

ISSN 1179-3113 (print version)
ISSN 1179-3121 (online version)

Phytotaxa

768
26 July 2018



Magnolia Press, Auckland, New Zealand



Floristic diversity and new records of Fabaceae in Semnan Province, Iran: From the Eastern Alborz Mountains to the Central Plateau

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Published: 2024-07-02

DOI: [10.1007/s13345-024-01010-0](https://doi.org/10.1007/s13345-024-01010-0)

Page range: 1-13

Abstract views: 27

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***Vararia subtropica* sp. nov. (Peniophoraceae, Russulales), a coriaceous fungus from Yunnan Province, SW China**

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Published: 2024-07-02

DOI: [10.1007/s13345-024-01010-0](https://doi.org/10.1007/s13345-024-01010-0)

Page range: 22-32

Abstract views: 24

PDF downloaded: 0

[PDF \(A: 228K\)](#)



***Campanula selenica* (Campanulaceae), a new species from western Iran**

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Published: 2024-07-02

DOI: [10.1007/s13345-024-01010-0](https://doi.org/10.1007/s13345-024-01010-0)

Page range: 37-47

Abstract views: 21

PDF downloaded: 0

[PDF \(A: 770K\)](#)



***Primulina lichuanensis* (Gesneriaceae), a new species from western Hubei, China**

ZHONG-BAO DONG, YONG ZENG, BONG-GWONG YUN, BEN-KUN LI, WEI-YI LIU, XUEJING-LONG LI

Published: 2024-07-02

DOI: [10.1007/s13345-024-01010-0](https://doi.org/10.1007/s13345-024-01010-0)

Page range: 62-69

Abstract views: 14

PDF downloaded: 0

[PDF \(A: 288K\)](#)



Vararia subtropica sp. nov. (Peniophoraceae, Russulales), a coriaceous fungus from Yunnan Province, SW China

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Abstract

A new species, *Vararia subtropica*, from Yunnan Province, SW China, is described and illustrated based on morphological characters and phylogenetic analyses. *Vararia subtropica* is characterized by the cream to buff hymenial surface, a dimitic hyphal system with generative hyphae with clamp connections, and cylindrical, slightly curved to allantoid basidiospores (7.1–11.3 × 2.7–5.2 µm). Sequences of ITS and nLSU were generated from the studied specimens, and phylogenetic analysis was performed with Maximum Likelihood and Bayesian Inference methods. The phylogenetic analysis indicated that the new species belongs to the genus *Vararia* and is the sister species of *V. daweishanensis*. A description, illustrations, and phylogenetic analysis results are provided. This discovery expands the known diversity of *Vararia* in subtropical Asia and improves our understanding of phylogenetic relationships within the genus.

Key words: Biodiversity, morphology, new taxon, taxonomy, wood-inhabiting fungi

Introduction

In forest ecosystems, wood-inhabiting fungi are found on living trees, standing dead trees, fallen decorticated trunks, fallen trunks and branches, stumps, and even manufactured woody products (Cui *et al.* 2019, Wu *et al.* 2022, Yuan *et al.* 2023, Zhou *et al.* 2023, Hibbett *et al.* 2025). These fungi secrete various enzymes that effectively decompose cellulose, hemicellulose, and lignin into simple inorganic substances (Si *et al.* 2011), and thus represent a key decomposer group that underpins nutrient turnover and carbon cycling in forest ecosystems (Dai *et al.* 2021, Zhao *et al.* 2023, 2026, Case *et al.* 2025).

Vararia P. Karst. (1898: 32) is a corticioid, wood-inhabiting genus within Peniophoraceae of the order Russulales, with a broad geographic distribution, and typified by *V. investiens* (Schwein.) P. Karst. (1898: 32) (Miller *et al.* 2006, Larsson 2007, Chen *et al.* 2015, Deng *et al.* 2026a, b). *Vararia* is the most species-rich genus in Peniophoraceae and plays fundamental ecological roles as a decomposer, contributing to carbon cycling in forest soils (Kirk *et al.* 2008, Tedersoo *et al.* 2014, Deng *et al.* 2024). *Vararia* is characterized by resupinate basidiomata, a dimitic hyphal structure with simple septa or clamped generative hyphae and often dextrinoid dichotomous hyphae in Melzer's reagent, presence of gloecystidia, and variously shaped smooth basidiospores with or without an amyloid reaction (Boidin & Lanquetin 1975, Boidin *et al.* 1980, Bernicchia & Gorjón 2010, Deng *et al.* 2026a, b). The species of *Vararia* are typically found on fallen angiosperm branches, dead wood, or herbaceous stems, and occasionally on gymnosperm wood (Yurchenko

et al. 2020). In recent years, integrative studies combining morpho-anatomical evidence and molecular phylogenetic data have constantly reported new *Vararia* species, most of which have been reported from tropical and subtropical regions (Nakasone 2015, Liu & He 2016, Deng *et al.* 2026b). Recently, ten *Vararia* species were discovered in China, namely, *V. asiana* Y.L. Deng & C.L. Zhao, *V. bambusicola* Y.L. Deng & C.L. Zhao, *V. bannaensis* Y.L. Deng & C.L. Zhao, *V. dehongensis* Y.L. Deng & C.L. Zhao, *V. ferruginosa* Y.L. Deng & C.L. Zhao, *V. lacerata* Y.L. Deng & C.L. Zhao, *V. membranacea* Y.L. Deng & C.L. Zhao, *V. muscicola* Y.L. Deng & C.L. Zhao, *V. tuberculata* K.S. Wang & C.L. Zhao, and *V. wumengshanensis* Y.L. Deng & C.L. Zhao, based on combined morphoanatomical characters and molecular phylogenetic data (Deng *et al.* 2026a, b, Wang *et al.* 2026).

Phylogenetic analyses of corticioid fungal species using ITS1-5.8S-ITS2-nrLSU nuclear rDNA revealed that Peniophoraceae is nested within the russuloid clade and currently comprises seventeen accepted genera, including *Vararia* (Larsson & Larsson 2003, Larsson *et al.* 2004, Leal-Dutra *et al.* 2018, Li *et al.* 2023, Deng *et al.* 2024, 2026a). Surveys of corticioid fungi in southern China have further clarified interspecific relationships within *Vararia* (Zou *et al.* 2022, Deng & Zhao 2023). Multi-gene phylogenetic analyses revealed that *Vararia* is paraphyletic; however, available morphological evidence remains insufficient to justify splitting the genus into separate genera (Deng *et al.* 2024, 2026a, b). Accordingly, the discovery and formal description of additional species are needed to better resolve species boundaries and evolutionary relationships within *Vararia*.

During recent investigations in Yunnan Province, China, we collected numerous samples of a coriaceous taxon, described here as a new species of *Vararia*. Morphological characters and molecular phylogenetic evidence, based on internal transcribed spacer (ITS) regions and the large subunit nuclear ribosomal RNA gene (nLSU), support its recognition. Detailed descriptions, illustrations, and phylogenetic analysis results for the new species are provided.

Materials and methods

Sample collection and herbarium specimen preparation

Fresh basidiomata were collected from Dali, Honghe, Pu'er, Wenshan, Yuxi, Yunnan Province, China. Field data were recorded (Rathnayaka *et al.* 2025), photographs of basidiomata were taken in situ, and specimens were transported to the laboratory in mushroom collection boxes. All specimens were dried in an electric food dehydrator at 40 °C (Hu *et al.* 2022), then sealed in an envelope bag and deposited in the herbarium of Southwest Forestry University (SWFC), Kunming, Yunnan Province, P.R. China. Macromorphological descriptions were prepared from field notes and photos collected in the field and in the lab. Color terminology follows Petersen (1996). Micromorphological data were obtained from the dried specimens by light microscopy, following the methods described in previous studies (Zhao *et al.* 2023, Dong *et al.* 2024). The following abbreviations are used: KOH = 5% potassium hydroxide water solution, CB = Cotton Blue, CB– = acyanophilous, IKI = Melzer's Reagent, IKI– = both inamyloid and indextrinoid, L = mean spore length (arithmetic average for all spores), W = mean spore width (arithmetic average for all spores), Q = variation in the L/W ratios between the specimens studied and $n = a/b$ (number of spores (a) measured from given number (b) of specimens).

Molecular procedures and phylogenetic analyses

The EZNA HP Fungal DNA Kit (Omega Biotechnologies Co., Ltd., Kunming, China) was used to extract DNA from the dried specimens, with some modifications. The nuclear ribosomal ITS region was amplified with primers ITS5 and ITS4 (White *et al.* 1990). The PCR procedure for ITS was as follows: initial denaturation at 95 °C for 3 min, followed by 35 cycles at 94 °C for 40 s, 58 °C for 45 s, and 72 °C for 1 min, and a final extension of 72 °C for 10 min. The nuclear LSU region was amplified with primer pair LR0R and LR7 (Vilgalys & Hester 1990). The PCR procedure for LSU was as follows: initial denaturation at 94 °C for 1 min, followed by 35 cycles at 94 °C for 30 s, 48 °C for 1 min, and 72 °C for 1.5 min, and a final extension of 72 °C for 10 min. The PCR procedure for ITS and LSU followed a previous study (Dong *et al.* 2024). All of the newly generated sequences were deposited in NCBI GenBank (<https://www.ncbi.nlm.nih.gov/genbank/>) (Table 1).

TABLE 1. List of species, specimens, and GenBank accession numbers of sequences used in this study. - and * refers to the data unavailability and type material, respectively.

Species name	Sample no.	GenBank accession No.		Country	References
		ITS	nLSU		
<i>Asterostroma bambusicola</i>	He4132	KY263865	KY263871	China	Liu & He (2016)
<i>Asterostroma cervicolor</i>	He2314	KY263859	KY263869	Sweden	Larsson & Larsson (2003)
<i>Asterostroma cervicolor</i>	He4020	KY263860	KY263868	Japan	Suhara <i>et al.</i> (2010)
<i>Asterostroma fimbriatum</i>	CLZhao 41500	PV940929	PX070093	China	Deng <i>et al.</i> (2026a)
<i>Asterostroma laxum</i>	EL33-99	AF506410	AF506410	Sweden	Larsson & Larsson (2003)
<i>Asterostroma macrosporum</i>	TMI:25696	AB439544	-	Japan	Suhara <i>et al.</i> (2010)
<i>Asterostroma macrosporum</i>	TMI:25697	AB439545	-	Japan	Suhara <i>et al.</i> (2010)
<i>Asterostroma muscicola</i>	KHL9537	AF506409	AF506409	Sweden	Larsson & Larsson (2003)
<i>Baltazaria galactina</i>	CBS 752.86	MH862034	MH873721	France	Vu <i>et al.</i> (2019)
<i>Baltazaria galactina</i>	He4999	MK625618	MK625547	France	Vu <i>et al.</i> (2019)
<i>Baltazaria neogalactina</i>	CBS 755.86	MH862037	MH873724	France	Vu <i>et al.</i> (2019)
<i>Baltazaria neogalactina</i>	CBS:758.86	MH862040	MH873727	France	Vu <i>et al.</i> (2019)
<i>Baltazaria pingbianensis</i>	CLZhao 17755*	OR048814	OR510674	China	Deng <i>et al.</i> (2026a)
<i>Baltazaria pingbianensis</i>	CLZhao 18294	OR048816	-	China	Deng <i>et al.</i> (2026a)
<i>Dichostereum boidinii</i>	He4410	MH538315	MH538331	China	Liu & He (2018)
<i>Dichostereum boidinii</i>	He5026	MH538324	MH538330	China	Liu & He (2018)
<i>Dichostereum pallescens</i>	CBS:718.81	MH861456	MH873198	USA	Vu <i>et al.</i> (2019)
<i>Dichostereum pallescens</i>	CBS:719.81	MH861457	MH873199	USA	Vu <i>et al.</i> (2019)
<i>Gloiothele citrina</i>	LE-BIN 2968	OL840636	-	Russia	Deng <i>et al.</i> (2026a)
<i>Gloiothele fragilima</i>	CLZhao 15980	PV147168	-	China	Deng <i>et al.</i> (2026a)
<i>Gloiothele globosa</i>	PERTH:8690790	MT536993	MT524528	Australia	Bougher & Barrett (2020)
<i>Gloiothele lactescens</i>	EL8-98	AF506453	AF506453	Sweden	Larsson & Larsson (2003)
<i>Gloiothele lamellosa</i>	KHL11031	AF506454	AF506454	Sweden	Larsson & Larsson (2003)
<i>Gloiothele lamellosa</i>	CBS:404.83	MH861620	MH873337	Madagascar	Vu <i>et al.</i> (2019)
<i>Gloiothele olearia</i>	BIO-Fungi11969	MT240525	-	Sweden	Larsson & Larsson (2003)
<i>Gloiothele torrendii</i>	JB18615	AF506455	AF506455	Sweden	Larsson & Larsson (2003)
<i>Gloiothele tuberculata</i>	CLZhao 29888	PV441135	PV441150	China	Deng <i>et al.</i> (2026a)
<i>Gloiothele tuberculata</i>	CLZhao 29919	PV441136	PV441151	China	Deng <i>et al.</i> (2026a)
<i>Lachnocladium schweinfurthianum</i>	KM49740	MH260033	MH260051	United Kingdom	Leal-Dutra <i>et al.</i> (2018)
<i>Peniophora cinerea</i>	He3725	MK588769	MK588809	China	Deng <i>et al.</i> (2024)
<i>Peniophora cinerea</i>	CBS:261.37	MH855905	MH867412	Netherlands	Vu <i>et al.</i> (2019)
<i>Peniophora incarnata</i>	NH10271	AF506425	AF506425	Sweden	Larsson & Larsson (2003)
<i>Peniophora incarnata</i>	CBS 430.72	MH860518	MH872230	Netherlands	Vu <i>et al.</i> (2019)
<i>Peniophora nuda</i>	LZ15-07	MT859929	-	China	Deng <i>et al.</i> (2026b)
<i>Peniophora quercina</i>	CBS 407.50	MH856687	MH868204	Netherlands	Vu <i>et al.</i> (2019)
<i>Peniophora quercina</i>	CBS:410.50	MH856690	MH868207	France	Vu <i>et al.</i> (2019)
<i>Peniophora tristicula</i>	He 4775	MH669235	MH669239	China	Liu & He (2018)
<i>Peniophora versiformis</i>	He 3029	MK588756	MK588796	China	Xu <i>et al.</i> (2023)
<i>Scytinostroma alutum</i>	CBS:766.81	MH861486	MH873225	France	Vu <i>et al.</i> (2019)
<i>Scytinostroma alutum</i>	CBS 762.81	MH861482	MH873221	France	Vu <i>et al.</i> (2019)
<i>Scytinostroma artocreas</i>	GHL-2016-Oct	MH204688	MH204691	China	Liu <i>et al.</i> (2019)
<i>Scytinostroma beijingense</i>	He 7768	OQ731943	OQ729731	China	Li <i>et al.</i> (2023)
<i>Scytinostroma boidinii</i>	He 5138	MK625572	MK625497	China	Li <i>et al.</i> (2023)
<i>Scytinostroma boidinii</i>	He 6911	OQ731934	OQ729724	China	Li <i>et al.</i> (2023)
<i>Scytinostroma daweshanense</i>	CLZhao 17926 *	OR096194	OR461462	China	Dong <i>et al.</i> (2024)
<i>Scytinostroma duriusculum</i>	CBS:758.81	MH861478	MH873217	France	Vu <i>et al.</i> (2019)

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TABLE 1. (Continued)

Species name	Sample no.	GenBank accession No.		Country	References
		ITS	nLSU		
<i>Scytinostroma incrustatum</i>	He 2841	MH142906	MH142910	China	Liu <i>et al.</i> (2019)
<i>Scytinostroma portentosum</i>	EL11-99	AF506470	AF506470	Sweden	Larsson & Larsson (2003)
<i>Scytinostroma portentosum</i>	CBS 503.48	MH856447	-	Netherlands	Vu <i>et al.</i> (2019)
<i>Scytinostroma renisporum</i>	CBS:770.86	MH862050	MH873737	Bali	Vu <i>et al.</i> (2019)
<i>Scytinostroma renisporum</i>	CBS:771.86	MH862051	MH873738	Bali	Vu <i>et al.</i> (2019)
<i>Scytinostroma subduriusculum</i>	He 7657	OQ731941	OQ729727	China	Li <i>et al.</i> (2023)
<i>Scytinostroma subrenisporum</i>	He 4384	MK625567	MK625495	China	Li <i>et al.</i> (2023)
<i>Scytinostroma subrenisporum</i>	He 4792	MK625566	MK625493	China	Li <i>et al.</i> (2023)
<i>Scytinostroma yunnanense</i>	CLZhao 10802	MT611446	-	China	Wang <i>et al.</i> (2020)
<i>Scytinostroma yunnanense</i>	CLZhao 11010	MT611447	-	China	Wang <i>et al.</i> (2020)
<i>Stereum hirsutum</i>	He3504	MK625629	MK625557	China	Deng <i>et al.</i> (2026a)
<i>Stereum ostrea</i>	He2067	KU559366	KU574826	China	Deng <i>et al.</i> (2026a)
<i>Vararia abortiphysa</i>	CBS:632.81	MH861387	MH873136	Gabon	Vu <i>et al.</i> (2019)
<i>Vararia ambigua</i>	CBS 634.81	MH861388	MH873137	France	Vu <i>et al.</i> (2019)
<i>Vararia amphithallica</i>	CBS:635.81	MH861389	MH873138	Gabon	Vu <i>et al.</i> (2019)
<i>Vararia amphithallica</i>	CBS:687.81	MH861431	MH873173	France	Vu <i>et al.</i> (2019)
<i>Vararia asiana</i>	CLZhao 25187*	OR102488	OR510680	China	Deng <i>et al.</i> (2026a)
<i>Vararia aurantiaca</i>	CBS:642.81	MH861394	MH873143	Gabon	Vu <i>et al.</i> (2019)
<i>Vararia aurantiaca</i>	CBS:641.81	MH861393		Netherlands	Vu <i>et al.</i> (2019)
<i>Vararia bambusicola</i>	CLZhao 35740*	PV637442	PV637449	China	Deng <i>et al.</i> (2026a)
<i>Vararia bambusicola</i>	CLZhao 35743	PV637443	PV637450	China	Deng <i>et al.</i> (2026a)
<i>Vararia bannaensis</i>	CLZhao 35714*	PV441143	PV441157	China	Deng <i>et al.</i> (2026a)
<i>Vararia bannaensis</i>	CLZhao 35720	PV441144	PV441158	China	Deng <i>et al.</i> (2026a)
<i>Vararia breviphysa</i>	CBS:643.81	MH873144	MH873144	Gabon	Vu <i>et al.</i> (2019)
<i>Vararia breviphysa</i>	CBS:644.81	MH861396	MH873145	Gabon	Vu <i>et al.</i> (2019)
<i>Vararia calami</i>	CBS:646.81	MH861398	-	France	Vu <i>et al.</i> (2019)
<i>Vararia calami</i>	CBS:648.81	MH861399	-	France	Vu <i>et al.</i> (2019)
<i>Vararia callichroa</i>	CBS:744.91	MH874000	MH874000	France	Vu <i>et al.</i> (2019)
<i>Vararia cinnamomea</i>	CBS:641.84	MH873487	MH873487	Madagascar	Vu <i>et al.</i> (2019)
<i>Vararia cinnamomea</i>	CBS:642.84	MH873488	MH873488	Madagascar	Vu <i>et al.</i> (2019)
<i>Vararia cremea</i>	CBS:651.81	MH873147	MH873147	France	Vu <i>et al.</i> (2019)
<i>Vararia daweshanensis</i>	CLZhao 17911	OP380613	OP615103	China	Zou <i>et al.</i> (2022)
<i>Vararia daweshanensis</i>	CLZhao 17936	OP380614	OP380688	China	Zou <i>et al.</i> (2022)
<i>Vararia dussii</i>	CBS:652.81	MH873148	MH873148	France	Vu <i>et al.</i> (2019)
<i>Vararia dussii</i>	CBS:655.81	MH861405	-	France	Vu <i>et al.</i> (2019)
<i>Vararia ellipsospora</i>	HHB-19503	MW740328	-	New Zealand	Zou <i>et al.</i> (2022)
<i>Vararia ferruginosa</i>	CLZhao 30551*	PV147175	-	China	Deng <i>et al.</i> (2026a)
<i>Vararia ferruginosa</i>	CLZhao 30574	PV147176	PV185860	China	Deng <i>et al.</i> (2026a)
<i>Vararia fissurata</i>	CLZhao 5218	OQ025218	OR539502	China	Deng <i>et al.</i> (2024)
<i>Vararia fissurata</i>	CLZhao 8171*	OQ025219	OR539503	China	Deng <i>et al.</i> (2024)
<i>Vararia fragilis</i>	CLZhao 16475	OP380612	OP380687	China	Zou <i>et al.</i> (2022)
<i>Vararia fragilis</i>	CLZhao 2628	OP380611	-	China	Zou <i>et al.</i> (2022)
<i>Vararia fusispora</i>	PDD:119539	OL709443	-	New Zealand	Zou <i>et al.</i> (2022)
<i>Vararia gallica</i>	CBS 234.91	MH862250	MH873932	Canada	Vu <i>et al.</i> (2019)
<i>Vararia gallica</i>	CBS 656.81	MH861406	MH873152	France	Vu <i>et al.</i> (2019)
<i>Vararia gillesii</i>	CBS:660.81	MH873153	MH873153	Cote d'Ivoire	Vu <i>et al.</i> (2019)
<i>Vararia gomezii</i>	CBS:661.81	MH873154	MH873154	France	Vu <i>et al.</i> (2019)

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TABLE 1. (Continued)

Species name	Sample no.	GenBank accession No.		Country	References
		ITS	nLSU		
<i>Vararia gracilispora</i>	CBS:663.81	MH861411	-	Gabon	Vu <i>et al.</i> (2019)
<i>Vararia gracilispora</i>	CBS:664.81	MH861412	-	Gabon	Vu <i>et al.</i> (2019)
<i>Vararia insolita</i>	CBS:668.81	MH861413	-	France	Vu <i>et al.</i> (2019)
<i>Vararia intricata</i>	CBS:673.81	MH861418	-	France	Vu <i>et al.</i> (2019)
<i>Vararia investiens</i>	He 2104	-	MH669236	USA	Liu & He (2018)
<i>Vararia investiens</i>	FP 151122	MH971976	MH971977	USA	Liu & He (2018)
<i>Vararia investiens</i>	UC2023140	KP814286	-	USA	Rosenthal <i>et al.</i> (2017)
<i>Vararia isabellina</i>	CLZhao 22852*	OR048789	OR506350	China	Deng <i>et al.</i> (2024)
<i>Vararia isabellina</i>	CLZhao 22887	OR048788	OR506351	China	Deng <i>et al.</i> (2024)
<i>Vararia lacerata</i>	CLZhao 33407*	PQ811403	PV185851	China	Deng <i>et al.</i> (2026a)
<i>Vararia lacerata</i>	CLZhao 33510	PQ811404	PV185852	China	Deng <i>et al.</i> (2026a)
<i>Vararia lincangensis</i>	CLZhao 22791*	OR048819	OR506348	China	Deng <i>et al.</i> (2024)
<i>Vararia lincangensis</i>	CLZhao 22799	OR048818	OR506349	China	Deng <i>et al.</i> (2024)
<i>Vararia malaysiana</i>	CBS:644.84	MH873490	MH873490	Singapore	Vu <i>et al.</i> (2019)
<i>Vararia membaranacea</i>	CLZhao 35709	PV637445	PV637452	China	Deng <i>et al.</i> (2026a)
<i>Vararia membaranacea</i>	CLZhao 35710*	PV637446	PV637453	China	Deng <i>et al.</i> (2026a)
<i>Vararia minispora</i>	CBS:682.81	MH861426	-	France	Vu <i>et al.</i> (2019)
<i>Vararia muscicola</i>	CLZhao 21669*	PV147167	PV185854	China	Deng <i>et al.</i> (2026a)
<i>Vararia ochroleuca</i>	JS24400	AF506485	AF506485	Norway	Larsson & Larsson (2003)
<i>Vararia ochroleuca</i>	CBS:465.61	MH858109	-	France	Vu <i>et al.</i> (2019)
<i>Vararia parmastoi</i>	CBS:879.84	MH861852	MH861852	Uzbekistan	Vu <i>et al.</i> (2019)
<i>Vararia perplexa</i>	CBS:695.81	MH861438	-	France	Vu <i>et al.</i> (2019)
<i>Vararia pingbianensis</i>	CLZhao 25157	OR195737	OR510677	China	Deng <i>et al.</i> (2026a)
<i>Vararia pirispora</i>	CBS:720.86	MH862016	-	France	Vu <i>et al.</i> (2019)
<i>Vararia punctata</i>	CLZhao 22439*	OR048812	OR510675	China	Deng <i>et al.</i> (2024)
<i>Vararia rhombospora</i>	CBS:743.81	MH861470	-	France	Vu <i>et al.</i> (2019)
<i>Vararia rosulenta</i>	CBS:743.86	MH862028	-	France	Vu <i>et al.</i> (2019)
<i>Vararia rugosispora</i>	CBS:697.81	MH861440	-	Gabon	Vu <i>et al.</i> (2019)
<i>Vararia sigmatospora</i>	CBS:748.91	MH874001	MH874001	Netherlands	Vu <i>et al.</i> (2019)
<i>Vararia sigmatospora</i>	CBS:748.91	MH874001	MH874001	Netherlands	Vu <i>et al.</i> (2019)
<i>Vararia sinensis</i>	CLZhao 25160*	OR102494	OR510678	China	Deng <i>et al.</i> (2024)
<i>Vararia sinensis</i>	CLZhao 25161	OR102495	OR510679	China	Deng <i>et al.</i> (2024)
<i>Vararia sphaericospora</i>	He4847	MK625592	MK625521	China	Deng <i>et al.</i> (2026a)
<i>Vararia sphaericospora</i>	CBS:700.81	MH873185	MH873185	Gabon	Vu <i>et al.</i> (2019)
<i>Vararia subtropica</i>	CLZhao 10234	PX903765	-	China	Present study
<i>Vararia subtropica</i>	CLZhao 10792	PX903766	-	China	Present study
<i>Vararia subtropica</i>	CLZhao 15541	PX903767	-	China	Present study
<i>Vararia subtropica</i>	CLZhao 15544	PX903768	PX915433	China	Present study
<i>Vararia subtropica</i>	CLZhao 17652	OQ025221	PX915434	China	Present study
<i>Vararia subtropica</i>	CLZhao 17729	PX903769	-	China	Present study
<i>Vararia subtropica</i>	CLZhao 17741	PX903770	-	China	Present study
<i>Vararia subtropica</i>	CLZhao 17796*	OQ025222	PX915435	China	Present study
<i>Vararia subtropica</i>	CLZhao 17801	PX903771	PX915436	China	Present study
<i>Vararia subtropica</i>	CLZhao 17815	PX903772	PX915437	China	Present study
<i>Vararia subtropica</i>	CLZhao 17821	PX903773	-	China	Present study
<i>Vararia subtropica</i>	CLZhao 17943	PX903774	PX915438	China	Present study
<i>Vararia subtropica</i>	CLZhao 17990	PX903775	-	China	Present study

.....continued on the next page

TABLE 1. (Continued)

Species name	Sample no.	GenBank accession No.		Country	References
		ITS	nLSU		
<i>Vararia subtropica</i>	CLZhao 18054	PX903776	PX915439	China	Present study
<i>Vararia subtropica</i>	CLZhao 18293	PX903777	-	China	Present study
<i>Vararia subtropica</i>	CLZhao 18535	PX903778	-	China	Present study
<i>Vararia subtropica</i>	CLZhao 18749	PX903779	-	China	Present study
<i>Vararia subtropica</i>	CLZhao 18970	PX903780	-	China	Present study
<i>Vararia subtropica</i>	CLZhao 18971	PX903781	-	China	Present study
<i>Vararia subtropica</i>	CLZhao 19004	PX903782	-	China	Present study
<i>Vararia subtropica</i>	CLZhao 19062	PX903783	-	China	Present study
<i>Vararia subtropica</i>	CLZhao 19091	PX903784	-	China	Present study
<i>Vararia subtropica</i>	CLZhao 3237	OQ025220	-	China	Present study
<i>Vararia subtropica</i>	CLZhao 6218	PX903785	PX915440	China	Present study
<i>Vararia subtropica</i>	CLZhao 6219	PX903786	PX915441	China	Present study
<i>Vararia subtropica</i>	CLZhao 6239	PX903787	PX915442	China	Present study
<i>Vararia subtropica</i>	CLZhao 6271	PX903788	PX915443	China	Present study
<i>Vararia subtropica</i>	CLZhao 6274	PX903789	PX915444	China	Present study
<i>Vararia subtropica</i>	CLZhao 945	PX903790	PX915445	China	Present study
<i>Vararia subtropica</i>	CLZhao 9671	PX903791	-	China	Present study
<i>Vararia trinidadensis</i>	CBS:650.84	MH873495	MH873495	Madagascar	Vu <i>et al.</i> (2019)
<i>Vararia trinidadensis</i>	CBS:651.84	MH861803	-	Madagascar	Vu <i>et al.</i> (2019)
<i>Vararia tropica</i>	CBS 704.81	MH861447	MH873189	France	Vu <i>et al.</i> (2019)
<i>Vararia tuberculata</i>	CLZhao 42901	PX097879	PX072023	China	Wang <i>et al.</i> (2026)
<i>Vararia tuberculata</i>	CLZhao 42927	PX097880	PX072024	China	Wang <i>et al.</i> (2026)
<i>Vararia vassilievae</i>	UC2022892	KP814203	-	USA	Deng <i>et al.</i> (2026b)
<i>Vararia verrucosa</i>	CBS:706.81	MH861449	MH861449	France	Vu <i>et al.</i> (2019)
<i>Vararia wumengshanensis</i>	CLZhao 31659*	PQ811405	PV185853	China	Deng <i>et al.</i> (2026a)
<i>Vararia yaoshanensis</i>	CLZhao 20565	PP091675	PP091683	China	Deng <i>et al.</i> (2024)
<i>Vararia yaoshanensis</i>	CLZhao 20693*	PP091665	PP091684	China	Deng <i>et al.</i> (2024)

The sequences were aligned in MAFFT version 7 using the G-INS-i strategy (Katoh *et al.* 2019). The alignment was adjusted manually using AliView version 1.27 (Larsson 2014). The dataset was initially aligned, and later, ITS and LSU sequences were combined using Mesquite version 3.51. Maximum Likelihood analyses were performed using the CIPRES Science Gateway (<https://www.phylo.org/portal2/login!input.action>; Miller *et al.* 2012) based on the dataset using the RAxML-HPC BlackBox tool, with 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 1,000 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 in ACCESS v2.1.6 (Kalyaanamoorthy *et al.* 2017) using the Bayesian Information Criterion, and the model was used for Bayesian analysis. Four Markov chains were run from random starting trees. Trees were sampled every 1,000th generation. The first 25% of sampled trees were discarded as burn-in, while the remaining trees were used to construct a 50% majority consensus tree and to calculate Bayesian posterior probabilities (BPPs).

Phylogenetic trees were visualized and adjusted using FigTree v1.4.4 (<http://tree.bio.ed.ac.uk/software/figtree>), and the exports were edited using Adobe Illustrator CS6 software (Adobe Systems, USA). Branches of the consensus tree that received bootstrap support for Maximum Likelihood (ML) equal to or above 70%, and Bayesian Inference (BI) equal to or above 0.95, respectively.

Results

Phylogenetic analyses

The combined ITS+nLSU dataset (Figure 1) comprised sequences from 157 fungal specimens representing 87 taxa, and *Stereum hirsutum* (Willd.) Pers. and *S. ostrea* (Blume & T. Nees) Fr. were retrieved as the outgroup taxa (Deng *et al.* 2026a). A total of four Markov chains were run for two independent runs from random starting trees, each with 1,000,000 generations for the ITS+nLSU dataset, with trees and parameters sampled every 1000 generations. Maximum Likelihood (ML) and Bayesian Inference (BI) analyses yielded similar topologies, with an effective sample size (ESS) average ESS (avg. ESS) = 3015.7. Eight genera within Peniophoraceae (Russulales) formed well-separated clades in the phylogenetic tree inferred from ITS+LSU data, and *Vararia* in Peniophoraceae formed five branches, which is consistent with the results of the previous study by Wang *et al.* (2026). The new species *Vararia subtropica*, is nested within *Vararia* and sister to *V. daweishanensis* L. Zou & C.L. Zhao (2022: 14).

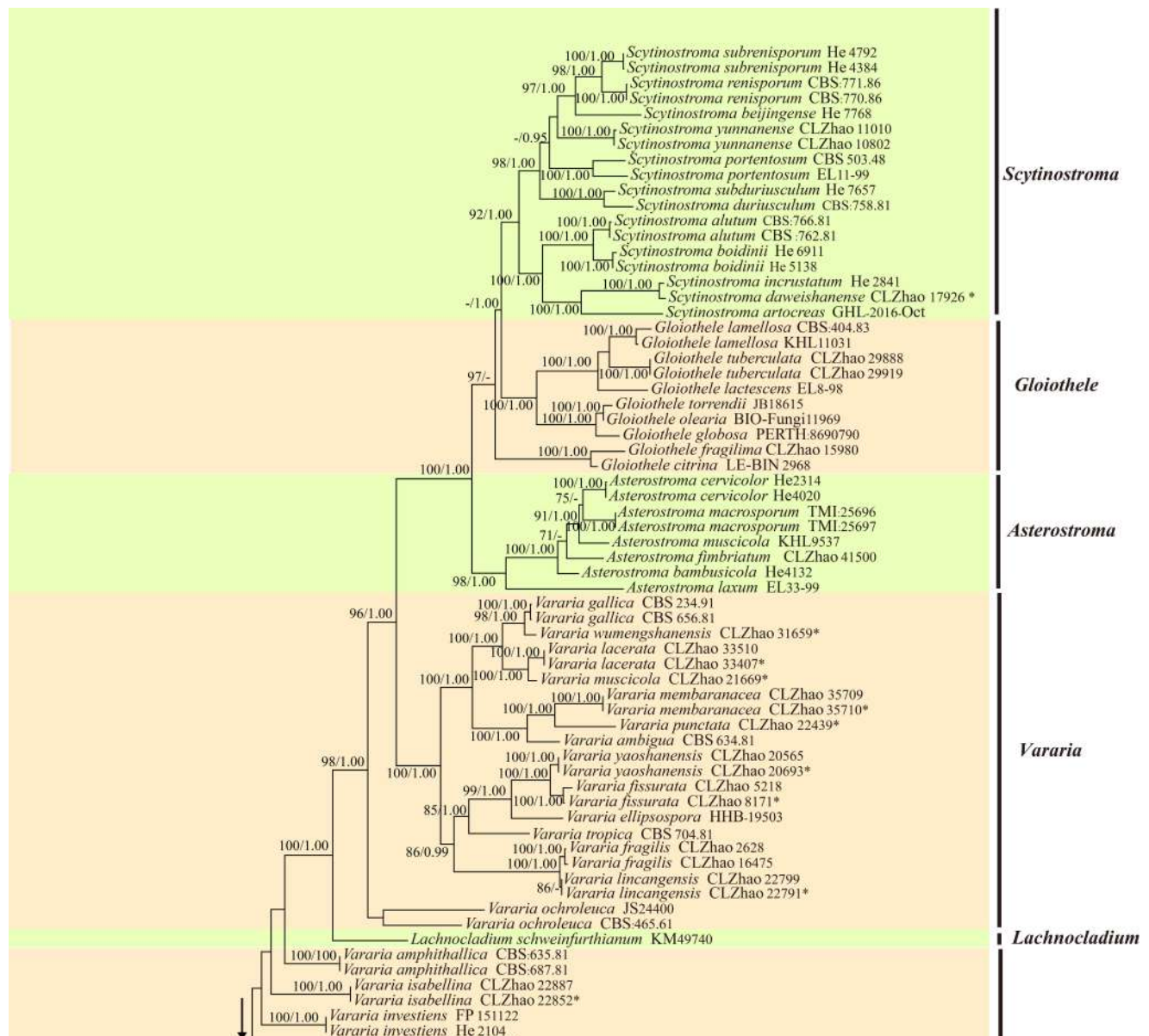


FIGURE 1. Maximum Likelihood tree illustrating phylogeny of the family Peniophoraceae and related species based on ITS and nLSU sequences. Branches are labeled with Maximum Likelihood Bootstrap values higher than 70% and Bayesian Posterior Probabilities more than 0.95, respectively. The new species is in bold, and type specimens are indicated with an asterisk (*).

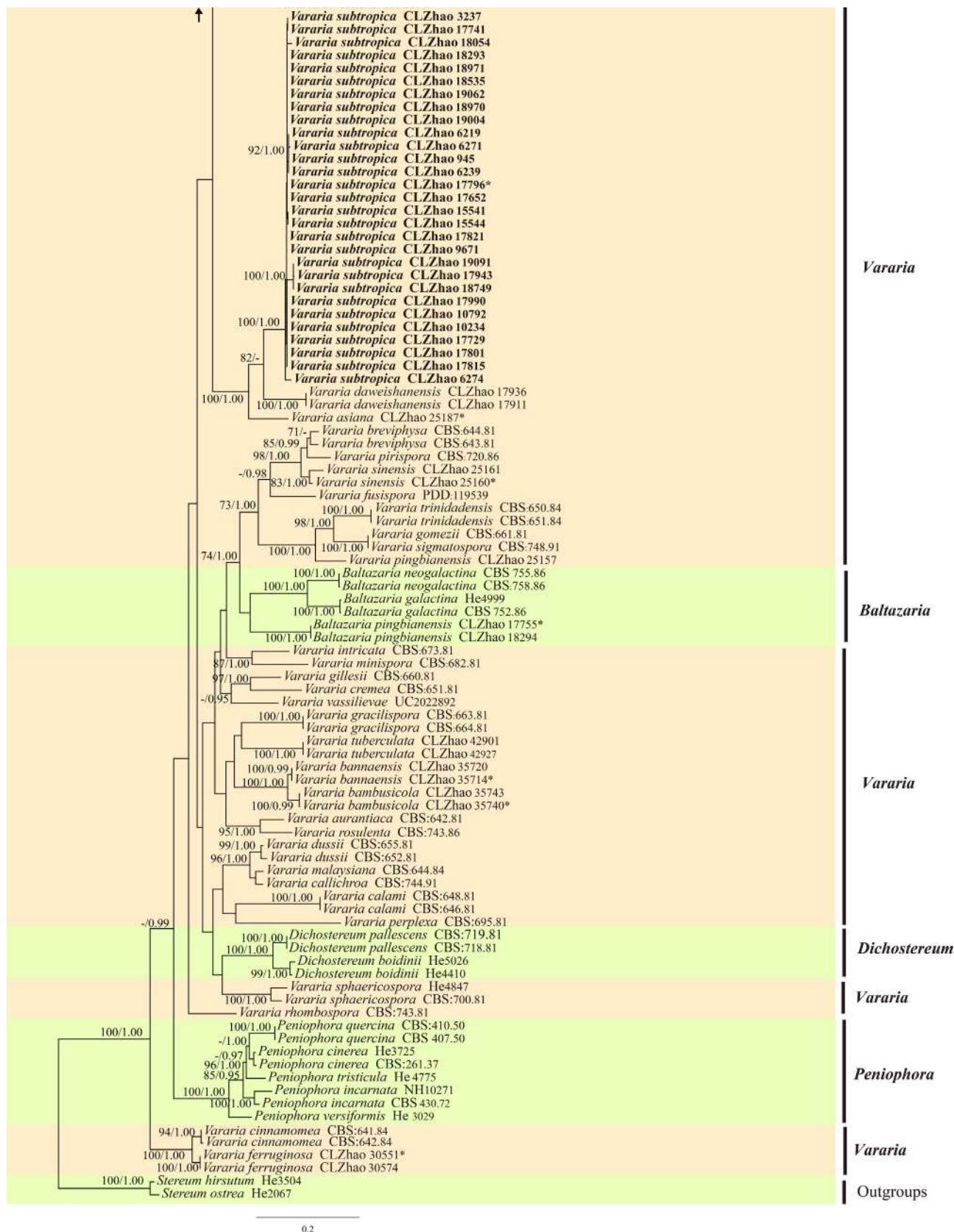


FIGURE 1. (Continued) Maximum Likelihood tree illustrating phylogeny of the family Peniophoraceae and related species based on ITS and nLSU sequences.

The combined ITS+nLSU dataset (Figure 2) included sequences from 108 fungal specimens representing 55 species, with *Peniophora incarnata* (Pers.) P. Karst. and *P. nuda* (Fr.) Bres. as the outgroups (Deng *et al.* 2024). A total of four markov chains were run for two independent runs from random starting trees, each with 280,000

generations for the ITS+nLSU dataset, with trees and parameters sampled every 1000 generations. The best model for the combined ITS+nLSU dataset, as estimated and applied in the Bayesian analysis, was TIM2+I+G. Maximum Likelihood (ML) and Bayesian Inference (BI) analyses yielded similar topologies, with an average standard deviation of split frequencies = 0.009934 (BI) and an effective sample size (ESS) average ESS (avg. ESS) = 1502.7. Phylogenetic analyses based on combined ITS+nLSU dataset (Figure 2), further confirmed that *Vararia subtropica* sp. nov. is sister to *V. dawweishanensis*.

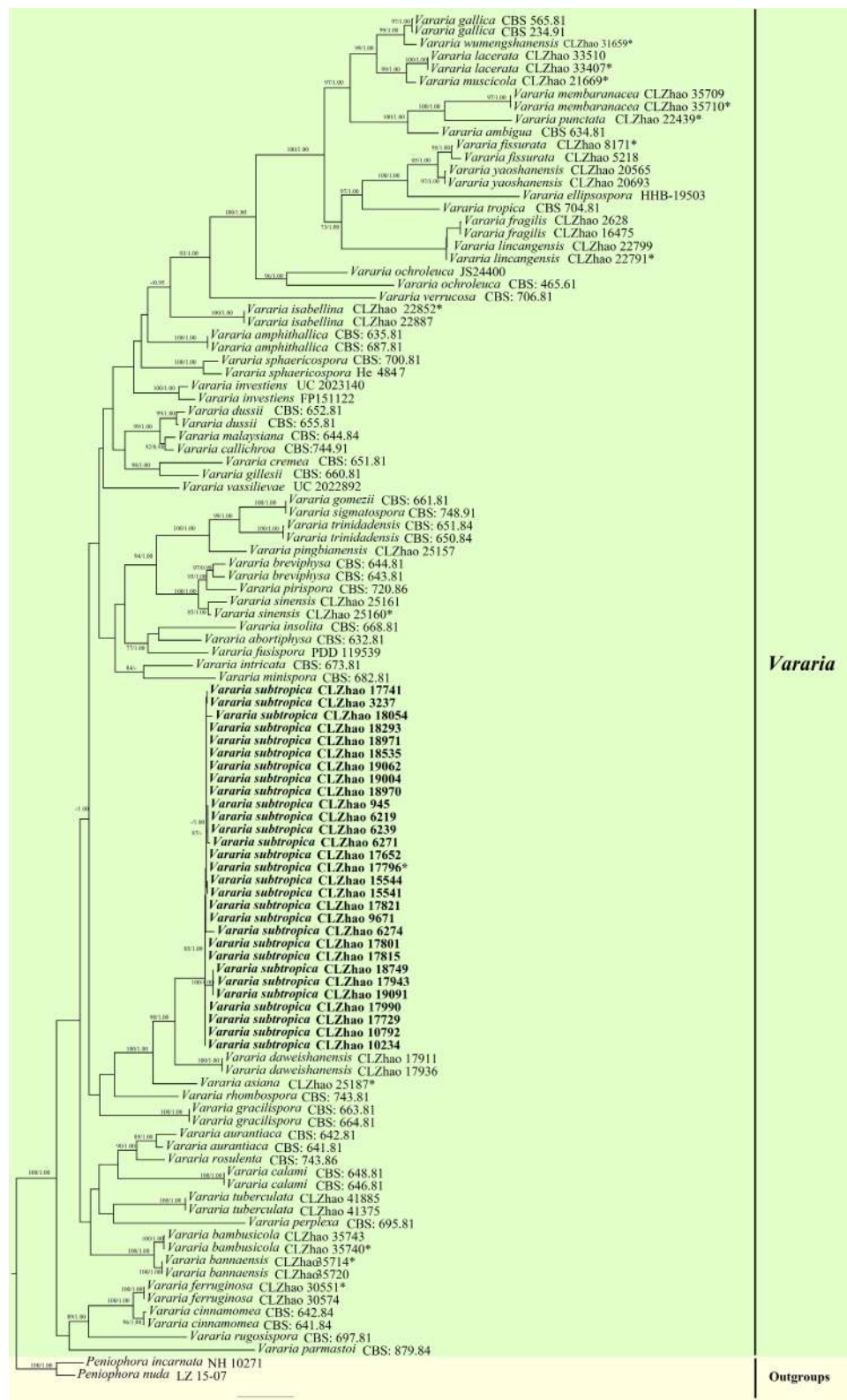


FIGURE 2. Maximum Likelihood tree illustrating phylogeny of genus *Vararia* and related species based on ITS and nLSU sequences. Branches are labeled with Maximum Likelihood Bootstrap values higher than 70% and Bayesian Posterior Probabilities more than 0.95, respectively. The new species is in bold, and type specimens are indicated with an asterisk (*).

Taxonomy

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

MycoBank No: MB 862039, Figures 3–5.

Etymology:—*Subtropica* (Lat.) refers to the species having a distribution in subtropical areas.

Holotype:—China, Yunnan Province, Honghe, Pingbian County, Daweishan National Nature Reserve, GPS coordinates 22°51' N, 103°41' E, elev. 2,360 m asl., on the fallen angiosperm branch, leg. C.L. Zhao, 1 August 2019, CLZhao 17796 (SWFC 00017796).

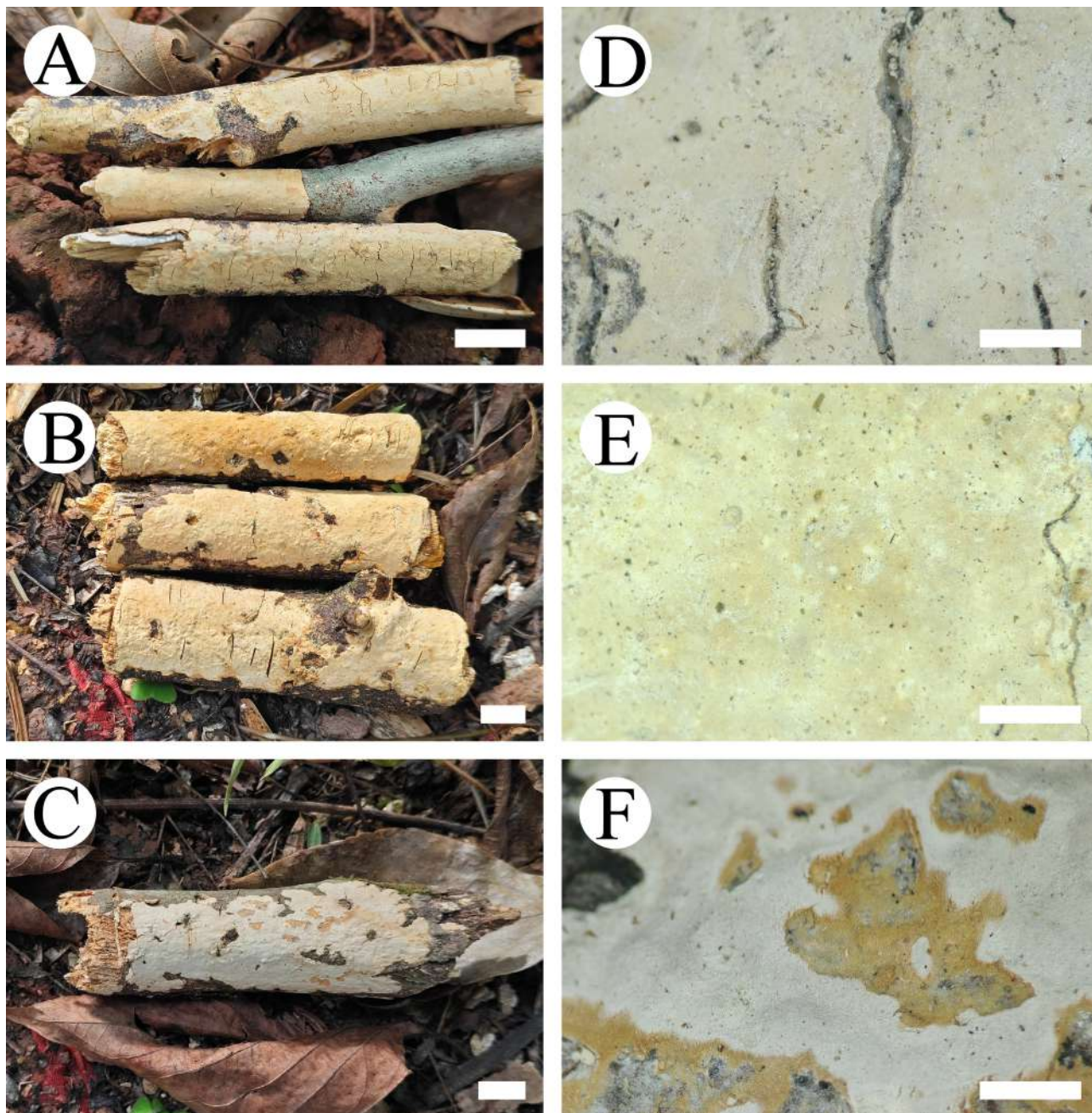


FIGURE 3. Basidiomata of *Vararia subtropica* (holotype, CLZhao 17796). **A–C** Basidiomata on the substrate. **D–F** Character hymenophore. Scale bars: **A–C** = 1 cm, **E–F** = 1 mm.

Diagnosis:—*Vararia subtropica* is characterized by the cream to buff hymenial surface, a dimittic hyphal system with generative hyphae with clamp connections, and cylindrical, slightly curved to allantoid basidiospores ($7.1\text{--}11.3 \times 2.7\text{--}5.2 \mu\text{m}$).

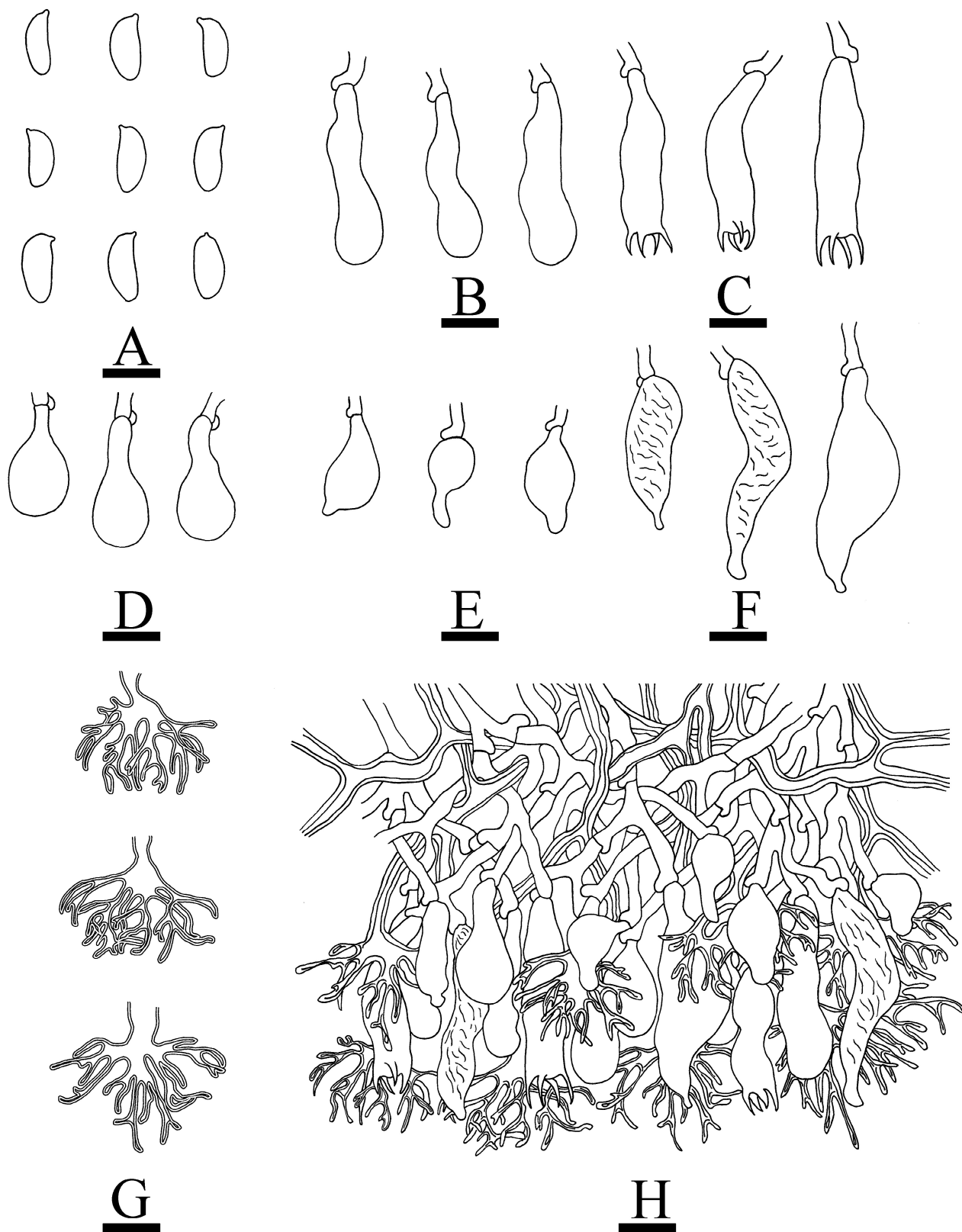


FIGURE 4. Microscopic structures of *Vararia subtropica* (holotype, CLZhao 17796). **A** Basidiospores. **B** Basidioles. **C** Basidia. **D** Clavate cystidia. **E** Urniform cystidia. **F** Fusiform gloeocystidia. **G** Dichohyphae. **H** A section of the hymenium. Scale bars: **A–H** = 10 μ m.

Basidiomata:—Annual, resupinate, cracked, coriaceous, without odor or taste when fresh, up to 5 cm long, 1.5 cm wide, and 150 μ m thick at the center. Hymenial surface smooth, cream to buff when fresh, buff upon drying. Sterile margin white, thinning out, up to 2 mm wide.

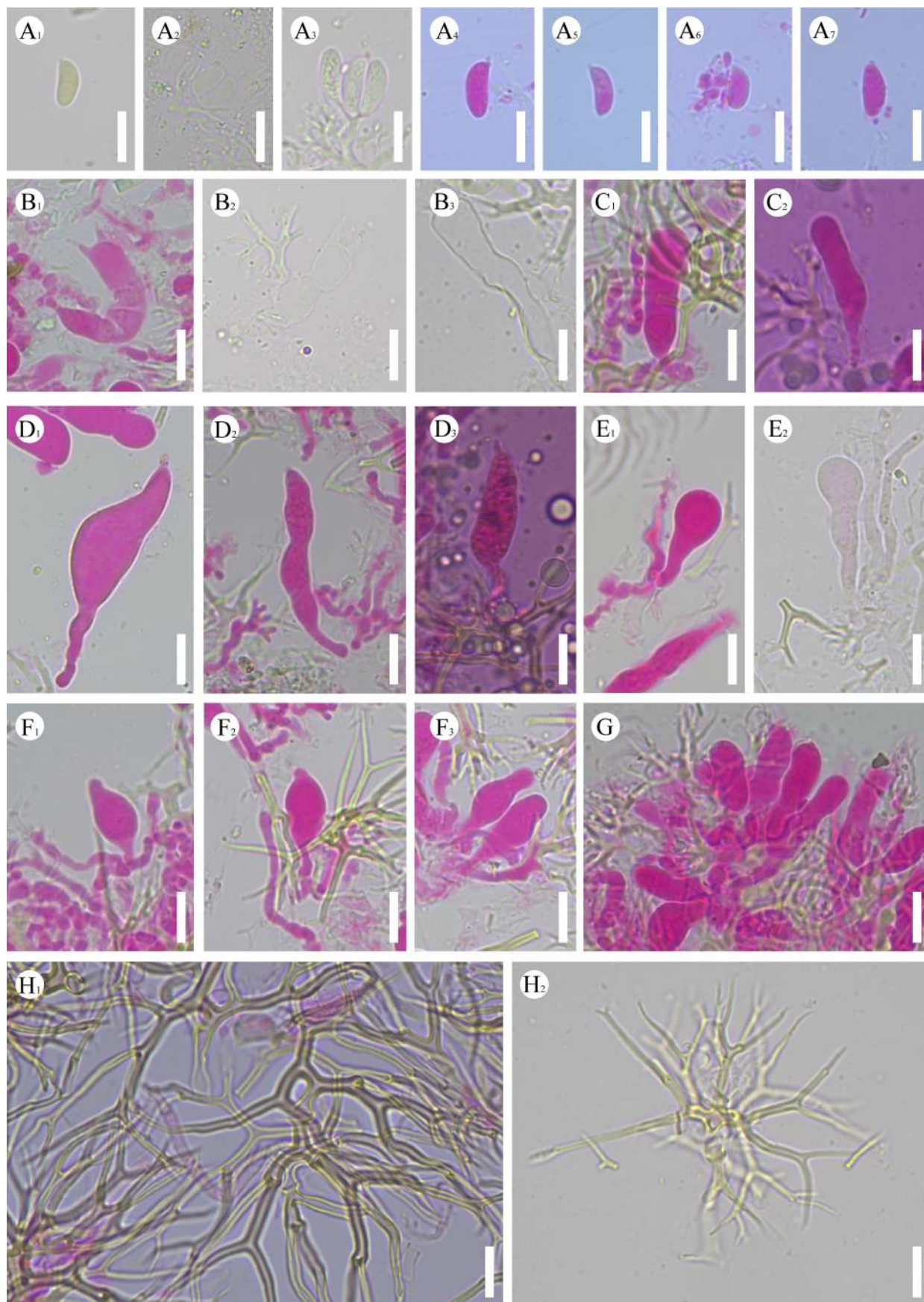


FIGURE 5. Microscopic structures of *Vararia subtropica* (holotype, CLZhao 17796). **A₁–A₇** Basidiospores. **B₁–B₃** Basidia. **C₁, C₂** Basidioles. **D₁–D₃** Fusiform gloecystidia. **E₁, E₂** Clavate cystidia. **F₁–F₃** Urniform cystidia. **G** A section of the hymenium. **H₁, H₂** Skeletal hyphae. Scale bars: **A–H** = 10 μ m.

Hyphal system:—Dimitic; generative hyphae with clamp connections, colorless, thin-walled, smooth, rarely branched, interwoven, 1–2.5 µm in diameter, CB–, IKI–; tissues unchanged in KOH. Skeletal hyphae colorless, smooth, 1.5–2.5 µm in diameter, extremely thick-walled. Dichohyphae predominant, yellowish, capillary, frequently branched, thick-walled, dichotomously to irregularly branched with main branches and acute tips, weakly to moderately dextrinoid in Melzer’s reagent, CB–. Gloeocystidia three types: 1) globose to clavate, colorless, thin-walled, smooth, 11–25 × 4.5–9 µm; 2) urniform, colorless, thin-walled, smooth, 12.5–22 × 3–8.5 µm; 3) fusiform, colorless, thin-walled, smooth, filled with some refractive matter, with a shizopapilla in the apical part, 19–50.5 × 5–12.5 µm. Basidia subcylindrical, flexuous, with four sterigmata and a basal clamp connection, colorless, thin-walled, smooth, 14–34 × 3–9 µm; basidioles numerous, in shape similar to basidia but smaller.

Spores:—Basidiospores cylindrical, slightly curved to allantoid, colorless, thin-walled, smooth, CB–, (6.5–)7.1–11.3(–11.8) × (2.3–)2.7–5.2(–5.6) µm, L = 9.30 µm, W = 3.92 µm, Q = 2.18–2.61 (n = 600/30).

Material examined specimens (paratypes):—China, Yunnan Province, Yuxi, Xiping County, Mopanshan National Forestry Park, GPS coordinates 23°51' N, 101°16' E, elev. 1,700 m asl., on the fallen angiosperm branch, leg. C.L. Zhao, 17 January 2017, CLZhao 945 (SWFC 00000945); on the angiosperm trunk, 18 January 2018, CLZhao 6218 (SWFC 00006218), on the fallen angiosperm branch, CLZhao 6219 (SWFC 00006219), CLZhao 6239 (SWFC 00006239), CLZhao 6271 (SWFC 00006271); Pu'er, Laoyang River National Forest Park, GPS coordinates 101°09' N, 22°60' E, elev. 1,200 m asl., on the fallen angiosperm branch, leg. C.L. Zhao, 30 September 2017, CLZhao 3237 (SWFC 00003237); Jingdong County, Wuliangshan National Nature Reserve, GPS coordinates 24°46' N, 100°58' E, elev. 2,500 m asl., on the fallen angiosperm branch, leg. C.L. Zhao, 6 January 2019, CLZhao 9671 (SWFC 00009671); Dali, Nanjian County, Lingbaoshan, GPS coordinates 24°76' N, 100°50' E, elev. 2,500 m asl., on the fallen angiosperm branch, leg. C.L. Zhao, 9 January 2019, CLZhao 10234 (SWFC 00010234); Wenshan, Xichou County, Xiaoqiaogou, National Nature Reserve, GPS coordinates 23°22' N, 104°45' E, elev. 2,500 m asl., on the fallen angiosperm branch, leg. C.L. Zhao, 14 January 2019, CLZhao 10792 (SWFC 00010792), on the fallen branch of *Quercus*, 21 July 2019, CLZhao 15541 (SWFC 00015541), on the angiosperm stump, 21 July 2019, CLZhao 15544 (SWFC 00015544); Honghe, Pingbian County, Daweishan National Nature Reserve, GPS coordinates 22°51' N, 103°41' E, elev. 2,360 m asl., on the fallen angiosperm branch, leg. C.L. Zhao, 1 August 2019, CLZhao 17652 (SWFC 00017652), CLZhao 17729 (SWFC 00017729), CLZhao 17741 (SWFC 00017741), CLZhao 17801 (SWFC 00017801), CLZhao 17815 (SWFC 00017815), CLZhao 17821 (SWFC 00017821), CLZhao 17943 (SWFC 00017943), 2 August 2019, CLZhao 17990 (SWFC 00017990), 17 April 2015, CLZhao 18054 (SWFC 00018054), 3 August 2019, CLZhao 18293 (SWFC 00018293), CLZhao 18535 (SWFC 00018535), 7 June 2020, CLZhao 18749 (SWFC 00018749), CLZhao 18751 (SWFC 00018751), on the angiosperm trunk, CLZhao 18970 (SWFC 00018970), on the fallen angiosperm branch, CLZhao 18971 (SWFC 00018971), on the angiosperm trunk, CLZhao 19004 (SWFC 00019004), on the fallen angiosperm branch, CLZhao 19062 (SWFC 00019062), CLZhao 19091 (SWFC 00019091).

Discussion

Phylogenetically, recent molecular studies of Peniophoraceae using concatenated ITS and nLSU sequences from global sampling have shown that *Vararia* species are distributed across multiple clades (Zou *et al.* 2022, Deng & Zhao 2023, Deng *et al.* 2026a, Wang *et al.* 2026). In the present study, the topology based on ITS+nLSU sequences (Figures 1, 2) revealed that *V. subtropica* formed a lineage and was a sister to *V. daweishanensis*. However, *V. daweishanensis* can be delimited from *V. subtropica* by its thin- to thick-walled generative hyphae, subcylindrical to elliptical to ovoid gloeocystidia, and longer basidiospores (9–13 × 3.5–5 µm vs. 7.1–11.3 × 2.7–5.2 µm, Zou *et al.* 2022).

Morphologically, *Vararia subtropica* resembles *V. amphithallica* Boidin *et al.*, *V. bispora* S.L. Liu & S.H. He, *V. fissurata* Y.L. Deng & C.L. Zhao, *V. investiens* (Schwein.) P. Karst., *V. montana* S.L. Liu & S.H. He and *V. sphaericospora* Gilb. possess generative hyphae with clamp connections. However, *V. amphithallica* is distinguished from *V. subtropica* by its basidia with 2 sterigmata and longer basidiospores (12–17 × 4.5–5.5 µm vs. 7.1–11.3 × 2.7–5.2 µm), slightly thick-walled, subglobose, subcylindrical or gradually narrower gloeocystidia (Boidin *et al.* 1980). *Vararia bispora* differentiates from *V. subtropica* by its basidia with 2 sterigmata and larger fusiform to cylindrical basidiospores (18–22 × 6–7.2 µm vs. 7.1–11.3 × 2.7–5.2 µm, Liu & He 2016). *Vararia fissurata* differs from *V. subtropica* due to its shorter basidia (20–27 × 4–8 µm vs. 29–56 × 5.5–10 µm), and ellipsoid to broadly ellipsoid basidiospores (5–10 × 3–7 µm vs. 7.1–11.3 × 2.7–5.2 µm, Deng *et al.* 2024). *Vararia investiens* is distinct from *V. subtropica* by its longer fusiform gloeocystidia (40–80 × 4–8 µm vs. 19–50.5 × 5–12.5 µm), longer fusiform basidia (30–50 × 4–5 µm vs. 14–34 × 3–9 µm, Boidin & Lanquetin 1975). In addition, *V. montana* differentiates from *V. subtropica* by having longer

clavate gloeocystidia (50–100 × 4–9 µm vs. 19–50.5 × 5–12.5 µm), both larger clavate basidia (70–110 × 10–16 µm vs. 29–56 × 5.5–10 µm), and broadly ellipsoid basidiospores (12–16 × 9.5–13 µm vs. 7.1–11.3 × 2.7–5.2 µm, Liu & He 2016). Moreover, *V. sphaericospora* can be distinguished from *V. subtropica* by longer subcylindric to fusiform gloeocystidia (48–80 × 7–11 µm vs. 19–50.5 × 5–12.5 µm), and wider basidiospores (8–10 × 7.5–8.5 µm vs. 7.1–11.3 × 2.7–5.2 µm, Gilbertson 1965).

Wood-inhabiting fungi represent an ecologically important branch of the fungal tree of life and exhibit diverse functional traits (Hibbett *et al.* 2025, Zhao *et al.* 2025). Given their ecological roles and potential value, improved documentation of fungal diversity is increasingly urgent for both conservation and future utilization (Wang *et al.* 2024, 2025, Liu *et al.* 2025, Wijesinghe *et al.* 2025, Zhao *et al.* 2026). To date, 27 *Vararia* species have been reported from China, including those newly described in the present study and other species described in recent studies. This paper refines our understanding of species diversity within *Vararia*, and continued field surveys coupled with multi-locus phylogenetic analyses will likely reveal additional taxa.

Acknowledgements

The research was supported by the China Scholarship Council (CSC) from Ministry of Education of China (Project No. 202407850024), the Forestry and Grass Science and Technology Innovation Joint Project of Yunnan Province (Project No. 202404CB090008), Yunnan Province Graduate Supervisor Team Project-Taxonomy and phylogeny of forest edible and medicinal fungi in Yunnan province (Changlin Zhao team: 503260614), the Science Foundation of Education Department of Yunnan Province (2025Y0845), Science and Technology Projects of Yunnan Universities Serving Key Industries (FWCY-BSPY2025093), and Southwest Forestry University Graduate Research Innovation Fund Project (YJS-KCJJ-2025-03).

Author contributions

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

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