



Clarification of some imperfectly understood characters in the Chinese species *Thalictrum przewalskii* (Ranunculaceae), with reduction of *T. lasiogynum* and *T. latistylum* to its synonymy

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Xylodon bambusinus and *X. xinpingensis spp. nov.* (Hymenochaetales) from southern China

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Abstract

Two new species, *Xylodon bambusinus* and *X. xinpingensis*, are proposed based on morphological and molecular evidences. Both species share the annual growth habit, resupinate basidiomata and monomitic hyphal system with clamped, colorless generative hyphae, smooth, thin-walled basidiospores, but *X. bambusinus* is characterized by the smooth to tuberculate hymenial surface, presence of capitate and fusiform cystidia, broad ellipsoid basidiospores, while *X. xinpingensis* by the reticulate hymenophore with cream hymenial surface, and subglobose basidiospores ($4.5-6 \times 3.5-5 \mu m$). 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. The phylogenetic analyses based on molecular data of ITS and ITS+nLSU sequences showed that *X. bambusinus* was sister to *X. subclavatus*, while *X. xinpingensis* grouped with *X. astrocystidiatus* and *X. paradoxus*. The nLSU dataset revealed that *X. bambusinus* grouped with *X. asperus* and *X. brevisetus* with lower supports, and that *X. xinpingensis* grouped with *X. astrocystidiatus* and *X. paradoxus* and then with *X. rimosissimus* without supports. Both morphological and molecular evidences confirmed the placement of two new species in *Xylodon*. Description and figures from the new species and a key to the known species of *Xylodon* from China are presented.

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

Introduction

The corticioid genus *Xylodon* (Pers. 1801: 522) Gray (1821: 649) (Schizoporaceae, Hymenochaetales) based on the generic type *X. quercinus* (Pers.) Gray (1821: 649), is characterized by the resupinate basidiomata with smooth, tuberculate, grandinioid, odontioid, coralloid, irpicoid or poroid hymenophore, a monomitic hyphal system with clamp connections on generative hyphae and bladder-like, bottle-shaped, capitate to subulate cystidia, suburniform basidia and globose to ellipsoid to cylindrical basidiospores and by causing a white rot (Gray 1821, Bernicchia & Gorjón 2010). Both MycoBank database (http://www.MycoBank.org) and Index Fungorum (http://www.indexfungorum.org) register 192 specific and infraspecific names in *Xylodon*, and recently more species enriched the diversity of this genus (Wu 1990, 2000, 2001, 2006, Hjortstam & Ryvarden 2009, Xiong *et al.* 2009, 2010, Dai 2011, 2012, Lee & Langer 2012, Yurchenko & Wu 2013, 2014, Zhao *et al.* 2014, Chen *et al.* 2016, 2018, Kan *et al.* 2017a, b, Riebesehl & Langer 2017, Wang & Chen 2017, Riebesehl *et al.* 2019, Shi *et al.* 2019).

Phylogeny inferred from nuclear DNA sequence data for *Hyphodontia* s.l. demonstrated 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, and *Xylodon* nested into the *Xylodon-Schizopora-Palifer* clade (Yurchenko & Wu 2014). Based on the morphological and phylogenetic information, Riebesehl & Langer (2017) studied *Hyphodontia* s.l. in which 13 new combinations in *Xylodon* were proposed. Recently, phylogenetic and morphological studies in *Xylodon* showed that 77 species were accepted in

Xylodon to date and *Palifer* Stalpers & P.K. Buchanan (1991: 339) and *Odontiopsis* Hjortstam & Ryvarden (1980: 180) are synonymised under *Xylodon* based on morphological and sequence data (Riebesehl *et al.* 2019).



FIGURE 1. Maximum Parsimony strict consensus tree illustrating the phylogeny of two new species and related species in *Xylodon* based on ITS sequences. Branches are labeled with maximum likelihood bootstrap values > 75%, parsimony bootstrap values > 75% and Bayesian posterior probabilities > 0.95, respectively.



FIGURE 2. Maximum Parsimony strict consensus tree illustrating the phylogeny of two new species and related species in *Xylodon* based on nLSU sequences. Branches are labeled with maximum likelihood bootstrap values > 75%, parsimony bootstrap values > 75% and Bayesian posterior probabilities > 0.95, respectively.



FIGURE 3. Maximum Parsimony strict consensus tree illustrating the phylogeny of two new species and related species in *Xylodon* based on ITS+nLSU sequences. Branches are labeled with maximum likelihood bootstrap values > 75%, parsimony bootstrap values > 75% and Bayesian posterior probabilities > 0.95, respectively.

During the investigations on wood-inhabiting fungi in Yunnan Province, P.R. China, specimens of *Xylodon* were found and could not be assigned to any described species. In this study, the authors examine taxonomy and phylogeny of these specimens within *Xylodon* based on the internal transcribed spacer (ITS) and the large subunit nuclear ribosomal RNA gene (nLSU) sequences and morphological characters.

Materials and methods

Morphological studies

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. Colour terms follow Petersen (1996). Micromorphological data were obtained from the dried specimens, and observed under a light microscope following Dai (2012). The following abbreviations are used: KOH = 5% potassium hydroxide, CB = Cotton Blue, CB- = acyanophilous, IKI = Melzer's reagent, IKI- = both inamyloid and non-dextrinoid, L = mean spore length (arithmetic average of all spores), W = mean spore width (arithmetic average of 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.

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 *et al.* 1990). 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 products were purified and directly sequenced at Kunming Tsingke Biological Technology Limited Company, Kunming, Yunnan Province, P.R. China. All newly generated sequences were deposited at GenBank (Table 1).

Sequencher 4.6 (GeneCodes, Ann Arbor, MI, USA) was used to edit the DNA sequences. Sequences were aligned in MAFFT 7 (http://mafft.cbrc.jp/alignment/server/) using the "G-INS-i" strategy and manually adjusted in BioEdit (Hall 1999). The sequence alignment was deposited in TreeBase (submission ID 26926). *Phellinus gabonensis* Decock & Yombiyeni (2011: 358) was selected as outgroup for phylogenetic analyses of ITS (Fig. 1), nLSU (Fig. 2) and ITS+nLSU (Fig. 3), phylogenetic trees, respectively (Riebesehl *et al.* 2019).

Maximum parsimony (MP) analyses were applied to the ITS, nLSU and ITS+nLSU dataset sequences. Approaches to phylogenetic analysis followed Zhao & Wu (2017) 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. Maxtrees 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 1000 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+I+G) 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 3500 thousand generations for ITS (Fig. 1), 2700 thousand generations for nLSU (Fig. 2), 1700 thousand generations for ITS+nLSU (Fig. 3) 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 values (BS) >75%, maximum parsimony bootstrap values (BT) >75%, or Bayesian posterior probabilities (BPP) >0.95.



FIGURE 4. Basidiomata of Xylodon bambusinus (holotype). Bars: A-2 cm, B-1 mm.



FIGURE 5. *Xylodon bambusinus* (holotype), microscopic structures: A: Basidiospores. B: Basidia and basidioles. C: Capitate cystidia. D: Fusiform cystidia. E: A section of hymenium. F: A section of subiculum. Bars: A—5 µm; B–F—10 µm.

Results

Molecular phylogeny

The ITS phylogenetic tree included sequences from 61 fungal specimens representing 43 taxa. The dataset had an aligned length of 724 characters in the dataset, of which 342 characters are constant, 112 are variable and parsimony-

uninformative, and 270 are parsimony-informative. Maximum parsimony analysis yielded 1 equally parsimonious tree (TL = 1717, CI = 0.3646, HI = 0.6354, RI = 0.5655, RC = 0.2062). 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 =0.009952 (BI).





FIGURE 6. Basidiomata of *Xylodon xinpingensis* (holotype). Bars: A-2 cm; B-1 mm.



FIGURE 7. Xylodon xinpingensis (holotype), microscopic structures: A: Basidiospores. B: Basidia and basidioles. C: Cystida. D: A section of hymenium. E: A section of subiculum. Bars: A—5 µm; B–E—10 µm.

The phylogenetic tree (Fig. 1) inferred from ITS sequences demonstrated that *X. bambusinus* was sister to *X. subclavatus* (Yurchenko, H.X. Xiong & Sheng H. Wu) Riebesehl, Yurchenko & Langer (2017: 650) and then grouped with several close species comprised *X. filicinus* Yurchenko & Riebesehl (2019: 110), *X. hastifer* Hjortstam & Ryvarden (2009: 37), *X. hyphodontinus* (Hjortstam & Ryvarden) Riebesehl, Yurchenko & G. Gruhn (2019: 117), and *X. pseudotropicus* (C.L. Zhao, B.K. Cui & Y.C. Dai) Riebesehl, Yurchenko & Langer (2017: 649). *Xylodon xinpingensis* grouped with *X. astrocystidiatus* (Yurchenko & Sheng H. Wu) Riebesehl, Yurchenko & Langer (2017: 641) and *X. paradoxus* (Schrad.) Chevall (1826: 274) with lower supports (- BS, 87% BT, - BPP).

TABLE 1. List of species, spec	imens and GenBank accession nu	mbers of sequences used	in this study.
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Success norma	Sample no.	GenBank accession no.		D - f
Species name		ITS	nLSU	Kelelences
Phellinus gabonensis	MUCL 52025	HM635715	HM635690	Yombiyeni et al. 2011
Xylodon apacheriensis	Canfield 180	KY081800	-	Riebesehl & Langer 2017
X. asperus	UC 2023169	KP814365	-	Rosenthal et al. 2017
X. asperus	KHL 8530	-	AY586675	Larsson et al. 2004
X. astrocystidiatus	Wu 9211-71	JN129972	JN129973	Yurchenko & Wu 2014
X. australis	CIEFAP-11041	-	MH884895	Riebesehl et al. 2019
X. bambusicola	CLZhao 11211	MW394658	MW394651	Present study
X. bambusicola	CLZhao 11215	MW394661	MW394652	Present study
X. bambusicola	CLZhao 11219	MW394659	MW394653	Present study
X. bambusicola	CLZhao 11224	MW394662	MW394654	Present study
X. bambusicola	CLZhao 11310	MW394660	MW394655	Present study
X. borealis	UC 2022850	KP814307	-	Rosenthal et al. 2017
X. borealis	JS 26064	-	AY586677	Larsson et al. 2004
X. brevisetus	KHL 12386	DQ873612	DQ873612	Larsson et al. 2006
X. bubalinus	Cui 12888	KY290983	-	Wang & Chen 2017
X. chinensis	Wu 1407-105	KX857804	KX857811	Chen et al. 2017
X. cystidiatus	FR-0249200	MH880195	-	Riebesehl et al. 2019
X. detriticus	UC 2023108	KP814412	-	Rosenthal et al. 2017
X. dimiticus	Dai 15321	KT989969	-	Chen et al. 2016
X. exilis	MSK-F 7431	-	MH884897	Riebesehl et al. 2019
X. exilis	TUB-FO 42450	MH880197	-	Riebesehl et al. 2019
X. exilis	TUB-FO 42565	MH880198	MH884898	Riebesehl et al. 2019
X. filicinus	MSK-F 12869	MH880199	MH884899	Riebesehl et al. 2019
X. filicinus	MSK-F 12870	MH880200	MH884900	Riebesehl et al. 2019
X. flaviporus	FCUG 1053	AF145575	-	Paulus et al. 2000
X. flaviporus	FR 0249797	MH880201	-	Riebesehl et al. 2019
X. flaviporus	KUC 2013080817	-	KJ668314	Jang <i>et al.</i> 2016
X. follis	FR-0249814	MH880204	MH884902	Riebesehl et al. 2019
X. hastifer	Ryvarden 19767	KY081801	-	Riebesehl & Langer 2017
X. heterocystidiatus	Wu 9209-27	JX175045	-	Yurchenko & Wu 2014
X. heterocystidiatus	Wu 9209-27	-	KX857821	Chen et al. 2017
X. hyphodontinus	LIP GG-MAR12-238	MH880207	MH884905	Riebesehl et al. 2019
X. hyphodontinus	LIP GG-MAR15-127	MH880208	MH884906	Riebesehl et al. 2019
X.kunmingensis	CLZhao 3019	MK404532	-	Shi <i>et al</i> . 2019
X. lenis	Wu 0808-32	-	KX857820	Chen et al. 2017
X. lenis	Wu 890714-3	KY081802	-	Riebesehl & Langer 2017
X. mollissimus	LWZ 20160318-3	KY007517	-	Kan <i>et al</i> . 2017b
X. nespori	KAS-GEL 3158	-	DQ340346	Riebesehl et al. 2019
X. nespori	KAS-JR 14	MH880210	-	Riebesehl et al. 2019
X. nespori	KUC 20161012-50	MF774797	-	Riebesehl et al. 2019
X. niemelaei	Dai 15358	KT989973	-	Chen <i>et al.</i> 2016
X. niemelaei	FR-0249178	-	MH884907	Riebesehl et al. 2019
X. niemelaei	FR-0249225	MH880213	-	Riebesehl et al. 2019
X. niemelaei	Wu 1010-62	-	KX857817	Chen <i>et al.</i> 2017

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TABLE 1 (Continued)

Species name	Sample no.	GenBank accession no.		Deferences
Species name		ITS	nLSU	Kererences
X. nothofagi	PDD:91630	GQ411524	-	Fukami et al. 2010
X. ovisporus	ICMP 13830	AF145584	-	Paulus et al. 2000
X. ovisporus	KAS-GEL 3493	EU583421	-	Riebesehl et al. 2019
X. ovisporus	KUC 20130725-29	-	KJ668365	Jang et al. 2016
X. paradoxus	FCUG 2425	AF145571	-	Paulus et al. 2000
X. paradoxus	KAS-GEL 2511	-	AF518647	Hibbett & Binder 2002
X. paradoxus	KAS-JR 06	MH880219	-	Riebesehl et al. 2019
X. paradoxus	KAS-JR 28	-	MH884908	Riebesehl et al. 2019
X. pseudolanatus	FP-150922	MH880220	MH884909	Riebesehl et al. 2019
X. pseudotropicus	Dai 10768	KF917543	-	Zhao et al. 2014
X. quercinus	OttoMiettinen 150501	KT361632	-	Ariyawansa et al. 2015
X. quercinus	KHL 11076	KT361633	AY586678	Larsson et al. 2004
X. raduloides	KAS-JR 26	MH880225	MH884910	Riebesehl et al. 2019
X. raduloides	LR 18813	MH880226	MH884911	Riebesehl et al. 2019
X. ramicida	Viacheslav Spirin 7664	KT361634	-	Ariyawansa et al. 2015
X. reticulatus	GC 1512-1	KX857808	KX857813	Chen et al. 2017
X. rhizomorphus	Dai 12354	KF917544	-	Zhao et al. 2014
X. rhizomorphus	Dai 12367	KF917545	-	Zhao et al. 2014
X. rimosissimus	Ryberg 021031	DQ873627	DQ873628	Larsson et al. 2006
X. serpentiformis	TUB-FO 40675	MH880228	-	Riebesehl et al. 2019
X. serpentiformis	TUB-FO 40985	-	MH884912	Riebesehl et al. 2019
X. serpentiformis	TUB-FO 42688	MH880229	MH884913	Riebesehl et al. 2019
X. spathulatus	KHL 7085	KY081804	-	Riebesehl & Langer 2017
X. spathulatus	MSK-F 12931	-	MH884914	Riebesehl et al. 2019
X. subclavatus	TUB-FO 42167	MH880232	-	Riebesehl et al. 2019
X. subflaviporus	KAS-GEL 3466	MH880233	-	Riebesehl et al. 2019
X. subflaviporus	Wu 0809-76	KX857803	KX857815	Chen et al. 2017
X. subtropicus	Wu 1508-2	KX857806	-	Chen et al. 2017
X. subtropicus	Wu 9806-105	KX857807	KX857809	Chen et al. 2017
X. verecundus	KHL 12261	DQ873642	-	Larsson et al. 2006
X. xinpingensis	CLZhao 9125	MW394656	MW394649	Present study
X. xinpingensis	CLZhao 9174	MW394657	MW394650	Present study

The nLSU dataset included sequences from 42 fungal specimens representing 30 species. The dataset had an aligned length of 949 characters, of which 804 characters are constant, 37 are variable and parsimony-uninformative, and 108 are parsimony-informative. Maximum parsimony analysis yielded 4 equally parsimonious trees (TL = 421, CI = 0.4276, HI = 0.5724, RI = 0.6281, RC = 0.2685). 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, and Bayesian analysis had an average standard deviation of split frequencies = 0.009893 (BI).

The nLSU phylogeny (Fig. 2) revealed that *X. bambusinus* grouped with *X. asperus* (Fr.) Hjortstam & Ryvarden (2009: 34) and *X. brevisetus* (P. Karst.) Hjortstam & Ryvarden (2009: 35) with a lower supports (- BS, 62% BT, - BPP). *Xylodon xinpingensis* grouped with *X. rimosissimus* (Peck) Hjortstam & Ryvarden (2009: 39), *X. astrocystidiatus*, *X. paradoxus* and *X. follis* Riebesehl, Yurchenko & E. Langer (2019: 112) without branch support.

The ITS+nLSU dataset included sequences from 61 fungal specimens representing 43 taxa. The dataset had an aligned length of 1683 characters in the dataset, of which 1061 characters are constant, 227 are variable and parsimony-

uninformative, and 395 are parsimony-informative. Maximum parsimony analysis yielded 1 equally parsimonious tree (TL = 2249, CI = 0.4149, HI = 0.5851, RI = 0.5509, RC = 0.2285). Best model for ITS+nLSU 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 =0.009983 (BI).

Further phylogenetic tree (Fig. 3) inferred from ITS+nLSU sequences demonstrated that *X. bambusinus* was sister to *X. subclavatus* (100 BS, 100 BT, 1.00 BPP), while *X. xinpingensis* grouped with *X. astrocystidiatus*, *X. paradoxus* and *X. follis* with lower supports.

Taxonomy

Xylodon bambusinus C.L. Zhao & X. Ma, *sp. nov.* Figs. 4, 5 *MycoBank no.*: MB 838334

Holotype:—CHINA. Yunnan Province, Wenshan, Xichou County, Xiaoqiaogou National Nature Reserve, E 104°41′, N 23°21′, alt. 1550 m, on dead bamboo, 16 January 2019, *CLZhao 11310* (SWFC!).

Etymology:-bambusinus (Lat.): referring to the host of dead bamboo.

Basidiomata:—Annual, adnate, ceraceous, without odor or taste when fresh, becoming ceraceous to corneus upon drying, up to 6.5 cm long, 2.5 cm wide, 100–500 μ m thick. Hymenial surface grandinoid, with 5–8 aculei per mm, aculei conical, acute, white to cream when fresh, turning cream to buff upon drying, cracking. Subiculum very thin, cream to buff. Margin sterile, 0.2 cm wide, cream.

Hyphal structure:--Hyphal system monomitic, generative hyphae with clamp connections, colorless, thick-walled, branched, interwoven, 2–6.5 µm in diameter, IKI-, CB-; tissues unchanged in KOH.

Hymenium:—Cystidia of two types, (i) fusiform cystidia smooth, colorless, thin-walled, $17.5-27 \times 4-6 \mu m$; (ii) capitate cystidia smooth, colorless, thin-walled, slightly constricted at the neck, with a globose head, $18.5-31 \times 3-4 \mu m$; basidia clavate to subclavate, constricted, with 4 sterigmata and a basal clamp connection, $15-28 \times 3.5-4.5 \mu m$.

Spores:—Basidiospores broad ellipsoid, colorless, thin-walled, smooth, IKI-, CB-, $(3.5-)4-5.5(-5.7) \times (2.6-)3-4(-4.4) \ \mu\text{m}$, L = 4.34 μm , W = 3.26 μm , Q = 1.28–1.4 (n = 150/5). Holytype: $(3.7-)4-5 \times 2.6-3.7 \ \mu\text{m}$, L = 4.29 μm , W = 3.22 μm , Q = 1.33 (n = 30/1).

Ecology and distribution:-Lignicolous, causing a white rot. Found in China.

Additional specimens (paratypes) examined:—CHINA, Yunnan Province, Wenshan, Xichou County, Xiaoqiaogou National Nature Reserve, E 104°41′, N 23°21′, alt. 1550 m, on dead bamboo, 16 January 2019, *CLZhao* 11211 (SWFC!), *CLZhao* 11215 (SWFC!), *CLZhao* 11219 (SWFC!), *CLZhao* 11224 (SWFC!).

Xylodon xinpingensis C.L. Zhao & X. Ma, *sp. nov.* Figs. 6, 7 *MycoBank no.*: MB 838335

Holotype:—CHINA. Yunnan Province, Yuxi, Xinping County, Jinshan Primeval Forest Park, E 101°30', N 23°56', alt. 2500 m, on fallen angiosperm trunk, 2 January 2019, *CLZhao 9174* (SWFC!).

Etymology:-xinpingensis (Lat.): referring to the locality (Xinping County) of the type specimens.

Basidiomata:—Annual, adnate, soft-membranaceous, without odor or taste when fresh, becoming cotton upon drying, up to 8 cm long, 4 cm wide, 500–1000 µm thick. Hymenial surface reticulate, white to cream when fresh, turn to cream upon drying. Subiculum very thin, cream. Margin sterile, 0.1 cm wide, white.

Hyphal structure:—Hyphal system monomitic, generative hyphae with clamp connections, colorless, thick-walled, branched, interwoven, 2–6 µm in diameter, IKI-, CB-; tissues unchanged in KOH.

Hymenium:—Cystidia fusiform, covered with crystal, colorless, thin-walled, $19.5-31 \times 2-6 \mu m$; basidia clavate, with 4 sterigmata and a basal clamp connection, $18.5-33 \times 3-6.5 \mu m$.

Spores:—Basidiospores subglobose, colorless, smooth, thin-walled, with oil drops, IKI-, CB-, $(4.1-)4.5-6(-6.4) \times (3-)3.5-5 \mu m$, L = 5.15 μm , W = 4.21 μm , Q = 1.23 (n = 60/2). Holytype: $(4.8-)5-6.4 \times (3.4-)3.5-5(5.1-) \mu m$, L = 5.4 μm , W = 4.43 μm , Q = 1.23 (n = 30/1).

Ecology and distribution:-Lignicolous, causing a white rot. Found in China.

Additional specimen (paratype) examined:—CHINA, Yunnan Province, Yuxi, Xinping County, Jinshan Primeval Forest Park, E 101°30', N 23°56', alt. 2500 m, on fallen angiosperm trunk, 2 January 2019, *CLZhao* 9125 (SWFC!).

Discussion

In the present study, two new species *X. bambusinus* and *X. xinpingensis* were described based on phylogenetic analyses and morphological characters.

According to our results based on present sequence data (Figs. 1, 2, 3), *X. bambusinus* and *X. xinpingensis* are nested into *Xylodon* with strong supports (100% BS, 100% BT, 1.00 BPP). *Xylodon* is also strongly supported as a genus, as previously observed (Yurchenko & Wu 2014, Riebeschl *et al.* 2019).

Phylogenetically, the usefulness of ITS sequences alone in defining and identifying species in Xylodon is approaching its limits. Riebesehl et al. (2019) called for further studies in Xylodon will require sequences from additional genetic markers with more variation. In the present study, based on the ITS and nLSU sequences, two new species formed a well-supported monophyletic lineage distinct from other Xylodon species. In ITS phylogenetic tree (Fig. 1), X. bambusinus was sister to X. subclavatus (100% BS, 100% BT, 1.00 BPP) and then grouped with related species comprised X. filicinus, X. hastifer, X. hyphodontinus and X. pseudotropicus without branch supports, but morphologically X. subclavatus differs from X. bambusinus by having the odontioid hymenophore and presence of moniliform and hyphoid cystidia (Yurchenko et al. 2013). Xylodon filicinus differs in the odontioid hymenophore with farinaceous or pruinose hymenial surface and hypha-like cystidia (Riebesehl et al. 2019). Xylodon hastifer differs in its odontioid hymenophore and subglobose basidiospores (Hjortstam & Ryvarden 2009). Xylodon hyphodontinus differs in its odontioid hymenophore with light ochraceous hymenial surface (Hjortstam & Ryvarden 1980). Xylodon pseudotropicus differs in the poroid hymenophore and narrower basidiospores (4.3-4.9 × 2.8-3 µm, Zhao et al. 2014). Xylodon xinpingensis grouped with X. astrocystidiatus (100% BS, 100% BT, 1.00 BPP) and X. paradoxus (- BS, 87% BT, - BPP), but X. astrocystidiatus differs from X. xinpingensis by having odontioid hymenophore and presence of moniliform and lecythiform cystidia; additionally, it grows on twig of Rhododendron formosanum (Yurchenko & Wu 2014). Xylodon paradoxus differs in the tubulose to irpicoid hymenophore, a dimitic hyphal system and the ovoid basidiospores, being a cosmopolitan taxon (Donk 1967).

In nLSU molecular analysis (Fig. 2), X. bambusinus grouped with X. asperus and X. brevisetus with lower supports (- BS, 62% BT, - BPP). However, morphologically X. asperus differs from X. bambusinus by having the odontioid hymenophore with yellowish to whitish cream hymenial surface and larger, broadly elliposoid basidiospores (5–6 × $3.5-4.5 \mu m$, Eriksson & Ryvarden 1976). Xylodon brevisetus differs in its odontioid hymenophore and gloeocystidia (Eriksson & Ryvarden 1976). Xylodon xinpingensis grouped with X. astrocystidiatus, X. paradoxus, X. rimosissimus and X. follis without branch support, but X. rimosissimus differs from X. xinpingensis by having the odontioid hymenophore with dark cream to ochraceous hymenial surface and subclavate basidia. In addition, it is distributed in Eurasia, Africa, North America and South America (Peck 1897, Hjortstam & Ryvarden 2009). Xylodon follis differs in its capitate cystidia and utriform basidia and larger, broadly globose basidiospores and larger, broadly globose basidiospores (8– $9.5 \times 7-8.5 \mu m$) and this species is so far known from La Réunion (Mascarene Archipelago) (Riebesehl *et al.* 2019).

Further study based on ITS+nLSU analysis (Fig. 3) revealed that *X. bambusinus* was sister to *X. subclavatus* (100% BS, 100% BT, 1.00 BPP); *X. xinpingensis* grouped with *X. astrocystidiatus* (78 BS, 80% BT, 0.94 BPP), *X. paradoxus* (- BS, 93% BT, 0.97 BPP) and *X. follis*, which showed a similar topology result with the ITS phylogenetic tree (Fig. 1).

Wood-rotting fungi is an extensively studied group of Basidiomycota (Gilbertson & Ryvarden 1987, Núñez & Ryvarden 2001, Bernicchia & Gorjón 2010, Dai 2012, Ryvarden & Melo 2014), nonetheless the diversity of the corticioid fungi is still not well known, especially in the subtropics and tropics, and many taxa were recently described from these areas in China (Shen *et al.* 2018, Liu *et al.* 2019, Luo *et al.* 2019, Ma & Zhao 2019, Guan *et al.* 2020, Zhao *et al.* 2021). *Xylodon bambusinus* and *X. xinpingensis* are also from the subtropics, and it is likely that more new wood-rotting fungi will be found after further investigations and molecular analyses.

A key to known species of Xylodon from China

1.	Generative hyphae simple-septa	X. poroideoefibulatus
1.	Generative hyphae clamp connections	2
2.	Hymenophore poroid or irpicoid	3
2.	Hymenophore odontioid to hydnoid or grandinoid	
3.	Hyphal system dimitic	4
3.	Hyphal system monomitic	6
4.	Pores size < 3 per mm	X. subtropicus
4.	Pores size > 3 per mm	5

5.	Basidiomata margin with fimbriate, basidiospores > 3.5 µm in width	X. mollissimus
5.	Basidiomata margin without fimbriate, basidiospores < 3.5µm in width	X. subflaviporus
6.	Cystidia of one or two types	
6.	Cystidia of three or four types	
7.	Basidia barrel-shaped to pyriform	X. pseudotropicus
7.	Basidia clavate or urniform	
8.	Basidia suburniform to urniform	X. taiwanianus
8.	Basidia clavate	9
9.	Basidiospores 3.5–4.5×3–3.5 µm	X. flaviporus
9.	Basidiospores 5–5.5×3.5–4 µm	X. niemelaei
10.	Capitate cystidia up to 40 µm in length, basidia 12–19×4–5 µm	X. reticulatus
10.	Capitate cystidia up to 26 µm in length, basidia 20-25×4-5 µm	
11.	Cystidia absent	X. bubalinus
11.	Cystidia present	
12.	Cystidia of one or two types	
12.	Cystidia of three or four types	
13.	Cystidia of one type	
13.	Cystidia of two types	
14.	Bladder-like cystidia present	X. rhizomorphus
14.	Bladder-like cystidia absent	
15.	Basidia suburniform, 15–20×3.5–4 µm	X. lenis
15.	Basidia clavate, 18.5–33×3–6.5 μm	X. xinpingensis
16.	Leptocystidia present	X. heterocystidiatus
16.	Leptocystidia absent	
17.	Grow on bamboo	X. bambusinus
17.	Grow on dead branch of angiosperm	X. subclavatus
18.	Cystidia of four types	X. astrocystidiatus
18.	Cystidia of three types	
19.	Basidia clavate	X. kunmingensis
19.	Basidia urnifrom	
20.	Basidiospores globose or subglobose, 4-5×4-4.5 µm	X. filicinus
20.	Basidiospores ellipsoid, 5.5–6×3.5–4 µm	X. anmashanensis

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