Phytotaxa
661

The wood-decaying fungal diversity unveiled by morphology and phylogeny in Ailaoshan Mountain, Yunnan, China

LU WANG, XIN YANG, CHANGLIN ZHAO

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Page range: 1-30

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Volvariella griseoalba (*Agaricales*, *Volvariellaceae*), a new species from Punjab, Pakistan

WASIQA ARSHAD, HIRA IJAZ, MEHBOOBULLAH KHAN, ANEELA YASMEEN, CHANG-LIN ZHAO, ANEEQA GHAFOOR, ESHA KOMAL, ABDUL RAHMAN NIAZI, SANA JABEEN

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DOI: 10.11646/phytotaxa.661.1.2

Page range: 31-46

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A new species of *Impatiens* (Balsaminaceae) from Southern Xizang, China with supplementary knowledge on *I. leptocarpa* Hook. f.

JING TIAN, TAO-HUA YUAN, SHUAI PENG, ZHU-ZHU YANG, GUANG-WAN HU, QING-FENG WANG

Published: 2024-07-18

DOI: 10.11646/phytotaxa.661.1.3

Page range: 47-62

PDF (12.20MB)

Morphological variation within *Solanum campylacanthum* (Solanaceae) in Uganda and its relationship with *S. cerasiferum*

CAROL KAWUMA, MARY NAMAGANDA, ESTHER KATUURA, PERPETUA IPULET, JOHN WASSWA MULUMBA, BIRTHAN KANSIIME, FELLY MOMBO TUNSIME, ANIFAT OLAYEMI BELLO, BRITA STEDJE

Published: 2024-07-18

DOI: 10.11646/phytotaxa.661.1.4

Page range: 63-74

PDF (5.62MB)

Molecular phylogeny and morphology reveal a new wood-inhabiting fungal species, *Hyphoderma guangdongense* (Polyporales, Basidiomycota), from China

JIANGQING SU, XUNCHI ZHANG, CHANGLIN ZHAO, HONGMIN ZHOU

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Page range: 75-86

PDF (5.22MB)

Two new species of *Syzygium* (Myrtaceae) from Wawonii Island, Southeastern Sulawesi, Indonesia

SITI SUNARTI, ROSADAH

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Page range: 87-96

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A new species of *Tarenna* (Rubiaceae: Ixoroideae) from Kerala, India

ROSE ALOOR JOSE, ANOOP PUTHUPARAMBIL BALAN, THOMAS VALIKATTIL PONNACHAN

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Lectotypification and new data on the distribution of the Philippine endemic *Liparis dumaguetensis* (Orchidaceae)

MA. KATRINA R. FULGENCIO, JIM COOTES, OLIVE A. AMPARADO, MARK ARCEBAL K. NAIVE

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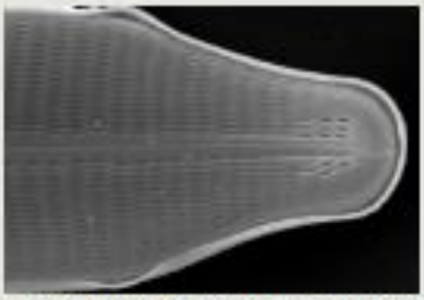

Geissleria triundulata sp.nov., a new freshwater diatom (Cymbellaceae, Bacillariophyta) from the Mula-Mutha River Basin, India

PRATYASHA NAYAK, MITAL THACKER, PAUL B. HAMILTON, BALASUBRAMANIAN KARTHICK

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Page range: 109-118

Abstract views: 7

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Dryopteris microlepioides, a new synonym of *Trichoneuron microlepioides* (Dryopteridaceae)

SHI-YONG DONG, ZHENG-YU ZUO, VAN THE PHAM

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Molecular phylogeny and morphology reveal a new wood-inhabiting fungal species, *Hyphoderma guangdongense* (Polyporales, Basidiomycota), from China

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Abstract

Hyphoderma is one of the most important representative groups of wood-inhabiting fungi. These fungi secrete various enzymes capable of degrading cellulose, hemicellulose, and lignin into simple inorganic substances. The taxa within the genus cause the white rot of wood, play a key role in the carbon cycle, and are the most efficient wood decomposers in the forest ecosystem. This study proposes a new wood-inhabiting fungal taxon, *Hyphoderma guangdongense,* based on morphological features and molecular evidence. It is characterized by the white hymenial surface, a monomitic hyphal system having the generative hyphae with clamp connections, the presence of the septate and tubular cystidia, and cylindrical basidiospores (6–10 × 3–5 µm). The phylogenetic tree inferred from a combination of the internal transcribed spacers (ITS) and large subunit (nrLSU) of the nuclear ribosomal DNA (rDNA) sequences revealed that *H. guangdongense* placed into the genus *Hyphoderma*, in which it is closely related to a clade comprising two taxa, *H. setigerum,* and *H. floccosum*. A full description, illustrations, and results of the new species' phylogenetic analysis are provided.

Key words: 1 new species, Biodiversity, Guangdong Province, Phylogenetic analysis, Taxonomy, Wood-inhabiting fungi

Introduction

Fungi are eukaryotic microorganisms that play fundamental ecological roles as decomposers, pathogens, and mutualists of plants and animals (Tedersoo *et al.* 2014, Yang *et al.* 2023). In forest ecosystems, the fungi drive carbon cycling in forest soils, mediate the mineral nutrition of plants, alleviate carbon limitations, and alleviate the carbon limitations (Tedersoo *et al.* 2014, Yang *et al.* 2024). Fungi have evolved numerous strategies to degrade hard-to-digest substrates for outcompeting other microbes while combating competitors using an arsenal of bioactive metabolites, such as the familiar antibiotics, ethanol, and organic acids (Rokas *et al.* 2018). To carry out the genome evolution and reconstruction of the phylogenetic relationships of fungi, an increasing number of species have been employed for the fungal tree of life by using genome-scale data in molecular systematics by mycologists (James *et al.* 2020, Luo *et al.* 2022). Molecular systematics has supported many existing lineages, which changed the traditional attribution of many fungal species and found many new taxa (Duan *et al.* 2023).

Wood-inhabiting fungi are a cosmopolitan group in kingdom fungi and have a rich diversity related to the high diversity of plants growing in boreal, temperate, subtropical, and tropical regions (Gilbertson & Ryvarden 1987, Núñez & Ryvarden 2001, Bernicchia & Gorjón 2010, Dai 2012, Ryvarden & Melo 2014, Dai *et al.* 2015, 2021, Wu *et al.* 2020, Luo *et al.* 2022, Duan *et al.* 2023, Yang *et al*. 2024). The taxa from the family Hyphodermataceae are continuously reported, with the frequent inclusion of data from DNA sequences and by employing both fresh material and cultures, and mycologists re-collect historic taxa and their types to accomplish taxonomy and molecular systematics in this family Hyphodermataceae (Yurchenko & Wu 2015, Luo *et al.* 2022, Wijayawardene *et al.* 2022, Yang *et al.* 2023).

The genus *Hyphoderma* Wallr. (1833: 576) (Hyphodermataceae, Polyporales) represents one of the most species-rich and taxonomically complicated genera among wood-inhabiting fungi, typified by *H. setigerum* (Fr.) Donk. (1957:

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15) (Donk 1957, Kirk *et al.* 2008, Yurchenko & Wu 2015). The species within the genus cause white- rot (Wu 1997), but it is one of the most important fungal groups in the forest ecosystem (Floudas *et al.* 2012, Duan *et al.* 2023). *Hyphoderma* is characterized by the resupinate to effuse-reflexed basidiomata with ceraceous consistency, smooth to tuberculate or hydnoid hymenophore, a monomitic hyphal structure (rarely dimitic) with clamp connections on generative hyphae, presence of cystidia or not, basidia suburniform to subcylindrical and cylindrical, smooth, thin-walled, ellipsoid to subglobose basidiospores (Wallroth 1833, Bernicchia & Gorjón 2010). Currently, 116 species have been accepted worldwide in *Hyphoderma* (Donk 1957, Nakasone 2008, Wu *et al.* 2010, Baltazar *et al.* 2016, Martín *et al.* 2018, Ma *et al.* 2021, Duan *et al.* 2023). *Hyphoderma* has registered 209 specific and infraspecific names in Index Fungorum (http://www.indexfungorum.org) and MycoBank (https://www.mycobank.org).

Molecular systematics covering *Hyphoderma* revealed the classification of corticioid fungi which showed that *H. obtusum* J. Erikss. (1958: 16) and *H. setigerum* clustered into the family Meruliaceae Rea, and then grouped with the taxon *Hypochnicium polonense* (Bres.) Donk (1957: 15) in this research, based on the internal transcribed spacer (ITS) regions and the large subunit nuclear ribosomal RNA gene (nLSU) sequences (Larsson 2007). Tellería *et al*. (2012) discussed the relationships between two genera *Hyphoderma* and *Peniophorella* P. Karst., in which some species from both genera were grouped and proposed a new species, *H. macaronesicum* Tellería, M. Dueñas, Beltrán-Tej., Rodr.-Armas & M.P. Martín (2012: 1125). The research focusing on the *H. setigerum* complex showed that *H. pinicola* Yurchenko. & Sheng H. Wu (2014a: 2) represented the fifth species in this complex, and the result revealed that this complex occurred worldwide from tropical to temperate regions (Yurchenko & Wu 2014b). A revised family-level classification of the order Polyporales revealed that four species of *Hyphoderma* nested into the residual polyporoid clade, belonging to the family Hyphodermataceae, and they were grouped with three related genera *Meripilus* P. Karst., *Physisporinus* P. Karst. and *Rigidoporus* Murrill (Justo *et al.* 2017). The research was carried out based on the morphology and phylogeny, in which two new species, *H. fissuratum* C.L. Zhao & X. Ma (2021: 37) and *H. mopanshanense* C.L. Zhao (2021: 39), were proposed, and the *Hyphoderma* species were compared with closely related taxa (Ma *et al.* 2021).

During the surveys of wood-inhabiting fungi, we discovered a species of this group in Guangdong Province, China, which was not consistent with any known species of wood-inhabiting fungi. To clarify the placement and relationships of the species, we carried out a phylogenetic and taxonomic study on *Hyphoderma* based on the ITS+nLSU sequences.

Materials and methods

Sample collection and herbarium specimen preparation

Fresh basidiomata of fungi growing on angiosperm branches were collected from the Shaoguan of Guangdong Province, P.R. China. The samples were photographed in situ, and fresh macroscopic details were recorded. Photographs were recorded using a Canon 80D camera (Tokyo, Japan). All photos were stacked and merged using Helicon Focus Pro 7.7.5 software. Specimens were dried in an electric food dehydrator at 40 °C (Hu *et al.* 2022), and then sealed and stored in an envelope bag and deposited in the herbarium of the Southwest Forestry University (SWFC), Kunming, Yunnan Province, P.R. China.

Morphology

Macromorphological descriptions were based on field notes and photos captured in the field and lab. Color terminology followed Petersen (1996). Micromorphological data were obtained from the dried specimens following observation under a light microscope (Zhao *et al.* 2023). The following abbreviations were used: KOH = 5% potassium hydroxide water solution, CB = cotton clue, 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 a given number (b) of specimens). Q_m represented the average Q of basidiospores measured ± standard deviation.

DNA extraction

The CTAB rapid plant genome extraction kit-DN14 (Aidlab Biotechnologies Co., Ltd., Beijing, P.R. China) was used to obtain genomic DNA from the dried specimens. The nuclear ribosomal ITS region was amplified with primers ITS5 and ITS4 (White *et al.* 1990). The nuclear nLSU region was amplified with primer pair LR0R and LR7 (Vilgalys & Hester 1990).

PCR amplification, sequencing

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 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 (Yunnan Province, P.R. China). All newly generated sequences were deposited in NCBI GenBank (https://www.ncbi.nlm.nih.gov/genbank/). These sequences, along with sequences from closely related taxa, are given in Table 1.

TABLE 1. Names, voucher numbers, references, and corresponding GenBank accession numbers of sequences used in this study. (The new species are in bold, * is shown type material, - is shown data without used)

Species name	Voucher number	GenBank accession number		References
		ITS	nLSU	
Diplomitoporus crustulinus	FD-137	KP135299	KP135211	Justo *et al*. 2017
Hyphoderma amoenum	USO 286622	HE577030	-	Tellería *et al*. 2012
H. assimile	CBS:125852	MH863808	MH875272	Vu *et al*. 2019
H. cremeoalbum	NH 11538 (GB)	DQ677492	DQ677492	Larsson 2007
H. cremeoalbum	CLZhao 17007	OM985716	OM985753	Duan *et al*. 2023
H. crystallinum	CLZhao 9338	MW917161	MW913414	Guan & Zhao 2021a
H. crystallinum	CLZhao 9374	MW917162	MW913415	Guan & Zhao 2021a
H. definitum	NH 12266 (GB)	DQ677493	DQ677493	Larsson 2007
H. fissuratum	CLZhao 6731	MT791331	-	Ma *et al*. 2021
H. fissuratum	CLZhao 6726	MT791330	MT791334	Ma *et al*. 2021
H. floccosum	CLZhao 17129	MW301683	MW293733	Guan & Zhao 2021b
H. floccosum	CLZhao 17215	MW301687	MW293735	Guan & Zhao 2021b
H. granuliferum	5273	JN710545	JN710545	Yurchenko & Wu 2014b
H. guangdongense	**CLZhao 12657**	**PP235513**	**PP235514**	**Present study**
H. incrustatum	KHL6685	-	AY586668	Yurchenko & Wu 2014b
H. litschaueri	NH 7603 (GB)	DQ677496	DQ677496	Larsson 2007
H. litschaueri	FP-101740-Sp	KP135295	KP135219	Duan *et al*. 2023
H. macaronesicum	MA:Fungi 90388	KC984327	-	Unpublished
H. macaronesicum	TFC:Mic 15115	HE577011	-	Yurchenko & Wu 2014b
H. marginatum	CLZhao 3404	OM985717	OM985754	Duan *et al*. 2023
H. medioburiense	FD-335	KP135298	KP135220	Floudas & Hibbett 2015
H. membranaceum	CLZhao 5844	MW917167	MW913420	Guan & Zhao 2021a
H. membranaceum	CLZhao 6971	MW917168	MW913421	Guan & Zhao 2021a
H. microporoides	CLZhao 6857	MW917169	MW913422	Guan & Zhao 2021a
H. microporoides	CLZhao 8695	MW917170	MW913423	Guan & Zhao 2021a
H. moniliforme	Wu 0211-42	KC928282	-	Yurchenko & Wu 2015
H. moniliforme	Wu 0211-46	KC928284	-	Yurchenko & Wu 2015
H. mopanshanense	CLZhao 6498	MT791329	MT791333	Ma *et al*. 2021
H. mopanshanense	CLZhao 6449	OM985720	OM985759	Duan *et al*. 2023
H. nemorale	TNM F3931	KJ885183	KJ885184	Yurchenko & Wu 2015
H. nemorale	Wu 9508-14	KC928280	KC928281	Yurchenko & Wu 2015
H. niveomarginatum	CLZhao 25078	OR141728	OR506179	Yang *et al*. 2023
H. nudicephalum	Wu9307_29	AJ534269	-	Nilsson *et al.* 2003

...continued on the next page

TABLE 1. (Continued)

Species name	Voucher number	GenBank accession number		References
		ITS	nLSU	
H. nudicephalum	CLZhao 17839	OM985721	OM985760	Duan *et al*. 2023
H. obtusiforme	KHL1464	JN572909	-	Yurchenko & Wu 2014a
H. obtusiforme	KHL11105	JN572910	-	Yurchenko & Wu 2014a
H. obtusum	JS17804	-	AY586670	Yurchenko & Wu 2014a
H. occidentale	KHL 8477 (GB)	DQ677499	DQ677499	Larsson 2007
H. paramacaronesicum	MA: Fungi 87736	KC984399	-	Martín *et al*. 2018
H. paramacaronesicum	MA: Fungi 87737	KC984405	-	Martín *et al*. 2018
H. prosopidis	ARIZ HHB 8479	HE577029	-	Yurchenko & Wu 2015
H. puerense	CLZhao 9476	MW443045	-	Guan *et al.* 2021
H. puerense	CLZhao 9583	MW443046	MW443051	Guan *et al*. 2021
*H. setigerum**	FCUG 1200	AJ534273	-	Nilsson *et al*. 2003
*H. setigerum**	FCUG 1688	AJ534272	-	Nilsson *et al*. 2003
H. sinense	CLZhao 7963	MW301679	MW293730	Guan & Zhao 2021b
H. sinense	CLZhao 17811	MW301682	MW293732	Guan & Zhao 2021b
H. sordidum	CLZhao 27379	OR141731	-	Yang *et al*. 2023
H. sordidum	CLZhao 27390	OR141732	OR506180	Yang *et al*. 2023
H. subsetigerum	HHB11620	GQ409521	-	Yurchenko & Wu 2014a
H. tenuissimum	CLZhao 7221	MW443049	MW443054	Guan *et al*. 2021
H. tenuissimum	CLZhao 16210	MW443050	MW443055	Guan *et al*. 2021
H. transiens	NH 12304 (GB)	DQ677504	DQ677504	Larsson 2007
H. tropicum	CLZhao 17308	OM985727	OM985768	Duan *et al*. 2023
H. variolosum	CBS: 734.91	MH862320	MH873992	Vu *et al.* 2019
H. variolosum	CBS: 735.91	MH862321	MH873993	Vu *et al.* 2019
H. weishanense	CLZhao 22403	OR141727	OR506181	Yang *et al*. 2023

Phylogenetic analyses

The sequences were aligned in 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). The dataset was aligned first and then ITS+nLSU sequences were combined with Mesquite version 3.51. The alignment datasets were deposited in TreeBASE (submission ID 31209). *Diplomitoporus crustulinus* (Bres.) Domanski (1970: 192) was selected as an outgroup taxon for the phylogenetic analyses of the ITS+nLSU following a previous study (Justo *et al*. 2017). Maximum parsimony (MP), Maximum Likelihood (ML), and Bayesian Inference (BI) analyses were applied to the combined three datasets. Approaches to phylogenetic analyses followed Zhao and Wu (2017). MP analysis 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 1000 random sequence additions. Maxtrees were set to 5000, branches of zero length were collapsed and all most parsimonious trees were saved. Clade robustness was assessed using bootstrap (BT) analysis with 1000 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 most-parsimonious tree generated. ML was inferred using RAxML-HPC2 through the Cipres Science Gateway (www.phylo.org) (Miller *et al*. 2012). Branch support (BS) for ML analysis was determined by 1,000 bootstrap replicates and evaluated under the gamma model.

MrModeltest 2.3 (Nylander 2004) was used to determine the best-fit evolution model for each data set for Bayesian inference (BI), which 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). A total of 4 Markov chains were run for 2 runs from random starting trees for 4 million generations for ITS+nLSU (Fig. 1), with trees and parameters sampled every 1000 generations. The first one-fourth of all generations were discarded as burn-in. The majority rule consensus tree of all remaining trees was calculated. Branches were considered as significantly supported if they received maximum

likelihood bootstrap value (BS) ≥70%, maximum parsimony bootstrap value (BT) ≥70%, or Bayesian posterior probabilities (BPP) ≥0.95.

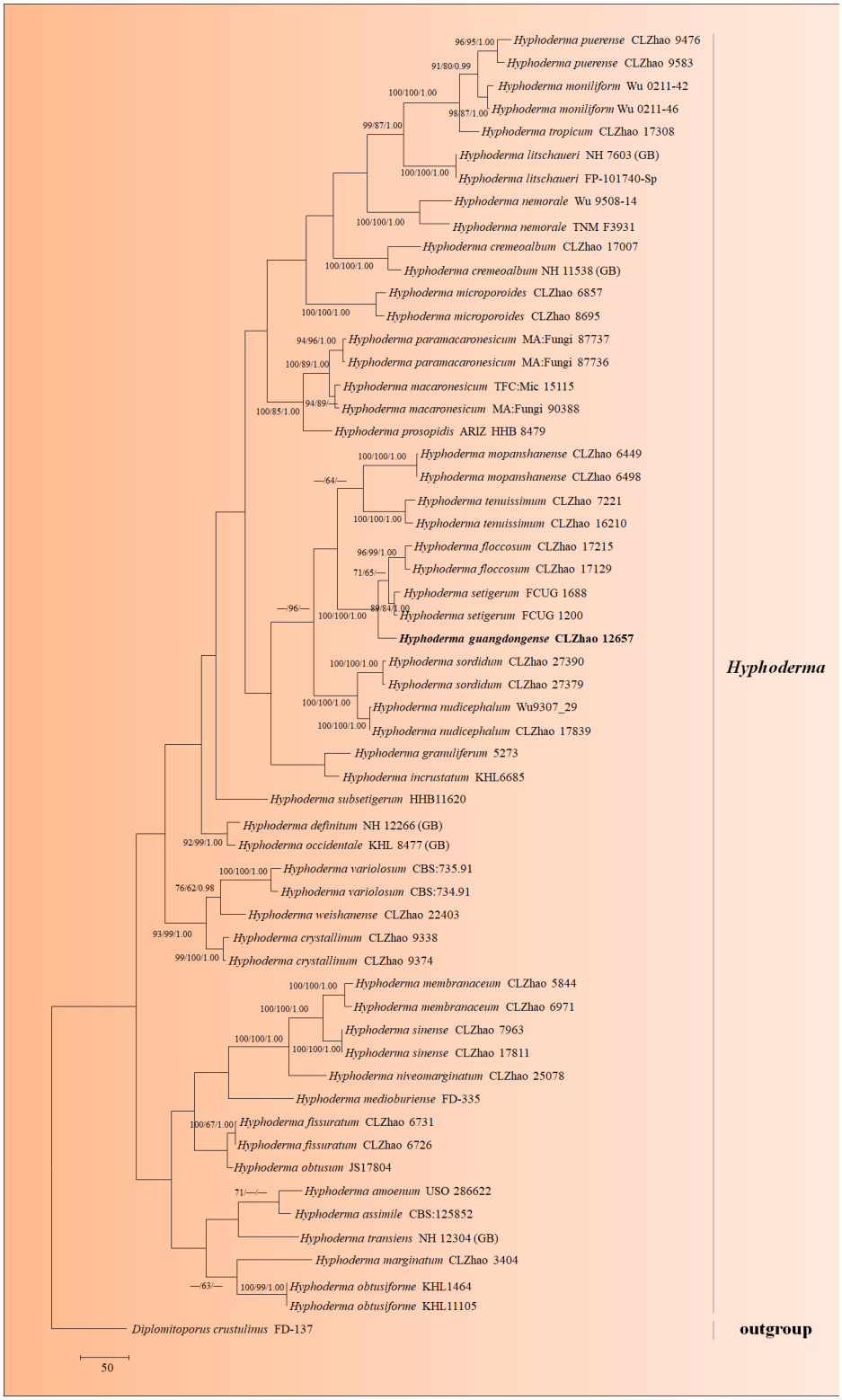

FIGURE 1. Maximum parsimony strict consensus tree illustrating the phylogeny of a new species and related species in *Hyphoderma* based on ITS+nLSU sequences. The branch is labeled with the maximum likelihood lead value equal to or greater than 70%, the reduced lead value equal to or greater than 50%, and the Bayesian posterior probability value equal to or greater than 95%. The new species is in bold.

Results

Phylogenetic analyses

The dataset based on ITS+nLSU comprises sequences from 57 fungal specimens representing 37 species. The dataset had an aligned length of 2030 characters, of which 1413 characters are constant, 135 are variable and parsimony-uninformative, and 482 are parsimony-informative. Maximum parsimony analysis yielded 2 equally parsimonious trees (TL = 3053, CI = 0.3344 HI = 0.6656, RI = 0.5881, and RC = 0.1967). Bayesian analysis and ML analysis resulted in a similar topology as MP analysis with an average standard deviation of split frequencies of 0.009838 (BI), and the effective sample size (ESS) across the two runs is double the average ESS (avg ESS) = 326.5. In addition, the results of BLAST queries in NCBI based on ITS and nLSU separately showed the sequences producing significant alignment descriptions: in ITS BLAST results, the top ten taxa are *Hyphoderma pinicola*, and *H. subsetigerum* (Maximum record descriptions: Max score 968; Total score 968; Query cover 100%; E value 0.0; Ident 96.43%). In nLSU BLAST results, the top ten taxa are *Hyphoderma floccosum*, *H. subsetigerum,* and *H. nudicephalum* (Maximum record descriptions: Max score 2508; Total score 2508; Query cover 99%; E value 0.0; Ident 99.56%). The phylogenetic tree (Fig. 1) inferred from ITS+nLSU sequences revealed that *Hyphoderma guangdongense* grouped into the genus *Hyphoderma*, in which it closely grouped with two taxa *H. setigerum* and *H. floccosum* C.L. Zhao & Q.X. Guan (2021: 455).

Taxonomy

Hyphoderma guangdongense J.Q. Su & C.L. Zhao, *sp. nov.* Figs. 2, 3

MycoBank no.: MB 852596

***Diagnosis*:—**Differs from other species in the genus by the white hymenophore surface, a monomitic hyphal system, and cylindrical basidiospores (7.4–9.0 × 3.2–4.0 µm).

Etymology*:—guangdongense* (Lat.): refers to "Guangdong Province" where the type specimen was collected.

***Holotype*:—**CHINA. Guangdong Province, Shaoguan, Danxiashan National Forest Park, GPS coordinates: 24°56′ N, 113°41′ E, altitude: 415 m asl., on a fallen branch of angiosperm, leg. C.L. Zhao, 4 June 2019, CLZhao 12657 (SWFC).

Gene sequences (from holotype):—PP235513 (ITS) and PP235514 (nrLSU)

***Basidiomata*:—**Annual, resupinate, farinaceous when fresh, turn brittle upon drying, without odor or taste, up to 10 cm long, 1 cm wide, 50–200 µm thick. Hymenial surface smooth, white when fresh, white upon drying. Sterile margin white, up to 1 mm.

***Hyphal system*:—**Monomitic, generative hyphae with clamp connections, colorless, thick-walled, frequently branched, interwoven, 3.5–6.0 µm in diameter; IKI–, CB–, tissues unchanged in KOH.

***Hymenium*:—**Cystidia of two types: (1) septate cystidia colorless, thick-walled, larger, presence of clamped septa with abundant encrustations, 93.0–144.0 × 8.0–10.4 µm; (2) tubular cystidia, colorless, thin-walled, 55.0–63.0 × 6.5–10.3 µm. Basidia barrelled, constricted, somewhat sinuous, with 4 sterigmata and a basal clamp connection, with oil drops, 15.5–18.0 × 5.5–7.0 µm; basidioles dominant, similar to basidia in shape, but slightly smaller.

***Spores*:—**Basidiospores cylindrical, colorless, thin-walled, smooth, IKI–, CB–, (6.5–)7.4–9.0(–9.8) × (3.1–)3.2–4.0(–4.6) µm, L = 8.19 µm, W = 3.63 µm, Q = 2.25 (n = 30/1), Q_m=2.26 ± 0.20.

***Type of rot*:**—White rot.

***Ecology and distribution*:**—The sample collection site had a subtropical wet monsoon climate with an evergreen angiosperm forest, and samples were collected on fallen angiosperm branches. So far, it has only been found in Guangdong, China.

Discussion

The present study describes the new species *Hyphoderma guangdongense* based on phylogenetic analyses and morphological characteristics.

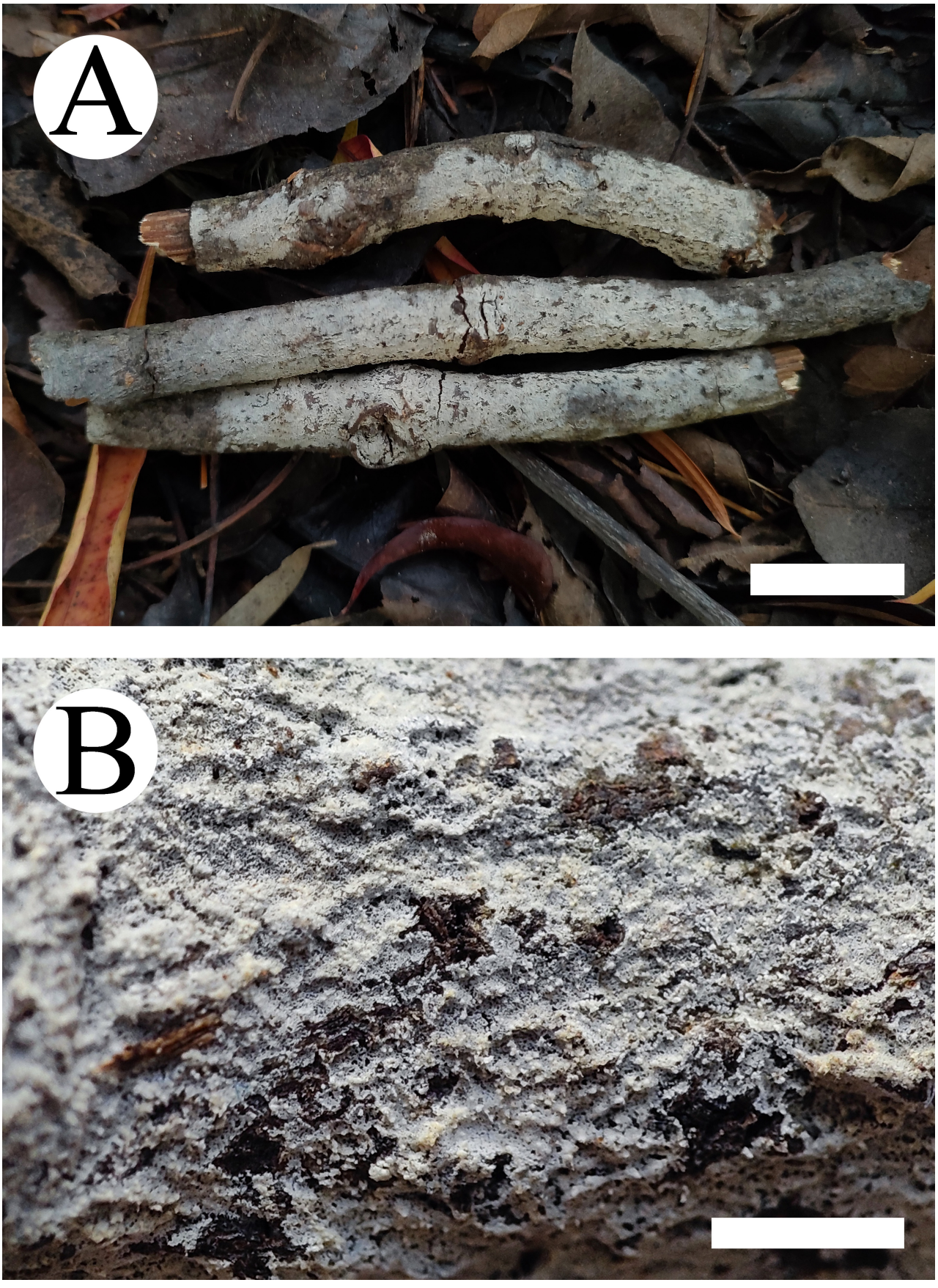

FIGURE 2. *Hyphoderma guangdongense* (holotype, CLZhao 12657): basidiomata on the substrate (A), macroscopic characteristics of hymenophore (B). Bars: (A) = 2 cm and (B) = 2 mm.

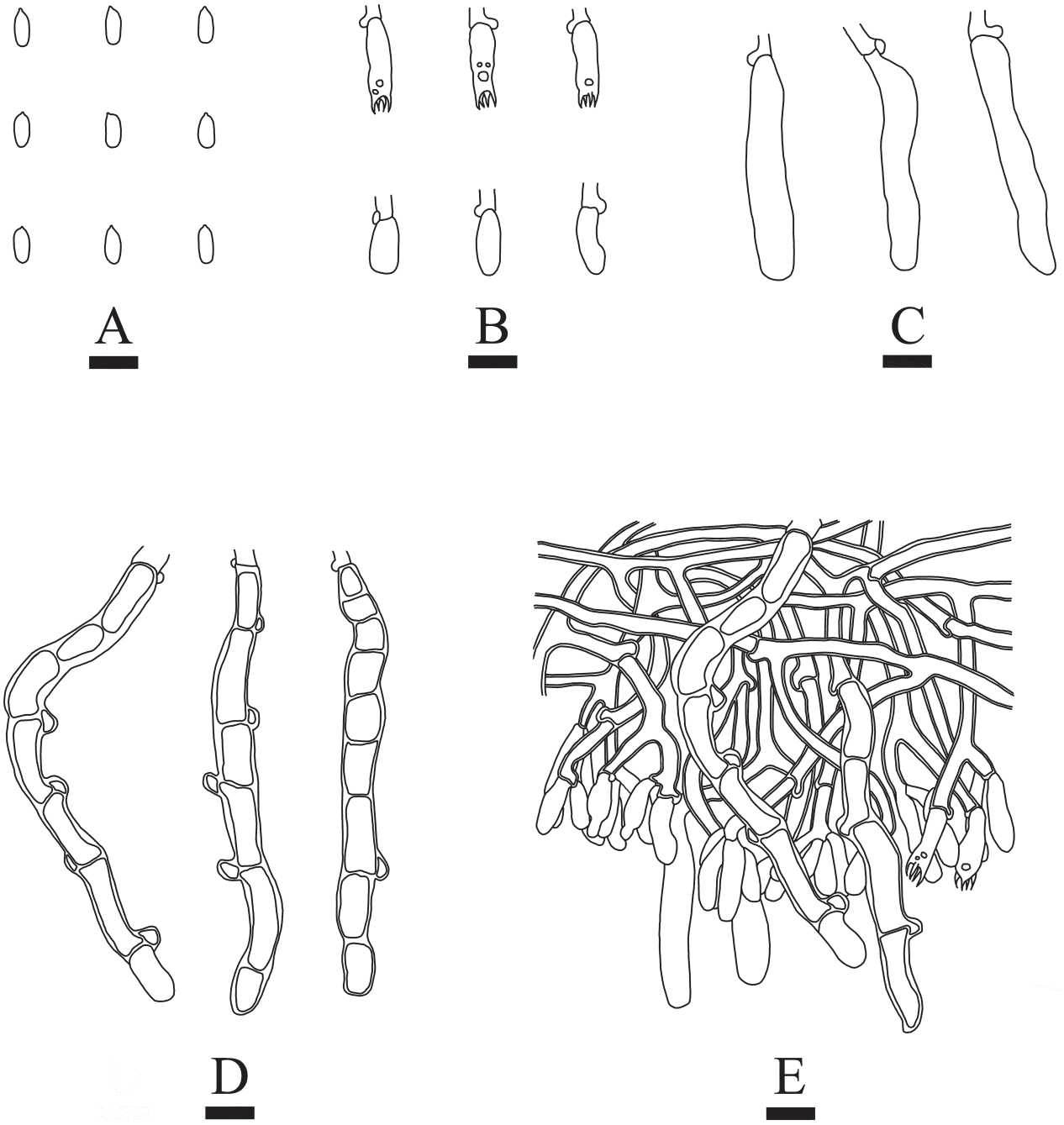

FIGURE 3. Microscopic structures of *Hyphoderma guangdongense* (holotype, CLZhao 12657): basidiospores (A), basidia and basidioles (B), tubular cystidia (C), septate cystidia (D), a section of the hymenium (E). Bars: (A–C) = 5 µm; (D–E) = 10 µm.

The family-level classification of Polyporales (Basidiomycota) based on nLSU, ITS, and RPBl genes revealed that four species *Hyphoderma macaronesicum*, *H. medioburiense* (Burt) Donk (1957: 15), *H. mutatum* (Peck) Donk (1957: 15), and *H. setigerum* nested in Hyphodermataceae within the residual polyporoid clade (Justo *et al*. 2017). In this study, the phylogram inferred from the ITS+nLSU gene regions (Fig. 1) revealed that the new species grouped into the genus *Hyphoderma*, in which *H. guangdongense* is closely related to two taxa *H. setigerum* and *H. floccosum*, and grouped with *H. mopanshanense* and *H. tenuissimum* C.L. Zhao & Q.X. Guan (2021: 153). Our meticulous morphological comparisons have shown that *H. setigerum* is distinct from *H. guangdongense* by having the tuberculate to the odontoid hymenial surface and the larger subclavate to clavate basidia (25–30 × 6–7 µm, Donk 1957). *Hyphoderma floccosum* differs from *H. guangdongense* by ceraceous to brittle basidiomata and its thin-walled generative hyphae (Guan & Zhao 2021b). Additionally, *H. mopanshanense* is separated from *H. guangdongense* by having the ceraceous to hard ceraceous basidiomata, porulose to pilose hymenial surface, and the wider septate cystidia

(86–171 × 10.5–13 µm, Ma *et al*. 2021). *Hyphoderma tenuissimum* differs from *H. guangdongense* by its tuberculate to minutely grandinioid to slightly buff hymenial surface and larger septate cystidia (50–220 × 6.5–13 µm, Guan *et al*. 2021).

Morphologically, *H. guangdongense* is similar to *H. membranaceum* C.L. Zhao & Q.X. Guan (2021: 8), *H. microporoides* C.L. Zhao & Q.X. Guan (2021: 9) and *H. sinense* C.L. Zhao & Q.X. Guan (2021: 454) by having the cylindrical, thin-walled and smooth basidiospores. However, *H. membranaceum* is distinguished from *H. guangdongense* by its membranous basidiomata, white to pale gray to cream tuberculate hymenial surface, the moniliform cystidia and thin-walled generative hyphae (Guan & Zhao 2021a). *Hyphoderma microporoides* differs from *H. guangdongense* by its cream to the pale hymenial surface, capitate cystidia, and thin-walled generative hyphae (Guan & Zhao 2021a). *Hyphoderma sinense* differs in the white to cream hymenial surface, and encrusted crystals cystidia (18.5–38 × 6–11 µm), and moniliform cystidia (30–60.5 × 6–10 µm, Guan & Zhao 2021b).

Wood-inhabiting fungi are generally found in dead tree trunks, inverted wood, and artificial wood products, which can secrete various biological enzymes degrading cellulose, hemicellulose, and lignin in wood into simple inorganic substances, and they play a pivotal role in forest ecosystems and are important members of ecosystem decomposition (Dai 2011). It is a cosmopolitan fungal group with a rich diversity in boreal, temperate, subtropical, and tropical vegetations (Tedersoo *et al.* 2014, James *et al.* 2020, Wu *et al.* 2020, 2022, Dai *et al.* 2021, Luo & Zhao 2023, Hussain *et al.* 2024). Based on the morphological and phylogenetic methods, several wood-inhabiting fungi were recorded in China (Wu *et al*. 2020, Dai *et al*. 2021, Wang *et al*. 2021, Luo & Zhao 2022, Mao *et al*. 2023, Zhao *et al*. 2023). *Hyphoderma* is one of the important representative groups of wood-inhabiting fungi (Bernicchia & Gorjón 2010). Currently, the species diversity of *Hyphoderma* in China is 38 (Guan & Zhao 2021a b; Guan *et al*. 2021, Ma & Zhao 2021, Zong *et al*. 2021, Gu & Zhao 2022, Deng & Zhao 2023, Duan *et al.* 2023, Yang *et al*. 2024). It is essential to enrich the species diversity of this genus with further fieldwork and molecular analyses.

This study concludes that the genus *Hyphoderma* is one of the most important representative groups of wood-inhabiting fungi. A new wood-inhabiting fungal taxon, *H. guangdongense*, is proposed based on its distinct morphological features and robust molecular evidence. It is characterized by the white hymenial surface, a monomitic hyphal system having generative hyphae with clamp connections, and cylindrical basidiospores. The phylogenetic tree inferred from a combination of the internal transcribed spacers (ITS) and large subunit (nrLSU) of the nuclear ribosomal DNA (rDNA) sequences revealed that *H. guangdongense* placed in the genus *Hyphoderma*, in which it is closely related to a clade comprising two taxa, *H. setigerum,* and *H. floccosum*.

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