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by Seunghyun Lee, Deokjea Cha, Yongwoo Nam and Jonkook Jung

Diversity 2021, 13(11), 582; <https://doi.org/10.3390/d13110582> – 14 Nov 2021

Abstract The red-necked longhorn beetle (RLB; *Aromia bungii* [Faldernmann, 1835]) is an emerging invasive pest. From its native range of East Asia, it invaded Europe and Japan in the early 2010s. Despite its increasing importance, the molecular resources of RLB are scarce, and its [...] [Read more](#). (This article belongs to the Special Issue [Diversity and Evolution of Coleoptera](#))

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Additions to the Knowledge of Corticioid *Xylodon* (Schizoporaceae, Hymenochaetales): Introducing Three New *Xylodon* Species from Southern China

by Kai-Yue Luo, Meng-Han Gu and Chang-Lin Zhao

Diversity 2021, 13(11), 581; <https://doi.org/10.3390/d13110581> (registering DOI) – 14 Nov 2021

Abstract Three wood-inhabiting fungal species, *Xylodon gossypinus*, *X. macrosporus*, and *X. sinensis* spp. nov. were collected from southern China, with the similar function to decompose rotten wood, which are here proposed as new taxa based on a combination of morphological features and molecular [...] [Read more](#).

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by Hongyi Liu, Yufeng Zhang, Wei Xu, Yu Fang and Honghua Ruan

Diversity 2021, 13(11), 580; <https://doi.org/10.3390/d13110580> – 14 Nov 2021

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by Lillian A. Palomino-Alvarez, Xochitl G. Vitas, Raúl E. Castillo-Cupul, Nanay Y. Suárez-Mozo, Diana Ugalde, Gabriel Cervantes-Campero, María R. Muñoz-Reyes, Pedro Homá-Cano, Yoalli Guetzalli Hernández-Díaz, Rosa Botello-Casas, Maryjose Garza-González, Yhuicán A. Avedaño-Peláez, Alejandro Hernández-González, Carlos E. Paz-Ríos, Jose M. Lizaso-Guillermo, Magdalena Garza-Venegas, Yasmín Dávila-Jiménez, Deneb Orfígota, Gema Hidalgo, José L. Tello-Muñiz, [Show full author list](#)

Diversity 2021, 13(11), 579; <https://doi.org/10.3390/d13110579> – 12 Nov 2021



Abstract Autonomous reef monitoring structures (ARMS) have been proposed as a standardized, passive, nondestructive sampling tool. This study assessed the ability of ARMS to capture the cryptic species diversity of two coral reefs by recording species richness and taxonomic representativeness using conventional taxonomy. The [...] [Read more](#).

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Article

Additions to the Knowledge of Corticioid *Xylodon* (Schizoporaceae, Hymenochaetales): Introducing Three New *Xylodon* Species from Southern China

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Abstract: Three wood-inhabiting fungal species, *Xylodon gossypinus*, *X. macrosporus*, and *X. sinensis* spp. nov. were collected from southern China, with the similar function to decompose rotten wood, which are here proposed as new taxa based on a combination of morphological features and molecular evidence. *Xylodon gossypinus* is characterized by the resupinate basidiomata with cotton hymenophore, and ellipsoid basidiospores; *X. macrosporus* is characterized by the resupinate basidiomata having the cracking hymenophore with pale yellowish hymenial surface, and larger basidiospores 8–10.5 × 7.5–9 µm; and *X. sinensis* differs by its grandinoid hymenial surface and subglobose basidiospores measuring as 3–5 × 2.5–4 µm. Sequences of ITS and nLSU rRNA markers of the studied samples were generated, and phylogenetic analyses were performed with maximum likelihood, maximum parsimony, and Bayesian inference methods. The ITS+nLSU analysis in Hymenochaetales revealed that the three new species clustered into the Schizoporaceae family, located in genus *Xylodon*; based on the ITS dataset, *X. gossypinus* was a sister to *X. ussuriensis*; *X. macrosporus* closely grouped with *X. follis* with a high support; and *X. sinensis* was retrieved as two sisters to *X. attenuatus* and *X. yarraensis* with a lower support.

Keywords: biodiversity; molecular systematics; taxonomy; white rot fungi; wood-decaying fungi; Yunnan Province



Citation: Luo, K.-Y.; Qu, M.-H.; Zhao, C.-L. Additions to the Knowledge of Corticioid *Xylodon* (Schizoporaceae, Hymenochaetales): Introducing Three New *Xylodon* Species from Southern China. *Diversity* **2021**, *13*, 581. <https://doi.org/10.3390/d13110581>

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1. Introduction

Corticioid fungi are mainly a diverse and heterogeneous group of basidiomycete fungi which display a considerable ability to transform or degrade different environmental contaminants on their extensive organic compound degradation abilities [1]. The corticioid genus *Xylodon* (Pers.) Gray (Schizoporaceae, Hymenochaetales) with the generic type *X. quercinus* (Pers.) Gray is characterized by the basidiomata having a smooth, tuberculate, grandinoid, odontoid, coralloid, irpicoid or poroid hymenophore, and a monomitic hyphal system with clamped generative hyphae and presence of multi-types cystidia, suburniform basidia, and globose to ellipsoid to cylindrical basidiospores, causing a white rot [2,3]. Both the MycoBank database (<http://www.Mycobank.org>, accessed on 5 November 2021) and the Index Fungorum (<http://www.indexfungorum.org>, accessed on 5 November 2021) have registered 203 specific and infraspecific names in the genus *Xylodon*, but the actual number of species reaches eighty-three [4–30].

Based on the early embrace of molecular systematics by mycologists, both the discovery and classification of fungi among the more basal branches of the tree are now coming to light from genomic analyses and environmental DNA surveys [31]. On the basis of the nuclear DNA sequence data, the molecular systematics for *Hyphodontia* s.l. demonstrated

that the polyphyletic genus consisted of six well-distinguished clades: *Lagarobasidium* clade, *Kneiffiella-Alutaceodontia* clade, *Hyphodontia* clade, *Hastodontia* clade, *Xylodon-Lyomyces-Rogersella* clade, and *Xylodon-Schizopora-Palifer* clade, in which the genera *Xylodon*, *Schizopora*, *Palifer*, *Lyomyces*, and *Rogersella* were mixed within the *Xylodon-Lyomyces-Rogersella* clade and the *Xylodon-Schizopora-Palifer* clade, and thus it had no phylogenetic support in their study [32]. Phylogenetic trees indicated that *Hyphodontia* s.l. consisted of various genera, which revealed that it hardly differentiated between the genera *Xylodon* and *Schizopora* with neither morphological nor molecular data; therefore, both should be summarized in one genus [20]. Inferred from a natural classification of *Hyphodontia sensu lato* with the trait evolution of basidiocarps within Hymenochaetales (Basidiomycota), six genera: *Fasciodontia*, *Hastodontia*, *Hyphodontia*, *Kneiffiella*, *Lyomyces*, and *Xylodon* were separated into four clades within Hymenochaetales, in which *Fasciodontia*, *Lyomyces*, and *Xylodon* were accepted as members of the family Schizoporaceae; however *Kneiffiella* and *Hyphodontia* were placed into monotypic families, Chaetoporellaceae and Hyphodontiaceae, respectively, and *Hastodontia* was considered to be an uncertain family rank within Hymenochaetales [23].

During investigations on corticioid fungi in southern China, three additional taxa were found which could not be assigned to any described species. In this study, the authors examine the taxonomy and phylogeny of the three new species within *Xylodon*. The aim of the current study is to further explore the species diversity of *Xylodon*, and more importantly, to construct a more natural taxonomic system of *Xylodon* within *Hyphodontia sensu lato*, based on the internal transcribed spacer (ITS) regions and the large subunit nuclear ribosomal RNA gene (nLSU) sequences.

2. Materials and Methods

2.1. Sample Collection and Herbarium Specimen Preparation

Fresh fruiting bodies of the fungi growing on the angiosperm stump, on the trunk of angiosperm, and on fallen angiosperm branches, were collected from the Dali, Puer, Wenshan, Yuxi of Yunnan Province, P.R. China. The samples were photographed in situ and fresh macroscopic details were recorded. Photographs were recorded by a Jianeng 80D camera. All photos were focus stacked and merged using Helicon Focus software. Macroscopic details were recorded and transported to a field station where the fruit body was dried on an electronic food dryer at 45 °C. Once dried, the specimens were sealed in envelope and zip lock plastic bags and labeled. The dried specimens were deposited in the herbarium of the Southwest Forestry University (SWFC), Kunming, Yunnan Province, P.R. China.

2.2. Morphology

Macromorphological descriptions are based on field notes and photos captured in the field and lab. Color terminology follows Petersen [33]. Micromorphological data were obtained from the dried specimens following observation under a light microscope [11]. 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 = means spore length (arithmetic average for all spores), W = means 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 given number (b) of specimens).

2.3. Molecular Phylogeny

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 using the manufacturer's instructions [34]. The nuclear ribosomal ITS region was amplified with primers ITS5 and ITS4 [35]. The nuclear nLSU region was amplified with primer pair LR0R and LR7 (<http://lutzonilab.org/nuclear-ribosomal-dna/>, accessed on 5 November 2021). 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/>, accessed on 20 October 2021) (Table 1).

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

Species Name	Specimen No.	GenBank Accession No.		References	Country
		ITS	nLSU		
<i>Fasciodontia brasiliensis</i>	MSK-F 7245a	MK575201	MK598734	[36]	Brazil
<i>F. bugellensis</i>	KAS-FD 10705a	MK575203	MK598735	[36]	France
<i>Hastodontia halonata</i>	HHB-17058	MK575207	MK598738	[36]	Mexico
<i>Hymenochaete cinnamomea</i>	He 2074	KU975460	KU975500	Unpublished	China
<i>Hym. rubiginosa</i>	He 1049	JQ716407	JQ279667	[37]	China
<i>Hyphodontia alutaria</i>	GEL3183	DQ340318	DQ340373	Unpublished	Germany
<i>Hyp. arguta</i>	KHL11938	EU118632	EU118633	[38]	Sweden
<i>Hyp. pallidula</i>	KAS-GEL2097	DQ340317	DQ340372	Unpublished	Germany
<i>Hyp. densispora</i>	LWZ20170908-5	MT319426	MT319160	[23]	China
<i>Hyp. zhixiangii</i>	LWZ20180903-5	MT319423	MT319158	[23]	China
<i>Kneiffiella barba-jovis</i>	KHL 11730	DQ873609	DQ873610	[30]	Sweden
<i>K. eucalypticola</i>	LWZ20180515-9	MT319411	MT319143	[23]	Australia
<i>K. palmae</i>	KAS-GEL 3456	DQ340333	DQ340369	[36]	China
<i>K. subalutacea</i>	GEL2196	DQ340341	DQ340362	[36]	Norway
<i>Lyomyces allantosporus</i>	FR 0249548	KY800397	KY795963	[39]	Réunion
<i>L. bambusinus</i>	CLZhao 4831	MN945968	MW264919	[40]	China
<i>L. fimbriatus</i>	Wu 911204-4	MK575210	MK598740	[36]	China
<i>L. mascarensis</i>	KAS-GEL 4833	KY800399	KY795964	[36]	Réunion
<i>L. orientalis</i>	LWZ20170909-7	MT319436	MT319170	[23]	China
<i>L. sambuci</i>	KAS-JR 7	KY800402	KY795966	[39]	Germany
<i>Xylodon acystidiatus</i>	LWZ20180514-9	MT319474	MT319211	[23]	Australia
<i>X. apacheriensis</i>	Wu 0910-58	KX857797	KX857822	[41]	China
<i>X. asper</i>	KHL8530	AY463427	AY586675	[42]	Sweden
<i>X. astrocystidiatus</i>	Wu 9211-71	JN129972	JN129973	[14]	China
<i>X. attenuatus</i>	Spirin 8775	MH324476		[26]	America
<i>X. australis</i>	LWZ20180509-8	MT319503		[23]	China
<i>X. bambusinus</i>	CLZhao 9174	MW394657	MW394650	[43]	China
<i>X. borealis</i>	JS26064	AY463429	AY586677	[42]	Norway
<i>X. brevisetus</i>	JS17863	AY463428	AY586676	[42]	Norway
<i>X. crystalliger</i>	LWZ20170816-33	MT319521	MT319269	[23]	China
<i>X. cystidiatus</i>	FR-0249200	MH880195	MH884896	[30]	Réunion
<i>X. damansaraensis</i>	LWZ20180417-23	MT319499		[23]	Malaysia
<i>X. detriticus</i>	Zibarová 30.10.17	MH320793	MH651372	[26]	Czech Republic
<i>X. filicinus</i>	MSK F 12869	MH880199	NG067836	[30]	China
<i>X. flaviporus</i>	FR-0249797	MH880201	MH884901	[30]	Réunion
<i>X. follis</i>	FR-0249814	MH880204	MH884902	[30]	Réunion
<i>X. gossypinus</i>	CLZhao 4465	MZ663803	MZ663812	Present study	China
<i>X. gossypinus</i>	CLZhao 8375 [T]	MZ663804	MZ663813	Present study	China
<i>X. hastifer</i>	K(M) 172400	NR166558		[20]	America
<i>X. heterocystidiatus</i>	Wei 17-314	MT731753	MT731754	Unpublished	China
<i>X. hyphodontinus</i>	KAS-GEL9222	MH880205	MH884903	[30]	Kenya
<i>X. kunmingensis</i>	TUB-FO 42565	MH880198	MH884898	[30]	China

Table 1. Cont.

Species Name	Specimen No.	GenBank Accession No.		References	Country
		ITS	nLSU		
<i>K. eucalypticola</i>	LWZ20180515-9	MT319411	MT319143	[23]	Australia
<i>K. palmae</i>	KAS-GEL 3456	DQ340333	DQ340369	[36]	China
<i>K. subalutacea</i>	GEL2196	DQ340341	DQ340362	[36]	Norway
<i>Lyomyces</i>	FR 0249548	KY800397	KY795963	[39]	Réunion
<i>allantosporus</i>					
<i>L. bambusinus</i>	CLZhao 4831	MN945968	MW264919	[40]	China
<i>L. fimbriatus</i>	Wu 911204-4	MK575210	MK598740	[36]	China
<i>L. mascarensis</i>	KAS-GEL 4833	KY800399	KY795964	[36]	Réunion
<i>L. orientalis</i>	LWZ20170909-7	MT319436	MT319170	[23]	China
<i>L. sambuci</i>	KAS-JR 7	KY800402	KY795966	[39]	Germany
<i>Xylodon acystidiatus</i>	LWZ20180514-9	MT319474	MT319211	[23]	Australia
<i>X. apacheriensis</i>	Wu 0910-58	KX857797	KX857822	[41]	China
<i>X. asper</i>	KHL8530	AY463427	AY586675	[42]	Sweden
<i>X. astrocystidiatus</i>	Wu 9211-71	JN129972	JN129973	[14]	China
<i>X. attenuatus</i>	Spirin 8775	MH324476		[26]	America
<i>X. australis</i>	LWZ20180509-8	MT319503		[23]	China
<i>X. bambusinus</i>	CLZhao 9174	MW394657	MW394650	[43]	China
<i>X. borealis</i>	JS26064	AY463429	AY586677	[42]	Norway
<i>X. brevisetus</i>	JS17863	AY463428	AY586676	[42]	Norway
<i>X. crystalliger</i>	LWZ20170816-33	MT319521	MT319269	[23]	China
<i>X. cystidiatus</i>	FR-0249200	MH880195	MH884896	[30]	Réunion
<i>X. damansaraensis</i>	LWZ20180417-23	MT319499		[23]	Malaysia
<i>X. detriticus</i>	Zibarová 30.10.17	MH320793	MH651372	[26]	Czech Republic
<i>X. filicinus</i>	MSK F 12869	MH880199	NG067836	[30]	China
<i>X. flaviporus</i>	FR-0249797	MH880201	MH884901	[30]	Réunion
<i>X. follis</i>	FR-0249814	MH880204	MH884902	[30]	Réunion
<i>X. gossypinus</i>	CLZhao 4465	MZ663803	MZ663812	Present study	China
<i>X. gossypinus</i>	CLZhao 8375 [T]	MZ663804	MZ663813	Present study	China
<i>X. hastifer</i>	K(M) 172400	NR166558		[20]	America
<i>X. heterocystidiatus</i>	Wei 17-314	MT731753	MT731754	Unpublished	China
<i>X. hyphodontinus</i>	KAS-GEL9222	MH880205	MH884903	[30]	Kenya
<i>X. kunmingensis</i>	TUB-FO 42565	MH880198	MH884898	[30]	China
<i>X. lagenicystidiatus</i>	LWZ20180513-16	MT319634	MT319368	[23]	Australia
<i>X. lenis</i>	Wu890714-3	KY081802		[20]	China
<i>X. macrosporus</i>	CLZhao 2379	MZ663805	MZ663814	Present study	China
<i>X. macrosporus</i>	CLZhao 2488	MZ663806	MZ663815	Present study	China
<i>X. macrosporus</i>	CLZhao 3238	MZ663807	MZ663816	Present study	China
<i>X. macrosporus</i>	CLZhao 8787	MZ663808		Present study	China
<i>X. macrosporus</i>	CLZhao 10226 [T]	MZ663809	MZ663817	Present study	China
<i>X. mollissimus</i>	LWZ20160318-3	KY007517	MT319347	[23]	China
<i>X. nesporii</i>	LWZ20180921-35	MT319655	MT319238	[23]	China
<i>X. niemelaei</i>	LWZ20150707-13	MT319630	MT319365	[23]	China
<i>X. nongravis</i>	GC1412-22	KX857801	KX857818	[41]	China
<i>X. nothofagi</i>	ICMP 13842	AF145583		[44]	China
<i>X. ovisporus</i>	LWZ20170815-31	MT319666	MT319346	[23]	China
<i>X. papillosus</i>	CBS 114.71	MH860026		[45]	The Netherlands
<i>X. paradoxus</i>	Dai14983	MT319519	MT319267	[23]	China
<i>X. pruinosis</i>	Spirin 2877	MH332700		[26]	Estonia
<i>X. pseudolanatus</i>	FP-150922	MH880220	NG067837	[30]	Belize
<i>X. pseudotropicus</i>	Dai16167	MT319509	MT319255	[23]	China
<i>X. quercinus</i>	KHL11076	KT361633	AY586678	[42]	Sweden
<i>X. ramicida</i>	Spirin 7664	NR138013		Unpublished	America
<i>X. rhododendricola</i>	LWZ20180513-9	MT319621	MT319357	[23]	Australia
<i>X. rimosissimus</i>	Ryberg 021031	DQ873627	DQ873628	[46]	Sweden
<i>X. serpentiformis</i>	LWZ20170816-15	MT319673	MT319218	[23]	China
<i>X. sinensis</i>	CLZhao 9197	MZ663810	MZ663818	Present study	China
<i>X. sinensis</i>	CLZhao 11120 [T]	OK560885	MZ663819	Present study	China

Table 1. Cont.

Species Name	Specimen No.	GenBank Accession No.		References	Country
		ITS	nLSU		
<i>X. spathulatus</i>	LWZ20180804-10	MT319646	MT319354	[23]	China
<i>X. subclavatus</i>	TUB-FO 42167	MH880232		[30]	China
<i>X. subflaviporus</i>	Wu 0809-76	KX857803	KX857815	[41]	China
<i>X. subserpentiformis</i>	LWZ20180512-16	MT319486	MT319226	[23]	Australia
<i>X. subtropicus</i>	LWZ20180510-24	MT319541	MT319308	[23]	China
<i>X. taiwanianus</i>	CBS 125875	MH864080	MH875537	[45]	The Netherlands
<i>X. ussuriensis</i>	KUN 1989	NR166241		Unpublished	America
<i>X. verecundus</i>	KHL 12261	DQ873642	DQ873643	[46]	Sweden
<i>X. victoriensis</i>	LWZ20180510-29	MT319487	MT319228	[23]	Australia
<i>X. xinpingensis</i>	CLZhao 11224	MW394662	MW394654	[43]	China
<i>X. yarraensis</i>	LWZ20180510-5	MT319639	MT319378	[23]	Australia
<i>X. yunnanensis</i>	LWZ20180922-47	MT319660		[23]	China

[T] is shown type material, holotype.

The sequences were aligned in MAFFT 7 (<https://mafft.cbrc.jp/alignment/server/>, accessed on 5 November 2021) using the “G-INS-i” strategy for the ITS and ITS+nLSU dataset. The alignment was adjusted manually using BioEdit [47]. The dataset was aligned first and then ITS and nLSU sequences were combined with Mesquite version 3.51. Alignment datasets were deposited in TreeBASE (submission ID 28877). ITS+nLSU sequences and ITS-only dataset were used to position the three new species among *Xylodon* and related taxa. Sequences of *Hymenochaete cinnamomea* (Pers.) Bres. and *H. rubiginosa* (Dicks.) Lév. retrieved from GenBank were used as an outgroup in the ITS+nLSU sequences (Figure 1); sequences of *Lyomyces orientalis* Riebesehl, Yurchenko & Langer, and *L. sambuci* (Pers.) P. Karst. retrieved from GenBank were used as an outgroup in the ITS-only sequences (Figure 2) [23].

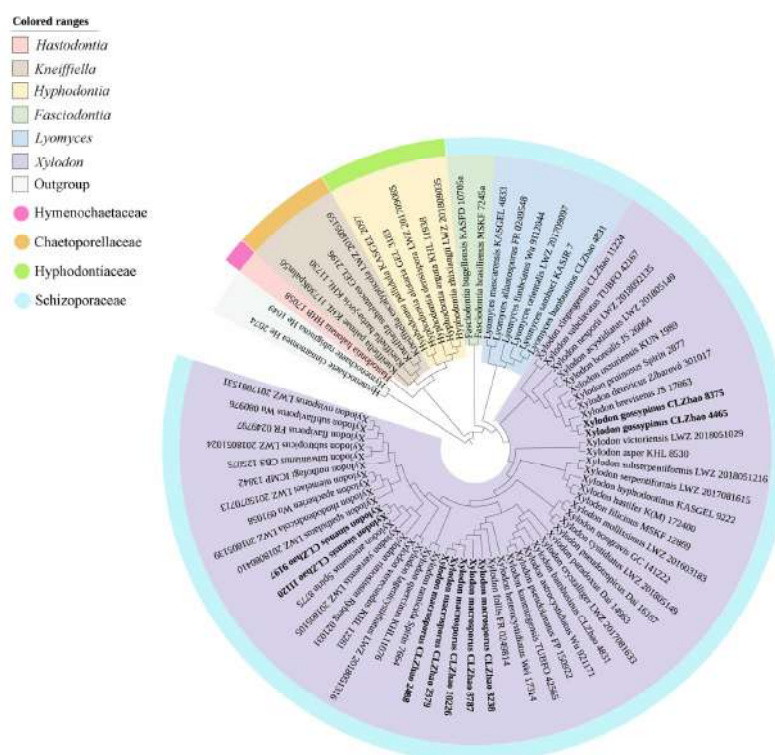


Figure 1. Maximum parsimony strict consensus tree illustrating the phylogeny of *Xylodon* and related genera in Hymenochaetales based on ITS+nLSU sequences. The families and genera represented by each color are indicated in the upper left of the phylogenetic tree.

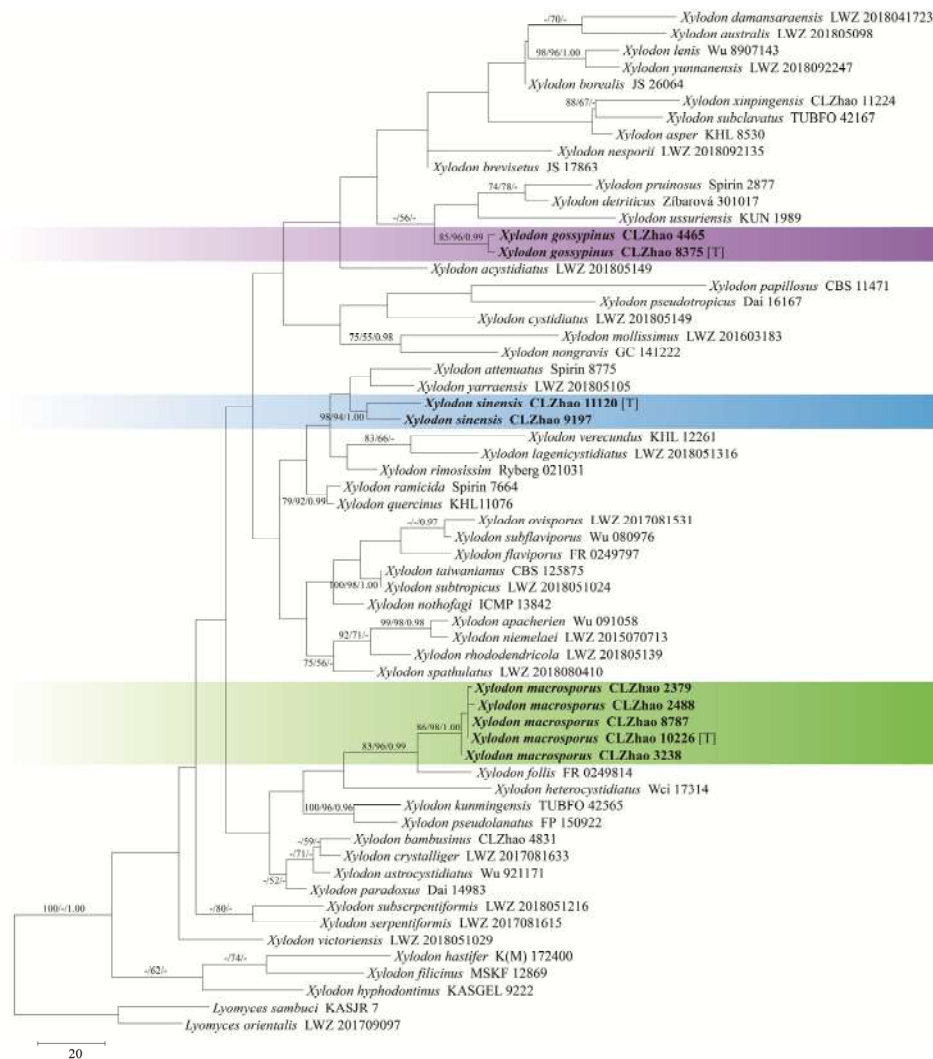


Figure 2. Maximum parsimony strict consensus tree illustrating the phylogeny of three new species and related species in *Xylodon* based on ITS sequences. Branches are labelled with maximum likelihood bootstrap value >70%, parsimony bootstrap value >50%, and Bayesian posterior probabilities >0.95, respectively. The new species are in bold; [T] is shown type material, holotype.

Maximum parsimony (MP), maximum likelihood (ML) and Bayesian inference (BI) analyses were applied to the combined three datasets following previous study, and the tree construction procedure was performed in PAUP* version 4.0b10 [48]. 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 bootstrap (BT) analysis with 1000 replicates [49]. 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. The multiple sequence alignment was also analyzed using maximum likelihood (ML) in RAXML-HPC2 through the Cipres Science Gateway [50]. Branch support (BS) for ML analysis was determined by 1000 bootstrap replicates.

MrModeltest 2.3 [51] 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 [52]. A total of 4 Markov chains were run for 2 runs from random starting trees for 920 thousand

generations for ITS+nLSU (Figure 1) and 13 million generations for ITS (Figure 2) with trees and parameters sampled every 1000 generations. The first one-fourth of all generations was discarded as burn-in. The majority rule consensus tree of all remaining trees was calculated. Branches were considered 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.

3. Results

3.1. Molecular Phylogeny

The ITS+nLSU dataset (Figure 1) included sequences from 74 fungal specimens representing 68 species. The dataset had an aligned length of 1421 characters, of which 744 characters are constant, 121 are variable and parsimony uninformative, and 556 are parsimony informative. Maximum parsimony analysis yielded 660 equally parsimonious trees (TL = 3859, CI = 0.2983, HI = 0.7017, RI = 0.5080, and RC = 0.1515). The best model for the ITS+nLSU dataset estimated and applied in the Bayesian analysis was 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 to MP analysis with an average standard deviation of split frequencies = 0.014909 (BI), and the effective sample size (ESS) across the two runs is the double of the average ESS (avg ESS) = 529.

The ITS-alone dataset (Figure 2) included sequences from 61 fungal specimens representing 55 species. The dataset had an aligned length of 589 characters, of which 257 characters are constant, 82 are variable and parsimony uninformative, and 250 are parsimony informative. Maximum parsimony analysis yielded 5000 equally parsimonious trees (TL = 1991, CI = 0.2823, HI = 0.7177, RI = 0.3947, and RC = 0.1114). The best model for the ITS dataset estimated and applied in the Bayesian analysis was 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 to MP analysis with an average standard deviation of split frequencies = 0.017958 (BI), and the effective sample size (ESS) across the two runs is the double of the average ESS (avg ESS) = 2396.5.

The phylogram inferred from the ITS+nLSU rDNA gene regions (Figure 1), based on the six genera, *Fasciodontia*, *Hastodontia*, *Hyphodontia*, *Kneiffiella*, *Lyomyces*, and *Xylodon*, were separated into 4 families within Hymenochaetales, in which three genera *Fasciodontia*, *Lyomyces*, and *Xylodon* were members of Schizoporaceae; three genera *Hastodontia*, *Hyphodontia*, and *Kneiffiella* clustered into monotypic families, Hymenochaetaceae, Hyphodontiaceae, and Chaetoporellaceae, respectively; in which our three new species clustered into family Schizoporaceae, divided into genus *Xylodon*. *Xylodon gossypinus* was sister to *X. brevisetus* (P. Karst.) Hjortstam & Ryvar den, *X. macrosporus* grouped with *X. follis* Riebesehl, Yurchenko & Langer, and *X. sinensis* formed a sister group to *X. attenuatus* Spirin & Viner.

Based on the ITS sequences analysis (Figure 2), three undescribed species grouped into *Xylodon*: the new species *X. gossypinus*, two specimens CLZhao 8375 and CLZhao 4465 with higher supports (85% BS, 96% BP, and 0.99 BPP) were sister to *X. ussuriensis* Viner with lower supports (-BS, 56% BP, and -BPP); *X. macrosporus*, five specimens CLZhao 2379, CLZhao 2488, CLZhao 10226, CLZhao 8787 and CLZhao 3238 with higher supports (86% BS, 98% BP, and 1.00 BPP) grouped closely with *X. follis* with higher supports (83% BS, 96% BP, and 0.99 BPP); and the new taxon *X. sinensis*, two specimens CLZhao 11120 and CLZhao 9197 with higher supports (98% BS, 94% BP, and 1.00 BPP) formed a sister group to *X. attenuatus* and *X. yarraensis* Xue W. Wang & L.W. Zhou with very low supports (-BS, -BP, and -BPP).

3.2. Taxonomy

Xylodon gossypinus C.L. Zhao & K.Y. Luo sp. nov. Figures 3–5.

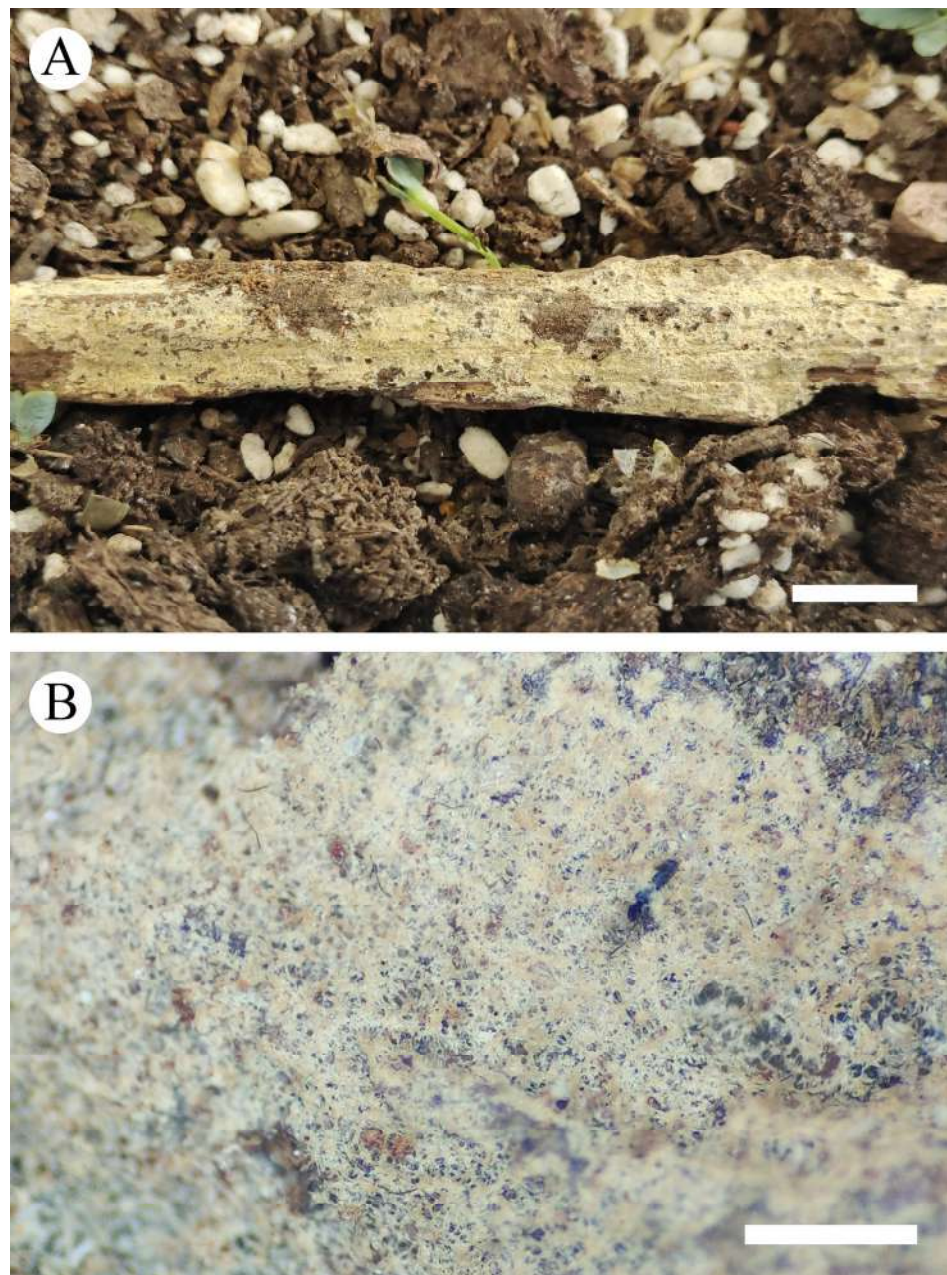


Figure 3. Basidiomata of *Xylodon gossypinus* (holotype). Bars: (A) = 1 cm and (B) = 1 mm.

Mycobank no.: 841268

Holotype—China. Yunnan Province, Puer, Jingdong County, Taizhong village, Ailaoshan Ecological Station, Ailaoshan National Nature Reserve, 24°32' N, 101°01' E, altitude 2450 m asl., on the angiosperm stump, leg. C.L. Zhao, 23 August 2018, CLZhao 8375 (SWFC).

Etymology—*gossypinus* (Lat.): referring to the cotton hymenophore of the specimens.

Fruiting body—Basidiomata annual, resupinate, without odor and taste when fresh, becoming flocculent when fresh, cotton upon drying, up to 9 cm long, 4 cm wide, 30–100 µm thick. Hymenial surface smooth, cream when fresh, buff upon drying, presence of some sort of projections. Sterile margin indistinct, cream to buff, 0.5–1 mm wide.

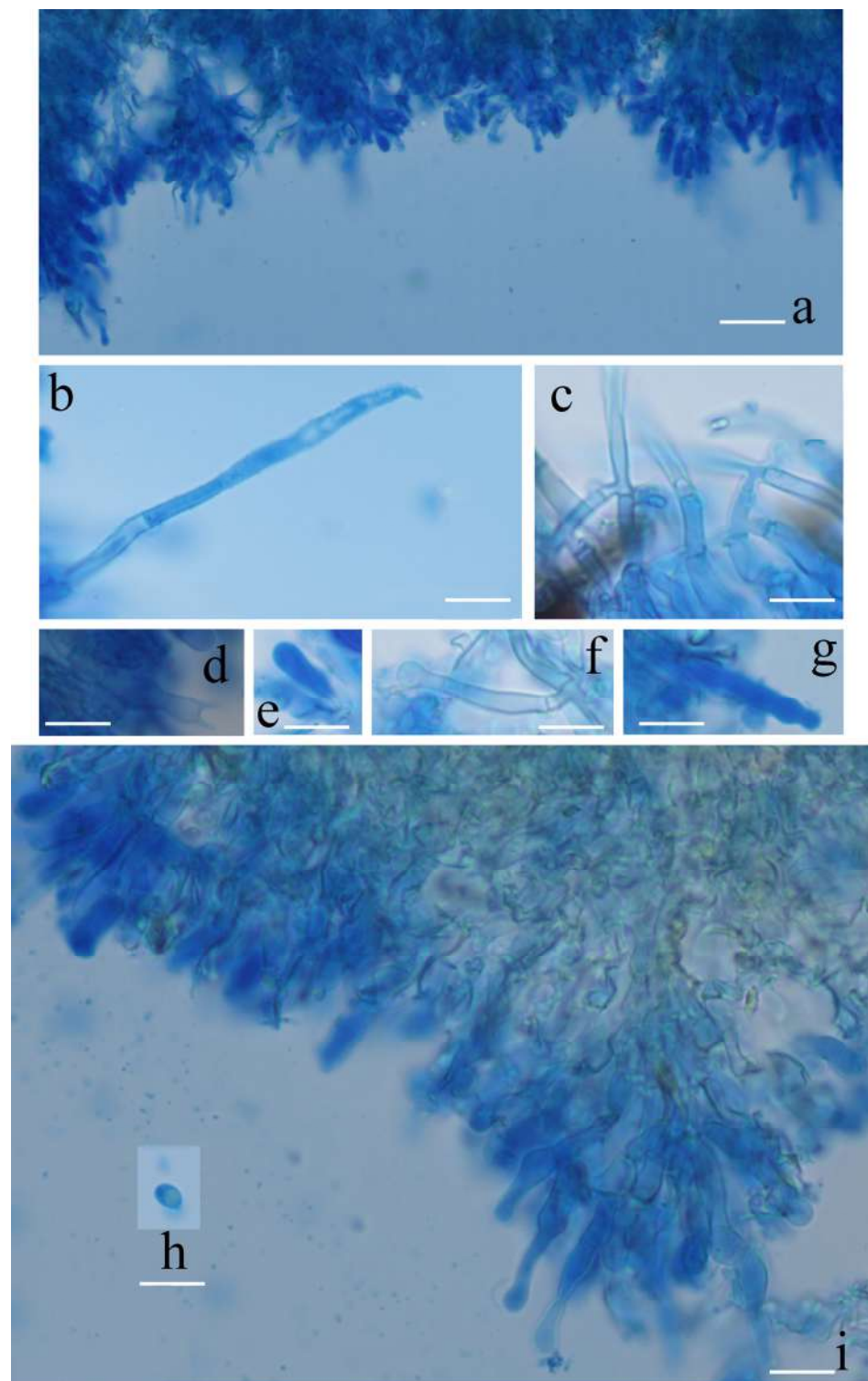


Figure 4. Microscopic structures of *Xylodon gossypinus* (holotype) (a): a section of hymenium (b), subulate cystidia to leptocystidia (c), generative hyphae (d), basidia (e), basidioles (f), capitate cystidia (g), moniliform cystidia (h), and basidiospores (i). A section of hymenium. Bars: (a–i) = 10 μ m, (a) 10 \times 40, (b–i) 10 \times 100 Oil.

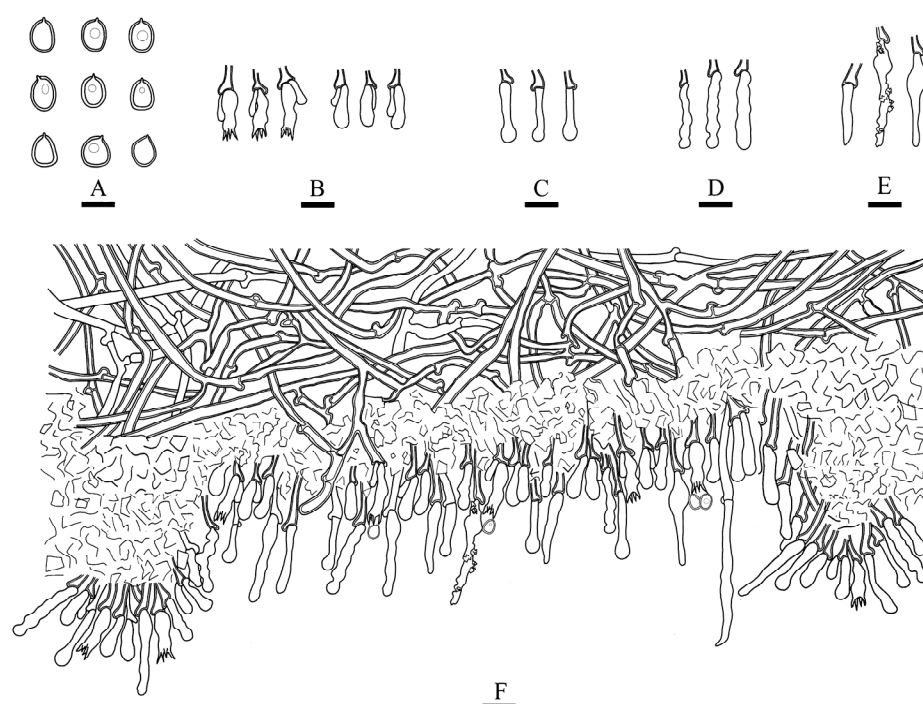


Figure 5. Microscopic structures of *Xylodon gossypinus* (holotype) (A): basidiospores (B), basidia and basidioles (C), capitate cystidia (D), moniliform cystidia (E), and subulate cystidia to leptocystidia (F). A section of hymenium. Bars: (A) = 5 μ m, (B–F) = 10 μ m.

Hyphal system—Monomitic, generative hyphae with clamps, colorless, thin- to thick-walled, frequently branched, interwoven, 2–4.5 μ m in diameter, IKI-, CB-; tissues unchanged in KOH; subhymenial hyphae densely covered by crystals.

Hymenium—Cystidia of three types: (1) capitate cystidia numerous, smooth, colorless, thin-walled, slightly constricted at the neck, with a globose head, 16–23.5 \times 2.5–5 μ m; (2) moniliform cystidia frequently, smooth, colorless, thin-walled, 17–45 \times 2–9 μ m; (3) subulate cystidia to leptocystidia lesser, thin-walled, with wider base, gradually thinning, 17.5–45.5 \times 2–5 μ m; basidia clavate to subcylindrical, constricted, with 4 sterigmata and a basal clamp connection, 11–13 \times 3–5.5 μ m.

Spores—Basidiospores ellipsoid, colorless, thick-walled, smooth, with one oil drop inside, IKI-, CB-, (2.5–)3–5.5(–6) \times (2–)2.5–4(–4.5) μ m, L = 4.34 μ m, W = 3.40 μ m, Q = 1.25–1.31 (n = 60/2).

Additional specimen examined—China. Yunnan Province, Puer, Jingdong County, Wuliangshan National Nature Reserve, GPS coordinates 22°46' N, 100°58' E, altitude 1400 m asl., on the trunk of angiosperm, leg. C.L. Zhao, 6 October 2017, CLZhao 4465 (SWFC).

Notes: Morphologically, *Xylodon gossypinus* is similar to *X. xinpingensis* C.L. Zhao & X. Ma based on the character of flocculent hymenophores. However, *Xylodon xinpingensis* differs from *X. gossypinus* by having the reticulate hymenial surface, the presence of fusiform cystidia, and subglobose, thin-walled basidiospores [43].

Xylodon gossypinus reminds *X. anmashanensis* (Yurchenko, H.X. Xiong & Sheng H. Wu) Riebesehl, Yurchenko & Langer, *X. crassispurus* (Gresl. & Rajchenb.) Hjortstam & Ryvarden, *X. pruinus* (Bres.) Spirin & Viner, *X. rickii* (Hjortstam & Ryvarden) K.H.

Larss. and *X. septocystidiatus* (H.X. Xiong, Y.C. Dai & Sheng H. Wu) Riebesehl & Langer based on the character of the thick-walled basidiospores. However, *Xylodon anmashanensis* is distinguished from *X. gossypinus* by having the irpicoid to odontoid hymenial surface and longer basidiospores (up to 7.5 μ m long) [13]; *X. crassispurus* differs from *X. gossypinus* by having only one type of capitate cystidia and wider basidiospores (5.5–6 \times 4–4.5 μ m) [53]; *X. pruinus* differs from *X. gossypinus* by its grandinioid to odontoid hymenial surface and the presence of clavate to spathuliform cystidia [26]; *X. rickii* is separated from *X. gossypinus*

by having the ochraceous hymenial surface with small brown dots and the presence of two types of cystidia: encrusted cystidia and capitate cystidia [54]; *X. septocystidiatus* is distinguished from *X. gossypinus* by its grandinioid hymenial surface and the presence of septocystidia [23].

Xylodon macrosporus C.L. Zhao & K.Y. Luo, sp. nov. Figures 6–8.

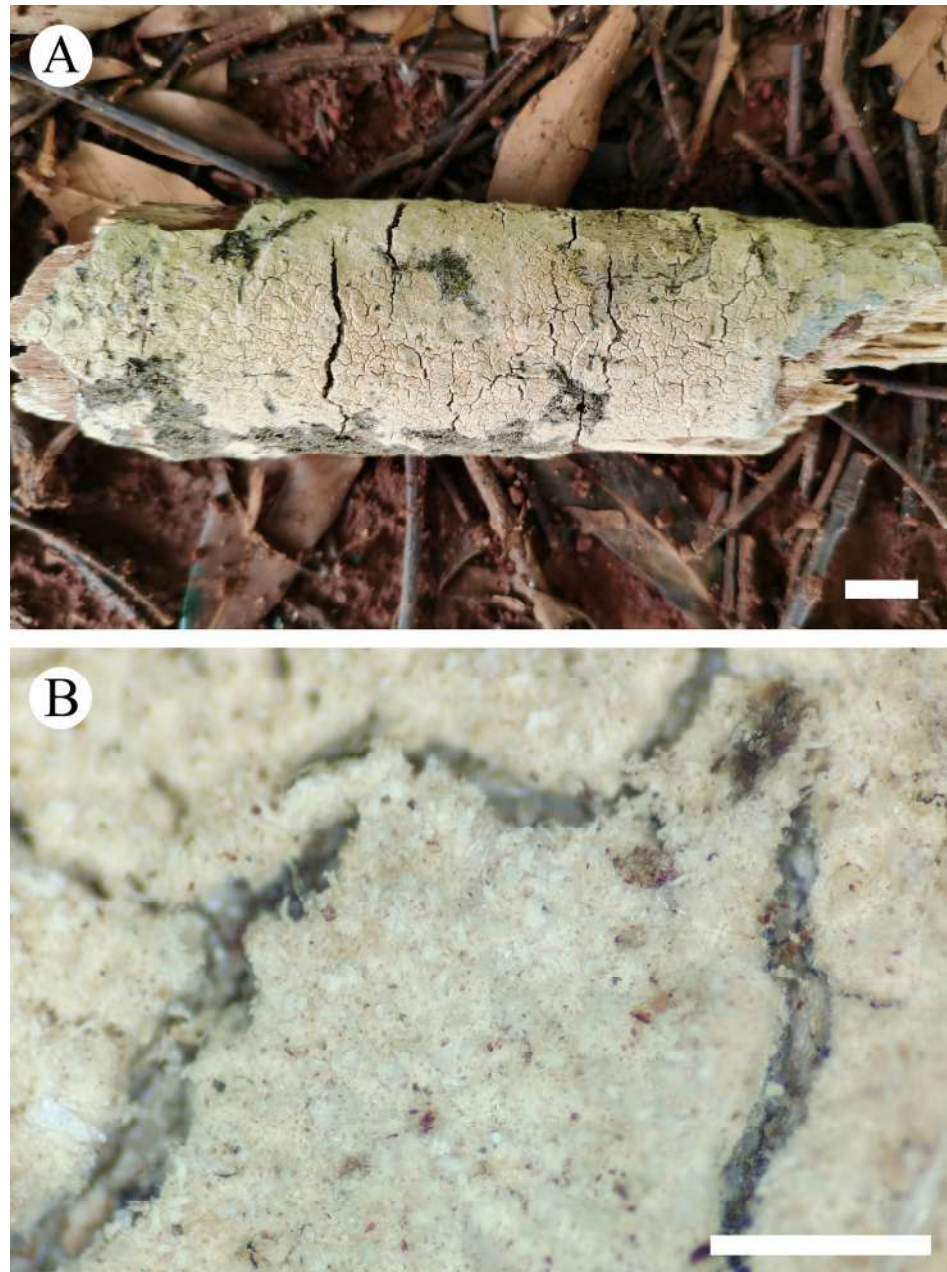


Figure 6. Basidiomata of *Xylodon macrosporus* (holotype). Bars: (A) = 1 cm and (B) = 1 mm.

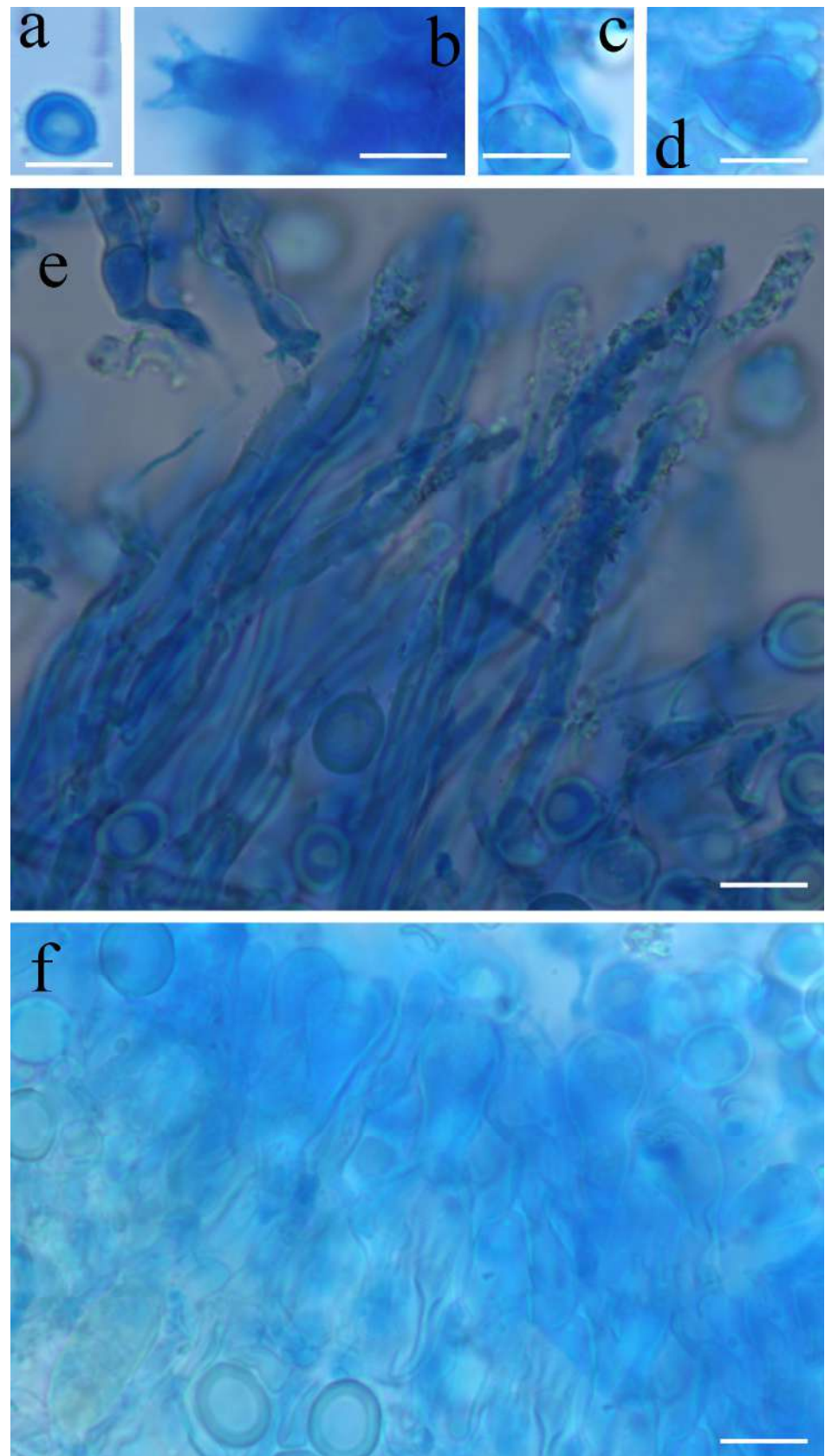


Figure 7. Microscopic structures of *Xylodon macrosporus* (holotype) (a): basidiospores (b), basidia (c), capitate cystidia (d), cystidia (e), and cylindrical cystidia (f). A section of hymenium. Bars: (a–f) = 10 μ m, 10 \times 100 Oil.

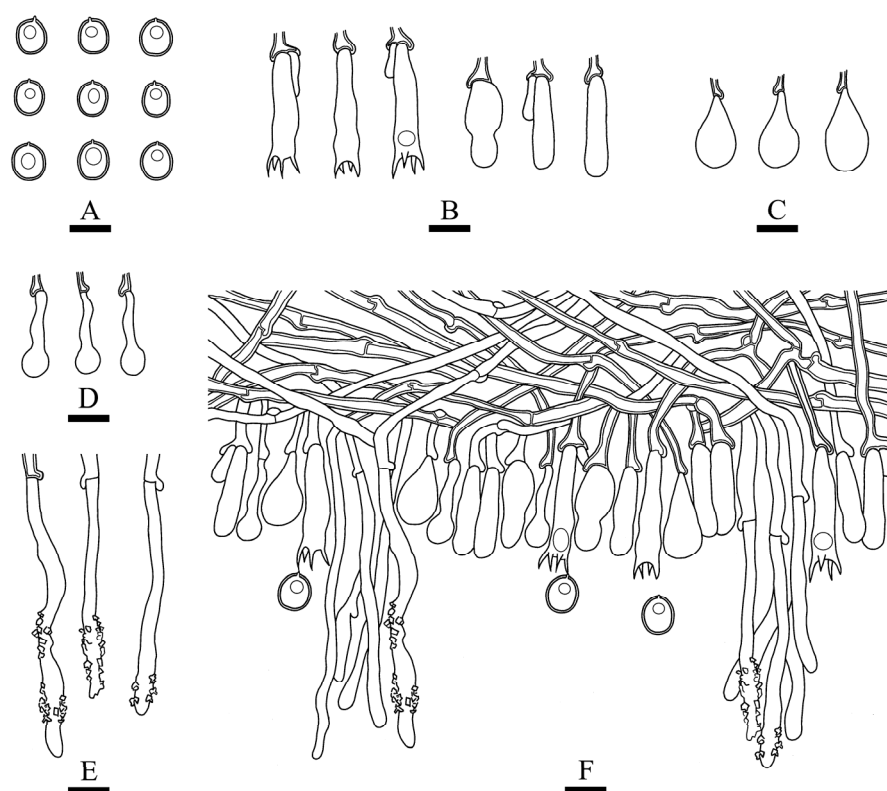


Figure 8. Microscopic structures of *Xylodon macrosporus* (holotype) (A): basidiospores (B), basidia and basidioles (C), cystidia (D), capitate cystidia (E), and cylindrical cystidia (F). A section of hymenium. Bars: (A–F) = 10 μ m.

Mycobank no.: 841269

Holotype—China. Yunnan Province, Dali, Nanjian County, Lingbaoshan National Forestry Park, GPS coordinates 24°48' N, 100°32' E, altitude 2400 m asl., on fallen angiosperm branch, leg. C.L. Zhao, 9 January 2019, CLZhao 10226 (SWFC).

Etymology—*macrosporus* (Lat.): referring to the larger basidiospores of the specimens.

Fruiting body—Basidiomata annual, resupinate, coriaceous when fresh, brittle when dry, up to 11 cm long, 4 cm wide, 70–150 μ m thick. Hymenial surface grandinioid under the lens, shorter, buff when fresh, pale yellowish upon drying, cracking. Sterile margin indistinct, cream to buff, about 1 mm wide.

Hyphal system—Monomitric, generative hyphae with clamps, colorless, thin- to thick-walled, occasionally branched, interwoven, 2–5 μ m in diameter, IKI-, CB-; tissues unchanged in KOH.

Hymenium—Cystidia of three types: (1) capitate cystidia rare, smooth, colorless, thin-walled, slightly constricted at the neck, with a globose head, 8–25.5 \times 3–10 μ m; (2) cylindrical cystidia numerous, strongly encrusted in the obtuse apex, 44–79.5 \times 3–6 μ m; (3) cystidia frequently, smooth, colorless, thin-walled, 11–21 \times 6–11 μ m; basidia subcylindrical, with 4 sterigmata and a basal clamp connection, 11.5–36 \times 5–11 μ m.

Spores—Basidiospores ellipsoid to broad ellipsoid, colorless, thick-walled, smooth, IKI-, CB-, 8–10.5(–11) \times (7–)7.5–9(–9.5) μ m, L = 9.25 μ m, W = 8.14 μ m, Q = 1.07–1.15 (n = 150/5).

Additional specimens examined. **China**—Yunnan Province, Yuxi, Xinping County, Mopanshan National Forestry Park, GPS coordinates 22°02' N, 101°20' E, altitude 2007 m asl., on the trunk of *Quercus semecarpifolia*, leg. C.L. Zhao, 18 August 2017, CLZhao 2379 (SWFC); on fallen angiosperm branch, leg. C.L. Zhao, 18 August 2017, CLZhao 2488 (SWFC); Puer, Laiyanghe National Forestry Park, GPS coordinates 22°36' N, 101°00' E, altitude 1500 m asl., on fallen angiosperm branch, leg. C.L. Zhao, 30 September 2017, CLZhao 3238 (SWFC);

Puer, Jingdong County, Taizhong village, Ailaoshan Ecological Station, Ailaoshan National Nature Reserve, GPS coordinates 24°32' N, 101°01' E, altitude 2450 m asl., on fallen angiosperm branch, leg. C.L. Zhao, 25 August 2018, CLZhao 8787 (SWFC).

Notes: Morphologically, *Xylodon macrosporus* is similar to *X. bambusinus* C.L. Zhao & X. Ma, *X. heterocystidiatus* (H.X. Xiong, Y.C. Dai & Sheng H. Wu) Riebesehl, Yurchenko & Langer, *X. lagenicystidiatus* Xue W. Wang & L.W. Zhou, *X. victoriensis* Xue W. Wang & L.W. Zhou and *X. yarraensis* Xue W. Wang & L.W. Zhou based on having the grandinoid hymenial surface. However, *Xylodon bambusinus* is separated from *X. macrosporus* by having the ceraceous basidiomata, the presence of two types of cystidia: fusiform cystidia and capitate cystidia, and smaller basidiospores ($4\text{--}5 \times 2.6\text{--}3.7 \mu\text{m}$) [43]; *X. heterocystidiatus* is distinguished from *X. macrosporus* by the presence of capitate and clavate to cylindrical cystidia, and smaller basidiospores ($4.2\text{--}5.6 \times 2.5\text{--}3.5 \mu\text{m}$) [8]; *X. lagenicystidiatus* differs from *X. macrosporus* by having the white to cream hymenial surface, the presence of leptocystidia and lagenocystidia, and smaller basidiospores ($4.6\text{--}5.3 \times 2.8\text{--}3.3 \mu\text{m}$); *X. victoriensis* differs from *X. macrosporus* by presence of leptocystidia and smaller basidiospores ($3.8\text{--}4.6 \times 3.2\text{--}3.7 \mu\text{m}$); *X. yarraensis* is separated from *X. macrosporus* by having capitate cystidia, thin-walled and smaller basidiospores ($4.5\text{--}5.3 \times 3.1\text{--}3.8 \mu\text{m}$) [23].

Xylodon macrosporus is similar to *X. echinatus* (Yurchenko & Sheng H. Wu) Riebesehl, Yurchenko & Langer, *X. rhizomorphus* (C.L. Zhao, B.K. Cui & Y.C. Dai) Riebesehl, Yurchenko & Langer, *X. subscopinellus* (G. Cunn.) Hjortstam & Ryvarden, *X. tuberculatus* (Kotir. & Saaren.) Hjortstam & Ryvarden and *X. ussuriensis* Viner in having ellipsoid to broad ellipsoid basidiospores. However, *Xylodon echinatus* is distinguished from *X. macrosporus* by its thick-walled tubular cystidia and smaller basidiospores ($4\text{--}6.5 \times 3.5\text{--}5 \mu\text{m}$) [11]; *X. rhizomorphus* differs from *X. macrosporus* by presence of margin rhizomorphs, bladder-like cystidia and smaller basidiospores ($4.1\text{--}5.9 \times 3.5\text{--}4.3 \mu\text{m}$) [15]; *X. subscopinellus* differs from *X. macrosporus* by having the odontoid hymenophore with cream to sulphur-yellow hymenial surface, the presence of cylindrical to moniliform gloeocystidia, and subclavate cystidia [55]; *X. tuberculatus* is separated from *X. macrosporus* by having the smooth to papillose or tuberculate hymenial surface, the presence of gloeocystidia, and smaller basidiospores ($4\text{--}5.2 \times 2.8\text{--}4.1 \mu\text{m}$) [56]; *X. ussuriensis* is distinguished from *X. macrosporus* by its sterile margin white to pale ochraceous, floccose, the presence of tramal hyphae, narrower basidia ($14.7\text{--}22.8 \times 3.4\text{--}4.9 \mu\text{m}$) and smaller basidiospores ($5.1\text{--}6 \times 3.8\text{--}4.6 \mu\text{m}$) [26].

Xylodon sinensis C.L. Zhao & K.Y. Luo, sp. nov. Figures 9–11.

Mycobank no.: 841270

Holotype—China. Yunnan Province, Wenshan, Xichou County, Xiaoqiaogou, Wenshan National Nature Reserve, GPS coordinates 23°22' N, 104°43' E, altitude 1500 m asl., on the trunk of angiosperm, leg. C.L. Zhao, 15 January 2019, CLZhao 11120 (SWFC).

Etymology—*sinensis* (Lat.): referring to provenance (China) of the specimens.

Fruiting body—Basidiomata annual, resupinate, adnate, coriaceous, without odor and taste when fresh, up to 5 cm long, 3.5 cm wide, 100–150 μm thick. Hymenial surface grandinoid, cream to buff when fresh, buff to brown on drying. Sterile margin indistinct, cream to buff, about 1 mm wide.

Hyphal system—Monomitic, generative hyphae with clamps, colorless, thin- to thick-walled, frequently branched, interwoven, 1.5–4 μm in diameter; IKI-, CB-; tissues unchanged in KOH.

Hymenium—Cystidia fusiform rare, $10\text{--}21 \times 3\text{--}6 \mu\text{m}$; basidia subclavate to barreled, slightly constricted in the middle to somewhat sinuous, with 4 sterigmata and a basal clamp, $9.5\text{--}17.5 \times 2.5\text{--}4.5 \mu\text{m}$.

Spores—Basidiospores subglobose, colorless, thin-walled, smooth, IKI-, CB-, $(2.5\text{--})3\text{--}5 \times (2\text{--})2.5\text{--}4\text{--}(4.5) \mu\text{m}$, $L = 3.75 \mu\text{m}$, $W = 3.17 \mu\text{m}$, $Q = 1.14\text{--}1.22$ ($n = 60/2$).

Additional specimen examined—China. Yunnan Province, Puer, Jinshan Original Forest, GPS coordinates 23°56' N, 101°31' E, altitude 2300 m asl., on the trunk of angiosperm, leg. C.L. Zhao, 2 January 2019, CLZhao 9197 (SWFC).

Notes: Morphologically, *Xylodon sinensis* resembles *X. capitatus* (G. Cunn.) Hjortstam & Ryvar den, *X. pseudotropicus* (C.L. Zhao, B.K. Cui & Y.C. Dai) Riebesehl, Yurchenko & Langer, *X. subflaviporus* C.C. Chen & Sheng H. Wu and *X. subserpentiniformis* Xue W. Wang & L.W. Zhou based on having the buff to brown hymenial surface. However, *Xylodon capitatus* differs from *X. sinensis* by having the capitate gloeocystidia and longer basidiospores ($5\text{--}6 \times 4\text{--}4.5 \mu\text{m}$) [55]; *X. pseudotropicus* is distinguished from *X. sinensis* by its poroid hymenial surface and the capitate cystidia [15]; *X. subflaviporus* differs from *X. sinensis* by having the poroid hymenophore and four kinds cystidia of present as capitate cystidia, acicular or cylindrical cystidia, subulate to ventricose cystidia, apically-encrusted cystidia [17]; *X. subserpentiniformis* is separated from *X. sinensis* by its tramacystidia [23].

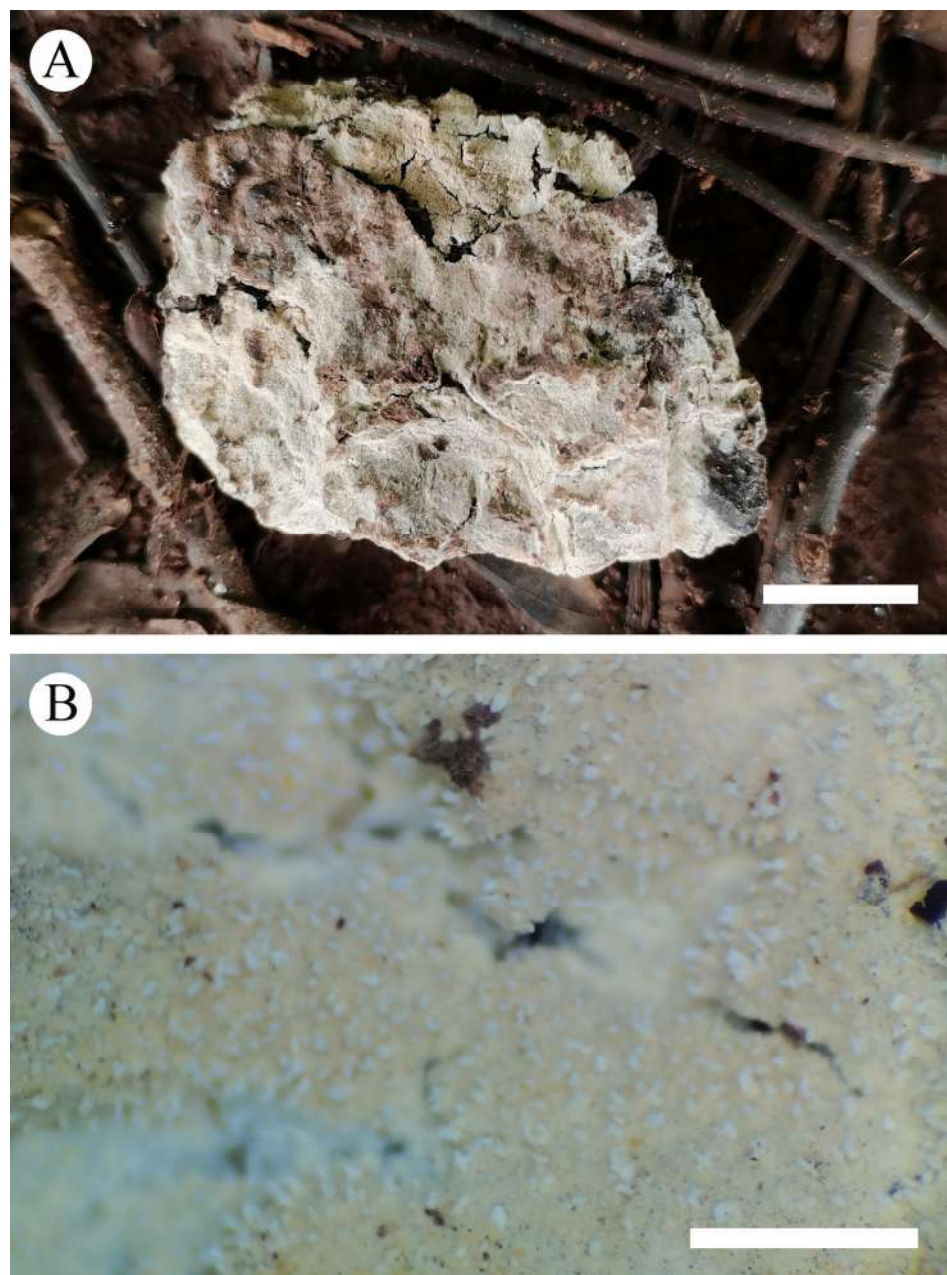


Figure 9. Basidiomata of *Xylodon sinensis* (holotype). Bars: (A) = 1 cm and (B) = 1 mm.

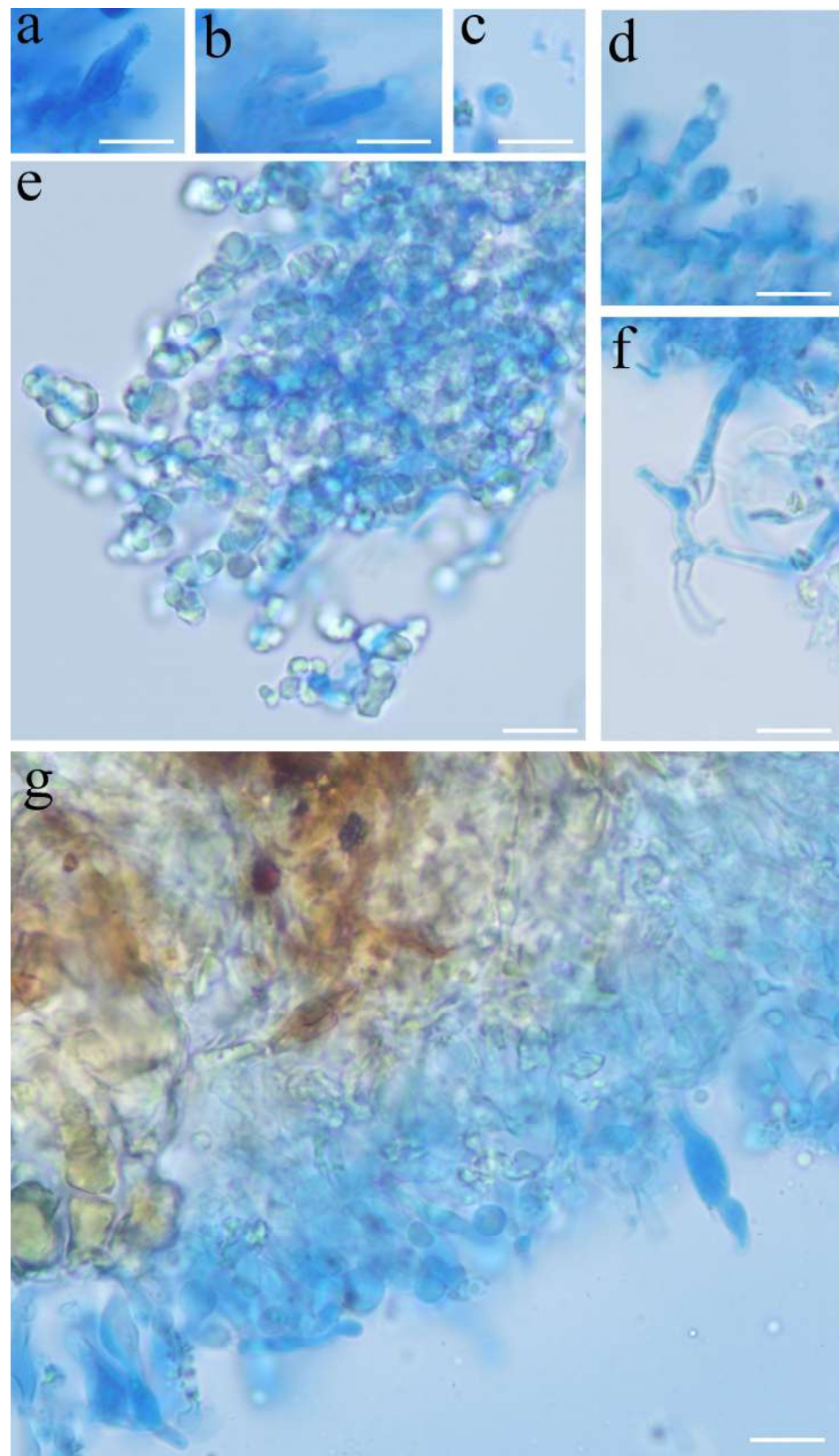


Figure 10. Microscopic structures of *Xylodon sinensis* (holotype) (a): fusiform cystidia (b), basidioles (c), basidiospores (d), basidia (e), crystal (f), and generative hyphae (g). A section of hymenium. Bars: (a–g) = 10 μ m, 10 \times 100 Oil.

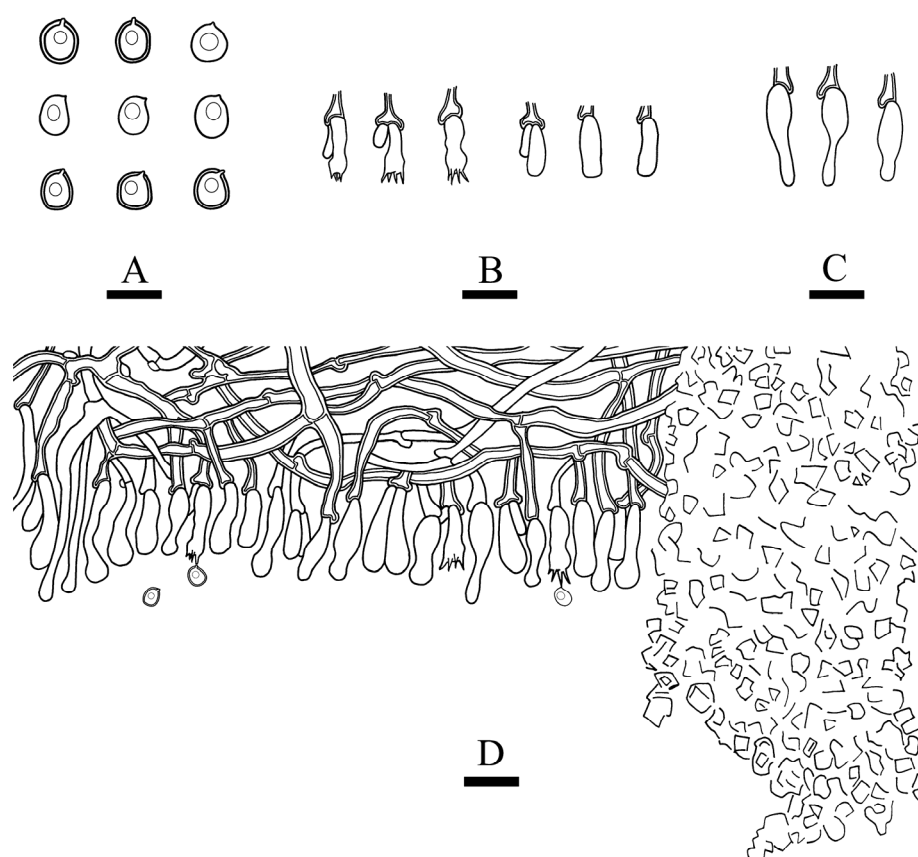


Figure 11. Microscopic structures of *Xylodon sinensis* (holotype) (A): basidiospores (B), basidia and basidioles (C), and fusiform cystidia (D). A section of hymenium. Bars: (A) = 5 μ m, (B–D) = 10 μ m.

Xylodon sinensis resembles *X. bisporus* (Boidin & Gilles) Hjortstam & Ryvarden, *X. crustosoglobosus* (Hallenb. & Hjortstam) Hjortstam & Ryvarden, *X. poroideoefibulatus* (Sheng H. Wu) Hjortstam & Ryvarden, *X. rudis* (Hjortstam & Ryvarden) Hjortstam & Ryvarden and *X. subglobosus* Samita, Sanyal & Dhingra ex L.W. Zhou & T.W. May based on having subglobose basidiospores. However, *Xylodon bisporus* differs from *X. sinensis* by having the smooth, milky white hymenial surface and bigger basidiospores ($5.5\text{--}7 \times 4.7\text{--}6.2 \mu\text{m}$) [57]; *X. crustosoglobosus* is separated from *X. sinensis* by its greyish-white to yellowish hymenial surface and the presence of subulate cystidia [58]; *X. poroideoefibulatus* differs from its cream to ivory-yellowish hymenial surface and longer basidiospores ($5\text{--}5.7 \times 4\text{--}4.5 \mu\text{m}$) [6]; *X. rudis* is separated from *X. sinensis* by its pale ochraceous hymenial surface and the absence of cystidia [59]; *X. subglobosus* is distinguished from *X. sinensis* by having odontoid hymenial surface and cystidia like hyphal ends [23].

4. Discussion

Phylogenetically, six genera, *Fasciodontia*, *Hastodontia*, *Hyphodontia*, *Kneiffiella*, *Lyomyces*, and *Xylodon* were nested into four families, Schizoporaceae, Chaetoporellaceae, Hyphodontiaceae, an uncertain family rank within Hymenochaetales, in which *Fasciodontia*, *Lyomyces*, and *Xylodon* grouped into the family Schizoporaceae; *Kneiffiella* and *Hyphodontia* placed into families Chaetoporellaceae and Hyphodontiaceae, respectively, and *Hastodontia* was considered to be an uncertain family rank within Hymenochaetales [23]. In the present study (Figure 1), our three undescribed taxa nested into family Schizoporaceae, located in the genus *Xylodon*. The previous research showed that *Xylodon* was strongly supported to be a monogenetic genus in *Hyphodontia* s.l. by the mycologists [14,23,30]. According to our result based on present sequence data (Figure 2), *X. gossypinus*, *X. macrosporus*, and *X. sinensis* are nested into *Xylodon* with strong supports.

The three new taxa were found to belong to *Xylodon* based on the ITS sequences (Figure 2), in which *X. gossypinus* was sister to *X. ussuriensis* with lower supports (-BS, 56% BP, and -BPP) and both taxa have the similar identify scores (88.12%) based on the BLAST analysis; the species *X. macrosporus* grouped with *X. follis* with higher supports (83% BS, 96% BP, and 0.99 BPP) and both taxa have similar identify scores (93.57%) based on the BLAST analysis; the taxon *X. sinensis* formed two sister groups to *X. attenuatus* and *X. yarraensis* with very low supports (-BS, -BP, and -BPP) and both taxa have lower identity scores, respectively (93.20%, -) based on the BLAST analysis. However, morphologically *Xylodon ussuriensis* differs from *X. gossypinus* by having a grandinioid to odontoid hymenial surface and the presence of tramal cystidia, subhymenial cystidia, and astrocystidia [26]; *X. follis* is distinguished from *X. macrosporus* by its soft-membranaceous basidiomata and the presence of capitate cystidia [30]; *X. attenuatus* is separated from *X. sinensis* by having effused basidiomata and the presence of subcapitate or capitate cystidia and hyphoid cystidia [26], *X. yarraensis* differs from *X. sinensis* by its the presence of capitate cystidia [23].

In the ecological habit and geographical distribution, the taxa of *Xylodon* are widespread and primarily wood decomposers, causing a white-rot of angiosperms and gymnosperms [14,60]. A few *Xylodon* taxa have been collected on rotten spruce stumps, palms or palm tree inflorescences, bamboo, and ferns [9,23,56,57,61–65].

The taxa of *Xylodon* are a typical example group of wood-rotting fungi, which is an extensively studied group of Basidiomycota [3,11,66–72]. Currently, 30 species of *Xylodon* were recorded in China [20,22,23,26,30,36,43,73]. Based on our present morphology and phylogeny study of *Xylodon*, all of these can be separated from the three new species (Figures 1 and 2).

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