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Full paper

Hyphoderma fissuratum and *H. mopanshanense* spp. nov. (*Polyporales*) from southern China

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ABSTRACT

Two new species, *Hyphoderma fissuratum* and *H. mopanshanense* spp. nov., are proposed based on morphological and molecular evidences. *Hyphoderma fissuratum* is characterized by resupinate basidiomata with cracking hymenial surface, a monomitic hyphal system with generative hyphae bearing clamp connections, IKI–, CB–, and cylindrical, colorless, thin-walled, smooth basidiospores measuring (8.5–10.3 × 3–4 µm). *Hyphoderma mopanshanense* is characterized by an annual growth habit, slight gray to cream hymenial surface, and fusiform, thick-walled cystidia apically encrusted with crystal. Sequences of ITS and LSU nrRNA gene regions of the studied samples were generated, and phylogenetic analyses were performed with maximum likelihood, maximum parsimony and Bayesian inference methods. These phylogenetic analyses based on molecular data of ITS and nLSU sequences showed that two *Hyphoderma* new species formed a well supported monophyletic lineage distinct from other related species and then *H. fissuratum* grouped with *H. medioburiense* and *H. roseocremeum*. *Hyphoderma mopanshanense* grouped with *H. setigerum*.

Keywords: corticioid fungi, *Hyphodermataceae*, molecular phylogeny, taxonomy, wood-rotting fungi, Yunnan Province

Article history: Received 6 May 2020, Revised 18 August 2020, Accepted 18 August 2020, Available online 20 January 2021.

1. Introduction

Hyphoderma Wallr. was typified by *H. setigerum* (Fr.) Donk (synonymy with *H. spiculosum* Wallr.) (Wallroth, 1833). The genus is characterized by resupinate to effuse-reflexed basidiomata with ceraceous consistencey, and smooth to tuberculate or hydnoid hymenophore and a monomitic hyphal structure (rarely dimitic) with clamp connections on generative hyphae, presence of cystidia or not, basidia suburniform to subcylindrial and cylindrical, ellipsoid to subglobose, smooth, thin-walled basidiospores (Wallroth, 1833; Bernicchia & Gorjón, 2010). So far 100 species have been accepted in the genus worldwide (Wallroth, 1833; http://www.indexfungorum.org/names/Names.asp; http://www.mycobank.org/Biolomics.aspx?Table=Mycobank).

Recently, molecular studies involving *Hyphoderma* based on single-gene or multi-gene datasets have been carried out (Larsson, 2007; Telleria, Dueñas, Beltrán-Tejera, Rodríguez-Armas & Martín, 2012; Binder et al., 2013; Yurchenko & Wu, 2014a, 2015; Justo et al., 2017). On the basis of the internal transcribed spacer (ITS) regions and the large subunit nuclear ribosomal RNA gene (nLSU) sequences, Larsson (2007) revealed the classification of corticioid fungi and showed that *Hyphoderma obtusum* J. Erikss. and *H. setigerum* (Fr.) Donk clustered into *Meruliaceae* Rea and then grouped with *Hypochnicium polonense* (Bres.) Å. Strid. Telleria, Dueñas, Beltrán-Tejera, Rodríguez-Armas & Martín. (2012) proposed a new species, *Hyphoderma macaronesicum* Tellería, M. Dueñas, Beltrán-Tej, Rodr.-Armas & M.P. Martín and then discussed the relationships with the closely related taxa in *Hyphoderma*. Binder et al. (2013) presented the molecular studies employing multi-gene datasets (5.8S, nLSU, translation elongation factor 1-α (TEF1) gene, mitochondrial rRNA gene sequences (mtSSU), the second-largest subunit of RNA polymerase II (RPB2) and the largest subunit of RNA polymerase II) to investigate the phylogenetic relationships within the *Polyporales*, in which *Hyphoderma cremeoalbum* (Höhn. & Litsch.) Jülich and *H. setigerum* were nested into the residual polyporoid clade and placed inside of *Hyphodermataceae* Jülich. Yurchenko & Wu (2014a) studied the *Hyphoderma setigerum* complex and showed that *H. pinicola* Yurchenko & Sheng H. Wu represented a fifth species of *H. setigerum* complex. Yurchenko & Wu (2015) reported that *Hyphoderma moniliforme* (P.H.B. Talbot) Manjón, G. Moreno & Hjortstam and *H. nemorale* K.H. Larss., saprobically growing on wood, were recorded as new for mycobiota in China. A revised family-level classification of the *Polyporales* revealed that four *Hyphoderma* species nested into the residual poly-

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poroid clade belonging to *Hyphodermataceae* and then grouped with three genera *Meripilus* P. Karst., *Physisporinus* P. Karst. and *Rigidoporus* Murrill (Justo et al., 2017).

Recently, we collected two undescribed taxa from Yunnan Province, P. R. China that could not be assigned to any described genera. We present morphological and molecular phylogenetic evidence that support the recognition of two new species within the *Hyphoderma*, based on the internal transcribed spacer (ITS) regions and the large subunit nuclear ribosomal RNA gene (nLSU) sequences.

2. Materials and methods

2.1. Morphology

The specimens studied are deposited at the herbarium of Southwest Forestry University (SWFC), Kunming, Yunnan Province, P.R. China. Macromorphological descriptions are based on field notes. Color terms follow Petersen (1996). Micromorphological data were obtained from the dried specimens, and observed under a light microscope following Dai (2012). The following abbreviations were used: KOH = 5% potassium hydroxide, CB = Cotton Blue, CB– = acyanophilous, IKI = Melzer's reagent, IKI– = both inamyloid and indextrinoid, L = mean spore length (arithmetic average for all spores), W = mean spore width (arithmetic average for all spores), Q = variation in the L/W ratios between the specimens studied, n (a/b) = number of spores (a) measured from given number (b) of specimens.

2.2. Molecular phylogeny

CTAB rapid plant genome extraction kit-DN14 (Aidlab Biotechnologies Co., Ltd, Beijing) was used to obtain genomic DNA from dried specimens, according to the manufacturer's instructions with some modifications that a small piece of dried fungal specimen (about 30 mg) was ground to powder with liquid nitrogen. The powder was transferred to a 1.5 mL centrifuge tube, suspended in 0.4 mL of lysis buffer, and incubated at 65 °C in a water bath for 60 min. After that, 0.4 mL phenol-chloroform (24:1) was added to each tube and the suspension was shaken vigorously. After centrifugation at 13,000 rpm for 5 min, 0.3 mL of supernatant was transferred to a new tube and mixed with 0.45 mL of binding buffer. The mixture was then transferred to an adsorbing column (AC) for centrifugation at 13,000 rpm for 0.5 min. Then, 0.5 mL of inhibitor removal fluid was added in AC for a centrifugation at 12,000 rpm for 0.5 min. After washing twice with 0.5 mL of washing buffer, the AC was transferred to a clean centrifuge tube, and 100 mL elution buffer was added to the middle of adsorbed film to elute the genome DNA. ITS region was amplified with primer pair ITS5 and ITS4 (White, Bruns, Lee & Taylor, 1990). Nuclear LSU region was amplified with primer pair LR0R and LR7 (http://www.biology.duke.edu/fungi/mycolab/primers.htm). 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 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 directly sequenced at Kunming Tsingke Biological Technology Limited Company. All newly generated sequences were deposited at GenBank (Table 1).

Sequences were aligned in MAFFT 7 (https://mafft.cbrc.jp/alignment/server/) using the "G-INS-I" strategy for nLSU, and manually adjusted in BioEdit (Hall 1999). Alignment datasets were deposited in TreeBase (submission ID 25203). *Phanerochaete sordida* (P. Karst.) J. Erikss. & Ryvarden was selected as outgroup for phylogenetic analyses of ITS and nLSU phylogenetic trees (Yurchenko & Wu, 2015).

Maximum parsimony analyses were applied to the ITS and nLSU dataset sequences. Approaches to phylogenetic analysis followed Chen, Cui & Dai, (2016), and the tree construction procedure was performed in PAUP* version 4.0b10 (Swofford, 2002). All 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. Max-trees were set to 5000, branches of zero length were collapsed and all parsimonious trees were saved. Clade robustness was assessed using a bootstrap (BT) analysis with 1,000 replicates (Felsenstein, 1985). Descriptive tree statistics tree length (TL), consistency index (CI), retention index (RI), rescaled consistency index (RC), and homoplasy index (HI) were calculated for each Maximum Parsimonious Tree generated. Datamatrix was also analyzed using Maximum Likelihood (ML) approach with RAxML-HPC2 through the Cipres Science Gateway (www.phylo.org; Miller et al., 2009). Branch support (BS) for ML analysis was determined by 1000 bootstrap replicates.

MrModeltest 2.3 (Nylander, 2004) was used to determine the best-fit evolution model for each data set for Bayesian inference (BI). BI was calculated with MrBayes3.1.2 with a general time reversible (GTR) model of DNA substitution and a gamma distribution rate variation across sites (Ronquist & Huelsenbeck, 2003). Four Markov chains were run for 2 runs from random starting trees for 400,000 generations for ITS (Fig. 1), 300,000 generations for nLSU (Fig. 2), and trees were sampled every 100 generations. The first one-fourth generations were discarded as burn-in. A majority rule consensus tree of all remaining trees was calculated. Branches were considered as significantly supported if they received maximum likelihood bootstrap (BS)>70%, maximum parsimony bootstrap (BT) >50%, or Bayesian posterior probabilities (BPP) >0.95.

3. Results

3.1. Taxonomy

Hyphoderma fissuratum C.L. Zhao & X. Ma, sp. nov. Figs. 3, 4.
MycoBank no.: MB 836259.

Holotype: China, Yunnan Province, Chuxiong, Zixishan Forestry Park, E 101°24′, N 25°0′, alt. 1950 m, on angiosperm stump, 26 Jun 2018, CLZhao 6726 (SWFC).

Etymology: *Fissuratum* (Lat.): referring to the cracking hymenial surface.

Basidiomata: Annual, resupinate, thin, ceraceous when fresh, turn to leathery upon drying, up to 12 cm long, 5 cm wide, 300–500 μm thick. Hymenial surface smooth, cream when fresh, cracking, cream to cinnamon-buff upon drying. Sterile margin distinct, white.

Hyphal structure: Hyphal system monomitic, generative hyphae with clamp connections, IKI–, CB–, tissues unchanged in KOH.

Subiculum: Generative hyphae colorless, thin-walled, rarely branched, 3.5–5.5 μm diam; larger crystal present.

Hymenial layer: Generative hyphae colorless, thin-walled, rarely branched, 3–5 μm diam.

Hymenium: Cystidia and cystidioles absent; basidia narrowly clavate, with four sterigmata and a basal clamp connection, 24–28 × 4–5.5 μm.

Basidiospores: Cylindrical, colorless, thin-walled, smooth, IKI–,

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

Species name	Sample no.	GenBank accession no.		References
		ITS	nLSU	
Hyphoderma cremeoalbum	NH 11538	DQ677492	DQ677492	Larsson (2007)
H. definitum	GEL 2898	—	AY515348	Yurchenko & Wu (2014a)
H. definitum	FCUG 2426	AJ534293	—	Nilsson et al. (2003)
H. definitum	NH 12266	DQ677493	DQ677493	Larsson (2007)
H. fissuratum	CLZhao 6726	MT791330	MT791334	Present study
H. fissuratum	CLZhao 6731	MT791331	MT791335	Present study
H. granuliferum	KHL 12561	JN710545	JN710545	Yurchenko & Wu (2014b)
H. incrustatum	KHL 6685	—	AY586668	Yurchenko & Wu (2014b)
H. litschaueri	NH 7603	DQ677496	DQ677496	Larsson (2007)
H. litschaueri	CFMR 2011050	KJ140573	—	Yurchenko & Wu (2014b)
H. macaronesicum	TFC 15981	HE577027	—	Yurchenko & Wu (2014b)
H. macaronesicum	MA 16099	HE577028	—	Yurchenko & Wu (2014b)
H. medioburiense	NH 10950	DQ677497	DQ677497	Larsson (2007)
H. moniliforme	TNM F14735	KC928282	KC928283	Yurchenko & Wu (2015)
H. moniliforme	TNM F14739	KC928284	KC928285	Yurchenko & Wu (2015)
H. mopanshanense	CLZhao 6493	MT791328	MT791332	Present study
H. mopanshanense	CLZhao 6498	MT791329	MT791333	Present study
H. nemorale	EM 2793	—	AY586669	Yurchenko & Wu (2014b)
H. nemorale	TNM F3910	KC928282	KC928283	Yurchenko & Wu (2015)
H. nemorale	TNM F3931	KJ885183	KJ885184	Yurchenko & Wu (2015)
H. nudicephalum	Wu 9508225	AJ534268	—	Nilsson et al. (2003)
H. nudicephalum	Wu 930729	AJ534269	—	Nilsson et al. (2003)
H. nudicephalum	GEL 4727	—	AJ406510	Yurchenko & Wu (2014b)
H. obtusiforme	KHL 1464	JN572909	—	Yurchenko & Wu (2014b)
H. obtusiforme	KHL 11105	JN572910	—	Yurchenko & Wu (2014b)
H. obtusum	JS 17804	—	AY586670	Yurchenko & Wu (2014b)
H. occidentale	KHL 8469	—	AY586674	Yurchenko & Wu (2014b)
H. occidentale	KHL 8477	DQ677499	DQ677499	Larsson (2007)
H. pinicola	TNM F13635	KJ885179	KJ885180	Yurchenko & Wu (2014b)
H. pinicola	TNM F13643	KC928278	KC928279	Yurchenko & Wu (2014b)
H. prosopidis	ARIZ 8479	HE577029	—	Yurchenko & Wu (2015)
H. roseocremeum	NH 10545	—	AY586672	Yurchenko & Wu (2014b)
H. setigerum	FCUG 1688	AJ534272	—	Nilsson et al. (2003)
H. setigerum	FCUG 1200	AJ534273	—	Nilsson et al. (2003)
H. setigerum	KHL 8544	—	AY586673	Yurchenko & Wu (2014b)
H. setigerum	NH 8544	—	FN907905	Yurchenko & Wu (2014b)
H. subtestaceum	HHB 11620	GQ409521	—	Yurchenko & Wu (2014b)
H. subtestaceum	MJL 1536	GQ409522	—	Yurchenko & Wu (2014b)
H. subtestaceum	Wu 920215	AJ534278	—	Nilsson et al. (2003)
H. subtestaceum	Wu 930418	AJ534277	—	Nilsson et al. (2003)
H. transiens	NH 12304	DQ677504	DQ677504	Larsson (2007)
Phanerochaete sordida	KHL 12054	EU118653	EU118653	Larsson (2007)

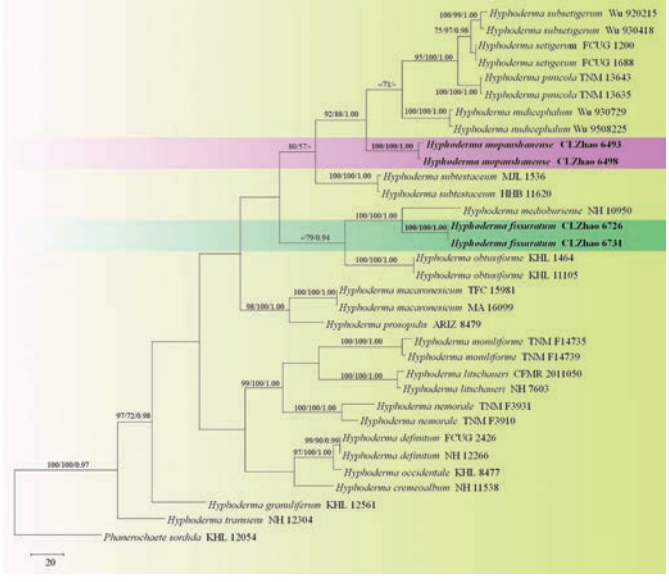

Fig. 1. – Maximum Parsimony strict consensus tree illustrating the phylogeny of two new species and related species in *Hyphoderma* based on ITS sequences. Branches are labelled with maximum likelihood bootstrap > 70%, parsimony bootstrap proportions > 50% and Bayesian posterior probabilities > 0.95, respectively.

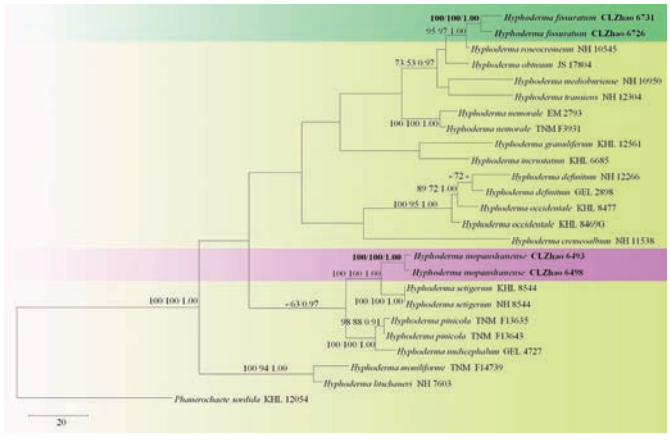

Fig. 2. – Maximum Parsimony strict consensus tree illustrating the phylogeny of two new species and related species in *Hyphoderma* based on nLSU sequences. Branches are labeled with maximum likelihood bootstrap > 70%, parsimony bootstrap proportions > 50% and Bayesian posterior probabilities > 0.95, respectively.

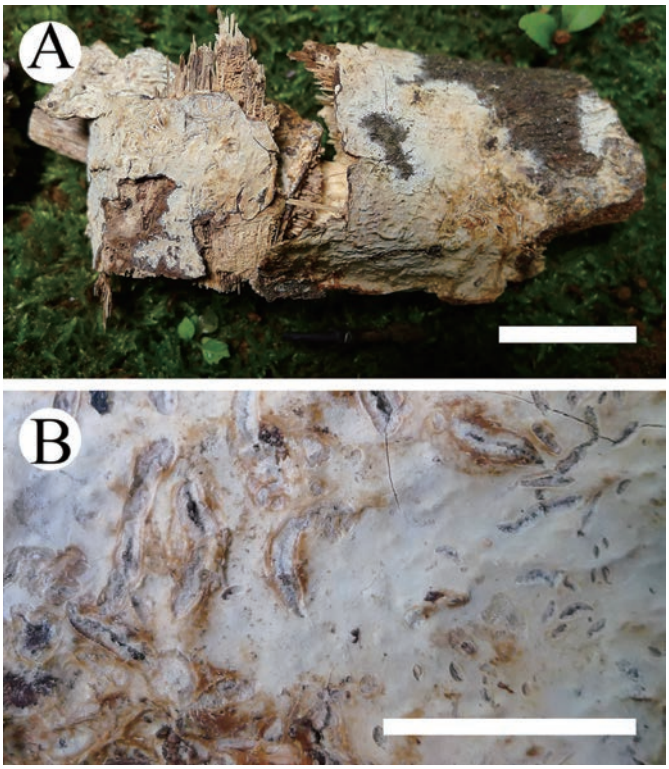

Fig. 3. – *Hyphoderma fissuratum* (holotype): basidiomata. *Bars*: A 2 cm; B 5 mm.

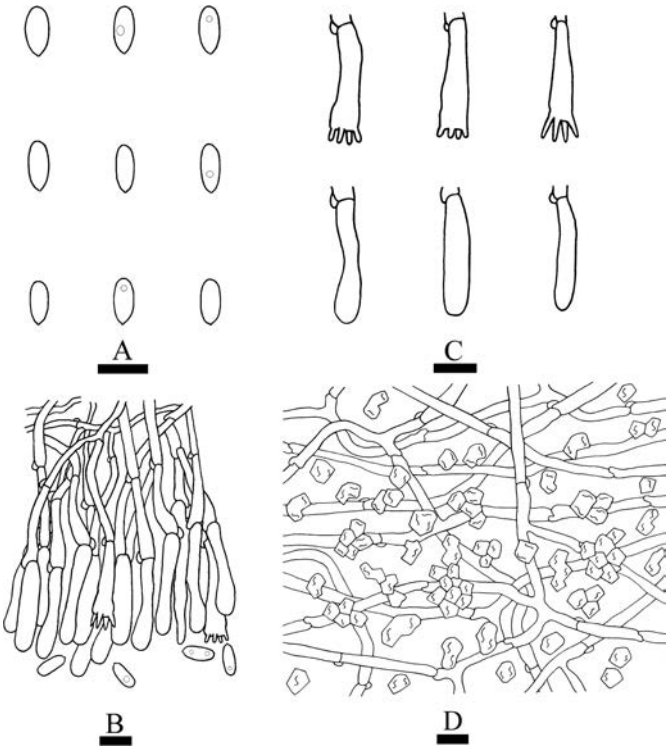

Fig. 4. – *Hyphoderma fissuratum* (holotype), microscopic structures: A: Basidiospores. B: A section of hymenium. C: Basidia and basidioles. D: Subculium. *Bars*: A–D 10 μm.

CB–, (8.2–)8.5–10.3(–10.5) × 3–4 μm, L = 9.40 μm, W = 3.66 μm, Q = 2.51–2.63 (n = 60/2).

Type of rot: White rot.

Additional specimens examined: CHINA, Yunnan Province, Chuxiong, Zixishan Forestry Park, E 101°24′, N 25°0′, alt. 1950 m, on angiosperm stump, 26 Jun 2018, CLZhao 6731 (SWFC).

Hyphoderma mopanshanense C.L. Zhao, sp. nov. Figs. 5, 6.

MycoBank no.: MB 836262.

Holotype: China, Yunnan Province, Yuxi, Xinping, Mopanshan National Forestry Park, E 101°29′, N 23°56′, alt. 2200m, on fallen angiosperm trunk, 19 Jan 2018, CLZhao 6498 (SWFC).

Etymology: *Mopanshanense* (Lat.): referring to the locality (Mopanshan) of the type specimens.

Basidiomata: Annual, resupinate, ceraceous when fresh, turn to hard ceraceous upon drying, up to 7 cm long, 5 cm wide, 100–300 μm thick. Hymenial surface porulose to pilose, white to slightly pale gray when fresh, slight gray to cream upon drying. Sterile margin indistinct, white to slightly gray.

Hyphal structure: Hyphal system monomitic, generative hyphae bearing clamp connections, IKI–, CB–, tissues unchanged in KOH.

Subiculum: Generative hyphae colorless, thick-walled, rarely branched, 4–6 μm diam.

Hymenial layer: Generative hyphae colorless, thick-walled, rarely branched, 3.5–6.5 μm diam.

Hymenium: Cystidia fusiform, numerous, thick-walled, septated, apically encrusted with crystal, 86–171 × 10.5–13 μm, cystidioles absent; basidia clavate, with four sterigmata and a basal clamp connection, 15–18.5 × 3–4.5 μm.

Basidiospores: Cylindrical, colorless, thin-walled, smooth, IKI–, CB–, (7.6–)7.8–9.7(–10) × 2.6–3.3 μm, L = 8.78 μm, W = 2.95 μm, Q = 2.77–2.98 (n = 60/2).

Additional specimens examined: CHINA, Yunnan Province, Yuxi, Xinping County, Mopanshan National Forestry Park, E 101°29′, N 23°56′, alt. 2200m, on the fallen branch of angiosperm, 4 Jan 2018, CLZhao 6493 (SWFC).

3.2. Molecular phylogeny

The ITS dataset included sequences from 33 fungal specimens representing 19 taxa. The dataset had an aligned length of 647 characters in the dataset, of which 310 characters are constant, 47 are variable and parsimony-uninformative, and 290 are parsimony-informative. Maximum parsimony analysis yielded 1 equally parsimonious tree (TL = 1238, CI = 0.459, HI = 0.541, RI =0.646, RC = 0.296). Best model for ITS estimated and applied in the Bayesian analysis: GTR+I+G, lset nst = 6, rates = invgamma; prset statefreqpr = dirichlet (1,1,1,1). Bayesian analysis resulted in the similar topology with an average standard deviation of split frequencies =0.009955.

The phylogeny (Fig. 1) inferred from ITS sequences demonstrated that two new species, *Hyphoderma fissuratum* and *H. mopanshanense*, clustered into the *Hyphoderma*. *Hyphoderma fissuratum* was sister to *H. medioburiense* (Burt) Donk, and *H. mopanshanense* formed a monophyletic lineage with a strong support (100% BS, 100% BP and 1.00 BPP).

The nLSU dataset included sequences from 25 fungal specimens representing 19 species. The dataset had an aligned length of 1300 characters, of which 931 characters are constant, 168 are variable and parsimony-uninformative, and 201 are parsimony-informative. Maximum parsimony analysis yielded 4 equally parsimonious trees (TL = 792, CI = 0.605, HI = 0.395, RI = 0.491, RC = 0.297). Best model for the nLSU dataset estimated and applied in the Bayesian analysis: GTR+I+G, lset nst = 6, rates = invgamma; prset statefreqpr = dirichlet (1,1,1,1). Bayesian analysis and ML analysis resulted in a similar topology as MP analysis, with an average stan-

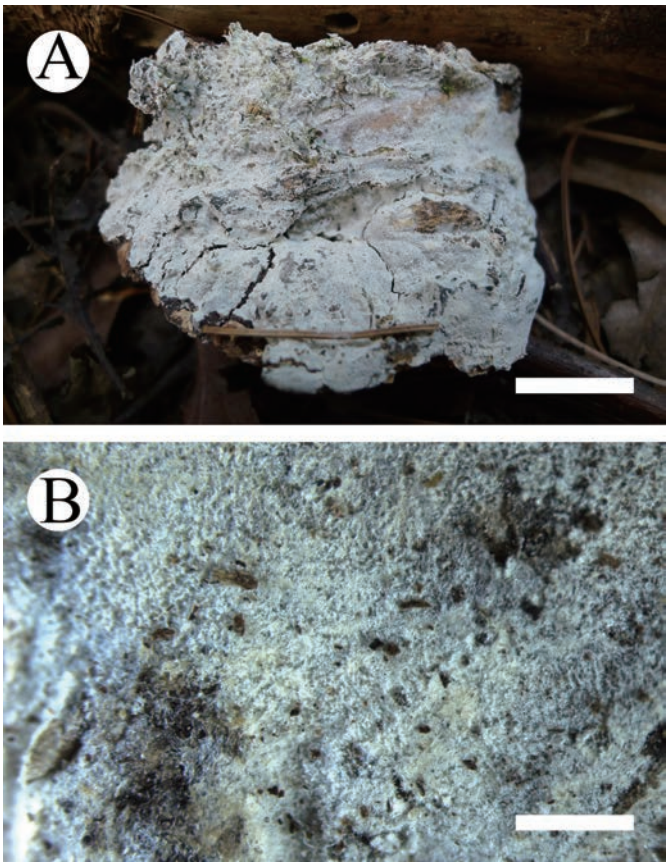

Fig. 5. – *Hyphoderma mopanshanense* (holotype): basidiomata. *Bars*: A 1 cm; B 1 mm.

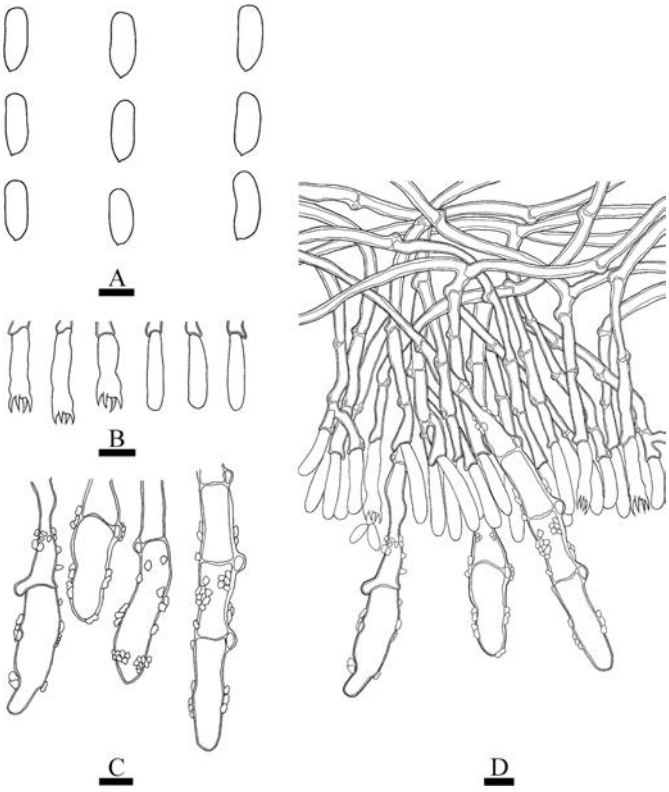

Fig. 6. – *Hyphoderma mopanshanense* (holotype), microscopic structures: A: Basidiospores. B: Basidia and basidioles. C: Cystida. D: A section of hymenium. *Bars*: A 5 μm; B–D 10 μm.

dard deviation of split frequencies = 0.009036 (BI).

The phylogenetic tree (Fig. 2) inferred from nLSU sequences revealed that *Hyphoderma fissuratum* grouped with *H. roseocremeum* (Bres.) Donk, and *H. mopanshanense* was sister to *H. setigerum*.

4. Discussion

In the present study, two new species *Hyphoderma fissuratum* and *H. mopanshanense* was described based on phylogenetic analyses and morphological characters.

Phylogenetically, *Hyphoderma fissuratum* was sister to *H. medioburiense* based on ITS sequence data (Fig. 1). However, morphologically, *Hyphoderma medioburiense* differs from *H. fissuratum* by its yellowish ochraceous hymenial surface, presence of cystidia and larger basidiospores (11–15 × 4–5 μm; Bernicchia & Gorjón, 2010). In the nLSU sequences, *Hyphoderma fissuratum* was grouped with *H. roseocremeum*, but morphologically *H. roseocremeum* differs in its whitish to yellowish ochraceous hymenial surface with rose tint and presence of tubular cystida (Bernicchia & Gorjón, 2010).

Morphologically, *Hyphoderma fissuratum* reminds on five species based on lacking cystidia, *H. acystidiatum* Sheng H. Wu, *H. cremeoalbum* (Höhn. & Litsch.) Jülich, *H. densum* Sheng H. Wu, *H. sibiricum* (Parmasto) J. Eriksss. & Å. Strid and *H. singularibasidium* Dhingra, Avn.P. Singh & Singla. However, *H. acystidiatum* differs in its white hymenial surface and grandinioid hymenophore and wider basidiospores (9–11.5 × 4.5–5.3 μm; Wu, 1997); *H. cremeoalbum* in its presence of paraphysoid hyphae among the basidia and larger basidiospores (10–14 × 5–6 μm; Jülich, 1974); *H. densum* in its ivory yellow hymenial surface and larger basidiospores (10.5–12.5 × 4.2–5 μm; Wu, 1997); *H. sibiricum* in its strikingly yellow hymenial surface and wider basidiospores (7–9 × 4–5 μm; Eriksson & Ryvarden, 1975); *H. singularibasidium* in its grayish white to yellowish white hymenial surface and presence of the lateral outgrowth from the middle of basidium (Dhingra, Singh, & Singla, 2009).

In phylogenetic study, *Hyphoderma mopanshanense* formed a single lineage with good support (100% BS, 100% BP and 1.00 BPP) and then grouped with *H. subtestaceum* (Litsch.) Donk and a clade comprising taxa of *H. nudicephalum* Gilb. & M. Blackw., *H. pinicola* Yurch. & Sheng H. Wu, *H. setigerum*, *H. subsetigerum* Sheng H. Wu on the basis of ITS sequences (Fig. 1). In the nLSU sequences, *H. mopanshanense* has sister to *H. setigerum* and then clustered with *H. nudicephalum* and *H. pinicola* (Fig. 2). However, *H. nudicephalum* differs from *H. mopanshanense* by having the farinaceous to odontioid hymenial surface, conspicuous capitate cystidia with nonincrusted apices and wider basidiospores (7–9 × 3.5–4 μm; Gilbertson & Blackwell, 1988). *Hyphoderma pinicola* differs in its chalky white hymenial surface and larger basidiospores (13–16 × 4–4.5 μm; Yurchenko & Wu, 2014b). *Hyphoderma setigerum* is separated from *H. mopanshanense* by the smooth to tuberculate hymenophore, larger basidia (25–30 × 6–75 μm) and basidiospores (7–11 × 3–4.5 μm; Bernicchia & Gorjón, 2010). *Hyphoderma subsetigerum* differs in its grandinioid hymenophore with whitish to ivory yellow hymenial surface and smaller basidiospores (6–8 × 2.8–3.2 μm; Wu, 1997). *Hyphoderma subtestaceum* differs from *H. mopanshanense* by having the membranaceous hymenophore with pallidus to cream to isabellinus hymenial surface (Litschauer, 1928).

In the geographical distribution, both new species, *Hyphoderma fissuratum* and *H. mopanshanense* were collected at the same spot (Yunnan Province). However, they are not grouped together in ITS and nLSU analyses (Figs. 1, 2), and *H. fissuratum* differs from *H.*

mopanshanense by having the cracking hymenial surface and larger basidiospores (8.5–10.3 × 3–4 μm).

Wood-rotting fungi is an extensively studied group of *Basidiomycota* (Núñez & Ryvarden, 2001; Bernicchia & Gorjón, 2010; Dai 2012; Ryvarden & Melo, 2014; Dai et al., 2015), but the Chinese wood-rotting fungus diversity is still not well known, especially in subtropics and tropics, many recently described taxa of this ecological group were from these areas (Dai, 2012; Chen, Korhonen, Li & Dai, 2014; Bian & Dai, 2015; Cui et al., 2019; Shen et al., 2019; Zhu, Song, Zhou, Si & Cui, 2019). Two new species in the present study are from subtropics, too. It is possible that a number of other new taxa will be found after further field studies and molecular analyses.

Disclosure

The authors declare no conflict of interest. All the experiments undertaken in this study comply with the current laws of the People's Republic of China.

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