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云南省的糙孢孔菌属(糙孢孔目，担子菌门)一新种

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摘　要：木生真菌在森林生态系统中作为分解者发挥着关键作用。本研究基于形态特征与分子证据从云南发现一种新的木生真菌—景谷糙孢孔菌 *Trechispora jingguensis*。该新种的主要特征为：担子果平伏，子实层表面具小短齿，新鲜时呈白色至淡米色，干燥后转为浅米色，菌丝系统一体系，生殖菌丝具锁状联合，担孢子椭圆形，具刺。通过 ITS 和 nLSU 分子片段测序，结合最大似然法、最大简约法与贝叶斯推断法，对研究标本进行了系统发育分析。分子系统学研究结果表明：景谷糙孢孔菌 *T. jingguensis* 聚类至糙孢孔菌属，并与晶体糙孢孔菌 *T. crystallina* 构成姊妹群。本文提供了该新种的详细形态描述、显微图片及系统发育分析结果，以支持其分类学地位。

关键词：刺孢菌科；木腐菌；分子系统学；分类学

A new species of *Trechispora* (Trechisporales, Basidiomycota) from Yunnan Province, China

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Abstract: Wood-inhabiting fungi play crucial roles as decomposers in forest ecosystems. In this study, a new wood-inhabiting fungus, *Trechispora jingguensis,* is proposed based on a

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combination of morphological features and molecular evidence. *Trechispora jingguensis* is characterized by resupinate basidiomata with grandinioid, white to slightly buff when fresh, turning slightly buff upon drying, a monomitic hyphal system, generative hyphae with clamp connections, and ellipsoid and aculeate basidiospores. Phylogenetic analysis was based on ITS and nLSU sequences, in combination with ML, MP, and BI methods. The results showed that the new species *T. jingguensis* was sister to *T. crystallina*. A full description, illustrations and phylogenetic analysis results of the new species are provided.

Keywords: Hydnodontaceae; wood-inhabiting fungi; molecular phylogeny; taxonomy

INTRODUCTION

Wood-inhabiting fungi occur on living trees, dead standing dead trees, fallen decorticated trunks, fallen trunks and branches, rotten wood, stumps, and even manufactured wood products (Dai *et al*. 2006; Dai 2010; Cui *et al.* 2019; Wu *et al.* 2022; Yuan *et al.* 2023; Hibbett *et al.* 2025). They represent a major group of decomposers in forest ecosystems (Dai *et al.* 2011; Si *et al*. 2011a, 2011b; Yuan *et al*. 2023; Yang *et al.* 2025). Wood-inhabiting fungi are widely studied Basidiomycota in China (Wu *et al.* 2022; Cui *et al.* 2023; Dong *et al.* 2023; Li *et al.* 2024; Zhao *et al.* 2024; Zhou *et al.* 2024; Dong *et al.* 2025; Wang *et al*. 2025).

Trechispora P. Karst. (Hydnodontaceae Jülich) is the largest genus in Trechisporales K.H. Larss (Hibbett *et al.* 2007). It was introduced by Karsten (1890) and typified by *T. onusta* P. Karst. Species of *Trechispora* are generally characterized by resupinate to effused basidiomata, a smooth to hydnoid to poroid hymenophore, ampullaceous septa, short cylindric basidia, and smooth to verrucose or aculeate basidiospores (Bernicchia & Gorjón 2010; Luo *et al.* 2024; Wijesinghe *et al.* 2025). Calcium oxalate crystals on subicular hyphae can provide additional diagnostic characters (Larsson 1992, 1994; Lin *et al.* 2025). Currently, 167 specific names in *Trechispora* are listed in MycoBank (2026) and Index Fungorum (2026).

Historically, taxonomic concepts in *Trechispora* were largely based on morphology. In 2002, based on interpretation of morphological characters, Ryvarden (2002) transferred *Hydnodon thelephorus* (Lév.) Banker to *Trechispora* as *Trechispora thelephora* (Lév.) Ryvarden. With the development of molecular systematics, DNA sequence data have become widely applied in *Trechispora* taxonomy. Larsson (2007) demonstrated that *T. farinacea* (Pers.) Liberta and *T. hymenocystis* (Berk. & Broome) K.H. Larss. clustered together and were nested within the family Hydnodontaceae. Up to the present, 14 new species were reported from China (Xu *et al.* 2019; Luo & Zhao 2022; Luo *et al.* 2024; Lin *et al.* 2025; Wijesinghe *et al.* 2025), viz. *T. yunnanensis* C.L. Zhao, *T. albofarinosa* K.Y. Luo & C.L. Zhao, *T. wenshanensis* K.Y. Luo & C.L. Zhao, *T. bisterigmata* K.Y. Luo & C.L. Zhao, *T. pileata* K.Y. Luo & C.L. Zhao, *etc*.

Most species of *Trechispora* are saprotrophs, typically occurring on decayed wood, bamboos, grasses, palms, tree ferns, mosses, or soil with litters (Larsson 1992; Liu *et al.* 2019; Chikowski *et al.*

2020; Lin *et al.* 2022). They play an important role as decomposers in forest ecosystems (Jülich 1976; Larsson 1992; de Meiras-Ottoni *et al.* 2021; Lin *et al.* 2025). While surveying wood-inhabiting fungi in Yunnan Province, China, specimens representing an undescribed taxon of *Trechispora* were collected. Morphological characters and molecular phylogenetic evidence of ITS and nLSU, support its recognition as a new species. Detailed descriptions, illustrations, and phylogenetic analysis results for the new species are provided.

1 MATERIALS AND METHODS

1.1 Morphology studies

Fresh specimens of wood-inhabiting fungi on angiosperm branches were collected from a broad-leaf forest in Pu'er, Yunnan Province, China. Specimens were deposited in the herbarium of Southwest Forestry University (SWFC), Kunming, Yunnan Province, China. Macromorphological descriptions and color terminology follow Petersen (1996) and subsequent studies (Dong *et al.* 2024; Yang *et al*. 2025). Standardized sampling of microstructures for measurement includes basidiospores (30), basidia, basidioles and cystidia (5), and hyphae diameters (10) (Cui *et al.* 2019; Zhao *et al.* 2023; Dong *et al.* 2024).

1.2 DNA extraction, polymerase chain reaction, and sequencing

Fungal specimens were processed for genomic DNA extraction with the HiPure Fungal DNA Mini KitⅡ(Meiji Biotechnologies Co. Ltd., Guangzhou), which employs a rapid CTAB-based method. The primer pair of ITS5 and ITS4 (White *et al.* 1990; Zhao *et al.* 2012) was amplified with ITS region. The primer pair LR0R and LR7 was amplified with nuclear LSU region. The PCR was performed following Dong *et al.* (2024) and Yang *et al.* (2025).

1.3 Phylogenetic Analyses

All the nucleotide sequences were systematically listed in Table 1. The sequences were aligned with MAFFT version 7 (Katoh *et al.* 2019) using the G-INS-I strategy. The alignment was adjusted manually using AliView version 1.27 (Larsson 2014). Each dataset was aligned separately at first, and then the ITS and nLSU regions were combined with Mesquite version 3.51.

Maximum parsimony analysis in PAUP* version 4.0b10 (http://phylosolutions. com/paup-test/) was applied to ITS and the combined ITS+nLSU dataset following a previous study (Zhao & Wu 2017). Trees were inferred using the heuristic search option with TBR branch swapping and 1 000 random sequence additions (Dong *et al.* 2023). The combined dataset was also analyzed using maximum likelihood (ML) in RAxMl-HPC2 through the CIPRES Science Gateway (Miller *et al.* 2012). Branch support (BS) in the ML analysis was assessed through 1 000 bootstrap pseudo-replicates. MrModeltest 2.3 was used to determine the best-fit evolutionary model for each dataset for Bayesian inference (BI) (https://github.com/nylander/MrModeltest2/releases). It was performed using MrBayes 3.2.7a with a GTR+I+G model of DNA substitution and a gamma distribution rate variation across sites (Ronquist *et al.* 2012). Four Markov chains were run for 2 runs from random starting trees for 500 million generations for ITS+nLSU (Fig. 1).

Table 1 Species, specimens, and GenBank accession numbers of sequences used in this study.

Species	**Sample no.**	**GenBank accessions no.**		**Country**	**References**
		ITS	**nLSU**		
Dextrinocystis calamicola	He 5693*	MK204533	MK204546	China	Liu *et al.* 2019
Trechispora acerosa	Chen 3186*	PV085797	PV085828	China	Lin *et al.* 2025
Trechispora acerosa	GC 1612-34	PV085798	PV085827	China	Lin *et al.* 2025
Trechispora acerosa	He 4641	OM523513	OM339319	China	Liu SL *et al.* 2022
Trechispora alba	CH21384*	OR557258	–	China	Liu *et al.* 2024
Trechispora albofarinosa	CLZhao 4356	OQ241383	OQ282703	China	Luo *et al.* 2024
Trechispora alborhizomorpha	CLZhao 37978*	PV591026	–	China	Wijesinghe *et al.* 2025
Trechispora alnicola	AFTOL-ID 665	DQ411529	AY635768	USA	Unpublished
Trechispora araneosa	KHL 8570	AF347084	AF347084	Sweden	Larsson *et al.* 2004
Trechispora bambusicola	CLZhao 3305*	MW544022	MW520172	China	Zhao & Zhao 2021
Trechispora bispora	CBS:142.63	MH858241	MH869842	Australia	Vu *et al.* 2019
Trechispora bisterigmata	CLZhao 2522*	OQ241386	–	China	Luo *et al.* 2024
Trechispora candidissima	Dai 7092	OM523407	OM339229	China	Liu SL *et al.* 2022
Trechispora chaibuxiensis	LWZ 20170814-34*	OM523409	OM339231	China	Liu SL *et al.* 2022
Trechispora clancularis	FRDBI 4426619	MW487976	–	UK	Unpublished
Trechispora cohaerens	HHB 19445	MW740327	–	New Zealand	Unpublished
Trechispora confinis	KHL 11064	AF347081	AF347081	Sweden	Larsson *et al.* 2004
Trechispora constricta	Dai 10534*	OM523416	–	China	Liu SL et al. 2022
Trechispora constricta	He 5899	OM523417	OM339236	China	Liu SL *et al.* 2022
Trechispora copiosa	AMO422*	MN701013	MN687971	Brazil	de Meiras-Ottoni *et al.* 2021
Trechispora cryptomerioides	0906RK10-23	KF679506	OK422242	China	Lin *et al.* 2022
Trechispora cryptomerioides	GC 2308-51	PV085817	–	China	Lin *et al.* 2025
Trechispora crystallina	LWZ 20171013-7*	OM523420	OM339239	Vietnam	Liu SL *et al.* 2022
Trechispora damansaraensis	LWZ 20180417-26*	–	OM339241	Malaysia	Liu SL *et al.* 2022
Trechispora damansaraensis	He 6415	OM523421	OM339240	Malaysia	Liu SL *et al.* 2022
Trechispora dentata	Dai 22565*	OK298491	OM049408	China	Liu ZB *et al.* 2022
Trechispora dimitica	FRDBI 13394362	MW487977	OR892779	UK	Unpublished
Trechispora dimitiella	Dai 21181	OK298493	OK298949	China	Liu ZB *et al.* 2022
Trechispora echinospora	MA-Fungi 82485	JX392845	JX392846	Equatorial Guinea	Tellería *et al.* 2013
Trechispora farinacea	KHL 8451	AF347082	AF347082	Sweden	Unpublished
Trechispora fimbriata	CLZhao 4154	MW544023	MW520173	China	Zhao & Zhao 2021
Trechispora fissurata	LWZ 20171015-35*	OM523431	OM339249	Vietnam	Liu SL *et al.* 2022
Trechispora floralis	Wu 1703-66*	PV085813	PV085822	China	Lin *et al.* 2025
Trechispora foetida	FLOR 56315	MK458769	–	Brazil	Furtado *et al.* 2021
Trechispora formosana	Chen 3151*	PV085800	PV085823	China	Lin *et al.* 2025

Species	Sample no.	GenBank accessions no.		Country	References
		ITS	nLSU		
Trechispora fragilis	Dai 20535	OK298494	OK298950	China	Liu ZB *et al.* 2022
Trechispora gelatinosa	AMO1139*	MN701021	MN687978	Brazil	de Meiras-Ottoni *et al.* 2021
Trechispora gracilis	LWZ 20210626-5b*	OM523436	OM339254	China	Liu SL *et al.* 2022
Trechispora havencampii	SFSU DED8300*	NR154418	KT253947	Africa	Desjardin & Perry 2015
Trechispora hondurensis	HONDURAS19-F016*	NR178152	NG081479	Honduras	Haelewaters *et al.* 2020
Trechispora hymenocystis	KHL 8795	AF347090	AF347090	Sweden	Larsson *et al.* 2004
Trechispora incisa	GB-0090648	KU747095	KU747087	Sweden	Unpublished
Trechispora invisitata	UC2023088	KP814425	–	USA	Unpublished
Trechispora jingguensis	**CLZhao 46306**	**PX844723**	**PX872115**	**China**	**Present study**
Trechispora jingguensis	**CLZhao 46451***	**PX844724**	**PX872116**	**China**	**Present study**
Trechispora kavinioides	KGN 981002	AF347086	AF347086	Norway	Larsson *et al.* 2004
Trechispora khokpasiensis	MEL2382623	KP012986	–	Australia	Deng *et al.* 2023
Trechispora khokpasiensis	MMCR00009*	MZ687107	MZ683197	Thailand	Deng *et al.* 2023
Trechispora khokpasiensis	ZP-1029	OM523532	–	China	Deng *et al.* 2023
Trechispora laevispora	Dai 21655*	OK298495	OM108710	China	Liu ZB *et al.* 2022
Trechispora larssonii	LWZ 20190817-11a*	OM523442	OM339259	China	Liu SL *et al.* 2022
Trechispora latehypha	He 3924	OM523443	OM339261	China	Liu SL *et al.* 2022
Trechispora latehypha	He 5438*	OM523445	–	China	Liu SL *et al.* 2022
Trechispora laxa	MHHNU10714*	OP959650	OP954661	China	Deng *et al.* 2023
Trechispora longiramosa	CH 19233*	OM523449	–	China	Liu SL *et al.* 2022
Trechispora longiramosa	HG 140168	OM523448	OM339264	China	Liu SL *et al.* 2022
Trechispora malayana	Dai 17876	OM523452	OM339265	Singapore	Liu SL *et al.* 2022
Trechispora mangensis	CLZhao 36340	PV591025	–	China	Wijesinghe *et al.* 2025
Trechispora microspora	FRDBI 18772216	OL828778	–	UK	Unpublished
Trechispora minispora	AM176	MK328886	MK328895	Mexico	Yuan *et al.* 2020
Trechispora mollis	URM85884*	MK514945	MH280003	Brazil	Chikowski *et al.* 2020
Trechispora mollusca	Dai 6191	OM523455	OM339269	China	Liu SL *et al.* 2022
Trechispora murina	CLZhao 11752*	OL615004	OL615009	China	Luo & Zhao 2022
Trechispora nivea	LWZ 20180804-3	OM523461	OM339273	China	Liu SL *et al.* 2022
Trechispora orchidophila	FM151.1	JF691276	–	Franch	Martos *et al.* 2012
Trechispora orchidophila	Wu 1703-55*	PV085812	PV085824	China	Lin *et al.* 2025
Trechispora orchidophila	Y453-2	LC327027	–	Japan	Ogura-Tsujita *et al.* 2018
Trechispora odontioidea	CLZhao 17890*	ON417458	OQ282713	China	Luo & Zhao 2022
Trechispora olivacea	CLZhao 17826	ON417457	OQ282714	China	Luo & Zhao 2022
Trechispora papillosa	AMO795	MN701023	MN687981	Brazil	de Meiras-Ottoni *et al.* 2021
Trechispora patawaensis	VPapp-GF1901*	OL314550	OL314546	French	Lin *et al.* 2025

Species	Sample no.	GenBank accessions no.		Country	References
		ITS	nLSU		
Trechispora perminispora	LWZ20190816-39a*	OM523525	OM339329	China	Liu SL *et al.* 2022
Trechispora regularis	KHL 10881	AF347087	AF347087	Jamaica	Larsson *et al.* 2004
Trechispora rigida	URM85754	MT406381	MH279999	Brazil	Chikowski *et al.* 2020
Trechispora robusta	FLOR 56179	MK458770	–	Brazil	Furtado *et al.* 2021
Trechispora saluangensis	MMCR00260*	MZ687104	MZ683201	Thailand	Sommai *et al.* 2023
Trechispora sanpapaoensis	MMCR00124.1	MZ687109	MZ683200	Thailand	Sommai *et al.* 2023
Trechispora sinensis	LWZ 20180804-19*	OM523482	OM339290	China	Liu SL *et al.* 2022
Trechispora stevensonii	MA-Fungi 70645	JX392843	JX392844	Spain	Tellería *et al.* 2013
Trechispora subaraneosa	LWZ 20210918-10a*	OM523529	OM339332	China	Liu *et al.* 2024
Trechispora subconfinis	LWZ 20230715-12a*	PP959670	–	China	Wang *et al.* 2024
Trechispora subfarinacea	LWZ 20200921-33a*	OM523528	OM339331	China	Liu *et al.* 2024
Trechispora subfissurata	He 3907	OM523490	OM339298	China	Liu SL *et al.* 2022
Trechispora subhymenocystis	LWZ 20190818-29b*	OM523492	OM339299	China	Liu SL *et al.* 2022
Trechispora subsinensis	LWZ 20190611-9	OM523497	OM339304	China	Liu SL *et al.* 2022
Trechispora subsphaerospora	KHL 8511	AF347080	AF347080	Sweden	Larsson *et al.* 2004
Trechispora taiwanensis	He 4571*	OM523498	OM339305	China	Liu SL *et al.* 2022
Trechispora termitophila	AMO396*	MN701025	MN687983	Brazil	de Meiras-Ottoni *et al.* 2021
Trechispora thailandica	He 4101*	OM523499	OM339307	Thailand	Liu SL *et al.* 2022
Trechispora tongdaoensis	MHHNU11083*	OP959651	OP954662	China	Deng *et al.* 2023
Trechispora torrendii	URM85886	MK515148	MH280004	Brazil	Chikowski *et al.* 2020
Trechispora tropica	LWZ 20170613-14*	OM523502	OM339310	China	Liu SL *et al.* 2022
Trechispora tuberculata	Dai 17433*	OM523507	OM339314	Brazil	Liu SL *et al.* 2022
Trechispora wenshanensis	CLZhao 11649*	OQ241389	OQ282716	China	Luo *et al.* 2024
Trechispora yunnanensis	CLZhao 210*	NR177488	MN654918	China	Xu *et al.* 2019
Trechispora yunnanensis	CLZhao 214	MN654922	MN654919	China	Xu *et al.* 2019

Asterisks (*) indicate holotype sequences.

2 RESULTS

2.1 Molecular phylogeny

Maximum parsimony analysis yielded 1 equally parsimonious tree (TL=6 500, CI=0.282 6, HI=0.717 4, RI=0.433 7, RC=0.122 6). The best model of nucleotide evolution for the ITS+nLSU dataset estimated and applied in the Bayesian analysis was found to be GTR+F+I+G4. The Bayesian and ML analyses resulted in topologies that mirrored the MP phylogeny. With respect to the Bayesian analysis, the mean standard deviation of split frequencies=0.051 282 (BI) and the effective sample size (ESS) across the two runs is double the average ESS (avg. ESS)=1 801.5. The topology based on ITS+nLSU sequences (Fig. 1) shows that *T. jingguensis* is grouped with the clade comprising *T. bambusicola* C.L. Zhao, *T. crystallina* S.L. Liu & L.W. Zhou, and *T. murina* K.Y. Luo & C.L. Zhao.


* Holotype
100/ - /1
Trechispora longiramosa CH 19233 China *
100/63/0.99
Trechispora longiramosa HG 140168 China
100/94/1
Trechispora laxa MHHNU10714 China *
96/85/ -
Trechispora sanpapaoensis MMCR00124.1 Thailand
Trechispora havencampii SFSU DED8300 Africa *
100/100/1
Trechispora robusta FLOR 56179 Brazi
Trechispora termitophila AMO396 Brazil *
Trechispora foetida FLOR 56315 Brazil *
98/63/ -
Trechispora fragilis Dai 20535 China
Trechispora bispora CBS:142.63 Australia
Trechispora perminispora LWZ20190816-39a China *
Trechispora mangensis CLZhao 36340 China
Trechispora malayana Dai 17876 Singapore
100/100/1
Trechispora yunnanensis CLZhao 210 China *
76/-/-
Trechispora yunnanensis CLZhao 214 China
Trechispora thailandica He 4101 Thailand *
100/99/1
Trechispora sinensis LWZ 20180804-19 China *
82/-/-
100/68/1
Trechispora odontioidea CLZhao 17890 China *
100/98/1
Trechispora subsinensis LWZ 20190611-9 China
100/71/1
Trechispora chaibuxiensis LWZ 20170814-34 China *
Trechispora nivea LWZ 20180804-3 China
100/99/1
Trechispora fimbriata CLZhao 4154 China
Trechispora rigida URM85754 Brazil
Trechispora tongdaoensis MHHNU11083 China *
Trechispora damansaraensis He 6415 Malaysia
100/94/1
Trechispora damansaraensis LWZ 20180417-26 Malaysia *
Trechispora wenshanensis CLZhao 11649 China *
Trechispora orchidophila Wu 1703-55 China *
Trechispora orchidophila Y453-2 Japan
100/100/1
Trechispora orchidophila FM151.1 Franch
100/100/1
Trechispora mollis URM85884 Brazil *
Trechispora hondurensis HONDURAS19-F016 Honduras *
Trechispora latehypha He 3924 China
100/100/1
Trechispora latehypha He 5438 China *
100/100/1
Trechispora subaraneosa LWZ 20210918-10a China *
100/99/1
Trechispora albofarinosa CLZhao 4356 China
-/-/1
Trechispora araneosa KHL 8570 Sweden
93/66/1
Trechispora hymenocystis KHL 8795 Sweden
100/100/1
Trechispora subhymenocystis LWZ 20190818-29b China *
-/-/1
Trechispora formosana Chen 3151 China *
Trechispora fissurata LWZ 20171015-35 Vietnam *
100/98/1
Trechispora subfissurata He 3907 China
Trechispora torrendii URM85886 Brazil
Trechispora farinacea KHL 8451
Trechispora subfarinacea LWZ 20200921-33a China *
82/55/ -
Trechispora echinospora MA-Fungi 82485 Equatorial Guinea
-/-/0.99
Trechispora olivacea CLZhao 17826 China
100/100/1
Trechispora larssonii LWZ 20190817-11a China *
70/-/-
Trechispora gelatinosa AMO1139 Brazil *
Trechispora papillosa AMO795 Brazil
Trechispora patawaensis VPapp-GF1901 French

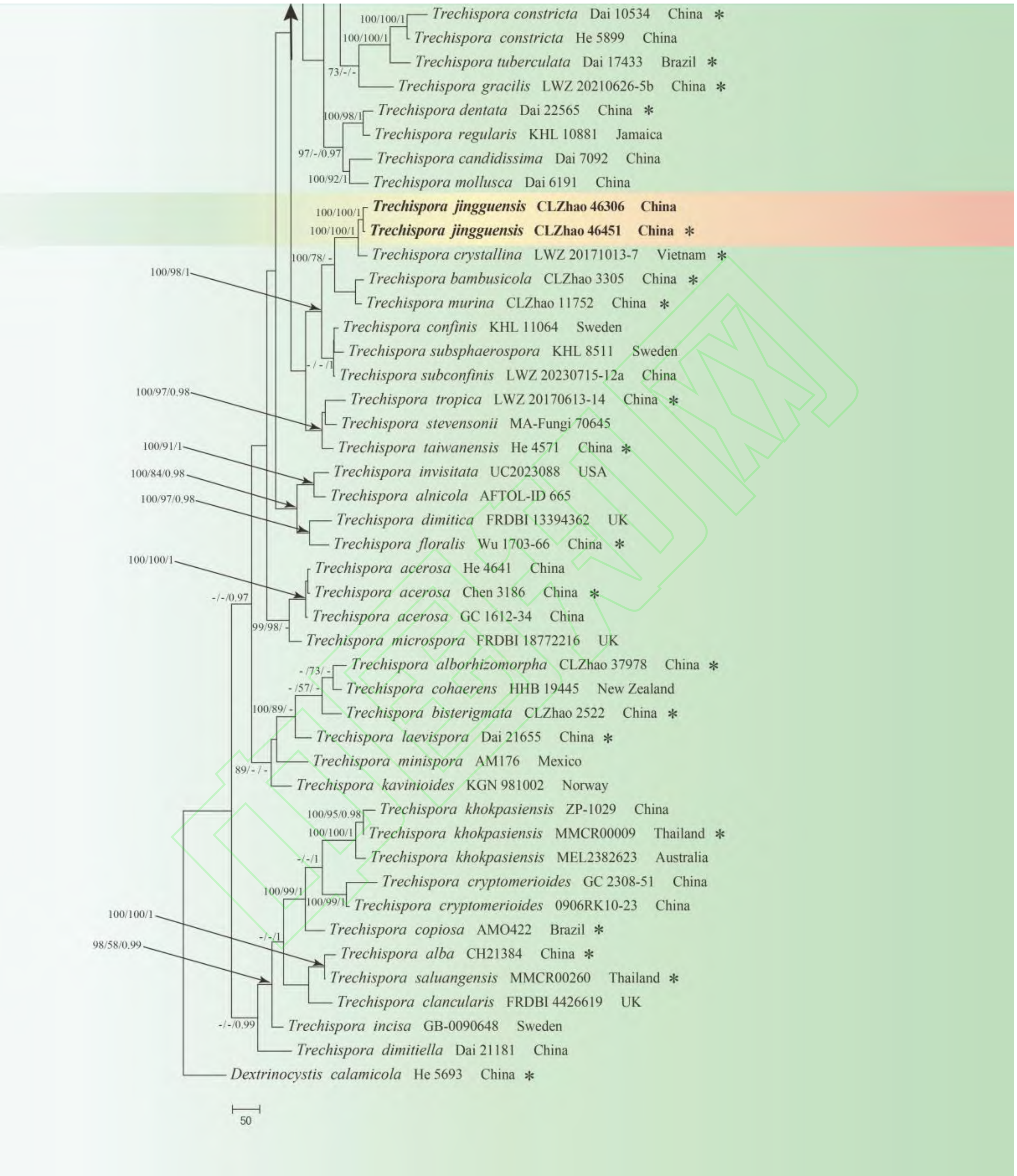

Fig. 1 Maximum parsimony strict consensus tree illustrating the *Trechispora jingguensis* and related species in the genus *Trechispora* based on the combined ITS+nLSU sequences. Branches are labeled with maximum likelihood bootstrap values ≥ 70%, parsimony bootstrap values ≥ 50%, and Bayesian posterior probabilities ≥ 0.95. The new species is in bold. Asterisks (*) indicate holotype sequences.

2.2 Taxonomy

Trechispora jingguensis Q. Li & C.L. Zhao, **sp. nov.** Figs. 2, 3 and 4

MycoBank no.: MB 862038

Holotype. China, Yunnan Province, Puer, Jinggu County, Mangyu Grand Canyon, GPS coordinates: 23°53′N, 100°67′E, elev. 1 151 m asl., on a fallen angiosperm branch, leg. C.L. Zhao, 20 August 2025, CLZhao 46451 (SWFC 00046451).

Etymology. *jingguensis* (Lat.): referring to the locality (Jinggu County) of the type specimen.

Diagnosis. It differs from other *Trechispora* species by its slightly buff basidiomata, a monomitic hyphal system with clamp connections, ellipsoid and aculeate basidiospores (2.9–4 × 2.2–2.9 µm).

Basidiomata. Annual, resupinate, farinose, without odor or taste when fresh, up to 9 cm long, 3 cm wide, 150 µm thick at center. Hymenial surface grandinioid, white to slightly buff when fresh, slightly buff on drying. Sterile margin narrow, slightly buff, and up to 1 mm wide.

Hyphal structure. Hyphal system monomitic, generative hyphae with clamp connections, frequently branched, colorless, thin-walled, 1.5–4.5 µm in diameter, IKI–, CB–, subhymenial hyphae densely covered by crystals; tissues unchanged in KOH.

Hymenium. Cystidia absent. Basidia clavate, slightly constricted, with four sterigmata and a basal clamp connection, 7–15 × 3.5–6 µm; basidioles dominant, in shape similar to basidia, but slightly smaller.

Basidiospores. Ellipsoid, colorless, thin-walled, aculeate, IKI–, CB–, 2.9–4(–4.3) × 2.2–2.9(–3.5) µm, L = 3.43 µm, W = 2.57 µm, Q = 1.32–1.35 (n = 60/2).

Type of rot: white rot.

Paratype – China, Yunnan Province, Puer, Jinggu County, Mangyu Grand Canyon, GPS coordinates: 23°53′N, 100°67′E, elev. 1 155 m asl., on a fallen angiosperm branch, leg. C.L. Zhao, 20 August 2025, CLZhao 46306 (SWFC 00046306).

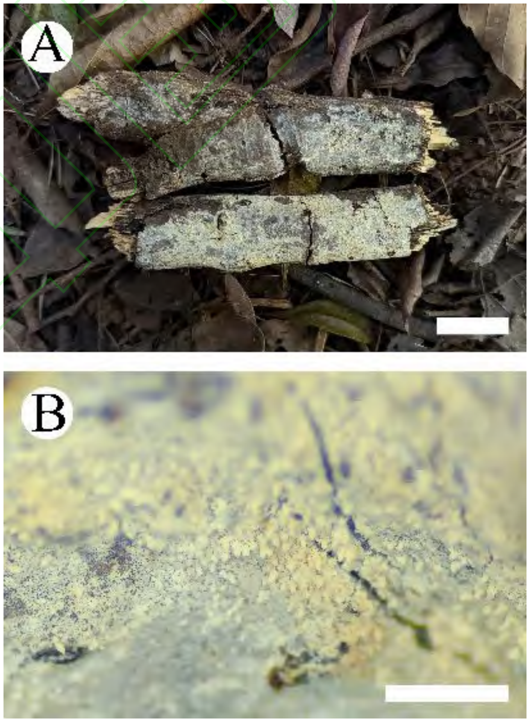

Fig. 2 Basidiomata of *Trechispora jingguensis* (SWFC 00046451, holotype). Bars: A = 2 cm; B = 1 mm.

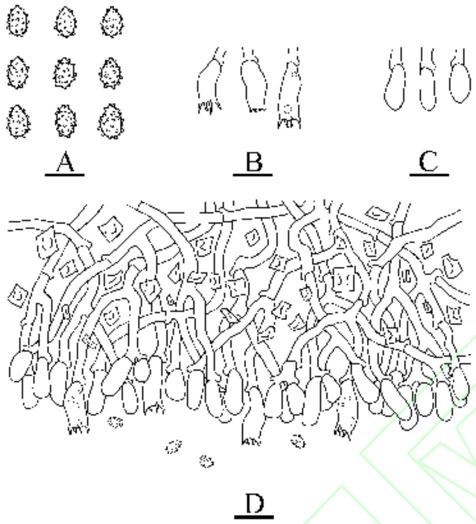

Fig. 3 Microscopic structures of *Trechispora jingguensis* (SWFC 00046451, holotype). A: Basidiospores; B: Basidia; C: Basidioles; D: A section of hymenium. Bars: A = 5 µm; B–D = 10 µm.

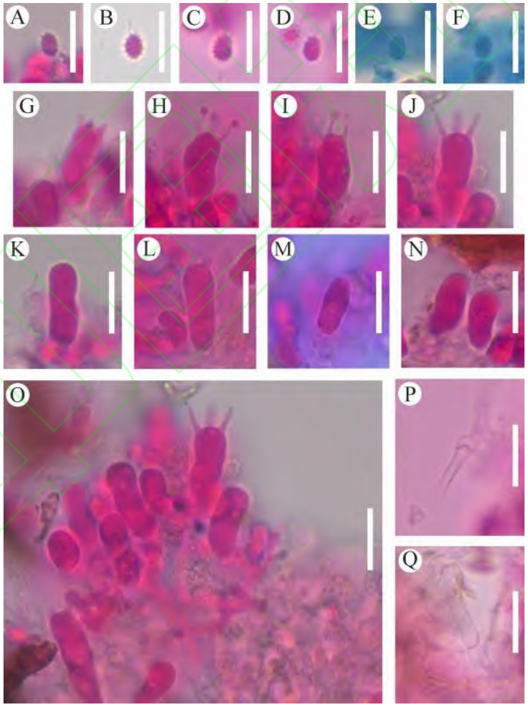

Fig. 4 Microscopic structures of *Trechispora jingguensis* (SWFC 00046451, holotype). A–F: Basidiospores; G–J: Basidia; K–N: Basidioles; O: A section of hymenium; P, Q: Generative hyphae with clamp connection. Scale bars: A–Q = 10 µm. 10×100 Oil.

3 DISCUSSIONS

Phylogenetically, *T. jingguensis* is grouped with the clade comprising *T. bambusicola*, *T. crystallina*, and *T. murina* in the ITS + nLSU phylogeny (Fig. 1). However, *T. bambusicola* is distinguished from *T. jingguensis* by its odontioid hymenial surface, thick-walled generative hyphae, shortly cylindrical to subclavate basidia and, thick-walled basidiospores (Zhao & Zhao 2021). *Trechispora crystallina* is readily distinguished from *T. jingguensis* by its cream to straw-yellow hymenial surface when drying, cylindrical basidia with a slight median constriction, and thin- to slightly thick-walled basidiospores (Liu SL *et al.* 2022). *Trechispora murina* is distinguished from *T. jingguensis* by its greyish hymenial surface wheSn drying and thick-walled generative hyphae (Luo & Zhao 2022).

Morphologically, *T. jingguensis* resembles *T. albofarinosa* K.Y. Luo & C.L. Zhao, *T. constricta* S.L. Liu, S.H. He & L.W. Zhou and *T. laevispora* Z.B. Liu, Y.D. Wu & Yuan Yuan in sharing a monomitic hyphal system and ellipsoid basidiospores. However, *T. albofarinosa* differs from *T. jingguensis* by its thick-walled generative hyphae (Luo *et al.* 2024). *Trechispora constricta* is distinguished from *T. jingguensis* by its odontioid hymenial surface, cylindrical basidia and hyaline to yellowish basidiospores (Liu SL *et al.* 2022). *Trechispora laevispora* differs from *T. jingguensis* by having a smooth and white hymenial surface, smooth and narrower basidiospores (2.6–3.2 × 1.9–2.2 μm vs. 2.9–4 × 2.2–2.9 μm, Liu ZB *et al.* 2022).

Author contributions

LI Qi: conducting field surveys and sampling, species identification, thesis conception and initial manuscript drafting; Peng Xiwen: species identification and data analysis; Wang Shunhong, Ma Zhiqiang: data analysis and literature search; Shu Chengwei, Zhou Ronglun: field survey and sampling; Zhao Changlin: providing guidance on species identification and manuscript writing; species identification, thesis conception, review, editorial oversight, funding acquisition, supervision.

Declaration of competing interests

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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