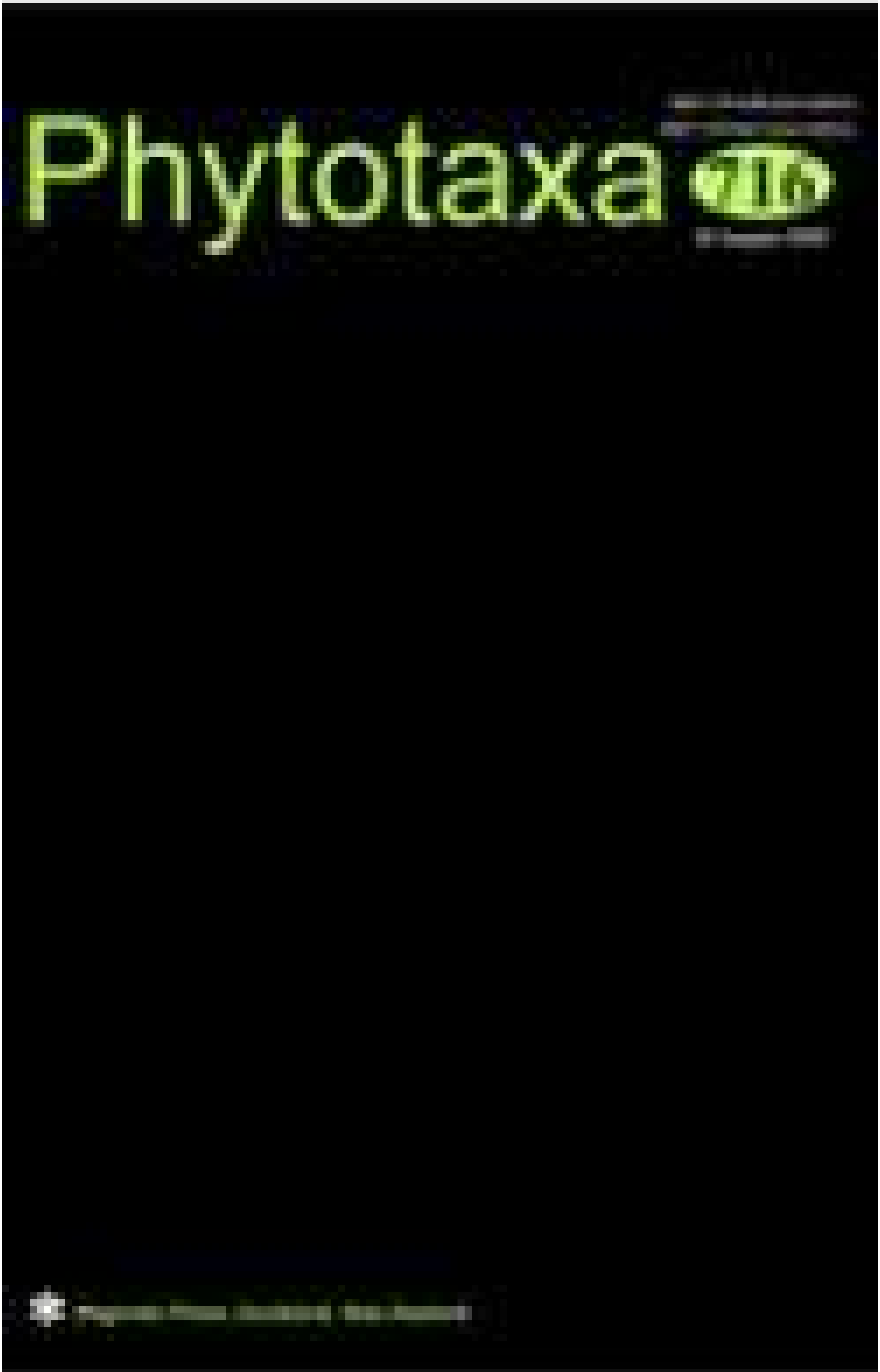
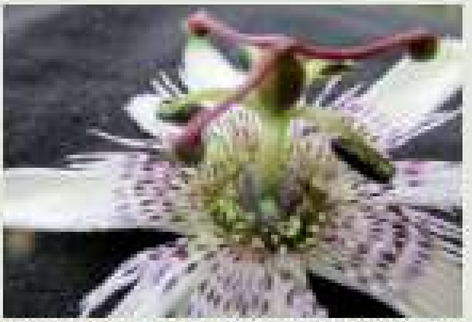


Phytotaxa



Five New Species of *Passiflora* (subgenus *Decaloba*, Passifloraceae) from Peru

TATIANA ERIKA ROJAS ESPINOZA, JOHN M. MACDOUGAL, PETER MØLLER JØRGENSEN

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A new species of *Gyroporus* (*Gyroporaceae*, *Boletales*) from Swat, Pakistan

SANA SANA, MUNAZZA KIRAN, WAJID ALI, ISHTIAQ TARAFDER

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Molecular phylogeny and morphology reveal a new species of *Phanerochaete* (*Phanerochaetaceae*, *Basidiomycota*) from Yunnan Province, China

YINGHAO LI, XIN YANG, ZIJUNSE ZHANG, JIANGQING SU, CHANGLIN ZHAO, HONGMIN ZHOU

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Conioscypha pruni sp. nov. (Conioscyphaceae, Conioscyphales), from sweet cherry (*Prunus avium*) from Sichuan Province, China

YUE-QIN LIAO, LI-PENG DENG, YAN-PENG CHEN, JIAN-XIN LIU, SAJEEWA S. N. MAHARACHCHIKUMBURA

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Leptochilus phanerophlebius (Polypodiaceae), a new species from Fenshuiling National Nature Reserve, southeastern Yunnan, China

ZHI-YONG YU, ZHEN-LONG LIANG, ZONG-LI LIANG, HAI-LONG HE, YAN-HONG LI, QIN-WEI ZHANG, LIANG ZHANG

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A new member (*Camellia dakplaoensis*) and new synonymization in *Camellia* section *Piquetia* (Theaceae)

THI THANH HUONG NGUYEN, THE NHIEN NGUYEN, TUAN ANH PHAM, DUC BINH NGUYEN, THE SON NGO, HOANG THUONG LUU

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Aristolochia guillermoi (Aristolochiaceae), a new species from Peru and a key to identify the *Aristolochia* taxa with branched trichomes

FAVIO GONZÁLEZ, BORIS ESQUERRE-IBAÑEZ

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Correspondence

The geographic distribution of *Pluteus xylophilus* (Pluteaceae) in the Americas

MATÍAS SEBASTIÁN TINGANI, NICOLÁS NIVEIRO, CARLOS ALBERTO SALVADOR-MONTOYA

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Molecular phylogeny and morphology reveal a new species of *Phanerochaete* (*Phanerochaetaceae*, *Basidiomycota*) from Yunnan Province, China

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Abstract

Wood-inhabiting fungi play a crucial role in forest ecosystems as an important group of decomposers, found in living trees, dead standing trees, decorticated trunks, fallen branches, and manufactured wood. A new wood-inhabiting fungus *Phanerochaete flavissima*, belonging to the family Phanerochaetaceae, is described and illustrated based on the morphological characteristics and molecular data. *Phanerochaete flavissima* is characterized by annual, resupinate basidiomata with pale yellow to yellow hymenial surface, a monomitic hyphal system having the simple-septate generative hyphae, and ellipsoid, colorless, thin-walled basidiospores measuring 4.5–5.5 × 2.0–3.0 µm. The phylogenetic analyses based on ITS+nLSU rDNA sequences confirmed that the new species belongs to the genus *Phanerochaete*, and revealed that the new taxon is closely related to *P. carnosa*. A full description, illustrations, and phylogenetic analysis results of the new species are provided.

Keywords: Basidiomycetes, Molecular phylogeny, New species, Wood-inhabiting fungi

Introduction

Fungi are well-known as a diverse group of microorganisms that play important roles in forest ecosystems (Hyde *et al.* 2024). Basidiomycota constitute a major phylum of the kingdom fungi and are second in number of described species to Ascomycota (Dai *et al.* 2021, Zhao *et al.* 2023, He *et al.* 2024, Wijayawardene *et al.* 2024).

Wood-inhabiting fungi are found in living trees, dead standing trees, decorticated trunks, fallen trunks and branches, stumps as well as manufactured wood products (Yuan *et al.* 2023, Qin *et al.* 2025), in which these fungi of the cell walls and the components within the living cells secrete various enzymes that effectively degrade cellulose, hemicellulose and lignin into simple inorganic substances, in which as an important group of decomposers, they play an essential role in forest ecosystems (Dai 2010, Cui *et al.* 2019, Wu *et al.* 2022b, Dong *et al.* 2024, Yang *et al.* 2025).

The family Phanerochaetaceae Jülich, belonging to the order Polyporales (Basidiomycota), was typified by *Phanerochaete* P. Karst (1889: 426). The genus *Phanerochaete* P. Karst., belonging to the family Phanerochaetaceae (Polyporales, Basidiomycota), was typified by *P. alnea* (Fr.) P. Karst. (1889: 427) (Deng *et al.* 2024). It is characterized by the membranaceous, smooth hymenial surface (some are tuberculate, odontioid-hydnoid or merulioid-poroid), mostly monomitic hyphal system, simple-septate generative hyphae or with rare clamp connections in the subiculum, clavate basidia and ellipsoid to cylindrical, thin-walled and smooth basidiospores, which are inamyloid and non-dextrinoid (Wu *et al.* 2018). The colorless subiculum is present in most species, but brownish subiculum also occurs (Chen *et al.* 2021). Based on the MycoBank database (http://www.MycoBank.org, accessed on 30 July 2025) and the Index Fungorum (www.indexfungorum.org; accessed on 30 July 2025), 223 names are added in the genus *Phanerochaete*,

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and 131 species have been accepted worldwide (Chen *et al.* 2021, Wang & Zhao 2021, Yu *et al.* 2023, Deng *et al.* 2024, Dong *et al.* 2024, Luo *et al*. 2024, Xu *et al.* 2025).

Pioneering studies have been conducted on the phylogenetic analysis of *Phanerochaete* (Floudas & Hibbett 2015, Miettinen *et al.* 2016, Xu *et al.* 2020, Chen *et al.* 2021, Wang *et al.* 2023, Deng *et al.* 2024, Dong *et al.* 2024, Xu *et al.* 2025). The research employed *RPB*1, *RPB*2, and the ITS and LSU ribosomal genes to investigate phanerochaetoid taxa and revealed that *Phanerochaete* was further divided into four smaller clades (*Phanerochaete* sensu stricto, *Bjerkandera*, *Hyphodermella,* and *Phlebiopsis*), but only *Phanerochaete* s.s. and *Phlebiopsis* clades have been previously identified (Floudas & Hibbett 2015). Miettinen *et al.* (2016) investigated the relationships among genera within Phanerochaetaceae based on phylogenetic analyses of ITS, LSU, and *rpb*1, as well as morphology, and they demonstrated that the macromorphology of basidiomata and hymenophore construction did not reflect monophyletic groups in *Phanerochaete*. In the phlebioid clade (Phanerochaetaceae*,* Irpicaceae*,* Meruliaceae) of Polyporales, species diversity, taxonomy, and multi-gene phylogeny revealed that the family Phanerochaetaceae comprises four main lineages with substantial support, including the *Donkia, Phanerochaete, Phlebiopsis,* and *Bjerkandera* clades, in which *Phanerochaete* s.l. was defined as a polyphyletic genus based on previous phylogeny results (Chen *et al*. 2021, Wang *et al.* 2023). Further phylogeny of the five corticioid genera of Phanerochaetaceae based on ITS1-5.8S-ITS2 and nrLSU sequence data indicated that the *Donkia*, *Phlebiopsis*, *Rhizochaete*, and *Phanerochaete* clades are distinct from *P. subsanguinea* Yue Li & S.H. He (2023: 20) (Li *et al*. 2023). In addition, *P. rhizomorpha* C.C. Chen, Sheng H. Wu & S.H. He (2021: 380) was replaced by *P. subsanguinea* based on molecular analyses (Li *et al*. 2023). Molecular systematics and taxonomy reveal three new taxa in *Phanerochaete* (Phanerochaetaceae, Polyporales) from the Yunnan–Guizhou Plateau, East Asia. This study generated sequences of the ITS and LSU rDNA markers for 12 genera related to the genus *Phanerochaete* within the family Phanerochaetaceae (Polyporales). Phylogenetic analyses revealed that the phylogram inferred from the ITS dataset showed that *P. subtuberculata* J. Yu & C.L. Zhao (2023: 9) was a sister group to *P. crystallina* C.C. Chen, Sheng H. Wu & S.H. He (2021: 378) and *P. subtropica* J. Yu & C.L. Zhao (2023: 8) grouped with *P. daliensis* Yu & C.L. Zhao (2023: 6) (Yu *et al*. 2023). The phylogenetic analyses of ITS+nLSU revealed that the *Phanerochaete tongbiguanensis* Y.L. Deng & C.L. Zhao (2024: 18) was nested into the genus *Phanerochaete* within the family Phanerochaetaceae (Polyporales), in which *Phanerochaete tongbiguanensis* was sister to *P. daliensis* (Deng *et al*. 2024). Based on the loci encompassed the internal transcribed spacer (ITS) regions, the large subunit nuclear ribosomal RNA gene (nLSU), small subunit mitochondrial rRNA gene sequences (mtSSU), translation elongation factor 1-α gene (TEF1), RNA polymerase II largest subunit (*rpb*1), and the second subunit of RNA polymerase II (*rpb*2), the species diversity, taxonomy, molecular systematics and divergence time of wood-inhabiting fungi in Yunnan-Guizhou Plateau, Asia showed that *Phanerochaete mopanshanensis* J.H. Dong & C.L. Zhao (2024: 1244) was grouped in the genera *Phanerochaete* (Dong *et al*. 2024). The phylogram based on the ITS+nLSU rDNA gene regions revealed that three species of *P. albocremea* Ying Xu & C.L. Zhao (2025:279), *P. fissurata* Ying Xu & C.L. Zhao (2025: 279), and *P. punctata* Ying Xu & C.L. Zhao (2025: 284), collected from southern China, belonged to the genus *Phanerochaete* in the family *Phanerochaetaceae*, in which the species *P. fissurata* was retrieved as a sister to *P. cinerea* Y.L. Xu & S.H. He (2020: 1535) (Xu *et al*. 2025).

During investigations on wood-inhabiting fungi in Yunnan Province, China, two specimens of *Phanerochaete* were collected. To clarify the placement and relationships of both specimens, we conducted a phylogenetic and taxonomic study on the genus *Phanerochaete*, based on ITS and nLSU sequences. Both specimens are identified as an undescribed species of *Phanerochaete*, and the detailed description and illustrations of the new species are provided here.

Materials and methods

Sample Collection and Herbarium Specimen Preparation

Fresh basidiomata growing on angiosperm branches were collected from Honghe, Yunnan Province, P.R. China, and the collection details were noted (Rathnayaka *et al.* 2024). The samples were photographed *in situ,* and macroscopic details of fresh basidiomata were recorded. Photographs were taken using a Jianeng 80D camera (Tokyo, Japan). Specimens were dried in an electric food dehydrator at 45°C (Hu *et al.* 2022). Once dried, the specimens were sealed in envelopes and zip-lock plastic bags and labeled (Zhao *et al.* 2023). The dried specimens were deposited in the herbarium of the Southwest Forestry University (SWFC), Kunming, Yunnan Province, China.

Morphology

The macromorphological descriptions were based on field notes and photos captured in the field and lab. The color terminology follows Petersen (1996). The micromorphological data were obtained from dried specimens observed under a Nikon Eclipse E100 light microscope, following the method described by Liu *et al.* (2025). The following abbreviations are used: KOH = 5% potassium hydroxide water solution, CB– = acyanophilous, 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).

Molecular Phylogeny

The CTAB rapid plant genome extraction kit-DN14 (Aidlab Biotechnologies Co., Ltd., Beijing, China) was used to obtain genomic DNA from the dried specimens according to the manufacturer's instructions. The nuclear ribosomal internal transcribed spacer (ITS) region was amplified with the primer pair ITS5/ITS4 (White *et al.* 1990), and the nuclear large subunit (nLSU) region with the primer pair LR0R/LR7 (Vilgalys & Hester 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 at 72°C for 10 min. The PCR procedure for nLSU was as follows: initial denaturation at 94°C for 1 min, followed by 35 cycles at 94°C for 30 s, 48°C for 1 min, and 72°C for 1.5 min, and a final extension at 72°C for 10 min. The PCR products were purified and sequenced at Kunming Tsingke Biological Technology Limited Company (Yunnan Province, P.R. China). All newly generated sequences were deposited in GenBank (Table 1).

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

Species Name	Sample No.	ITS	nLSU	Country	References
Crepatura ellipsospora	CLZhao 1265	MK343692	MK343696	China	Ma & Zhao (2019)
Phanerochaete aculeata	Wu 1809-278	MZ422786	MZ637178	China	Chen *et al*. (2021)
Phanerochaete aculeata	GC 1703-117	MZ422785	MZ637177	China	Chen *et al*. (2021)
Phanerochaete albida	WEI 18-365	MZ422789	MZ637180	China	Chen *et al*. (2021)
Phanerochaete albida	GC 1407-14	MZ422788	MZ637179	China	Chen *et al*. (2021)
Phanerochaete alnea *	Larsson 12054	KX538924	—	Norway	Spirin *et al*. (2017)
Phanerochaete alpina	Wu 1308-61	MZ422790	MZ637182	China	Chen *et al*. (2021)
Phanerochaete alpina	Wu 1308-77	MZ422791	MZ637183	China	Chen *et al*. (2021)
Phanerochaete arizonica	RLG-10248-Sp	KP135170	KP135239	USA	Floudas & Hibbett (2015)
Phanerochaete australis	He 6013	MT235656	MT248136	China	Phookamsak *et al*. (2019)
Phanerochaete australis	HHB-7105-Sp	KP135081	KP135240	USA	Floudas & Hibbett (2015)
Phanerochaete australosanguinea	MA:Fungi:91308	MH233925	MH233928	Chile	Phookamsak *et al*. (2019)
Phanerochaete australosanguinea	MA:Fungi:91309	MH233926	MH233929	Chile	Phookamsak *et al*. (2019)
Phanerochaete bambusicola	He 3606	MT235657	MT248137	China	Xu *et al*. (2020)
Phanerochaete bambusicola	Wu 0707-2	MF399404	MF399395	China	Wu *et al*. (2017)

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TABLE 1. (Continued)

Species Name	**Sample No.**	**ITS**	**nLSU**	**Country**	**References**
Phanerochaete brunnea	He 4192	MT235658	MT248138	China	Xu *et al*. (2020)
Phanerochaete burdsallii	He 2066	MT235690	MT248177	USA	Xu *et al*. (2020)
Phanerochaete burtii	HHB-4618-Sp	KP135117	KP135241	USA	Floudas & Hibbett (2015)
Phanerochaete canobrunnea	He 5726	MT235659	MT248139	Sri Lanka	Wu *et al*. (2017)
Phanerochaete canobrunnea	CHWC1506-66	LC412095	LC412104	China	Xu *et al*. (2020)
Phanerochaete fissurata	CLZhao 35311	PQ454013	PQ454678	China	Xu *et al*.(2025)
Phanerochaete fissurata	CLZhao 35321	PQ454014	PQ454679	China	Xu *et al*.(2025)
Phanerochaete punctata	CLZhao 30365	PQ454015	PQ454680	China	Xu *et al*.(2025)
Phanerochaete punctata	CLZhao 30512	PQ454016	PQ454681	China	Xu *et al*.(2025)
Phanerochaete albocremea	CLZhao 31998	PQ454009	PQ454675	China	Xu *et al*.(2025)
Phanerochaete albocremea	CLZhao 32032	PQ454010	PQ454676	China	Xu *et al*.(2025)
Phanerochaete carnosa	He 5172	MT235660	MT248140	China	Xu *et al*. (2020)
Phanerochaete carnosa	HHB-9195	KP135129	KP135242	USA	Floudas & Hibbett (2015)
Phanerochaete chrysosporium	He 5778	MT235661	MT248141	Sri Lanka	Xu *et al*. (2020)
Phanerochaete chrysosporium	HHB-6251-Sp	KP135094	KP135246	USA	Floudas & Hibbett (2015)
Phanerochaete cinerea	He 5998	—	MT248171	China	Xu *et al*. (2020)
Phanerochaete cinerea	He 6003	—	MT248172	China	Xu *et al*. (2020)
Phanerochaete citrinosanguinea	FP-105385-Sp	KP135100	—	USA	Floudas & Hibbett (2015)
Phanerochaete concrescens	He 4657	MT235662	MT248142	China	Chen *et al*. (2021)
Phanerochaete concrescens	H Spirin 7322	KP994380	KP994382	Russia	Volobuev *et al*. (2015)
Phanerochaete crystallina	Chen 3823	MZ422802	—	China	Chen *et al*. (2021)
Phanerochaete cumulodentata	He 2995	MT235664	MT248144	China	Phookamsak (2019)
Phanerochaete cumulodentata	LE<RUS>:298935	KP994359	KP994386	Russia	Volobuev *et al*. (2015)
Phanerochaete cystidiata	He 4224	MT235665	MT248145	China	Xu *et al*. (2020)
Phanerochaete cystidiata	Wu 1708-326	LC412097	LC412100	China	Wu *et al*. (2018)
Phanerochaete ericina	HHB-2288	KP135167	KP135247	USA	Floudas & Hibbett (2015)

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TABLE 1. (Continued)

Species Name	Sample No.	ITS	nLSU	Country	References
Phanerochaete ericina	He 4285	MT235666	MT248146	China	Xu *et al*. (2020)
Phanerochaete flavissima	**CLZhao 17997***	**PV175887**	**PV203435**	**China**	**Present study**
Phanerochaete flavissima	**CLZhao 40600**	**PV175888**	**PV203436**	**China**	**Present study**
Phanerochaete fusca	Wu1409-163	LC412099	LC412106	China	Wu *et al*. (2018)
Phanerochaete fusca	Wu 1409-161	LC412098	LC412105	China	Wu *et al*. (2018)
Phanerochaete granulata	Chen 2835	MZ422808	MZ637194	China	Chen *et al*. (2021)
Phanerochaete granulata	GC 1703-5	MZ422809	MZ637195	China	Chen *et al*. (2021)
Phanerochaete granulata	Wu 9210-57	MZ422810	MZ637196	China	Chen *et al*. (2021)
Phanerochaete guangdongensis	Wu 1809-348	MZ422813	MZ637199	China	Chen *et al*. (2021)
Phanerochaete guangdongensis	Wu 1809-319	MZ422811	MZ637197	China	Chen *et al*. (2021)
Phanerochaete hainanensis	He 3562	MT235692	MT248179	China	Boonmee *et al*. (2021)
Phanerochaete hymenochaetoides	He 5988	—	MT248173	China	Xu *et al*. (2020)
Phanerochaete incarnata	He 20120728-1	MT235669	MT248149	China	Xu *et al*. (2020)
Phanerochaete incarnata	WEI 16-075	MF399406	MF399397	China	Wu *et al*. (2017)
Phanerochaete laevis	He 20120917-8	MT235670	MT248150	China	Xu *et al*. (2020)
Phanerochaete laevis	HHB-15519	KP135149	KP135249	USA	Floudas & Hibbett (2015)
Phanerochaete leptocystidiata	He 5853	MT235685	MT248168	China	Xu *et al*. (2020)
Phanerochaete leptocystidiata	Dai 10468	MT235684	MT248167	China	Xu *et al*. (2020)
Phanerochaete livescens	He 5010	MT235671	MT248151	China	Xu *et al*. (2020)
Phanerochaete metuloidea	He 2766	MT235682	MT248164	China	Xu *et al*. (2020)
Phanerochaete minor	He 3988	MT235686	MT248170	China	Xu *et al*. (2020)
Phanerochaete mopanshanensis	CLZhao 2357	OR096190	OR461450	China	Dong *et al*. (2024)
Phanerochaete parmastoi	He 4570	MT235673	MT248153	China	Xu *et al*. (2020)
Phanerochaete parmastoi	Wu 880313-6	MZ422823	GQ470654	China	Chen *et al*. (2021)
Phanerochaete porostereoides	He1902	KX212217	KX212221	China	Liu & He (2016)
Phanerochaete porostereoides	He1908	KX212218	KX212222	China	Liu & He (2016)

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TABLE 1. (Continued)

Species Name	Sample No.	ITS	nLSU	Country	References
Phanerochaete pruinosa	CLZhao 7112	MZ435346	MZ435350	China	Wang & Zhao (2021)
Phanerochaete pruinosa	CLZhao 7113	MZ435347	MZ435351	China	Wang & Zhao (2021)
Phanerochaete pseudosanguinea	FD-244	KP135098	KP135251	USA	Floudas & Hibbett (2015)
Phanerochaete rhizomorpha	GC 1708-335	MZ422824	MZ637208	China	Chen *et al*. (2021)
Phanerochaete rhizomorpha	GC 1708-354	MZ422825	MZ637209	China	Chen *et al*. (2021)
Phanerochaete rhodella	FD-18	KP135187	KP135258	USA	Floudas & Hibbett (2015)
Phanerochaete robusta	Wu 1109-69	MF399409	MF399400	China	Wu *et al*. (2018)
Phanerochaete robusta	MG265	KP127068	KP127069	China	Ghobad-Nejhad *et al*. (2015)
Phanerochaete sanguineocarnosa	FD-359	KP135122	KP135245	USA	Floudas & Hibbett (2015)
Phanerochaete sinensis	He4660	MT235688	MT248175	China	Xu *et al*. (2020)
Phanerochaete sinensis	GC1809-56	MT235689	MT248176	China	Xu *et al*. (2020)
Phanerochaete sordida	FD-241	KP135136	KP135252	USA	Floudas & Hibbett (2015)
Phanerochaete spadicea	Wu 0504-15	MZ422837	MZ637219	China	Chen *et al*. (2021)
Phanerochaete spadicea	Wu 0504-11	MZ422836	—	China	Chen *et al*. (2021)
Phanerochaete stereoides	He 5824	MT235677	MT248158	Sri Lanka	Xu *et al*. (2020)
Phanerochaete stereoides	He 2309	KX212219	KX212223	China	Liu & He (2016)
Phanerochaete subcarnosa	Wu 9310-3	MZ422841	GQ470642	China	Chen *et al*. (2021)
Phanerochaete subcarnosa	GC 1809-90	MZ422840	MZ637222	China	Chen *et al*. (2021)
Phanerochaete subceracea	FP-105974-R	KP135162	KP135255	USA	Floudas & Hibbett (2015)
Phanerochaete subceracea	HHB-9434	KP135163	—	USA	Floudas & Hibbett (2015)
Phanerochaete subrosea	He 2421	MT235687	MT248174	China	Xu *et al*. (2020)
Phanerochaete subsanguinea	CLZhao 10470	MZ435348	MZ435352	China	Wang & Zhao (2021)
Phanerochaete subsanguinea	CLZhao 10477	MZ435349	MZ435353	China	Wang & Zhao (2021)
Phanerochaete subtropica	CLZhao F8716	OP605486	OQ195089	China	Yu *et al*. (2023)
Phanerochaete subtropica	CLZhao F2763	OP605518	OQ195090	China	Yu *et al*. (2023)
Phanerochaete subtuberculata	CLZhao F5130	OP605484	OQ195088	China	Yu *et al*. (2023)

...continued on the next page

TABLE 1. (Continued)

Species Name	Sample No.	ITS	nLSU	Country	References
Phanerochaete subtuberculata	CLZhao F6838	OP605485	OQ195087	China	Yu *et al*. (2023)
Phanerochaete taiwaniana	He 5269	MT235680	MT248161	Vietnam	Xu *et al*. (2020)
Phanerochaete taiwaniana	Wu 0112-13	MF399412	MF399403	China	Chen *et al*. (2021)
Phanerochaete tongbiguanensis	CLZhao 30606	OR917875	OR921222	China	Deng *et al*.(2024)
Phanerochaete velutina	He 3079	MT235681	MT248162	China	Xu *et al*. (2020)
Phanerochaete velutina	H:7022032 Kotiranta 25567	KP994354	KP994387	Russia	Volobuev *et al*. (2015)
Phanerochaete yunnanensis	He 2719	MT235683	MT248166	China	Xu *et al*. (2020)
Phanerochaete yunnanensis	He 2697	—	MT248165	China	Xu *et al*. (2020)

* Indicates type specimen; new sequences are in bold and — represents the data unavailability.

The sequences were aligned using MAFFT version 7 (Katoh *et al.* 2019) with the G-INS-i strategy. The alignment was adjusted manually using AliView version 1.27 (Larsson 2014). The dataset was first aligned, and then the sequences of ITS+nLSU were combined using Mesquite version 3.51. The combined ITS+nLSU sequence datasets were used to infer the position of the new species in the *Hymenochaete* and related species.

Maximum Parsimony (MP), Maximum Likelihood (ML), and Bayesian Inference (BI) analyses were applied to the combined datasets, following a previous study (Zhao & Wu 2017). The tree construction procedure was performed in PAUP* version 4.0b10 (Swofford 2002). All of the characters were equally weighted, and gaps were treated as missing data. Using the heuristic search option with TBR branch swapping and 1,000 random sequence additions, trees were inferred. Max trees were set to 5,000, branches of zero length were collapsed, and all parsimonious trees were saved. Clade robustness was assessed using bootstrap (BT) analysis with 1000 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 generated. The multiple sequence alignment was also analyzed using maximum likelihood (ML) in RAxML-HPC2 (Miller *et al.* 2012). Branch support (BS) for ML analysis was determined by 1,000 bootstrap replicates.

MrModeltest 2.3 (Nylander 2004) was used to determine the best-fit evolution model for each dataset for Bayesian inference (BI), which was performed using MrBayes 3.2.7a with a GTR+I+G model of DNA substitution and a gamma distribution rate variation across sites (Ronquist & Huelsenbeck 2003). A total of four Markov chains were run for two independent runs from random starting trees, each with 16 million generations, for the combined ITS+nLSU sequences. Trees and parameters were sampled every 1,000 generations. The first one-fourth of all the generations were discarded as burn-ins. The majority-rule consensus tree of all the remaining trees was calculated. Branches were considered significantly supported if they received a maximum likelihood bootstrap value (BS) of ≥70%, a maximum parsimony bootstrap value (BT) of ≥70%, or Bayesian posterior probabilities (BPP) of ≥0.95.

Results

Phylogenetic analyses

The phylogenetic tree (Figure 1) inferred from ITS+nLSU sequences revealed that *Phanerochaete flavissima* was nested within the *Phanerochaete* (Hymenochaetaceae). The dataset based on ITS+nLSU (Figure 1) comprises sequences from 94 fungal specimens representing 61 species. The dataset had an aligned length of 3,032 characters, of which 2,165 characters were constant, 210 were variable and parsimony-uninformative, and 506 were parsimony-informative. Maximum parsimony analysis yielded one equally parsimonious tree (TL = 2891, CI = 0.4358, HI = 0.5642, RI = 0.6415, RC = 0.2796). Bayesian analysis and ML analysis yielded a topology similar to that of MP analysis, with the effective sample size (ESS) across the two runs being double the average ESS (avg ESS) of 455.

The phylogenetic tree (Figure 1) inferred from ITS+nLSU sequences revealed that *Phanerochaete flavissima* was closely related to *P. carnosa* Parmasto (1986: 375).

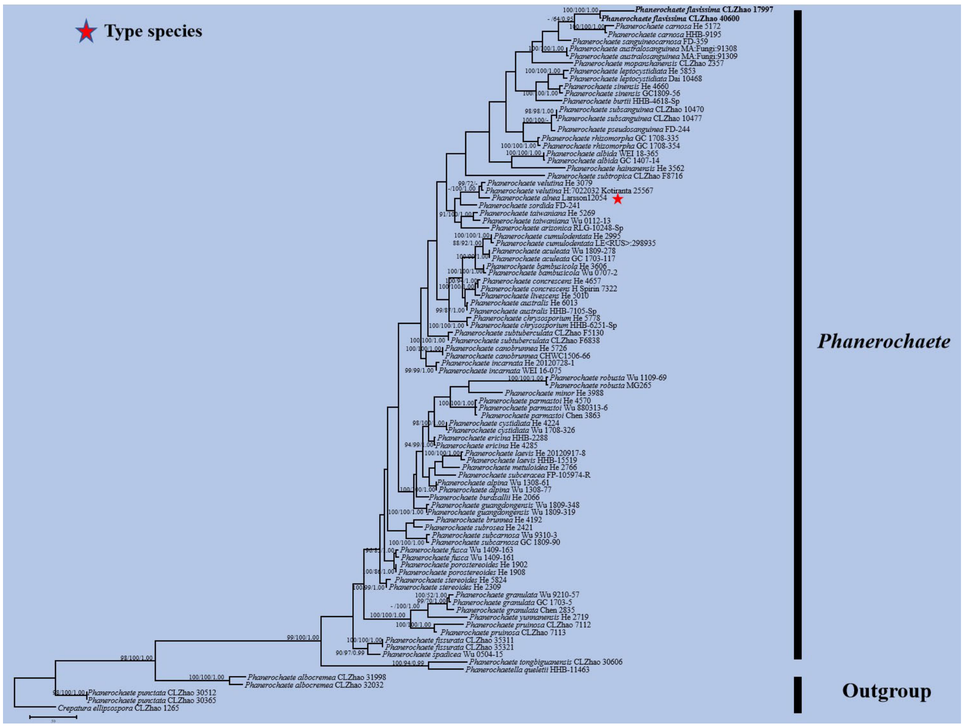

FIGURE 1. Maximum parsimony strict consensus tree illustrating the phylogeny of one new species and related species in *Phanerochaete* based on ITS+nLSU sequences. The branch is labeled with a maximum likelihood lead value greater than 70%, a reduced lead value greater than 50% and a Bayesian posterior probability greater than 0.95. The red star represents the type species. New species are in bold.

Taxonomy

Phanerochaete flavissima Y.C. Li & C.L. Zhao, *sp. nov.* Figures 1 and 2

MycoBank no.: MB 859084

***Etymology*:**—Refers to the yellow hymenial surface of the type specimen when fresh.

***Holotype*:**—China. Yunnan Province, Honghe, Pingbian County, Daweishan National Nature Reserve, 22°51' N, 103°41' E, altitude 2360 m, on the angiosperm trunk, leg. C.L. Zhao, 2 August 2019, CLZhao 17997 (SWFC).

***Basidiomata*:**—Annual, resupinate, adnate, without odor or taste when fresh, soft leather when fresh, leather upon drying, up to 6.8 cm long, 2.7 cm wide, 600–900 µm thick. Hymenial surface smooth, lemon-yellow when fresh, pale yellow to yellow when dry. Sterile margin pale yellow, 0.3 mm wide.

***Hyphal system*:**—Monomitic, generative hyphae mostly simple septate, clamp connections occasionally present in subiculum; tissues unchanged in KOH; generative hyphae mainly horizontal, colorless, thin to thick-walled, straight, occasionally branched, interwoven, sometimes encrusted with crystals, IKI–, CB–, 4.0–7.5 µm in diameter.

***Hymenium*:**—Cystidia and cystidioles absent. Basidia and basidioles not observed.

***Spores*:**—Basidiospores ellipsoid, colorless, thin-walled, smooth, occasionally with small oil drops, IKI–, CB–, 4.5–5.5 × 2.0–3.0 µm, L = 4.94 µm, W = 2.47 µm, Q = 1.89–2.00 (n = 60/2).

***Additional specimen examined (paratype)*:**—China. Yunnan Province, Honghe, Pingbian District, Daweishan Forest Park, GPS coordinates: 22°91' N, 103°70' E, altitude: 2075 m, on the fallen branch of an angiosperm tree, leg. C.L. Zhao, 3 October 2024, CLZhao 40600 (SWFC).

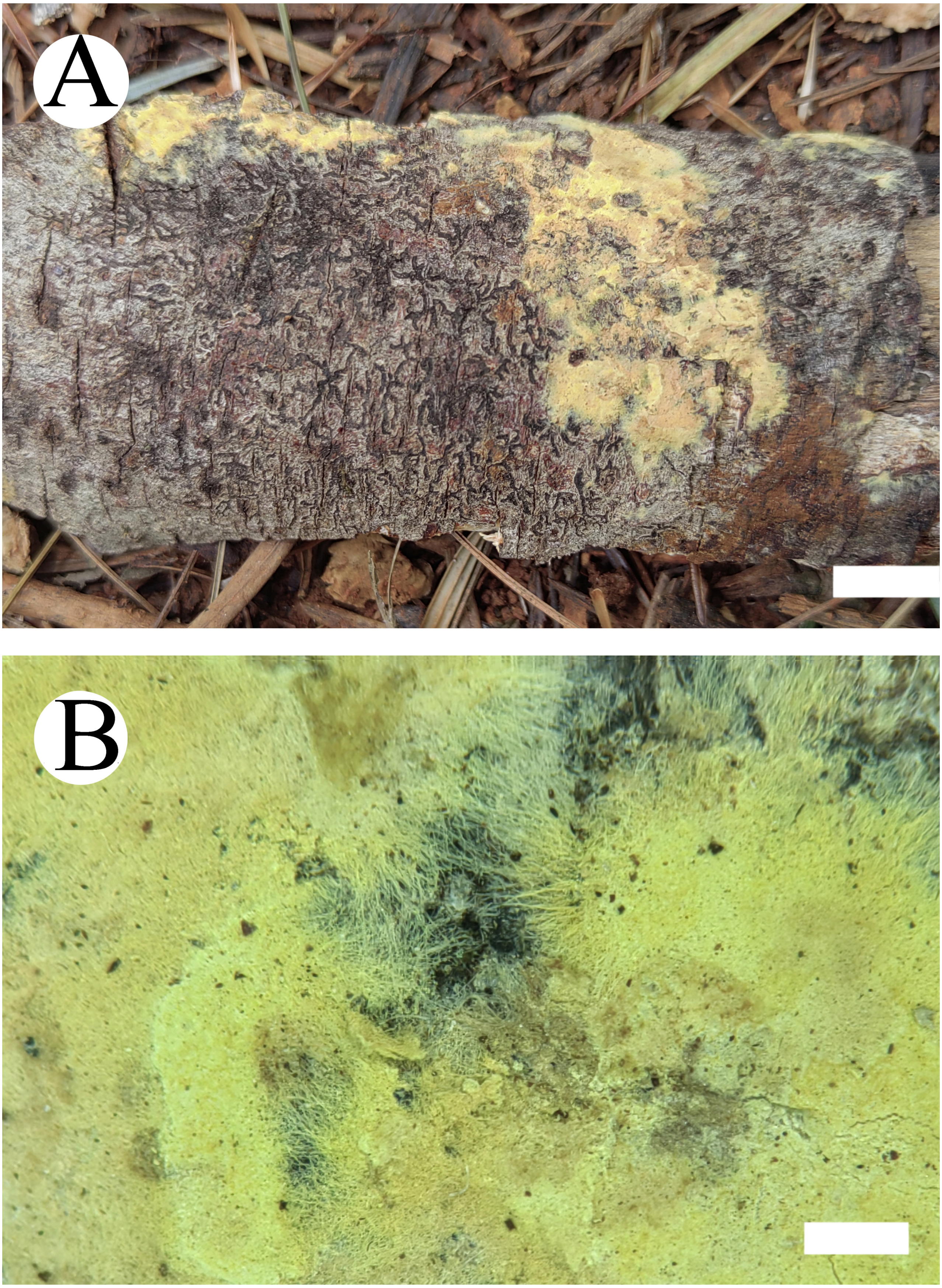

FIGURE 2. *Phanerochaete flavissima* (holotype, CLZhao 17997): basidiomata on the substrate (A), macroscopic characteristics of hymenophore (B). Bars: (A) = 1 cm and (B) = 1 mm.

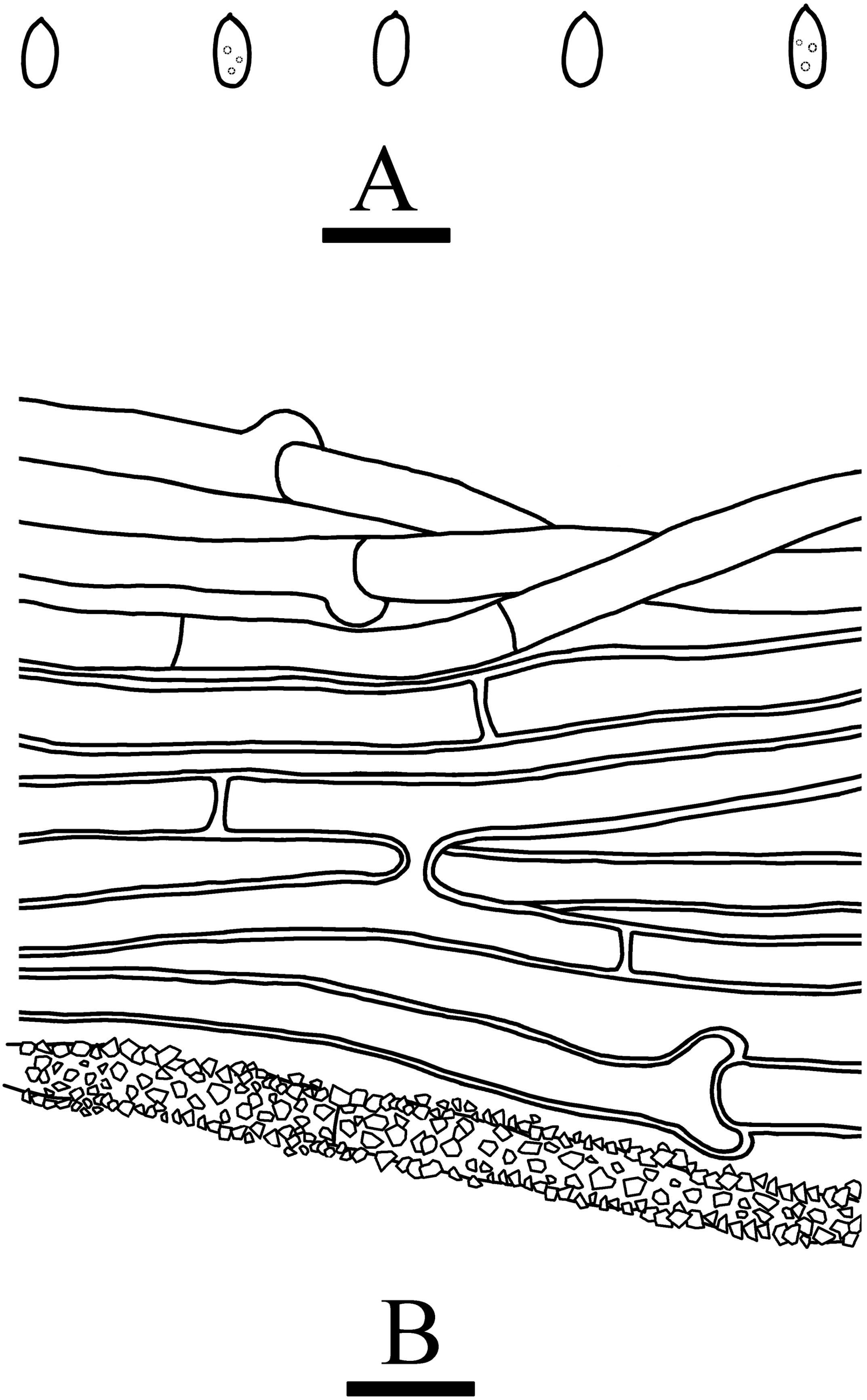

FIGURE 3. Microscopic structures of *Phanerochaete flavissima* (holotype, CLZhao 17997): basidiospores (A), a section of the hymenium (B). Bars: (A–B) = 10 µm.

Discussion

In the present study, *Phanerochaete flavissima* is described as a new species based on phylogenetic analyses and morphological characteristics. Currently, 60 species of *Phanerochaete*, including the present new species, have been reported in China.

In our study, the phylogenetic tree of ITS+nLSU (Figure 1) shows that the new species *Phanerochaete flavissima* is closely related to *P. carnosa.* However, *Phanerochaete carnosa* is distinct from *P. flavissima* by having a white hymenial surface and longer basidiospores (4.5–6 × 2–3 µm, Burdsall *et al.* 1985).

Morphologically, *Phanerochaete carnosa* (Burt) Parmasto (1967:388) and *P. punctata* are similar to *P. flavissima* by having ellipsoid basidiospores. However, *Phanerochaete carnosa* is distinguished from *P. flavissima* by its longer basidiospores (4.5–6 × 2–3 µm, Parmasto 1967). *Phanerochaete punctata* differs from *P. flavissima* by a white to pale buff hymenial surface (Xu *et al.* 2025); this new species enriches the fungal diversity in the Honghe area.

Fungi are one of the most diverse groups of organisms on earth and play a crucial role in ecosystem processes and functions (Hyde 2022). New DNA sequencing techniques have revolutionized the research of fungal taxonomy and diversity, with approximately 165,000 species of fungi having been described (Hyde *et al.* 2024). In recent years, the wood-inhabiting fungi have become an extensively studied group of Basidiomycota, which includes a number of poroid, smooth, grandinoid, odontioid, and hydnoid basidiomata in China (Dai *et al*. 2021, Wu *et al*. 2022a, 2022b, Dong *et al*. 2023a, 2023b, Zhao *et al*. 2024, Zhou *et al*. 2024); however, many new taxa have not yet been discovered. Therefore, the corticioid species diversity of the order *Phanerochaete* remains poorly understood in China, particularly in subtropical and tropical areas. This paper enhances our understanding of fungal diversity in this region. We anticipate that more undescribed corticioid taxa will be discovered throughout China after extensive collection combined with morphological and molecular analyses.

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