

Helvellosebacina sclerotica (Sebacinaceae, Sebacinales), a new species from China, based on morphology and phylogeny

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Abstract

Helvellosebacina sclerotica sp. nov. was found in Yunnan Province, China, which is described here as a new species based on the morphological characteristics and molecular evidence. It is characterized by the resupinate basidiomata, smooth hymenial surface, a monomitic hyphal system with septate generative hyphae, and broadly ellipsoid to ellipsoid, smooth basidiospores (11–15 × 5.5–8.0 µm). Phylogenetic analyses of the combined internal transcribed spacer (ITS) and large subunit ribosomal RNA (nrLSU) sequence dataset confirmed that the new species belongs to *Helvellosebacina*. The phylogenetic tree inferred from ITS sequences showed that *Helvellosebacina sclerotica* was recovered as a sister group to *H. granulate*. Detailed descriptions, illustrations, and phylogenetic analyses of one new species are provided.

Key words: Molecular phylogeny, New taxon, Taxonomy, Wood-inhabiting fungi, Yunnan Province

Introduction

Fungi are one of the most diverse and ecologically important groups of organisms on Earth (Martin & Tan 2025). About 155,000 species of fungi have been described, and possibly millions more remain to be named (Hibbett *et al.* 2025).

The genus *Helvellosebacina* (Sebacinaceae, Sebacinales) was established by Oberwinkler *et al.* (2014), with *H. conrescens* (Schwein.) Oberw. as the type species, and this species is characterized by resupinate to upright merulioid-helvelloid, gelatinous, granular basidiomata, a monomitic hyphal system with septate generative hyphae, and longitudinally septate basidia (Oberwinkler *et al.* 2014, Dong *et al.* 2025b). Members of this genus typically occur either solitarily or in groups in deciduous forests, where they form associations with diverse plant hosts (Sesli 2021). The genus is widely distributed in Asia, Europe, North America, and South America (Dong *et al.* 2025b). According to the MycoBank database and Index Fungorum (Accessed on 25 April 2026), the genus *Helvellosebacina* has 6 specific names. With the advancement of molecular techniques, DNA-based phylogenetic analysis has become a powerful tool for resolving taxonomic ambiguities and the diversity of Sebacinaceae (Oberwinkler *et al.* 2014, Sesli 2021). Previously, taxonomic studies on Sebacinaceae have utilized phylogenetic approaches, but they lacked comprehensive sampling or included environmental sequences without taxonomic annotation (Moyersoen & Weiß 2014, Oberwinkler

et al. 2014). Recently, the study has emphasized the use of additional protein-coding markers, which provide improved species resolution and broad taxonomic coverage in Sebacinaceae (Suh *et al.* 2026).

The aim of this study is to explore the diversity and phylogeny of wood-inhabiting fungi in China. During our investigations into the diversity of wood-inhabiting fungi in China, two specimens morphologically resembling *Helvellosebacina* were collected in Yunnan Province. To clarify the placement and relationships of the two specimens, we conducted a phylogenetic and taxonomic study of the genus *Helvellosebacina* based on ITS and ITS+nrLSU sequences, assigning them to the genus *Helvellosebacina*. Therefore, the new species *Helvellosebacina sclerotica*, is proposed, based on the morphological characteristics and phylogenetic analyses.

Materials and methods

Sample collection and herbarium specimen preparation

The fresh basidiomata were collected from fallen branches of *Pinus* in Zhaotong of Yunnan Province, P.R. China. The samples were photographed in situ, and fresh macroscopic details, as well as other important collection information, were recorded (Zhang *et al.* 2024, Zhou *et al.* 2024, Qu *et al.* 2022, Rathnayaka *et al.* 2025). The photographs were captured with a Nikon D7100. All the photos were focus stacked using Helicon Focus software. Macroscopic details were recorded and transported to a field station, where the basidiomata were dried on an electronic food dryer at 40 °C (Dong *et al.* 2025a). Once dried, the specimens were placed in a labeled envelope and then put in zip-lock plastic bags (Dong *et al.* 2024). The dried specimens were deposited in the herbarium of the Southwest Forestry University (SWFC), Kunming, Yunnan Province, P.R. China. The MycoBank number was registered in the MycoBank database (<http://www.mycobank.org>).

Morphological studies

The macro-morphological descriptions were based on field notes and photos captured in the field and lab. Petersen (1996) was followed in the use of color terminology. The micro-morphological data were obtained from dried specimens observed under a light microscope at 1000× oil immersion (Dong *et al.* 2024). Sections mounted in 5% KOH and 2% phloxine B (C₂₀H₂Br₄C₁₄Na₂O₅), and other reagents were also used, including Cotton Blue and Melzer's reagent to observe micro-morphology following Wang *et al.* (2026). To show the variation in spore sizes, 5% of measurements were excluded from each end of the range and shown in parentheses. At least thirty basidiospores from each specimen were measured. Stalks were excluded from basidia measurements, and the hilar appendage was excluded from basidiospore measurements. The following abbreviations are used: KOH = 5% potassium hydroxide water solution, CB– = acyanophilous, IKI– = both inamyloid and non-dextrinoid, 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, Q_m represented the average Q of basidiospores measured ± standard deviation, and n = a/b (number of spores (a) measured from given number (b) of specimens).

Molecular procedures and phylogenetic analyses

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 ITS region was amplified with primer pair ITS5 and ITS4 primers (White *et al.* 1990). The nuclear nrLSU region was amplified with primer pair LR0R and LR7 (Vilgalys & Hester 1990, Rehner & Samuels 1994).

The PCR procedure for ITS was as follows: initial denaturation at 95 °C for 3 min, followed by 35 cycles of denaturation at 94 °C for 40 s, annealing at 58 °C for 45 s, extension at 72 °C for 1 min, and a final extension at 72 °C for 10 min. The PCR protocol for nrLSU 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 (Chen & Zhao 2020, Guan & Zhao 2023). The PCR products were purified and sequenced at Kunming Tsingke Biological Technology Limited Company (Yunnan Province, P.R. China). The newly generated sequences were deposited in NCBI GenBank (Table 1).

Phylogenetic analyses followed the methods in Dissanayake *et al.* (2020). Newly generated sequence data were initially subjected to a BLAST search in NCBI to obtain the most probable closely related taxa in the GenBank (<http://blast.ncbi.nlm.nih.gov/>). Sequence data were retrieved from GenBank based on recent publications (<https://www.ncbi.nlm.nih.gov/nuccore/>).

TABLE 1. A list of species, specimens, and GenBank accession numbers of sequences used in this study. Accession numbers of all sequences generated in this study are in bold, and – refers to the data unavailability.

Species Name	Sample No.	GenBank Accession No.		Country	References
		ITS	nrLSU		
<i>Chaetospermum artocarpi</i>	MFLUCC12-0536	KF516968	KF516974	France	Tangthirasunun <i>et al.</i> (2014)
<i>Chaetospermum camelliae</i>	MFLUCC12-0318	KF516964	KF516970	France	Tangthirasunun <i>et al.</i> (2014)
<i>Chaetospermum camelliae</i>	MFLUCC12-0433	KF516965	KF516971	France	Tangthirasunun <i>et al.</i> (2014)
<i>Chaetospermum chaetosporum</i>	Soil_F52	PQ552916	–	India	Unpublished
<i>Chaetospermum chaetosporum</i>	CBS:154.59	KJ710461	KJ710439	Switzerland	Crous <i>et al.</i> (2014)
<i>Ditangium altaicum</i>	LE 231836	MH836338	–	Russia	Malysheva <i>et al.</i> (2019)
<i>Ditangium cerasi</i>	TUB 0(2020)3	KF061265	KF061265	Germany	Oberwinkler <i>et al.</i> (2014)
<i>Ditangium cerasi</i>	TUB 0(2020)2	KF061264	KF061264	Germany	Oberwinkler <i>et al.</i> (2014)
<i>Ditangium incarnatum</i>	LE 303419	MH836337	–	Russia	Malysheva <i>et al.</i> (2019)
<i>Ditangium incarnatum</i>	LE 206311	MH836336	–	Russia	Malysheva <i>et al.</i> (2019)
<i>GlobuliSebacina rolleyi</i>	RJB794	AY509550	AY509550	Canada	Wells <i>et al.</i> (2004)
<i>GlobuliSebacina chenii</i>	R.Kirschner Wu 3653	–	KY304488	China	Wells <i>et al.</i> (2004)
<i>Helvellosebacina chrysalidodoma</i>	CLZhao 20782	PX436028	PX956475	China	Present study
<i>Helvellosebacina chrysalidodoma</i>	CLZhao 20792	PX436029	PX956476	China	Present study
<i>Helvellosebacina chrysalidodoma</i>	SFC (2023)0908-01	PV399946	PV399908	Republic of Korea	Suh <i>et al.</i> (2026)
<i>Helvellosebacina chrysalidodoma</i>	SFC (2023)1006-06	PV399956	PV399918	Republic of Korea	Suh <i>et al.</i> (2026)
<i>Helvellosebacina concrescens</i>	TUB 019706	JQ665516	JQ665516	Germany	Riess <i>et al.</i> (2013)
<i>Helvellosebacina filicata</i>	Dai 20449	PQ877259	PQ877258	China	Dong <i>et al.</i> (2025b)
<i>Helvellosebacina filicata</i>	SeqID 44	OR482700	OR482700	China	Dong <i>et al.</i> (2025b)
<i>Helvellosebacina granulata</i>	KATOF.4080	MT302587	MT302588	Turkey	Sesli (2021)
<i>Helvellosebacina granulata</i>	KATO F.4080	MT302587	MT302588	Turkey	Sesli (2021)
<i>Helvellosebacina helvelloides</i>	TUB 019983	KF000415	KF000415	Germany	Oberwinkler <i>et al.</i> (2014)
<i>Helvellosebacina helvelloides</i>	TUB 019984	KF000416	KF000416	Germany	Oberwinkler <i>et al.</i> (2014)
<i>Helvellosebacina helvelloides</i>	TUB 019983	KF000415	KF000415	Germany	Oberwinkler <i>et al.</i> (2014)
<i>Helvellosebacina helvelloides</i>	TUB 019984	KF000416	KF000416	Germany	Oberwinkler <i>et al.</i> (2014)
<i>Helvellosebacina koreana</i>	SFC (2023)1005-04	PV399955	PV399917	Republic of Korea	Suh <i>et al.</i> (2026)

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TABLE 1. (Continued)

Species Name	Sample No.	GenBank Accession No.		Country	References
		ITS	nrLSU		
<i>Helvellosebacina koreana</i>	SFC (2023)1028-04	PV399957	PV399919	Republic of Korea	Suh <i>et al.</i> (2026)
<i>Helvellosebacina koreana</i>	SFC (2023)1005-04	PV399955	PV399917	Republic of Korea	Suh <i>et al.</i> (2026)
<i>Helvellosebacina koreana</i>	SFC (2023)1028-04	PV399957	PV399919	Republic of Korea	Suh <i>et al.</i> (2026)
<i>Helvellosebacina sclerotica</i>	CLZhao 20885	PX436025	–	China	Present study
<i>Helvellosebacina sclerotica</i>	CLZhao 20859	PX436024	–	China	Present study
<i>Helvellosebacina</i> sp.	TUB 020021	KF000449	KF000449	Germany	Oberwinkler <i>et al.</i> (2014)
<i>Helvellosebacina</i> sp.	TUB 020028	KF000456	KF000456	Germany	Oberwinkler <i>et al.</i> (2014)
<i>Helvellosebacina</i> sp.	TUB 020021	KF000449	KF000449	Germany	Oberwinkler <i>et al.</i> (2014)
<i>Helvellosebacina</i> sp.	TUB 020028	KF000456	KF000456	Germany	Oberwinkler <i>et al.</i> (2014)
<i>Sebacina aciculicola</i>	Dai 25793	PQ877260	–	China	Dong <i>et al.</i> (2025b)
<i>Sebacina aciculicola</i>	Seq ID43	OR482699	OR482699	China	Dong <i>et al.</i> (2025b)
<i>Sebacina caducifoliicola</i>	SFC (2023)0704-04	PV399930	PV399892	Republic of Korea	Suh <i>et al.</i> (2026)
<i>Sebacina caducifoliicola</i>	SFC (2023)0704-05	PV399931	PV399893	Republic of Korea	Suh <i>et al.</i> (2026)
<i>Sebacina caducifoliicola</i>	SFC (2023)0817-41	PV399940	PV399902	Republic of Korea	Suh <i>et al.</i> (2026)
<i>Sebacina caducifoliicola</i>	SFC (2023)0817-45	PV399942	PV399904	Republic of Korea	Suh <i>et al.</i> (2026)
<i>Sebacina c&ida</i>	TUB 020330	KF061277	KF061277	USA	Oberwinkler <i>et al.</i> (2014)
<i>Sebacina c&ida</i>	TUB 020331	KF061278	KF061278	USA	Oberwinkler <i>et al.</i> (2014)
<i>Sebacina confusa</i>	437	KP783467	–	Russia	Unpublished
<i>Sebacina crystallina</i>	NIBRFG 0000504700	PV399921	PV399884	Republic of Korea	Suh <i>et al.</i> (2026)
<i>Sebacina crystallina</i>	SFC (2019)0919-11	PV399927	PV399890	Republic of Korea	Suh <i>et al.</i> (2026)
<i>Sebacina crystallina</i>	SFC (2023)0729-09	PV399934	PV399896	Republic of Korea	Suh <i>et al.</i> (2026)
<i>Sebacina cystidiata</i>	TUB 020024	KF000452	KF000452	Germany	Oberwinkler <i>et al.</i> (2014)
<i>Sebacina cystidiata</i>	TUB 020025	KF000453	KF000453	Germany	Oberwinkler <i>et al.</i> (2014)
<i>Sebacina dimitica</i>	TUB 019987	KF061271	KF061271	Austria	Oberwinkler <i>et al.</i> (2014)
<i>Sebacina dimitica</i>	TUB 019988	KF061272	KF061272	Austria	Oberwinkler <i>et al.</i> (2014)
<i>Sebacina epigaea</i>	TUB 019979	KF000411	KF000411	Austria	Oberwinkler <i>et al.</i> (2014)
<i>Sebacina epigaea</i>	TUB 020003	KF000432	KF000432	Austria	Oberwinkler <i>et al.</i> (2014)
<i>Sebacina flagelliformis</i>	TUB 020035	KF000463	KF000463	Germany	Oberwinkler <i>et al.</i> (2014)
<i>Sebacina flagelliformis</i>	TUB 020036	KF000464	KF000464	Germany	Oberwinkler <i>et al.</i> (2014)
<i>Sebacina incarnata</i>	SFC (2020)0821-21	PV399928	PV399891	Republic of Korea	Suh <i>et al.</i> (2026)
<i>Sebacina incarnata</i>	SFC (2020)0821-26	PV399929	–	Republic of Korea	Suh <i>et al.</i> (2026)

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TABLE 1. (Continued)

Species Name	Sample No.	GenBank Accession No.		Country	References
		ITS	nrLSU		
<i>Sebacina incrustans</i>	TUB 019991	KF000420	KF000420	Austria	Oberwinkler <i>et al.</i> (2014)
<i>Sebacina incrustans</i>	TUB 020018	KF000446	KF000446	Austria	Oberwinkler <i>et al.</i> (2014)
<i>Sebacina orientalis</i>	CLZhao 20735	PX436026	PX956474	China	Present study
<i>Sebacina orientalis</i>	CLZhao 20791	PX436027	–	China	Present study
<i>Sebacina orientalis</i>	SFC (2023)0907-02	PV399944	PV399906	Republic of Korea	Suh <i>et al.</i> (2026)
<i>Sebacina orientalis</i>	SFC (2023)0907-03	PV399945	PV399907	Republic of Korea	Suh <i>et al.</i> (2026)
<i>Sebacina orientalis</i>	SFC (2023)0908-03	PV399948	PV399910	Republic of Korea	Suh <i>et al.</i> (2026)
<i>Sebacina orientalis</i>	SFC (2023)0908-05	PV399950	PV399912	Republic of Korea	Suh <i>et al.</i> (2026)
<i>Sebacina orientalis</i>	SFC (2023)0908-13	PV399952	PV399914	Republic of Korea	Suh <i>et al.</i> (2026)
<i>Sebacina orientalis</i>	SFC (2023)0908-19	PV399953	PV399915	Republic of Korea	Suh <i>et al.</i> (2026)
<i>Sebacina pallida</i>	TUB 019649	JQ665564	JQ665564	Germany	Oberwinkler <i>et al.</i> (2014)
<i>Sebacina pallida</i>	TUB 0(2020)9	KF061276	KF061276	Germany	Oberwinkler <i>et al.</i> (2014)
<i>Sebacina schweinitzii</i>	OMDLiNat#176490182	OR824654	–	USA	Unpublished
<i>Sebacina spongicarpa</i>	ZGCAT 302	OQ918288	OQ918308	India	Crous <i>et al.</i> (2024)
<i>Sebacina spongicarpa</i>	ZGCAT 301	PP388210	–	India	Crous <i>et al.</i> (2024)
<i>Sebacina tomentosa</i>	10 PDM3	KF773782	KF773781	Venezuela	Moyersoen & Weiß (2014)
<i>Sebacina tomentosa</i>	PD 10	KF773779	KF773779	Venezuela	Moyersoen & Weiß (2014)
<i>Serendipita vermifera</i>	MAFF 305835	DQ983814	DQ983814	Australia	Deshmukh <i>et al.</i> (2006)

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 initially aligned and later, ITS and nrLSU sequences were combined using Mesquite version 3.51. FASTA data file formats were converted to PHYLIP and NEXUS formats using the online tool available on the ALTER website (<http://sing.ei.uvigo.es/ALTER/>, Glez-Peña *et al.* 2010). Phylogenetic trees were constructed based on randomized accelerated Maximum Likelihood (ML) and Bayesian Inference (BI) analyses.

Maximum Likelihood (ML) analysis was performed using the CIPRES Science Gateway (<https://www.phylo.org/portal2/login!input.action>, Miller *et al.* 2012) based on the dataset using the RA × ML-HPC BlackBox tool, with RA × ML halt bootstrapping automatically and 0.25 for maximum hours and obtaining the best tree using ML search. Other parameters in ML analysis used default settings, and statistical support values were obtained using nonparametric bootstrapping with 1,000 replicates. Bayesian inference (BI) analysis was performed on the dataset using MrBayes v3.2.7a (Ronquist *et al.* 2012). The best substitution model for the dataset was selected using ModelFinder v2.2.0 (Kalyaanamoorthy *et al.* 2017) with the Bayesian Information Criterion, and the model was used for Bayesian analysis. Four Markov chains were run from random starting trees. Trees were sampled every 1,000th generation. The first 25% of sampled trees were discarded as burn-in, while the remaining trees were used to construct a 50% majority consensus tree and to calculate Bayesian posterior probabilities (BPPs).

Phylogenetic trees were visualized and adjusted using FigTree v1.4.4 (<http://tree.bio.ed.ac.uk/software/figtree/>), and the exports were edited using Adobe Illustrator CS6 software (Adobe Systems, USA). Branches were considered significantly supported if they received a maximum likelihood bootstrap value (BS) of ≥ 70% or a Bayesian posterior probability (BPP) of ≥ 0.95.

Pairwise homoplasy test

The Genealogical Concordance Phylogenetic Species Recognition Analysis (GCPSR) is a tool used to check significant recombinant events. The data were analysed using SplitsTree 4 with the pairwise homoplasy Φ_w, PHI test to determine

the recombination level within closely related species (Bruen *et al.* 2006, Quaedvlieg *et al.* 2014). A one-locus dataset (ITS) with closely related species was used for the analyses. PHI results below 0.05 ($\Phi_w < 0.05$) indicate significant recombination in the dataset. The relationships between closely related taxa were visualised by constructing split graphs from the concatenated datasets, using the LogDet transformation and splits decomposition options.

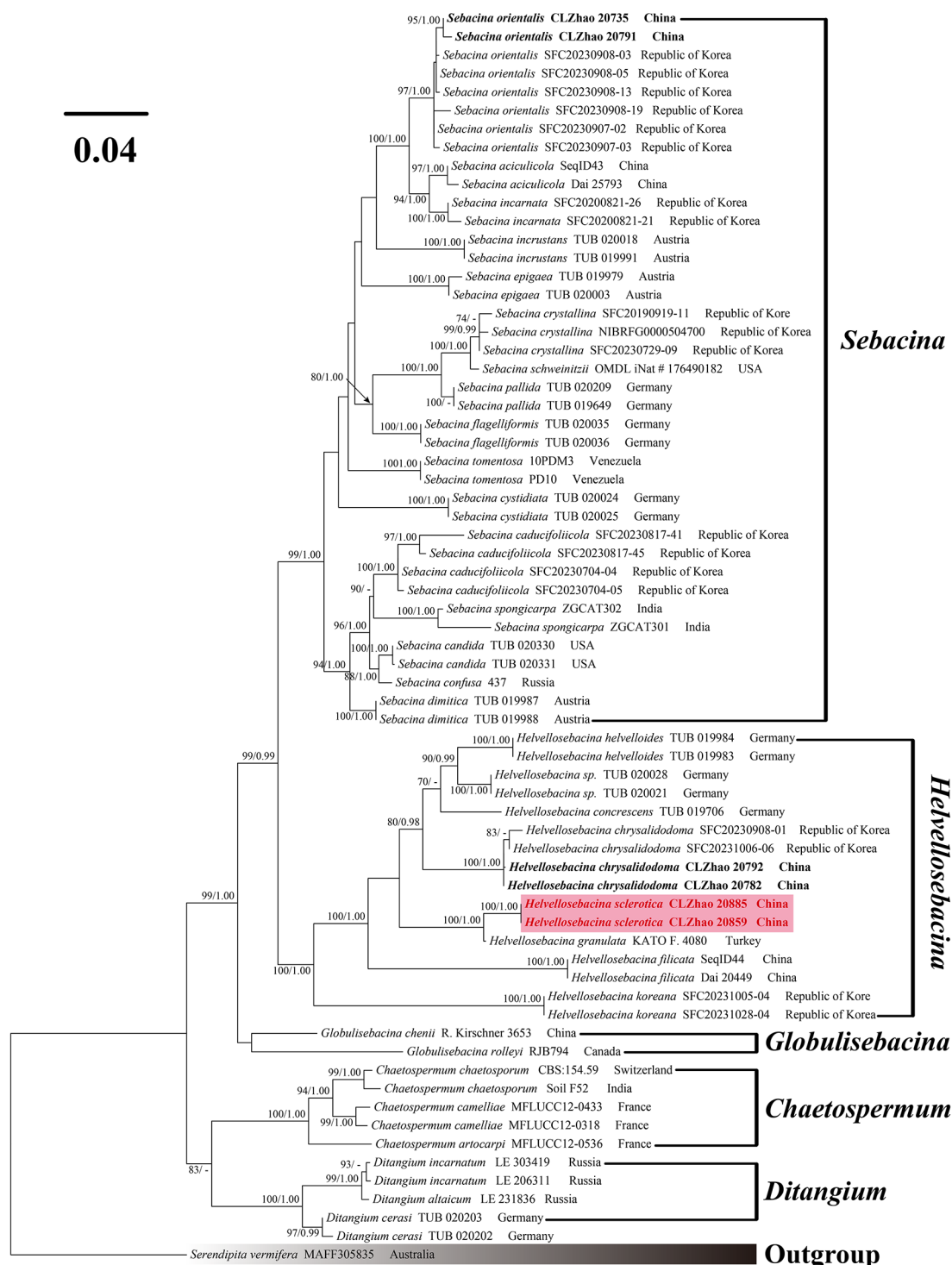


FIGURE 1. Maximum Likelihood strict consensus tree illustrating the phylogeny of the new species *Helvellosebacina sclerotica* in the family Sebacinaceae based on the combined ITS+nrLSU sequences. Branches are labeled with Maximum Likelihood bootstrap values equal to or above 70% and Bayesian posterior probabilities equal to or above 0.95. Newly generated sequences and new species are indicated in bold and red bold, respectively.

Results

Molecular phylogeny

The aligned dataset comprised 68 specimens representing 33 species, including a new species, in the order Sebacinaceae (Fig. 1), and the taxa *Serendipita vermifera* (Oberw.) P. Roberts was retrieved from GenBank as the outgroup for analysis, following a previous study (Dong *et al.* 2025b). Four Markov chains were run for 2,000 generations from random starting trees, each for two million generations, for the combined ITS+nrLSU (Fig. 1) data set, with trees and parameters sampled every 1,000 generations. The best model for the ITS+nrLSU dataset, estimated and applied in the Bayesian analysis, was HKY+F+I+G4. Both Maximum Likelihood (ML) and Bayesian Inference (BI) analyses generated similar topologies, with an average standard deviation of split frequencies = 0.006271 (BI) and an effective sample size (ESS) for Bayesian analysis across the two runs that is double the average ESS (avg. ESS) = 1232.5. The phylogenetic tree, based on ITS+nrLSU sequences analysis (Fig. 1), showed that the new species *Helvellosebacina sclerotica* was assigned to the genus *Helvellosebacina* within the family Sebacinaceae.

The aligned dataset comprised 17 specimens representing nine species of the new species *Helvellosebacina sclerotica* and related species in the genus *Helvellosebacina* (Fig. 2), and the taxa *Globulisebacina rolleyi* (L.S. Olive) Oberw., Garnica & K. Riess. were retrieved from GenBank as outgroup for analysis, following a previous study (Dong *et al.* 2025b). Four Markov chains were run for two independent runs from random starting trees, each for 0.5 million generations, on the ITS (Fig. 2) data set, with trees and parameters sampled every 1,000 generations. The best model for the ITS dataset, estimated and applied in the Bayesian analysis, was HKY+F+G4. Both Maximum Likelihood (ML) and Bayesian Inference (BI) analyses generated similar topologies, with an average standard deviation of split frequencies = 0.010249 (BI) and an effective sample size (ESS) for Bayesian analysis across the two runs that is double the average ESS (avg. ESS) = 444. The phylogram based on ITS sequences (Fig. 2) analysis, the new species *Helvellosebacina sclerotica* is classified within *Helvellosebacina* and identified as a sister to *H. granulata* Sesli.

Application of the PHI test to the ITS tree-locus sequences revealed no recombination level within phylogenetically related species with new taxa (Fig. 3). The PHI test results of the ITS sequence dataset show that (Fig. 3) $\Phi_w = 0.8623$ ($\Phi_w > 0.05$), no recombination in *Helvellosebacina sclerotica* compared with the closely related taxa.

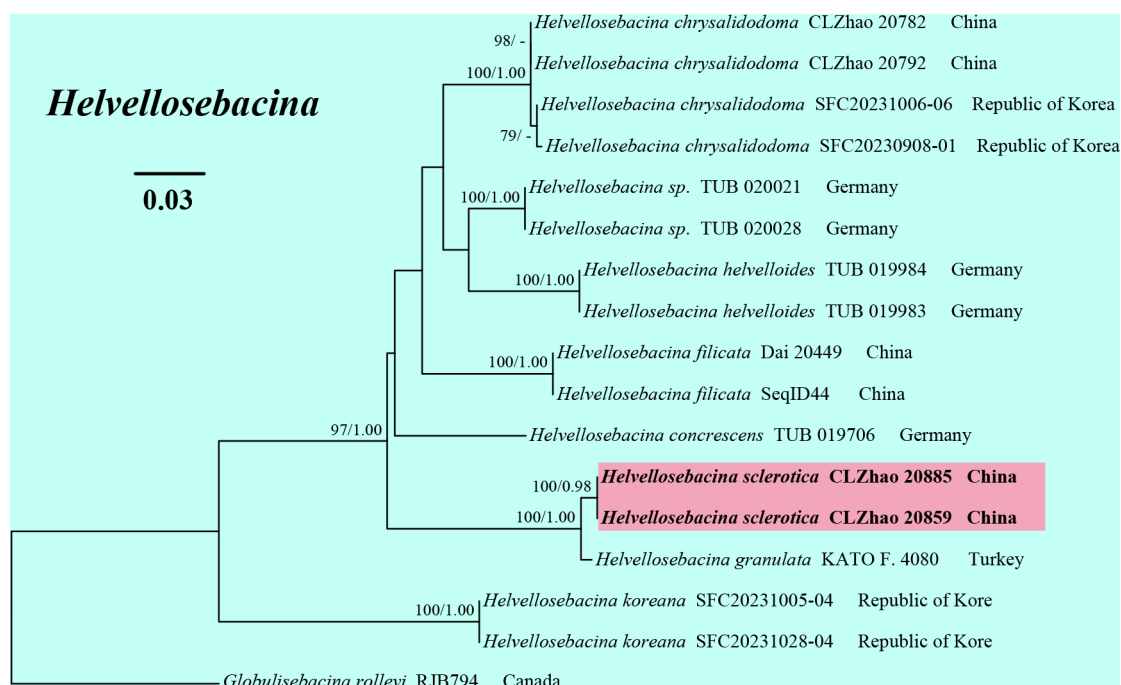


FIGURE 2. Maximum Likelihood strict consensus tree illustrating the phylogeny of the new species *Helvellosebacina sclerotica* and related species in the genus *Helvellosebacina* based on ITS sequences. Branches are labeled with Maximum Likelihood bootstrap values equal to or above 70% and Bayesian posterior probabilities equal to or above 0.95. The new species are in bold.

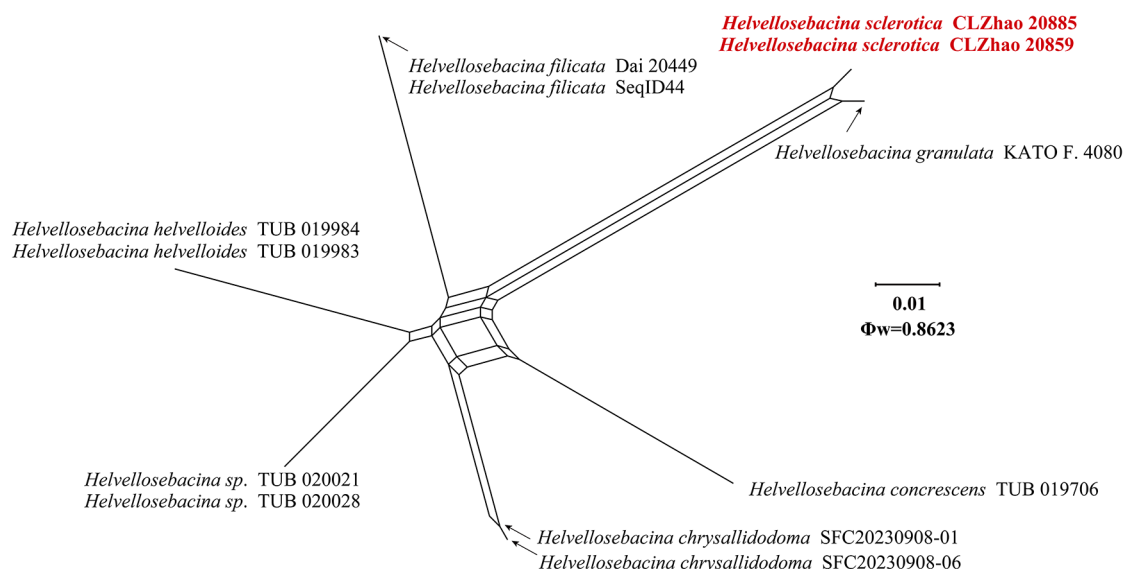


FIGURE 3. Split graphs showing the results of the pairwise homoplasy index (PHI) test of the new taxa and closely related taxa using LogDet transformation and splits decomposition. PHI test result P-value (Φ_w) ≤ 0.05 indicates that there is significant recombination between the isolates included in the alignment. The new taxa are in red, and each PHI test values and scale bars are given in the bottom right corner.

Taxonomy

Helvellosebacina sclerotica Y.J. Zhu & C.L. Zhao, *sp. nov.* Figs. 4–6.

MycoBank no.: MB863657

Etymology:—*sclerotica* (Lat.) refers to the sclerotic basidiomata of the type specimen.

Diagnosis:—*Helvellosebacina sclerotica* differs from other *Helvellosebacina* species by its smooth hymenial surface, septate generative hyphae, and broadly ellipsoid to ellipsoid basidiospores ($11\text{--}15 \times 5.5\text{--}8\ \mu\text{m}$).

Holotype:—CHINA. Yunnan Province, Zhaotong, Qiaojia County, Yaoshan Town, Yaoshan National Nature Reserve, $27^\circ 15' 52''\text{N}$, $103^\circ 07' 11''\text{E}$, elev. 3,200 m, on the fallen branch of *Pinus*, leg. C.L. Zhao, 23 August 2020, CLZhao 20885 (SWFCF00020885).

Basidiomata:—Annual, resupinate, cartilaginous to gelatinous, closely adnate on substrate, not easily separable, widely effused with a gelatinous texture on upper surface, up to 14 mm long, 2 mm wide, up to 120 μm thick. Hymenial surface smooth, white to cream, semi-transparent when fresh, distinctly shrinking to a film and becoming cream when dry. Sterile margin thinning out, white to cream, and up to 1 mm wide.

Hyphal structure:—Monomitic, generative hyphae with simple septa, hyphae simple or branched, interwoven, colorless, thick-walled, 2–4 μm in diameter; IKI–, CB–; tissues unchanged in KOH.

Hymenium:—Cystidia and cystidioles absent. Basidia thin-walled, obovate to subglobose, $14.5\text{--}18.2 \times 13.3\text{--}16.4\ \mu\text{m}$, longitudinally septate, 4-celled, usually with oil drops; sterigmata up to 25 μm long, $2.5\text{--}3\ \mu\text{m}$ in diameter, with tapered apex; basidioles dominant, similar to basidia in shape, but slightly smaller.

Basidiospores:—Allantoid, colorless, smooth, thin-walled, occasionally with 1–2 oil drops inside, IKI–, CB–, $(10\text{--})11\text{--}15\text{--}(16) \times 5.5\text{--}8.0\ \mu\text{m}$, $L = 12.75\ \mu\text{m}$, $W = 6.83\ \mu\text{m}$, $Q = 1.50\text{--}2.27$, $Q_m = 1.88 \pm 0.25$ ($n = 60/2$).

Additional specimen examined (paratype):—CHINA • Yunnan Province, Zhaotong, Qiaojia County, Yaoshan Town, Yaoshan National Nature Reserve, $27^\circ 15'\text{N}$, $103^\circ 07'\text{E}$, elev. 3200 m, on a fallen branch of *Pinus*, leg. C.L. Zhao, 23 August 2020, CLZhao 20859 (SWFCF00020859).



FIGURE 4. Basidiomata of *Helvellosebacina sclerotica* (holotype, CLZhao 20885).

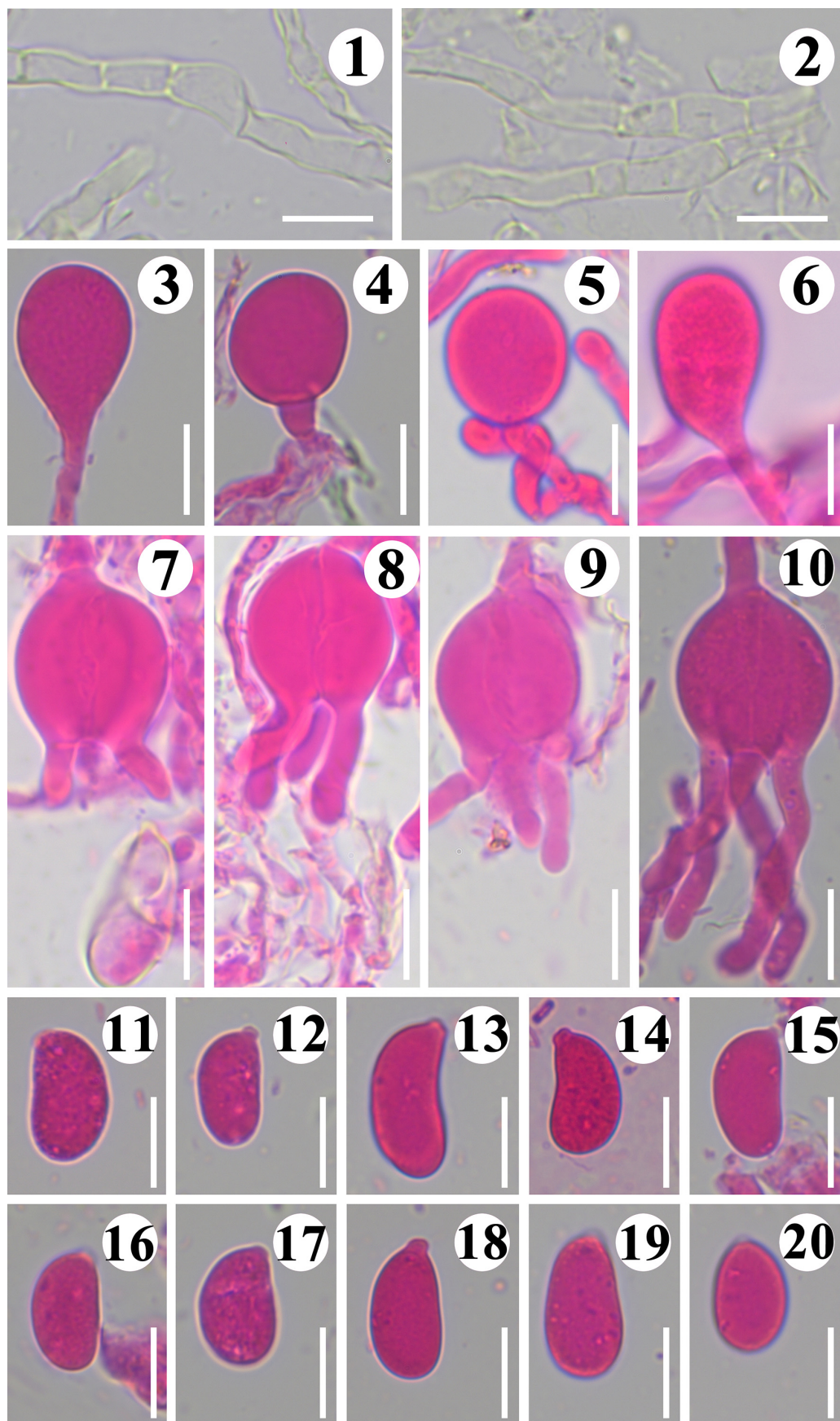


FIGURE 5. Sections of the hymenium of *Helvellosebacina sclerotica* (holotype, CLZhao 20885). (1–2) Hyphae; (3–6) Basidioles; (7–10) Basidia; (11–20) Basidiospores. Scale bars: 1–20 = 10 μ m; 1000 $\times$ Oil.

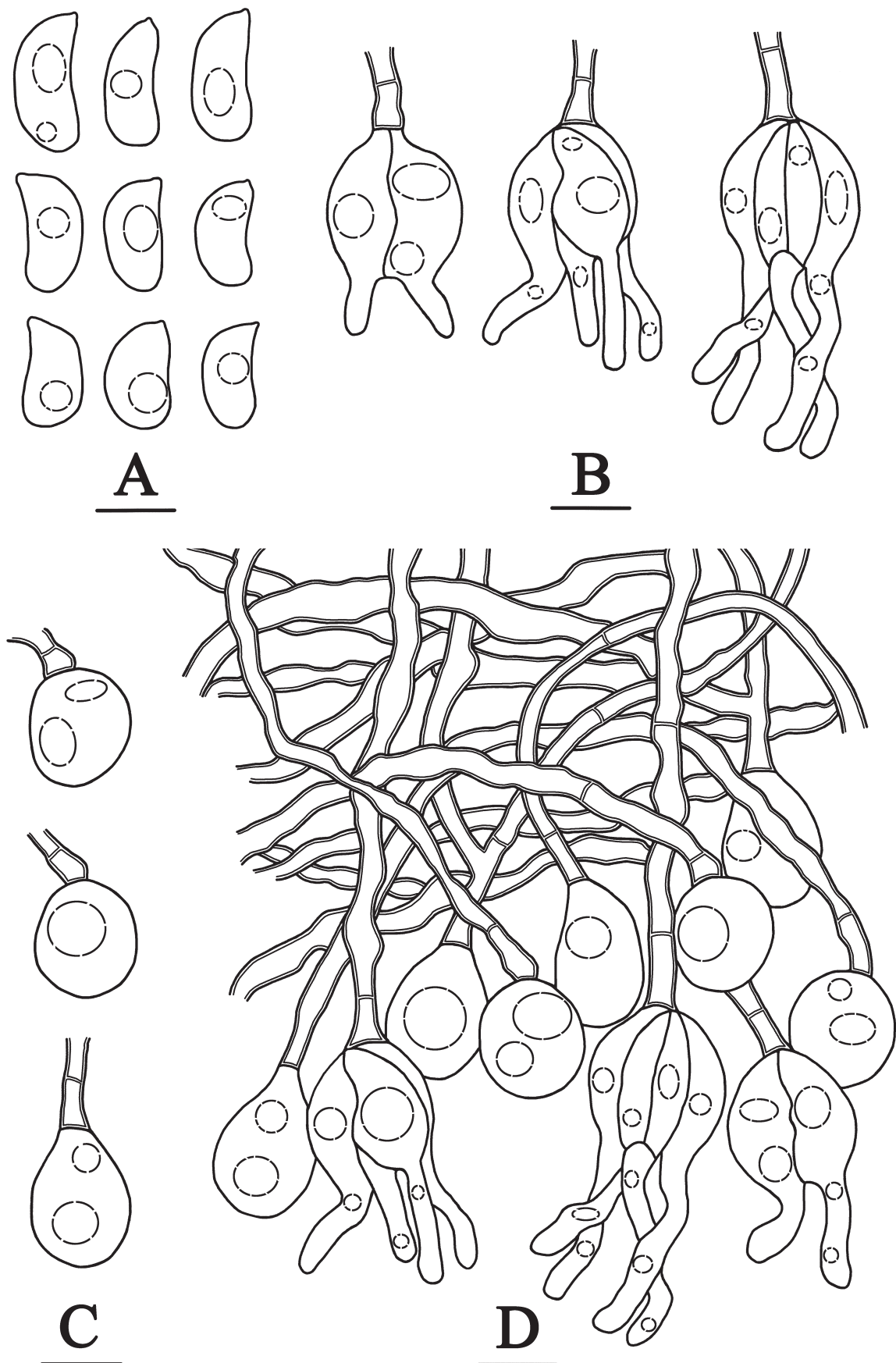


FIGURE 6. Microscopic structures of *Helvellosebacina sclerotica* (holotype, CLZhao 20885). (A) Basidiospores; (B) Basidia; (C) Basidioles; (D) Part of the vertical section of the hymenium. Scale bars: A–D = 10 μ m.

Discussion

In the present study, a new species *Helvellosebacina sclerotica*, is described based on phylogenetic analyses and morphological characteristics.

Phylogenetic analyses based on combined ITS + nrLSU sequences (Fig 1) and separate ITS sequences (Fig 2) both placed the new species *Helvellosebacina sclerotica* in the genus *Helvellosebacina* of the family Sebacinaceae, with the ITS phylogeny further resolving *H. sclerotica* as the sister species of *H. granulata*. However, morphologically, *H. granulata* differs from *H. sclerotica* by having sordid grayish or pale buff basidiomata, ellipsoid to subglobose or pyriform basidia, and ellipsoid to cylindrical basidiospores (Sesli 2021).

Morphologically, *Helvellosebacina sclerotica* resembles *H. chrysalidodoma* H. Suh, D. Kim & Y.W. Lim, *H. filicata* J.H. Dong, X. Zhang, Y.C. Dai & F. Wu, and *H. koreana* H. Suh, D. Kim & Y.W. Lim by sharing gelatinous and granular basidiomata, monomitic hyphal system, and smooth basidiospores. However, *H. chrysalidodoma* differentiates from *H. sclerotica* by its narrower basidia ($14.4\text{--}18.2 \times 11.4\text{--}13.1\ \mu\text{m}$ vs. $14.5\text{--}18.2 \times 13.3\text{--}16.4\ \mu\text{m}$) and elliptical or allantoid basidiospores (Suh *et al.* 2026). *Helvellosebacina filicata* differs from *H. sclerotica* by its slightly shorter basidiospores ($8.6\text{--}9.9 \times 5.8\text{--}7.6\ \mu\text{m}$ vs. $11\text{--}15 \times 5.5\text{--}8.0\ \mu\text{m}$, Dong *et al.* 2025b). *Helvellosebacina koreana* is distinguished from *H. sclerotica* by its wider basidia ($14.6\text{--}17.0 \times 8.0\text{--}10.8\ \mu\text{m}$ vs. $14.5\text{--}18.2 \times 13.3\text{--}16.4\ \mu\text{m}$) and thick-walled basidiospores (Suh *et al.* 2026).

In recent years, the wood-inhabiting fungi are an extensively studied group of Basidiomycota, which includes a number of poroid, smooth, grandinoid, odontoid and hydroid basidiomata in China (Floudas & Hibbett 2015, Miettinen *et al.* 2016, Spirin *et al.* 2017, Yuan *et al.* 2021, Luo *et al.* 2022, Wu *et al.* 2022, Zhang *et al.* 2023, Zhou *et al.* 2023, Yuan *et al.* 2023, Yang *et al.* 2023, 2024, Deng *et al.* 2025, Larsson *et al.* 2025, Zhao *et al.* 2025). This paper enriches our knowledge of fungal diversity in China. We anticipate that more undescribed wood-inhabiting fungal taxa will be discovered throughout China following extensive collections combined with morphological and molecular analyses.

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References

- Bruen, T.C., Philippe, H. & Bryant, D.A. (2006) A simple and robust statistical test for detecting the presence of recombination. *Genetics* 172 (4): 2665–2681.
<https://doi.org/10.1534/genetics.105.048975>
- Chen, J.Z. & Zhao, C.L. (2020) Morphological and molecular identification of four new resupinate species of *Lyomyces* (Hymenochaetales) from southern China. *MycKeys* 65: 101–118.
<https://doi.org/10.3897/mycokeys.65.48660>
- Crous, P.W., Giraldo, A., Hawksworth, D.L., Robert, V., Kirk, P.M., Guarro, J., Robbertse, B., Schoch, C.L., Damm, U., Trakunyingcharoen, T. & Groenewald, J.Z. (2014) The genera of fungi: fixing the application of type species of generic names. *IMA Fungus* 5 (1): 141–160.
<https://doi.org/10.5598/imafungus.2014.05.01.14>
- Crous, P.W., Wingfield, M.J., Jurjević, Ž., Balashov, S., Osieck, E.R., Marin-Felix, V., Luangsa-ard, J.J., Mejia, L.C., Cappelli, A., Parra, L.A., Lucchini, G., Chen, J., Moreno, G., Faraoni, M., Zhao, R.L., Weholt, O., Borovička, J., Jansen, G.M., Shivas, R.G., Tan, Y.P., Akulov, A., Alfenas, A.C., Alfenas, R.F., Altés, A., Avchar, R., Barreto, R.W., Catcheside, D.E.A., Chi, T.Y., Esteve-Raventós, H., L.T.M., Fryar, S.C., Larsbrink, J., Oberlies, N.H., Olsson, L., Pancorbo, F., Raja, H.A., Thanh, V.N., Thuy, N.T., Ajithkumar, K.,

- Akram, W., Alvarado, P., Angeletti, B., Arumugam, E., Atashi Khalaji, A., Bandini, D., Banniza, S., Baral, H.O., Barreto, M.C., Bellanger, J.M., Bezerra, J.D.P., Bezerra, J.L., Bianchin, V., Bibi, S., Boonmee, S., Braun, U., Brien, C., Brodt, T., Cano-Lira, J.F., Carriconde, F., Cazabonne, J., Cheewangkoon, R., Chethana, K.W.T., Cline, E.T., Cruz, A.C.R., Czachura, P., De Souza, J.T., Denchev, C.M., Denchev, T.T., Duong, T.A., Eyssartier, G., Flakus, A., Fournier, J., Frisullo, S., García-Jiménez, J., Gardiennet, A., Gené, J., Gryta, H., Hernández-Restrepo, M., Hirooka, Y., Hospenthal, D.R., Hubka, V., Illescas, T., Kezo, K., Kumar, S., Larsson, E., Lebel, T., Lechat, C., Lombard, L., Maciá Vicente, J.G., Mahadevakumar, S., Mang, S.M., Marbach, P.A.S., Marincowitz, S., Mateos, A., Mehrabi Koushki, M., Miglio, B.V., Mombert, A., Montañó-Mata, N.J., Murugadoss, R., Noor, A., Obermayer, E., Oliveira, J.A., Pereira, O.L., Piątek, M., Pinto, A., Pugh, T.A.M., Ramírez, G.H., Raphael, B., Rawat, G., Renuka, M., Reschke, K., Riebesehl, J., Ruiz Mateo, A., Saar, I., Saba, M., Safi, A., Sánchez, R.M., Sandoval Denis, M., Savitha, A.S., Sharma, A., Shelke, D., Soliz Santander, F.F., Sonawane, H., Souza, M.G.A.P., Starink-Willemse, M., Stryjak-Bogacka, M., Thines, M., Torres García, D., Traba, J.M., Vauras, J., Vermaas, M., Villarreal, M., Vu, D., Whiteside, E.J., Zafari, D. & Groenewald, J.Z. (2024) Fungal Planet description sheets: 1697–1780. *Fungal Systematics and Evolution* 14: 325–577.
<https://doi.org/10.3114/fuse.2024.14.19>
- Deng, Y.L., Chen, M., Wang, K.S., Liu, W.T., Chen, D.X., Yang, S.Q., Li, W.L., Zhou, H.M. & Zhao, C.L. (2025) Morphological and phylogenetic analyses reveal one new genus and six new species in Irpicaceae and Steccherinaceae (Polyporales, Basidiomycota) from the Yunnan–Guizhou Plateau, Asia. *IMA Fungus* 16: e172367.
<https://doi.org/10.3897/imafungus.16.172367>
- Deshmukh, S., Hückelhoven, R., Schäfer, P., Imani, J., Sharma, M., Weiss, M., Waller, F. & Kogel, K.H. (2006) The root endophytic fungus *Piriformospora indica* requires host cell death for proliferation during mutualistic symbiosis with barley. *Proceedings of the National Academy of Sciences of the United States of America* 103 (49): 18450–18457.
<https://doi.org/10.1073/pnas.0605697103>
- Dissanayake, A.J., Bhunjun, C.S., Maharachchikumbura, S.S. & Liu, J.K. (2020) Applied aspects of methods to infer phylogenetic relationships amongst fungi. *Mycosphere* 11: 2652–2676.
<https://doi.org/10.5943/mycosphere/11/1/-18>
- Dong, J.H., Chen, M.L., Chen, M., Li, Q., Zhu, Y.J., Zhang, X.C., Zhou, C.Q., Li, W., Muhammad, A., Zhou, H.M., Jabeen, S. & Zhao, C.L. (2025a) Notes, outline, taxonomy and phylogeny of wood-inhabiting Agaricales. *Mycosphere* 16 (1): 2599–2711.
<https://doi.org/10.5943/mycosphere/16/1/16>
- Dong, J.H., Li, Q., Yuan, Q., Luo, Y.X., Zhang, X.C., Dai, Y.F., Zhou, Q., Liu, X.F., Deng, Y.L., Zhou, H.M., Muhammad, A. & Zhao, C.L. (2024) Species diversity, taxonomy, molecular systematics and divergence time of wood-inhabiting fungi in Yunnan-Guizhou Plateau, Asia. *Mycosphere* 15: 1110–1293.
<https://doi.org/10.5943/mycosphere/15/1/10>
- Dong, J.H., Zhang, X., Guan, Q.X. & Wu, F. (2025b) Morphological characteristics and phylogenetic analysis reveal *Helvellosebacina filicata* sp. nov. and *Sebacina aciculicola* sp. nov. in Sebacinales from southwest China. *MycKeys* 118: 105–118.
<https://doi.org/10.3897/mycokeys.118.152160>
- Floudas, D. & Hibbett, D.S. (2015) Revisiting the taxonomy of *Phanerochaete* (Polyporales, Basidiomycota) using a four gene dataset and extensive ITS sampling. *Fungal Biology* 119: 679–719.
<https://doi.org/10.1016/j.funbio.2015.04.003>
- Glez-Peña, D., Gómez-Blanco, D., Reboiro-Jato, M., Fdez-Riverola, F. & Posada, D. (2010) ALTER: program oriented conversion of DNA and protein alignments. *Nucleic Acids Research* 38: 14–18.
<https://doi.org/10.1093/nar/gkq321>
- Guan, Q.X. & Zhao, C.L. (2023) Five new species of Schizoporaceae (Basidiomycota, Hymenochaetales) from East Asia. *MycKeys* 96: 25–56.
<https://doi.org/10.3897/mycokeys.96.99327>
- Hibbett, D., Nagy, L. & Nilsson, R. (2025) Fungal diversity, evolution, and classification. *Current Biology* 35: 463–469.
<https://doi.org/10.1016/j.cub.2025.01.053>
- Kalyaanamoorthy, S., Minh, B.Q., Wong, T.K.F., von Haeseler, A. & Jermin, L.S. (2017) ModelFinder: Fast model selection for accurate phylogenetic estimates. *Nature Methods* 14 (6): 587–589.
<https://doi.org/10.1038/nmeth.4285>
- Katoh, K., Rozewicki, J. & Yamada, K.D. (2019) MAFFT online service: Multiple sequence alignment, interactive sequence choice and visualization. *Briefings in Bioinformatics* 20 (4): 1160–1166.
<https://doi.org/10.1093/bib/bbx108>
- Larsson, A. (2014) AliView: A fast and lightweight alignment viewer and editor for large data sets. *Bioinformatics* 30 (22): 3276–3278.
<https://doi.org/10.1093/bioinformatics/btu531>
- Larsson, K.H., Viner, Ilya V.S. & Spirin, V. (2025) Additions to the taxonomy of *Phanerochaete* sensu lato (Polyporales, Basidiomycota);

- one new genus, two new species and twelve new combinations. *Mycological Progress* 24: 74.
<https://doi.org/10.1007/s11557-025-02094-z>
- Luo, K.Y., Chen, Z.Y. & Zhao, C.L. (2022) Phylogenetic and taxonomic analyses of three new wood-inhabiting fungi of *Xylodon* (Basidiomycota) in a forest ecological system. *Journal of Fungi* 8: 405.
<https://doi.org/10.3390/jof8040405>
- Malysheva, V., Spirin, V.A., Miettinen, O., Kout, J., Savchenko, A. & Larsson, K. (2019) On *Craterocola* and *Ditangium* (Sebacinales, Basidiomycota). *Mycological Progress* 18: 753–762.
<https://doi.org/10.1007/s11557-019-01485-3>
- Martin, F. & Tan, H. (2025) Saprotrophy-to-symbiosis continuum in fungi. *Current Biology* 35 (11): 469–475.
<https://doi.org/10.1016/j.cub.2025.01.032>
- Miettinen, O., Spirin, V., Vlasak, J., Rivoire, B., Stenroos, S. & Hibbett, D. (2016) Polypores and genus concepts in Phanerochaetaceae (Polyporales, Basidiomycota). *MycoKeys* 17: 1–46.
<https://doi.org/10.3897/mycokeys.17.10153>
- Miller, M.A., Pfeiffer, W. & Schwartz, T. (2012) The CIPRES science gateway. [In Proceedings of the 1st Conference of the Extreme Science and Engineering Discovery Environment: Bridging from the Extreme to the Campus and Beyond, Chicago, IL, 1–39.]
<https://doi.org/10.1145/2335755.2335836>
- Moyersoen, B. & Weiß, M. (2014) New neotropical Sebacinales species from a *Pakaraimaea dipterocarpacea* forest in the Guayana region, Southern Venezuela: structural diversity and phylogeography. *PLoS One* 9 (7): 1–17.
<https://doi.org/10.1371/journal.pone.0103076>
- Oberwinkler, F., Riess, K., Bauer, R. & Garnica, S. (2014) Morphology and molecules: the Sebacinales, a case study. *Mycological Progress* 13 (3): 445–470.
<https://doi.org/10.1007/s11557-014-0983-1>
- Petersen, J.H. (1996) *Farvekort. The Danish Mycological Society's Colour-Chart*. Foreningen til Svampekundskabens Fremme, Greve, pp. 1–6.
- Quaedvlieg, W., Binder, M., Groenewald, J.Z., Summerell, B.A., Carnegie, A.J., Burgess, T.I. & Crous, P.W. (2014) Introducing the consolidated species concept to resolve species in the Teratosphaeriaceae. *Persoonia* 33 (1): 1–40.
<https://doi.org/10.3767/003158514X681981>
- Qu, M.H., Wang, D.Q. & Zhao, C.L. (2022) A Phylogenetic and taxonomic study on *Xylodon* (Hymenochaetales): focusing on three new *Xylodon* species from southern China. *Journal of Fungi* 8: 35.
<https://doi.org/10.3390/jof8010035>
- Rathnayaka, A.R., Tennakoon, D.S., Jones, G.E., Wanasinghe, D.N., Bhat, D.J., Priyashantha, A.H., Stephenson, S.L., Tibpromma, S. & Karunarathna, S.C. (2025) Significance of precise documentation of hosts and geospatial data of fungal collections, with an emphasis on plant-associated fungi. *New Zealand Journal of Botany* 63 (2-3): 462–489.
<https://doi.org/10.1080/0028825X.2024.2381734>
- Rehner, S.A. & Samuels, G.J. (1994) Taxonomy and phylogeny of *Gliocladium* analysed from nuclear large subunit ribosomal DNA sequences. *Mycological Research* 98 (6): 625–634.
[https://doi.org/10.1016/S0953-7562\(09\)80409-7](https://doi.org/10.1016/S0953-7562(09)80409-7)
- Riess, K., Oberwinkler, F., Bauer, R. & Garnica, S. (2013) High genetic diversity at the regional scale and possible speciation in *Sebacina epigaea* and *S. incrustans*. *BMC Evolutionary Biology* 13: 102.
<https://doi.org/10.1186/1471-2148-13-102>
- Ronquist, F., Teslenko, M., van der Mark, P., Ayres, D.L., Darling, A., Höhna, S., Larget, B., Liu, L., Suchard, M.A. & Huelsenbeck, J.P. (2012) MrBayes 3.2: Efficient bayesian phylogenetic inference and model choice across a large model space. *Systematic Biology* 61 (3): 539–542.
<https://doi.org/10.1093/sysbio/sys029>
- Sesli, E. (2021) *Helvellosebacina granulata* sp. nov. (Basidiomycota: Sebacinaceae) from the East Black Sea Region of Turkey. *Nordic Journal of Botany* 39 (6): e03189.
<https://doi.org/10.1111/njb.03189>
- Spirin, V., Volobuev, S., Okun, M., Miettinen, O. & Larsson, K.H. (2017) What is the type species of *Phanerochaete* (Polyporales, Basidiomycota). *Mycological Progress* 16: 171–183.
<https://doi.org/10.1007/s11557-016-1267-8>
- Suh, H., Seo, C.W., Park, K.H., Yoo, S., Kim, D., Cho, Y. & Lim, Y.W. (2026) Hidden diversity of crust-like Sebacinaceae (Sebacinales, Agaricomycetes) in Asia. *IMA Fungus* 17: e168486.
<https://doi.org/10.3897/imafungus.17.168486>
- Tangthirasunun, N., Silar, P., Bhat, D.J., Chukeatirote, E., Wikee, S., Maharachchikumbura, S., Hyde, K. & Wang, Y. (2014) Morphology

- and phylogeny of *Chaetospermum* (asexual coelomycetous Basidiomycota). *Phytotaxa* 175: 61–72.
<https://doi.org/10.11646/phytotaxa.175.2.1>
- Vilgalys, R. & Hester, M. (1990) Rapid genetic identification and mapping of enzymatically amplified ribosomal DNA from several *Cryptococcus* species. *Journal of Bacteriology* 172 (8): 4238–4246.
<https://doi.org/10.1128/jb.172.8.4238-4246.1990>
- Wang, L., He, S.Y., Lambert, C., Zhu, Y.G., Zhang, J.L., Yang, Y., Li, W.L., Zhou, H.M. & Zhao, C.L. (2026) Comprehensive morphological and phylogenetic analyses of Hymenochaetales (Basidiomycota) unveil one new genus and twenty-six novel wood-inhabiting species from southwestern China. *Persoonia* 56: 328–380.
<https://doi.org/10.3114/persoonia.2026.56.05>
- Wells, K., Bandoni, R.J., Lim, S.H. & Berbee, M.L. (2004) Observations on some species of *Myxarium* and reconsideration of the Auriculariaceae and Hyaloriaceae Auriculariales. 237.
- White, T.J., Bruns, T., Lee, S. & Taylor, J. (1990) Amplification and direct sequencing of fungal ribosomal RNA genes for phylogenetics. In: Innis, M.A., Gelfand, D.H., Sninsky, J.J. & White, T.J. (Eds.) *PCR protocols: A guide to methods and applications*. Academic Press, San Diego, pp. 315–322.
<https://doi.org/10.1016/B978-0-12-372180-8.50042-1>
- Wu, F., Zhou, L.W., Vlasák, J. & Dai, Y.C. (2022) Global diversity and systematics of Hymenochaetaceae with poroid hymenophore. *Fungal Diversity* 113: 1–192.
<https://doi.org/10.1007/s13225-021-00496-4>
- Yang, Y., Li, R., Jiang, Q.Q., Zhou, H.M., Muhammad, A., Wang, H.J. & Zhao, C.L. (2024) Phylogenetic and taxonomic analyses reveal three new wood-inhabiting fungi (Polyporales, Basidiomycota) in China. *Journal of Fungi* 10: 55.
<https://doi.org/10.3390/jof10010055>
- Yang, Y., Li, R., Liu, C.M. & Zhao, C.L. (2023) Morphological and molecular identification for two new species of wood-inhabiting macrofungi (Basidiomycota) from Yunnan-Guizhou Plateau, China. *Phytotaxa* 591 (1): 1–18.
<https://doi.org/10.11646/phytotaxa.591.1.1>
- Yuan, Q., Luo, K.Y., Zhang, Y. & Zhao, C.L. (2023) Morphological characteristics and phylogenetic analyses revealed three new wood-inhabiting fungi (Agaricomycetes, Basidiomycota) in Southern China. *Phytotaxa* 592 (3): 179–195.
<https://doi.org/10.11646/phytotaxa.592.3.1>
- Yuan, Y., Chen, J.J., Korhonen, K., Martin, F. & Dai, Y.C. (2021) An updated global species diversity and phylogeny in the forest pathogenic genus *Heterobasidion* (Basidiomycota, Russulales). *Frontiers in Microbiology* 11: 596393.
<https://doi.org/10.3389/fmicb.2020.596393>
- Zhang, Q.Y., Liu, H.G., Papp, V., Zhou, M., Dai, Y.C. & Yuan, Y. (2023) New insights into the classification and evolution of *Favolaschia* (Agaricales, Basidiomycota) and its potential distribution, with descriptions of eight new species. *Mycosphere* 14: 777–814.
<https://doi.org/10.5943/mycosphere/14/1/10>
- Zhang, X.C., Li, Y.C., Wang, Y.Y., Xu, Z., Zhao, C.L. & Zhou, H.M. (2024) *Xylodon asiaticus* (Hymenochaetales, Basidiomycota), a new species of corticioid fungus from southern China. *Phytotaxa* 634 (1): 1–15.
<https://doi.org/10.11646/phytotaxa.634.1.1>
- Zhao, H., Cui, Y.J., Guan, Q.X., Wang, K., Zhuang, L., Zeng, G.Y., Wei, Y.L., Wu, F. & Yuan, H.S. (2025) Global species diversity and distribution patterns within the order Hymenochaetales (Agaricomycetes, Basidiomycota). *Mycosphere* 16 (1): 3257–3280.
<https://doi.org/10.5943/mycosphere/16/1/24>
- Zhou, H.M., Gu, Z.R. & Zhao, C.L. (2024) Molecular phylogeny and morphology reveal a new species of *Asterostroma* from Guizhou Province, China. *Phytotaxa* 635 (2): 173–181.
<https://doi.org/10.11646/phytotaxa.635.2.7>
- Zhou, M., Dai, Y.C., Vlasák, J., Liu, H.G. & Yuan, Y. (2023) Updated systematics of *Trichaptum s.l.* (Hymenochaetales, Basidiomycota). *Mycosphere* 14: 815–917.
<https://doi.org/10.5943/mycosphere/14/1/11>