

Phytotaxa

ISSN 1179-3113 print edition
ISSN 1179-3121 online edition



Vol. 100 Number 1 2015

Published by
 Magnolia Press, Auckland, New Zealand



Lamiaceae in Parque Estadual do Juquery (PEJY), Southeast Brazil

THAÍS TEIXEIRA CONEIRO, CARLA POLESSELI BRUNIERA

Published: 2025-11-25

DOI: [10.11646/phytotaxa.731.1.1](https://doi.org/10.11646/phytotaxa.731.1.1)

Page range: 1-23

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The occurrence of Scandinavian *Hieracium oistophyllum* (Asteraceae) in Central Europe confirmed by morphological, cytogenetic and molecular evidence

ALEKSANDRA GRABOWSKA-JOACHIMIAK, GRZEGOŹ GÓRAŁSKI, DAGMARA KWOLEK, ZBIGNIEW SZELĄG

Published: 2025-11-25

DOI: [10.11646/phytotaxa.731.1.2](https://doi.org/10.11646/phytotaxa.731.1.2)

Page range: 24-34

Abstract views: 101

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Rediscovery of *Clematis liboensis* (Ranunculaceae) from southeastern Guizhou, China, an imperfectly known species previously known only from its type material, with a geographical extension and an amended description

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Published: 2025-11-25

DOI: [10.11646/phytotaxa.731.1.3](https://doi.org/10.11646/phytotaxa.731.1.3)

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Molecular phylogeny and morphology reveal a new wood-inhabiting fungal species, *Stereum tongbiguanense* (Stereaceae, Russulales) from China

MENG CHEN, YINGLIAN DENG, KAISHENG WANG, YONGGAO ZHU, RONGCONG YANG, SHIHUI ZHANG, QIDONG SU, CHANGLIN ZHAO

Published: 2025-11-25

DOI: [10.11646/phytotaxa.731.1.4](https://doi.org/10.11646/phytotaxa.731.1.4)

Page range: 51-66

Abstract views: 90

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Published: 2025-11-25

DOI: [10.11646/phytotaxa.751.1.5](https://doi.org/10.11646/phytotaxa.751.1.5)

Page range: 67-77

Abstract views: 67

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Notes about *Basella alba* (Basellaceae) with description of a new variety from West Bengal (India)

SAUBHIK DAS

Published: 2025-11-25

DOI: [10.11646/phytotaxa.751.1.6](https://doi.org/10.11646/phytotaxa.751.1.6)

Page range: 78-86

Abstract views: 102

PDF downloaded: 6

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Mitreola sinhoensis (Loganiaceae), a new species from northwestern Vietnam

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Published: 2025-11-25

DOI: [10.11646/phytotaxa.751.1.7](https://doi.org/10.11646/phytotaxa.751.1.7)

Page range: 87-95

Abstract views: 74

PDF downloaded: 11

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Molecular phylogeny and morphology reveal a new wood-inhabiting fungal species, *Stereum tongbiguanense* (Stereaceae, Russulales) from China

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Abstract

Taxonomy plays a central role in understanding the diversity of life, translating the products of biological exploration and discovery (specimens and observations) into systems of names that establish a “classification home” for taxa. In this study, a new species, *Stereum tongbiguanense*, is proposed based on the morphological features and molecular evidence. The new species is characterized by coriaceous basidiomata with smooth, white to cream hymenial surface, a dimitic hyphal system with generative hyphae bearing simple septa, and allantoid basidiospores measuring $5.4\text{--}6.8 \times 2.5\text{--}3.5\ \mu\text{m}$. The phylogenetic tree inferred from ITS+nLSU sequences reveals that *S. tongbiguanense* is nested within the family Stereaceae of the order Russulales, forms a sister lineage with *S. tropicum*, and is also closely related to *S. insigne*. A full description, illustrations, and phylogenetic analysis results of the new species are provided.

Key words: Basidiomycota, Classification, Molecular systematics, New Taxon, Wood-inhabiting fungi, Yunnan Province

Introduction

Fungi are crucial components of life on Earth with essential ecological and economic impacts (Wu *et al.* 2016, 2019, Hyde *et al.* 2024, Yang *et al.* 2025). Their interactions with other organisms significantly contribute to the proper functioning of terrestrial ecosystems, and previous studies indicated that they have promoted the evolution of many terrestrial clades (Berbee *et al.* 2017, Loron *et al.* 2019, Gan *et al.* 2021, Yuan *et al.* 2023, Zhao *et al.* 2023a, 2024, Hyde *et al.* 2024, Wang *et al.* 2025).

The phylum Basidiomycota R.T. Moore (1980: 371) is one of the major branches of the fungal tree of life (Dai 2010, Vainio *et al.* 2011, Tedersoo *et al.* 2021, Baldrian *et al.* 2022, He *et al.* 2022, Niskanen *et al.* 2023, Liu *et al.* 2025). The Russulales Kreisel ex P.M. Kirk, P.F. Cannon & J.C. David. (2001) is one of the major lineages of Basidiomycota, which is morphologically the most diverse order, containing a remarkable variety of basidiomata forms, including resupinate, discoid, effused-reflexed, clavarioid, pileate, or gasteroid and hymenophore configurations from smooth, poroid, hydroid, lamellate, to labyrinthoid. Functionally, these fungi are primarily saprotrophs, as well as ectomycorrhizal, root parasites, and insect symbionts (Miller *et al.* 2006, Cui *et al.* 2018, 2019, Wu *et al.* 2020, Qin *et al.* 2025, Xu *et al.* 2025, Zhou *et al.* 2025).

The family Stereaceae Pilát (1930: 34), belonging to the Russulales, is typified by *Stereum* Hill ex Pers. (1974: 110). So far, the family contains only corticioid and stereoid wood-inhabiting fungi with smooth or occasionally tuberculate or merulioid hymenophores. Micromorphologically, all species in the family possess gloeocystidia (skeletocystidia in *Stereum*) and amyloid basidiospores with smooth or ornamented walls (Larsson & Larsson 2003, Bernicchia & Gorjón 2010, Xu *et al.* 2025). Stereaceae formed a well-supported monophyletic clade within Russulales, causing white rot (or white pocket rot in some species) on both conifers and hardwoods (Eriksson *et al.* 1984, Xu *et al.* 2025). Up to now, the family includes 21 genera, among them, *Stereum* and *Xylobolus* P. Karst. (1881: 11) are considered to be closely related genera that form the core of the family Stereaceae Pilát, which share pseudocystidia, but the latter have shorter, more ellipsoid basidiospores. Furthermore, *Xylobolus* has a brown context and a dense zone separating the context from a usually brown tomentum (Ghobad-Nejhad *et al.* 2025).

The genus *Stereum* (Stereaceae, Russulales) was established by Hill ex Pers. (1794), typified by *S. hirsutum* (Willd.) Pers. It is characterized by annual to perennial, resupinate, effuse-reflexed to pileate basidiomata, hyphal system dimitic; generative hyphae simple-septate, thin- to thick-walled; present skeletocystidia, acutocystidia, acanthocystidia; clavate to tubular basidia with 4-sterigmata; ellipsoid to cylindrical, amyloid basidiospores (Persoon 1794, Xu *et al.* 2025). According to the MycoBank database (<http://www.mycobank.org>, accessed on 12 August 2025) and the Index Fungorum (<http://www.indexfungorum.org>, accessed on 12 August 2025), 730 names of *Stereum* have been registered, of which 234 names are legitimate because many species have been moved to other genera (Larsson & Larsson 2003, Miller *et al.* 2006, Larsson 2007, Vu *et al.* 2019; He *et al.* 2024, Wang *et al.* 2025a, Xu *et al.* 2025).

During investigations of wood-inhabiting fungi, we collected five specimens morphologically according to *Stereum* Russulales in Yunnan Province, China, which did not match any known species. We conducted morphological and molecular analyses using the ITS and nLSU DNA markers, and our results support the proposal of a new species, *Stereum tongbiguanense*.

Materials and methods

Morphological studies

Fresh basidiomata of fungus growing on angiosperm branches in Dehong, Yunnan Province, China, were photographed *in situ*. After the collection information was recorded (Rathnayaka *et al.* 2024), the specimens were taken to the laboratory and dried in an electric food dehydrator at 50 °C (Itu *et al.* 2022, Dong *et al.* 2024). The dried specimens were sealed in an envelope bag, stored, and deposited in the herbarium of Southwest Forestry University (SWFC), Kunming, Yunnan Province, P.R. China. The macro-morphological descriptions were based on field notes and photos taken in the field and in the lab. The color terminology followed Petersen (1996) and was confirmed in general terms according to the CMYK color code (Deep White Printing Team 2022).

The micro-morphological data were obtained from dried specimens observed under a light microscope, following the method described by Zhao *et al.* (2023b). The following abbreviations were used: KOH = 5% potassium hydroxide water solution, CB = Cotton Blue, CB- = acyanophilous, IKI = Melzer's reagent, L = mean spores' length (arithmetic average for all spores), W = mean spores' 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), Q = the average of Q (arithmetic average for all spores).

Molecular procedures and phylogenetic analyses

The CTAB rapid plant genome extraction kit-DN14 (Aidlab Biotechnologies Co., Ltd., Beijing, China) was used to obtain genomic DNA from the dried specimens following the manufacturer's instructions (Dong *et al.* 2024, Wang *et al.* 2024, Yang *et al.* 2025). The nuclear ribosomal internal transcribed spacer (ITS) region was amplified using the primer pair ITS5/ITS4 (White *et al.* 1990), and the nuclear large subunit (nLSU) region was amplified with the primer pair LR0R/LR7 (Vilgalys & 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, 58 °C for 45 s, and 72 °C for 1 min, and a final extension of 72 °C for 10 min. The PCR procedure for nLSU was as follows: initial denaturation at 94 °C for 1 min, followed by 35 cycles of denaturation at 94 °C for 30 s, annealing at 48 °C for 1 min, extension at 72 °C for 1.5 min, and a final extension at 72 °C for 10 min. The PCR products were purified and sequenced at Kunming Tsingke Biological Technology Limited Company (Yunnan Province, P.R. China). All of the newly generated sequences were deposited in GenBank (Table 1).

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

Species name	Sample no.	Country	GenBank accession numbers		References
			ITS	nLSU	
<i>Acanthobasidium bambusicola</i>	He2357	China	KU559343	KU574833	Dai & He 2016
<i>Ac. delicatum</i>	CBS 233.86	France	-	MH873638	Vu <i>et al.</i> 2018
<i>Ac. norvegicum</i>	T623	France	-	AY039328	Wu <i>et al.</i> 2001
<i>Ac. quila</i>	SPG3088	Chile	MT831059	-	Rajchenberg <i>et al.</i> 2021
<i>Ac. weirii</i>	HHB13132	Italy	KX306882	-	Dai <i>et al.</i> 2017a
<i>Ac. weirii</i>	HHB13499	Canada	KX306883	-	Dai <i>et al.</i> 2017a
<i>Acanthofungus rimosus</i>	Wu9601-1	China	MF043521	AY039333	Wu <i>et al.</i> 2019a
<i>Aleurocystidiellum bernicchia</i>	MR12636	Chile	MT831037	MT831017	Rajchenberg <i>et al.</i> 2021
<i>Al. subcruentatum</i>	He2886	China	KU559341	KU574847	Dai & He 2016
<i>Aleurobotrys botryosus</i>	He2712	China	KX306877	KY450788	Dai <i>et al.</i> 2017b
<i>As. botryosus</i>	DAOM211598	Canada	AF506398	AF506398	Larsson & Larsson 2003
<i>Aleurodiscus amorphus</i>	Hc4937	China	MW533080	MW528916	Xu <i>et al.</i> 2025
<i>A. amorphus</i>	HHB15282	USA	-	AY039312	Wu <i>et al.</i> 2001
<i>A. effusus</i>	Hc2261	China	KU559344	KU574834	Dai & Hc 2016
<i>A. fujii</i>	Hc2919	China	-	KU574846	Dai & Hc 2016
<i>A. fujii</i>	Hc2921	China	KC505571	KU574845	Dai & Hc 2016
<i>A. gigasporus</i>	He2865	China	MW533081	MW528917	Xu <i>et al.</i> 2025
<i>A. gigasporus</i>	Wu0108-15	China	KY706205	KY706213	Dai & He 2017
<i>A. grantii</i>	T569	USA	-	AY039326	Wu <i>et al.</i> 2001
<i>A. grantii</i>	Hc2895	China	KU559347	KU574837	Dai & Hc 2016
<i>A. penicillatus</i>	T322	Canada	-	AY039315	Wu <i>et al.</i> 2001
<i>A. pinicola</i>	Wu1106-16	China	MF043524	MF043529	Wu <i>et al.</i> 2019a
<i>A. pinicola</i>	Wu1308-54	China	MF043525	MF043530	Wu <i>et al.</i> 2019a
<i>A. subroseus</i>	Hc4807	China	M11109054	M11109048	Tian <i>et al.</i> 2018
<i>A. wakefieldiae</i>	Hc2579	China	KU559355	KU574843	Dai & Hc 2016
<i>Conferticium ochraceum</i>	He2900	China	KY860409	KY860467	Liu 2017
<i>Cm. ochraceum</i>	He2932	China	KY860411	KY860470	Liu 2017
<i>Cm. subtropicum</i>	He1827*	China	KY860405	KY860463	Liu 2017
<i>Cm. subtropicum</i>	Hc1804	China	KY860404	MW528922	Xu <i>et al.</i> 2025
<i>Confertotrama macrospora</i>	Wu9202-21*	China	AF506377	AF506377	Larsson & Larsson 2003
<i>Ca. rajchenbergii</i>	NH16358	Chile	JQ716940	-	Gorjón & Hallenberg 2013
<i>Ca. rugulosa</i>	He5997	China	-	MW528924	Xu <i>et al.</i> 2025
<i>Ca. rugulosa</i>	He3427	China	MW533086	MW528925	Xu <i>et al.</i> 2025

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TABLE 1. (Continued)

Species name	Sample no.	Country	GenBank accession numbers		References
			ITS	nLSU	
<i>Gelatinostereum phlebioides</i>	He1951	China	MW533097	MW528943	Xu <i>et al.</i> 2025
<i>Gm. phlebioides</i>	Dai14965*	China		MW528940	Xu <i>et al.</i> 2025
<i>Gloeocystidiopsis heimii</i>	He5830	Sri Lanka	MW533085	MW528921	Xu <i>et al.</i> 2025
<i>Gs. heimii</i>	CBS 321.66	Central African Republic	AF506381	AF506381	Larsson & Larsson 2003
<i>Gs. ravum</i>	NH13291	Estonia	AF506382	AF506382	Larsson & Larsson 2003
<i>Gs. ravum</i>	CBS 125849	Estonia	MH863805	MH875269	Vu <i>et al.</i> 2018
<i>Gs. shenghuai</i>	He5411*	China	MW533083	MW528919	Xu <i>et al.</i> 2025
<i>Gs. tenuissimus</i>	He4816	China	-	MW528923	Xu <i>et al.</i> 2025
<i>Gs. tenuissimus</i>	He3575*	China	KX306880	KY706214	Dai <i>et al.</i> 2017a
<i>Gloeomyces bambusinus</i>	He4263	China	KY706208	KY706218	Tian <i>et al.</i> 2018
<i>G. bicornis</i>	Wu1308-101	China	LC433893	LC433900	Wu <i>et al.</i> 2022
<i>G. bicornis</i>	Wu1308-125*	China	LC433899	LC433906	Wu <i>et al.</i> 2022
<i>G. cerussatum</i>	EL25-97	Spain	AF506401	AF506401	Larsson & Larsson 2003
<i>G. dextrinoideophyses</i>	He4078*	Thailand	-	KY450783	Dai <i>et al.</i> 2017b
<i>G. formosanus</i>	Chen2736*	China	LC433894	LC433901	Wu <i>et al.</i> 2022
<i>G. formosanus</i>	Chen2748	China	LC433895	LC433902	Wu <i>et al.</i> 2022
<i>G. graminicola</i>	He2606	China	KY860401	KY860459	Liu 2017
<i>G. parvisporus</i>	Wu1307-84	China	LC433897	LC433904	Wu <i>et al.</i> 2022
<i>G. parvisporus</i>	Wu1307-88	China	LC433898	LC433905	Wu <i>et al.</i> 2022
<i>G. persicus</i>	Ghobad-Nejhad3173*	China	KU213590	KU213591	Ghobad-Nejhad & Langer 2018
<i>G. subcerussatus</i>	He6964	China	MW533099	MW528948	Xu <i>et al.</i> 2025
<i>G. subcerussatus</i>	Ghobad-Nejhad2360*	China	MI1109051	MI1109045	Tian <i>et al.</i> 2018
<i>G. thailandicus</i>	He5307	China	MW533082	MW528918	Xu <i>et al.</i> 2025
<i>G. thoenii</i>	CBS 236.86	Netherlands	MH861950	MH873640	Vu <i>et al.</i> 2018
<i>G. tropicus</i>	He3830*	China	KX553875	KX578720	Dai <i>et al.</i> 2017a
<i>Gloeosoma decorticans</i>	MR12666	Chile	MT831041	MT831021	Rajchenberg <i>et al.</i> 2021
<i>Ga. decorticans</i>	MR12665	Chile	MT831042	MT831022	Rajchenberg <i>et al.</i> 2021
<i>Ga. mirabilis</i>	He3733	China	KY450787	KY450791	Dai <i>et al.</i> 2017b
<i>Ga. zealandicus</i>	PDD106668	New Zealand	MN044063	-	
<i>Ga. viellinum</i>	646cc	Argentina	MT831039	MT831019	Rajchenberg <i>et al.</i> 2021
<i>Laurilia sulcata</i>	Dai15889	China	KY172895	KY172911	Liu <i>et al.</i> 2017
<i>Megalocystidium brunneum</i>	He3407	China	MW533077	MW528912	Xu <i>et al.</i> 2025

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TABLE 1. (Continued)

Species name	Sample no.	Country	GenBank accession numbers		References
			ITS	nLSU	
<i>M. brunneum</i>	He3447*	China	MW533078	MW528913	Xu <i>et al.</i> 2025
<i>M. chinense</i>	He4655	China	MW533076	MW528910	Xu <i>et al.</i> 2025
<i>M. chinense</i>	Dai14769	China	-	MW528909	Xu <i>et al.</i> 2025
<i>M. diffisum</i>	Spirin 4244 H	Russia	MT477147	MT477147	Spirin <i>et al.</i> 2021
<i>M. effusum</i>	He2526*	China	MT121215	MW528911	Zhao 2018
<i>M. leucoxanthum</i>	CBS 269.54	France	MH857325	MH868866	Vu <i>et al.</i> 2018
<i>M. leucoxanthum</i>	HK9808	Spain	AF506420	AF506420	Larsson & Larsson 2003
<i>M. luridum</i>	KIL8635	Norway	AF506422	AF506422	Larsson & Larsson 2003
<i>M. luridum</i>	CBS 270.54	France	MH857326	MH868867	Vu <i>et al.</i> 2018
<i>M. wakullum</i>	Oslo-930107	USA	AF506443	AF506443	Larsson & Larsson 2003
<i>Stereodiscus antarcticus</i>	MR11265	Argentina	MT831048	-	Rajchenberg <i>et al.</i> 2021
<i>St. limonisorus</i>	PDD16691	Australia	MF631156	MF631179	Unpublished
<i>St. parmiformis</i>	SPG3104	Chile	MT831051	MT831031	Rajchenberg <i>et al.</i> 2021
<i>St. patagonicus</i>	MA-Fungi 90714	Chile	MF631177	MF631193	—
<i>St. trivialis</i>	MR11264	Argentina	MT831047	-	Rajchenberg <i>et al.</i> 2021
<i>Stereum complicatum</i>	He2234	USA	KU559368	KU574828	Dai & He 2016
<i>S. gausapatum</i>	He1629	China	MH121178	MW263956	Zhao 2018
<i>S. hirsutum</i>	He3000	China	MH121188	MW263959	Zhao 2018
<i>S. insigne</i>	He1608	China	MW263980	MW263961	Cao 2022
<i>S. insigne</i>	He3333	China	MW263981	MW263962	Cao 2022
<i>S. lithocarp</i>	He2704	China	MH121196	MW263963	Zhao 2018
<i>S. ochraceoflavum</i>	He3405	China	MW263982	MW263965	Cao 2022
<i>S. ostrea</i>	He2067	USA	KU559366	KU574826	Dai & He 2016
<i>S. rhododendri</i>	He4483*	China	MW263992	MW263976	Xu <i>et al.</i> 2025
<i>S. rhododendri</i>	He4459	China	MW263993	MW263977	Xu <i>et al.</i> 2025
<i>S. rugosum</i>	He5586	China	MW263984	MW263969	Cao 2022
<i>S. sanguinolentum</i>	He2111	USA	KU559367	KU574827	Dai & He 2016
<i>S. subtomentosum</i>	He4965	China	MW533090	MW528931	Xu <i>et al.</i> 2025
<i>S. tropicum</i>	He5968*	China	MW263990	MW263974	Xu <i>et al.</i> 2025
<i>S. tropicum</i>	He6050	China	MW263991	MW263975	Xu <i>et al.</i> 2025
<i>S. tongbiguanense</i>	CLZhao 42617	China	PV962798	PV962803	Present study
<i>S. tongbiguanense</i>	CLZhao 42627*	China	PV962799	PV962804	Present study
<i>S. tongbiguanense</i>	CLZhao 42631	China	PV962800	-	Present study
<i>S. tongbiguanense</i>	CLZhao 42697	China	PV962801	-	Present study
<i>S. tongbiguanense</i>	CLZhao 42740	China	PV962802	-	Present study
<i>Xyloholus annosus</i>	He3986	China	MH121207	MW263978	Cao & He 2020
<i>X. austrosinense</i>	He4239	China	MT121217	MW528945	Cao & He 2020

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TABLE 1. (Continued)

Species name	Sample no.	Country	GenBank accession numbers		References
			ITS	nLSU	
<i>X. frustulatus</i>	He2231	USA	MH121216	KU574825	Dai & He 2016
<i>X. lividocoeruleus</i>	MB1825	USA	-	AY039314	Wu <i>et al.</i> 2001
<i>X. lividocoeruleus</i>	FP100292	USA	-	AY039319	Wu <i>et al.</i> 2001
<i>X. princeps</i>	He3335	China	-	MW528946	Xu <i>et al.</i> 2025
<i>X. subpileatus</i>	FP106735	USA	-	AY039309	Wu <i>et al.</i> 2001

To determine the phylogeny, we compiled an ITS+nLSU dataset. In the combined dataset, Sequences of *Laurilia sulcata* (Burt) Pouzar (1959: 14) were selected as the outgroup in the ITS+nLSU analysis (Figure 1), following the previous study (Xu *et al.* 2025). The sequences were initially aligned using MAFFT (<https://mafft.cbrc.jp/alignment/server/>) with the “G-INS-I” strategy (Kato *et al.* 2019), and then manually optimized in AliView version 1.27 (Larsson 2014). Finally, the two gene fragments were concatenated with Mesquite v3.70 (Maddison & Maddison 2021; <https://www.mesquiteproject.org>) for further phylogenetic analyses.

Maximum Parsimony (MP), Maximum Likelihood (ML), and Bayesian Inference (BI) analyses were applied to the combined datasets following a previous study (Dong *et al.* 2024), and the tree construction procedure was performed in PAUP* version 4.0b10 (Swofford 2002). All of the characters were equally weighted, and gaps were treated as missing data. Trees were inferred using the heuristic search option with TBR branch swapping and 1,000 random sequence additions. Max trees were set to 5000, branches of zero length were collapsed, and all parsimonious trees were saved. Clade robustness was assessed using bootstrap (BT) analysis with 1,000 replicates (Felsenstein 1985). Descriptive tree statistics, tree length (TL), the consistency index (CI), the retention index (RI), the rescaled consistency index (RC), and the homoplasy index (HI) were calculated for each maximum parsimonious tree generated. The multiple sequence alignment was also analyzed using maximum likelihood (ML) in RAxML-HP2 (Miller *et al.* 2012). Branch support (BS) for ML analysis was determined by 1,000 bootstrap replicates.

Bayesian Inference (BI) phylogenies were inferred using MrBayes v3.2.7a with a general time-reversible model of DNA substitution and a gamma distribution of rate variation across sites (Ronquist *et al.* 2012). Four Markov chains were run twice from a random starting tree for 0.652 million generations on the datasets (Figure 1), with trees and parameters sampled every 1,000 generations. The first one-fourth of all generations was discarded as burn-in. The majority rule consensus tree of all remaining trees was calculated. Branches were considered significantly supported if they received a maximum likelihood bootstrap value (BS) $\geq 70\%$, a maximum parsimony bootstrap value (BT) $\geq 50\%$, or a Bayesian posterior probability (BPP) ≥ 0.95 .

Results

Phylogenetic analyses

The dataset, based on ITS+nLSU (Figure 1), comprises sequences from 107 fungal specimens representing 73 different species. The dataset had an aligned length of 2,111 characters, of which 1,325 characters were constant, 263 were variable and parsimony-uninformative, and 523 were parsimony-informative. Maximum parsimony analysis yielded 1 equally parsimonious tree (TL = 3,796, CI = 0.3351, HI = 0.6649, RI = 0.6109, RC = 0.2047). Bayesian analysis and ML analysis yielded a similar topology to the MP analysis, with an average standard deviation of split frequencies of 0.009981 (BI), and the effective sample size (ESS) across the two runs was double the average ESS (avg ESS) = 1742.

The phylogenetic tree inferred from ITS+nLSU sequences revealed that the new species *Stereum tongbiguanense* was nested within the genus *Stereum* located in the family Stereaceae, forming a sister lineage to *S. tropicum* S.H. He, Y.F. Cao & Yun L. Xu (2025: 143), and it is also closely related to *S. insigne* Bres. (1891: 158).

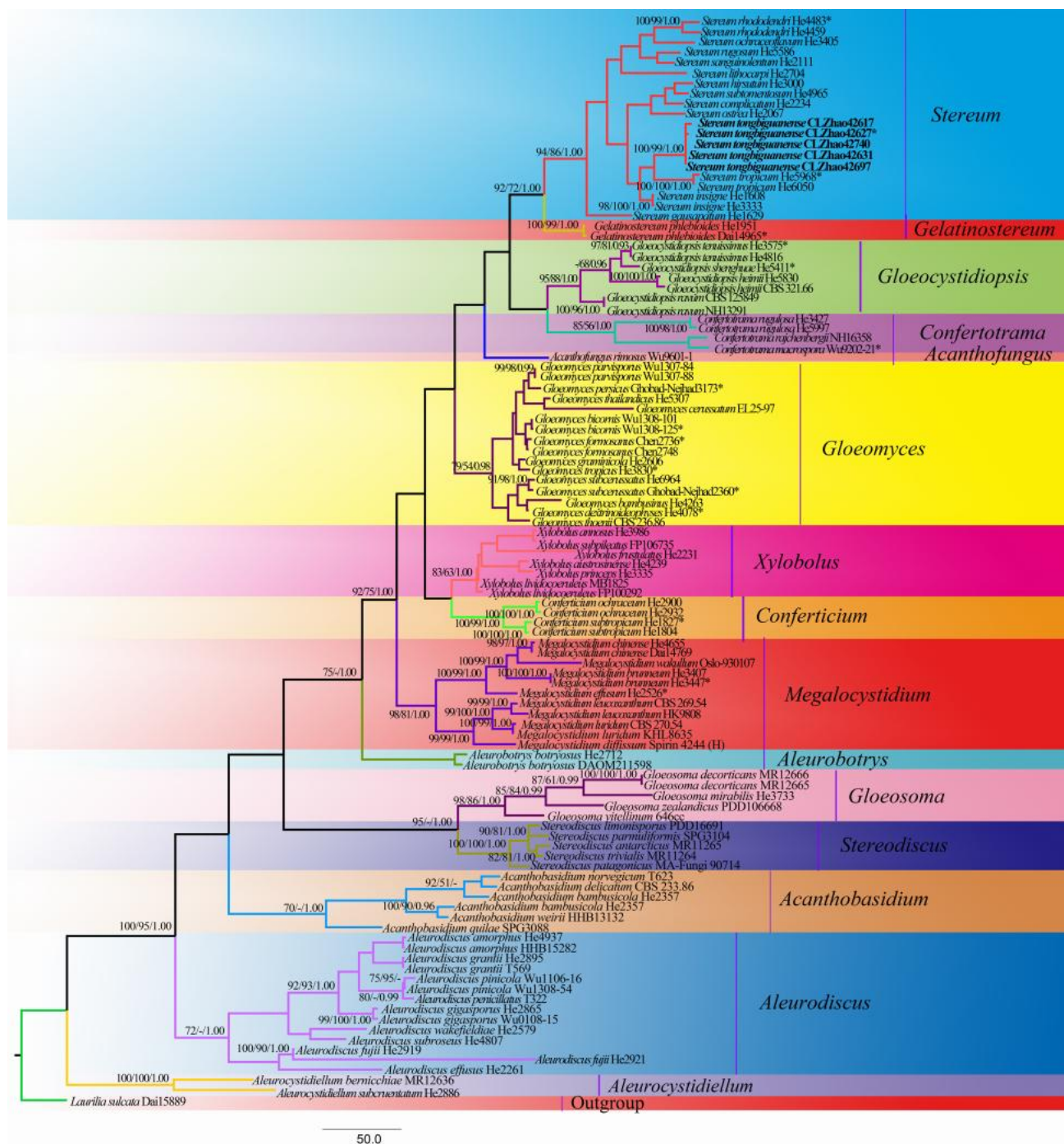


FIGURE 1. Maximum parsimony strict consensus tree illustrating the phylogeny of the new species *Stereum tongbiguanense* and related species in the family Stereaceae within the order Russulales based on ITS–nLSU sequences. The branch is labeled with a maximum-likelihood lead value of 70% or higher, a reduced lead value of 50% or higher, and a Bayesian posterior probability of 0.95 or higher.

Taxonomy

Stereum tongbiguanense M. Chen & C.L. Zhao, *sp. nov.* Figs. 2, 3, 4

Mycobank no.: MB 860442

Etymology:—*Tongbiguanense* (Lat.) refers to the type locality “Tongbiguan Nature Reserve” in China.

Holotype:—CHINA. Yunnan Province, Dchong, Ruili, Tongbiguan Provincial Nature Reserve, GPS coordinates 23°38'N, 97°51'E, altitude 1,500 m asl., on the fallen angiosperm branch, leg. C.L. Zhao, 24 November 2024, CLZhao 42627 (SWFC).

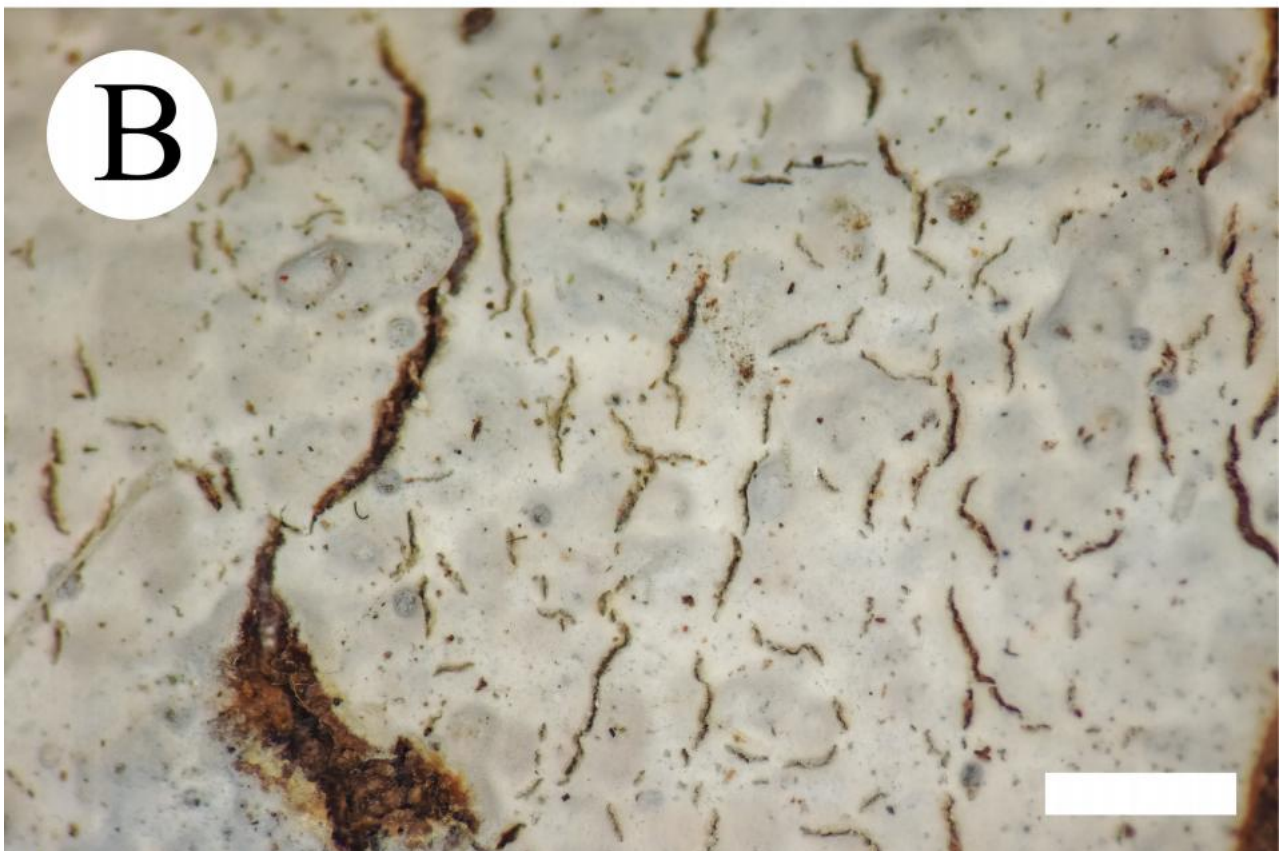


FIGURE 2. Basidiomata of *Stereum tongbiguanense*. (Holotype, CLZhao 42627): Basidiomata on the substrate (A). Macroscopic characteristics of hymenophore (B). Bars: (A) = 1 cm and (B) = 1 mm.

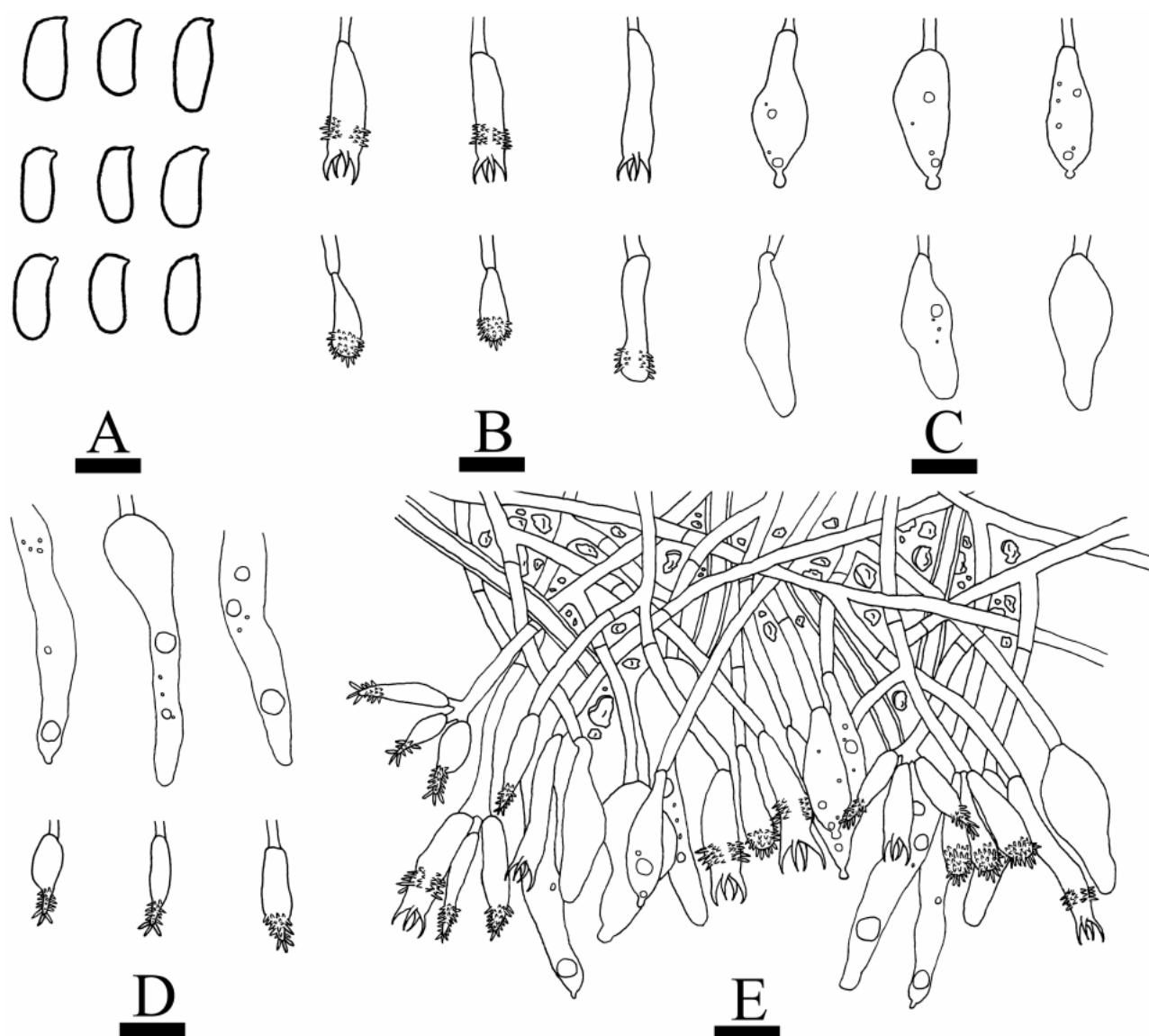


FIGURE 3. Microscopic structures of *Stereum tongbiguanense* (Holotype, CLZhao 42627): (A). Basidiospores. (B). Basidia and basidioles. (C). Bottled cystidia. (D). Acanthohyphidia. (E). A section of the hymenium. Bars: A – 5 μ m, B–E – 10 μ m.

Basidiomata:—Annual, resupinate, coriaceous, densely and deeply cracked when mature, without odor or taste when fresh, and up to 11 cm long, 1.5 cm wide, and 100 μ m thick. Hymenial surface smooth, white when fresh, turning to white to cream upon drying. Sterile margin thin, white, up to 1 mm wide.

Hyphal structure:—Hyphal system dimitic; generative hyphae bearing simple septa, colorless, thin-walled, frequently branched, interwoven, with some crystals, 2–3 μ m in diameter; skeletal hyphae, thick-walled, colorless, 3.5–4 μ m in diameter; IKI–, CB–; tissues unchanged in KOH.

Hymenium:—Cystidia two types: 1) bottled cystidia smooth, colorless, thin-walled, usually filled with refractive oil-like matter, swelling at base, slightly constricted at the neck, 19–42 $\times$ 4–11 μ m; 2) acanthohyphidia numerous, subcylindrical, colorless, with numerous spines, 11–20.5 $\times$ 3–7 μ m. Basidia subcylindrical, with many spines at the middle part, colorless, thin-walled, with 4 sterigmata and a basal simple septum, 17–27 $\times$ 4–6 μ m; basidioles dominant, in shape similar to basidia, but slightly smaller.

Spores:—Basidiospores allantoid, colorless, smooth, thin-walled, IKI+, CB–, (4.5–)5.4–6.8(–7.4) $\times$ (2.2–)2.5–3.5(–3.7) μ m, L = 6.22 μ m, W = 3.00 μ m, Q = 2.02–2.14 (n = 150/5).

Type of rot:—White rot.

Additional specimens examined (paratypes):—CHINA. Yunnan Province, Dehong, Tongbiguan Nature Reserve, GPS coordinates 23°38' N, 97°51' E, altitude 1,500 m asl., on the fallen angiosperm branch, leg. C.L. Zhao, 24 November 2024, CLZhao 42617, CLZhao 42631, CLZhao 42697, CLZhao 42740 (SWFC).

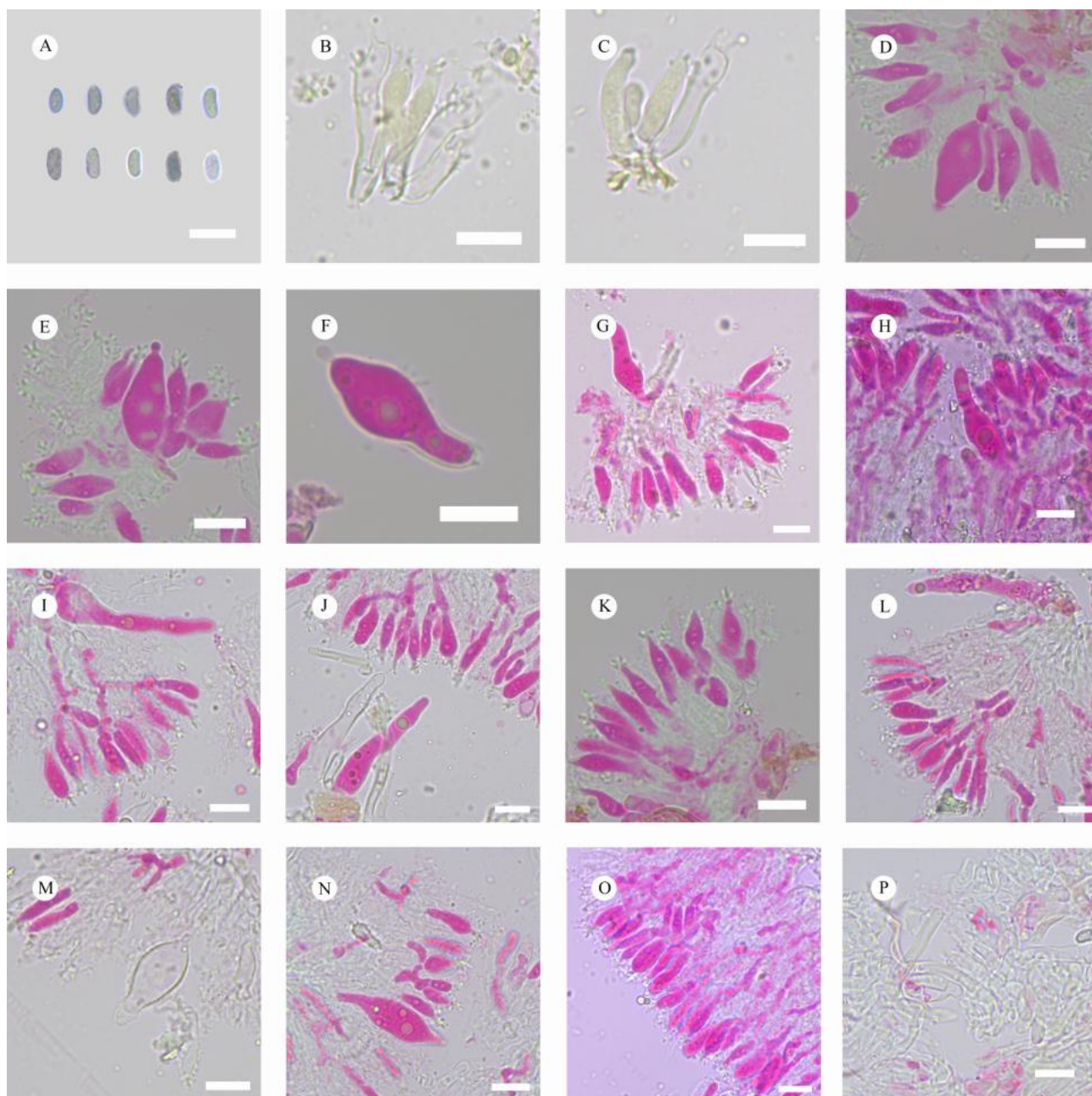


FIGURE 4. Microscopic structures of *Stereum tongbiguanense* (Holotype, CLZhao 42627): (A). Basidiospores. (B–C). Basidia and basidioles. (D–J). Bottled cystidia. (K–N). Acanthohyphae. (O). A section of the hymenium. (P). Skeletal hyphae. Bars: A–P = 10 μ m.

Discussion

In the present study, a new species, *Stereum tongbiguanense*, is proposed based on a combination of morphological features and molecular evidence.

For many years, the genus *Stereum* represented a heterogeneous assemblage of distantly related fungi (Chamuris 1988). After several taxonomic revisions, the genus represents a natural, monophyletic group (Chamuris 1988). *Xyloholus* and *Stereum* are considered to be closely related genera that share pseudocystidia (Chamuris 1988). At least two members of *Stereum* subg. *Stereum* has developed a narrow substratum preference, as seen in *S. gausapatum* (Fr.) Fr. (1874: 638) on *Quercus* species, and *S. striatum* (Fr.) Fr. (1838: 548) on *Carpinus caroliniana*; *S. sanguinolentum* (Fr.) Fr. (1838: 549) (subg. *Aculeatostereum*) is the only species that specially inhabits the gymnosperm wood. Species of *Xyloholus*, such as *X. frustulatus* (Pers.) P. Karst. (1881: 11) and *X. subpileatus* (Berk. & M.A. Curtis) Boidin (1958: 341), as well as the Asian *S. spectabile* Klotzsch (1843: 238), were recorded to be especially inhabiting in *Quercus*,

occasionally *Castanea* (Boidin *et al.* 1979, Chamuris 1988, O’Kennon *et al.* 2018, Felegyi *et al.* 2024). In the present study, based on the ITS+nLSU analysis (Figure 1), the genus *Stereum* is closely related to *Gelatinostereum* S.H. He, S.L. Liu & Y.C. Dai (2025: 132). However, morphologically, *Gelatinostereum* is distinguished from *Stereum* by its gelatinous, hygrophanous, soft basidiomata, radiate plicate, abhymenial surface with zonate and sulcate, tuberculate to meruloid, grayish orange to brown hymenophore (Xu *et al.* 2025). Phylogenetically (Figure 1), *S. tongbiguanense* forms a sister taxon with *S. tropicum* and is closely related to *S. insigne*. However, morphologically, *S. tropicum* can be distinguished from *S. tongbiguanense* by its bright yellow hymenophore and thick-walled basidia (Xu *et al.* 2025), and *S. insigne* can be distinguished from *S. tongbiguanense* by its monomitric hyphal system with thick-walled generative hyphae and thick-walled cystidia (Cao 2022).

In ecology and biogeography, the macro-fungi are an extensively studied group of Basidiomycota, which are an important group in the forest ecosystems (Wu *et al.* 2022, Deng & Zhao 2023, Zhang *et al.* 2023, Dong *et al.* 2024, Zhang *et al.* 2024, Zhou *et al.* 2024, Liu *et al.* 2025, Yang *et al.* 2025). However, the diversity of *Stereum* in China remains largely unknown, particularly in subtropical and tropical areas. This paper reports a new species, *S. tongbiguanense*, which enriches our knowledge of fungal diversity in this area. The discovery of *S. tongbiguanense* underscores the need for further fieldwork and molecular analyses to identify new taxa and enhance our understanding of fungal diversity.

Acknowledgements

The research was supported by the National Natural Science Foundation of China (Project No. 32170004), Forestry and Grass Science and Technology Innovation Joint Project of Yunnan Province (Project No. 202404CB090008), Modern Industry School of Edible-fungi, Southwest Forestry University (SYJ25), Yunnan Province College Students Innovation and Entrepreneurship Training Program (Project no. S202510677111, S202510677002), the Science Foundation of Education Department of Yunnan Province (2025Y0845) and the Forestry Innovation Programs of Southwest Forestry University (Grant No: LXXK-2025D20).

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