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***Hyphoderma jingguense* sp. nov.**
(Hyphodermataceae, Polyporales), a wood-inhabiting fungus from Yunnan Province, China

QI LI, XIWEN FENG, CHENGWEI SHU, RONGLUN ZHOU, XINYU LI, CHANGLIN ZHAO

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Taxonomic novelties in *Onosma* (Boraginaceae): two new endemic species from the Zagros Mountains, Iran

FARZANEH KHAJOEI NASAB, AMIN ZERAATEGAR, HAMZEH ALI SHIRMARDI

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The natural hybrid between *Aloe arborescens* and *A. petricola* (Asphodelaceae [subfam. Asphodeloideae] tr. Aloee) described as *A. ×attwoodii*

GIDEON F. SMITH

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***Peliosanthes hainanensis* (Asparagaceae), a new species from Hainan Province, China**

XING XING MAO, HUAN TANG, JIN LIN YU, LI LI, QIANG FAN, HUI ZHE FENG

Published: 2026-09-23

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***Bulbine pauciflora* (Asphodelaceae: Asphodeloideae), a new cremnohyte from Scarp Forest in the Eastern Cape, South Africa**

GIDEON F. SMITH, NEIL R. CROUCH, ANDREW MCKAY, DAVID G.A. STYLES

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***Camellia nganiana*: a new species of Theaceae from Vietnam**

NGA NGUYEN-PHI, HONG TRUONG LUU

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Hyphoderma jingguense sp. nov. (Hyphodermataceae, Polyporales), a wood-inhabiting fungus from Yunnan Province, China

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Abstract

A new corticioid fungal species, *Hyphoderma jingguense* sp. nov., collected from a forest habitat in Yunnan Province, China, is described and illustrated based on morphological and molecular evidence. Morphologically, the species is characterized by ceraceous basidiomata with a farinaceous hymenial surface, a monomitic hyphal system with clamped generative hyphae, and allantoid basidiospores measuring $7.3\text{--}9.1 \times 3\text{--}3.9\ \mu\text{m}$. Phylogenetic analyses based on combined ITS and nLSU sequence data using Maximum Likelihood and Bayesian Inference placed *H. jingguense* within *Hyphoderma* (Hyphodermataceae), which forms a sister clade to *H. tenuissimum*. A description, illustrations, and phylogenetic analysis results are provided. In addition, we compare the new species with closely related taxa.

Key words: Fungal classification, Molecular data, Morphology, Phylogenetic analyses, Wood-inhabiting fungi

Introduction

In the Forest ecosystem, wood-decaying fungi secrete various enzymes that effectively degrade wood components such as cellulose, hemicellulose, and lignin into simple compounds by contributing to nutrient cycling, and consequently functioning as important decomposers in forest ecosystems (Kirk *et al.* 2008, Si *et al.* 2011, Floudas *et al.* 2012, Dai *et al.* 2021, Spirin *et al.* 2021, Wijesinghe *et al.* 2025).

Hyphoderma Wallr. (1833: 576) was established by Wallroth (1833) and is typified by *H. setigerum* (Fr.) Donk (1957: 15); it is one of the groups of wood-inhabiting fungi (Donk 1957, Yurchenko & Wu 2015, Li *et al.* 2026). Taxonomically, the generic delimitation of *Hyphoderma* and its related genera has long been controversial. Traditional classification included a broad assemblage of corticioid fungi in *Hyphoderma*, but subsequent molecular phylogenetic studies demonstrated that the traditionally circumscribed genus was polyphyletic, leading to the transfer of several species to related genera such as *Peniophorella* P. Karst. (1889: 427) (Larsson 2007, Justo *et al.* 2017, Li *et al.* 2026, Wan *et al.* 2026). Subsequent molecular phylogenetic studies have refined the circumscription of *Hyphoderma* and confirmed the independent phylogenetic position of the core *Hyphoderma* lineage within Hyphodermataceae Jülich (1982: 373) (Justo *et al.* 2017, Yang *et al.* 2025, Li *et al.* 2026, Wan *et al.* 2026). The genus is morphologically characterized by resupinate to effuse-reflexed basidiomata with a ceraceous consistency; smooth, tuberculate or hydroid hymenophores; a monomitic (rarely dimitic) hyphal structure with clamp connections on generative hyphae, and present or absent cystidia, suburniform to subcylindrical to cylindrical basidia bearing ellipsoid to subglobose,

smooth, thin-walled basidiospores (Bernicchia & Gorjón 2010). Species in this genus cause a white rot (Floudas *et al.* 2012, Guan *et al.* 2021, Duan *et al.* 2023). Based on the Index Fungorum (<http://www.indexfungorum.org>, accessed on 6 September 2026), *Hyphoderma* includes 224 specific and infraspecific names, of which 132 are accepted worldwide, and 55 species are accepted in China. In addition, for the hosts and substrates of these fungal species, *Hyphoderma* species were previously mainly reported on angiosperms, with few taxa on gymnosperms (such as *Hyphoderma alboarachnum*, and *Hyphoderma fulgens*), and were also found on bamboo (*Hyphoderma bambusinum*).

Molecular phylogenetic studies have played a pivotal role in elucidating the evolutionary relationships of *Hyphoderma*, integrated with morphology, too. Recent studies have used molecular data, particularly the internal transcribed spacer (ITS) region and the large subunit nuclear ribosomal RNA gene (nLSU) sequences, Nilsson *et al.* (2003) highlighted the phylogeography of *Hyphoderma setigerum* in the Northern Hemisphere based on molecular, morphological and crossing tests, and revealed nine preliminary taxa within the *H. setigerum* complex. Larsson (2007) revealed the classification of corticioid fungi and showed that *H. obtusum* J. Erikss. (1958: 97) and *H. setigerum* formed a clade within the family Meruliaceae Rea, and were recovered as sister to *Hypochnicium polonense* (Bres.) Å. Strid (1975: 68). Tellería *et al.* (2012) described *Hyphoderma macaronesicum* Tellería, M. Dueñas *et al.* (2012: 1125) and explored its phylogenetic affinities with allied taxa within *Hyphoderma*. Molecular systematic analyses have since provided a family-level phylogenetic framework for the order Polyporales and demonstrated that Hyphodermataceae contained only a single genus, *Hyphoderma* (Li *et al.* 2026). Multi-marker (ITS, nLSU, mtSSU, *rpb1*, and *rpb2*) phylogenetic analyses also revealed that *Hyphoderma* comprises several well-supported subclades (Yang *et al.* 2023a, 2025). Recent biogeographical studies and molecular clock estimates indicated that the ancestor of *Hyphoderma* likely originated in the Cretaceous, with a mean stem age of 117.76 Mya, and biogeographic reconstruction further suggested that Asia is the most probable ancestral area of *Hyphoderma* species (Li *et al.* 2026).

In a fungal survey of wood-inhabiting fungi in forest habitats of Yunnan Province, China, one undescribed corticioid fungal species was collected. To confirm the taxonomic affinities of the species, molecular phylogenetic analyses based on combined ITS and nLSU sequence data on the genus *Hyphoderma*, along with morphological characterization, were carried out. Accordingly, we propose a new species, *Hyphoderma jingguense*, with a detailed description and illustrations based on macro- and micro-morphological characteristics and molecular data.

Materials and methods

Sample collection and herbarium specimen preparation

Fresh basidiomata of lignicolous fungi were collected from fallen angiosperm branches in a broad-leaved forest located in Pu'er, Yunnan Province, China. Macromorphological features and important collection details were documented immediately in the field (Rathnayaka *et al.* 2025), and additional observations were made in the laboratory (Dong *et al.* 2024). Macro-morphological descriptions were based on field notes and photos captured in the field and lab. Micro-morphological data were obtained from dried specimens using a light microscope (Nikon Ni, Tokyo, Japan), and images were captured with a Nikon D7100 camera. All images were subsequently focus-stacked using Helicon Focus software. Specimens were dehydrated at 40 °C in an electric food dehydrator (Dong *et al.* 2025), then stored in paper envelopes and deposited in the herbarium of Southwest Forestry University (SWFC), Kunming, Yunnan, China.

Morphology

Macromorphological descriptions were based on field notes and photos captured in the field and laboratory. Petersen (1996) was followed for the color terminology. The micromorphological characters were obtained from the dried specimens using a light microscope with a 1000× magnification using a 100× oil immersion objective with a 10× ocular lens (Zhao *et al.* 2023, Dong *et al.* 2024), in which the measurements (e.g., spore sizes) did not change in water, CB, IKI and KOH.

The following abbreviations are used:

CB = Cotton Blue, CB– = acyanophilous.

IKI = Melzer's Reagent. IKI– = both inamyloid and indextrinoid.

KOH = 5% potassium hydroxide water solution

L = mean spore length (average for all spores)

W = mean spore width (average for all spores)

Q = variation in the L/W ratios between the specimens studied

Qm = mean of the individual Q values of all measured basidiospores $\pm$ standard deviation
n = a/b (number of spores (a) measured from given number (b) of specimens).

Molecular-Phylogenetic study

The CTAB rapid fungal genome extraction HiPure Fungal DNA Mini Kit II (Meiji Biotechnologies Co. Ltd., Guangzhou) was used to obtain genomic DNA from dried specimens following the manufacturer's instructions. The ITS region was amplified with the primer pair ITS5 and ITS4 (White *et al.* 1990). The nuclear ribosomal LSU gene was amplified with the primers LR0R and LR7 (Vilgalys & Hester 1990, Rehner & Samuels 1994). 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; while the PCR procedure for nLSU 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 products were purified and sequenced at Kunming Tsingke Biological Technology Limited Company, Kunming, Yunnan Province, China. All newly generated sequences were deposited in NCBI GenBank (Table 1).

TABLE 1. A list of species, specimens and GenBank accession numbers of sequences used in this study. The new species are shown in bold; * refers to type material (holotype) of relevant species and — refers to the missing data.

Species Name	Sample No.	GenBank Accession No.		Country	References
		ITS	nLSU		
<i>Diplomitoporus crustulinus</i>	FD-137	KP135299	KP135211	USA	Justo <i>et al.</i> 2017
<i>Hyphoderma alboarachnum</i>	CLZhao 30488*	PV470563	—	China	Li <i>et al.</i> 2026
<i>H. amoenum</i>	USO 286622	HE577030	—	Canada	Telleria <i>et al.</i> 2012
<i>H. asianum</i>	CLZhao 18091*	OR141726	PP826262	China	Yang <i>et al.</i> 2025
<i>H. assimile</i>	CBS:125852	MH863808	MH875272	New Zealand	Vu <i>et al.</i> 2019
<i>H. australosetigerum</i>	MA:Fungi 92235*	MN963764	—	Chile	Boonmee <i>et al.</i> 2021
<i>H. australosetigerum</i>	MA:Fungi 92240	MN963760	—	Chile	Boonmee <i>et al.</i> 2021
<i>H. bambusinum</i>	CLZhao 29903*	PV469674	PV819428	China	Li <i>et al.</i> 2026
<i>H. cinereofuscum</i>	CLZhao 30341	PQ492371	PQ511128	China	Li <i>et al.</i> 2025
<i>H. cinereofuscum</i>	CLZhao 30283	PQ492372	PQ511129	China	Li <i>et al.</i> 2025
<i>H. cremeoalbum</i>	NH 11538 (GB)	DQ677492	DQ677492	Sweden	Larsson 2007
<i>H. cremeoalbum</i>	CLZhao 17007	OM985716	OM985753	China	Duan <i>et al.</i> 2023
<i>H. crystallinum</i>	CLZhao 9338*	MW917161	MW913414	China	Guan & Zhao 2021a
<i>H. crystallinum</i>	CLZhao 9374	MW917162	MW913415	China	Guan & Zhao 2021a
<i>H. definitum</i>	NH 12266 (GB)	DQ677493	DQ677493	China	Larsson 2007
<i>H. fissuratum</i>	CLZhao 6731	MT791331	—	China	Ma <i>et al.</i> 2021
<i>H. fissuratum</i>	CLZhao 6726*	MT791330	MT791334	China	Ma <i>et al.</i> 2021
<i>H. floccosum</i>	CLZhao 17129*	MW301683	MW293733	China	Guan & Zhao 2021b
<i>H. floccosum</i>	CLZhao 17215	MW301687	MW293735	China	Guan & Zhao 2021b
<i>H. fulgens</i>	CLZhao 37429*	PV829544	PV810095	China	Li <i>et al.</i> 2026
<i>H. fulgens</i>	CLZhao 36600	PV829546	PV810096	China	Li <i>et al.</i> 2026
<i>H. granuliferum</i>	5273	JN710545	JN710545	Canada	Yurchenko & Wu 2014a
<i>H. grandineum</i>	CLZhao 30046*	PV470561	PV819429	China	Li <i>et al.</i> 2026
<i>H. guangdongense</i>	CLZhao 12657*	PP235513	PP235514	China	Su <i>et al.</i> 2024

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TABLE 1. (Continued)

Species Name	Sample No.	GenBank Accession No.		Country	References
		ITS	nLSU		
<i>H. incrustatum</i>	KHL 6685	—	AY586668	Spain	Yurchenko & Wu 2014a
<i>H. jingguense</i>	CLZhao 46043*	PZ688829	PZ10594	China	Present study
<i>H. jingguense</i>	CLZhao 46110	PZ688830	PZ10595	China	Present study
<i>H. laceratum</i>	CLZhao 34242*	PV829552	PV810101	China	Li <i>et al.</i> 2026
<i>H. laceratum</i>	CLZhao 34672	PV829553	PV810103	China	Li <i>et al.</i> 2026
<i>H. litschaueri</i>	NH 7603 (GB)	DQ677496	DQ677496	Sweden	Larsson 2007
<i>H. litschaueri</i>	FP-101740-Sp	KP135295	KP135219	USA	Floudas & Hibbett 2015
<i>H. macaronesicum</i>	MA:Fungi 90388	KC984327	—	USA	Telleria <i>et al.</i> 2012
<i>H. marginatum</i>	CLZhao 3404*	OM985717	OM985754	China	Duan <i>et al.</i> 2023
<i>H. medioburiense</i>	FD-335	KP135298	KP135220	China	Floudas & Hibbett 2015
<i>H. membranaceum</i>	CLZhao 5844*	MW917167	MW913420	China	Guan & Zhao 2021a
<i>H. membranaceum</i>	CLZhao 6971	MW917168	MW913421	China	Guan & Zhao 2021a
<i>H. microporoides</i>	CLZhao 6857	MW917169	MW913422	China	Guan & Zhao 2021a
<i>H. microporoides</i>	CLZhao 8695	MW917170	MW913423	China	Guan & Zhao 2021a
<i>H. moniliform</i>	Wu 0211-42*	KC928282	—	China	Yurchenko & Wu 2015
<i>H. moniliforme</i>	Wu 0211-46	KC928284	—	China	Yurchenko & Wu 2015
<i>H. mopanshanense</i>	CLZhao 6498*	MT791329	MT791333	China	Ma <i>et al.</i> 2021
<i>H. mopanshanense</i>	CLZhao 6449	OM985720	OM985759	China	Duan <i>et al.</i> 2023
<i>H. nemorale</i>	TNM F3931	KJ885183	KJ885184	China	Yurchenko & Wu 2015
<i>H. nemorale</i>	Wu 9508-14	KC928280	KC928281	China	Yurchenko & Wu 2015
<i>H. nitidum</i>	CLZhao 37195*	PV470533	—	China	Yuan <i>et al.</i> 2026
<i>H. nitidum</i>	CLZhao 37232	PV470534	—	China	Yuan <i>et al.</i> 2026
<i>H. niveomarginatum</i>	CLZhao 25078*	OR141728	OR506179	China	Yang <i>et al.</i> 2023
<i>H. nudicephalum</i>	Wu9307-29	AJ534269	—	China	Nilsson <i>et al.</i> 2003
<i>H. nudicephalum</i>	CLZhao 17839	OM985721	OM985760	China	Duan <i>et al.</i> 2023
<i>H. obtusiforme</i>	KHL1464	JN572909	—	Spain	Yurchenko & Wu 2014b
<i>H. obtusiforme</i>	KHL11105	JN572910	—	Spain	Yurchenko & Wu 2014b
<i>H. obtusum</i>	JS17804	—	AY586670	China	Yurchenko & Wu 2014b
<i>H. occidentale</i>	KHL 8477 (GB)	DQ677499	DQ677499	China	Larsson 2007
<i>H. paramacaronesicum</i>	MA:Fungi 87736*	KC984399	—	USA	Martín <i>et al.</i> 2018
<i>H. paramacaronesicum</i>	MA:Fungi 87737	KC984405	—	China	Martín <i>et al.</i> 2018
<i>H. pinicola</i>	TNM F13637	KJ885181	KJ885182	China	Yurchenko & Wu 2014b
<i>H. pinicola</i>	Wu 0108-36	KC928278	KC928279	China	Yurchenko & Wu 2014b

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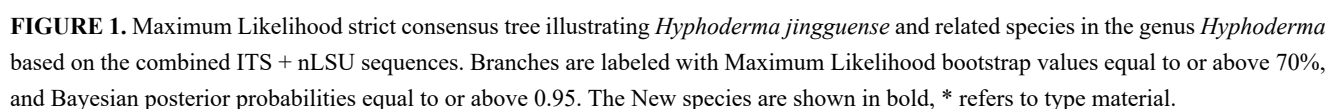
TABLE 1. (Continued)

Species Name	Sample No.	GenBank Accession No.		Country	References
		ITS	nLSU		
<i>H. prosopidis</i>	ARIZ HHB 8479	HE577029	—	China	Yurchenko & Wu 2015
<i>H. puerense</i>	CLZhao 9476*	MW443045	—	China	Guan <i>et al.</i> 2021
<i>H. puerense</i>	CLZhao 9583	MW443046	MW443051	China	Guan <i>et al.</i> 2021
<i>H. qujingense</i>	CLZhao 26018*	OR141729	PP826263	China	Yang <i>et al.</i> 2025
<i>H. setigerum</i>	FCUG 1200	AJ534273	—	Sweden	Nilsson <i>et al.</i> 2003
<i>H. setigerum</i>	FCUG 1688	AJ534272	—	Sweden	Nilsson <i>et al.</i> 2003
<i>H. sinense</i>	CLZhao 7963*	MW301679	MW293730	China	Guan & Zhao 2021b
<i>H. sinense</i>	CLZhao 17811	MW301682	MW293732	China	Guan & Zhao 2021b
<i>H. sordidum</i>	CLZhao 27379	OR141731	—	China	Yang <i>et al.</i> 2023
<i>H. sordidum</i>	CLZhao 27390*	OR141732	OR506180	China	Yang <i>et al.</i> 2023
<i>H. subsetigerum</i>	HHB11620	GQ409521	—	China	Yurchenko & Wu 2014a
<i>H. tenuissimum</i>	CLZhao 7221*	MW443049	MW443054	China	Guan <i>et al.</i> 2021
<i>H. tenuissimum</i>	CLZhao 16210	MW443050	MW443055	China	Guan <i>et al.</i> 2021
<i>H. tongbiguanense</i>	CLZhao 39574	PV470531	—	China	Yuan <i>et al.</i> 2026
<i>H. tongbiguanense</i>	CLZhao 39575*	PV470532	—	China	Yuan <i>et al.</i> 2026
<i>H. transiens</i>	NH 12304	DQ677504	DQ677504	Sweden	Larsson 2007
<i>H. tropicum</i>	CLZhao 17308*	OM985727	OM985768	China	Duan <i>et al.</i> 2023
<i>H. variolosum</i>	CBS:734.91	MH862320	MH873992	China	Vu <i>et al.</i> 2019
<i>H. variolosum</i>	CBS:735.91	MH862321	MH873993	China	Vu <i>et al.</i> 2019
<i>H. weishanense</i>	CLZhao 22403*	OR141727	OR506181	China	Yang <i>et al.</i> 2023
<i>H. yunnanense</i>	CLZhao 8845	OM985728	OM985769	China	Duan <i>et al.</i> 2023

Sequence quality was assessed, and BLAST searches were conducted against GenBank to identify closely related taxa. Reference sequences were retrieved from GenBank based on the BLAST search results. The ITS and nLSU datasets were aligned separately using MAFFT v.7, refined in AliView, and concatenated in Mesquite. All sequences are provided in Table 1. 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. Sequences of *Podoscypha vespillonea* (Berk.) Boidin & Lanq. (1973:143) and *Podoscypha yunnanensis* C.L. Zhao (2019: 214) were selected as an outgroup in the ITS + nLSU analysis (Fig. 1) as inspired by a previous study (Justo *et al.* 2017).

Maximum likelihood (ML) and Bayesian inference (BI) analyses were applied to the combined dataset following a previous study (Yang *et al.* 2025). Phylogenetic reconstructions were performed using ML tools implemented in the PhyloSuite v1.2.3 platform (Zhang *et al.* 2020). ML phylogenies were inferred with IQ-TREE v2.2.0, with 5,000 ultrafast bootstrap replicates and 1,000 SH-aLRT tests to assess branch support (Nguyen *et al.* 2015). 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 ModelFinder v2.2.0 (Kalyaanamoorthy *et al.* 2017) using a Bayesian Information Criterion, and the model was used for Bayesian analysis. The best model for the combined ITS+nLSU dataset estimated and applied in the Bayesian analysis was GTR+I+G+F. Four Markov chains were run from random starting trees. Trees were sampled every 1000th generation. The first 25% of sampled trees were discarded as burn-in, while the remaining trees were used to construct a 50% majority consensus tree and to calculate Bayesian posterior probabilities (BPPs).

- * Holotype
- ▲ Type species



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

Molecular phylogeny

The combined ITS+nLSU dataset (Fig. 1) included sequences from 78 fungal specimens representing 51 species. Maximum likelihood analysis was performed using IQ-TREE on the combined dataset under the GTR+R5+F model, which was selected as the best-fit substitution model according to the Akaike Information Criterion (AIC). The resulting best-scoring ML tree (Fig. 1) had a final optimized likelihood value of -22657.977. For Bayesian Inference (BI) analysis, a total of four Markov chains were run for two independent runs from random starting trees, each with 2.4 million generations for the ITS+nLSU dataset, with trees and parameters sampled every 1000 generations, with an average standard deviation of split frequencies = 0.006754 (BI) and an effective sample size (ESS) average ESS (avg. ESS) = 1003.5. Maximum Likelihood (ML) and Bayesian Inference (BI) analyses yielded similar topologies.

Phylogenetic analyses based on a combined ITS+LSU dataset (Fig. 1) revealed that the new species, *Hyphoderma jingguense*, was nested within the genus *Hyphoderma*, forming a separate clade sister to *H. tenuissimum* C.L. Zhao & Q.X. Guan (2021: 153) with 100% BS and 1.00 BPP support.

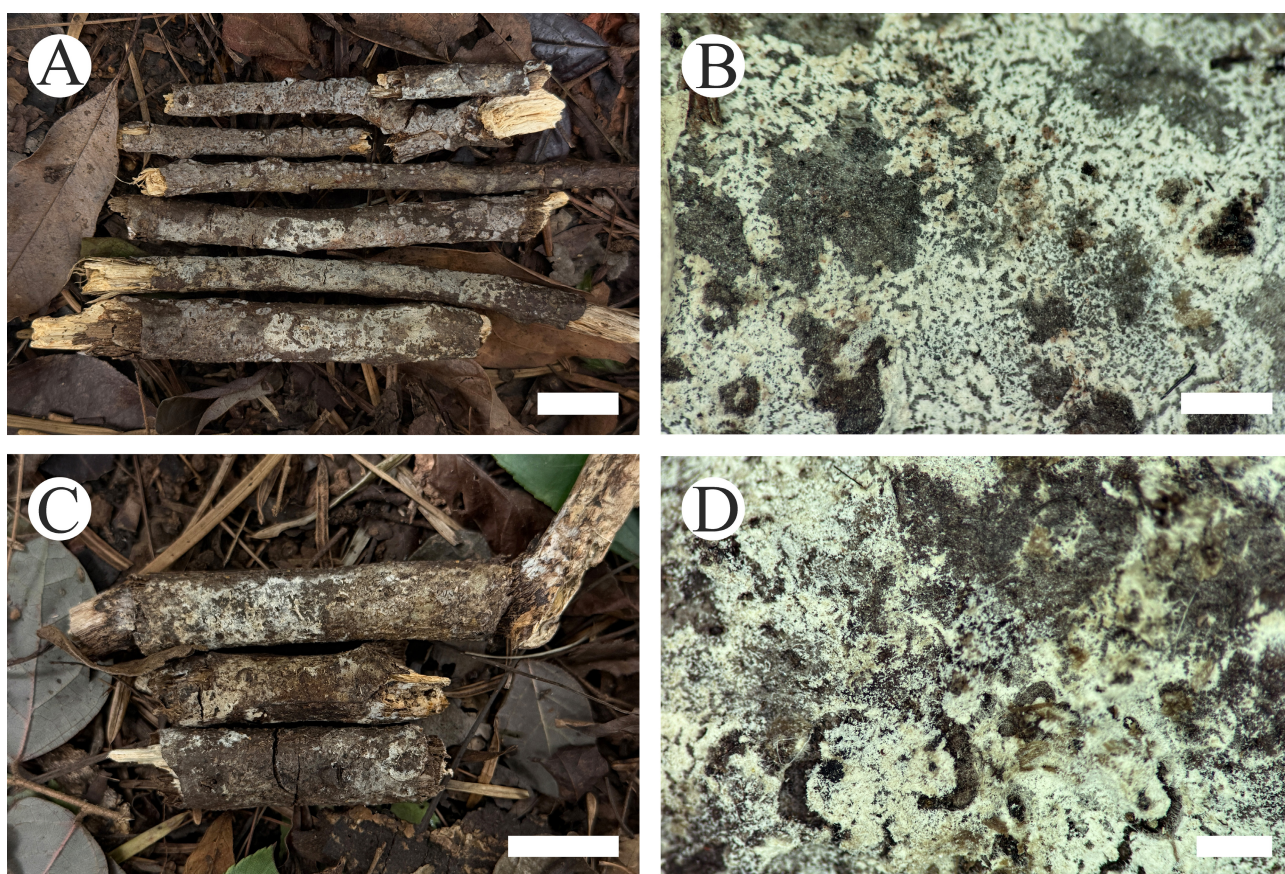


FIGURE 2. Basidiomata of *Hyphoderma jingguense* (A, B) CLZhao 46043 (holotype); (C, D) CLZhao 46110 (paratype). Scale bars: A–B = 1 cm; C–D = 1 mm.

Taxonomy

Hyphoderma jingguense Q. Li & C.L. Zhao, *sp. nov.* Figs. 2–4

Mycobank no.: MB864825

Etymology:—*Jingguense* (Lat.): refers to the type locality, Jinggu County of Yunnan Province.

Diagnosis:—*Hyphoderma jingguense* differs from *H. tenuissimum* by ceraceous basidiomata, a farinaceous hymenial surface, and cylindrical to allantoid basidiospores ($7.3\text{--}9.1 \times 3\text{--}3.9\ \mu\text{m}$).

Holotype:—CHINA. Yunnan Province, Pu'er, Jinggu County, Xiaoheijiang virgin Forest Park, GPS coordinates $23^{\circ}02'\text{N}$, $100^{\circ}43'\text{E}$, elevation 1210 m asl., on fallen angiosperm branch, leg. C.L. Zhao, 19 August 2025, CLZhao 46043 (SWFC 00046043).

Basidiomata:—Annual, resupinate, adnate, without odor or taste when fresh, soft ceraceous when fresh, becoming ceraceous upon drying, up to 10 cm long, 1.5 cm wide and 100 μm thick. Hymenial surface farinaceous, slightly buff when fresh, buff upon drying. Sterile margin narrow, pale buff, up to 1 mm.

Hyphal structure:—Hyphal system monomitic, generative hyphae with clamp connections, colorless, thick-walled, rarely branched, interwoven, 2.5–5 μm in diameter; IKI–, CB–; tissues unchanged in KOH.

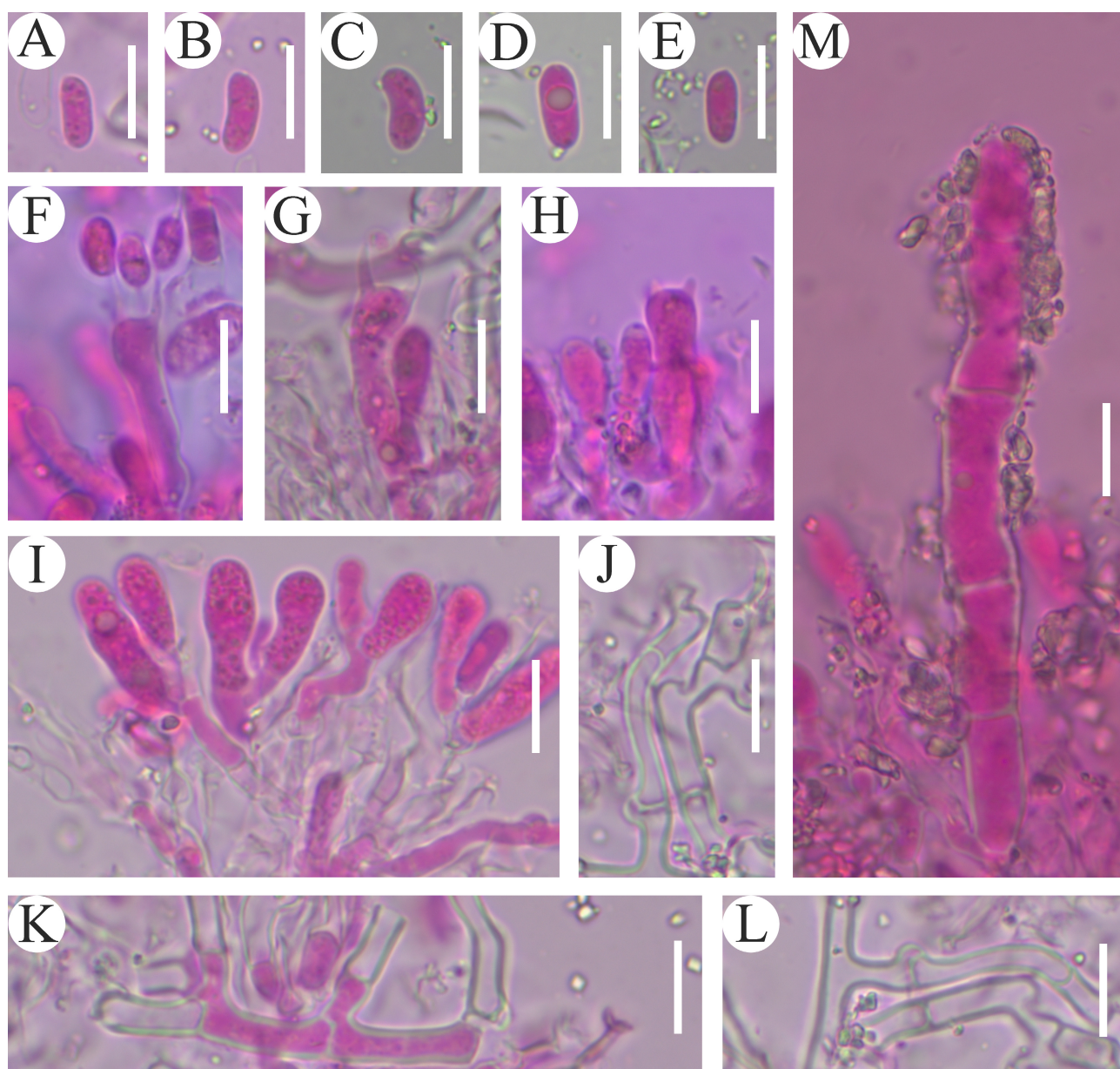


FIGURE 3. Sections of hymenium of *Hyphoderma jingguense* (holotype, CLZhao 46043). (A–E) Basidiospores; (F–H) Basidia; (I) Basidioles; (J–L) Generative hyphae; (M) Cystidia. Scale bars: A–M = 10 μm .

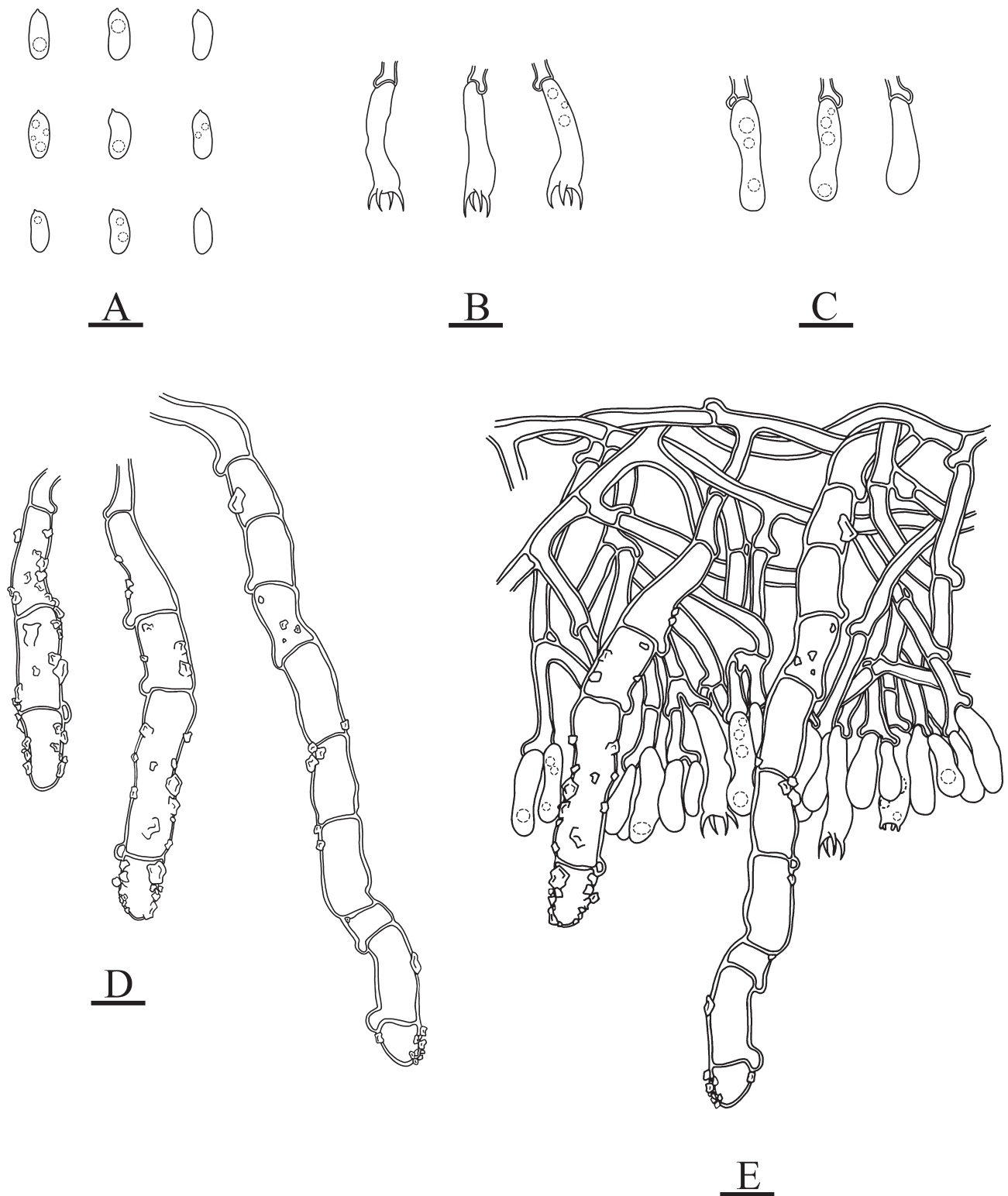


FIGURE 4. Microscopic structures of *Hyphoderma jingguense* (holotype, CLZhao 46043). (A) Basidiospores; (B) Basidia; (C) Basidioles; (D) Cystidia; (E) A section of the hymenium. Scale bars: A–E = 10 μ m.

Hymenium:—Cystidia cylindrical, thick-walled, with 2–9 septa and encrusted with abundant crystals, $37\text{--}145 \times 7\text{--}10 \mu\text{m}$. Basidia clavate, slightly sinuous or constricted in the middle, with 4 sterigmata and a basal clamp connection, $11\text{--}21 \times 3.5\text{--}7 \mu\text{m}$; basidioles dominant, similar to basidia in shape, but slightly smaller.

Basidiospores:—Allantoid, thin-walled, smooth, colorless, IKI–, CB–, $(6.5\text{--})7.3\text{--}9.1(-10) \times (2.9\text{--})3\text{--}3.9(-4) \mu\text{m}$, $L = 8.24 \mu\text{m}$, $W = 3.46 \mu\text{m}$, $Q = 2.36\text{--}2.46$, $Q_m = 2.38 \pm 0.2$ ($n = 60/2$).

Additional specimen examined (paratype):—CHINA. Yunnan Province, Pu'er, Jinggu County, Xiaoheijiang Original Forest Park, GPS coordinates $23^{\circ}02'N$, $100^{\circ}56'E$, elevation 1104 m asl., on a fallen angiosperm branch, leg. C.L. Zhao, 20 August 2025, CLZhao 46110 (SWFC 00046110).

Discussion

Wood-rotting fungi play essential roles in ecosystem functioning, which have substantial economic value, and are of considerable importance in scientific research (Vainio *et al.* 2011, Dai & Cui 2014, Shen *et al.* 2018, Ma & Zhao 2019, Yang *et al.* 2023b, Bhunjun *et al.* 2024, Deng *et al.* 2026, Wang *et al.* 2026). Geographically, southwest China, including Yunnan Province, is recognized as a major center of fungal diversity (Dai *et al.* 2004, 2007, 2021; Yuan *et al.* 2021; Zhang *et al.* 2023; Cui *et al.* 2025). In this study, we describe a new species of *Hyphoderma* based on morphological and molecular evidence, expanding the taxonomic framework and diversity of *Hyphoderma* in subtropical Asia.

Phylogenetically, *Hyphoderma jingguense* is closely related to *H. tenuissimum* and *H. yunnanense* Z.Y. Duan & C.L. Zhao (2023: 12) based on ITS+nLSU gene analyses (Fig. 1). *Hyphoderma tenuissimum* differs from *H. jingguense* by its membranaceous basidiomata when fresh, tuberculate to minutely granuloid hymenial surface, clavate to subcylindrical basidia, and cylindrical basidiospores (Guan *et al.* 2021). However, *H. yunnanense* differs from *H. jingguense* by a tuberculate hymenial surface, thin-walled generative hyphae, and narrowly ellipsoid to cylindrical basidiospores ($10\text{--}11.5 \times 4\text{--}5.5 \mu\text{m}$ vs. $7.3\text{--}9.1 \times 3\text{--}3.9 \mu\text{m}$, Duan *et al.* 2023).

Further, morphologically, *Hyphoderma jingguense* resembles *H. microporoides* C.L. Zhao & Q.X. Guan (2021: 9), *H. pinicola* Yurchenko & Sheng H. Wu (2014: 2) and *H. sinense* C.L. Zhao & Q.X. Guan (2021: 454) in sharing clamp connections, generative hyphae, and allantoid basidiospores. However, *H. microporoides* differs from *H. jingguense* by its smooth hymenial surface, thin-walled generative hyphae, and capitate and smooth cystidia (Guan & Zhao 2021a). *Hyphoderma pinicola* is distinguished from *H. jingguense* by its membranaceous hymenial surface, thin-walled generative hyphae, and scattered, aseptate cystidia (Yurchenko & Wu 2014a). *Hyphoderma sinense* differs from *H. jingguense* by a membranaceous hymenial surface, encrusted and moniliform cystidia, and larger basidia ($20.5\text{--}34 \times 6\text{--}9.5 \mu\text{m}$ vs. $11\text{--}21 \times 3.5\text{--}7 \mu\text{m}$, Guan & Zhao 2021b).

In recent years, numerous new species of *Hyphoderma* have been reported from Yunnan province (Guan *et al.* 2021, Yang *et al.* 2023a, Li *et al.* 2025, 2026), reflecting the high species diversity of this region. The high diversity of *Hyphoderma* is likely associated with the region's complex topography, diverse vegetation types, and heterogeneous climatic conditions. This also suggests that more undescribed species likely remain to be discovered in forest habitats in Yunnan Province. The discovery of *H. jingguense* in Asia is consistent with Li *et al.* (2026), which proposed that Asia is the most probable ancestral area of the genus.

Although our study provides robust morphological and molecular evidence for species delimitation, the phylogenetic analyses relied solely on ITS and nLSU sequences. Future studies incorporating protein-coding markers, such as *rpb1*, *rpb2*, and *tef1- α* , together with broader taxon sampling, may provide better resolution of relationships among closely related species of *Hyphoderma*. *Hyphoderma* remains a taxonomically challenging group with diverse cystidia morphology, and a comprehensive revision of this genus will require global sampling and more in-depth phylogenomic studies.

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