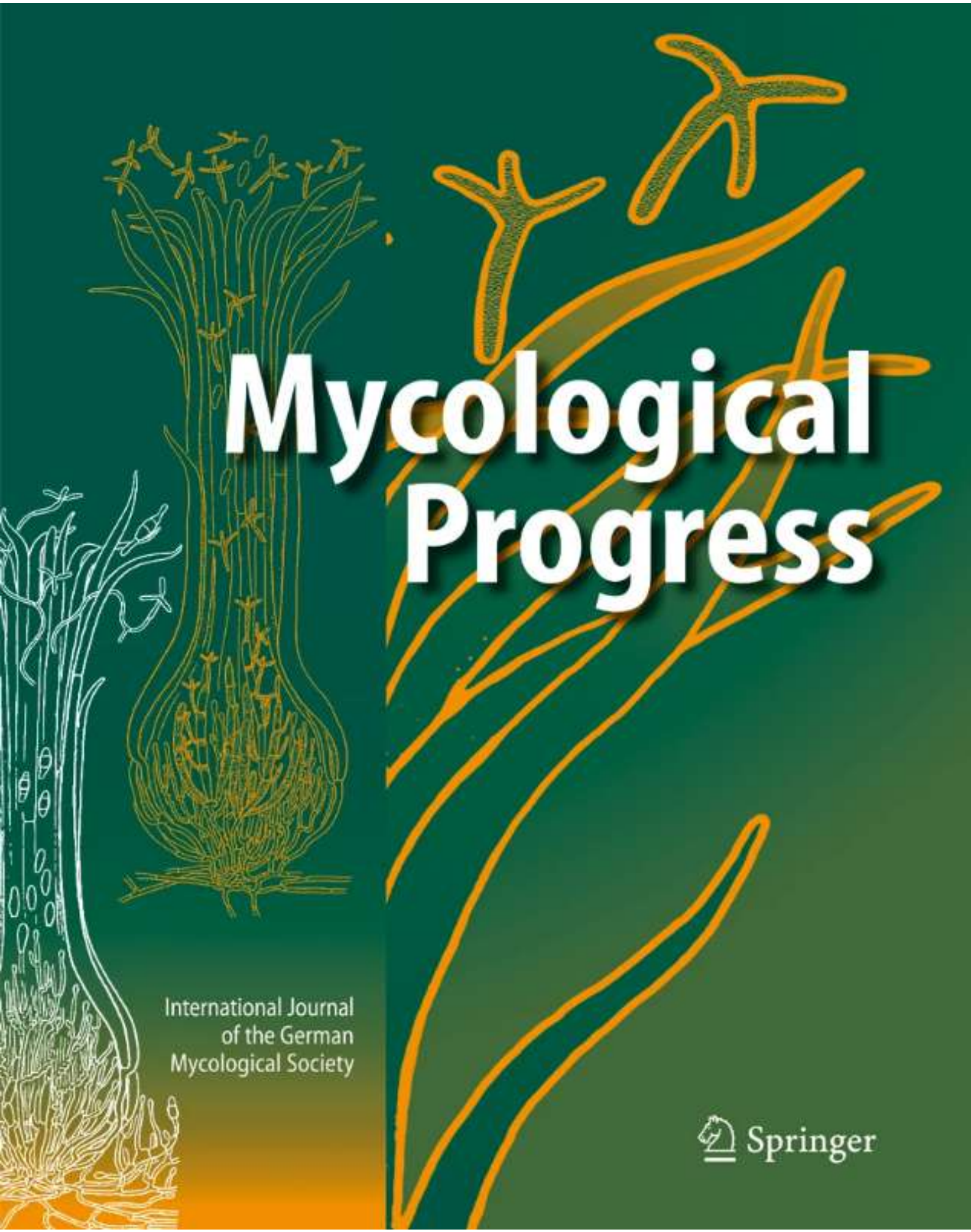

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ORIGINAL ARTICLE

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

Yinglian Deng[1,4] · Wanting Liu[1,4] · Qi Li[1,4] · Zhonglong Zhu[3] · Changlin Zhao[1,2,4]

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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 the 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*, *Vararia farinacea* and *V. ruiliensis*. Combining morphological observations and molecular phylogenetic analyses, we detected and determined the taxonomic position of these three new species, which are grouped within the two families *Gloeocystidiellaceae* and *Peniophoraceae* (*Russulales*). 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; Wu et al. 2022; Liu et al. 2025; Wang et al. 2025a, b, c; Yuan et al. 2026). They exhibit striking morphological, phylogenetic, and ecological diversity (Park et al. 2020; Ghobad-Nejhad et al. 2024; Zhao et al. 2025), yet global fungal diversity remains poorly known and increasingly threatened (Niskanen et al. 2023; Hyde et al. 2024; Zhao et al. 2025, 2026).

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). The two genera *Gloeocystidiellum* Donk (*Gloeocystidiellaceae*) and *Vararia* P. Karst. (*Peniophoraceae*) contain the highest number of species and taxonomic gaps persist within them, most studies revealed that they are recognized as highly polyphyletic within the order *Russulales* (Kirk et al. 2008; Leal-Dutra et al. 2018; Deng et al. 2024).

The corticioid genus *Gloeocystidiellum* was established by Donk with *G. porosum* (Berk. & M.A. Curtis) Donk as its type (Donk 1931). 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. 2025a, b, c). The phylogenetic analyses have confirmed that the core clade belongs to the resurrected

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✉ Changlin Zhao
changlin.zhao@helmholtz-hzi.de; fungi@swfu.edu.cn

[1] The Key Laboratory of Forest Resources Conservation and Utilization in the Southwest Mountains of China Ministry of Education, Yunnan Provincial Key Laboratory for Conservation and Utilization of In-Forest Resource, Southwest Forestry University, Kunming 650224, China

[2] Department of Microbial Drugs, Helmholtz Centre for Infection Research (HZI), Inhoffenstrasse 7, Brunswick 38124, Germany

[3] Hubei Three Gorges Polytechnic Research Center for Germplasm Innovation and Ecological Cultivation of Chinese Medicinal Materials in Wuling Mountain Area, Yichang 443000, People's Republic of China

[4] College of Forestry, Southwest Forestry University, Kunming 650224, People's Republic of China

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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

Taxa	Voucher	GenBank accession		Locality	Reference
		ITS	nLSU		
Asterostroma bambusicola	He 4132	KY263865	KY263871	China	Liu and He 2016
Asterostroma cervicolor	He 2314	KY263859	KY263869	Sweden	Larsson and Larsson 2003
Asterostroma cervicolor	He 4020	KY263860	KY263868	Japan	Suhara et al. 2010
Asterostroma fimbriata	CLZhao 41500 *	PV940929	PX070093	China	Deng et al. 2026a
Asterostroma laxum	EL33-99	AF506410	AF506410	Sweden	Larsson and Larsson 2003
Asterostroma macrosporum	TMI:25696	AB439544	—	Japan	Suhara et al. 2010
Asterostroma macrosporum	TMI:25697 *	AB439545	—	Japan	Suhara et al. 2010
Asterostroma muscicola	KHL9537	—	AF506409	Sweden	Larsson and Larsson 2003
Baltazaria galactina	CBS 752.86	MH862034	MH873721	France	Vu et al. 2019
Baltazaria galactina	He 4999	MK625618	MK625547	France	Vu et al. 2019
Baltazaria neogalactina	CBS 755.86 *	MH862037	MH873724	France	Vu et al. 2019
Baltazaria neogalactina	CBS:758.86	MH862040	MH873727	France	Vu et al. 2019
Dichostereum boidinii	He 4410	MH538315	MH538331	China	Liu and He 2018
Dichostereum boidinii	He 5026 *	MH538324	MH538330	China	Liu and He 2018
Dichostereum pallescens	CBS:718.81	MH861456	MH873198	USA	Vu et al. 2019
Dichostereum pallescens	CBS:719.81 *	MH861457	MH873199	USA	Vu et al. 2019
Gloeocystidiellum fissuratum	CLZhao 32247	PQ287849	PQ295865	China	Wang et al. 2025a, b, c
Gloeocystidiellum fissuratum	CLZhao 32303	PQ287850	PQ295866	China	Wang et al. 2025a, b, c
Gloeocystidiellum formosanum	Wu 9404–19	AF506439	AF506439	China	Larsson and Larsson 2003
Gloeocystidiellum graminicola	GB/WU9210-12	AF506448	AF506448	China	Larsson and Larsson 2003
Gloeocystidiellum heimii	LY/CBS321.66	AF506381	AF506381	African	Jaramillo-Riofrío et al. 2023
Gloeocystidiellum porosum	CBS/51085	AF310097	—	Netherlands	Larsson and Hallenberg 2001
Gloeocystidiellum porosum	CBS/27154	AF310098	—	France	Larsson and Hallenberg 2001
Gloeocystidiellum punctatum	CLZhao 20755 *	PP356586	PP785346	China	Deng et al. 2026a
Gloeocystidiellum sinense	CLZhao 25040	PQ453516	PQ453518	China	Zhang et al. 2025
Gloeocystidiellum sinense	CLZhao 25320 *	PQ453517	PQ453519	China	Zhang et al. 2025
Gloeocystidiellum tenuissimum	**CLZhao 42660***	**PZ244094**	**PZ253254**	**China**	**Present study**
Gloeocystidiellum tenuissimum	**CLZhao 48991**	**PZ244095**	**—**	**China**	**Present study**
Gloeocystidiellum triste	KHL10334 *	AF506442	AF506442	Sweden	Jaramillo-Riofrío et al. 2023
Gloeocystidiellum yunnanense	CLZhao 7165	MZ710569	MZ710571	China	Zhao and Zhao 2023
Gloeocystidiellum yunnanense	CLZhao 7202 *	MZ710570	MZ710572	China	Zhao and Zhao 2023
Gloiothele citrina	LE -BIN 2968	OL840636	—	Russia	Deng et al. 2026b
Gloiothele fragilima	CLZhao 15980 *	PV147168	—	China	Deng et al. 2026a
Gloiothele globosa	PERTH:8690790	MT536993	MT524528	Australia	Bougher et al. 2020
Gloiothele lactescens	EL8-98	AF506453	AF506453	Sweden	Larsson and Larsson 2003
Gloiothele lamellosa	CBS:404.83 *	MH861620	MH873337	Madagascar	Vu et al. 2019
Gloiothele lamellosa	KHL11031	AF506454	AF506454	Venezuela	Larsson and Larsson 2003
Gloiothele olearia	BIO-Fungi11969 *	MT240525	—	Spain	Larsson et al. 2020
Gloiothele torrendii	JB18615	AF506455	AF506455	Sweden	Larsson and Larsson 2003
Gloiothele tuberculata	CLZhao 29888	PV441135	PV441150	China	Deng et al. 2026a
Gloiothele tuberculata	CLZhao 29919 *	PV441136	PV441151	China	Deng et al. 2026a
Lachnocladium schweinfurthianum	KM49740	MH260033	MH260051	Cameroon	Leal-Dutra et al. 2018
Laurilia sulcata	Dai15889	KY172895	KY172911	China	Unpublished
Peniophora cinerea	CBS:261.37 *	MH855905	MH867412	France	Vu et al. 2019
Peniophora cinerea	He 3725	MK588769	MK588809	China	Xu et al. 2023
Peniophora incarnata	CBS 430.72	MH860518	MH872230	Netherlands	Vu et al. 2019
Peniophora incarnata	NH10271	AF506425	AF506425	Sweden	Larsson and Larsson 2003

Table 1 (continued)

Taxa	Voucher	GenBank accession		Locality	Reference
		ITS	nLSU		
Peniophora quercina	CBS:407.50	MH856687	MH868204	France	Vu et al. 2019
Peniophora quercina	CBS:410.50	MH856690	MH868207	France	Vu et al. 2019
Peniophora tristicula	He 4775	MH669235	MH669239	China	Liu and He 2018
Peniophora versiformis	He 3029	MK588756	MK588796	China	Xu et al. 2023
Scytinostroma alutum	CBS:762.81	NR170738	MH873221	France	Vu et al. 2019
Scytinostroma alutum	CBS:766.81	MH861486	MH873225	France	Vu et al. 2019
Scytinostroma artocreas	GHL-2016-Oct	MH204688	MH204691	China	Liu et al. 2018
Scytinostroma beijingense	He 7768 *	OQ731943	OQ729731	China	Li et al. 2023
Scytinostroma boidinii	He 5138	MK625572	MK625497	China	Li et al. 2023
Scytinostroma boidinii	He 6911 *	OQ731934	OQ729724	China	Li et al. 2023
Scytinostroma daweishanense	CLZhao 17926 *	OR096194	OR461462	China	Dong et al. 2024
Scytinostroma duriusculum	CBS:758.81	MH861478	MH873217	France	Vu et al. 2019
Scytinostroma duriusculum	He 3590	MK625571	MK625499	China	Dong et al. 2024
Scytinostroma incrustatum	He 2841 *	MH142906	MH142910	China	Liu et al. 2019
Scytinostroma incrustatum	He 5368	MH204689	MH204690	China	Liu et al. 2019
Scytinostroma ostrea	He 2067	KU559366	KU574826	China	Dai et al. 2017
Scytinostroma renisporum	CBS:770.86	MH862050	MH873737	China	Vu et al. 2019
Scytinostroma renisporum	CBS:771.86	MH862051	MH873738	China	Vu et al. 2019
Scytinostroma subrenisporum	He 4384	MK625567	MK625495	China	Li et al. 2023
Scytinostroma subrenisporum	He 4792	MK625566	MK625493	China	Li et al. 2023
Stereum hirsutum	He 3504	MK625629	MK625557	China	Deng et al. 2026b
Vararia abortiphysa	CBS:632.81	MH861387	MH873136	Gabon	Vu et al. 2019
Vararia ambigua	CBS:634.81	MH861388	MH873137	France	Vu et al. 2019
Vararia amphithallica	CBS:635.81	MH861389	MH873138	Gabon	Vu et al. 2019
Vararia amphithallica	CBS:687.81	MH861431	MH873173	France	Vu et al. 2019
Vararia asiana	CLZhao 25187 *	OR102488	OR510680	China	Deng et al. 2026a
Vararia aurantiaca	CBS:642.81 *	MH861394	MH873143	Gabon	Vu et al. 2019
Vararia aurantiaca	CBS:641.81	MH861393	—	France	Vu et al. 2019
Vararia bambusicola	CLZhao 35740 *	PV637442	PV637449	China	Deng et al. 2026a
Vararia bambusicola	CLZhao 35743	PV637443	PV637450	China	Deng et al. 2026a
Vararia bannaensis	CLZhao 35714 *	PV441143	PV441157	China	Deng et al. 2026a
Vararia bannaensis	CLZhao 35720	PV441144	PV441158	China	Deng et al. 2026a
Vararia breviphysa	CBS:643.81	MH873144	MH873144	Gabon	Vu et al. 2019
Vararia breviphysa	CBS:644.81 *	MH861396	MH873145	Gabon	Vu et al. 2019
Vararia calami	CBS:646.81	MH861398	—	France	Vu et al. 2019
Vararia calami	CBS:648.81 *	MH861399	—	France	Vu et al. 2019
Vararia callichroa	CBS:744.91 *	MH874000	MH874000	France	Vu et al. 2019
Vararia cinnamomea	CBS:641.84	MH873487	MH873487	Madagascar	Vu et al. 2019
Vararia cinnamomea	CBS:642.84 *	MH873488	MH873488	Madagascar	Vu et al. 2019
Vararia cremea	CBS:651.81 *	MH873147	MH873147	France	Vu et al. 2019
Vararia daweishanensis	CLZhao 17911	OP380613	OP615103	China	Zou et al. 2022
Vararia daweishanensis	CLZhao 17936 *	OP380614	OP380688	China	Zou et al. 2022
Vararia denghongensis	CLZhao 37632	PZ013428	PZ013453	China	Deng et al. 2026b
Vararia denghongensis	CLZhao 37729*	PZ013429	PZ013454	China	Deng et al. 2026b
Vararia dussii	CBS:652.81 *	MH873148	MH873148	France	Vu et al. 2019
Vararia dussii	CBS:655.81	MH861405	—	France	Vu et al. 2019
Vararia ellipsospora	HHB-19503	MW740328	—	New Zealand	Zou et al. 2022
Vararia farinacea	**CLZhao 41965***	**PZ251038**	**PZ253260**	**China**	**Present study**

Table 1 (continued)

Taxa	Voucher	GenBank accession		Locality	Reference
		ITS	nLSU		
Vararia farinacea	**CLZhao 41596**	**PZ251039**	**PZ253261**	**China**	**Present study**
Vararia farinacea	**CLZhao 41793**	**PZ251040**	**PZ253262**	**China**	**Present study**
Vararia farinacea	**CLZhao 45978**	**PZ251041**	**—**	**China**	**Present study**
Vararia ferruginosa	CLZhao 30551 *	PV147175	—	China	Deng et al. 2026a
Vararia ferruginosa	CLZhao 30240	PV147172	PV185858	China	Deng et al. 2026a
Vararia fissurata	CLZhao 8171 *	OQ025219	OR539503	China	Deng et al. 2024
Vararia fissurata	CLZhao 5218	OQ025218	OR539502	China	Deng et al. 2024b
Vararia fragilis	CLZhao 16475 *	OP380612	OP380687	China	Zou et al. 2022
Vararia fragilis	CLZhao 2628	OP380611	—	China	Zou et al. 2022
Vararia fusispora	PDD:119539	OL709443	—	New Zealand	Zou et al. 2022
Vararia gallica	CBS:234.91 *	MH862250	MH873932	Canada	Vu et al. 2019
Vararia gallica	CBS:656.81	MH861406	MH873152	France	Vu et al. 2019
Vararia gillesii	CBS:660.81	MH873153	MH873153	Netherlands	Vu et al. 2019
Vararia gomezii	CBS:661.81 *	MH873154	MH873154	France	Vu et al. 2019
Vararia gracilispora	CBS:663.81	MH861411	—	Gabon	Vu et al. 2019
Vararia gracilispora	CBS:664.81	MH861412	—	Gabon	Vu et al. 2019
Vararia insolita	CBS:668.81	MH861413	—	France	Vu et al. 2019
Vararia intricata	CBS:673.81	MH861418	—	France	Vu et al. 2019
Vararia investiens	FP 151122	MH971976	MH971977	USA	Liu and He 2018
Vararia investiens	He 2104	—	MH669236	USA	Liu and He 2018
Vararia investiens	UC2023140	KP814286	—	USA	Rosenthal et al. 2017
Vararia isabellina	CLZhao 22852 *	OR048789	OR506350	China	Deng et al. 2024
Vararia isabellina	CLZhao 22887	OR048788	OR506351	China	Deng et al. 2024
Vararia lacerata	CLZhao 33407 *	PQ811403	PV185851	China	Deng et al. 2026a
Vararia lacerata	CLZhao 33510	PQ811404	PV185852	China	Deng et al. 2026a
Vararia lincangensis	CLZhao 22791 *	OR048819	OR506348	China	Deng et al. 2024
Vararia lincangensis	CLZhao 22799	OR048818	OR506349	China	Deng et al. 2024
Vararia malaysiana	CBS:644.84 *	MH873490	MH873490	Singapore	Vu et al. 2019
Vararia membaranacea	CLZhao 35709	PV637445	PV637452	China	Deng et al. 2026a
Vararia membaranacea	CLZhao 35710*	PV637446	PV637453	China	Deng et al. 2026a
Vararia minispora	CBS:682.81	MH861426	—	France	Vu et al. 2019
Vararia muscicola	CLZhao 21669 *	PV147167	PV185854	China	Deng et al. 2026a
Vararia ochroleuca	CBS:465.61	MH858109	—	France	Vu et al. 2019
Vararia ochroleuca	JS24400	AF506485	AF506485	Norway	Larsson and Larsson 2003
Vararia parmastoi	CBS:879.84	MH861852	MH861852	Uzbekistan	Vu et al. 2019
Vararia perplexa	CBS:695.81 *	MH861438	—	France	Vu et al. 2019
Vararia pingbianensis	CLZhao 25157	OR195737	OR510677	China	Deng et al. 2026a
Vararia pirispora	CBS:720.86	MH862016	—	France	Vu et al. 2019
Vararia punctata	CLZhao 22439 *	OR048812	OR510675	China	Deng et al. 2024
Vararia rhombospora	CBS:743.81	MH861470	—	France	Vu et al. 2019
Vararia rosulenta	CBS:743.86 *	MH862028	—	France	Vu et al. 2019
Vararia rugosispora	CBS:697.81 *	MH861440	—	Gabon	Vu et al. 2019
Vararia ruiliensis	**CLZhao 41930 ***	**PZ244096**	**PZ253255**	**China**	**Present study**
Vararia ruiliensis	**CLZhao 42739**	**PZ244097**	**PZ253256**	**China**	**Present study**
Vararia ruiliensis	**CLZhao 42841**	**PZ244098**	**PZ253257**	**China**	**Present study**
Vararia ruiliensis	**CLZhao 42880**	**PZ244099**	**PZ253258**	**China**	**Present study**
Vararia ruiliensis	**CLZhao 41506**	**PZ244100**	**PZ253259**	**China**	**Present study**
Vararia sigmatospora	CBS:748.91	MH874001	MH874001	Netherlands	Vu et al. 2019

Table 1 (continued)

Taxa	Voucher	GenBank accession		Locality	Reference
		ITS	nLSU		
Vararia sinensis	CLZhao 25160 *	OR102494	OR510678	China	Deng et al. 2024
Vararia sinensis	CLZhao 25161	OR102495	OR510679	China	Deng et al. 2024
Vararia sphaericospora	CBS:700.81	MH873185	MH873185	Gabon	Vu et al. 2019
Vararia sphaericospora	He 4847	MK625592	MK625521	China	Deng et al. 2026b
Vararia subtropica	CLZhao 17652	OQ025221	PX915434	China	Deng et al. 2026b
Vararia subtropica	CLZhao 17796*	OQ025222	PX915435	China	Deng et al. 2026b
Vararia trinidadensis	CBS:650.84	MH873495	MH873495	Madagascar	Vu et al. 2019
Vararia trinidadensis	CBS:651.84 *	MH861803	—	Madagascar	Vu et al. 2019
Vararia tropica	CBS 704.81 *	MH861447	MH873189	France	Vu et al. 2019
Vararia tuberculata	CLZhao 41375	PX097866	PX072010	China	Wang et al. 2026a, b
Vararia tuberculata	CLZhao 41885*	PX097865	PX072017	China	Wang et al. 2026a, b
Vararia vassilievae	UC2022892	KP814203	—	USA	Deng et al. 2026b
Vararia verrucosa	CBS:706.81 *	MH861449	MH861449	France	Vu et al. 2019
Vararia wumengshanensis	CLZhao 31659 *	PQ811405	PV185853	China	Deng et al. 2026a
Vararia yaoshanensis	CLZhao 20565	PP091675	PP091683	China	Deng et al. 2024
Vararia yaoshanensis	CLZhao 20693 *	PP091665	PP091684	China	Deng et al. 2024

family *Gloeocystidiellaceae*, containing the generic type *G. porosum* (Larsson and Hallenberg 2001; Larsson and Larsson 2003; Gorjón and Hallenberg 2013; Jaramillo-Riofrío et al. 2023; Deng et al. 2026a). Recently, on the basis of morphological examinations and multi-locus phylogenetic analyses (ITS, nLSU, *RPB*2, and *TEF1-α*), some *Gloeocystidiellum* species had been transferred to a new family *Camptocystidiellaceae* Xin Zhang bis, Y.C. Dai & Yuan Yuan, which is separated from *Gloeocystidiellaceae* (Zhang et al. 2026). *Gloeocystidiellum* is now restricted to its core clade within *Gloeocystidiellaceae*, including the generic type *G. porosum* together with *G. cremeum* Lu Wang & C.L. Zhao, *G. fissuratum* Lu Wang & C.L. Zhao, *G. permixtum* (Boidin, Lanq. & Gilles) E. Larss. & K.H. Larss., *G. sinense* S.Cheng Zhang & C.L. Zhao, *G. monocotyledonum* Xin Zhang bis, Y.C. Dai, Y.L. Zhao & Yuan Yuan, and *G. yunnanense* Y.L. Zhao & C.L. Zhao in subtropical China (Zhang et al. 2026). 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, 127 specific and infraspecific names are recorded in Index Fungorum (accessed on 28 August 2026), of which 104 are accepted worldwide, 36 species of *Vararia* in China (Bernicchia and Gorjón 2010; Deng et al. 2026a, b, c; Wang et al. 2026a; Zhang et al. 2026). 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; Zhang et al. 2026). 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

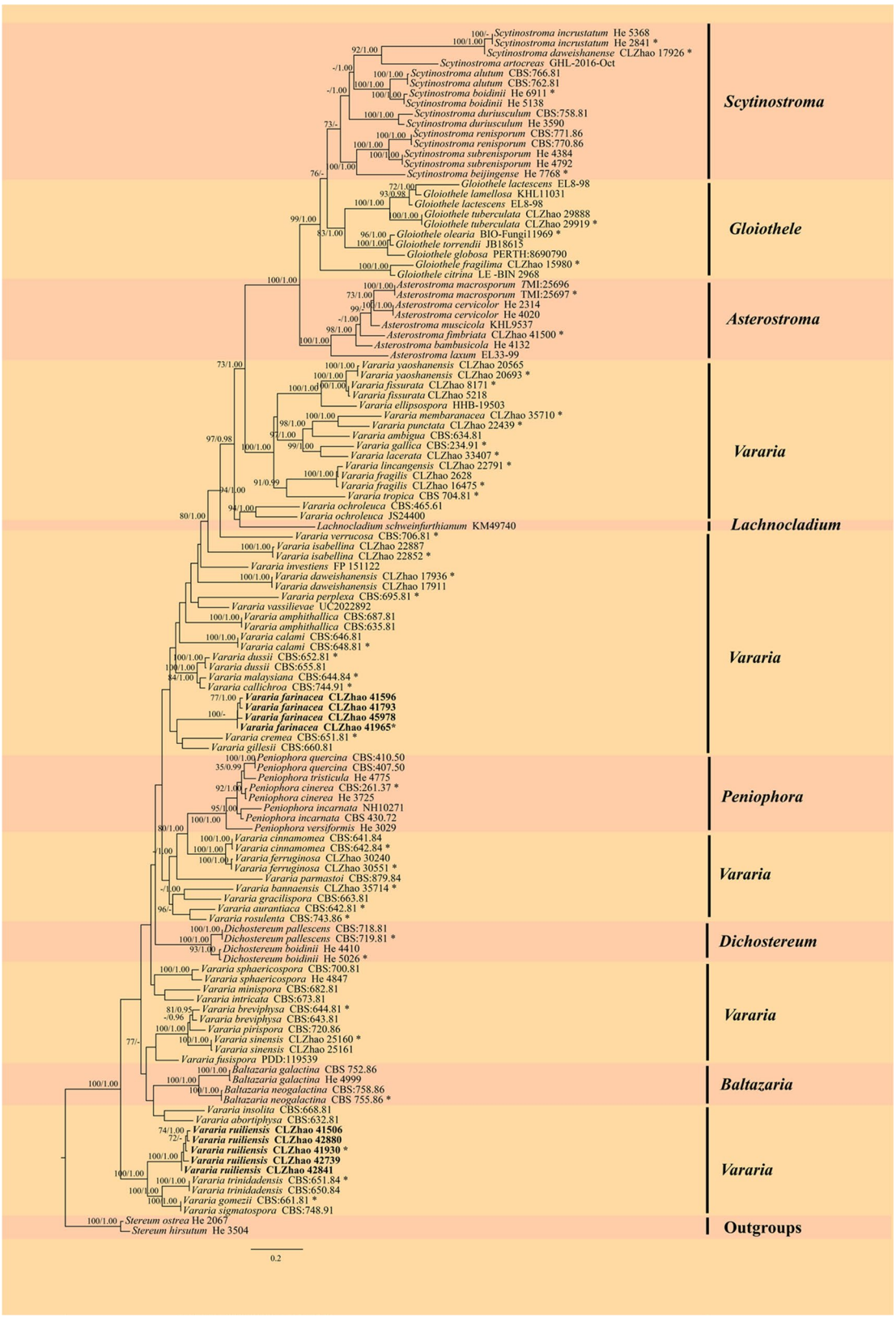


Fig. 1 Phylogram generated from maximum likelihood analysis of family *Peniophoraceae* based on combined ITS and nrLSU sequence data; branches are labelled with maximum likelihood bootstrap value ≥ 70% and Bayesian posterior probabilities ≥ 0.95. New species are shown in bold, * refers to type material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

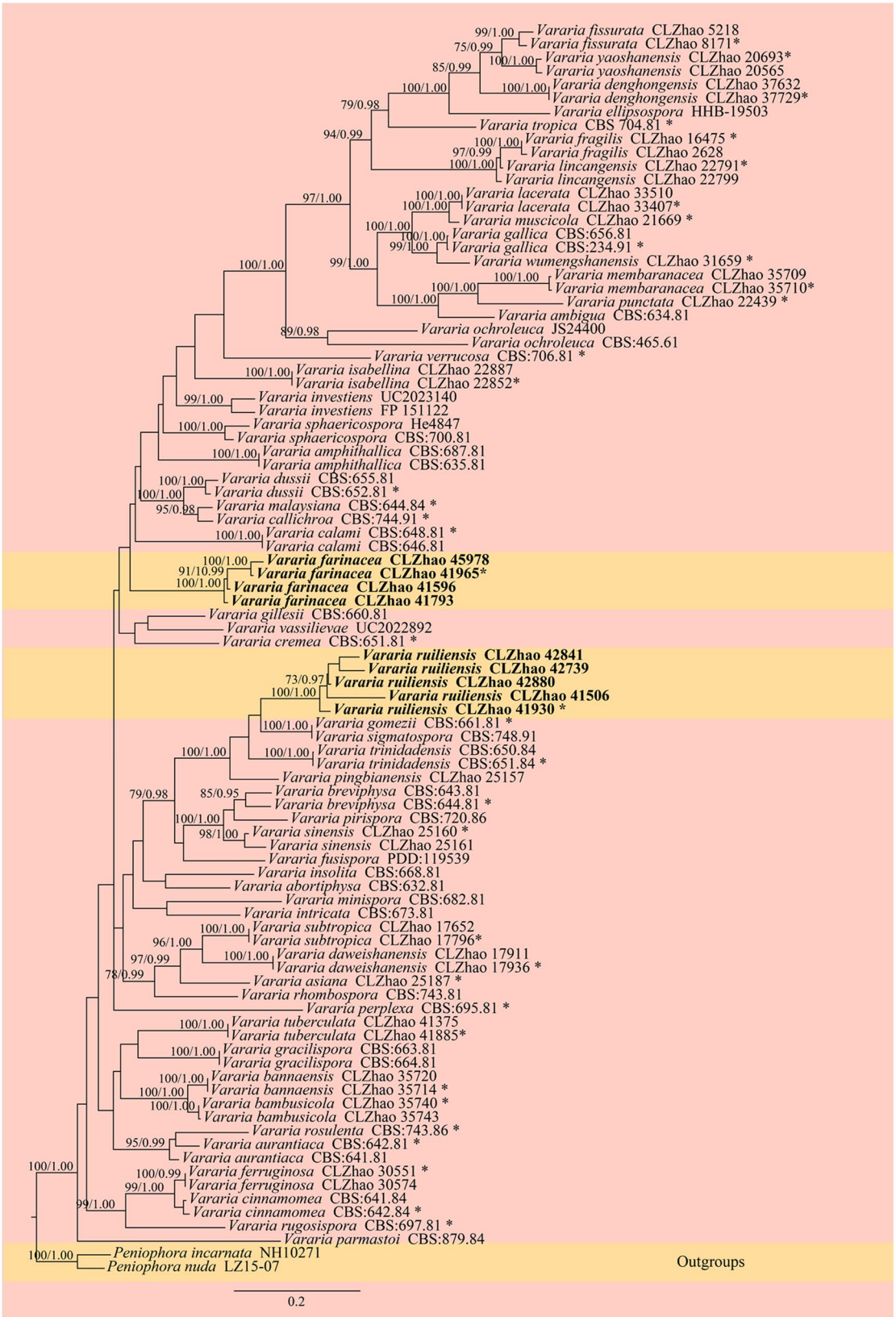


Fig. 2 Phylogram generated from maximum likelihood analysis of genus *Vararia* based on combined ITS and nrLSU sequence data; branches are labelled with maximum likelihood bootstrap value ≥ 70% and Bayesian posterior probabilities ≥ 0.95. New species are shown in bold, * refers to type material (holotype)

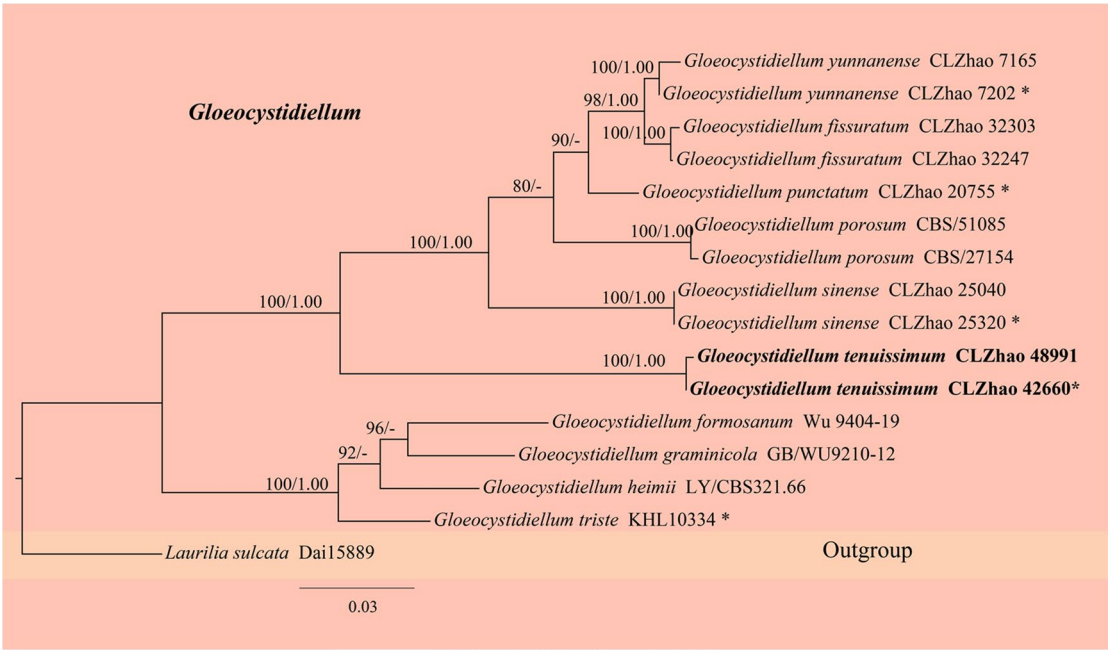


Fig. 3 Phylogram generated from maximum likelihood analysis of genus *Gloeocystidiellum* based on combined ITS and nrLSU sequence data; branches are labelled with maximum likelihood bootstrap value ≥ 70% and Bayesian posterior probabilities ≥ 0.95. New species are shown in bold, * refers to type material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

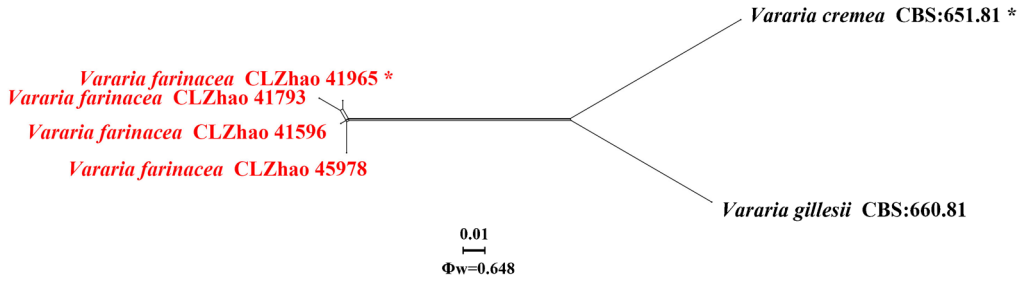


Fig. 4 Split graphs showing the results of PHI test for the ITS data of *Vararia farinacea* and closely related species using LogDet transformation and splits decomposition. PHI test results with Φw ≤ 0.05 indicate that there is significant recombination within the dataset. The new taxa are in red type

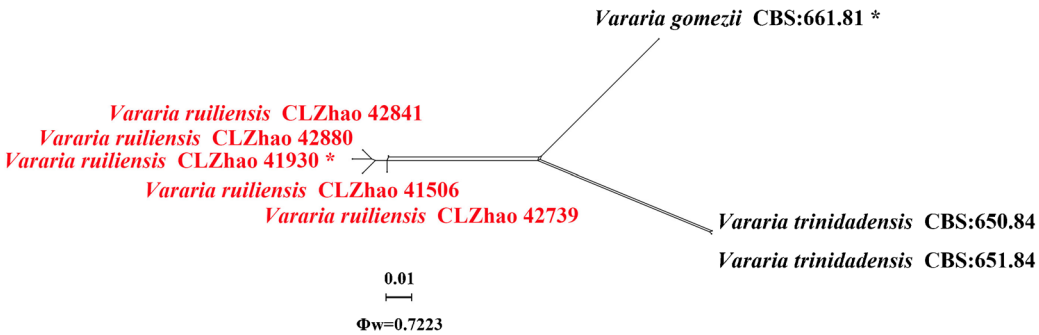


Fig. 5 Split graphs showing the results of PHI test for the ITS data of *Vararia ruiliensis* and closely related species using LogDet transformation and splits decomposition. PHI test results with Φw ≤ 0.05 indicate that there is significant recombination within the dataset. The new taxa are in red type

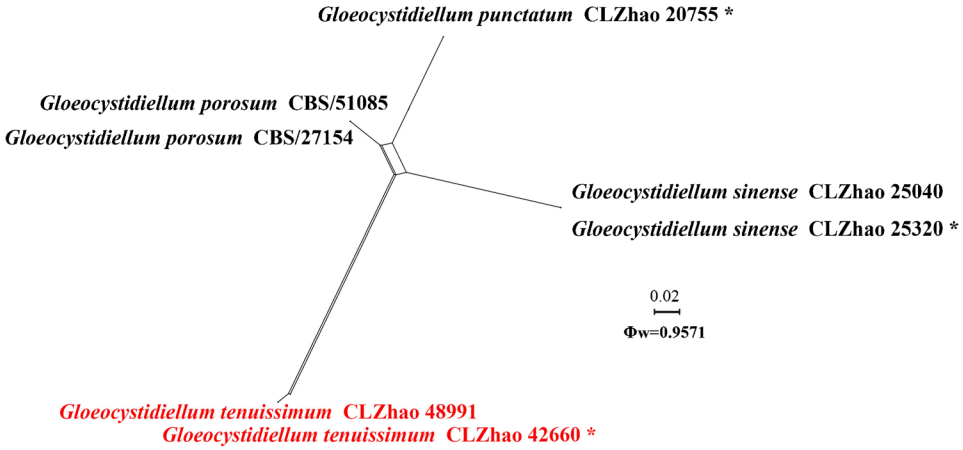


Fig. 6 Split graphs showing the results of PHI test for the ITS data of *Gloeocystidiellum tenuissimum* and closely related species using LogDet transformation and splits decomposition. PHI test results with $\Phi w \leq 0.05$ indicate that there is significant recombination within the dataset. The new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

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 ℃ for 40 s, 54 ℃ for 45 s, and 72 ℃ for 1 min; and a final extension at 72 ℃ for 10 min. The PCR procedure for nrLSU was as follows: initial denaturation at 94 ℃ for 1 min, followed by 35 cycles at 94 ℃ for 30 s, 50 ℃ for 1 min, and 72 ℃ for 1.5 min; and a final extension at 72 ℃ 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 (https://doi.org/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

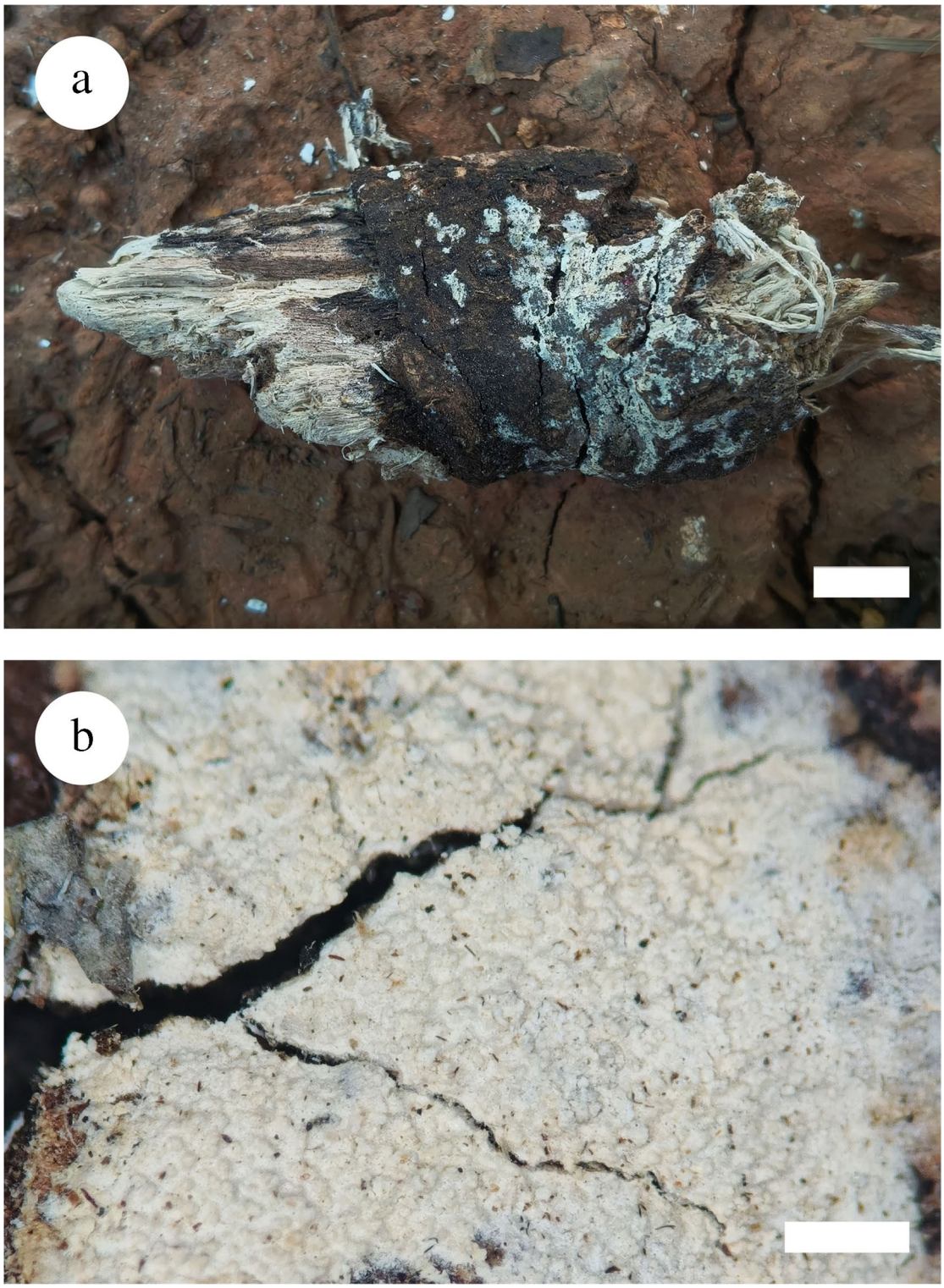


Fig. 7 Basidiomata of *Gloeocystidiellum tenuissimum* (holotype, SWFC 00042660). **a** Basidiomata on the substrate. **b** Character hymenophore. Scale bars: a = 1 cm, b = 1 mm

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 0.1.6 (Kalyaanamoorthy et al. 2017) using a Bayesian Information criterion, and

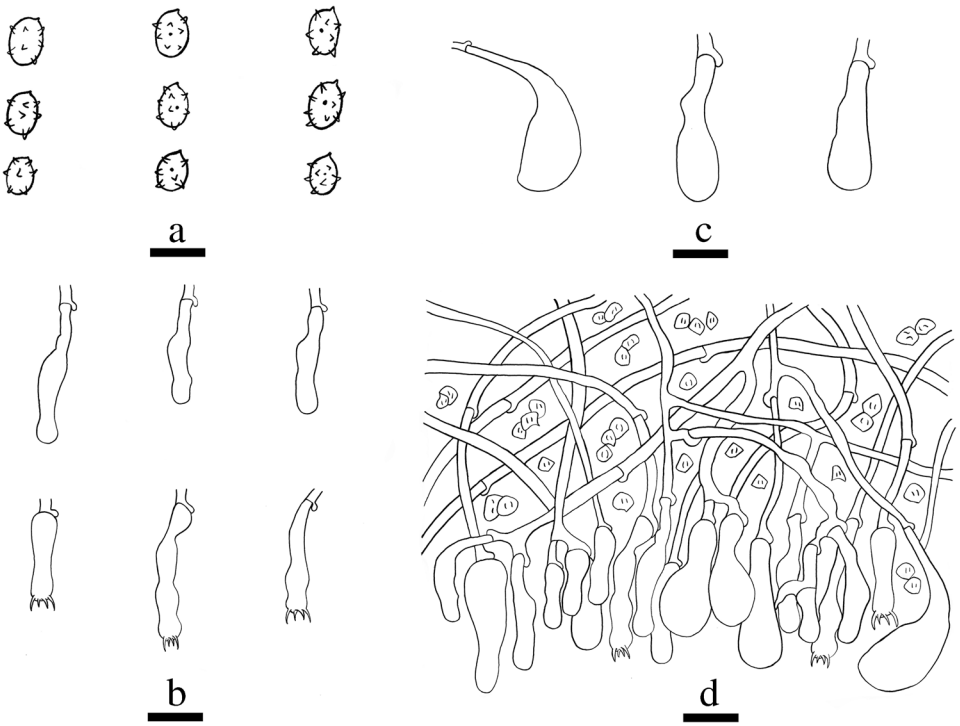


Fig. 8 Microscopic structures of *Gloeocystidiellum tenuissimum* (holotype, SWFC 00042660). **a** Basidiospores. **b** basidioles and Basidia. **c** Gloeocystidia. **d** A section of the hymenium. Scale bars: **a** = 5 μm, **b–d** = 10 μm

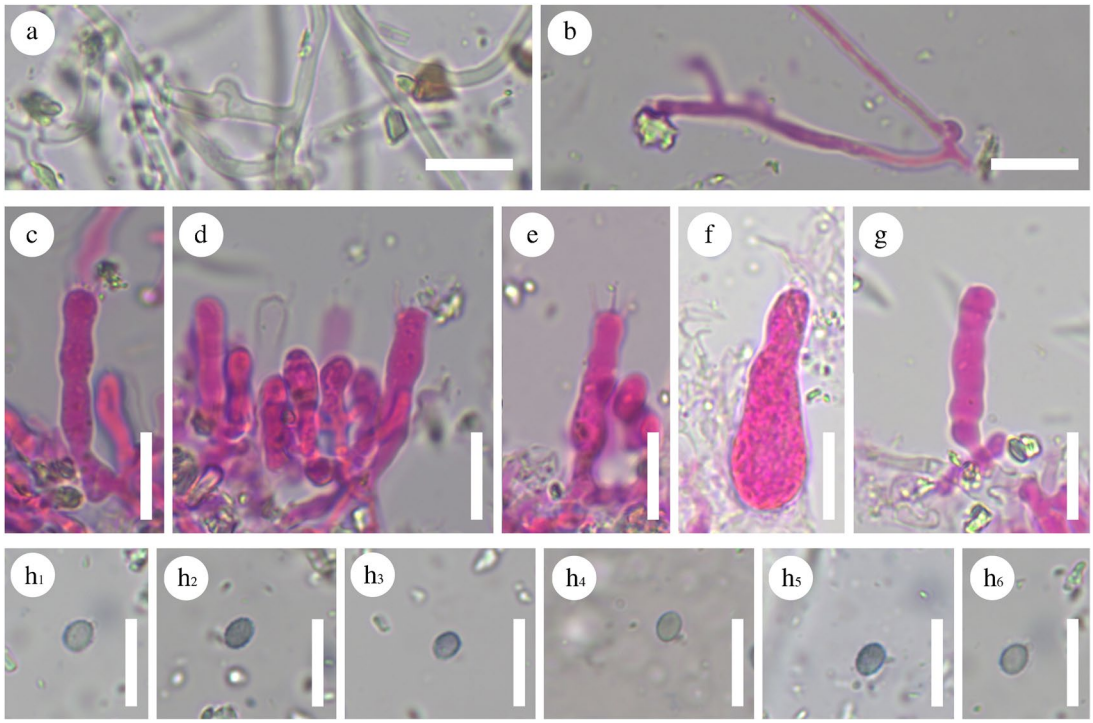


Fig. 9 Microscopic structures of *Gloeocystidiellum tenuissimum* (holotype, SWFC 00042660). **a–b** Generative hyphae. **c–e** Basidia. **f** Gloeocystidia. **g** basidioles. **h1–h6** Basidiospores. Scale bars: **a–h** = 10 μm

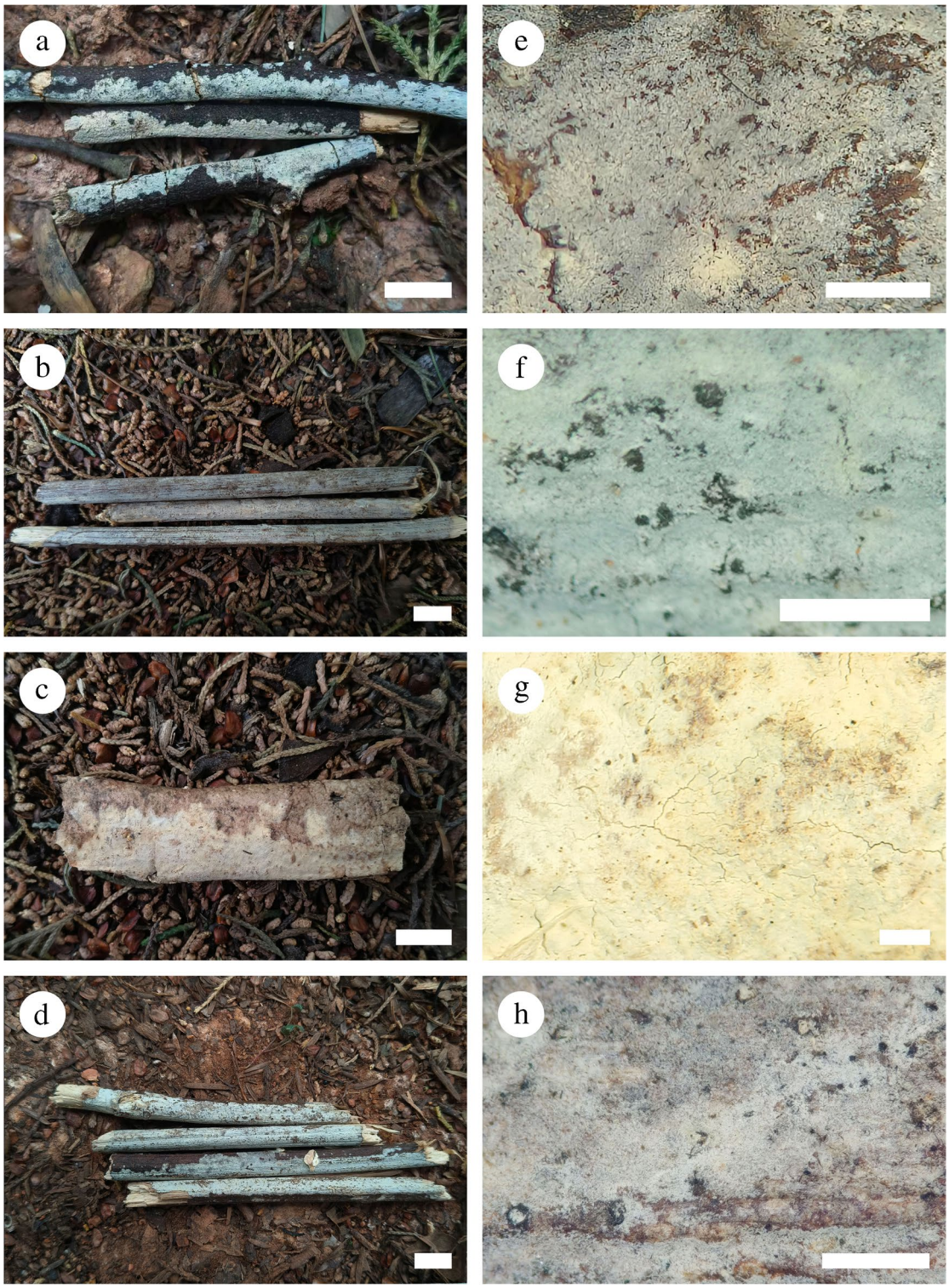


Fig. 10 Basidiomata of *Vararia farinacea* (holotype, SWFC 00041965). **a–g** Basidiomata on the substrate. **b–h** Character hymenophore. **a, e** (paratype, CLZhao 41965); **b, f** (paratype, CLZhao 41793); **c, g** (paratype, CLZhao 45978); **d, h** (paratype, CLZhao 41596). Scale bars: **a–g** = 1 cm, **b–h** = 1 mm

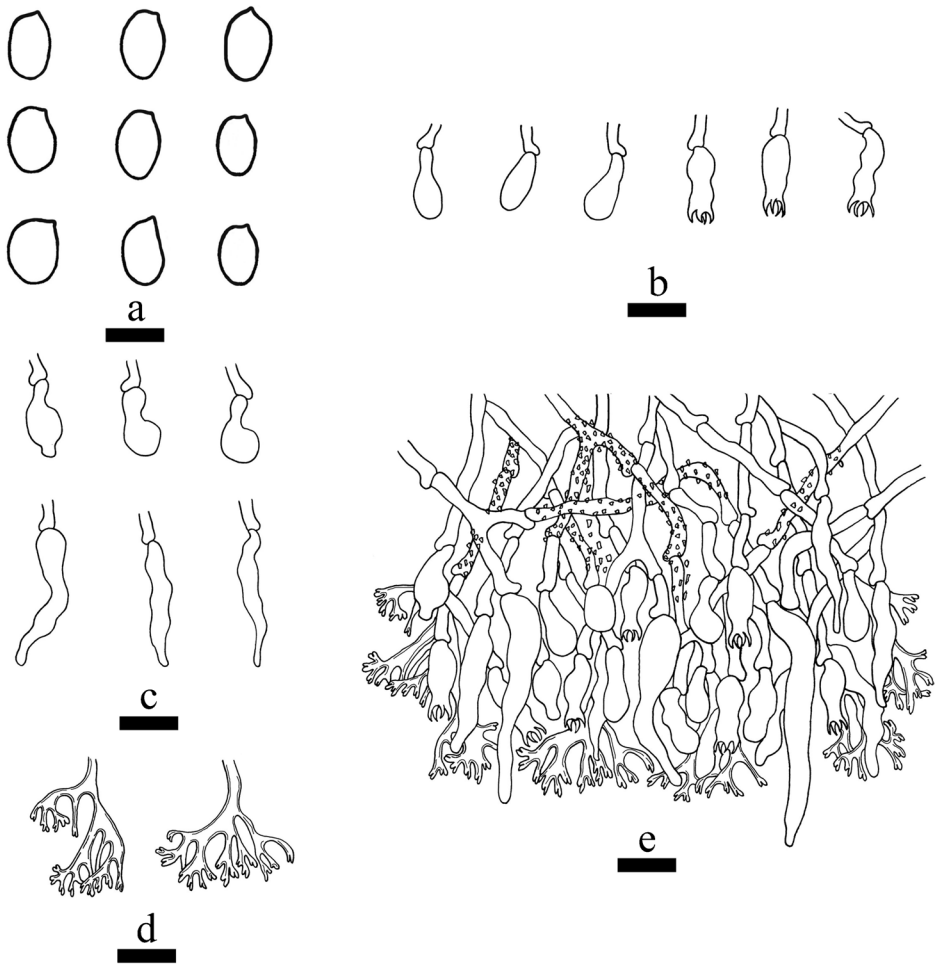


Fig. 11 Microscopic structures of *Vararia farinacea* (holotype, SWFC 00041965). **a** Basidiospores. **b** Basidioles and basidia. **c** Gloeocystidia. **d** Hyphidia. **e** A section of the hymenium. Scale bars: **a** = 5 μm, **b–e** = 10 μm

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 (Φw) and the PHI test, implemented in SplitsTree 4, were used to evaluate recombination levels among closely related species (Bruen et al. 2006; Quaedvlieg 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 eight 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

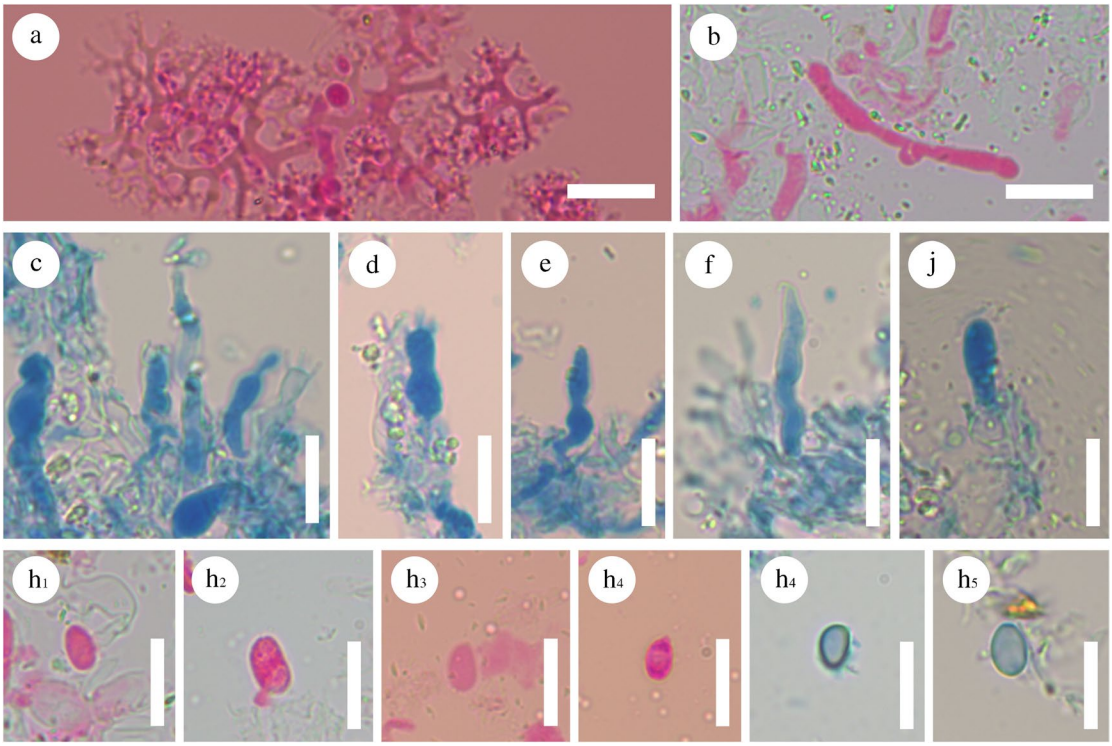


Fig. 12 Microscopic structures of *Vararia farinacea* (holotype, SWFC 00041965). **a** Hyphidia. **b** Generative hyphae. **c–d** Basidia. **e, f** Gloeocystidia. **j** Basidioles. **h1–h5** Basidiospores. Scale bars: **a–h** = 10 µm

(ITS = 1245 and 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* Massee, *Baltazaria* Leal-Dutra, Dentinger & G.W. Griff., *Dichostereum* Pilát, *Gloiothele* Bres., *Lachnocladium* Lév., *Peniophora* Cooke, *Scytinostroma* Donk and *Vararia*. Two independent lineages, *V. farinacea* and *V. ruiliensis*, were recovered within the genus *Vararia*, each forming a distinct and well-supported monophyletic clade.

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 and 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*, each forming a distinct.

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 and 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 closely related with *G. sinense*, *G. porosum*, *G. punctatum* Y.L. Deng & C.L. Zhao, *G. fissuratum* and *G. yunnanense*.

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* Boidin, Lanq. & Gilles and *V. gillesii* Boidin & Lanq. The test results show Φw = 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* A.L. Welden and *V. gomezii* Boidin & Lanq. The test results show Φw = 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* and *G. sinense*. The test results show Φw = 0.9571 for ITS data (Fig. 6), indicating that no recombination is present between the new species and related three *Gloeocystidiellum* species.

The BLAST results of *Gloeocystidiellum tenuissimum* for the top ten taxa were *G. inconstans* (G. Cunn.) Stalpers & P.K. Buchanan (ICMP 16491), *Gloeodontia subasperispora* (Litsch.) E. Larss. & K.H. Larss. (UC2022874, 20190913–24), *Gloeodontia* sp., *Ga. sinensis* Y.L. Deng & C.L. Zhao (CLZhao 34280) and *G. yunnanense* (CLZhao 7165) (Maximum record descriptions: Max score 675;Total score 750; Query cover 100%; E value 0.0; Ident 86.73%). The BLAST result of *Vararia farinacea* for the closest top 10 taxa were *Scytinostroma decidens* Boidin, Gilles & Lanq. (CBS 714.86), *Vararia* sp., *V. callichroa* Boidin, Gilles & Lanq. (CBS 746.91, CBS 744.91), *V. aurantiaca* Boidin & Lanq. (CBS 642.81) (Maximum record descriptions: Max score 492, Total score 492, Query cover 64%, E value 4e-134, Per. Ident. 88.02%, Acc. len. 772). The BLAST result of *V. ruiliensis* for the closest top 10 taxa were *Agaricomycetes* sp., *V. pingbianensis* Y.L. Deng & C.L. Zhao (CLZhao 25157, CLZhao18609, CLZhao 5053), *V. trinidadensis* (CBS 651.84, CBS 650.84), *Scytinostroma crispulum* Boidin, Gilles & Lanq. (CBS 776.86, CBS 718.86, CBS 717.86) (Maximum record descriptions: Max score 527, Total score 527, Query cover 97%, E value 9e-145, Per. Ident. 84.96%, Acc. len. 633).

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.
Figures 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 (3.5–4.5 × 2.5–3 µm).

Holotype: CHINA, Yunnan Province, Dehong, Ruili City, Tongbiguan Provincial Nature Reserve, 24°01′ N, 97°83′ E, elevation 1100 m asl., on 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 cream when fresh, turning to cream upon drying. Sterile margin white, thinning out, up to 1 mm wide.

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

Hymenium: Gloeocystidia numerous, subclavate, colorless, thin-walled, 21–29 × 5–14 µm. Basidia subclavate to subcylindrical, slightly flexuous, with a basal clamp connection and four sterigmata, 14–23 × 3–5 µm, basidioles dominant, in shape similar to basidia, but slightly smaller.

Basidiospores: Ellipsoid, colorless, thin-walled, verrucose, IKI +, CB–, 3.5–4.5 × 2.5–3 µm, L = 3.93 µm, W = 2.90 µm, Q = 1.18–1.61 (n = 60/2).

Additional specimen (paratype) examined: CHINA, Yunnan Province, Dehong, Ruili, Tongbiguan Provincial Nature Reserve, 24°01′ N, 97°83′ E, elevation 1100 m asl., on fallen angiosperm branch, leg. C.L. Zhao, 24 September 2024, CLZhao 48991 (SWFC 00048991).

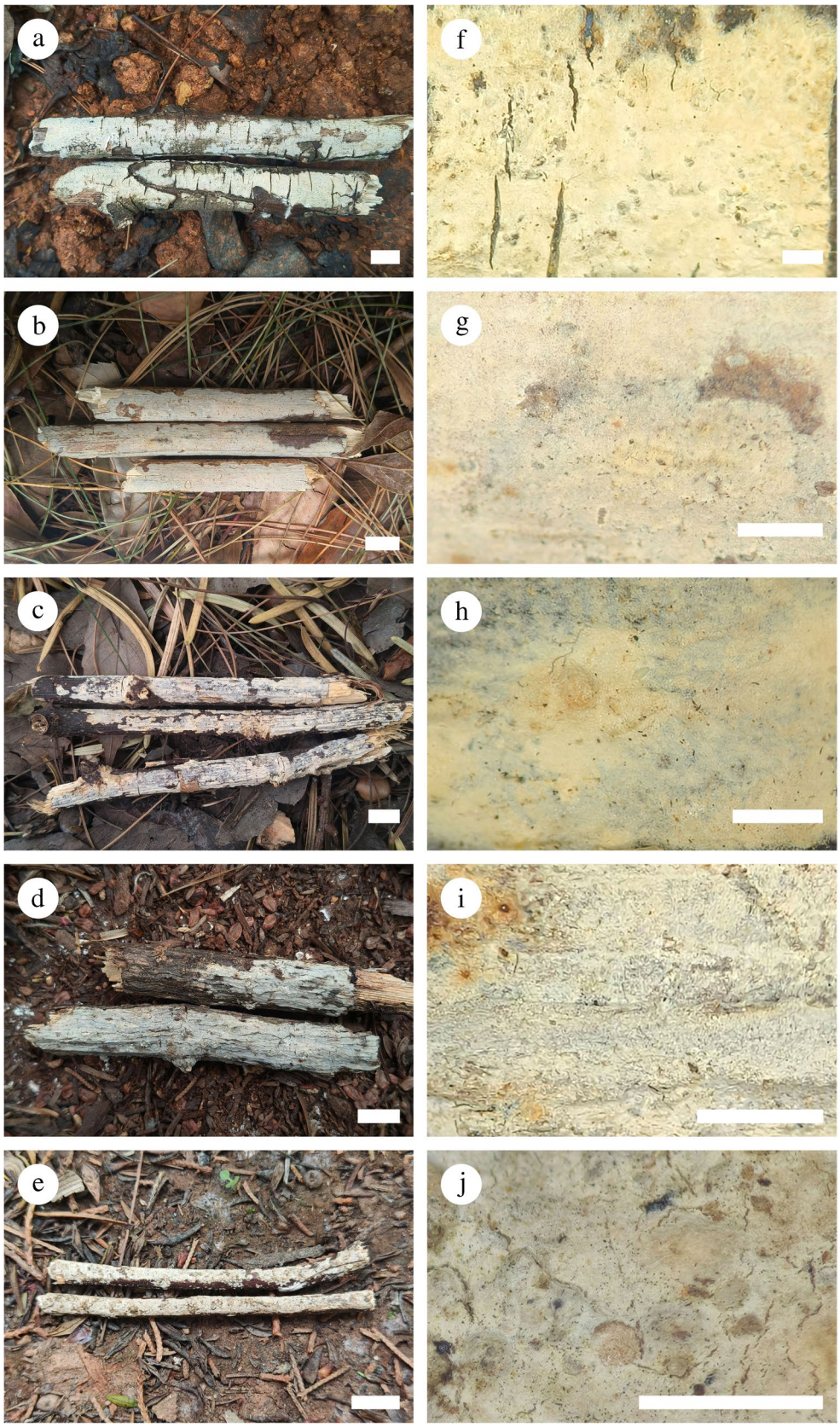
Vararia farinacea Y.L. Deng & C.L. Zhao, sp. nov.
Chinese name. 粉状叉丝革菌 (fen zhuang cha si ge jun).
MycoBank No.: 863624.
Figures 10, 11, 12

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

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

Holotype: CHINA, Yunnan Province, Dehong, Ruili, Tongbiguan Provincial Nature Reserve, Huyu village, 24°37′ N, 97°39′ E, elevation 1300 m asl., on 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, white to cream when fresh, turning to cream to pale yellow upon drying. Sterile margin narrow, thinning out, up to 1 mm wide.


a
f
b
g
c
h
d
i
e
j

◂**Fig. 13** Basidiomata of *Vararia ruiliensis* (holotype, SWFC 00041930). **a–e** Basidiomata on the substrate. **f–j** Character hymenophore. **a, f** (paratype, SWFC 00041930); **b, g** (paratype, SWFC 00042841); **c, h** (paratype, SWFC 00041506); **d, i** (paratype, SWFC 00042739); **e, j** (paratype, SWFC 00042880). Scale bars: **a–e** = 1 cm, **f–j** = 1 mm

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. Hyphidia predominate, thin-walled to thick-walled, 1–1.8 µm diameter, frequently branched, dichotomously to irregularly branched with main branches and obtuse tips.

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

Basidiospores: Ellipsoid, colorless, thin-walled, smooth, sometimes containing 1–2 oil droplets, IKI–, CB–, 4.5–6.5(–7) × 3–4.5 µm, L = 5.61 µm, W = 3.55 µm, Q = 1.29–2.00 (n = 80/4).

Additional specimens (paratypes) examined: CHINA, Yunnan Province, Dehong, Ruili, Tongbiguan Provincial Nature Reserve, 24°37′ N, 97°39′ E, elevation 1300 m asl., on 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°30′ N, 100°30′ E, elevation 1500 m asl., on fallen angiosperm branch, leg. C.L. Zhao, 19 August 2025, CLZhao 45978 (SWFC 00045978).

Vararia ruiliensis Y.L. Deng & C.L. Zhao, sp. nov.
Chinese name. 瑞丽叉丝革菌 (rui li cha si ge jun).
MycoBank No.: 863623.
Figures 13, 14, 15

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

Diagnosis: It is characterized by its cream to slightly yellowish hymenial surface, a dimitic hyphal system with generative hyphae bearing simple-septa and oblong ellipsoid basidiospores (5–7.5 × 2–3.5 µm).

Holotype: CHINA, Yunnan Province, Dehong, Ruili City, Tongbiguan Provincial Nature Reserve, Huyu village, 24°37′ N, 97°39′ E, elevation 1300 m asl., on fallen angiosperm branch, leg. C.L. Zhao, 22 September 2024, CLZhao 41930 (SWFC 00041930).

Basidiomata: Annual, resupinate, membranous, without odor or taste when fresh, up to 12 cm long, 2 cm wide, up to 200 µm thick. Hymenial surface smooth, cream when fresh, turning to cream to slightly yellowish upon drying. Sterile margin distinct, narrow, thinning out, up to 1 mm wide.

Hyphal system: Dimitic; generative hyphae bearing simple-septa, branched, colorless, thin-walled, 2–3.5 µm in diameter, IKI–, CB–; tissues unchanged in KOH. Subhymenial hyphae densely covered by crystals. Hyphidia predominate, thin-walled, frequently branched, 1–1.5 µm diameter, frequently branched, dichotomously to irregularly branched with main branches and obtuse tips.

Hymenium: Gloeocystidia fusiform to subcylindrical, colorless, smooth, thin-walled, usually containing refractive materials, 15–23 × 3.5–6.5 µm. Basidia subcylindrical, slightly flexuous, with four sterigmata and a basal simple septum, thin-walled, smooth, 14.5–21 × 3.5–6.5 µm; basidioles in shape similar to basidia, but slightly smaller.

Basidiospores: Cylindrical, colorless, thin-walled, smooth, usually containing 1–2 oil droplets, IKI–, CB–, (4.5–)5–7.5(–8) × (1.5–)2–3.5(–4) µm, L = 6.30 µm, W = 2.50 µm, 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, elevation 1300 m asl., on 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 the 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 recovered as monophyletic based on the phylogenetic evidence inferring from ITS, nrLSU, *RPB*2 and *TEF-α* sequences (Larsson and Hallenberg 2001; Deng et al. 2026a; Zhang et al. 2026). Based on the ITS + nrLSU data (Fig. 3), *G. tenuissimum* is grouped into the genus *Gloeocystidiellum*, and is closely related with *G. sinense*, *G. porosum*, *G. punctatum*, *G. fissuratum* and *G. yunnanense*. However, morphologically, *G. sinense* differs from *G. tenuissimum* by its smooth hymenial surface, generative hyphae with simple septa and longer tubular cystidia (44–52 µm vs. 21–29 µm) (Zhang et al. 2025); *G. porosum* differs in its both longer gloeocystidia (50–180 µm vs. 21–29 µm) and basidiospores (4.5–6 µm vs. 3.5–4.5 µm) (Boidin et al. 1997). Species *G. punctatum* is distinguished from *G. tenuissimum* by its both longer tubular gloeocystidia (51.5–106 µm vs. 21–29 µm) and basidiospores (4–6.5 µm

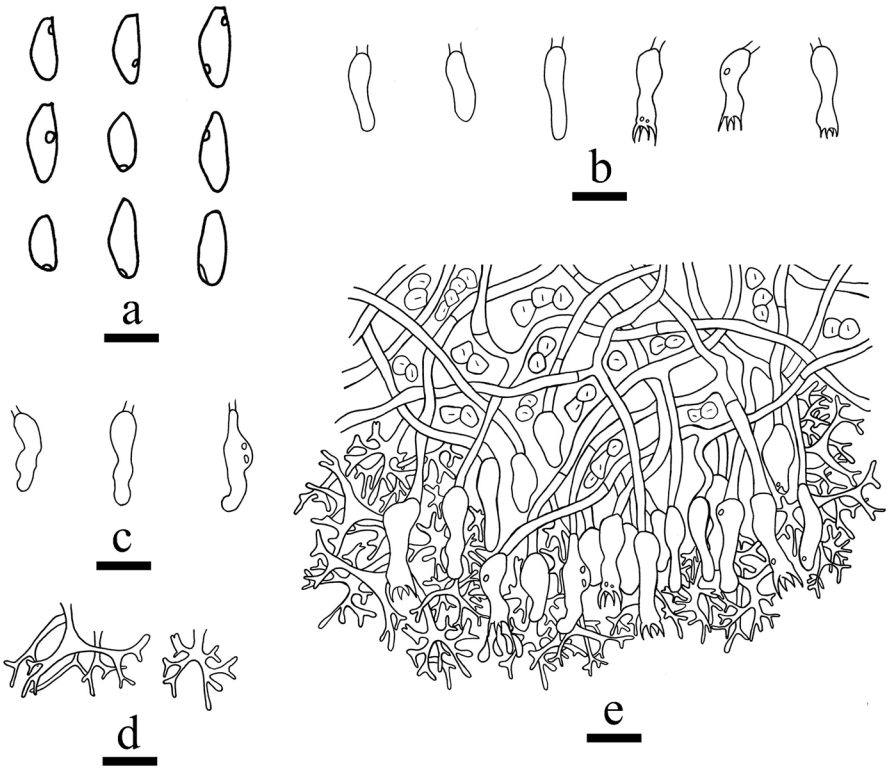


Fig. 14 Microscopic structures of *Vararia ruiliensis* (holotype, SWFC 00041930). **a** Basidiospores. **b** Basidioles and basidia. **c** Gloeocystidia. **d** Hyphidia. **e** A section of the hymenium. Scale bars: **a** = 5 μm, **b–e** = 10 μm

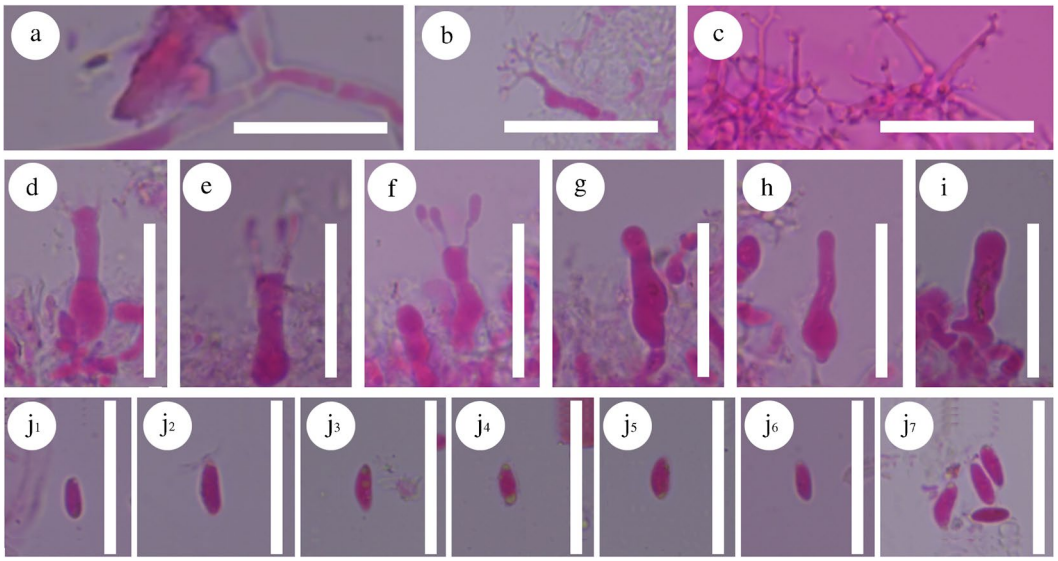


Fig. 15 Microscopic structures of *Vararia ruiliensis* (holotype, SWFC 00041930). **a** Generative hyphae. **b–c** Hyphidia. **d–f** Basidia. **g–h** Gloeocystidia. **i** Basidioles. **j1–j7** Basidiospores. Scale bars: **a–j** = 20 μm

vs. 3.5–4.5 μm) (Deng et al. 2026a). *Gloeocystidiellum fissuratum* is different from *G. tenuissimum* by having white to cinnamon-buff basidiomata, longer gloeocystidia, subclavate to obclavate (57–88 μm vs. 21–29 μm) and subglobose basidiospores (Wang et al. 2025a, b, c). *Gloeocystidiellum yunnanense* can be distinguished from *G. tenuissimum* by longer clavate and tubular gloeocystidia (25–48.2 μm and 22.6–47.2 μm vs. 21–29 μm) and thick-walled basidiospores (Zhao and Zhao 2023). In ITS BLAST results, *G. tenuissimum* is closely related to *G. inconstans*, but the latter is different from *G. tenuissimum* by having perennial, ceraceous basidiomata, wider gloeocystidia (12–16 μm vs. 5–14 μm) and

larger globose or subglobose basidiospores (5–6 × 5–5.5 µm vs. 3.5–4.5 × 2.5–3 µm) (Stalpers and Buchanan 1991).

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) reveal that two new taxa, *Vararia farinacea* and *V. ruiliensis* are grouped into the genus *Vararia* within the family *Peniophoraceae*. Additionally, the result of the PHI test showed that *V. farinacea* is phylogenetically closely related to *V. cremea*, *V. gillesii* and *V. sphaericospora.* However, morphologically, *V. cremea* is distinguished from *V. farinacea* by its larger subcylindrical gloeocystidia (40–90 × 7–15 µm vs. 23–40 × 4–6 µm), and both longer basidia (25–35 µm vs. 10–13 µm) and basidiospores (15–20 µm vs. 4.5–6.5 µm) (Boidin et al. 1980). *Vararia gillesii* is different from *V. farinacea* by having larger basidia (30–40 × 6–7 µm vs. 10–13 × 3–5 µm) and longer fusiform basidiospores (14–17 µm vs. 4.5–6.5 µm) (Boidin and Lanquetin 1975). *Vararia sphaericospora* can be distinguished from *V. farinacea* by its larger subcylindrical to fusiform gloeocystidia (48–105 × 7–11 µm vs. 23–40 × 4–6 µm), basidia (35–45 × 5.5–7 µm vs. 10–13 × 3–5 µm) and wider basidiospores (6.5–7 µm vs. 3–4.5 µm) (Boidin and Lanquetin 1975).

In addition, the result of the PHI test showed that *V. ruiliensis* is phylogenetically closely related with *V. trinidadensis* and *V. gomezii*. However, morphologically, *V. trinidadensis* is distinguished from *V. ruiliensis* by its larger gloeocystidia (27–50 × 7–12 µm vs. 15–23 × 3.5–7 µm) and longer basidiospores (13–17 µm vs. 5–7.5 µm) (Welden 1965). *Vararia gomezii* can be distinguished from *V. ruiliensis* by thicker dichohyphae (2–2.5 µm vs. 1–1.5 µm), both larger basidia (30–45 × 7–8 µm vs. 14.5–23 × 3.5–7 µm) and basidiospores (30–45 × 7–8 µm vs. 11–15 × 4.2–6 µm) (Boidin and Lquetin 1975).

Morphologically, *Vararia yaoshanensis* Y.L. Deng & C.L. Zhao is similar to *V. farinacea* by having two types of gloeocystidia. However, *V. yaoshanensis* differs from *V. farinacea* in its both larger basidia (23–46 × 5–8 µm vs. 10–13 × 3–5 µm) and basidiospores (7.6–10.8 × 5.7–7.8 µm vs. 4.5–6.5 × 3–4.5 µm) (Deng et al. 2024). *Vararia punctata* Y.L. Deng & C.L. Zhao is similar to *V. ruiliensis* by having subcylindrical basidia. However, *V. punctata* is distinguished from *V. ruiliensis* by its white to cream hymenial surface and larger ellipsoid basidiospores (6–10 × 4–6 µm vs. 5–7.5 × 2–3.5 µm) (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 (Yuan et al. 2008; James et al. 2020; Dai et al. 2021; Wang et al. 2025a, b, c, 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*.

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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.

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

Competing interests The authors declare no competing interests.

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