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Molecular phylogeny and morphology reveal a new species of *Gloeocystidiellum* (Stereaceae, Russulales) from Southwestern China

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Abstract

Gloeocystidiellum yaoshanense sp. nov., found in Yunnan Province, Southwestern China, is described here as a new species based on its morphology and phylogenetic analyses. *Gloeocystidiellum yaoshanense* is characterized by its membranaceous basidiomata with cracked, grandinioid hymenial surface, a monomitic hyphal system bearing simple septa on generative hyphae, and broadly ellipsoid to ellipsoid basidiospores measuring 4–4.6 × 3–3.5 µm. Phylogenetic analyses of the new species were carried out based on the nuclear ribosomal internal transcribed spacer (nrITS) and the nuclear large subunit (nrLSU) of ribosomal DNA. The phylogenetic analyses indicated that the new species belongs to the genus *Gloeocystidiellum* and forms a monophyletic lineage. A full description, illustrations, and phylogenetic analysis results of the new species are provided.

Key words: Biodiversity, Phylogenetically, Taxonomy, Wood-inhabiting fungi, Yunnan Province

Introduction

Fungi exhibit enormous species diversity in terms of morphological, ecological, and nutritional modes (Cui *et al.* 2018, Wu *et al*. 2016, Dai *et al.* 2021, Zhao *et al.* 2023b, Song *et al*. 2024). Wood-inhabiting fungi play a crucial role in ecosystem processes, particularly in the degradation of wood and the recycling of organic matter (Dong *et al*. 2024).

The corticioid genus *Gloeocystidiellum* Donk (1931: 156), belonging to the order Russulales, was established by Donk (1931) with *Gc. porosum* (Berk & MA Curtis) Donk (1931: 156) as its type species. The genus is characterized by resupinate, membranaceous or ceraceous basidiomata, smooth, rarely grandinioid or odontioid hymenial surface, a monomitic hyphal system with clamped or simple-septate generative hyphae, present gloeocystidia, subcylindrical to clavate basidia with four sterigmata and suballantoid, ellipsoid, subglobose or globose, verrucose or aculeate basidiospores (Donk 1931, 1957, Bernicchia & Gorjón 2010). The Index Fungorum (http://www.indexfungorum.org, accessed June 28, 2025) lists 38 species in the genus *Gloeocystidiellum* (Larsson & Larsson 2003, Gorjón & Hallenberg 2013, Zhao & Zhao 2023, Zhang *et al*. 2025).

Molecular studies involving the genus *Gloeocystidiellum* based on single-gene or multi-gene datasets have been carried out (Larsson & Hallenberg 2001, Larsson & Larsson 2003, Gorjón & Hallenberg 2013, Jaramillo-Riofrío *et al*. 2023, Zhao & Zhao 2023, Zhang *et al*. 2025, Zhou *et al.* 2025). Based on phylogenetic analyses of nuclear 5.8S, ITS2, and nrLSU rDNA genes, the taxa of *Gloeocystidiellum* formed two clades, where the generic type species, *Gc. porosum* is grouped into clade I (Larsson & Larsson 2003). The high phylogenetic diversity among corticioid

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homobasidiomycetes showed that the taxon *Gc. subasperisporum* (Litsch.) J. Erikss. & Ryvarden (1975: 443) nested into the russuloid clade and closely grouped with *Gloeodontia discolor* (Berk. & M.A. Curtis) Boidin (1966: 22) (Larsson *et al*. 2004). Molecular phylogenetic analyses based on nrITS+nrLSU sequences within the order Russulales indicated that the genus *Gloeocystidiellum* nested into the family Russulaceae and clustered with the genus *Gloeodontia* (Leal-Dutra *et al*. 2018). The result of phylogenetic analyses showed that the genus *Gloeodontia* formed a single clade grouped with *Gloeocystidiellum* within the order Russulales (Chen *et al*. 2020, Zhao & Zhao 2023). In a recent study, the genus *Gloeocystidiellum* was classified within the family Stereaceae, belonging to the order Russulales (He *et al*. 2024, Zhang *et al*. 2025).

During investigations on the corticioid fungi in Yunnan Province, southwestern China, two specimens of *Gloeocystidiellum* were collected. To clarify the placement and relationships of these specimens, we conducted a phylogenetic and taxonomic study on the genus *Gloeocystidiellum* based on combined nrITS and nrITS+nrLSU sequence data. These specimens are identified as a new species of *Gloeocystidiellum*. Detailed descriptions, illustrations, and phylogenetic analysis results of the new species are provided.

Materials and methods

Sample collection and herbarium specimen preparation

The fresh basidiomata were collected from fallen angiosperm branches in Zhaotong, Yunnan Province, southwest China. The samples were photographed in situ, and fresh macroscopic details, as well as other important collection information, were recorded (Rathnayaka *et al*. 2024). The photographs were recorded using a Nikon D7100 camera. 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 (Hu *et al*. 2022). 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, China. The MycoBank number was registered in the MycoBank database (http://www.mycobank.org).

Morphology

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 with a magnification of 1000× oil (Zhao *et al.* 2023a, Dong *et al*. 2024, Zhang *et al*. 2025). Sections mounted in 5% KOH and 2% phloxine B ($C_{20}H_2Br_4C_{14}Na_2O_5$), and other reagents were also used, including Cotton Blue and Melzer's reagent to observe micro-morphology following Wu *et al*. (2022a). 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, CB+ = cyanophilous, IKI– = both inamyloid and non-dextrinoid, IKI+ =amyloid, 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 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 (nrITS) region was amplified with ITS5 and ITS4 primers (White *et al*. 1990), while the nuclear large subunit (nrLSU) region was amplified with the LR0R and LR7 primer pair (Vilgalys & Hester 1990, Rehner & Samuels 1994). The PCR procedure for nrITS 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 procedure for nrLSU was as follows: initial denaturation at 94 °C for 1 min, followed by 35 cycles of denaturation at 94 °C for 30 s, annealing at 48 °C for 1 min, extension at 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). The newly generated sequences were deposited in NCBI GenBank (Table 1).

TABLE 1. A list of species, specimens, and GenBank accession numbers of sequences used in this study. The new species is in bold.

Species Name	Sample No.	GenBank Accession No.		Country	References
		ITS	nrLSU		
Aleurobotrys botryosus	He 2712	KX306877	KY450788	China	Maekawa *et al.* 2023
Aleurobotrys botryosus	Wu 9302-61	—	AY039331	China	Maekawa *et al.* 2023
Aleurodiscus bambusinus	He 4261	KY706207	KY706219	China	Dai & He 2017
Aleurodiscus canadensis	Wu1207-90	KY706203	KY706225	China	Dai & He 2017
Conferticium heimii	LY/CBS321.66	AF506381	AF506381	Central African Republic	Jaramillo-Riofrío *et al.* 2023
Conferticium heimii	CBS321.66	MH858805	MH858805	Central African Republic	Vu *et al.* 2019
Conferticium ravum	CBS:125849	MH863805	MH875269	Estonia	Vu *et al.* 2019
Conferticium ravum	NH13291	AF506382	AF506382	USA	Larsson & Larsson 2003
Conferticium tuberculatum	CLZhao 29376	PQ166602	PQ295861	China	Wang *et al.* 2025
Conferticium tuberculatum	CLZhao 29390	PQ166603	PQ295862	China	Wang *et al.* 2025
Gloeocystidiellum aspellum	LIN 625	AF506432	—	China	Larsson & Lrsson 2003
Gloeocystidiellum bisporum	CBS/961.96	AY048875	AY048875	Sweden	Jaramillo-Riofrío *et al.* 2023
Gloeocystidiellum bisporum	KHL11135	AY048877	AY048877	Norway	Larsson & Lrsson 2003
Gloeocystidiellum clavuligerum	GB/NH11185	AF310088	AF310088	Spain	Jaramillo-Riofrío *et al.* 2023
Gloeocystidiellum cremeum	CLZhao 33623	PQ287847	PQ295864	China	Wang *et al.* 2025
Gloeocystidiellum cremeum	CLZhao 33690	PQ287848	—	China	Wang *et al.* 2025
Gloeocystidiellum fissuratum	CLZhao 32247	PQ287849	PQ295865	China	Wang *et al.* 2025
Gloeocystidiellum fissuratum	CLZhao 32303	PQ287850	PQ295866	China	Wang *et al.* 2025
Gloeocystidiellum formosanum	Wu9404-19	AF506439	—	China	Maekawa *et al.* 2023
Gloeocystidiellum kenyense	TFC/15278	FR878082	—	Portugal	Jaramillo-Riofrío *et al.* 2023
Gloeocystidiellum kenyense	TFC/15309	FR878083	—	Portugal	Jaramillo-Riofrío *et al.* 2023
Gloeocystidiellum lojanense	HUTPL(F)/2181	OP377059	—	Ecuador	Jaramillo-Riofrío *et al.* 2023
Gloeocystidiellum lojanense	HUTPL(F)/550	OP377083	—	Ecuador	Jaramillo-Riofrío *et al.* 2023
Gloeocystidiellum luridum	HK9808	AF506421	—	Germany	Maekawa *et al.* 2023
Gloeocystidiellum porosum	CBS/51085	AF310097	AF310097	Netherlands	Jaramillo-Riofrío *et al.* 2023
Gloeocystidiellum porosum	NH 10434	AF310094	AF310094	Denmark	Larsson & Hallenberg 2001
Gloeocystidiellum rajchenbergii	GB/NH16353	JQ734555	—	Chile	Jaramillo-Riofrío *et al.* 2023
Gloeocystidiellum rajchenbergii	GB/NH16348	JQ734554	—	Chile	Jaramillo-Riofrío *et al.* 2023
Gloeocystidiellum sinense	CLZhao 25040	PQ453516	PQ453518	China	Zhang *et al.* 2025
Gloeocystidiellum sinense	CLZhao 25320	PQ453517	PQ453519	China	Zhang *et al.* 2025
Gloeocystidiellum triste	KHL10334	AF506442	—	Sweden	Maekawa *et al.* 2023
Gloeocystidiellum yaoshanense	**CLZhao 20850***	**PV682890**	**PV682892**	**China**	**Present study**
Gloeocystidiellum yaoshanense	**CLZhao 45465**	**PV682891**	**PV682893**	**China**	**Present study**
Gloeocystidiellum yunnanense	CLZhao 7165	MZ710569	MZ710571	China	Zhao & Zhao 2023
Gloeocystidiellum yunnanense	CLZhao 7202	MZ710570	MZ710572	China	Zhao & Zhao 2023

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TABLE 1. (Continued)

Species Name	Sample No.	GenBank Accession No.		Country	References
		ITS	nrLSU		
Lentinellus cochleatus	GB/KGN96-09-28	AF506417	—	Sweden	Jaramillo-Riofrío *et al.* 2023
Megalocystidium diffissum	V.Spirin4244	MT477147	MT477147	Sweden	Maekawa *et al.* 2023
Megalocystidium leucoxanthum	HK9808	AF506420	AF506420	Sweden	Maekawa *et al.* 2023
Neoaleurodiscus fujii	He 2921	KU559357	KU574845	China	Dai *et al.* 2017
Neoaleurodiscus fujii	Wu0807-41	—	FJ799924	China	Dai *et al.* 2017
Stereum complicatum	He 2234	KU559368	KU574828	China	Maekawa *et al.* 2023
Stereum hirsutum	Wu1109—127	LC430906	LC430909	China	Maekawa *et al.* 2023
Stereum sanguinolentum	He 2111	KU559367	KU574827	China	Maekawa *et al.* 2023
Vararia investiens	FP-151122	MH971976	—	USA	Liu & He 2018
Xylobolus frustulatus	He 2231	KU881905	KU574825	China	Maekawa *et al.* 2023
Xylobolus subpileatus	FP-106735	—	AY039309	USA	Maekawa *et al.* 2023

* is shown type material, holotype; — means the data unavailability.

The sequences were aligned using MAFFT version 7 (Katoh *et al*. 2019) with the G-INS-i strategy, and then manually adjusted using AliView version 1.27 (Larsson 2014). After trimming, the sequences of nrITS and nrLSU were combined using Mesquite version 3.51. Sequence of *Vararia investiens* (Schwein.) P. Karst. (1898: 32). The sequence obtained from GenBank was used as an outgroup to root trees in the nrITS+nrLSU analysis for the family Stereaceae (Fig. 1, Zhao & Zhao 2023), and *Lentinellus cochleatus* (Pers.) P. Karst. (1879: 247) was used as an outgroup in the nrITS analysis in the genus *Gloeocystidiellum* (Fig. 2, Zhang *et al*. 2025).

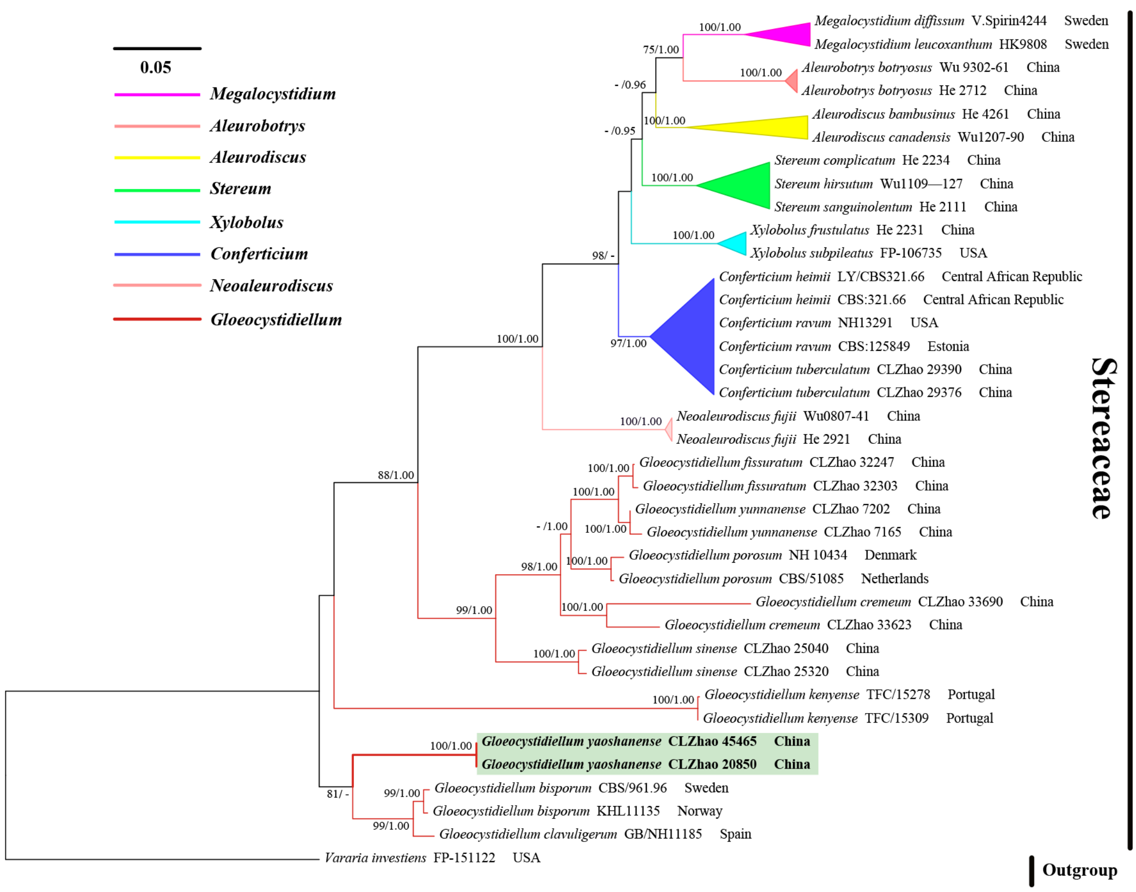

FIGURE 1. Maximum Likelihood strict consensus tree illustrating the *Gloeocystidiellum* and related genera in the family Stereaceae based on the combined nrITS+nrLSU sequences. Branches are labeled with Maximum Likelihood bootstrap values equal to or above 70% and Bayesian posterior probabilities equal to or above 0.95. The new species is in bold.

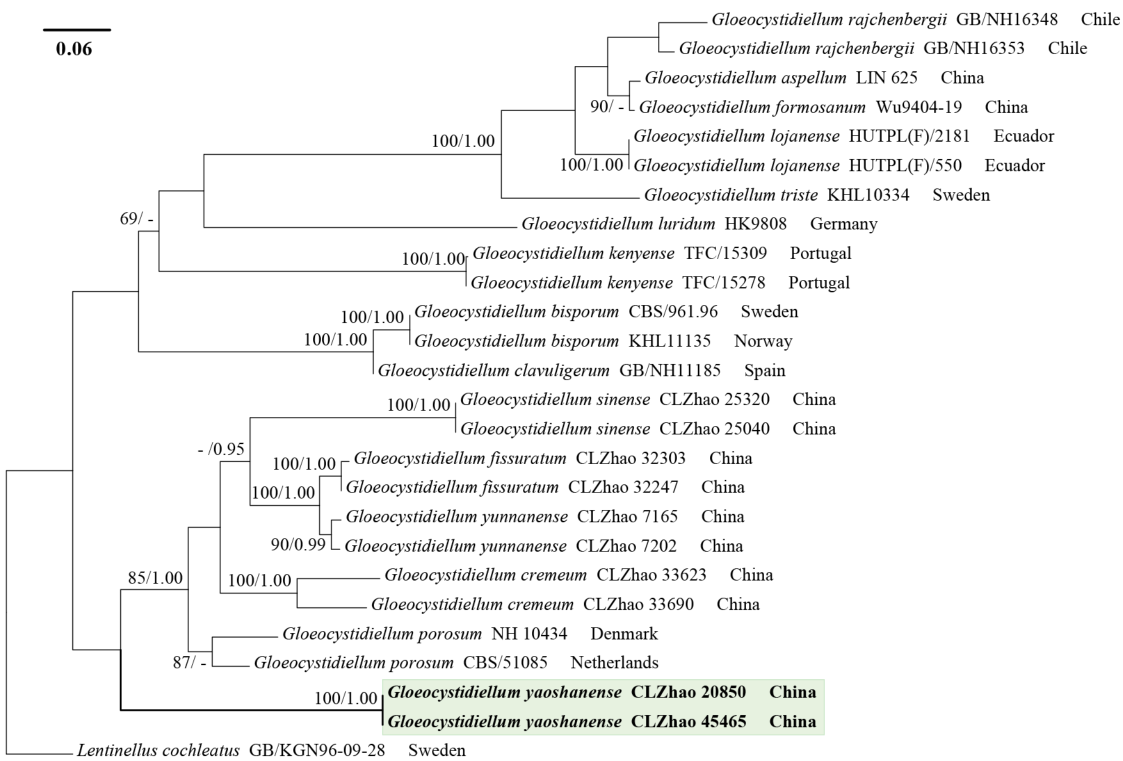

FIGURE 2. Maximum Likelihood strict consensus tree illustrating the phylogeny of the new species *Gloeocystidiellum yaoshanense,* and related species in the genus *Gloeocystidiellum* based on nrITS sequences. Branches are labeled with Maximum Likelihood bootstrap values equal to or above 70% and Bayesian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

Maximum Likelihood (ML), and Bayesian Inference (BI) analyses were applied to the combined two datasets following a previous study (Dong *et al*. 2024). Maximum Likelihood (ML) analysis was performed using RAxML-HPC BlackBox in the CIPRES Science Gateway (https://www.phylo.org/portal2/login!input.action, Miller *et al.* 2012) with a GTRCAT model of evolution and 1,000 bootstrap replicates (Felsenstein 1985). jModelTest v2 (Darriba *et al*. 2012) was used to determine the best-fit evolution model for each dataset for the purposes of Bayesian inference (BI), Bayesian inference was performed using MrBayes 3.2.7a (Ronquist *et al*. 2012). Four Markov chains were run from random starting trees. Trees were sampled every 1,000 generations. 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 (BPP).

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%, Bayesian posterior probabilities (BPP) of ≥ 0.95.

Results

Molecular phylogeny

The aligned nrITS+nrLSU dataset comprised 37 specimens representing 24 species. Four Markov chains were run for two independent runs from random starting trees, each for one million generations, using the combined nrITS+nrLSU (Fig. 1) data set, with trees and parameters sampled every 1,000 generations. The best model for the nrITS+nrLSU dataset, estimated and applied in the Bayesian analysis, was SYM+I+G. Maximum Likelihood (ML) and Bayesian Inference (BI) analysis yielded a similar topology, with an average standard deviation of split frequencies of 0.002328 (BI). The effective sample size (ESS) for Bayesian analysis across the two runs was approximately double the average ESS (avg. ESS) of 246.5.

The aligned nrITS dataset comprised 24 specimens representing 16 species. Four Markov chains were run for two runs from random starting trees, each for 0.3 million generations, for the nrITS-only (Fig. 2) data set with trees and parameters sampled every 1000 generations. The best model for the nrITS dataset, estimated and applied in the Bayesian analysis, was HKY+G. Maximum Likelihood (ML) and Bayesian Inference (BI) analysis yielded a similar topology, with an average standard deviation of split frequencies of 0.006831 (BI). The ESS for Bayesian analysis across the two runs was approximately double the average ESS (avg. ESS) of 210.5.

The phylogram based on the combined nrITS+nrLSU sequences (Fig. 1) indicated that the new species *Gloeocystidiellum yaoshanense* was assigned to the genus *Gloeocystidiellum*. The topology based on nrITS sequences (Fig. 2) revealed that the new species *Gc. yaoshanense*, formed a monophyletic lineage.

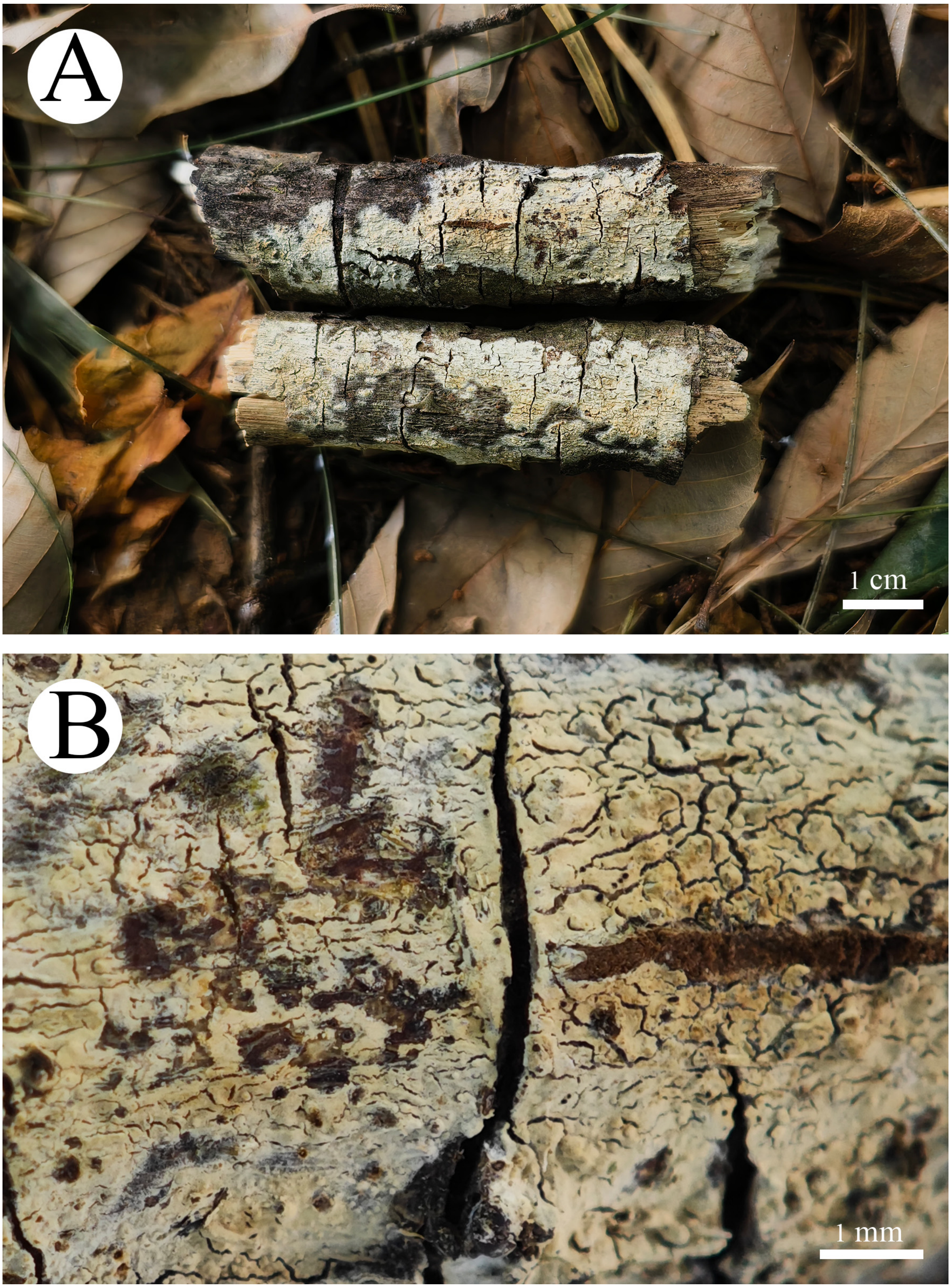

FIGURE 3. Basidiomata of *Gloeocystidiellum yaoshanense* (holotype, CLZhao 20850).

Taxonomy

Gloeocystidiellum yaoshanense Y.J. Zhu & C.L. Zhao, *sp. nov.* Figs. 3–5.
MycoBank no.: MB859528

Etymology:*—yaoshanense* (Lat.) refers to the type locality, Yaoshan National Nature Reserve.

Diagnosis:—Differs from *Gloeocystidiellum porosum* by its grandinoid hymenial surface, septate generative hyphae, and broadly ellipsoid to ellipsoid basidiospores (4–4.6 × 3–3.5 µm).

Holotype:—CHINA. Yunnan Province, Zhaotong, Qiaojia County, Yaoshan Town, Yaoshan National Nature Reserve, 27°15′52″N, 103°07′11″E, elev. 3,200 m, on the fallen angiosperm branch, 23 August 2020, CLZhao 20850 (SWFC!).

Basidiomata:—Annual, resupinate, adnate, membranaceous, becoming hard coriaceous upon drying, very hard to separate from substrate, without odor or taste when fresh, up to 15 cm long, 3 cm wide, 100–150 µm thick. Hymenial surface grandinioid, cracked with numerous crevices, cream (4A2) when fresh, turning to pinkish buff (5A3) to straw yellow (3A/B3) upon drying. Sterile margin narrow, cream (4A2), up to 1 mm wide.

Hyphal structure:—Hyphal system monomitic, generative hyphae with simple septa, colorless, thin-walled, branched, interwoven, 2–3 µm in diameter, IKI–, CB–; tissues unchanged in KOH.

Hymenium:—Gloeocystidia numerous, tubular, colorless, thin-walled, 17–25 × 3.5–5 µm; cystidioles absent. Basidia subclavate, occasionally sinuous or constricted in the middle, with four sterigmata, and a basal simple septum, 14–18 × 3–5 µm; basidioles dominant, similar to basidia in shape, but slightly smaller.

Basidiospores:—Broadly ellipsoid to ellipsoid, colorless, verrucose, slightly thick-walled, IKI+, CB+, (3.8–)4–4.6(–4.8) × 3–3.5(–3.7) µm, L = 4.34 µm, W = 3.31 µm, Q = 1.21–1.43, Q_m = 1.31 ± 0.07 (n = 60/2).

Additional specimen examined:—CHINA. Yunnan Province, Zhaotong, Qiaojia County, Yaoshan Town, Yaoshan National Nature Reserve, 27°15′52″N, 103°07′11″E, elev. 3,200 m, on the fallen angiosperm branch, 25 April 2025, CLZhao 45465 (SWFC!).

Discussion

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

Phylogenetically, the combined nrITS+nrLSU sequences (Fig. 1) indicated that the new species, *Gloeocystidiellum yaoshanense*, was assigned to the genus *Gloeocystidiellum*. The topology based on nrITS sequences (Fig. 2) revealed that the new species *Gc. yaoshanense*, formed a monophyletic lineage, and it seems that the new species is not related to other taxa in *Gloeocystidiellum.* The species *Gloeocystidiellum yaoshanense* has 75 base differences with the type species *Gc. porosum* in the genus *Gloeocystidiellum* based on the nrITS sequences. However, *Gc. porosum* can be distinguished from *Gc. yaoshanense* by its smooth hymenial surface, longer basidia (20–25× 3.5–4.5 µm *vs.* 14–18 × 3–5 µm), and thin-walled, longer basidiospores (5–6 × 2.5–3 µm *vs.* 4–4.6 × 3–3.5 µm, Bernicchia & Gorjón 2010).

Morphologically, the species *Gloeocystidiellum yaoshanense* resembles *Gc. fimbriatum* Burds. *et al*. (1981: 422), *Gc. lojanense* A. Jaram. *et al*. (2023: 9), *Gc. rajchenbergii* Gorjón & Hallenberg (2013: 186) and *Gc. sinense* S.C. Zhang & C.L. Zhao (2025: 6) in sharing the ellipsoid basidiospores. However, *Gloeocystidiellum fimbriatum* is different from *Gc. yaoshanense* by its fimbriate sterile margin, larger basidia (18–26 × 5–6.5 µm *vs.* 14–18 × 3–5 µm) (Ginns & Freeman 1994). The species *Gc. lojanense* differs from *Gc. yaoshanense* by having a ceraceous basidiomata with smooth and slightly tuberculate hymenial surface, larger basidia (25–35 × 5–6 µm *vs.* 14–18 × 3–5 µm) and thin-walled, longer basidiospores (6.5–8 × 3.4–4.5 µm *vs.* 4–4.6 × 3–3.5 µm, Jaramillo-Riofrío *et al*. 2023). The taxon *Gc. rajchenbergii* differs from *Gc. yaoshanense* by having a ceraceous basidiomata with the smooth hymenial surface, wider basidia (15–20 × 5–5.5 µm *vs.* 14–18 × 3–5 µm) and longer basidiospores (6–7 × 3–3.5 µm *vs.* 4–4.6 × 3–3.5 µm, Gorjón & Hallenberg 2013). The species *Gc. sinense* can be distinguished from *Gc. yaoshanense* by its coriaceous basidiomata and thin-walled, smooth basidiospores (Zhang *et al*. 2025).

The Wood-inhabiting fungi are an extensively studied group of Basidiomycota, which includes a number of poroid, smooth, grandinioid, odontioid and hydnoid basidiomata, and previously many new taxa were described from China (Dai 2010, Cui *et al*. 2019, Wu *et al.* 2020, 2022a, b, Wang *et al*. 2021, 2023, 2024, Liu *et al*. 2022, 2023, 2024, Zhao *et al*. 2023a, 2024, Yuan *et al.* 2023, Zhou *et al.* 2023, 2024, Dong *et al*. 2024, 2025a, b, Liu *et al.* 2025a, b, Qin *et al.* 2025). Fungi are closer to humans than to plants, and therefore can be treated as a kind of strategic biological resource (Ming *et al*. 2023). Scientific research on the biodiversity of fungi and their applications is important, as it may lead to the development of new products (Wu *et al.* 2019, Hyde *et al.* 2024a, b). Therefore, for future utilization, it is now urgent to recognize and conserve fungi. The species diversity of *Gloeocystidiellum* is still poorly understood in China, particularly in the subtropical region. This paper enriches our knowledge of fungal diversity in this area, and it is likely that more new taxa will be found with further fieldwork and molecular analyses.

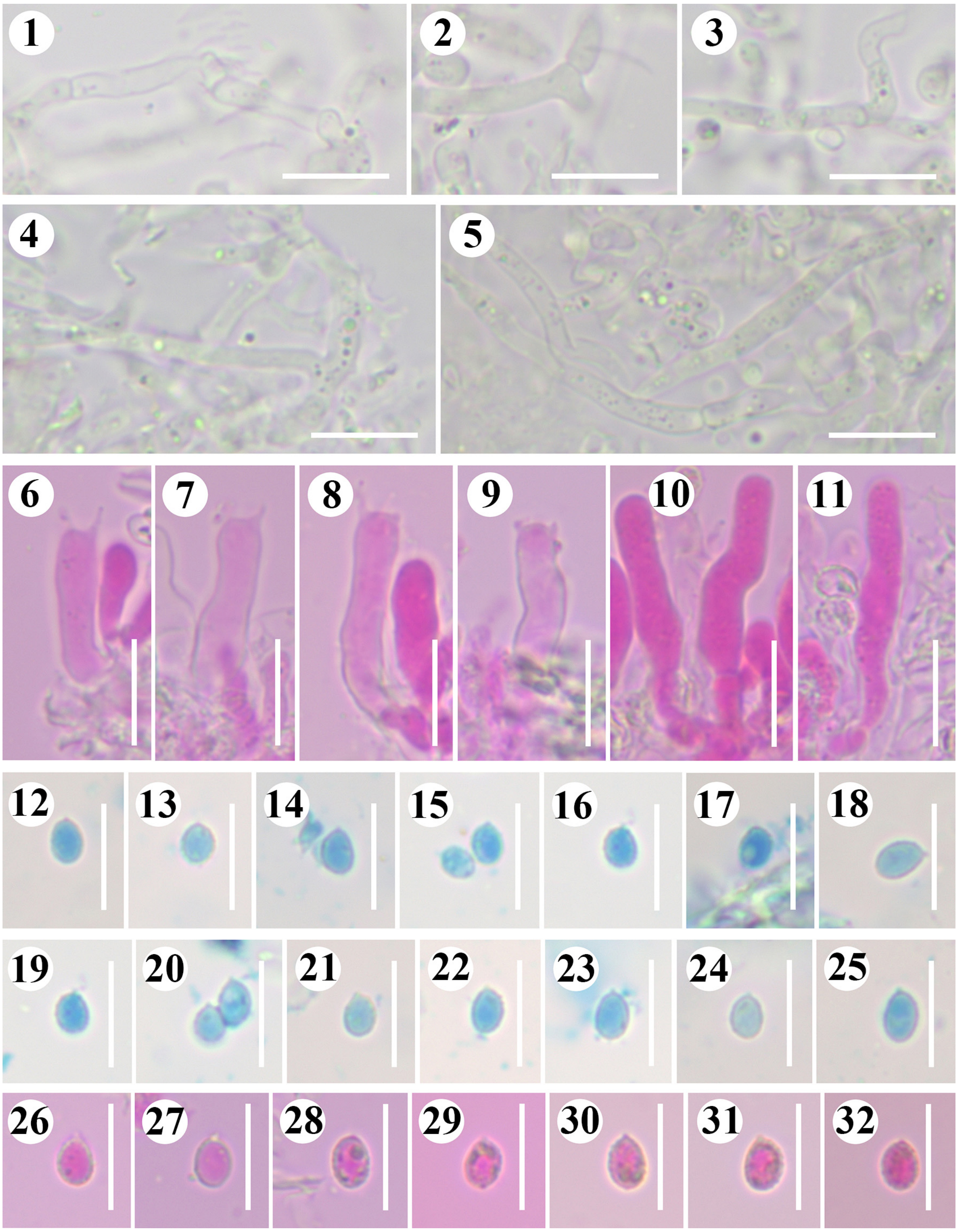

FIGURE 4. Sections of the hymenium of *Gloeocystidiellum yaoshanense* (holotype, CLZhao 20850). (1–5) Hyphae; (6–9) Basidia; (10–11) Gloeocystidia; (12–32) Basidiospores. Scale bars: 1–32 = 10 µm.

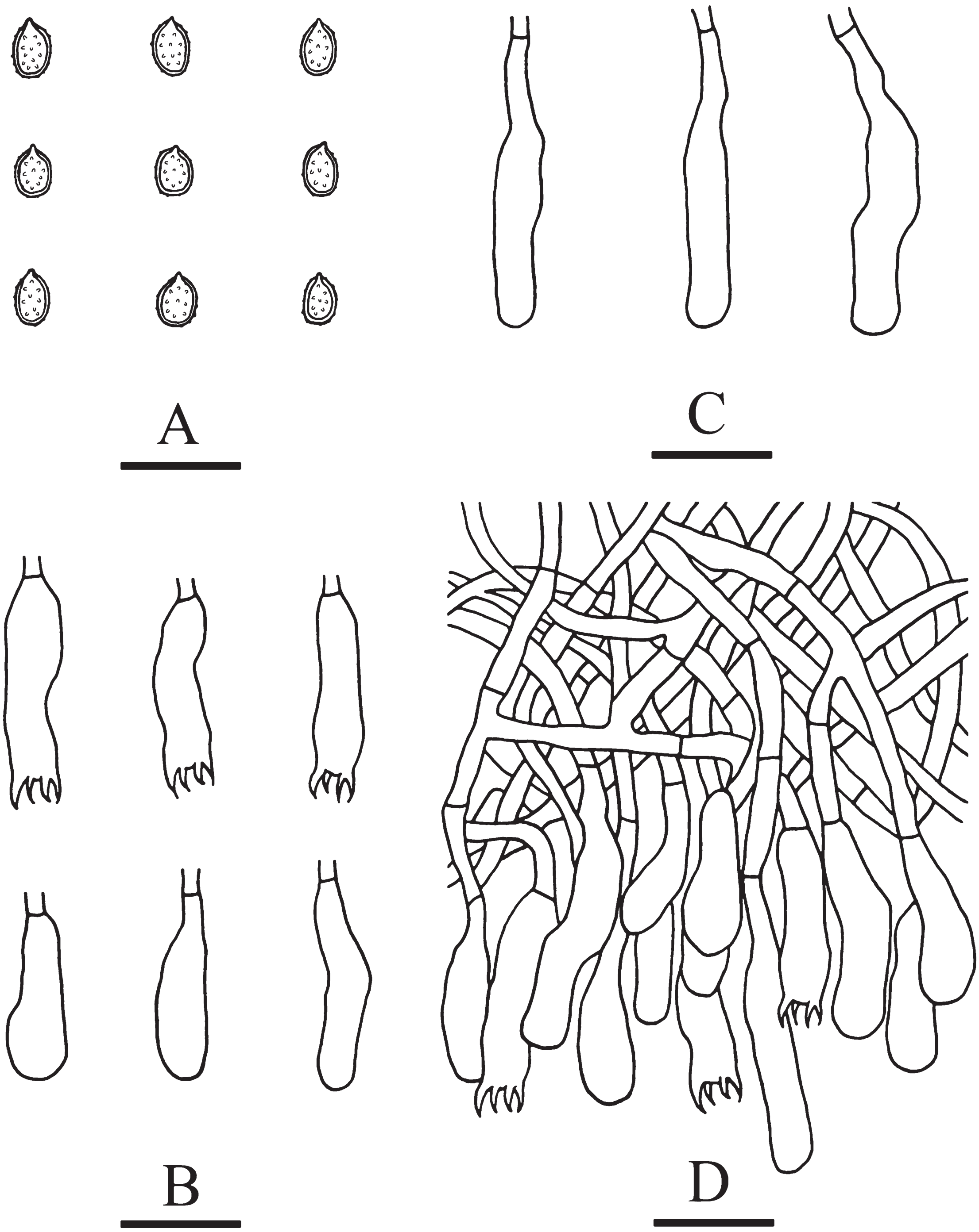

FIGURE 5. Microscopic structures of *Gloeocystidiellum yaoshanense* (holotype, CLZhao 20850). (A) Basidiospores; (B) Basidia and basidioles; (C) Gloeocystidia; (D) Part of the vertical section of the hymenium. Scale bars: A–D = 10 µm.

Acknowledgements

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References

Bernicchia, A. & Gorjón, S.P. (2010) *Fungi Europaei 12: Corticiaceae s.l.*. Edizioni Candusso, Lomazzo, 1007 pp.

Chen, L., Shi, Z.J., Wu, C.H. & Zhao, C.L. (2020) *Gloeodontia yunnanensis* sp. nov. (Russulales, Basidiomycota) from China, evidenced by morphological characters and phylogenetic analyses. *Phytotaxa* 432 (2): 111–118. https://doi.org/10.11646/phytotaxa.432.2.1

Cui, B.K., Li, H.J., Ji, X., Zhou, J.L., Song, J., Si, J., Yang, Z.L. & Dai, Y.C. (2019) Species diversity, taxonomy and phylogeny of Polyporaceae (Basidiomycota) in China. *Fungal Diversity* 97: 137–392. https://doi.org/10.1007/s13225-019-00427-4

Cui, Y.Y., Cai, Q., Tang, L.P., Liu, J.W. & Yang, Z.L. (2018) The family Amanitaceae: Molecular phylogeny, higher-rank taxonomy and the species in China. *Fungal Diversity* 91: 5–230. https://doi.org/10.1007/s13225-018-0405-9

Dai, L.D. & He, S.H. (2017) A new species and a new combination of *Aleurodiscus* s.l. (Russulales, Basidiomycota). *Mycosphere* 8 (7): 908–916. https://doi.org/10.5943/mycosphere/8/7/7

Dai, L.D., Wu, S.H., Nakasone, K.K., Burdsall, H.H. & He, S.H. (2017) Two new species of *Aleurodiscus* s.l. (Russulales, Basidiomycota) on bamboo from tropics. *Mycoscience* 58 (3): 213–220. https://doi.org/10.1016/j.myc.2017.02.001

Dai, Y.C. (2010) Hymenochaetaceae (Basidiomycota) in China. *Fungal Diversity* 45: 131–343. https://doi.org/10.1007/s13225-010-0066-9

Dai, Y.C., Yang, Z.L., Cui, B.K., Wu, G., Yuan, H.S., Zhou, L.W., He, S.H., Ge, Z.W., Wu, F., Wei, Y.L., Yuan, Y. & Si, J. (2021) Diversity and systematics of the important macrofungi in Chinese forests. *Mycosystema* 40: 770–805. https://doi.org/10.13346/j.mycosystema.210036

Darriba, D., Taboada, G.L., Doallo, R. & Posada, D. (2012) jModelTest 2: more models, new heuristics and parallel computing. *Nature Methods* 9: 772. https://doi.org/10.1038/nmeth.2109

Dong, J., Deng, Q., Chen, M., Chen, D., Zhou, C. & Zhao, C. (2025a) Molecular phylogeny and morphology reveal four new wood-inhabiting fungi of *Asterostroma* and *Radulomyces* (Basidiomycota) from Southwestern China. *MycoKeys* 112: 35–58. https://doi.org/10.3897/mycokeys.112.137098

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. (2025b) 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 (1): 1110–1293. https://doi.org/10.5943/mycosphere/15/1/10

Donk, M.A. (1931) Revisie van de Nederlandse Heterobasidiomycetae en Homobasidiomycetae-Aphyllophoraceae I. *Mededelingen van de Nederlandse Mycologische Vereeniging* 18: 67–200.

Donk, M.A. (1957) The generic names proposed for Hymenomycetes. vii: “Thelephoraceae”. *Taxon* 6: 17–28. https://doi.org/10.23071217865

Felsenstein, J. (1985) Confidence intervals on phylogenetics: an approach using bootstrap. *Evolution* 39: 783–791. https://doi.org/10.1111/j.1558-5646.1985.tb00420.x

Ginns, J. & Freeman, G.W. (1994) The Gloeocystidiellaceae (Basidiomycota, Hericiales) of North America. *Bibliotheca Mycologica* 157: 1–118.

Gorjón, S.P. & Hallenberg, N. (2013) Some new species and a first checklist of corticioid fungi (Basidiomycota) from Chile. *Mycological Progress* 12 (2): 185–192. https://doi.org/10.1007/s11557-012-0824-z

He, M.Q., Cao, B., Liu, F., Boekhout, T., Denchev, T.T., Schoutteten, N., Denchev, C.M., Kemler, M., Gorjón, S.P., Begerow, D., Valenzuela, R., Davoodian, N., Niskanen, T., Vizzini, A., Redhead, S.A., Ramírez-Cruz, V., Papp, V., Dudka, V.A., Dutta, A.K., García-Sandoval, R., Liu, X.Z., Kijpornyongpan, T., Savchenko, A., Tedersoo, L., Theelen, B., Trierveiler-Pereira, L., Wu, F., Zamora, J.C., Zeng, X.Y., Zhou, L.W., Liu, S.L., Ghobad-Nejhad, M., Giachini, A.J., Li, G.J., Kakishima, M., Olariaga, I., Haelewaters, D., Sulistyo, B., Sugiyama, J., Svantesson, S., Yurkov, A., Alvarado, P., Antonín, V., da Silva, A.F., Druzhinina, I., Gibertoni, T.B., Guzmán-Dávalos, L., Justo, A., Karunarathna, S.C., Galappaththi, M.C.A., Toome-Heller, M., Hosoya, T., Liimatainen, K., Márquez, R., Mešić, A., Moncalvo, J.M., Nagy, L.G., Varga, T., Orihara, T., Raymundo, T., Salcedo, I., Silva-Filho, A.G.S., Tkalčec, Z., Wartchow, F., Zhao, C.L., Bau, T., Cabarroi-Hernández, M., Cortés-Pérez, A., Decock, C., Lange, R.D., Weiss, M., Jr. Menolli, N., Nilsson, R.H., Fan, Y.G., Verbeken, A., Gafforov, Y., Meiras-Ottoni, A., Mendes-Alvarenga, R.L., Zeng, N.K., Wu, Q., Hyde, K.D., Kirk, P.M. & Zhao, R.L. (2024) Phylogenomics, divergence times and notes of orders in Basidiomycota. *Fungal Diversity* 126: 127–406. https://doi.org/10.1007/s13225-024-00535-w

Hu, Y., Karunarathna, S.C., Li, H., Galappaththi, M.C., Zhao, C.L., Kakumyan, P. & Mortimer, P.E. (2022) The impact of drying temperature on basidiospore size. *Diversity* 14 (4): 239. https://doi.org/10.3390/d14040239

Hyde, K.D., Baldrian, P., Chen, Y., Chethana, K.W.T., Hoog, S.D., Doilom, M., de Farias, A.R.G., Gonçalves, M.F.M., Gonkhom, D., Gui, H., Hilário, S., Hu, Y.W., Jayawardena, R.S., Khyaju, S., Kirk, P.M., Kohout, P., Luangharn, T., Maharachchikumbura, S.S.N., Manawasinghe, I.S., Mortimer, P.E., Niego, A.G.T., Phonemany, M., Sandargo, B., Senanayake, I.C., Stadler, M., Surup, F., Thongklang, N., Wanasinghe, D.N., Bahkali, A.H. & Walker, A. (2024a) Current trends, limitations and future research in the fungi? *Fungal Diversity* 125: 1–71. https://doi.org/10.1007/s13225-023-00532-5

Hyde, K.D., Saleh, A., Aumentado, H.D.R., Boekhout, T., Bera, I., Khyaju, S., Bhunjun, C.S., Chethana, K.W.T., Phukhamsakda, C., Doilom, M., Thiyagaraja, V., Mortimer, P.E., Maharachchikumbura, S.S.N., Hongsanan, S., Jayawardena, R.S., Dong, W., Jeewon, R., Al-Otibi, F., Wijesinghe, S.N. & Wanasinghe, D.N. (2024b) Fungal numbers: global needs for a realistic assessment. *Fungal Diversity* 128: 191–225. https://doi.org/10.1007/s13225-024-00545-8

Jaramillo-Riofrío, A., Decock, C., Suárez, J.P., Benítez, Á., Castillo, G. & Cruz, D. (2023) Screening of antibacterial activity of some resupinate fungi, reveal *Gloeocystidiellum lojanense* sp. nov. (Russulales) against *E. coli* from Ecuador. *Journal of Fungi* 9: 54. https://doi.org/10.3390/jof9010054

Katoh, K., Rozewicki, J. & Yamada, K.D. (2019) MAFFT online service: multiple sequence alignment, interactive sequence choice and visualization. *Briefings in Bioinformatics* 20: 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: 3276–3278. https://doi.org/10.1093/bioinformatics/btu531

Larsson, E. & Hallenberg, N. (2001) Species delimitation in the *Gloeocystidiellum porosum-clavuligerum* complex inferred from compatibility studies and nuclear rDNA sequence data. *Mycologia* 93: 907–914. https://doi.org/10.1080/00275514.2001.12063225

Larsson, E. & Larsson, K.H. (2003) Phylogenetic relationships of russuloid basidiomycetes with emphasis on aphyllophoralean taxa. *Mycologia* 95 (6): 1037–1065. https://doi.org/10.1080/15572536.2004.11833020

Larsson, K.H., Larsson, E. & Kõljalg, U. (2004) High phylogenetic diversity among corticioid Homobasidiomycetes. *Mycological Research* 108: 983–1002. https://doi.org/10.1017/s0953756204000851

Leal-Dutra, C.A., Neves, M.A., Griffith, G.W., Reck, M.A., Clasen, L.A. & Dentinger, B.T.M. (2018) Reclassification of *Parapterulicium* Corner (Pterulaceae, Agaricales), contributions to Lachnocladiaceae and Peniophoraceae (Russulales) and introduction of *Baltazaria* gen. nov. *MycoKeys* 37: 39–56. https://doi.org/10.3897/mycokeys.37.26303

Liu, S., Chen, Y.Y., Sun, Y.F., He, X.L., Song, C.G., Si, J., Liu, D.M., Gates, G. & Cui, B.K. (2022) Systematic classification and phylogenetic relationships of the brown-rot fungi within the Polyporales. *Fungal Diversity* 118: 1–94. https://doi.org/10.1007/s13225-022-00511-2

Liu, S., Shen, L.L., Xu, T.M., Song, C.G., Gao, N., Wu, D.M., Sun, Y.F. & Cui, B.K. (2023) Global diversity, molecular phylogeny and divergence times of the brown-rot fungi within the Polyporales. *Mycosphere* 14: 1564–1664. https://doi.org/10.5943/mycosphere/14/1/18

Liu, S.L. & He, S.H. (2018) Taxonomy and phylogeny of *Dichostereum* (Russulales), with descriptions of three new species from southern China. *MycoKeys* 10 (40): 111–126. https://doi.org/10.3897/mycokeys.40.28700

Liu, S.L., Liu, D.M. & Zhou, L.W. (2024) The future is now: how to conserve fungi. *Biological Diversity* 1: 6–8. https://doi.org/10.1002/bod2.12003

Liu, Z.B., Liu, H.G., Vlasák, J., Gates, G.M., Dai, Y.C. & Yuan, Y. (2025a) Global diversity and phylogeny of Incrustoporiaceae (Polyporales, Basidiomycota) with an emphasis on *Skeletocutis*. *Mycology* 16: 1083–1140. https://doi.org/10.1080/21501203.2024.2448145

Liu, Z.B., Yuan, Y., Dai, Y.C., Liu, H.G., Vlasák, J., Zeng, G.Y., He, S.H. & Wu, F. (2025b) Global diversity and systematics of Hymenochaetaceae with non-poroid hymenophore. *Fungal Diversity* 131: 1–97.
https://doi.org/10.1007/s13225-025-00552-3

Maekawa, N., Sugawara, R., Nakano, R., Shino, R., Sotome, K., Nakagiri, K. & Oba, Y. (2023) A new species of the genus *Aleurodiscus* sensu lato (Russulales, Basidiomycota) from Hachijo Island, Japan. *Mycoscience* 64: 109–115.
https://doi.org/10.47371/mycosci.2023.06.001

Ming, B., Zhou, L.W., Tong, Y.J. & Yin, F. (2023) "Risk assessment and warning system for strategic biological resources in China." *The Innovation Life* 1: 100004.
https://doi.org/10.59717/j.xinn-life.2023.100004

Miller, M.A., Pfeiffer, W. & Schwartz, T. (2012) The CIPRES Science Gateway: Enabling High-impact Science for Phylogenetics Researchers with Limited Resources. *Proceedings of the 1st Conference of the Extreme Science and Engineering Discovery Environment: Bridging from the Extreme to the campus and beyond*. Association for Computing Machinery, New York, pp. 1–8.
https://doi.org/10.1145/2335755.2335836

Petersen, J.H. (1996) Farvekort. *In*: *The Danish Mycological Society's Colour-Chart.* Foreningen til Svampekundskabens Fremme: Greve, Germany, pp. 1–6.

Qin, G.F., Qin, W.M., Wang, H.C., Zhao, J., Korhonen, K., Chen, J., Dai, Y.C. & Yuan, Y. (2025) Phylogeny and species diversity of *Armillaria* in China based on morphological, mating test, and GCPSR criteria. *Mycology* 16: 777–811.
https://doi.org/10.1080/21501203.2024.2404121

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. (2024) 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

Ronquist, F., Teslenko, M., van der Mark, P., Ayres, D.L., Darling, A., Hohna, S., Larget, B., Liu, L., Suchard, M.A. & Huelsenbeck, J.P. (2012) Mrbayes 3.2: efficient bayesian phylogenetic inference and model choice across a large model space. *Molecular Systems Biology* 61: 539–542.
https://doi.org/10.1093/sysbio/sys029

Song, J., Karunarathna, S.C., Senanayake, I.C. & Yu, F.Q. (2024) *Thyridium livistonae* sp. nov. from Yunnan Province, China, with two new combinations. *New Zealand Journal of Botany* 63 (2–3): 184–198.
https://doi.org/10.1080/0028825X.2024.2384470

Vilgalys, R. & Hester, M. (1990) Rapid genetic identification and mapping of enzymaticallyamplified ribosomal DNA from several *Cryptococcus* species. *Journal of Bacteriology* 172 (8): 4238–4246.
https://doi.org/10.1128/jb.172.8.4238-4246.1990

Vu, D., Groenewald, M., de Vries, M., Gehrmann, T., Stielow, B., Eberhardt, U., Al-Hatmi, A., Groenewald, J.Z., Cardinali, G., Houbraken, J., Boekhout, T., Crous, P.W., Robert, V. & Verkley, G.J.M. (2019) Large-scale generation and analysis of filamentous fungal DNA barcodes boosts coverage for kingdom fungi and reveals thresholds for fungal species and higher taxon delimitation. *Studies in Mycology* 92: 135–154.
https://doi.org/10.1016/j.simyco.2018.05.001

Wang, C.G., Zhao, H., Liu, H.G., Zeng, G.Y., Yuan, Y. & Dai, Y.C. (2023) A multi-gene phylogeny clarifies species diversity, taxonomy, and divergence times of *Ceriporia* and other related genera in Irpicaceae (Polyporales, Basidiomycota). *Mycosphere* 14 (1): 1665–1729.
https://doi.org/10.5943/mycosphere

Wang, C.G., Dai, Y.C., Kout, J., Gates, G.M., Liu, H.G., Yuan, Y. & Vlasák, J. (2024) Multi-gene phylogeny and taxonomy of *Physisporinus* (Polyporales, Basidiomycota). *Mycosphere* 15: 1455–1521.
https://doi.org/10.1080/21501203.2024.2379476

Wang, Y.R., Wu, Y.D., Vlasák, J., Yuan, Y. & Dai, Y.C. (2021) Phylogenetic analysis demonstrating four new species in *Megasporoporia* sensu lato (Polyporales, Basidiomycota). *Mycosphere* 12 (1): 1012–1037.
https://doi.org/10.5943/mycosphere/12/1/11

Wang, L., Zhu, Y., He, S., Jabeen, S. & Zhao, C. (2025) Additions to the coriaceous families Peniophoraceae and Stereaceae (Russulales): Six novel wood-inhabiting taxa in the genera *Conferticium*, *Gloeocystidiellum* and *Peniophora* from southwest China. *MycoKeys* 115: 273–308.
https://doi.org/10.3897/mycokeys.115.147044

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. (Ed.) *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., Yang, Z.L., Bau, T., Li, T.H. & Dai, Y.C. (2019) Resource diversity of Chinese macrofungi: edible, medicinal and poisonous species. *Fungal Diversity* 98: 1–76.
https://doi.org/10.1007/s13225-019-00432-7

Wu, F., Man, X.W., Tohtirjap, A. & Dai, Y.C. (2022a) A comparison of polypore fungal and species composition in forest ecosystems of China, North America, and Europe. *Forest Ecosystems* 9: 100051.
https://doi.org/10.1016/j.fecs.2022.100051

Wu, F., Yuan, Y., Chen, J.J., Cui, B.K., Zhou, M. & Dai, Y.C. (2020) Terrestriporiaceae fam. nov., a new family of Russulales (Basidiomycota). *Mycosphere* 11: 2755–2766.
https://doi.org/10.5943/mycosphere/11/1/21

Wu, F., Zhou, L.W., Vlasák, J. & Dai, Y.C. (2022b) Global diversity and systematics of Hymenochaetaceae with poroid hymenophore. *Fungal Diversity* 113: 1–192.
https://doi.org/10.1007/s13225-021-00496-4

Wu, G., Li, Y.C., Zhu, X.T., Kuan, Zhao, K., Han, L.H., Cui, Y.Y., Li, F., Xu, J.P. & Yang, Z.L. (2016) One hundred noteworthy boletes from China. *Fungal Diversity* 81: 25–188.
https://doi.org/10.1007/s13225-016-0375-8

Yuan, Y., Bian, L.S., Wu, Y.D., Chen, J.J., Wu, F., Liu, H.G., Zeng, G.Y. & Dai, Y.C. (2023) Species diversity of pathogenic wood-rotting fungi (Agaricomycetes, Basidiomycota) in China. *Mycology* 14: 204–226.
https://doi.org/10.1080/21501203.2023.2238779

Zhang, S.C., Dong, J.H., Zhang, X.J., Li, Y.C., Liu, R. & Zhao, C.L. (2025) *Gloeocystidiellum sinense* sp. nov. (Stereaceae, Russulales), a wood-inhabiting fungus from Yunnan Province, China. *New Zealand Journal of Botany* 63 (2-3): 370–381.
https://doi.org/10.1080/0028825X.2025.2454589

Zhao, C.L., Qu, M.H., Huang, R.X. & Karunarathna, S.C. (2023a) Multi-Gene Phylogeny and taxonomy of the wood-rotting fungal genus *Phlebia* sensu lato (Polyporales, Basidiomycota). *Journal of Fungi* 9: 320.
https://doi.org/10.3390/jof9030320

Zhao, H., Nie, Y., Zong, T.K., Wang, K., Lv, M.L., Cui, Y.J., Tohtirjap, A., Chen, J.J., Zhao, C.L., Wu, F., Cui, B.K., Yuan, Y., Dai, Y.C. & Liu, X.Y. (2023b) Species diversity, updated classification and divergence times of the phylum Mucoromycota. *Fungal Diversity* 123: 49–157.
https://doi.org/10.1007/s13225-023-00525-4

Zhao, H., Wu, Y.D., Yang, Z.R., Liu, H.G., Wu, F., Dai, Y.C. & Yuan, Y. (2024) Polypore funga and species diversity in tropical forest ecosystems of Africa, America and Asia, and a comparison with temperate and boreal regions of the Northern Hemisphere. *Forest Ecosystems* 11: 100200.
https://doi.org/10.1016/j.fecs.2024.100200

Zhao, Y.L. & Zhao, C.L. (2023) A corticioid fungus, *Gloeocystidiellum yunnanense* sp. nov. (Russulales) with characteristic gloeocystidia from southern China. *Nova Hedwigia* 116 (1-2): 155–170.
https://doi.org/10.1127/nova_hedwigia/2023/0725

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* 634 (1): 1–15.
https://doi.org/10.11646/phytotaxa.635.2.7

Zhou, H.M., Dai, Y.C., Bian, L.S., Liu, H.G., Vlasák, J. & Yuan, Y. (2025) Diversity, divergence time, and biogeography of the genus *Albatrellus* (Agaricomycetes, Russulales). *Mycology* 16: 738–776.
https://doi.org/10.1080/21501203.2024.2386021

Zhou, M., Dai, Y.C., Vlasák, J., Liu, H.G. & Yuan, Y. (2023) Updated systematics of *Trichaptum* s.l. (Hymenochaetales, Basidiomycota). *Mycosphere* 14 (1): 815–917.
https://doi.org/10.5943/mycosphere/14/1/11