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**Taxonomic and phylogenetic studies reveal three new species of corticioid fungi
(*Russulales*, *Basidiomycota*) from Southwestern China**

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Abstract

The southwestern region of China is a global biodiversity hotspot, yet the macrofungal diversity of *Russulales* (*Basidiomycota*) remains poorly documented, with numerous undescribed species expected from forest ecosystem. In present study, detailed morphological characteristics and a two-marker phylogenetic inference using the nuclear ribosomal internal transcribed spacers (ITS) and the large subunit (nrLSU) gene revealed three new species in *Russulales*, viz., *Gloeocystidiellum tenuissimum* sp. nov., *Vararia farinacea* sp. nov. and *V. ruiliensis* sp. nov. Combining morphological observations and molecular phylogenetic analyses, we detected and determined the taxonomic position of these three new species, which are grouped within two families *Gloeocystidiellaceae* and *Peniophoraceae* (*Russulales*), in which three new species clustered into genera of *Gloeocystidiellum* and *Vararia*. Descriptions, illustrations, and phylogenetic analyses results of the new taxa are provided. Our results augment the knowledge of species diversity and taxonomy of fungi in southwest China.

Keywords: Biodiversity · Taxonomy · Wood-inhabiting fungi · Yunnan Province

Introduction

Wood-inhabiting fungi (WIF) are key decomposers of plant and environmental contaminants (Stenlid et al. 2008; James et al. 2020; Wiens et al. 2026), colonizing diverse substrates from living trees to stumps (M'Barek et al. 2020). They exhibit striking morphological, phylogenetic, and ecological diversity (Park et al. 2020; Ghobad-Nejhad et al. 2024), yet global fungal diversity remains poorly known and increasingly threatened (Niskanen et al. 2023).

Within *Agaricomycetes*, the taxonomy and phylogeny of the order *Russulales* remains understudied, with many species awaiting discovery (Spirin et al. 2024; Yurchenko et al. 2025). Two genera of *Gloeocystidiellum* Donk (*Gloeocystidiellaceae*) and *Vararia* P. Karst. (*Peniophoraceae*) contain the highest number of species and the taxonomic gaps persist within them, which are recognized as highly polyphyletic within the order *Russulales* (Kirk et al. 2008; Leal-Dutra et al. 2018; Deng et al. 2024).

A corticioid genus *Gloeocystidiellum* belonging to order *Russulales* was established by Donk with *G. porosum* (Berk. & M.A. Curtis) Donk as its type species (Donk 1931). According to Index Fungorum (www.indexfungorum.org; accessed on 29 June 2026), and Mycobank (<https://www.mycobank.org/>; accessed on 29 June 2026), *Gloeocystidiellum* has registered 91 specific and infraspecific names, and the actual number of the species has reached up to 43, currently known, and they occur mainly in the tropical and subtropical areas of the world (Larsson and Hallenberg 2001; Jaramillo-Riofrío et al. 2023; Deng et al. 2026a). The genus *Gloeocystidiellum* s. lat. was originally placed in *Gloeocystidiellaceae* (Boidin et al. 1997), but species in the genus were later often assigned to *Stereaceae* based on morphological similarities and limited phylogenetic sampling (Wang et al. 2025). Recent phylogenetic analyses have confirmed that the core clade belongs to the resurrected family *Gloeocystidiellaceae*, containing the type species *G. porosum* (Larsson and Larsson 2003; Gorjón and Hallenberg 2013; Jaramillo-Riofrío et al. 2023). However, other lineages remain distributed across distinct

families within *Russulales*, reflecting the long-standing complexity of this group. Further introduction of additional species is still required to identify definitive defining characteristics of them.

The genus *Vararia* is a corticioid wood-inhabiting genus with a wide distribution, typified by *V. investiens* (Schwein.) P. Karst. (Welden 1965; Larsson and Larsson 2003; Karasinski 2010). In recent years, many new species of *Vararia* have been reported from tropical and subtropical regions, indicating a high potential diversity of this genus in low-latitude areas (Wang et al. 2026a). Currently, 118 specific and infraspecific names are recorded in Index Fungorum (accessed on 29 June 2026), of which 95 are accepted worldwide (Bernicchia and Gorjón 2010; Wang et al. 2026a). Taxonomic gaps persist within *Vararia*, which is recognized as highly polyphyletic (Leal-Dutra et al. 2018; Deng et al. 2024). Due to the limited availability of molecular sequence data and the absence of stable morphological or molecular characteristics, a detailed taxonomic classification of *Vararia* cannot currently be established (Boidin and Lanquetin 1975, 1984, 1987; Boidin et al. 1987; Leal-Dutra et al. 2018; Deng et al. 2026a, b). There is an urgent need to collect more *Vararia* specimens and obtain additional molecular markers to better clearly define the relationships among them.

During investigations on wood-inhabiting fungi in Yunnan province, China, three potentially new species were collected. To clarify the placement and relationships of these specimens, we carried out phylogenetic and taxonomic study based on ITS+nrLSU sequences. These specimens were assigned to the genera *Vararia* and *Gloeocystidiellum* of *Russulales*. The Pairwise Homoplasy Index (PHI) analyses were conducted to confirm the new species with related taxa.

Materials and methods

Sample collection and herbarium specimen preparation

Fresh basidiomata were collected from Dehong and Puer in Yunnan Province, China. The samples were photographed in situ and fresh macroscopic details were recorded (Deng et al. 2025). Photographs were recorded using a Nikon D7100 camera. Macroscopic details were recorded and transported to a field station where the fruiting bodies were dried on an electronic food dryer at 45 °C (Dong et al. 2024). Once dried, the specimens were sealed in an envelope and zip-lock plastic bags and labelled. The dried specimens were deposited in the herbarium of the Southwest Forestry University (SWFC), Kunming, Yunnan Province, China.

Morphological study

Macromorphological descriptions are based on field notes and photos captured in the field and laboratory and follow the color terminology of Petersen (1996). Micromorphological data were obtained from the dried specimens following observation under a light microscope (Deng et al. 2025). The following abbreviations were used: KOH = 5% potassium hydroxide water solution, CB+ = cyanophilous, CB = cotton clue, CB– = acyanophilous, IKI = Melzer’s reagent, IKI– = both inamyloid and indextrinoid, L = means spore length (arithmetic average for all spores), W = means 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 a given number (b) of specimens).

DNA extraction, amplification, and sequencing

CTAB rapid plant genome extraction kit-DN14 (Aidlab Biotechnologies Co., Ltd, Beijing) was used to obtain genomic DNA from dried specimens following the procedure of a previous study (Wang et al. 2026b). The ITS region was amplified with the primer pair ITS5 and ITS4 (White et al. 1990). The nuclear nrLSU region was amplified with the primer pair LR0R and LR7 (Vilgalys and Hester 1990). The PCR procedure for ITS was as follows: initial denaturation at

95 °C for 3 min, followed by 35 cycles at 94 °C for 40 s, 54 °C for 45 s, and 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 at 94 °C for 30 s, 50 °C for 1 min, and 72 °C for 1.5 min; and a final extension at 72 °C for 10 min. The PCR products were purified and sequenced at Kunming Tsingke Biological Technology Limited Company, Kunming, Yunnan Province, P.R. China. All newly generated sequences were deposited in GenBank (Table 1).

Sequence alignment and phylogenetic analyses

Newly generated sequences were initially subjected to BLAST searches in NCBI to identify the most closely related taxa in GenBank (<http://blast.ncbi.nlm.nih.gov/>), with type specimens or authoritative sequences referenced. Additional sequence data were retrieved from GenBank based on recent publications.

Sequences were aligned using MAFFT version 7 (<https://mafft.cbrc.jp/alignment/server/>), adjusting the direction of nucleotide sequences according to the first sequence and selecting the G-INS-i iterative refinement method (Katoh et al. 2019). The alignment was adjusted manually using AliView version 1.27 (Larsson 2014). A dataset of concatenated ITS and nrLSU sequences were combined using Mesquite version 3.51 to determine the phylogenetic position of the three new species. The multiple sequence alignments were deposited in Figshare (DOI: 10.6084/m9.figshare.32260929).

Maximum likelihood analyses were performed using the CIPRES Science Gateway (Miller et al. 2012) based on the dataset using the RAxML-HPC BlackBox tool, with setting RAxML 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 1000 replicates. Bayesian

inference (BI) analysis was performed on the same dataset using MrBayes v3.2.7a (Ronquist et al. 2012). The best substitution model for the dataset was selected by jModelTest2 on ACCESS v2 .1.6 (Kalyaanamoorthy et al. 2017) using a Bayesian Information criterion, and the model was used for Bayesian analysis. There were four independent runs, each of which had four chains for 8.915 million (Fig. 1), 4.1 million (Fig. 2) and 7.5 thousand (Fig. 3) generations sampling from the posterior distribution every 1000th 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 of the consensus tree that received ML bootstrap support equal to or above 70%, and Bayesian posterior probabilities equal to or above 0.95, respectively, were considered strongly supported.

Pairwise homoplasy test

The Genealogical Concordance Phylogenetic Species Recognition (GCPSR) analysis was employed to detect significant recombination events. Pairwise homoplasy index (Φ_w) and the PHI test, implemented in SplitsTree 4, were used to evaluate recombination levels among closely related species (Bruen et al. 2006; Quaadvlieg et al. 2014). The analysis was performed on a single-locus dataset (ITS) of closely related species. A PHI test result below 0.05 ($\Phi_w < 0.05$) indicates the presence of significant recombination in the dataset. Split graphs were constructed from the concatenated datasets using the LogDet transformation and splits decomposition options to visualize the relationships among closely related taxa.

Results

Phylogenetic placement

The ITS+nrLSU dataset comprised (Fig. 1) and encompassed 118 fungal specimens representing 67 taxa of the family *Peniophoraceae*, covering 8 genera. *Stereum hirsutum* (Willd.) Pers. and *S. ostrea* (Blume & T. Nees) Fr. were retrieved from GenBank as the outgroups following a previous study analysis (Deng et al. 2026a). The dataset had an aligned length of 2663 characters with gaps (ITS = 1245, LSU = 1418). The best model for the combined ITS+nrLSU dataset estimated and applied in the Bayesian analysis was GTR+I+G. Analyses of the dataset generated a final likelihood value of -41176.116744 for the best ML tree and a final average standard deviation of split frequencies of 0.009982 (BI) and an effective sample size (ESS) average ESS (avg. ESS) = 4293.

The topology (Fig. 1) shows that the family *Peniophoraceae* includes the genera *Asterostroma* Masee, *Baltazaria* Leal-Dutra, Dentinger & G.W. Griff, *Dichostereum* Pilát, *Gloiothele* Bres., *Lachnocladium* Lév., *Peniophora* Cooke, *Scytinostroma* Donk and *Vararia*. Two new species *V. farinacea* Y.L. Deng & C.L. Zhao and *V. ruiliensis* Y.L. Deng & C.L. Zhao form separate monophyletic and strongly supported clades inside *Vararia*. In which, *V. farinacea* is closely related to two taxa, namely *V. cremea* Boidin, Lanq. & Gilles and *V. gillesii* Boidin & Lanq. Moreover, *V. ruiliensis* is closely related to three taxa, namely *V. trinidadensis* A.L. Welden, *V. gomezii* Boidin & Lanq. and *V. sigmatospora* Boidin, Gilles & Lanq.

In the alignment of the genus *Vararia* sequences (Fig. 2), the concatenated dataset of ITS and nrLSU sequences comprised a total of 2232 characters with gaps (ITS = 842, LSU = 1388) characters, and 92 sequences representing 58 species, including *Peniophora incarnata* (Pers.) P. Karst. and *P. nuda* (Fr.) Bres. were retrieved from GenBank as the outgroups following a

previous study analysis (Deng et al. 2026b). The best model for the combined ITS+nrLSU dataset estimated and applied in the Bayesian analysis was TIM2+I+G. Analyses of the dataset generated a final likelihood value of -28080.717462 for the best ML tree and a final average standard deviation of split frequencies of 0.009934 (BI) and an effective sample size (ESS) average ESS (avg. ESS) = 1557.4 in the BI analysis. The phylogenetic tree (Fig. 2) reveals that two new species, *Vararia ruiliensis* and *V. farinacea* are grouped into the genus *Vararia*. In which, *V. farinacea* is fomed a lone clade, *V. ruiliensis* is closely with three taxa, *V. trinidadensis*, *V. gomezii* and *V. sigmatospora*.

A combined ITS+nrLSU dataset (Fig. 3) that included sequences from 15 fungal specimens representing 10 taxa of the genus *Gloeocystidiellum* were used for the phylogenetic treatment of that genus. *Laurilia sulcata* (Burt) Pouzar was retrieved from GenBank as the outgroup following a previous study analysis (Deng et al. 2026a). The dataset had an aligned length of 2130 characters with gaps (ITS = 772, LSU = 1356). The best model for the combined ITS+nrLSU dataset estimated and applied in the Bayesian analysis was TrNef+G. Analyses of the dataset generated a final likelihood value of -5997.936609 for the best ML tree and a final average standard deviation of split frequencies of 0.009795 (BI) and an effective sample size (ESS) average ESS (avg. ESS) = 212. Phylogenetic analysis (Fig. 3) reveals that the new species, *Gloeocystidiellum tenuissimum* C.L. Zhao is grouped into the genus *Gloeocystidiellum*, and is closley with *G. sinense* S. C. Zhang & C.L. Zhao.

Application of the PHI test to the ITS sequences revealed no recombination among phylogenetically related species. No significant recombination events were observed between *Vararia farinacea* and its phylogenetically closely related species, namely *V. cremea* and *V. gillesii*. The test results show $\Phi_w = 0.648$ for ITS data (Fig. 4), indicating that no recombination

is present between the new species and *V. cremea* and *V. gillesii*. No significant recombination events were observed between *V. ruiliensis* and its phylogenetically closely related species, namely *V. trinidadensis* and *V. gomezii*. The test results show $\Phi_w = 0.7223$ for ITS data (Fig. 5), indicating that no recombination is present between the new species and *V. trinidadensis* and *V. gomezii*. No significant recombination events were observed between *Gloeocystidiellum tenuissimum* and its phylogenetically closely related species, namely *G. porosum*, *G. punctatum* Y.L. Deng & C.L. Zhao and *G. sinense* S.Cheng Zhang & C.L. Zhao. The test results show $\Phi_w = 0.9571$ for ITS data (Fig. 6), indicating that no recombination is present between the new species and related three *Gloeocystidiellum* species.

Taxonomy

Gloeocystidiellum tenuissimum Y.L. Deng & C.L. Zhao, sp. nov.

Chinese name. 薄胶囊伏革菌 (bo jiao nang fu ge jun)

Mycobank No.: 863622

Figs. 7, 8, 9

Etymology: *tenuissimum* (Lat.): referring to the thin basidiomata of the type specimen.

Diagnosis: It is characterized by white to cream hymenial surface with tuberculata, a monomitic hyphal system with clamped generative hyphae, thin-walled, and subglobose basidiospores ($3.5\text{--}4.5 \times 2.5\text{--}3 \mu\text{m}$).

Holotype: CHINA, Yunnan Province, Dehong, Ruili City, Tongbiguan Provincial Nature Reserve, $24^{\circ}01' \text{ N}$, $97^{\circ}83' \text{ E}$, altitude 1100 m asl., on the fallen angiosperm branch, leg. C.L. Zhao, 24 September 2024, CLZhao 42660 (SWFC 00042660).

Basidiomata: Annual, resupinate, membranous, closely adnate, without odor or taste when fresh, up to 7 cm long, 3 cm wide, up to 100 μm thick. Hymenial surface grandinoid, white to

235 cream when fresh, turning to cream upon drying. Sterile margin white, thinning out, up to 1 mm
236 wide.

237 *Hyphal system*: Monomitic; generative hyphae with clamp connections, colorless, thin-
238 walled to slightly thick-walled, branched, interwoven, 2–3 μm in diameter; IKI–, CB–; tissues
239 unchanged in KOH. Subhymenial hyphae densely covered by crystals.

240 *Hymenium*: Gloeocystidia numerous, subclavate, colorless, thin-walled, $21\text{--}29 \times 5\text{--}14 \mu\text{m}$.
241 Basidia subclavate to subcylindrical, slightly flexuous, with a basal clamp connection and four
242 sterigmata, $14\text{--}23 \times 3\text{--}5 \mu\text{m}$, basidioles dominant, in shape similar to basidia, but slightly
243 smaller.

244 *Basidiospores*: Ellipsoid, colorless, thin-walled, verrucose, IKI+, CB–, $3.5\text{--}4.5 \times 2.5\text{--}3$
245 μm , $L = 3.93 \mu\text{m}$, $W = 2.90 \mu\text{m}$, $Q = 1.18\text{--}1.61$ ($n = 60/2$).

246 *Additional specimen (paratype) examined*: CHINA, Yunnan Province, Dehong, Ruili,
247 Tongbiguan Provincial Nature Reserve, $24^{\circ}01' \text{ N}$, $97^{\circ}83' \text{ E}$, altitude 1100 m asl., on the fallen
248 angiosperm branch, leg. C.L. Zhao, 24 September 2024, CLZhao 48991 (SWFC 00048991).

249

250 *Vararia farinacea* Y.L. Deng & C.L. Zhao, sp. nov.

251 **Chinese name.** 粉状叉丝革菌 (fen zhuang cha si ge jun)

252 *Mycobank No.*: 863624

253 Figs. 10, 11, 12

254 *Etymology*: *farinacea* (Lat.): referring to the farinaceous hymenial surface of the type
255 specimen.

256 *Diagnosis*: It is characterized by white to pale yellow hymenial surface, basidiomata, a
257 dimitic hyphal system with clamped generative hyphae, and ellipsoid basidiospores.

258 *Holotype*: CHINA, Yunnan Province, Dehong, Ruili, Tongbiguan Provincial Nature
259 Reserve, Huyu village, $24^{\circ}37' \text{ N}$, $97^{\circ}39' \text{ E}$, altitude 1300 m asl., on the fallen angiosperm

branch, leg. C.L. Zhao, 22 September 2024, CLZhao 41965 (SWFC 00041965).

Basidiomata: Annual, resupinate, farinaceous, thin, without odor or taste when fresh, up to 7 cm long, 0.8 cm wide, and 100 μm thick. Hymenial surface smooth, with white to cream when fresh, turning to cream to pale yellow upon drying. Sterile margin narrow, thinning out, up to 1 mm wide.

Hyphal system: Dimitic, generative hyphae with clamp connections, branched, colorless, thin-walled, 2–3 μm in diameter, IKI–, CB–, tissues unchanged in KOH. subhymenial hyphae densely covered by some crystals. Dichohyphae predominate, thin-walled to thick-walled, frequently branched, dichotomously to irregularly branched with main branches and obtuse tips, 1–1.8 μm diameter, IKI–, CB–, tissues unchanged in KOH.

Hymenium: Gloeocystidia numerous, variable in size and shape, with two types, (1) capitate, colorless, smooth, thin-walled, $8\text{--}12 \times 4\text{--}6 \mu\text{m}$; (2) fusiform, colorless, smooth, tapered or gradually elongated apex, $23\text{--}40 \times 4\text{--}6 \mu\text{m}$. Basidia cylindrical, slightly flexuous, with four sterigmata and a clamp connection, thin-walled, smooth, $10\text{--}13 \times 3\text{--}5 \mu\text{m}$; basidioles in shape similar to basidia, but slightly smaller.

Basidiospores: Ellipsoid, colorless, thin-walled, smooth, sometimes containing 1–2 oil droplets, IKI–, CB–, $4.5\text{--}6.5(-7) \times 3\text{--}4.5 \mu\text{m}$, $L = 5.61 \mu\text{m}$, $W = 3.55 \mu\text{m}$, $Q = 1.29\text{--}2.00$ ($n = 80/4$).

Additional specimens (paratypes) examined: CHINA, Yunnan Province, Dehong, Ruili, Tongbiguan Provincial Nature Reserve, $24^{\circ}37' \text{N}$, $97^{\circ}39' \text{E}$, altitude 1300 m asl., on the fallen angiosperm branch, leg. C.L. Zhao, 22 September 2024, CLZhao 41596 (SWFC 00041596), CLZhao 41793 (SWFC 00041793); Puer, Jinggu County, Xiaoheijiang Original Forest Park, $22^{\circ}30' \text{N}$, $100^{\circ}30' \text{E}$, altitude 1500 m asl., on the fallen angiosperm branch, leg. C.L. Zhao, 19 August 2025, CLZhao 45978 (SWFC 00045978).

285 *Vararia ruiliensis* Y.L. Deng & C.L. Zhao, sp. nov.

286 **Chinese name.** 瑞丽叉丝革菌 (rui li cha si ge jun)

287 *Mycobank No.:* 863623

288 Figs. 13, 14, 15

289 *Etymology:* *ruiliensis* (Lat.): referring to the locality (Ruili City) of the type specimens.

290 *Diagnosis:* It is characterized by its cream to slightly yellowish hymenial surface, a dimitic
291 hyphal system with generative hyphae bearing simple-septa and oblong ellipsoid basidiospores
292 ($5\text{--}7.5 \times 2\text{--}3.5 \mu\text{m}$).

293 *Holotype:* CHINA, Yunnan Province, Dehong, Ruili City, Tongbiguan Provincial Nature
294 Reserve, Huyu village, $24^{\circ}37' \text{ N}$, $97^{\circ}39' \text{ E}$, altitude 1300 m asl., on the fallen angiosperm
295 branch, leg. C.L. Zhao, 22 September 2024, CLZhao 41930 (SWFC 00041930).

296 *Basidiomata:* Annual, resupinate, membranous, without odor or taste when fresh, up to 12
297 cm long, 2 cm wide, up to $200 \mu\text{m}$ thick. Hymenial surface smooth, cream when fresh, turning
298 to cream to slightly yellowish upon drying. Sterile margin distinct, narrow, thinning out, up to
299 1 mm wide.

300 *Hyphal system:* Dimitic; generative hyphae bearing simple-septa, branched, colorless,
301 thin-walled, $2\text{--}3.5 \mu\text{m}$ in diameter, IKI–, CB–, tissues unchanged in KOH. Subhymenial hyphae
302 densely covered by crystals. Dichohyphae predominate, thin-walled, frequently branched, 1--
303 $1.5 \mu\text{m}$ diameter, IKI–, CB–, tissues unchanged in KOH.

304 *Hymenium:* Gloeocystidia fusiform to subcylindrical, colorless, smooth, thin-walled,
305 usually containing refractive materials, $15\text{--}23 \times 3.5\text{--}6.5 \mu\text{m}$. Basidia subcylindrical, slightly
306 flexuous, with four sterigmata and a basal simple septum, thin-walled, smooth, $14.5\text{--}21 \times 3.5\text{--}$
307 $6.5 \mu\text{m}$; basidioles in shape similar to basidia, but slightly smaller.

308 *Basidiospores:* Cylindrical, colorless, thin-walled, smooth, usually containing 1–2 oil
309 droplets, IKI–, CB–, $(4.5\text{--})5\text{--}7.5(\text{--}8) \times (1.5\text{--})2\text{--}3.5(\text{--}4) \mu\text{m}$, $L = 6.30 \mu\text{m}$, $W = 2.50 \mu\text{m}$, $Q =$

1.52–1.71(n = 150/5).

Additional specimens (paratypes) examined: CHINA, Yunnan Province, Dehong, Ruili City, Tongbiguan Provincial Nature Reserve, 24°01' N, 97°83' E, altitude 1300 m asl., on the fallen angiosperm branch, leg. C.L. Zhao, 22 September 2024, CLZhao 41506 (SWFC 00041506); 24 September 2024, CLZhao 42841 (SWFC 00042841), CLZhao 42739 (SWFC 00042739), CLZhao 42880 (SWFC 00042880).

Discussion

In present study, three new species, *Gloeocystidiellum tenuissimum*, *Vararia farinacea* and *V. ruiliensis* are described as new species based on phylogenetic analyses and morphological characteristics.

The family Gloeocystidiellaceae includes only the genus *Gloeocystidiellum*, and it is not recovered as monophyletic based on the phylogenetic evidence inferring from ITS and nrLSU sequences (Larsson and Hallenberg 2001; Deng et al. 2026a). In present study, based on the ITS+nrLSU data (Fig. 3), *G. tenuissimum* is grouped into the genus *Gloeocystidiellum*, and is closely with *G. sinense*. However, morphologically, *G. sinense* differs from *G. tenuissimum* by its smooth hymenial surface, generative hyphae with simple-septa, longer tubular cystidia ($44\text{--}52 \times 7\text{--}9.5 \mu\text{m}$ vs. $21\text{--}29 \times 5\text{--}14 \mu\text{m}$) (Zhang et al. 2025). Morphologically, *G. tenuissimum* is similar to *G. porosum* (Berk. & M.A. Curtis) Donk by having subclavate to subcylindrical basidia and generative hyphae with clamp connections. However, *G. porosum* differs in its larger gloeocystidia ($50\text{--}180 \times 6\text{--}12 \mu\text{m}$ vs. $21\text{--}29 \times 5\text{--}14 \mu\text{m}$) and basidiospores ($4.5\text{--}6 \times 2.6\text{--}3.5 \mu\text{m}$ vs. $3.5\text{--}4.5 \times 2.5\text{--}3$) (Boidin et al. 1997).

Based on the multiple loci, nine genera as *Asterostroma*, *Baltazaria*, *Dichostereum*, *Gloiothele*, *Lachnocladium*, *Michenera*, *Peniophora*, *Vesiculomyces* and *Vararia* were divided in the family *Peniophoraceae* (Larsson and Larsson 2003, Larsson et al. 2004; Leal-Dutra et al.

2018; Wang et al. 2026a). The ITS+nrLSU analyses (Figs. 1, 2) reveals that two new taxa, *Vararia farinacea* and *V. ruiliensis* are grouped into genus *Vararia* within the family *Peniophoraceae*. In which, *V. farinacea* is closely related to two taxa, *V. cremea* and *V. gillesii*. However, morphologically, *V. cremea* is distinguished from *V. farinacea* by its both larger subcylindrical gloecystidia ($40\text{--}90 \times 7\text{--}15 \mu\text{m}$ vs. $23\text{--}40 \times 4\text{--}6 \mu\text{m}$), basidia ($25\text{--}35 \times 4\text{--}5 \mu\text{m}$ vs. $10\text{--}13 \times 3\text{--}5 \mu\text{m}$) and basidiospores ($15\text{--}20 \times 2.7\text{--}3.5 \mu\text{m}$ vs. $4.5\text{--}6.5 \times 3\text{--}4.5 \mu\text{m}$) (Boidin et al. 1980). *Vararia gillesii* is differs from *V. farinacea* by having both larger basidia ($30\text{--}40 \times 6\text{--}7 \mu\text{m}$ vs. $10\text{--}13 \times 3\text{--}5 \mu\text{m}$) and fusiformibus basidiospores ($14\text{--}17 \times 4\text{--}4.75 \mu\text{m}$ vs. $4.5\text{--}6.5 \times 3\text{--}4.5 \mu\text{m}$) (Boidin and Lanquetin 1975). In addition, *V. ruiliensis* is closely with three taxa, *V. trinidadensis*, *V. gomezii* and *V. sigmatospora*. However, morphologically, *V. trinidadensis* is distinguished from *V. ruiliensis* by its both larger gloecystidia ($27\text{--}50 \times 7\text{--}12 \mu\text{m}$ vs. $15\text{--}23 \times 3.5\text{--}7 \mu\text{m}$) and basidiospores ($13\text{--}17 \times 2.5\text{--}3.2 \mu\text{m}$ vs. $5\text{--}7.5 \times 2\text{--}3.5 \mu\text{m}$) (Welden 1965). *Vararia gomezii* can be distinguished from *V. ruiliensis* by thicker dichohyphae ($2\text{--}2.5 \mu\text{m}$ vs. $1\text{--}1.5 \mu\text{m}$), both larger basidia ($30\text{--}45 \times 7\text{--}8 \mu\text{m}$ vs. $14.5\text{--}23 \times 3.5\text{--}7 \mu\text{m}$) and basidiospores ($30\text{--}45 \times 7\text{--}8 \mu\text{m}$ vs. $11\text{--}15 \times 4.2\text{--}6 \mu\text{m}$) (Boidin and Lquetin 1975). The taxon *V. sigmatospora* is different from *V. ruiliensis* by its larger basidiospores ($13\text{--}22 \times 2.5\text{--}3.5 \mu\text{m}$ vs. $5\text{--}7.5 \times 2\text{--}3.5 \mu\text{m}$) (Boidin et al. 1987).

Morphologically, *Vararia yaoshanensis* Y.L. Deng & C.L. Zhao is similar to *V. farinacea* by similiar two types of gloecystidia. However, *V. yaoshanensis* differs from *V. farinacea* in its both larger basidia ($23\text{--}46 \times 5\text{--}8 \mu\text{m}$ vs. $10\text{--}13 \times 3\text{--}5 \mu\text{m}$) and basidiospores ($7.6\text{--}10.8 \times 5.7\text{--}7.8 \mu\text{m}$ vs. $4.5\text{--}6.5 \times 3\text{--}4.5 \mu\text{m}$) (Deng et al. 2024). *Vararia punctata* Y.L. Deng & C.L. Zhao is similar to *V. ruiliensis* by having subcylindrica basidia. However, *V. punctata* is distinguished from *V. ruiliensis* by its white to cream hymenial surface and larger ellipsoid basidiospores ($6\text{--}10 \times 4\text{--}6 \mu\text{m}$ vs. $5\text{--}7.5 \times 2\text{--}3.5 \mu\text{m}$) (Deng et al. 2024).

WIF are an important part of forest ecosystems, which are mainly composed of most

members of *Basidiomycota*, and they possess important economic values and ecological functions (James et al. 2020; Dai et al. 2021; Wang et al. 2026a,b). Although in *Basidiomycota*, there has been a clear evolutionary trend in the development of different types of basidiomata, the taxonomy and phylogeny of some taxa in the order *Russulales* are still unresolved (Miller et al. 2001; Larsson and Larsson 2003; Spirin et al. 2024). In the present study, these data are also crucial as a supplement to the global knowledge of wood-inhabiting of the order *Russulales*.

References

- Bernicchia A, Gorjón SP (2010) *Corticiaceae* s.l. Fungi Europaei 12. Edizioni Candusso. Alassio, Italia.
- Boidin J, Gilles G, Lanquetin P (1987) *Basidiomycètes Apophyllophorales* de l'île de la Réunion. IX: Les genres *Dichostereum* Pilát et *Vararia* Karsten. Bulletin trimestriel de la Société mycologique de France 103: 119–135.
- Boidin J, Lanquetin P (1984) Compléments au genre *Vararia* P. Karst. (*Basidiomycetes*). Persoonia. 12(3):243–262.
- Boidin J, Lanquetin P (1987) Le genre *Scytinostroma* Donk (*Basidiomycetes, Lachnocladiaceae*). Bibliotheca Mycologica 114: 1–130.
- Boidin J, Lanquetin P, Gilles G (1980) Application du concept biologique de l'espèce aux Basidiomycètes. Le genre *Vararia* section *Vararia* au Gabon. Cryptogamie, Mycologie 1(4): 265–384.
- Boidin J, Lanquetin P, Gilles G (1997) Le genre *Gloeocystidiellum* sensu lato (Basidiomycotina). Bulletin de la Société Mycologique de France 113(1):1–80.
- Boidin J, Lanquetin P (1975) *Vararia* subgenus *Vararia* (*Basidiomycetes Lachnocladiaceae*): étude spéciale des espèces d'Afrique intertropicale. Bulletin de la Société Mycologique de France 91(4): 457–513.

385 Bougher NL, Barrett MD (2020) Fungi and slime moulds recorded in surveys at Kings Park
386 and Bold Park-urban bushlands Perth, Western Australia. *Western Australian Naturalist*
387 31: 191–251.

388 Bruen TC, Philippe H, Bryant DA (2006) A simple and robust statistical test for detecting the
389 presence of recombination. *Genetics* 172: 2665–2681.
390 <https://doi.org/10.1534/genetics.105.048975>

391 Dai LD, Wu SH, Nakasone KK, Burdsall HH Jr, He SH (2017) Two new species of *Aleurodiscus*
392 s.l. (*Russulales*, *Basidiomycota*) on bamboo from tropics. *Mycoscience* 58(3): 213–220.
393 <https://doi.org/10.1016/j.myc.2017.02.001>

394 Dai YC, Yang ZL, Cui BK, Wu G, Yuan HS, Zhou LW, He SH, Ge ZW, Wu F, Wei YL (2021)
395 Diversity and systematics of the important macrofungi in Chinese forests. *Mycosystema*
396 40: 770–805.

397 Deng YL, Chen M, Wang KS, Liu WT, Chen DX, Yang SQ, Li WL, Zhou HM, Zhao CL (2025)
398 Morphological and phylogenetic analyses reveal one new genus and six new species in
399 *Irpicaceae* and *Steccherinaceae* (*Polyporales*, *Basidiomycota*) from the Yunnan-
400 Guizhou Plateau, Asia. *IMA Fungus* 16: e172367.
401 <https://doi.org/10.3897/ima fungus.16.172367>

402 Deng YL, Chen M, Zhang SC, Wang KS, Liu WT, Qiu YH, Dou YT, Liu XF, Wijesinghe ASN,
403 Zhou HM, Jabeen S, Zhao CL (2026a) Notes, taxonomy, and phylogeny of wood-
404 inhabiting fungi in *Russulales*. *Mycosphere* 17: e003.
405 <https://doi.org/10.48130/mycosphere-0026-0003>

406 Deng YL, Jabeen S, Zhao CL (2024) Species diversity and taxonomy of *Vararia* (*Russulales*,
407 *Basidiomycota*) with descriptions of six species from Southwestern China. *Mycosphere*
408 103: 97–128. <https://doi.org/10.3897/mycokeys.103.118980>

409 Deng YL, Wang KS, Chen M, Qiu YH, Liu WT, Jabeen S, Liu XF, Zhao CL (2026b) Addition
 410 of four new wood-inhabiting fungi of *Russulales* (*Agaricomycetes*, *Basidiomycota*)
 411 from southwestern China. *MycKeys* 133: 1–40. [https://doi.org/10.3897/](https://doi.org/10.3897/mycokeys.133.193737)
 412 [mycokeys.133.193737](https://doi.org/10.3897/mycokeys.133.193737)
 413 Dong JH, Li Q, Yuan Q, Luo YX, Zhang XC, Dai YF, Zhou Q, Liu XF, Deng YL, Zhou HM,
 414 Zhao CL, Akmal M (2024) Species diversity, taxonomy, molecular systematics and
 415 divergence time of wood-inhabiting fungi in Yunnan-Guizhou Plateau, Asia.
 416 *Mycosphere* 15(1): 1110–1293. <https://doi.org/10.5943/mycosphere/15/1/10>
 417 Donk MA (1931) Revisie van de Nederlandse *Heterobasidiomycetae* en *Homobasidiomycetae*
 418 *–Aphylllophoraceae* I. Mededelingen van de Nederlandse Mycologische Vereeniging
 419 18–20: 67–200.
 420 Ghobad-Nejhad M, Zhou LW, Tomšovský M, Angelini P, Cusumano G, Angeles Flores G,
 421 Venanzoni R, Wang XW, Chaharmiri-Dokhaharani S, Moridi Farimani M, Pärtel K, Dai
 422 YC, Wu F (2024) Unlocking nature’s pharmacy: diversity of medicinal properties and
 423 mycochemicals in the family *Hymenochaetaceae* (*Agaricomycetes*, *Basidiomycota*).
 424 *Mycosphere* 15(1): 6347–6438. <https://dx.doi.org/10.5943/mycosphere/15/1/27>
 425 Gorjón SP, Hallenberg N (2013) Some new species and a first checklist of corticioid fungi
 426 (*Basidiomycota*) from Chile. *Mycological Progress* 12: 185–192.
 427 <https://doi.org/10.1007/s11557-012-0824-z>
 428 James TY, Stajich JE, Hittinger CT, Rokas A (2020) Toward a fully resolved fungal tree of life.
 429 *Annual Review of Microbiology* 74: 291–313. [https://doi.org/10.1146/annurev-micro-](https://doi.org/10.1146/annurev-micro-022020-051835)
 430 [022020-051835](https://doi.org/10.1146/annurev-micro-022020-051835)
 431 Jaramillo-Riofrío A, Decock C. Suárez JP, Benítez Á, Castillo G, Cruz D (2023) Screening of
 432 antibacterial activity of some resupinate fungi, reveal *Gloeocystidiellum lojanense* sp.

433 nov. (*Russulales*) against *E. coli* from Ecuador. Journal of Fungi 9: 54.
 434 <https://doi.org/10.3390/jof9010054>
 435 Kalyaanamoorthy S, Minh BQ, Wong TKF, Von Haeseler A, Jermiin LS (2017) ModelFinder:
 436 fast model selection for accurate phylogenetic estimates. Nature Methods
 437 14(6):587–589. <https://doi.org/10.1038/nmeth.4285>
 438 Karasinski D (2010) Polish resupinate *Russulales*: the genus *Vararia*. Acta Mycologica 45(1).
 439 <https://doi.org/10.5586/am.2010.007>
 440 Katoh K, Rozewicki J, Yamada KD (2019) MAFFT online service: multiple sequence
 441 alignment, interactive sequence choice and visualization. Brief Bioinform 20: 1160–
 442 1166. <https://doi.org/10.1093/bib/bbx108>
 443 Kirk PM, Cannon PF, Minter DW, Stalpers JA (2008) Dictionary of the Fungi. 10th Edition.
 444 Wallingford, UK: 1–771.
 445 Larsson A (2014) AliView: a fast and lightweight alignment viewer and editor for large datasets.
 446 Bioinformatics. 30(22): 3276–3278. <https://doi.org/10.1093/bioinformatics/btu531>
 447 Larsson E, Hallenberg N (2001) Species delimitation in the *Gloeocystidiellum porosum-*
 448 *clavuligerum* complex inferred from compatibility studies and nuclear rDNA sequence
 449 data. Mycologia 93: 907–914. <https://doi.org/10.1080/00275514.2001.12063225>
 450 Larsson E, Larsson KH (2003) Phylogenetic relationships of russuloid basidiomycetes with
 451 emphasis on aphyllorphorean taxa. Mycologia 95: 1037–1065.
 452 <https://doi.org/10.1080/15572536.2004.11833020>
 453 Larsson KH, Larsson E, Kõljalg U (2004) High phylogenetic diversity among corticioid ho-
 454 mobasidiomycetes. Mycological Research 108: 983–1002.
 455 <https://doi.org/10.1017/S0953756204000851>
 456 Larsson KH, Larsson E, Ryvarden L, Spirin V (2020) Some new combinations of corticioid
 457 fungi (*Basidiomycota*, *Agaricomycetes*). Synopsis Fungorum 40: 113–117.

458 Leal-Dutra CA, Neves MA, Griffith GW, Reck MA, Clasen LA. Dentinger BT (2018) Re-
 459 classification of *Parapterulicium* Corner (*Pterulaceae*, *Agaricales*), contributions to
 460 Lachnocladiaceae and *Peniophoraceae* (*Russulales*) and introduction of *Baltazaria* gen.
 461 nov. MycoKeys 37: 39–56. <https://doi.org/10.3897/mycokeys.37.26303>
 462 Li Y, Xu WQ, Liu SL, Yang N, He SH (2023) Species diversity and taxonomy of *Scytinostroma*
 463 sensu stricto (*Russulales*, *Basidiomycota*) with descriptions of four new species from
 464 China. MycoKeys 98:133–152. <https://doi.org/10.3897/mycokeys.98.105632>
 465 Liu SL, He SH (2016) The genus *Vararia* (*Russulales*, *Basidiomycota*) in China. Two new
 466 species and two new Chinese records. Nordic Journal of Botany 1756–1051. [https://](https://doi.org/10.1111/njb.01170)
 467 doi.org/10.1111/njb.01170
 468 Liu SL, He SH (2018) Taxonomy and phylogeny of *Dichostereum* (*Russulales*), with
 469 descriptions of three new species from southern China. MycoKeys 40: 111–126.
 470 <https://doi.org/10.3897/mycokeys.40.28700>
 471 Liu SL, Nakasone KK, He SH (2019) *Michenera incrustata* sp. nov. (*Peniophoraceae*,
 472 *Russulales*) from southern China. Nova Hedwigia 108(1-2): 197–206.
 473 https://doi.org/10.1127/nova_hedwigia/2018/0500
 474 M'Barek HN, Arif S, Taidi B, Hajjaj H (2020) Consolidated bioethanol production from olive
 475 mill waste: wood-decay fungi from central Morocco as promising decomposition and
 476 fermentation biocatalysts. Biotechnology Reports 28: e00541.
 477 <https://doi.org/10.1016/j.btre.2020.e00541>
 478 Miller MA, Pfeiffer W, Schwartz T (2012) The CIPRES science gateway: enabling high-impact
 479 science for phylogenetics researchers with limited resources. Proceedings of the 1st
 480 Conference of the Extreme Science and Engineering Discovery Environment: Bridging
 481 from the extreme to the campus and beyond 39:1–8.
 482 <https://doi.org/10.1145/2335755.2335836>

483 Miller SL, McClean TM, Walker JF, Buyck B (2001) A molecular phylogeny of the *Russulales*
 484 including agaricoid, gasteroid and pleurotoid taxa. *Mycologia* 93(2): 344–354.
 485 <https://doi.org/10.1080/00275514.2001.12063166>

486 Niskanen T, Lücking R, Dahlberg A, Gaya E, Suz LM, Mikryukov V, Liimatainen K,
 487 Druzhinina I, Westrip JRS, Mueller GM, Martins-Cunha K, Kirk P, Tedersoo L,
 488 Antonelli A (2023) Pushing the frontiers of biodiversity research: unveiling the global
 489 diversity, distribution, and conservation of fungi. *Annual Review of Environment and*
 490 *Resources* 48: 149–176. <https://doi.org/10.1146/annurev-environ-112621-090937>

491 Park JH, Pavlov IN, Kim MJ, Park MS, Oh SY, Park KH, Fong JJ, Lim YW (2020) Investigating
 492 wood decaying fungi diversity in Central Siberia, *Russia* using ITS sequence analysis
 493 and interaction with host trees. *Sustainability* 12(6): 2535.
 494 <https://doi.org/10.3390/su12062535>

495 Petersen JH (1996) Farvekort. The Danish Mycological Society's Colour-Chart. Foren-in-gen til
 496 Svampekundskabens Fremme, Greve, Denmark: 1–6.

497 Quaedvlieg W, Binder M, Groenewald JZ, Summerell BA, Carnegie AJ, Burgess TI, Crous PW
 498 (2014) Introducing the consolidated species concept to resolve species in the
 499 *Teratosphaeriaceae*. *Persoonia* 33: 1–40. <https://doi.org/10.3767/003158514X681981>

500 Ronquist F, Teslenko M, van der Mark P, Ayres DL, Darling A, Hohna S, Larget B, Liu L,
 501 Suchard MA, Huelsenbeck JP (2012) MrBayes 3.2: Efficient bayesian phylogenetic
 502 inference and model choice across a large model space. *Systematic Biology* 61(3): 539–
 503 542. <https://doi.org/10.1093/sysbio/sys029>

504 Rosenthal LM, Larsson KH, Branco S, Chung JA, Glassman SI, Liao HL, Peay KG, Smith DP,
 505 Talbot JM, Taylor JW, Vellinga EC, Vilgalys R, Bruns TD (2017) Survey of corticioid
 506 fungi in North American pinaceous forests reveals hyperdiversity, underpopulated

sequence databases, and species that are potentially ectomycorrhizal. *Mycologia* 109(1): 115–127. <https://doi.org/10.1080/00275514.2017.1281677>

Spirin V, Runnel K, Vlasák J, Viner I, Barrett M, Ryvarden L, Bernicchia A, Rivoire B, Ainsworth A, Grebenc T (2024) The genus *Fomitopsis* (*Polyporales*, *Basidiomycota*) reconsidered. *Studies in Mycology* 107: 149–249. <https://doi.org/10.3114/sim.2024.107.03>

Stenlid J, Penttilä R, Dahlberg A (2008) Chapter 13 Wood-decay basidiomycetes in boreal forests: Distribution and community development. *British Mycological Society Symposia Series* 28: 239–262. [https://doi.org/10.1016/S0275-0287\(08\)80015-X](https://doi.org/10.1016/S0275-0287(08)80015-X)

Suhara H, Maekawa N, Ushijima S, Kinjo K, Hoshi Y (2010) *Asterostroma* species (*Basidiomycota*) from mangrove forests in Japan. *Mycoscience* 51(1):75–80. <https://doi.org/10.1007/S10267-009-0006-2>

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>

Vu D, Groenewald M, De Vries M, Gehrman T, Stielow B, Eberhardt U, Al-Hatmi A, Groenewald JZ, Cardinali G, Houbraken J, Boekhout T, Crous PW, Robert V, Verkley GJM (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(1): 135–154. <https://doi.org/10.1016/j.simyco.2018.05.001>

Wang KS, Deng YL, Zhu YG, Chen M, Zhao CL (2026a) Molecular phylogeny and morphology reveal a new wood-inhabiting fungal species, *Vararia tuberculata* (*Peniophoraceae*, *Russulales*) from China. *Phytotaxa* 740(3): 248–262. <https://doi.org/10.11646/phytotaxa.740.3.3>

532 Wang L, He SY, Lambert C, Zhu YG, Zhang JL, Yang Y, Li WL, Zhou HM, Zhao CL (2026b)
 533 Comprehensive morphological and phylogenetic analyses of *Hymenochaetales*
 534 (*Basidiomycota*) unveil one new genus and twenty-six novel wood-inhabiting species
 535 from southwestern China. *Persoonia* 56: 328–380.
 536 <https://doi.org/10.3114/persoonia.2026.56.05>

537 Wang L, Zhu YG, He SY, Jabeen S, Zhao CL (2025) Additions to the coriaceous families
 538 *Peniophoraceae* and *Stereaceae* (*Russulales*): Six novel wood-inhabiting taxa in the
 539 genera *Conferticium*, *Gloeocystidiellum*, and *Peniophora* from southwest China.
 540 *MycKeys* 115: 273–308. <https://doi.org/10.3897/mycokeys.115.147044>

541 Welden A (1965) West Indian species of *Vararia* with notes on extralimital species. *Mycologia*
 542 57: 502–520. <https://doi.org/10.1080/00275514.1965.12018236>

543 White TJ, Bruns T, Lee S, Taylor J (1990) Amplification and direct sequencing of fungal
 544 ribosomal RNA genes for phylogenetics. *PCR Protocols: A Guide to Methods and*
 545 *Applications*. Academic Press, San Diego 18(1): 315–322.
 546 <https://doi.org/10.1016/B978-0-12-372180-8.50042-1>

547 Wiens JJ, Blomenkamp EG, Corliss M, Li X (2026) Global biodiversity and the expanding Tree
 548 of Life. *Proceedings of the National Academy of Sciences* 123(12): e2530656123.
 549 <https://doi.org/10.1073/pnas.2530656123>

550 Xu YL, Tian Y, He SH (2023) Taxonomy and phylogeny of *Peniophora* sensu lato (*Russulales*,
 551 *Basidiomycota*). *Journal of Fungi* 9(1): 93. <https://doi.org/10.3390/jof9010093>

552 Yurchenko E, Krasowska M, Kowczyk-Sadowy M, Zapora E (2025) Investigation of the
 553 possible antibacterial effects of corticioid fungi against different bacterial species.
 554 *International Journal of Molecular Sciences* 26: 3292.
 555 <https://doi.org/10.3390/ijms26073292>

556 Zhang SC, Dong JH, Zhang XJ, Li YC, Liu R, Liu R Zhao CL (2025) *Gloeocystidiellum sinense*
 557 sp. nov. (*Stereaceae*, *Russulales*), a wood-inhabiting fungus from Yunnan Province,
 558 China. New Zealand Journal of Botany 63(2-3): 370–381.
 559 <https://doi.org/10.1080/0028825X.2025.2454589>
 560 Zhao YL, Zhao CL (2023) A corticioid fungus, *Gloeocystidiellum yunnanense* sp. nov.
 561 (*Russulales*) with characteristic gloeocystidia from southern China. Nova Hedwigia 116:
 562 1–2. https://doi.org/10.1127/nova_hedwigia/2023/0725
 563 Zou L, Zhang XL, Deng YL, Zhao CL (2022) Four new wood-inhabiting fungal species of
 564 *Peniophoraceae* (*Russulales*, *Basidiomycota*) from the Yunnan-Guizhou Plateau, China.
 565 Journal of Fungi 8(11): 1227. <https://doi.org/10.3390/jof8111227>
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Statements and Declarations

Author contributions Conceptualization, CZ; methodology, CZ and YD; software, CZ, YD, QL and WL; validation, CZ and YD; formal analysis, CZ and YD; investigation, CZ, ZZ and YD; resources CZ and YD; writing—original draft preparation, CZ, YD, WL, and ZZ; writing—review and editing, CZ, ZZ, YD, QL and WL; visualization, CZ and ZZ; supervision, CZ; project administration, CZ; funding acquisition, CZ. All authors have read and agreed to the published version of the manuscript.

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Data availability Publicly available datasets were analyzed in this study. This data can be found here: [<https://www.ncbi.nlm.nih.gov/>; <https://doi.org/10.6084/m9.figshare.32260929>].

Declarations

Ethics approval and consent to participate All authors confirm that no research involving humans or animals was involved in the current study, that there are no issues relating to animal welfare relating to the current study and that they have approval to participate in the current study.

593 **Consent for publication** All authors have given explicit consent to the submitted paper and to
594 the inclusion of their data in it.

595 **Competing interests** The authors declare no competing interests.

Table

Table 1 List of species, specimens and GenBank accession numbers of sequences used in this study. — indicates data unavailability; * refers to type material (holotype); Newly generated sequences are in bold

Figure legends

Figure 1 Phylogram generated from maximum likelihood analysis of family *Peniophoraceae* based on combined ITS and nrLSU sequence data; branches are labeled with maximum likelihood bootstrap value $\geq 70\%$ and Bayesian posterior probabilities ≥ 0.95 . New species are shown in bold, * refers to type material (holotype)

Figure 2 Phylogram generated from maximum likelihood analysis of genus *Vararia* based on combined ITS and nrLSU sequence data; branches are labeled with maximum likelihood bootstrap value $\geq 70\%$ and Bayesian posterior probabilities ≥ 0.95 . New species are shown in bold, * refers to type material (holotype)

Figure 3 Phylogram generated from maximum likelihood analysis of genus *Gloeocystidiellum* based on combined ITS and nrLSU sequence data; branches are labeled with maximum likelihood bootstrap value $\geq 70\%$ and Bayesian posterior probabilities ≥ 0.95 . New species are shown in bold, * refers to type material (holotype)

Figure 4 Split graphs showing the results of PHI test for the ITS data of *Vararia farinacea* and closely related species using LogDet transformation and splits decomposition. PHI test results with $\Phi_w \leq 0.05$ indicate that there is significant recombination within the dataset. The new taxa are in red type.

Figure 5 Split graphs showing the results of PHI test for the ITS data of *Vararia ruiliensis* and closely related species using LogDet transformation and splits decomposition. PHI test results with $\Phi_w \leq 0.05$ indicate that there is significant recombination within the dataset. The new taxa are in red type.

Figure 6 Split graphs showing the results of PHI test for the ITS data of *Gloeocystidiellum tenuissimum* and closely related species using LogDet transformation and splits decomposition. PHI test results with $\Phi_w \leq 0.05$ indicate that there is significant recombination within the dataset. The new taxa are in red type.

Figure 7 Basidiomata of *Gloeocystidiellum tenuissimum* (holotype, CLZhao 42660). **a** Basidiomata on the substrate. **b** Character hymenophore. Scale bars: **a** = 1 cm, **b** = 1 mm.

Figure 8 Microscopic structures of *Gloeocystidiellum tenuissimum* (holotype, CLZhao 42660). **a** Basidiospores. **b** basidioles and Basidia. **c** Gloeocystidia. **d** A section of the

1 hymenium. Scale bars: **a** = 5 μ m, **b–d** = 10 μ m.

2
3 **Figure 9** Microscopic structures of *Gloeocystidiellum tenuissimum* (holotype, CLZhao
4 42660). **a–b** Generative hyphae. **c–e** Basidia. **f** Gloeocystidia. **g** basidioles. **h1–h6**
5 Basidiospores. Scale bars: **a–h** = 10 μ m.

6
7 **Figure 10** Basidiomata of *Vararia farinacea* (holotype, CLZhao 41965). **a–g**
8 Basidiomata on the substrate. **b–h** Character hymenophore. **a, e** (paratype, CLZhao
9 41965); **b, f** (paratype, CLZhao 41793); **c, g** (paratype, CLZhao 45978); **d, h** (paratype,
10 CLZhao 41596). Scale bars: **a–g** = 1 cm, **b–h** = 1 mm

11
12 **Figure 11** Microscopic structures of *Vararia farinacea* (holotype, CLZhao 41965). **a**
13 Basidiospores. **b** Basidioles and basidia. **c** Gloeocystidia. **d** Dichohyphae. **e** A section
14 of the hymenium. Scale bars: **a** = 5 μ m, **b–e** = 10 μ m.

15
16 **Figure 12** Microscopic structures of *Vararia farinacea* (holotype, CLZhao 41965). **a**
17 Dichohyphae. **b** Generative hyphae. **c–d** Basidia. **e, f** Gloeocystidia. **j** basidioles. **h1–**
18 **h5** Basidiospores. Scale bars: **a–h** = 10 μ m.

19
20 **Figure 13** Basidiomata of *Vararia ruiliensis* (holotype, CLZhao 41930). **a–e**
21 Basidiomata on the substrate. **f–j** Character hymenophore. **a, f** (paratype, CLZhao
22 41930); **b, g** (paratype, CLZhao 42841); **c, h** (paratype, CLZhao 41506); **d, i** (paratype,
23 CLZhao 42739); **e, j** (paratype, CLZhao 42880). Scale bars: **a–e** = 1 cm, **f–j** = 1 mm

24
25 **Figure 14** Microscopic structures of *Vararia ruiliensis* (holotype, CLZhao 41930). **a**
26 Basidiospores. **b** Basidioles and basidia. **c** Gloeocystidia. **d** Dichohyphae. **e** A section
27 of the hymenium. Scale bars: **a** = 5 μ m, **b–e** = 10 μ m.

28
29 **Figure 15** Microscopic structures of *Vararia ruiliensis* (holotype, CLZhao 41930). **a**
30 Generative hyphae. **b–c** Dichohyphae. **d–f** Basidia. **g–h** Gloeocystidia. **i** basidioles.
31 **j1–j7** Basidiospores. Scale bars: **a–j** = 20 μ m.

1 **Table 1** List of species, specimens and GenBank accession numbers of sequences used
2 in this study. — indicates data unavailability; * refers to type material (holotype);
3 Newly generated sequences are in bold

Taxa	Voucher	GenBank accession		Locality	Reference
		ITS	nLSU		
<i>Asterostroma bambusicola</i>	He 4132	KY263865	KY263871	China	Liu and He 2016
<i>Asterostroma cervicolor</i>	He 2314	KY263859	KY263869	Sweden	Larsson and Larsson 2003
<i>Asterostroma cervicolor</i>	He 4020	KY263860	KY263868	Japan	Suhara et al. 2010
<i>Asterostroma fimbriata</i>	CLZhao 41500 *	PV940929	PX070093	China	Deng et al. 2026a
<i>Asterostroma laxum</i>	EL33-99	AF506410	AF506410	Sweden	Larsson and Larsson 2003
<i>Asterostroma macrosporum</i>	TMI:25696	AB439544	—	Japan	Suhara et al. 2010
<i>Asterostroma macrosporum</i>	TMI:25697 *	AB439545	—	Japan	Suhara et al. 2010
<i>Asterostroma muscicola</i>	KHL9537	—	AF506409	Sweden	Larsson and Larsson 2003
<i>Baltazaria galactina</i>	CBS 752.86	MH862034	MH873721	France	Vu et al. 2019
<i>Baltazaria galactina</i>	He 4999	MK625618	MK625547	France	Vu et al. 2019
<i>Baltazaria neogalactina</i>	CBS 755.86 *	MH862037	MH873724	France	Vu et al. 2019
<i>Baltazaria neogalactina</i>	CBS:758.86	MH862040	MH873727	France	Vu et al. 2019
<i>Dichostereum boidinii</i>	He 4410	MH538315	MH538331	China	Liu and He 2018
<i>Dichostereum boidinii</i>	He 5026 *	MH538324	MH538330	China	Liu and He 2018
<i>Dichostereum pallescens</i>	CBS:718.81	MH861456	MH873198	USA	Vu et al. 2019
<i>Dichostereum pallescens</i>	CBS:719.81 *	MH861457	MH873199	USA	Vu et al. 2019
<i>Gloeocystidiellum fissuratum</i>	CLZhao 32247	PQ287849	PQ295865	China	Wang et al. 2025
<i>Gloeocystidiellum fissuratum</i>	CLZhao 32303	PQ287850	PQ295866	China	Wang et al. 2025
<i>Gloeocystidiellum formosanum</i>	Wu 9404-19	AF506439	AF506439	China	Larsson and Larsson 2003
<i>Gloeocystidiellum graminicola</i>	GB/WU9210-12	AF506448	AF506448	China	Larsson and Larsson 2003
<i>Gloeocystidiellum heimii</i>	LY/CBS321.66	AF506381	AF506381	African	Jaramillo-Riofrío et al. 2023
<i>Gloeocystidiellum porosum</i>	CBS/51085	AF310097	—	Netherlands	Larsson and Hallenberg 2001
<i>Gloeocystidiellum porosum</i>	CBS/27154	AF310098	—	France	Larsson and Hallenberg 2001
<i>Gloeocystidiellum punctatum</i>	CLZhao 20755 *	PP356586	PP785346	China	Deng et al. 2026a
<i>Gloeocystidiellum sinense</i>	CLZhao 25040	PQ453516	PQ453518	China	Zhang et al. 2025
<i>Gloeocystidiellum sinense</i>	CLZhao 25320 *	PQ453517	PQ453519	China	Zhang et al. 2025
<i>Gloeocystidiellum tenuissimum</i>	CLZhao 42660*	PZ244094	PZ253254	China	Present study
<i>Gloeocystidiellum tenuissimum</i>	CLZhao 48991	PZ244095	—	China	Present study

<i>Gloeocystidiellum triste</i>	KHL10334 *	AF506442	AF506442	Sweden	Jaramillo-Riofrío et al. 2023
<i>Gloeocystidiellum yunnanense</i>	CLZhao 7165	MZ710569	MZ710571	China	Zhao and Zhao 2023
<i>Gloeocystidiellum yunnanense</i>	CLZhao 7202 *	MZ710570	MZ710572	China	Zhao and Zhao 2023
<i>Gloiothele citrina</i>	LE -BIN 2968	OL840636	—	Russia	Deng et al. 2026b
<i>Gloiothele fragilima</i>	CLZhao 15980 *	PV147168	—	China	Deng et al. 2026a
<i>Gloiothele globosa</i>	PERTH:8690790	MT536993	MT524528	Australia	Bougher et al. 2020
<i>Gloiothele lactescens</i>	EL8-98	AF506453	AF506453	Sweden	Larsson and Larsson 2003
<i>Gloiothele lamellosa</i>	CBS:404.83 *	MH861620	MH873337	Madagascar	Vu et al. 2019
<i>Gloiothele lamellosa</i>	KHL11031	AF506454	AF506454	Venezuela	Larsson and Larsson 2003
<i>Gloiothele olearia</i>	BIO-Fungi11969 *	MT240525	—	Spain	Larsson et al. 2020
<i>Gloiothele torrendii</i>	JB18615	AF506455	AF506455	Sweden	Larsson and Larsson 2003
<i>Gloiothele tuberculata</i>	CLZhao 29888	PV441135	PV441150	China	Deng et al. 2026a
<i>Gloiothele tuberculata</i>	CLZhao 29919 *	PV441136	PV441151	China	Deng et al. 2026a
<i>Lachnocladium schweinfurthianum</i>	KM49740	MH260033	MH260051	Cameroon	Leal-Dutra et al. 2018
<i>Laurilia sulcata</i>	Dai15889	KY172895	KY172911	China	Unpublished
<i>Peniophora cinerea</i>	CBS:261.37 *	MH855905	MH867412	France	Vu et al. 2019
<i>Peniophora cinerea</i>	He 3725	MK588769	MK588809	China	Xu et al. 2023
<i>Peniophora incarnata</i>	CBS 430.72	MH860518	MH872230	Netherlands	Vu et al. 2019
<i>Peniophora incarnata</i>	NH10271	AF506425	AF506425	Sweden	Larsson and Larsson 2003
<i>Peniophora quercina</i>	CBS:407.50	MH856687	MH868204	France	Vu et al. 2019
<i>Peniophora quercina</i>	CBS:410.50	MH856690	MH868207	France	Vu et al. 2019
<i>Peniophora tristicula</i>	He 4775	MH669235	MH669239	China	Liu and He 2018
<i>Peniophora versiformis</i>	He 3029	MK588756	MK588796	China	Xu et al. 2023
<i>Scytinostroma alutum</i>	CBS:762.81	NR170738	MH873221	France	Vu et al. 2019
<i>Scytinostroma alutum</i>	CBS:766.81	MH861486	MH873225	France	Vu et al. 2019
<i>Scytinostroma artocreas</i>	GHL-2016-Oct	MH204688	MH204691	China	Liu et al. 2018
<i>Scytinostroma beijingense</i>	He 7768 *	OQ731943	OQ729731	China	Li et al. 2023
<i>Scytinostroma boidinii</i>	He 5138	MK625572	MK625497	China	Li et al. 2023
<i>Scytinostroma boidinii</i>	He 6911 *	OQ731934	OQ729724	China	Li et al. 2023
<i>Scytinostroma dawuishanense</i>	CLZhao 17926 *	OR096194	OR461462	China	Dong et al. 2024
<i>Scytinostroma duriusculum</i>	CBS:758.81	MH861478	MH873217	France	Vu et al. 2019
<i>Scytinostroma duriusculum</i>	He 3590	MK625571	MK625499	China	Dong et al. 2024
<i>Scytinostroma incrustatum</i>	He 2841 *	MH142906	MH142910	China	Liu et al. 2019
<i>Scytinostroma incrustatum</i>	He 5368	MH204689	MH204690	China	Liu et al. 2019
<i>Scytinostroma ostrea</i>	He 2067	KU559366	KU574826	China	Dai et al. 2017
<i>Scytinostroma renisporum</i>	CBS:770.86	MH862050	MH873737	China	Vu et al. 2019

<i>Scytinostroma renisporum</i>	CBS:771.86	MH862051	MH873738	China	Vu et al. 2019
<i>Scytinostroma subrenisporum</i>	He 4384	MK625567	MK625495	China	Li et al. 2023
<i>Scytinostroma subrenisporum</i>	He 4792	MK625566	MK625493	China	Li et al. 2023
<i>Stereum hirsutum</i>	He 3504	MK625629	MK625557	China	Deng et al. 2026b
<i>Vararia abortiphysa</i>	CBS:632.81	MH861387	MH873136	Gabon	Vu et al. 2019
<i>Vararia ambigua</i>	CBS:634.81	MH861388	MH873137	France	Vu et al. 2019
<i>Vararia amphithallica</i>	CBS:635.81	MH861389	MH873138	Gabon	Vu et al. 2019
<i>Vararia amphithallica</i>	CBS:687.81	MH861431	MH873173	France	Vu et al. 2019
<i>Vararia asiana</i>	CLZhao 25187 *	OR102488	OR510680	China	Deng et al. 2026a
<i>Vararia aurantiaca</i>	CBS:642.81 *	MH861394	MH873143	Gabon	Vu et al. 2019
<i>Vararia aurantiaca</i>	CBS:641.81	MH861393	—	France	Vu et al. 2019
<i>Vararia bambusicola</i>	CLZhao 35740 *	PV637442	PV637449	China	Deng et al. 2026a
<i>Vararia bambusicola</i>	CLZhao 35743	PV637443	PV637450	China	Deng et al. 2026a
<i>Vararia bannaensis</i>	CLZhao 35714 *	PV441143	PV441157	China	Deng et al. 2026a
<i>Vararia bannaensis</i>	CLZhao 35720	PV441144	PV441158	China	Deng et al. 2026a
<i>Vararia breviphysa</i>	CBS:643.81	MH873144	MH873144	Gabon	Vu et al. 2019
<i>Vararia breviphysa</i>	CBS:644.81 *	MH861396	MH873145	Gabon	Vu et al. 2019
<i>Vararia calami</i>	CBS:646.81	MH861398	—	France	Vu et al. 2019
<i>Vararia calami</i>	CBS:648.81 *	MH861399	—	France	Vu et al. 2019
<i>Vararia callichroa</i>	CBS:744.91 *	MH874000	MH874000	France	Vu et al. 2019
<i>Vararia cinnamomea</i>	CBS:641.84	MH873487	MH873487	Madagascar	Vu et al. 2019
<i>Vararia cinnamomea</i>	CBS:642.84 *	MH873488	MH873488	Madagascar	Vu et al. 2019
<i>Vararia cremea</i>	CBS:651.81 *	MH873147	MH873147	France	Vu et al. 2019
<i>Vararia dawweishanensis</i>	CLZhao 17911	OP380613	OP615103	China	Zou et al. 2022
<i>Vararia dawweishanensis</i>	CLZhao 17936 *	OP380614	OP380688	China	Zou et al. 2022
<i>Vararia denghongensis</i>	CLZhao 37632	PZ013428	PZ013453	China	Deng et al. 2026b
<i>Vararia denghongensis</i>	CLZhao 37729*	PZ013429	PZ013454	China	Deng et al. 2026b
<i>Vararia dussii</i>	CBS:652.81 *	MH873148	MH873148	France	Vu et al. 2019
<i>Vararia dussii</i>	CBS:655.81	MH861405	—	France	Vu et al. 2019
<i>Vararia ellipsospora</i>	HHB-19503	MW740328	—	New Zealand	Zou et al. 2022
<i>Vararia farinacea</i>	CLZhao 41965*	PZ251038	PZ253260	China	Present study
<i>Vararia farinacea</i>	CLZhao 41596	PZ251039	PZ253261	China	Present study
<i>Vararia farinacea</i>	CLZhao 41793	PZ251040	PZ253262	China	Present study
<i>Vararia farinacea</i>	CLZhao 45978	PZ251041	—	China	Present study
<i>Vararia ferruginosa</i>	CLZhao 30551 *	PV147175	—	China	Deng et al. 2026a
<i>Vararia ferruginosa</i>	CLZhao 30240	PV147172	PV185858	China	Deng et al. 2026a
<i>Vararia fissurata</i>	CLZhao 8171 *	OQ025219	OR539503	China	Deng et al. 2024
<i>Vararia fissurata</i>	CLZhao 5218	OQ025218	OR539502	China	Deng et al. 2024b
<i>Vararia fragilis</i>	CLZhao 16475 *	OP380612	OP380687	China	Zou et al. 2022
<i>Vararia fragilis</i>	CLZhao 2628	OP380611	—	China	Zou et al. 2022
<i>Vararia fusispora</i>	PDD:119539	OL709443	—	New Zealand	Zou et al. 2022
<i>Vararia gallica</i>	CBS:234.91 *	MH862250	MH873932	Canada	Vu et al. 2019

<i>Vararia gallica</i>	CBS:656.81	MH861406	MH873152	France	Vu et al. 2019
<i>Vararia gillesii</i>	CBS:660.81	MH873153	MH873153	Netherlands	Vu et al. 2019
<i>Vararia gomezii</i>	CBS:661.81 *	MH873154	MH873154	France	Vu et al. 2019
<i>Vararia gracilispora</i>	CBS:663.81	MH861411	—	Gabon	Vu et al. 2019
<i>Vararia gracilispora</i>	CBS:664.81	MH861412	—	Gabon	Vu et al. 2019
<i>Vararia insolita</i>	CBS:668.81	MH861413	—	France	Vu et al. 2019
<i>Vararia intricata</i>	CBS:673.81	MH861418	—	France	Vu et al. 2019
<i>Vararia investiens</i>	FP 151122	MH971976	MH971977	USA	Liu and He 2018
<i>Vararia investiens</i>	He 2104	—	MH669236	USA	Liu and He 2018
<i>Vararia investiens</i>	UC2023140	KP814286	—	USA	Rosenthal et al. 2017
<i>Vararia isabellina</i>	CLZhao 22852 *	OR048789	OR506350	China	Deng et al. 2024
<i>Vararia isabellina</i>	CLZhao 22887	OR048788	OR506351	China	Deng et al. 2024
<i>Vararia lacerata</i>	CLZhao 33407 *	PQ811403	PV185851	China	Deng et al. 2026a
<i>Vararia lacerata</i>	CLZhao 33510	PQ811404	PV185852	China	Deng et al. 2026a
<i>Vararia lincangensis</i>	CLZhao 22791 *	OR048819	OR506348	China	Deng et al. 2024
<i>Vararia lincangensis</i>	CLZhao 22799	OR048818	OR506349	China	Deng et al. 2024
<i>Vararia malaysiana</i>	CBS:644.84 *	MH873490	MH873490	Singapore	Vu et al. 2019
<i>Vararia membaranacea</i>	CLZhao 35709	PV637445	PV637452	China	Deng et al. 2026a
<i>Vararia membaranacea</i>	CLZhao 35710*	PV637446	PV637453	China	Deng et al. 2026a
<i>Vararia minispora</i>	CBS:682.81	MH861426	—	France	Vu et al. 2019
<i>Vararia muscicola</i>	CLZhao 21669 *	PV147167	PV185854	China	Deng et al. 2026a
<i>Vararia ochroleuca</i>	CBS:465.61	MH858109	—	France	Vu et al. 2019
<i>Vararia ochroleuca</i>	JS24400	AF506485	AF506485	Norway	Larsson and Larsson 2003
<i>Vararia parmastoi</i>	CBS:879.84	MH861852	MH861852	Uzbekistan	Vu et al. 2019
<i>Vararia perplexa</i>	CBS:695.81 *	MH861438	—	France	Vu et al. 2019
<i>Vararia pingbianensis</i>	CLZhao 25157	OR195737	OR510677	China	Deng et al. 2026a
<i>Vararia pirispora</i>	CBS:720.86	MH862016	—	France	Vu et al. 2019
<i>Vararia punctata</i>	CLZhao 22439 *	OR048812	OR510675	China	Deng et al. 2024
<i>Vararia rhombospora</i>	CBS:743.81	MH861470	—	France	Vu et al. 2019
<i>Vararia rosulenta</i>	CBS:743.86 *	MH862028	—	France	Vu et al. 2019
<i>Vararia rugosisporea</i>	CBS:697.81 *	MH861440	—	Gabon	Vu et al. 2019
<i>Vararia ruiliensis</i>	CLZhao 41930 *	PZ244096	PZ253255	China	Present study
<i>Vararia ruiliensis</i>	CLZhao 42739	PZ244097	PZ253256	China	Present study
<i>Vararia ruiliensis</i>	CLZhao 42841	PZ244098	PZ253257	China	Present study
<i>Vararia ruiliensis</i>	CLZhao 42880	PZ244099	PZ253258	China	Present study
<i>Vararia ruiliensis</i>	CLZhao 41506	PZ244100	PZ253259	China	Present study
<i>Vararia sigmatospora</i>	CBS:748.91	MH874001	MH874001	Netherlands	Vu et al. 2019
<i>Vararia sinensis</i>	CLZhao 25160 *	OR102494	OR510678	China	Deng et al. 2024
<i>Vararia sinensis</i>	CLZhao 25161	OR102495	OR510679	China	Deng et al. 2024
<i>Vararia sphaericospora</i>	CBS:700.81	MH873185	MH873185	Gabon	Vu et al. 2019
<i>Vararia sphaericospora</i>	He 4847	MK625592	MK625521	China	Deng et al. 2026b

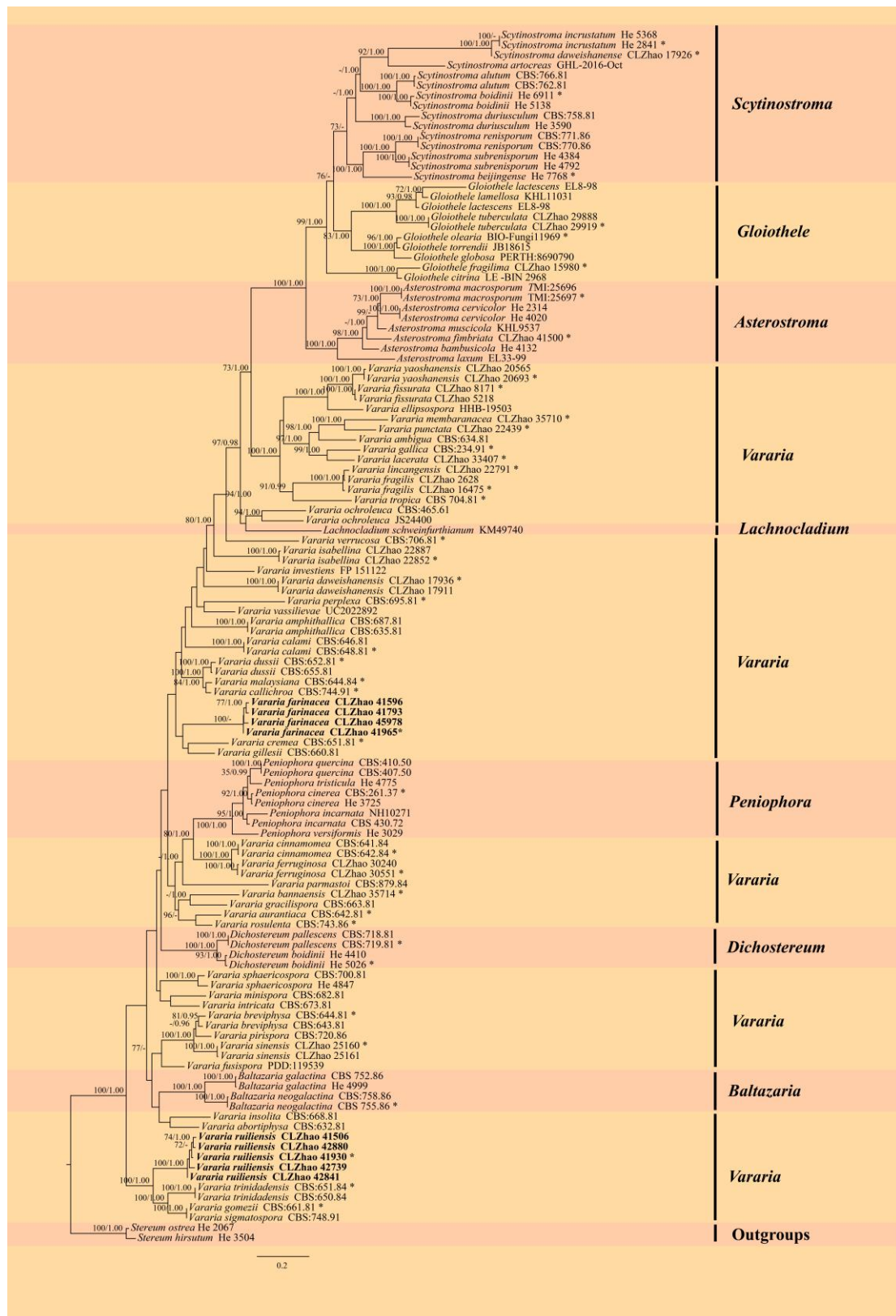
<i>Vararia subtropica</i>	CLZhao 17652	OQ025221	PX915434	China	Deng et al. 2026b
<i>Vararia subtropica</i>	CLZhao 17796*	OQ025222	PX915435	China	Deng et al. 2026b
<i>Vararia trinidadensis</i>	CBS:650.84	MH873495	MH873495	Madagascar	Vu et al. 2019
<i>Vararia trinidadensis</i>	CBS:651.84 *	MH861803	—	Madagascar	Vu et al. 2019
<i>Vararia tropica</i>	CBS 704.81 *	MH861447	MH873189	France	Vu et al. 2019
<i>Vararia tuberculata</i>	CLZhao 41375	PX097866	PX072010	China	Wang et al. 2026
<i>Vararia tuberculata</i>	CLZhao 41885*	PX097865	PX072017	China	Wang et al. 2026
<i>Vararia vassilievae</i>	UC2022892	KP814203	—	USA	Deng et al. 2026b
<i>Vararia verrucosa</i>	CBS:706.81 *	MH861449	MH861449	France	Vu et al. 2019
<i>Vararia wumengshanensis</i>	CLZhao 31659 *	PQ811405	PV185853	China	Deng et al. 2026a
<i>Vararia yaoshanensis</i>	CLZhao 20565	PP091675	PP091683	China	Deng et al. 2024
<i>Vararia yaoshanensis</i>	CLZhao 20693 *	PP091665	PP091684	China	Deng et al. 2024

1

2

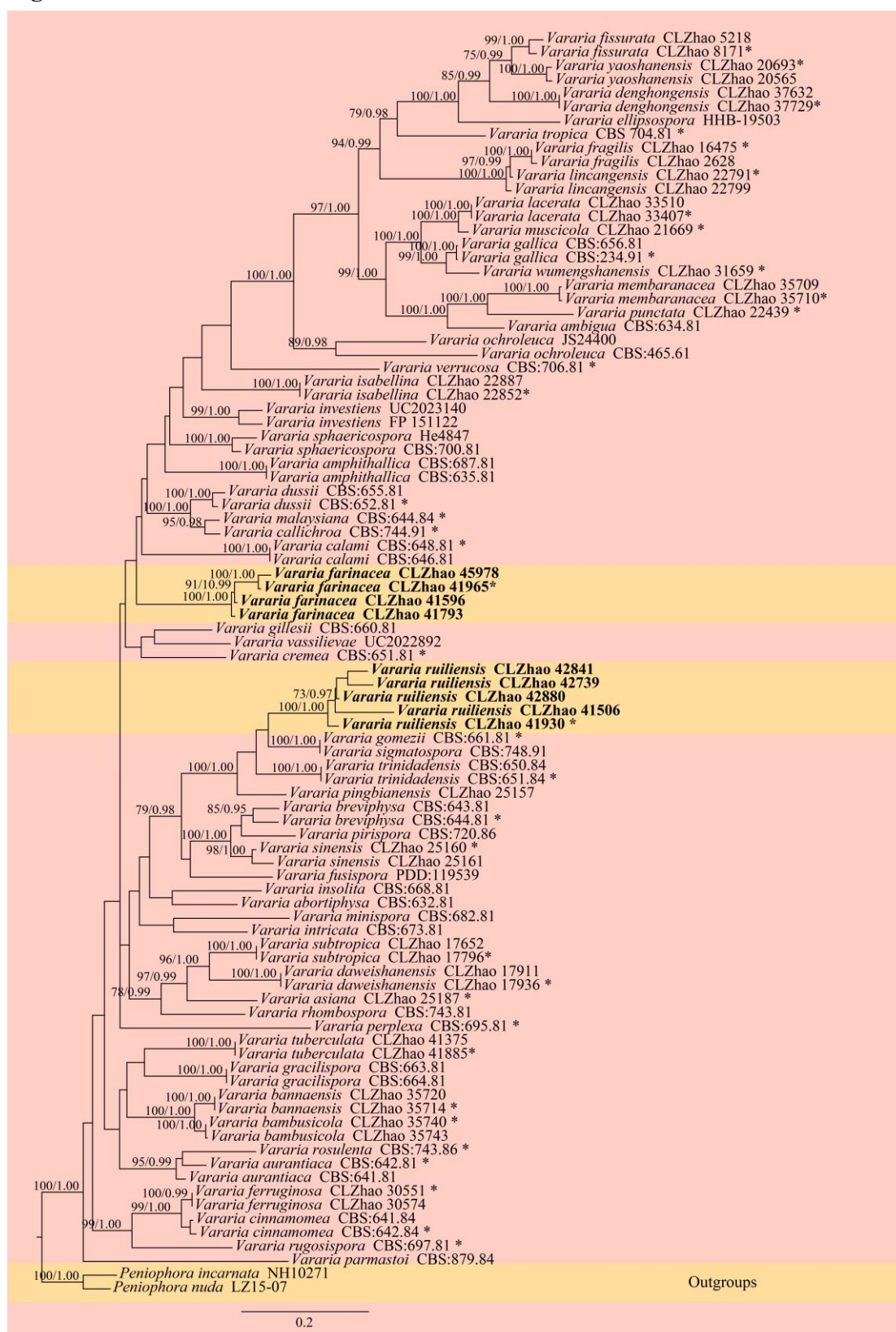
3

1 Fig. 1



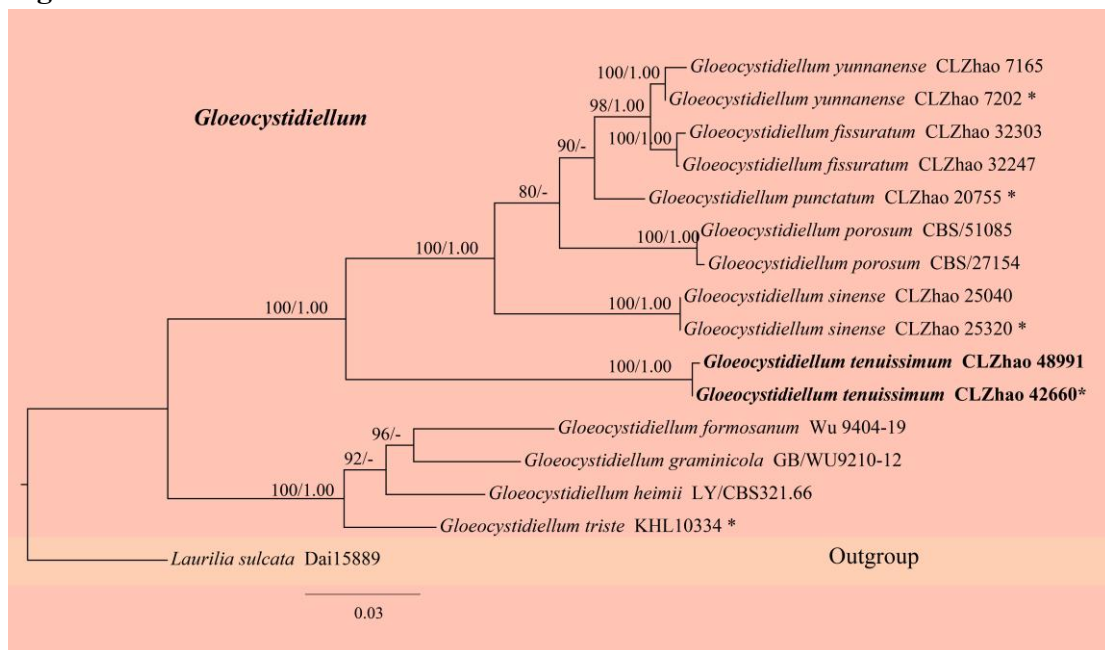
2
3

1 Fig. 2



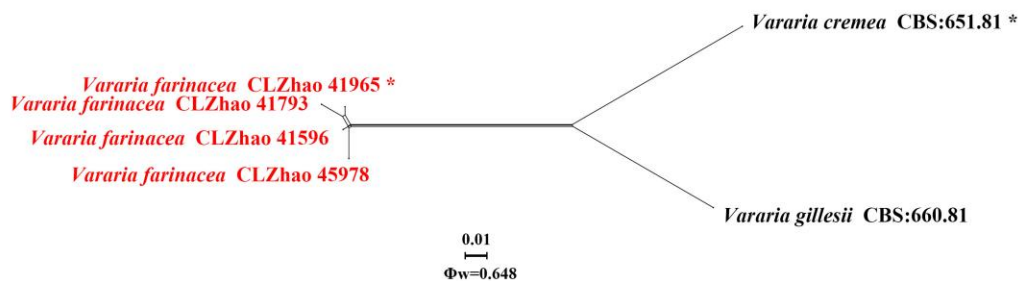
2
3

1 **Fig. 3**



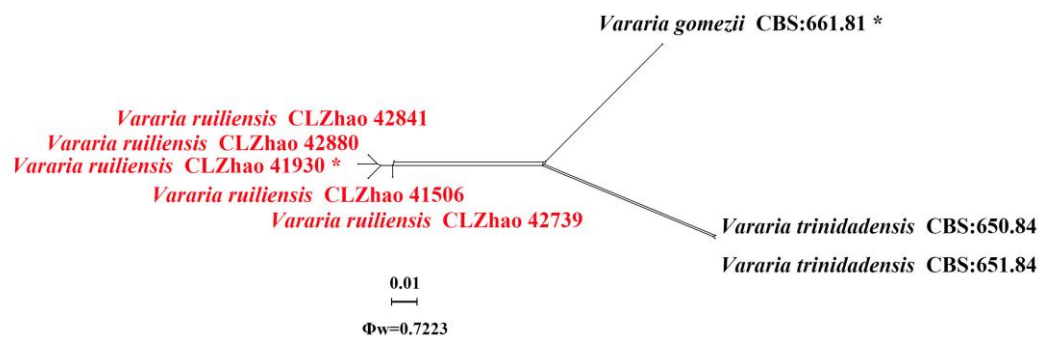
2
3
4

5 **Fig. 4**



6
7
8

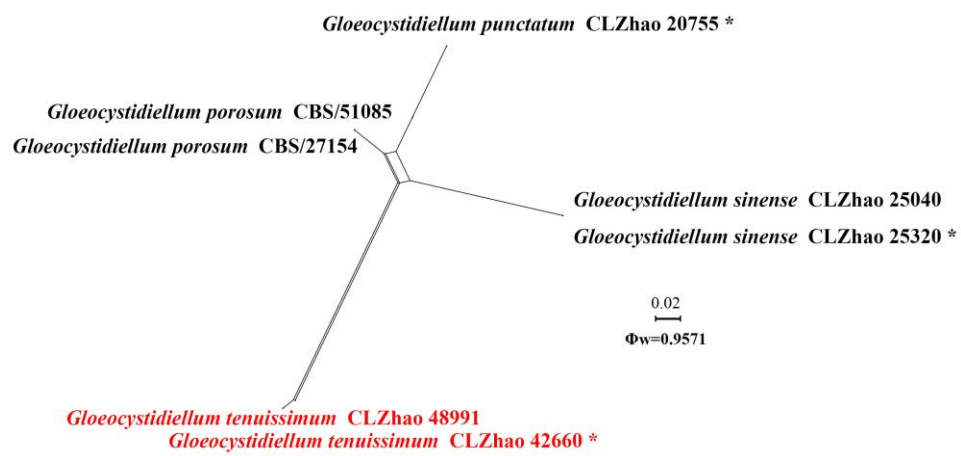
1 **Fig. 5**



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4 **Fig. 6**



5

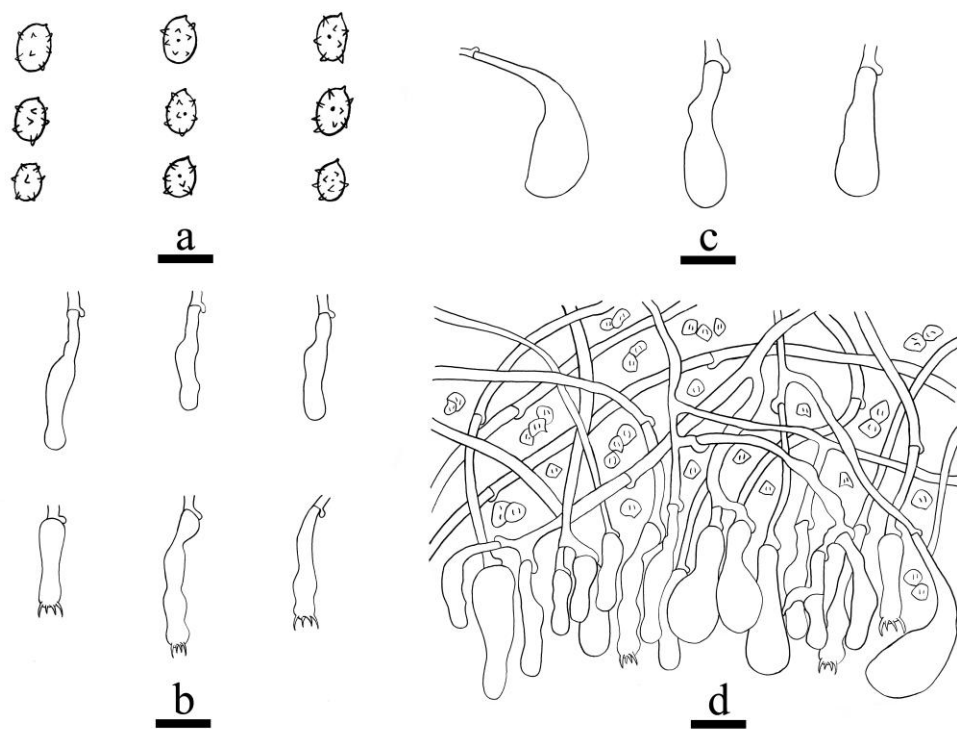
6

1 Fig. 7



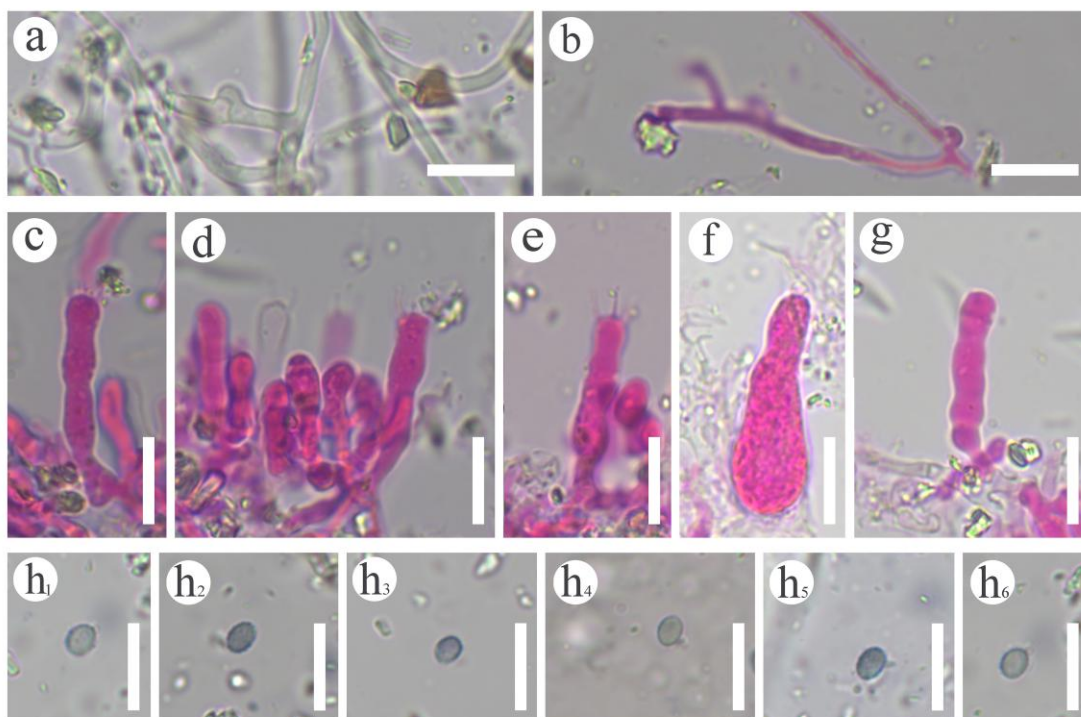
2
3

1 **Fig. 8**



2

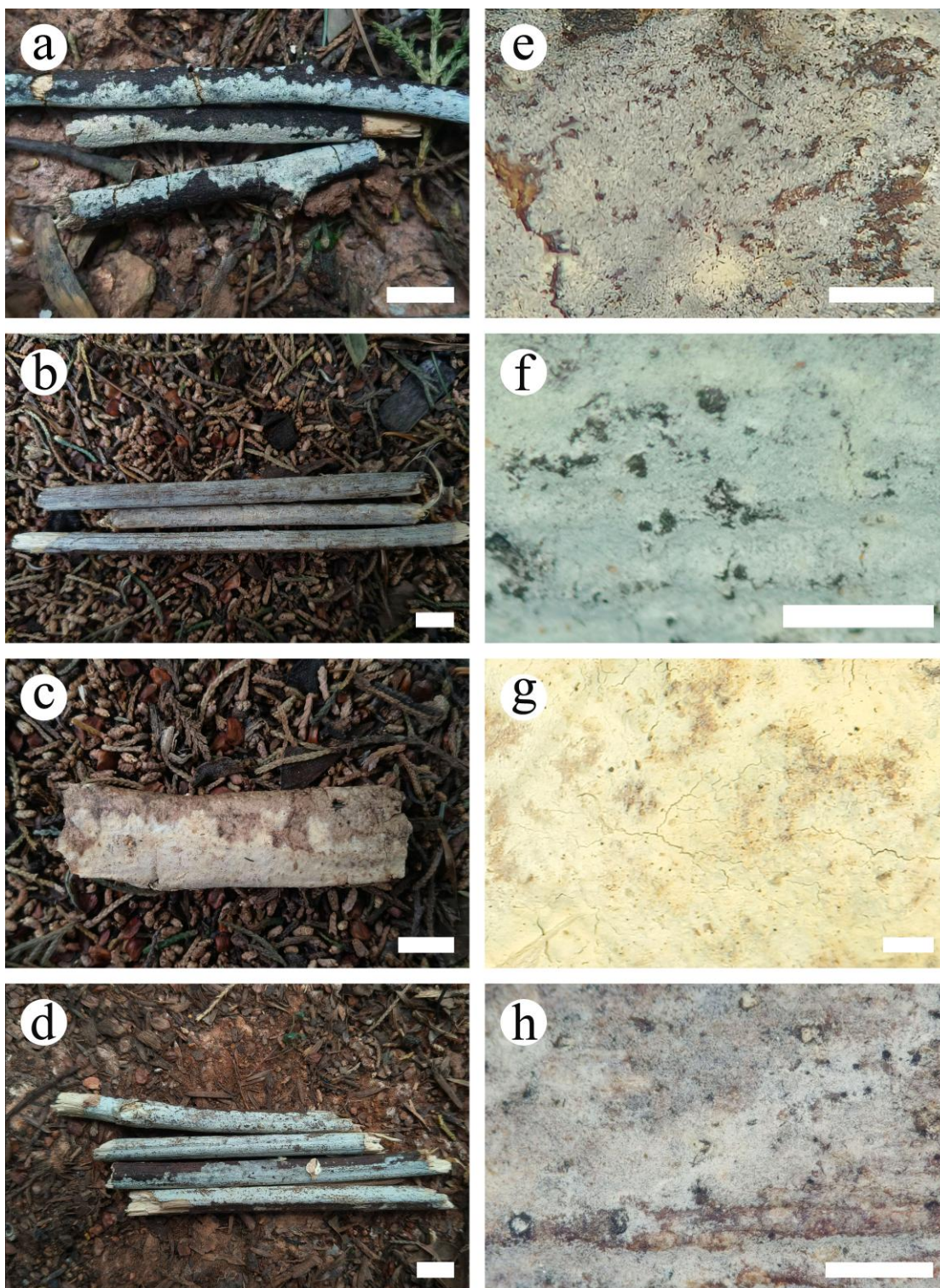
3 **Fig. 9**



4

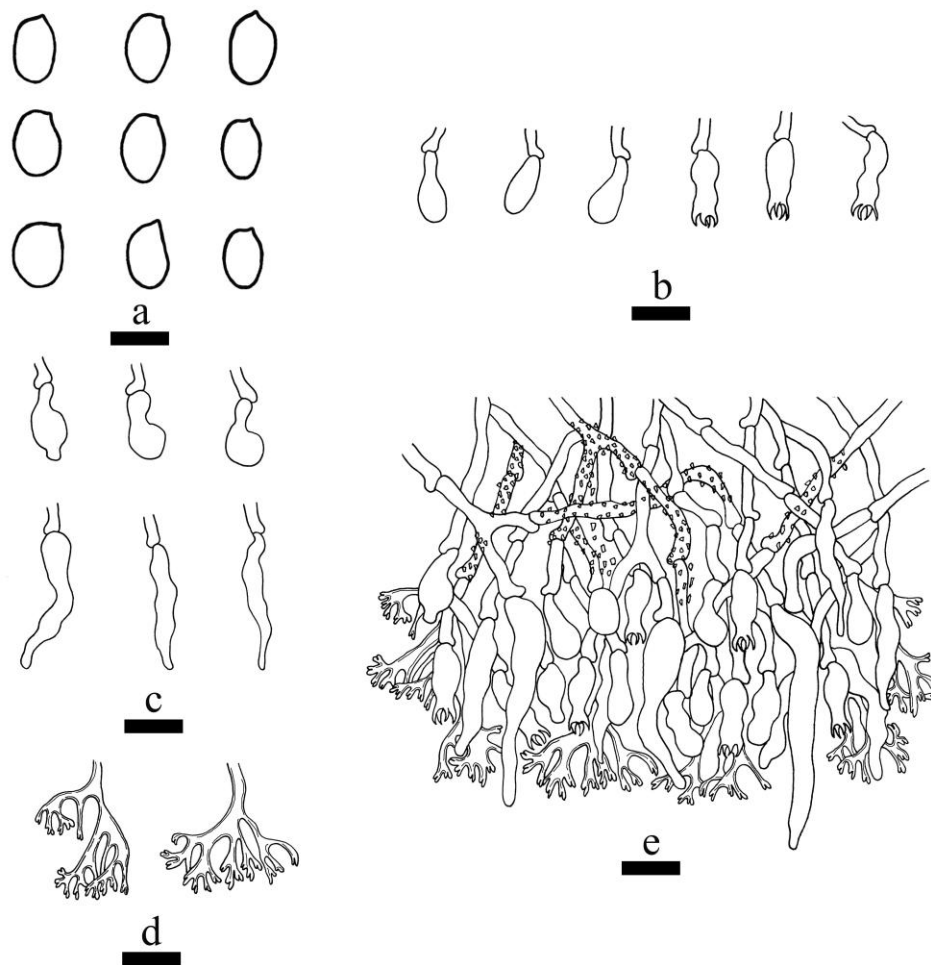
5

1 Fig. 10



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4

1 **Fig. 11**

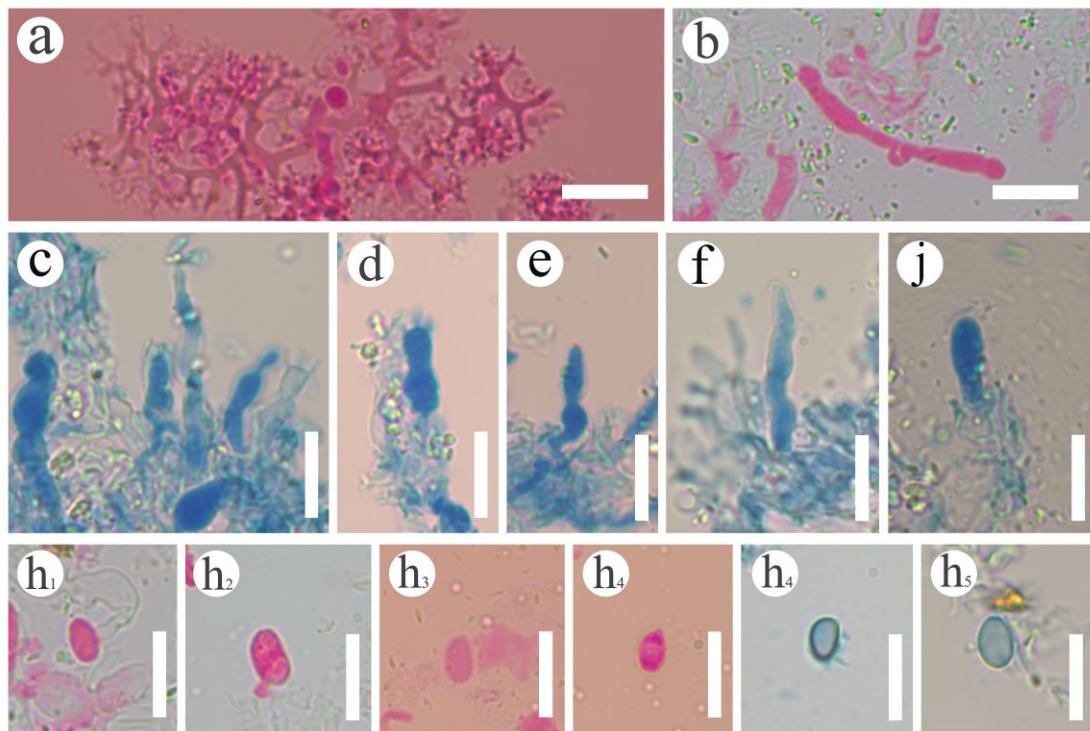


2

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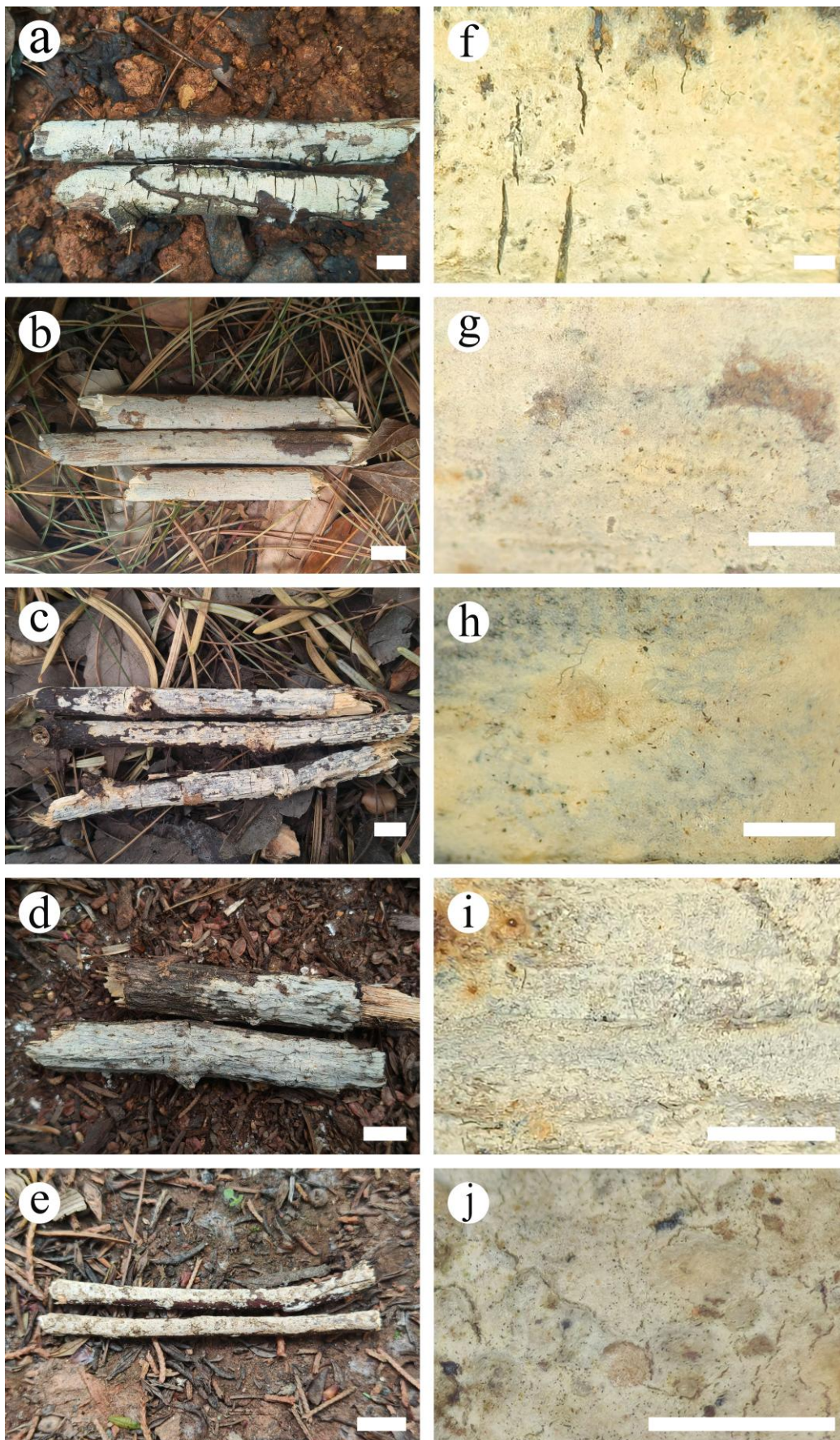
1 **Fig. 12**



2

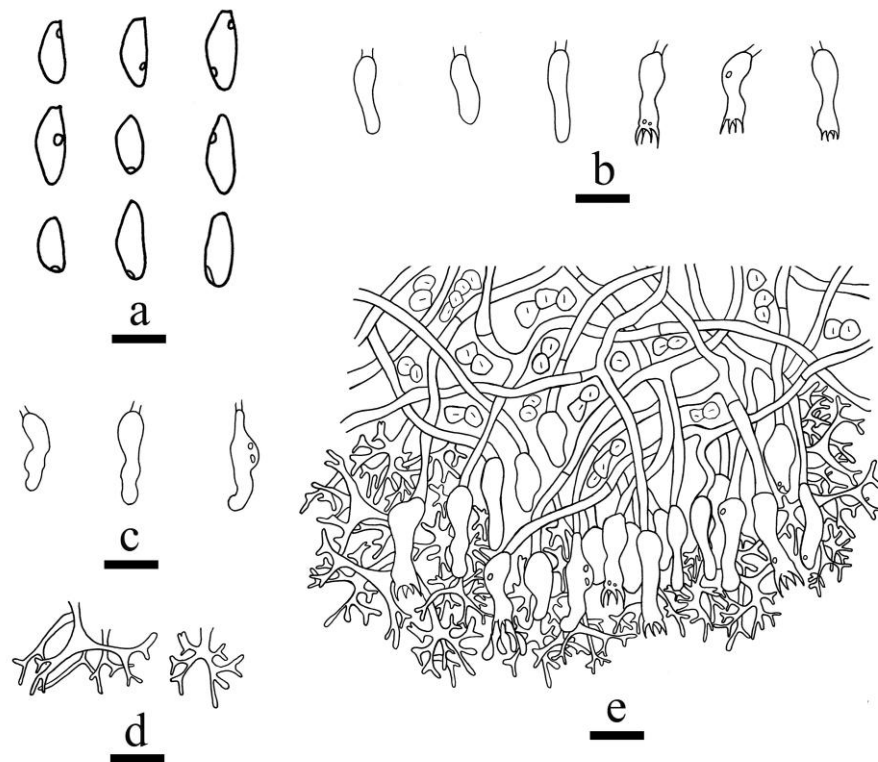
3

1 Fig. 13



2

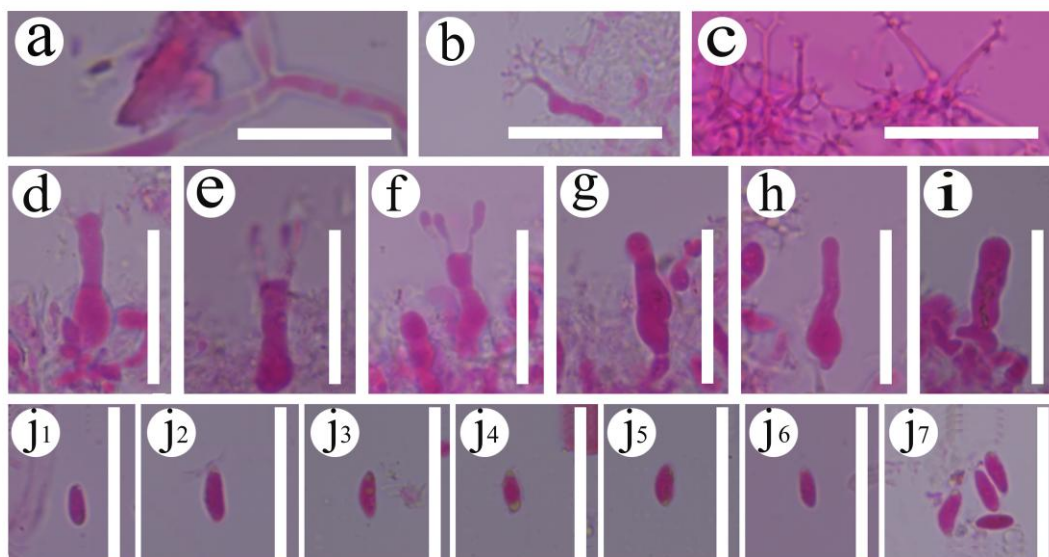
1 **Fig. 14**



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3

4 **Fig. 15**



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