Phytotaxa

755

Magnolia Press, Auckland, New Zealand

Notes on the diatom collection of the Natural History Museum, London (BM) X: Roper's species of *Biddulphia* (Bacillariophyta)

[illegible]

***Hymenochaete yaoshanensis* sp. nov. (Hymenochaetaceae, Hymenochaetales), a wood-inhabiting fungus from Yunnan Province, southwest China**

[illegible]

The taxonomy and nomenclature of *Kalanchoe* ser. *Rotundifoliae*, a cluster of small-growing to medium-sized species with narrowly urceolate flowers here included in *K.* sect. *Kalanchoe* (Crassulaceae [subfam. Cotyledonoideae] tr. Kalanchoeae), with the description of a new series, *K.* ser. *Hirtae*

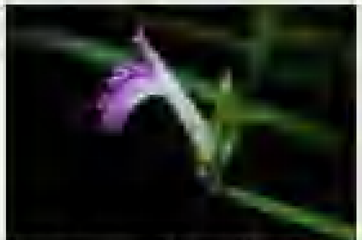
[illegible]

Morphological and ITS-based phylogenetic assessment of *Euphorbia* sect. *Pithyusa* (Euphorbiaceae) in Türkiye with taxonomic notes

[illegible]

Unveiling a novel *Menisporopsis* species (Chaetosphaeriaceae) from Thailand

[illegible]

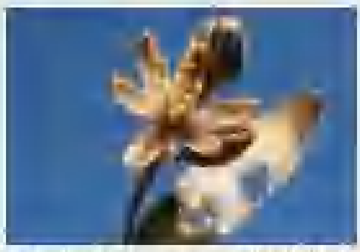


***Justicia zappiana* (Acanthaceae), a new species from the Atlantic Forest of Bahia, Brazil**

[illegible]

***Solanum altoserranum* (Solanaceae): a new species endemic from high-altitude grasslands of North-western Argentina**

[illegible]



***Trimelopter pterocarpum* (Hyacinthaceae subfam. Ornithogaloideae), a new species from South Africa**

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Hymenochaete yaoshanensis sp. nov. (Hymenochaetaceae, Hymenochaetales), a wood-inhabiting fungus from Yunnan Province, southwest China

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Abstract

The fungi constitute a highly diverse group distinct from plants and animals, and accurately determining the taxonomic placement of newly discovered taxa is essential for understanding fungal evolution and ecological function. In this study, a new species, *Hymenochaete yaoshanensis,* is proposed based on a combination of morphological features and molecular evidence of ITS and nLSU. The phylogenetic analysis inferred from ITS+nLSU sequence data placed *H. yaoshanensis* within the family Hymenochaetaceae and showed it to be closely related to *H. pinnatifida* and *H. longispora. Hymenochaete yaoshanensis* is characterized by a tuberculate to locally verruculose hymenial surface, a monomitic hyphal system, slightly thick-walled generative hyphae with simple septa, and oblong ellipsoid basidiospores (4–6 × 2–3 µm). A full description, illustrations, and phylogenetic analysis are provided to facilitate future taxonomic and systematic studies of *Hymenochaete* taxa.

Key words: Basidiomycota, Morphology, New species, Phylogeny, Taxonomy

Introduction

The origin and evolution of species is an important topic in biology, and biogeographic studies have been used to infer speciation processes, ancestral-state origins, and distribution patterns across diverse organismal groups (Wiens 2004, Seehausen *et al.* 2014). Fungi are crucial components of life on Earth and exert profound ecological and economic impacts (Hyde *et al.* 2024). However, compared with animals and plants, fungal biogeographical research remains limited (Zhao *et al.* 2024), largely because species delimitation is still incomplete, the fossil record is sparse (Taylor & Berbee 2006), and sampling is geographically and taxonomically uneven (Schmit & Mueller 2007). Through their interactions with other organisms significantly contribute to the proper functioning of terrestrial ecosystems, and growing evidence suggests that fungi have played important roles in shaping the evolution of multiple terrestrial clades (Berbee *et al.* 2017, Loron *et al.* 2019, Gan *et al.* 2021, Yuan *et al.* 2023, Liu *et al.* 2025b, Zhao *et al.* 2025). Basidiomycota R.T. Moore. (1980: 371) is the second largest branch in the fungal tree of life (Dai 2010, Vainioa *et al.* 2011, He *et al.* 2022, Niskanen *et al.* 2023, Hyde *et al.* 2024). The order Hymenochaetales Oberw. (1977: 89) comprises predominantly wood-inhabiting macrofungi in Agaricomycetes and was introduced with Hymenochaetaceae Donk (1948: 474) as the type family (Frey *et al.* 1997, Liu *et al.* 2025b, Zhao *et al.* 2025). All species in Hymenochaetales are white-rot fungi responsible for decomposing dead wood, and the order also includes renowned medicinal mushrooms, *Inonotus obliquus* (Fr.) Pilát (1942: 572) and *Sanghuangporus sanghuang* (Sheng, H. Wu *et al.*) Sheng H. Wu *et al.* (2015: 340), as well as economically important tree pathogens, such as species in the genera *Onnia* P. Karst. (1889:

326) and *Porodaedalea* Murrill (Dai 2010, Wu *et al.* 2022). Species of Hymenochaetales exhibit diverse basidiomata, comprising poroid, hydnoid, corticioid, and agaricoid morphologies (Larsson *et al.* 2006, Dai 2010, Korotkin *et al.* 2018, Liu *et al.* 2025b, Wijesinghe *et al.* 2025). Moreover, a subset of species displays marked host specificity, which can be broadly categorized into taxa associated exclusively with angiosperms, exclusively with gymnosperms, with both angiosperms and gymnosperms, or with bryophytes (Dai 2010, Purahong *et al.* 2018, Wijesinghe *et al.* 2025).

The family Hymenochaetaceae Donk is one of the clades within Hymenochaetales, and it comprises three major genera: *Phellinus* Quél. (1886: 172) sensu lato, *Hymenochaete* Lév. (1846: 150) and *Inonotus* P. Karst. (1879: 39) sensu lato (Larsen & Cobb-Poulle 1990, Léger 1998, Ryvarden 2005, Wu *et al.* 2022, Deng *et al.* 2025). Members of Hymenochaetaceae are characterized by annual to perennial, resupinate, effused-reflexed, pileate to stipitate, poroid or non- poroid, brownish basidiomata with a xanthochroic reaction in KOH, a monomitic, dimitic or trimitic hyphal system with simple septate generative hyphae, presence or absence of setal elements, and smooth, thin- to thick-walled, hyaline or brownish, indextrinoid or dextrinoid, cyanophilous or acyanophilous basidiospores, and all species cause white-rot (Liu *et al.* 2025b). Recently, the diversity and systematics of Hymenochaetaceae with poroid hymenophore were studied, and thirty-two poroid genera with 672 species were recognized (Wu *et al.* 2022). Many family members are economically significant; some species are forest pathogens, such as species in *Coniferiporia* L.W. Zhou & Y.C. Dai (1955: 388), *Onnia,* and *Pyrrhoderma* Imazeki. (1955: 388) (Zhou *et al.* 2016, Ji *et al.* 2017, Wu *et al.* 2022, Zhou *et al.* 2023). Notably, *Hymenochaete microcycla* (Zipp. ex Lév.) (2019: 86) Spirin & Miettinen (= *H. porioides* T. Wagner & M. Fisch.) has been reported to possess antitumor qualities and can also act as a pathogen of living angiosperm trees in native forests and plantations (Wu *et al.* 2019, Yuan *et al.* 2023).

Hymenochaete (Hymenochaetaceae, Hymenochaetales) Lév. is an aphyllophoroid genus of Agaricomycotina Doweld. (2001: LXXVIII) which was long considered readily distinguishable but has undergone substantial taxonomic re-evaluation since the beginning of 2002, when it was erected in 1846 (Parmasto *et al.* 2014, Li *et al.* 2024). *Hymenochaete* is the type genus of Hymenochaetaceae, and typified by *H. rubiginosa* (Dicks.) Lév. (1846: 150) (Léger 1998). *Hymenochaete* is characterized by annual to perennial, resupinate, effused-reflexed to pileate basidiomata with smooth, tuberculate, lamellate, poroid or hydnoid hymenophores; a monomitic or dimitic hyphal system; presence of setae, and hyaline, thin-walled, narrowly cylindrical to globose basidiospores (Léger 1998, Parmasto 2001, He & Dai 2012, Dai *et al.* 2025, Deng *et al.* 2025). According to Index Fungorum (www.index fungorum. org; accessed on 19 April 2026), *Hymenochaete* includes 399 registered names, of which 266 species are currently accepted worldwide (Léger 1998, Parmasto 2001, Parmasto & Gilbertson 2005, He & Dai 2012, Parmasto 2012, He *et al.* 2017, Pacheco *et al.* 2018, Miettinen *et al.* 2019, Dai *et al.* 2025, Deng *et al.* 2025).

During surveys of wood-inhabiting fungi in Yunnan Province, China, we collected specimens of a *Hymenochaete* taxon that did not match any previously described. In the present study, the taxonomic framework of Hymenochaetales is updated using ITS+nLSU sequence analyses, which support the taxonomy and phylogenetics of *Hymenochaete* species.

Materials and methods

Morphological studies

Fresh basidiomata of the fungus were photographed in situ from Zhaotong, Yunnan Province, China; collection details were recorded (Rathnayaka *et al.* 2025), and the specimens were taken to the laboratory in mushroom collection boxes. Specimens were dried in an electric food dehydrator at 40 °C (Hu *et al.* 2022), then sealed 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 collected in the field and in the lab. Color terminology follows Petersen (1996).

Micromorphological data were obtained from the dried specimens by light microscopy, following the methods described in previous studies (Zhao *et al.* 2023, Dong *et al.* 2024). 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).

Molecular procedures and phylogenetic analyses

The EZNA HP Fungal DNA Kit (Omega Biotechnologies Co., Ltd., Kunming, China) was used to extract DNA from the dried specimens, with some modifications. The nuclear ribosomal ITS region was amplified with primers ITS5 and ITS4 (White *et al.* 1990). The PCR procedure for ITS was as follows: initial denaturation at 95 °C for 3 min, followed by 35 cycles at 94 °C for 40 s, 58 °C for 45 s, and 72 °C for 1 min, and a final extension of 72 °C for 10 min. The nuclear LSU region was amplified with primer pair LR0R and LR7 (Vilgalys & Hester 1990, Rehner & Samuels 1994). The PCR procedure for LSU 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 of 72 °C for 10 min. The PCR procedure for ITS and LSU followed a previous study (Dong *et al.* 2024). All the newly generated sequences were deposited in NCBI GenBank (https://www.ncbi.nlm.nih.gov/genbank/) (Table 1).

To determine the phylogeny, we compiled an ITS+nLSU dataset. The sequences were initially aligned with MAFFT (https://mafft.cbrc.jp/alignment/server/) using the "G-INS-I" strategy (Katoh *et al.* 2019), and then manually optimized in AliView version 1.27 (Larsson 2014). Finally, the two gene fragments were concatenated with Mesquite v3.70 (Maddison & Maddison 2021, https://www.mesquiteproject.org/) for further phylogenetic analyses.

Maximum parsimony (MP), Maximum Likelihood (ML), and Bayesian Inference (BI) analyses were applied to the combined datasets following a previous study (Dong *et al.* 2024), and the tree construction procedure was performed in PAUP* version 4.0b10 (Swofford 2002). All the characters were equally weighted, and gaps were treated as missing data. Trees were inferred using the heuristic search option with TBR branch swapping and 1,000 random sequence additions. Max trees were set to 5000, branches of zero length were collapsed, and all parsimonious trees were saved. Clade robustness was assessed using bootstrap (BT) analysis with 1,000 replicates (Felsenstein 1985). Descriptive tree statistics, tree length (TL), the consistency index (CI), the retention index (RI), the rescaled consistency index (RC), and the homoplasy index (HI) were calculated for each maximum parsimonious tree 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.

TABLE 1. A list of species, specimens, and GenBank accession numbers of sequences used in this study; "–" indicates data unavailability, and "*" represents the type specimens.

Species name	Specimen No.	GenBank accession No.		Country	References
		ITS	nLSU		
Hydnoporia olivacea	Miettinen X3403	MK514612	–	USA	Liu *et al.* (2025b)
Hymenochaete acerosa	He 338	JQ279543	JQ279657	China	He & Li (2011)
H. acerosa	He 344*	JQ279544	–	China	He & Li (2011)
H. adhaerens	Spirin 4994	KM017411	–	Russia	Liu *et al.* (2025b)
H. adhaerens	Spirin 6246*	KM017412	–	Russia	Liu *et al.* (2025b)
H. adnata	He 655	OR287568	OR287643	China	Liu *et al.* (2025b)
H. adusta	He 207	JQ279523	KU975497	China	He & Dai (2012)
H. alpina	He 1388*	OR287604	OR287674	China	Liu *et al.* (2025b)
H. alpina	He 4918	OR287605	OR287675	China	Liu *et al.* (2025b)
H. ametzii	ARAN-Fungi 19941*	PP337720	PP337778	Spain	Olariaga *et al.* (2024)
H. ametzii	ARAN-Fungi 20108	PP337723	PP337781	Spain	Olariaga *et al.* (2024)
H. angustispora	Dai 17045	MF370592	MF370598	China	He & Liu (2017)
H. angustispora	Dai 17049*	MF370593	MF370599	China	He & Liu (2017)
H. anomala	He 135	JQ279567	–	China	He & Dai (2012)
H. anomala	He 592	JQ279566	JQ279650	China	He & Dai (2012)
H. asetosa	Dai 10756*	JQ279559	JQ279642	China	He & Dai (2012)
H. asetosa	He 545	JQ279558	–	China	He & Dai (2012)
H. asiatica	He 1270*	OR287593	OR287663	China	Liu *et al.* (2025b)
H. asiatica	He 5800	OR287594	–	Sri Lanka	Liu *et al.* (2025b)
H. atrobrunnea	Dai 18810	OR287608	OR287656	Australia	Liu *et al.* (2025b)

......*continued on the next page*

TABLE 1. (Continued)

Species name	Specimen No.	GenBank accession No.		Country	References
		ITS	nLSU		
H. atrobrunnea	Dai 18821*	OR287591	OR287657	Australia	Liu *et al.* (2025b)
H. attenuata	He 15	JQ279525	–	China	He & Dai (2012)
H. attenuata	He 28	JQ279526	JQ279633	China	He & Dai (2012)
H. australis	TAAM171362*	KM017414	–	Argentina	Liu *et al.* (2025b)
H. austrosinensis	He 1009*	OR287589	OR287660	China	Liu *et al.* (2025b)
H. austrosinensis	He 7078	OR287590	OR287661	China	Liu *et al.* (2025b)
H. bambusicola	He 4116*	KY425674	KY425681	Thailand	Nie *et al.* (2017)
H. bambusicola	He 4121	KY425675	KY425682	Thailand	Nie *et al.* (2017)
H. berteroi	He 133	JQ279524	–	China	He & Dai (2012)
H. berteroi	He 1488	KU975459	KU975498	China	He & Liu (2017)
H. biformisetosa	He 1445*	KF908247	KU975499	China	Yang & He (2014)
H. bispora	He 4993	OR287532	OR287617	China	Liu *et al.* (2025b)
H. boddingii	MEH 66068*	MN030343	MN030345	India	Rossi *et al.* (2020)
H. boddingii	MEH 66150	MN030344	MN030346	India	Rossi *et al.* (2020)
H. boidinii	CBS 765.91	MH862335	–	Réunion	Vu *et al.* (2019)
H. borbonica	CBS 731.86*	MH862026	MH873716	Réunion	Vu *et al.* (2019)
H. brunnea	He 591	OR287581	OR287654	China	Liu *et al.* (2025b)
H. brunnea	He 581*	OR287582	OR287655	China	Liu *et al.* (2025b)
H. campylopora	Cui 7393	JQ279513	JQ279629	China	Liu *et al.* (2025b)
H. cana	He 1305*	KF438169	KF438172	China	He & Li (2014)
H. cana	He 1315	KF438170	KF438173	China	He & Li (2014)
H. cervinoidea	CBS 736.86	MH862027	AF385157	Réunion	Vu *et al.* (2019)
H. cinerea	He 1432*	OR287602	OR287672	China	Liu *et al.* (2025b)
H. cinerea	He 1483	OR287603	OR287673	China	Liu *et al.* (2025b)
H. cinereoalba	CLZhao 4252	OR287567	OR287642	China	Liu *et al.* (2025b)
H. cinereoalba	He 6162*	OR287559	OR287636	China	Liu *et al.* (2025b)
H. cinnamomea	He 755	JQ279548	JQ279658	China	Nie *et al.* (2017)
H. cinnamomea	He 2074	KU975460	KU975500	USA	Nie *et al.* (2017)
H. coffeana	He 250	OR287533	–	China	Liu *et al.* (2025b)
H. colliculosa	Dai 16428	MF370596	MF370603	China	He & Liu (2017)
H. conchata	LWZ 20140728-11	KX258959	–	Thailand	Pan & Zhou (2016)
H. conchata	LWZ 20140728-13*	KX258960	–	Thailand	Pan & Zhou (2016)
H. conifericola	He 788	JQ279539	OR287666	China	Liu *et al.* (2025b)
H. conifericola	He 779*	JQ279538	JQ279641	China	Liu *et al.* (2025b)
H. contiformis	He 1166	KU975461	KU975501	China	He & Liu (2017)
H. cruenta	He 766	JQ279595	JQ279681	China	He & Liu (2017)
H. cupulata	Spirin 6245*	KM017417	–	Russia	Liu *et al.* (2025b)
H. cupulata	Spirin 6249	KM017418	–	Russia	Liu *et al.* (2025b)
H. curtisii	He 2061	KU975462	KU975502	USA	Olariaga *et al.* (2024)
H. cylindrospora	Dai 14890	OR287562	–	China	Liu *et al.* (2025b)
H. cylindrospora	He 773*	OR287563	OR287638	China	Liu *et al.* (2025b)
H. damicornis	URM 84261	KC348466	–	Brazil	Liu *et al.* (2025b)
H. denticulata	CBS 780.91*	MH862336	AF385155	Réunion	Vu *et al.* (2019)
H. denticulata	He 1271	KF438171	KF438174	China	He & Li (2014)

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TABLE 1. (Continued)

Species name	Specimen No.	GenBank accession No.		Country	References
		ITS	nLSU		
H. dichotoma	Dai 18649	OR287573	OR287647	Australia	Liu *et al.* (2025b)
H. dichotoma	Dai 18779*	OR287574	OR287648	Australia	Liu *et al.* (2025b)
H. dracaenicola	Dai 22090*	MW559797	MW559802	China	Du *et al.* (2021)
H. duportii	AFTOL-ID 666	DQ404386	AY635770	–	He & Liu (2017)
H. epichlora	He 525	JQ279549	JQ279659	China	He & Dai (2012)
H. epichlora	CLZhao 6083	MK795138	–	China	Unpublished
H. erastii	He 1639*	OR287569	OR287644	China	Liu *et al.* (2025b)
H. erastii	He 1644	OR287570	–	China	Liu *et al.* (2025b)
H. fissurata	He 1193*	OR287535	OR287619	China	Liu *et al.* (2025b)
H. fissurata	CLZhao 890	MG231570	–	China	Unpublished
H. flava	Dai 27359*	PV191160	PV191251	China	Liu *et al.* (2025b)
H. flava	He 346	OR287587	OR287658	China	Liu *et al.* (2025b)
H. floridea	He 529	JQ279598	–	China	He & Dai (2012)
H. floridea	He 536	JQ279597	JQ279683	China	He & Dai (2012)
H. fuliginosa	He 1188	KU975465	KU975506	China	He & Dai (2012)
H. fulva	He 620	JQ279564	–	China	He & Dai (2012)
H. fulva	He 640	JQ279565	JQ279648	China	He & Dai (2012)
H. globispora	He 911	OR287536	KU975508	China	Liu *et al.* (2025b)
H. granulata	He 1472*	KU975495	KU975547	China	Liu *et al.* (2025b)
H. hainanensis	He 1509	OR287595	OR287664	China	Liu *et al.* (2025b)
H. hainanensis	He 1534*	OR287596	OR287665	China	Liu *et al.* (2025b)
H. huangshanensis	He 432*	JQ279533	JQ279671	China	He & Dai (2012)
H. huangshanensis	He 441	JQ279535	JQ279669	China	He & Dai (2012)
H. hubeiensis	He 5084	OR287610	OR287678	China	Liu *et al.* (2025b)
H. hubeiensis	Dai 17959*	OR287611	OR287679	China	Liu *et al.* (2025b)
H. hydnoides	Cui 8806	JQ279589	–	China	He & Dai (2012)
H. hydnoides	He 245	JQ279590	JQ279680	China	He & Dai (2012)
H. iliensis	Yuan 374	PP769636	–	China	Liu *et al.* (2025b)
H. iliensis	Yuan 386*	PP769637	–	China	Liu *et al.* (2025b)
H. innexa	He 446	JQ279585	JQ279673	China	He & Dai (2012)
H. innexa	He 555	JQ279584	JQ279674	China	He & Dai (2012)
H. jobii	He 2077	KU975468	KU975510	USA	Yang & He (2014)
H. koeljalgii	TAAM 159464*	–	HE651003	Tanzania	Liu *et al.* (2025b)
H. legeri	He 960	KU975469	KU975511	China	Liu *et al.* (2025b)
H. legeri	He 1021	OR287538	OR287621	China	Liu *et al.* (2025b)
H. leveillei	CLZhao 10443	OR287547	–	China	Liu *et al.* (2025b)
H. leveillei	He 6202*	OR287549	OR287629	China	Liu *et al.* (2025b)
H. lictor	He 20140723-2	KU975470	KU975512	China	Liu *et al.* (2025b)
H. lictor	He 20140723-11	KU975471	KU975513	China	Unpublished
H. liyiriana	ARFR260*	OR584222	OR569028	India	Liu *et al.* (2025b)
H. liyiriana	ARFR260a	PQ182942	–	India	Liu *et al.* (2025b)
H. longispora	He 101	JQ279536	–	China	He & Dai (2012)
H. longispora	He 217	JQ279537	KU975514	China	He & Dai (2012)
H. subluteobadia	He 8	JQ279569	KU975515	China	He & Dai (2012)

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TABLE 1. (Continued)

Species name	Specimen No.	GenBank accession No.		Country	References
		ITS	nLSU		
H. subluteobadia	He 10*	JQ279568	–	China	He & Dai (2012)
H. luteomarginata	He 1457*	OR287614	OR287680	China	Liu *et al.* (2025b)
H. luteomarginata	He 1849	OR287615	OR287681	China	Liu *et al.* (2025b)
H. macrospora	Dai 488*	KM017413	–	China	Liu *et al.* (2025b)
H. major	CLZhao 5136	OR287558	–	China	Liu *et al.* (2025b)
H. major	He 1942*	KU975489	KU975541	China	Liu *et al.* (2025b)
H. megaspora	He 302	JQ279553	JQ279660	China	He & Dai (2012)
H. megaspora	He 328*	JQ279554	–	China	He & Dai (2012)
H. membranacea	He 1899*	KU975491	KU975543	China	Liu *et al.* (2025b)
H. membranacea	He 1903	KU975492	KU975544	China	Liu *et al.* (2025b)
H. microcycla	CLZhao 9903	OM959418	OM967407	China	Unpublished
H. microcycla	CLZhao 9910	OM959419	–	China	Unpublished
H. minor	He 933*	JQ279555	JQ279654	China	He & Dai (2012)
H. minor	He 936	JQ279556	–	China	He & Dai (2012)
H. minuscula	He 253	JQ279546	KU975516	China	He & Dai (2012)
H. minuscula	He 877	JQ279547	–	China	He & Dai (2012)
H. moniliformis	He 916*	OR287555	OR287633	China	Liu *et al.* (2025)
H. moniliformis	He 1321	OR287556	OR287634	China	Liu *et al.* (2025b)
H. montana	He 1172	OR287606	OR287676	China	Liu *et al.* (2025b)
H. montana	He 1380*	OR287607	OR287677	China	Liu *et al.* (2025b)
H. mougeotii	CBS 289.54	MH857337	MH868878	France	Vu *et al.* (2019)
H. muroiana	He 172	JQ279541	–	China	He & Dai (2012)
H. muroiana	He 405	JQ279542	KU975517	China	He & Dai (2012)
H. nanospora	CBS 924.96*	MH862622	MH874244	Central Africa Republic	Liu *et al.* (2025b)
H. nanospora	He 475	JQ279531	JQ279672	China	He & Dai (2012)
H. niveomarginata	Dai 24611	PP769638	PP769648	China	Liu *et al.* (2025b)
H. niveomarginata	He 1611*	PP769639	–	China	Liu *et al.* (2025b)
H. yaoshanensis	**CLZhao 20626**	**PP356584**	**PP785350**	**China**	**Present Study**
H. yaoshanensis	**CLZhao 20661***	**PP356585**	**–**	**China**	**Present Study**
H. nothofagicola	He 503	JQ279530	JQ279632	China	Liu *et al.* (2025b)
H. ochromarginata	Cui 8197	JQ279578	–	China	He & Dai (2012)
H. ochromarginata	He 47	JQ279579	JQ279666	China	He & Dai (2012)
H. odontoides	Dai 11635	JQ279563	JQ279647	China	Nie *et al.* (2017)
H. orientalis	He 1057	KY425678	KY425686	China	Nie *et al.* (2017)
H. orientalis	He 4601*	KY425677	KY425685	China	Nie *et al.* (2017)
H. parmastoi	He 367*	JQ780061	–	China	Nie *et al.* (2017)
H. parmastoi	He 867	JQ780063	KU975518	China	Nie *et al.* (2017)
H. paucisetigera	Cui 7845	JQ279560	JQ279644	China	He & Dai (2012)
H. paucisetigera	Dai 10478	JQ279561	–	China	He & Dai (2012)
H. peroxydata	JMB1819	KF371644	KF371647	Brazil	Baltazar *et al.* (2014)
H. peroxydata	JMB2102	KF371646	KF371649	Brazil	Baltazar *et al.* (2014)
H. piceae	He 1203*	OR287571	OR287645	China	Liu *et al.* (2025b)

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TABLE 1. (Continued)

Species name	Specimen No.	GenBank accession No.		Country	References
		ITS	nLSU		
H. piceae	He 1200	OR287572	OR287646	China	Liu *et al.* (2025b)
H. pinnatifida	He 2193	KU975472	KU975519	USA	He & Dai (2012)
H. puerensis	He 692*	OR287612	–	China	Liu *et al.* (2025b)
H. puerensis	He 708	OR287613	–	China	Liu *et al.* (2025b)
H. quercicola	He 373	KU975474	KU975521	China	He & Li (2011)
H. quercicola	He 377*	OR287542	–	China	He & Li (2011)
H. ramicola	He 1897*	KU975494	KU975546	China	Liu *et al.* (2025b)
H. ramicola	He 1703	KU975493	KU975545	China	Liu *et al.* (2025b)
H. resupinata	TU 100039	–	HE650988	Costa Rica	Liu *et al.* (2025b)
H. rhabarbarina	He 280	JQ279574	KY425688	China	Nie *et al.* (2017)
H. rhabarbarina	He 4636	KY425680	KY425689	China	Nie *et al.* (2017)
H. rheicolor	CLZhao 22819	PV243176	–	China	Unpublished
H. rhododendricola	He 392*	JQ279576	–	China	He & Dai (2012)
H. rhododendricola	He 1121	KU975476	KU975523	China	Olariaga *et al.* (2024)
H. rubiginosa	Miettinen X3422	MK757158	–	Switzerland	Liu *et al.* (2025b)
H. rubrobrunnea	He 1982*	OR287579	KU975549	China	Liu *et al.* (2025b)
H. rubrobrunnea	He 5346	OR287580	OR287653	China	Liu *et al.* (2025b)
H. rufomarginata	He 1489	KU975477	KU975524	China	Yang & He (2014)
H. senatoumbrina	He 2437	KU975478	KU975525	China	Olariaga *et al.* (2024)
H. separabilis	He 460	JQ279572	JQ279655	China	Nie *et al.* (2017)
H. separabilis	He 1479	KU975479	KU975526	China	Yang & He (2014)
H. separata	He 934	OR287544	OR287626	China	Liu *et al.* (2025b)
H. setulohypha	He 5602	OR287560	–	China	Liu *et al.* (2025b)
H. setulohypha	He 5570*	OR287561	OR287637	China	Liu *et al.* (2025b)
H. setipora	Cui 6301	JQ279515	JQ279639	China	Nie *et al.* (2017)
H. setipora	Cui 8349	JQ279516	JQ279638	China	Olariaga *et al.* (2024)
H. sharmae	CAL 1535*	KY929017	KY929018	India	Wang *et al.* (2019)
H. sharmae	66088	MK588753	MK588836	India	Liu *et al.* (2025b)
H. sichuanensis	He 1385*	OR287585	OR287652	China	Liu *et al.* (2025b)
H. sichuanensis	He 1340	OR287577	OR287641	China	Liu *et al.* (2025b)
H. sinensis	CLZhao 26040*	OR659001	PP425893	China	Li *et al.* (2024)
H. sinensis	CLZhao 26652	PQ060540	–	China	Li *et al.* (2024)
H. spathulata	He 685	JQ279591	KU975529	China	He & Dai (2012)
H. spathulata	He 704	JQ279592	–	China	He & Dai (2012)
H. sphaerospora	He 715	JQ279594	KU975531	China	He & Dai (2012)
H. sphaerospora	CLZhao 3206	MH114716	–	China	Unpublished
H. stereoidea	He 1661*	KU975488	KU975540	China	Liu *et al.* (2025b)
H. stereoidea	CLZhao 4321	OR287609	–	China	Liu *et al.* (2025b)
H. stratura	HHB-19391	MW740246	–	New Zealand	Liu *et al.* (2025b)
H. subepichlora	He 556	OR287554	OR287632	China	Liu *et al.* (2025b)
H. subepichlora	He 716*	PP769642	–	China	Liu *et al.* (2025b)
H. subferruginea	CLZhao 3325	MK269013	–	China	Unpublished

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TABLE 1. (Continued)

Species name	Specimen No.	GenBank accession No.		Country	References
		ITS	nLSU		
H. subferruginea	Cui 8122	JQ279521	–	China	He & Dai (2012)
H. subinnexa	He 1213	OR287597	OR287667	China	Liu *et al.* (2025b)
H. subinnexa	He 1007*	OR287598	OR287668	China	Liu *et al.* (2025b)
H. subluteobadia	He 8	JQ279569	KU975515	China	Liu *et al.* (2025b)
H. subluteobadia	He 10*	JQ279568	OR287662	China	Liu *et al.* (2025b)
H. subporioides	Cui 10163*	KT283051	OR287627	China	Liu *et al.* (2025b)
H. subrhabarbarina	He 737*	OR287575	OR287649	China	Liu *et al.* (2025b)
H. subrhabarbarina	He 860	OR287576	–	China	Liu *et al.* (2025b)
H. tasmanica	He 449	JQ279582	JQ279663	China	He & Dai (2012)
H. tasmanica	He 455	JQ279583	–	China	He & Dai (2012)
H. tongbiguanensis	He 1552	KF908248	KU975532	China	Nie *et al.* (2017)
H. tropica	He 574	JQ279587	JQ279675	China	He & Dai (2012)
H. tropica	He 661*	JQ279588	–	China	He & Dai (2012)
H. unicolor	He 450	JQ279552	–	China	He & Dai (2012)
H. unicolor	He 468a	JQ279551	JQ279662	China	He & Dai (2012)
H. ustulata	He 104	JQ780066		China	He & Liu (2017)
H. vaginata	He 2558	KU975483	KU975535	China	Liu *et al.* (2025b)
H. vaginata	He 2599	KU975484	KU975536	China	Olariaga *et al.* (2024)
H. variabilis	He 1610	OR287592	OR287650	China	Liu *et al.* (2025b)
H. variabilis	Dai 19779*	OR287584	OR287651	China	Liu *et al.* (2025b)
H. verruculosa	Dai 17047*	–	MF370600	China	He & Liu (2017)
H. verruculosa	Dai 17052	MF370594	MF370601	China	He & Liu (2017)
H. villosa	He 537	JQ279528	JQ279634	China	He & Dai (2012)
H. villosa	He 1739	KU975485	KU975537	China	Olariaga *et al.* (2024)
H. vitellina	CLZhao 17846	OR287550	–	China	Liu *et al.* (2025b)
H. vitellina	He 5061*	OR287551	OR287630	China	Liu *et al.* (2025b)
H. vivida	He 5288*	OR287599	OR287669	China	Liu *et al.* (2025b)
H. vivida	He 4986	OR287600	OR287670	China	Liu *et al.* (2025b)
H. weishanensis	CLZhao 22615*	PQ523357	PQ523363	China	Dai *et al.* (2025)
H. xerantica	CLZhao 4168	OM959451	OM967411	China	Unpublished
H. xerantica	Cui 9209	JQ279519	JQ279635	China	Nie *et al.* (2017)
H. yunnanensis	He 709*	JQ279571	–	China	He & Dai (2012)
H. yunnanensis	He 1447	KU975486	KU975538	China	Olariaga *et al.* (2024)

JModelTest 2 on the ACCESS server was used to determine the best-fit evolutionary model for each data set in the CIPRES Science Gateway (Miller *et al.* 2012). The best model for the ITS+nLSU dataset, as estimated and applied in the Bayesian analysis, was GTR+I+G. Bayesian Inference (BI) phylogenies were inferred using MrBayes v3.2.7a with a general time-reversible model of DNA substitution and a gamma distribution of rate variation across sites (Ronquist *et al.* 2012). A total of 4 Markov chains were run for 2 runs from random starting trees for 19 million generations for ITS+nLSU (Fig. 1), with trees and parameters sampled every 1,000 generations. The first one-fourth of all generations was discarded as burn-in. The majority rule consensus tree of all remaining trees was calculated. Branches were considered significantly supported if they received a maximum likelihood bootstrap value (BS) ≥70%, a maximum parsimony bootstrap value (BT) ≥50%, or a Bayesian posterior probability (BPP) ≥0.95.

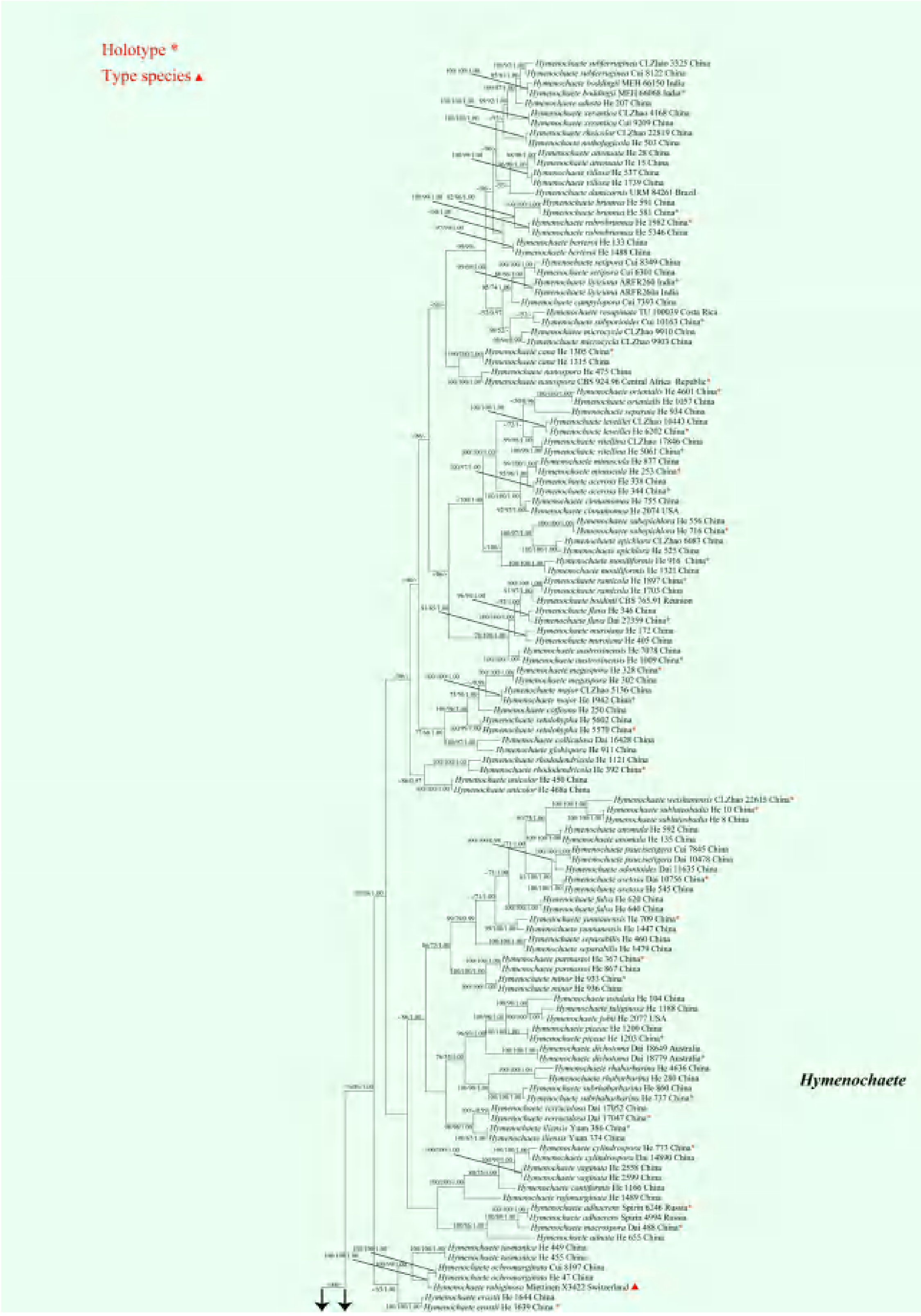

FIGURE 1. Maximum parsimony strict consensus tree illustrating the phylogeny of the new species *Hymenochaete yaoshanensis* and related species in the genus within the family Peniophoraceae based on ITS+nLSU sequences. The branch is labeled with a maximum-likelihood lead value of 70% or higher, a reduced lead value of 50% or higher, and a Bayesian posterior probability of 0.95 or higher.

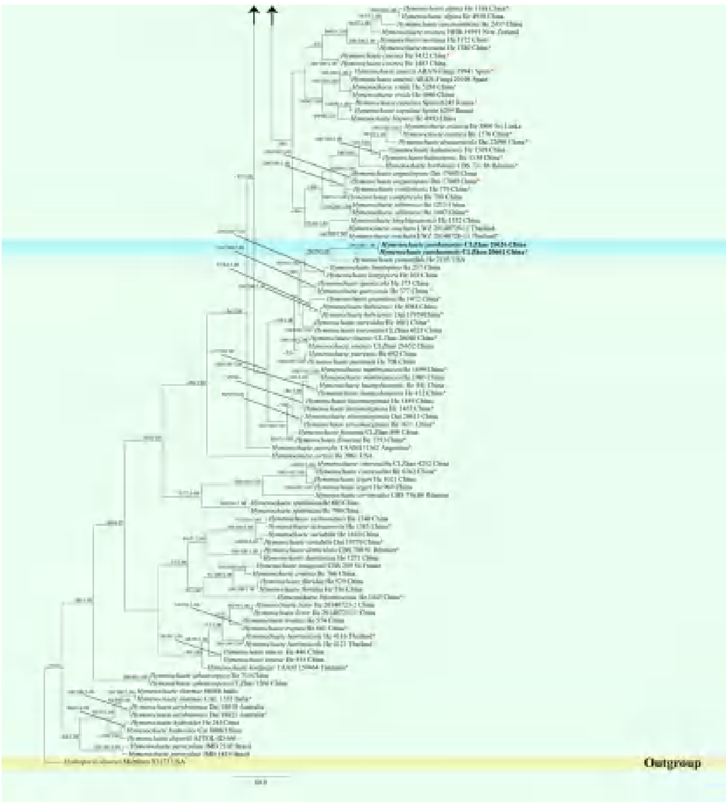

FIGURE 1. (Continued)

Phylogenetic analyses

The dataset based on ITS+nLSU (Figure 1), comprises sequences from 225 fungal specimens representing 132 different species. The dataset had an aligned length of 2,372 characters, of which 1,471 characters were constant, 200 were variable and parsimony-uninformative, and 701 were parsimony-informative. Maximum parsimony analysis yielded 1 equally parsimonious tree (TL = 5,270, CI = 0.2816, HI = 0.7184, RI = 0.7459, RC = 0.2100). Bayesian analysis and ML analysis yielded a similar topology to the MP analysis, with an average standard deviation of split frequencies of 0.037445 (BI), and the effective sample size (ESS) across the two runs was double the average ESS (avg ESS) = 304.5.

The phylogram based on the ITS+nLSU sequences indicates that the new species *Hymenochaete yaoshanensis* is recovered as a sister to *H. pinnatifida* Burt and is clustered with *H. longispora* Parmasto and *H. quercicola* S. H. He & Hai J. Li.

Taxonomy

Hymenochaete yaoshanensis X.M. Xu & C.L. Zhao, *sp. nov.*

MycoBank no.: MB852413

Etymology*:—*Yaoshanensis (Lat.): refers to the type locality, Yaoshan.

Diagnosis*:—Hymenochaete yaoshanensis* differs from other species in the genus *Hymenochaete* by grayish brownish to slightly brown hymenial surface with tuberculate to locally verruculose, subclavate to subcylindrical basidia, and oblong ellipsoid basidiospores measuring 4–6 × 2–3 µm.

***Holotype*:—**CHINA. Yunnan Province, Zhaotong, Qiaojia County, Yaoshan, Yaoshan National Nature Reserve, GPS coordinates: 27°08′ N, 103°09′ E, altitude 2,220 m asl., on the fallen angiosperm branch, leg. C.L. Zhao, 21 August 2020, CLZhao 20661 (SWFC 00020661).

***Basidiomata*:—**Annual, resupinate, adnate, hard corky, up to 9.3 cm long, 2.2 cm wide, and 0.1 mm thick. Hymenial surface tuberculate to locally verruculose, grayish brownish when fresh, grayish brownish to slightly brown upon drying. Margin grayish brownish, up to 1 mm.

FIGURE 2. *Hymenochaete yaoshanensis* (holotype, CLZhao 20661): Basidiomata (a), Macroscopic characteristics of hymenophore (b). Bars: (a) = 1 cm and (b) = 1mm.

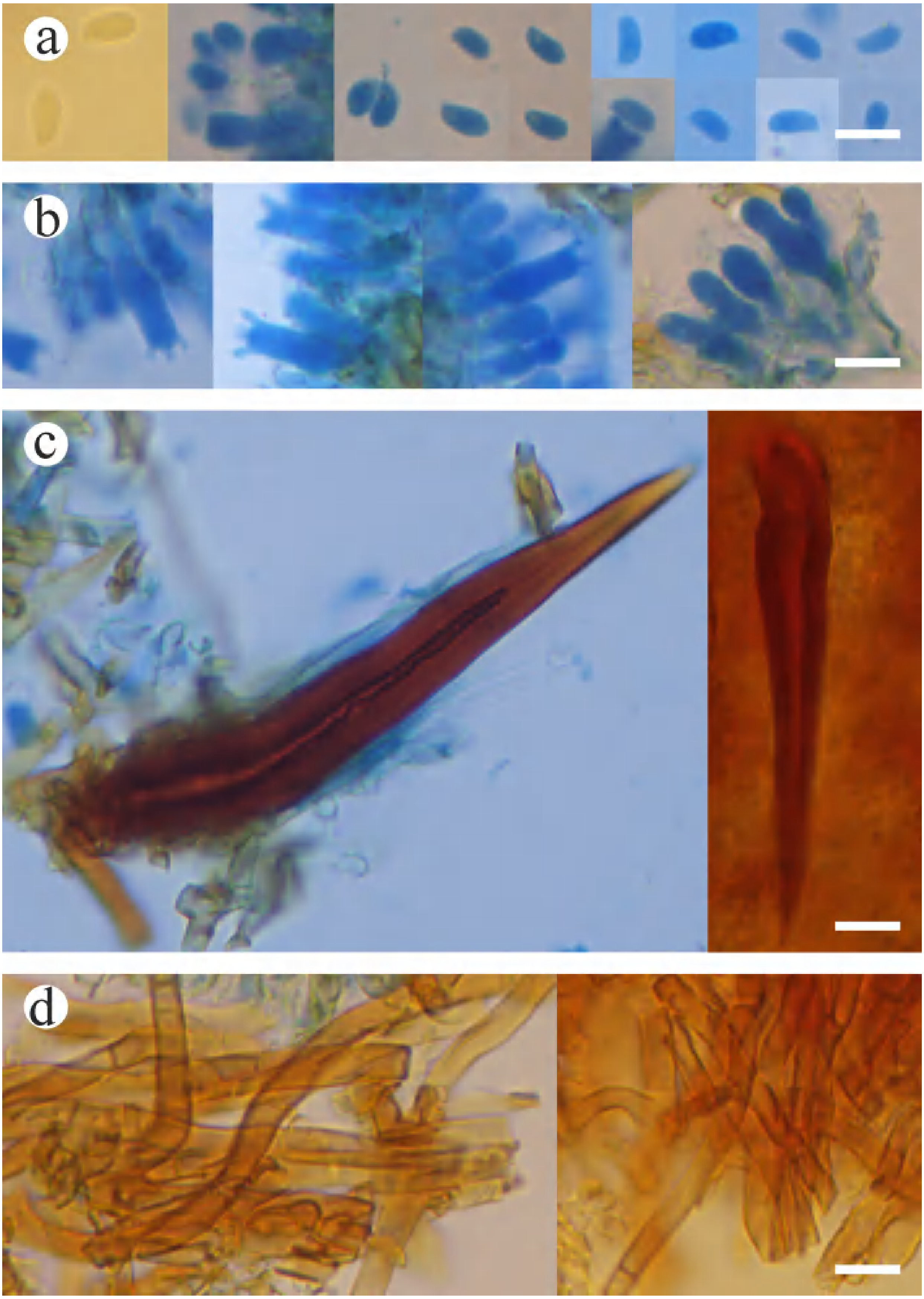

FIGURE 3. Microscopic structures of *Hymenochaete yaoshanensis* (holotype, CLZhao 20661): Basidiospores (a), Basidia and basidioles (b), Setae (c), A section of the hymenium (d). Bars: (a–d) = 10 µm.

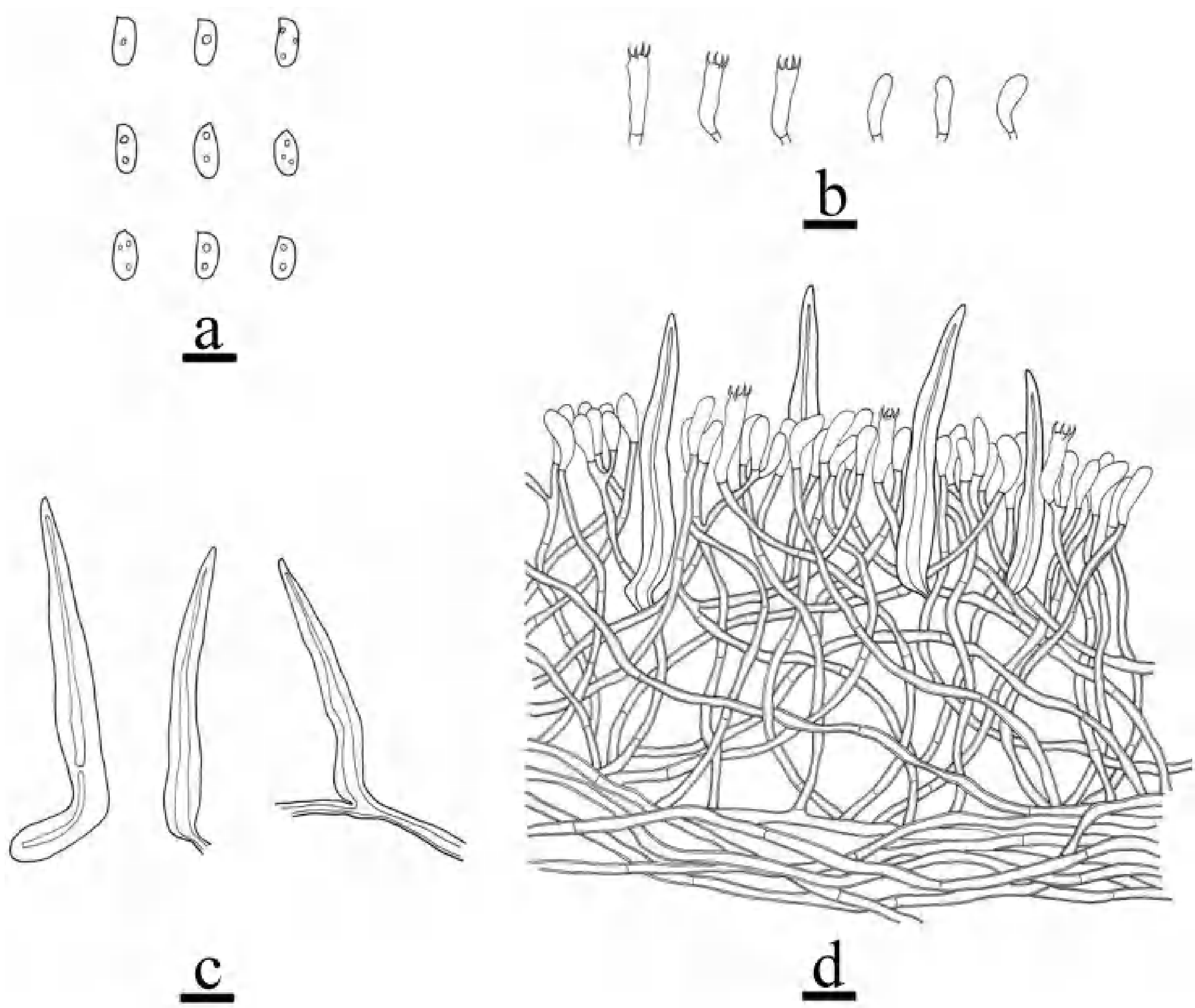

FIGURE 4. Microscopic structures of *Hymenochaete yaoshanensis* (holotype, CLZhao 20661): Basidiospores (a), Basidia and basidioles (b), Setae (c), A section of the hymenium (d). Bars: (a) = 5 µm and (b–d) = 10 µm.

Results

***Hyphal structure*:**—Hyphal system monomitic, generative hyphae colorless to golden brown, slightly thick-walled, with simple septa, rarely branched, interwoven, 1.5–3.5 µm in diameter, hyphal layer yellowish brown, IKI–, CB–; tissues darkening in KOH.

***Setae*:**—Numerous, subulate, reddish brown to dark brown, smooth, distinctly thick-walled with a narrow lumen, with an acute tip, 45–70 × 5.5–9 µm, embedded or projecting up to 30 µm beyond the hymenium.

***Hymenium*:**—Cystidia and cystidioles absent. Basidia subclavate to subcylindrical, colorless, thin-walled, with a basal simple septum and four sterigmata, 11–17 × 3–4 µm, basidioles dominant, in shape similar to basidia, but slightly smaller.

Basidiospores:—Basidiospores oblong ellipsoid, colorless, thin-walled, smooth, some with a guttule, IKI–, CB–, 4–6 × 2–3 µm, L = 4.59 µm, W = 2.31 µm, Q = 1.95–2 (n = 60/2).

***Additional specimen examined (paratype)*:**—CHINA. Yunnan Province, Zhaotong, Qiaojia County, Yaoshan, Yaoshan National Nature Reserve, GPS coordinates: 27°08′ N, 103°09′ E, altitude 2220 m asl., on fallen angiosperm branch, leg. C.L. Zhao, 21 August 2020, CLZhao 20626 (SWFC 00020626).

Discussion

Technological advancements from the 1990s onward enabled routine DNA-based analyses in fungal systematics (Parmasto *et al.* 2014), which in turn prompted extensive taxonomic revisions within Hymenochaetaceae. One major outcome was the recognition that *Hymenochaete* comprises two distinct lineages, *Hymenochaete* sensu stricto and *Pseudochaete* T. Wagner & M. Fisch (Wagner & Fischer 2002a, Zhao *et al.* 2025). Phylogenetic studies based on the nLSU rDNA sequence data of 150 species, including 17 poroid genera of Hymenochaetaceae, including types of *Hymenochaete* and *Pseudochaete*, confirmed the general classification of *Hymenochaete* and related genera, and research confirms *Hymenochaete* and *Pseudochaete* as two fully supported distinct clades (Wagner & Fischer 2001, 2002a, b; Parmasto *et al.* 2014). Despite these advances, research on the taxonomy of *Hymenochaete* remains ongoing. In the present study, a new species, *H. yaoshanensis,* is proposed based on an integrated assessment of morphological features and molecular evidence.

Phylogenetically, analyses of the combined ITS+nLSU sequences (Fig. 1) place our two collections within *Hymenochaete*. The two collections form a distinct lineage, are sister to *H. pinnatifida*, and are clustered with *H. longispora*. However, morphologically, *H. pinnatifida* is distinct from *H. yaoshanensis* by a hyphal system subdimitic and basidiospores cylindrical (Parmasto 2001). *Hymenochaete longispora* is distinct from *H. yaoshanensis* by having both longer setae (80–130 × 8–13 µm vs 45–70 × 5.5–9 µm) and basidia (20–25 × 5 µm 11–17 × 3–4 µm), and larger, cylindrical basidiospores (8–10 × 3–3.5 µm vs 4–6 × 2–3 µm) (Parmasto 1986). Morphological differences between *H. yaoshanensis* and its two sibling species, *H. pinnatifida* and *H. longispora*, are supplemented in Table 2.

Morphologically, *H. quercicola* S.H. He & Hai J. Li, *H. granulata* S.H. He, Z.B. Liu, Y.C. Dai, Yuan Yuan & F. Wu, *H. hubeiensis* S.H. He, Z.B. Liu, Y.C. Dai, Yuan Yuan & F. Wu, *H. stereoidea* S.H. He, Z.B. Liu, Y.C. Dai, Yuan Yuan & F. Wu, *H. puerensis* S.H. He, Z.B. Liu, Y.C. Dai, Yuan Yuan & F. Wu and *H. sinensis* Yan C. Li & C.L. Zhao are similar to *H. yaoshanensis* by the tuberculate to locally verruculose hymenial surface. The morphological distinctions among *Hymenochaete* species, including the newly described taxon *H. yaoshanensis*, are delineated through the comparative analysis presented in Table 2.

Wood-inhabiting fungi constitute a well-studied ecological guild within Basidiomycota, encompassing poroid, smooth, grandinioid, odontioid, and hydnoid basidiomata, and numerous new taxa have been described from China in recent years (He *et al.* 2022, Dong *et al.* 2024, Dai *et al.* 2025, Liu *et al.* 2025a, b, Wang *et al.* 2025a, b, Wijesinghe *et al.* 2025, Yang *et al.* 2025, Zhao *et al.* 2025). Therefore, the diversity of *Hymenochaete* in China remains insufficiently documented, particularly in subtropical and tropical regions. This study contributes to a greater understanding of fungal diversity in these areas, and continued field surveys coupled with molecular analyses will likely reveal additional undescribed taxa.

TABLE 2. A morphological comparison of *Hymenochaete yaoshanensis* and eight similar species in the genus *Hymenochaete*.

Species name	Basidiomata	Hyphal system	Basidia	Setae	Basidiospores	References
Hymenochaete granulata	Hymenophore surface smooth or locally verruculose.	Monomitic; generative hyphae thick-walled with simple septa, 2–4.5 µm in diameter.	Basidia clavate; 25–35 × 4–5 µm.	Setae abundant, subulate, thick-walled to subsolid, 45–60 × 5–7 µm.	Basidiospores cylindrical, thin-walled, 6–8 × 2.2–2.8 µm.	Liu *et al.* (2025b)
H. hubeiensis	Hymenophore surface smooth or locally verruculose.	Monomitic; generative hyphae thick-walled with simple septa, 1–2 µm in diameter.	Basidia clavate; 19–30 × 4.5–5.8 µm.	Setae abundant, subulate, thick-walled, 48–84 × 7–11 µm.	Basidiospores oblong-ellipsoid, thin-walled, 6–6.5 × 2.6–3 µm.	Liu *et al.* (2025b)
H. longispora	Hymenophore smooth.	Monomitic; generative hyphae thin-to-slightly thick-walled with simple septa, 1.5–4 µm in diameter.	Basidia clavata; 20–25 × 5 µm.	Setae smooth, without teeth, acute, not spathulate, 80–130 × 8–13 µm.	Basidiospores cylindrical, thin-walled, 8–10 × 3–3.5 µm.	Parmasto (1986)

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TABLE 2. (Continued)

Species name	Basidiomata	Hyphal system	Basidia	Setae	Basidiospores	References
H. pinnatifida	Hymenium smooth or with scattered low tubercles.	Subdimitic; generative hyphae hyaline or subhyaline, thin-walled, 1.8–2.7 µm in diameter.	Basidia not numerous, clavate or subclavate; 14–18 × 3–4.5 µm.	Setae not numerous, large, 40–70 × 5–8 µm, projecting up to 40 µm, conical to fusiform, with acute apex.	Basidiospores cylindrical, slightly curved, thin-walled, 4–7 × 1.5–2.8 µm.	Parmasto (2001)
H. puerensis	Hymenophore surface locally verruculose.	Monomitic; generative hyphae hyaline, thin- to thick-walled with simple septa, 2–4 µm in diameter.	Basidia clavate; 22–30 × 4–7 µm.	Setae abundant, usually subulate, 80–110 × 10–13 µm.	Basidiospores subcylindrical, thin-walled, 8–10 × 3.4–5 µm.	Liu *et al.* (2025b)
H. quercicola	Hymenophore smooth or tuberculate.	Monomitic; generative hyphae thin-to-slightly thick-walled with simple septa, 2.5–5 µm in diameter.	Basidia clavata; 17–36 × 4.5–6 µm.	Setae adsunt, subulatae, acutae, 85–120 × 6–10 µm.	Basidiospores oblong-ellipsoid to cylindrical, thin-walled, 6–8 × 3–3.6 µm.	He & Li (2011)
H. sinensis	Hymenophore surface brunneus to brown.	Monomitic; generative hyphae simple-septate, distinctly thick-walled, 2.5–3.5 µm in diameter.	Basidia barrelled; 10–12 × 3.1–3.8 µm.	Setae abundant, distinctly thick-walled, subulate, with an acute tip, 49–63 × 6.7–7.5 µm.	Basidiospores ellipsoid to broadly ellipsoid, distinctly thick-walled, 4–5× 2.5–3.5 µm.	Li *et al.* (2024)
H. stereoidea	Hymenophore surface smooth or locally verruculose.	Monomitic; generative hyphae hyaline, thick-walled, 2–4.5 µm in diameter.	Basidia clavate; 25–34 × 5–7.5 µm.	Setae abundant, usually subulate, 85–185 × 8–20 µm.	Basidiospores oblong-ellipsoid, thin-walled, usually with a guttule, 8–12 × 3–5 µm.	Liu *et al.* (2025b)
H. yaoshanensis	Hymenophore surface with tuberculate to locally verruculose.	Monomitic; generative hyphae slightly thick-walled, with simple septa, 1.5–3.5 µm in diameter.	Basidia subclavate to subcylindrical; 11–17 × 3–4 µm.	Setae Numerous, subulate, distinctly thick-walled, 45–70 × 5.5–9 µm.	Basidiospores oblong ellipsoid, thin-walled, 4–6 × 2–3 µm.	Present Study

Acknowledgements

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