef]
63. Hall, T.A. BioEdit: A user-friendly biological sequence alignment editor and analysis program for Windows 95/98/NT. *Nucleic Acids Symp. Ser.* **1999**, *41*, 95–98.
64. Wang, D.Q.; Zhao, C.L. Morphological and phylogenetic evidence for recognition of two new species of *Phanerochaete* from East Asia. *J. Fungi* **2021**, *7*, 1063. [CrossRef] [PubMed]
65. Leal-Dutra, C.A.; Neves, M.A.; Griffith, G.W.; Reck, M.A.; Clasen, L.A.; Dentinger, B.T.M. Reclassification of *Parapterulicium* Corner (*Pterulaceae*, *Agaricales*), contributions to *Lachnocladiaceae* and *Peniophoraceae* (*Russulales*) and introduction of *Baltazaria* gen. nov. *MycoKeys* **2018**, *37*, 39–56. [CrossRef] [PubMed]
66. Zhao, C.L.; Wu, Z.Q. *Ceriporiopsis kunmingensis* sp. nov. (*Polyporales*, *Basidiomycota*) evidenced by morphological characters and phylogenetic analysis. *Mycol. Prog.* **2017**, *16*, 93–100. [CrossRef]
67. Swofford, D.L. *PAUP*: Phylogenetic Analysis Using Parsimony (* and Other Methods)*, Version 4.0b10; Sinauer Associates: Sunderland, MA, USA, 2002.
68. Felsenstein, J. Confidence intervals on phylogenetics: An approach using bootstrap. *Evolution* **1985**, *39*, 783–791. [CrossRef]
69. Miller, M.A.; Pfeiffer, W.; Schwartz, T. The CIPRES Science Gateway: Enabling high-impact science for phylogenetics researchers with limited resources. *Assoc. Comput. Mach.* **2012**, *39*, 1–8. [CrossRef]
70. Vu, D.; Groenewald, M.; Vries, M.; Gehrmann, T.; Stielow, B.; Eberhardt, U.; Al-Hatmi, A.; Groenewald, J.Z.; Cardinali, G.; Houbraken, J.; et al. 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. *Stud. Mycol.* **2019**, *92*, 135–154. [CrossRef]
71. Liu, S.L.; Nakasone, K.K.; He, S.H. *Michenera incrustata* sp. nov. (*Peniophoraceae*, *Russulales*) from southern China. *Nova Hedwig.* **2019**, *108*, 197–206. [CrossRef]
72. Liu, S.L.; He, S.H. Taxonomy and phylogeny of *Dichostereum* (*Russulales*), with descriptions of three new species from southern China. *MycoKeys* **2018**, *40*, 111–126. [CrossRef]
73. Spirin, V.; Malysheva, V.; Miettinen, O.; Vlasák, J.; Alvarenga, R.L.M.; Gibertoni, T.B.; Ryvarden, L.; Larsson, K.K. On *Protomerulius* and *Heterochaetella* (*Auriculariales*, *Basidiomycota*). *Mycol. Prog.* **2019**, *18*, 1079–1099. [CrossRef]
74. Phookamsak, R.; Hyde, K.D.; Jeewon, R.; Bhat, D.J.; Jones, E.B.G.; Maharachchikumbura, S.; Raspé, O.; Karunarathna, S.C.; Wanasinghe, D.; Hongsanan, S.; et al. Fungal diversity notes 929–1035: Taxonomic and phylogenetic contributions on genera and species of fungi. *Fungal Divers.* **2019**, *95*, 1–273. [CrossRef]
75. Wu, S.H.; Chen, Y.P.; Wei, C.L.; Floudas, D.; Dai, Y.C. Two new species of *Phanerochaete* (*Basidiomycota*) and redescription of *P. robusta*. *Mycol. Prog.* **2017**, *17*, 425–435. [CrossRef]
76. Xu, Y.L.; Cao, Y.F.; Nakasone, K.K.; Chen, C.C.; He, S.H. Taxonomy and phylogeny of *Phanerochaete sensu stricto* (*Polyporales*, *Basidiomycota*) with emphasis on Chinese collections and descriptions of nine new species. *Mycosphere* **2020**, *11*, 1527–1552. [CrossRef]
77. Volobuev, S.; Okun, M.; Ordynets, A.; Spirin, V. The *Phanerochaete sordida* group (*Polyporales*, *Basidiomycota*) in temperate Eurasia, with a note on *Phanerochaete pallida*. *Mycol. Prog.* **2015**, *14*, 80. [CrossRef]
78. Wu, S.H.; Chen, C.C.; Wei, C.L. Three new species of *Phanerochaete* (*Polyporales*, *Basidiomycota*). *MycoKeys* **2018**, *41*, 91–106. [CrossRef] [PubMed]
79. Lima, V.X.; Lira, C.S.; Chikowski, R.S.; Santos, C.; Lima, N.; Gibertoni, T.B. Additions to neotropical stereoid fungi (*Polyporales*, *Basidiomycota*): One new species of *Lopharia* and one new combination in *Phlebiopsis*. *Mycol. Prog.* **2020**, *19*, 31–40. [CrossRef]
80. Miettinen, O.; Spirin, V.; Vlasák, J.; Rivoire, B.; Stenroos, S.; Hibbett, D. Polypores and genus concepts in *Phanerochaetaceae* (*Polyporales*, *Basidiomycota*). *MycoKeys* **2016**, *17*, 1–46. [CrossRef]
81. Zhao, C.L.; Liu, X.F.; Ma, X. *Phlebiopsis yunnanensis* sp. nov. (*Polyporales*, *Basidiomycota*) evidenced by morphological characters and phylogenetic analysis. *Nova Hedwig.* **2019**, *108*, 265–279. [CrossRef]
82. Nakasone, K.K.; Draeger, K.R.; Ortiz-Santana, B. A contribution to the taxonomy of *Rhizochaete* (*Polyporales*, *Basidiomycota*). *Cryptogam. Mycol.* **2017**, *38*, 81–99. [CrossRef]
83. Chikowski, R.S.; Larsson, K.H.; Gibertoni, T.B. Three new combinations in *Rhizochaete* (*Agaricomycetes*, *Fungi*) and a new record to the Brazilian Amazonia. *Nova Hedwig.* **2016**, *102*, 185–196. [CrossRef]
84. Nylander, J.A.A. *MrModeltest v2*; Program Distributed by the Author; Evolutionary Biology Centre, Uppsala University: Upp-sala, Sweden, 2004.
85. Ronquist, F.; Teslenko, M.; van der Mark, P.; Ayres, D.L.; Darling, A.; Hohna, S.; Larget, B.; Liu, L.; Suchard, M.A.; Huelsenbeck, J.P. Mrbayes 3.2: Efficient bayesian phylogenetic inference and model choice across a large model space. *Syst. Biol.* **2012**, *61*, 539–542. [CrossRef]
86. Massee, G.E. A monograph of the Thelephoraceae. *Part I Bot. J. Linn. Soc.* **1889**, *25*, 107–155. [CrossRef]
87. Karasiński, D. Polish resupinate Russulales: The genus *Vararia*. *Acta Mycol.* **2010**, *45*, 45–56. [CrossRef]
88. Welden, A.L. West Indian species of *Vararia* with notes on extralimital species. *Mycologia* **1965**, *57*, 502–520. [CrossRef]

89. Yang, Y.Y.; Jiang, Q.Q.; Li, Q.; Yang, J.W.; Cha, L.J.; Cheng, L.; Yang, S.Q.; Zhao, C.L.; Zhou, H.M. Molecular systematics and taxonomic analyses of three new wood-inhabiting fungi of *Hyphoderma* (*Hyphodermataceae*, *Basidiomycota*). *J. Fungi* **2023**, *9*, 1044. [CrossRef] [PubMed]
90. Bian, L.S.; Wu, F.; Dai, Y.C. Two new species of *Coltricia* (*Hymenochaetaceae*, *Basidiomycota*) from Southern China based onevidence from morphology and DNA sequence data. *Mycol. Prog.* **2016**, *15*, 27. [CrossRef]
91. Zhao, C.L.; Wu, F.; Dai, Y.C. *Leifiporia rhizomorpha* gen. et sp. nov. and *L. eucalypti* comb. nov. in Polyporaceae (*Basidiomycota*). *Mycol. Prog.* **2016**, *15*, 799–809. [CrossRef]
92. Guan, Q.X.; Zhao, T.J.; Zhao, C.L. Morphological characters and phylogenetic analyses reveal two new species of *Peniophorella* from Southern China. *Mycol. Prog.* **2020**, *19*, 397–404. [CrossRef]