



Xylodon asiaticus (Hymenochaetales, Basidiomycota), a new species of corticioid fungus from southern China

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Abstract

The corticioid fungi are a cosmopolitan group and show a rich diversity, growing in the vegetation of boreal, temperate, subtropical, and tropical regions. *Xylodon asiaticus* specimens were found in the Yunnan Province, China, which identified here to be a new species by their morphology and phylogeny. *Xylodon asiaticus* is characterized by its coriaceous basidiomata with a hydroid hymenophore and a monomitic hyphal system bearing generative hyphae with clamp connections, and ellipsoid to subcylindrical basidiospores measuring as 4–5.2 × 2.8–3.5 μm. Phylogenetic analyses of the order Hymenochaetales and the genus *Xylodon* based on the ITS and nLSU rRNA sequences were performed using the Maximum Likelihood, Maximum Parsimony, and Bayesian Inference methods. The phylogenetic analysis indicated that the new species nested into the family Schizoporaceae, and was retrieved as a sister to *X. pseudotropicus*. However, morphologically, *X. pseudotropicus* differs from *X. asiaticus* by its poroid hymenial surface and oblong-ellipsoid basidiospores (Zhao *et al.* 2014).

Key words: Molecular systematics, Taxonomy, Wood-inhabiting fungi, Yunnan Province

Introduction

In forest ecosystems, fungi play an essential ecological role to drive carbon cycling in forest soils, mediate mineral nutrition of plants, and alleviate carbon limitations (Tedersoo *et al.* 2014). The corticioid fungi are a cosmopolitan group and have a rich diversity related to the high diversity of plants growing in boreal, temperate, subtropical, and tropical regions (Gilbertson & Ryvarden 1987, Bernicchia & Gorjón 2010, Dai *et al.* 2015, 2021, Zhao *et al.* 2023). The order Hymenochaetales Oberw. comprises many representative corticioid fungal taxa, including hydroid, corticioid, and polyporoid fungi possessing basidiomata with diverse hymenophoral and cystidial morphology (Riebesehl *et al.* 2019, Wu *et al.* 2020, Guan *et al.* 2023). Members of the family Schizoporaceae Jülich are widely found in different countries and areas, causing white rot (Langer *et al.* 1994, Luo *et al.* 2022, Guan *et al.* 2023).

The corticioid fungal genus *Xylodon* (Pers.) Gray (Schizoporaceae, Hymenochaetales) is typified by *X. quercinus* (Pers.) Gray (1821: 649) (Bernicchia & Gorjón 2010). This genus is characterized by the resupinate or effuse basidiomata with a smooth, tuberculate, grandinoid, odontoid, coralloid, irpicoid, or poroid hymenophore; a monomitic or dimitic hyphal system with clamped generative hyphae; the presence of different types of cystidia; utriform or suburniform basidia; and cylindrical to ellipsoid to globose basidiospores, and causing white rot (Gray 1821, Bernicchia & Gorjón 2010). Based on the MycoBank database (<http://www.Mycobank.org>, accessed on 27 September 2023) and the Index Fungorum (<http://www.indexfungorum.org>, accessed on 27 September 2023), the genus *Xylodon* has been registered 228 specific and infraspecific names, but the actual number of the species is only 103 (Wu 1990, Wu *et al.* 2000, 2001, 2006, Hjortstam & Ryvarden 2007, 2009, Bernicchia & Gorjón 2010, Tura 2011, Dai 2012, Lee & Langer 2012,

Yurchenko *et al.* 2013, Zhao *et al.* 2014, Chen *et al.* 2016, Riebesehl & Langer 2017, Wang & Chen 2017, Chen *et al.* 2018, Riebesehl *et al.* 2019, Shi *et al.* 2019, Viner 2018, 2021, Luo *et al.* 2021, 2022, Qu *et al.* 2022, Guan *et al.* 2023).

In recent years, the genus *Xylodon* was generally studied by molecular systematics and it was included in the *Hyphodontia* s.l. (Hjortstam & Ryvarden 2009, Yurchenko & Wu 2016, Riebesehl & Langer 2017, Wang & Chen 2017, Riebesehl *et al.* 2019, Qu *et al.* 2022, Guan *et al.* 2023). *Hyphodontia* s.l. was shown to be a polyphyletic genus, and a broad concept employed by some mycologists due to a lack of rDNA sequences for many taxa, in which *Xylodon* and *Kneiffiella* P. Karst included rich species (Hjortstam & Ryvarden 2009, Riebesehl & Langer 2017, Riebesehl *et al.* 2019, Luo *et al.* 2022). Based on the molecular systematics research, two clades, the *Xylodon-Lyomyces-Rogersella* and the *Xylodon-Schizopora-Palifer* clades, were described, and the related species of *Lyomyces* P. Karst., *Palifer* Stalpers & P.K. Buchanan, *Rogersella* Libert & A.J. Navas *Schizopora* Velen., and *Xylodon*, within both clades were suggested to be mixed (Yurchenko *et al.* 2013). The research comprised the representative sequences and taxa of *Hyphodontia* s.l., such as *Lyomyces*, *Palifer*, *Rogersella*, *Schizopora*, and *Xylodon* in which the result demonstrated that it was hard to distinguish the two genera *Xylodon* and *Schizopora* on the basis of the morphological and phylogenetic information, therefore, the authors proposed that the related species of *Schizopora* should be united into the genus *Xylodon* (Riebesehl & Langer 2017). For the phylogenetic relationship of *Xylodon* species, it was confirmed that the two genera *Lagarobasidium* Jülich and *Xylodon* should be synonymous based on the molecular data from the ITS and nLSU regions, in which the three species *X. pumilius* (Gresl. & Rajchenb.) K.H. Larss. (2018: 84), *X. magnificus* (Gresl. & Rajchenb.) K.H. Larss. (2018: 80), and *X. rickii* (Gresl. & Rajchenb.) K.H. Larss. (2018: 84) were combined into *Xylodon* (Viner *et al.* 2018). All the members of the genera *Odontopsis* Hjortstam & Ryvarden and *Palifer* were placed in the genus *Xylodon* based on the molecular analyses of 28S and ITS data, in which they proposed four new species of *Xylodon* as *X. exilis* Yurchenko, Riebesehl & Langer (2019: 107), *X. filicinus* Yurchenko & Riebesehl (2019: 110), *X. follis* Riebesehl, Yurchenko & Langer (2019: 112), and *X. pseudolanatus* Nakasone, Yurchenko & Riebesehl (2019: 115) (Riebesehl *et al.* 2019). Based on the multiple loci in *Hyphodontia* s.l., *Fasciodontia* Yurchenko & Riebesehl, *Hastodontia* (Parmasto) Hjortstam & Ryvarden, *Hyphodontia* J. Erikss., *Lyomyces*, *Kneiffiella*, and *Xylodon* in the order Hymenochaetales, they were divided into four clades and three new taxa were found from China, in which *X. gossypinus* C.L. Zhao & K.Y. Luo (2021: 8) and *X. brevisetus* (P. Karst.) Hjortstam & Ryvarden (2009: 35) grouped together (Luo *et al.* 2021). Based on the morphological descriptions and molecular analyses, three new species, namely *Xylodon angustisporus* Viner & Ryvarden (2021: 173), *X. dissiliens* Viner & Ryvarden (2021: 173), and *X. laxiusculus* Viner & Ryvarden (2021: 175), were described in Africa and placed in the genus *Xylodon* (Viner *et al.* 2021). A phylogenetic and taxonomic study focusing on the genus *Xylodon* (Hymenochaetales) newly described three species of this genus from southern China, and this research enriched the fungal diversity worldwide (Qu *et al.* 2022).

During investigations on corticioid fungi in Yunnan Province, China, several specimens of *Xylodon* were collected. To clarify the placement and relationships of these specimens, we carried out a phylogenetic and taxonomic study on *Xylodon*, based on the ITS and nLSU sequences. These specimens are identified as an undescribed species of *Xylodon*, and the detailed description and illustrations of the new species are provided here.

Materials and methods

Sample Collection and Herbarium Specimen Preparation

The fresh fruiting bodies on the trunk of *Quercus semecarpifolia* and fallen angiosperm branches were collected from Dali, Wenshan, and Yuxi of Yunnan Province, China. The samples were photographed in situ, and fresh macroscopic details were recorded. Photographs were recorded by a Nikon D7100 camera. 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 an envelope and zip-lock plastic bags and labeled (Qu *et al.* 2022). The dried specimens were deposited in the herbarium of the Southwest Forestry University (SWFC), Kunming, Yunnan Province, China.

Morphology

The macromorphological descriptions were based on field notes and photos captured in the field and lab. The

color terminology follows Petersen (1996). The micromorphological data were obtained from the dried specimens after observation under a light microscope with a magnification of 10×100 oil (Zhao *et al.* 2023). The following abbreviations are used: KOH = 5% potassium hydroxide water solution, CB– = acyanophilous, IKI– = both inamyloid and indextrinoid, L = mean spore length (arithmetic average for all spores), W = mean spore width (arithmetic average for all spores), Q = variation in the L/W ratios between the specimens studied, and n = a/b (number of spores (a) measured from given number (b) of specimens).

Molecular Phylogeny

The CTAB rapid plant genome extraction kit-DN14 (Aidlab Biotechnologies Co., Ltd., Beijing, China) was used to obtain genomic DNA from the dried specimens according to the manufacturer's instructions. The nuclear ribosomal of the internal transcribed spacer (ITS) region was amplified with ITS5 and ITS4 primers (White *et al.* 1990). The nuclear large subunit (nLSU) region was amplified with the LR0R and LR7 primer pair (<http://lutzonilab.org/nuclear-ribosomal-dna/>, accessed on 22 January 2022). 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 of the newly generated sequences were deposited in NCBI GenBank (Table 1).

TABLE 1. List of species, specimens, and GenBank accession numbers of sequences used in this study. The new species are in bold.

Species name	Specimen number	Country	GenBank accession number		References
			ITS	nLSU	
<i>Fasciodontia brasiliensis</i>	MSKF 7245a*	Brazil	MK575201	MK598734	Yurchenko <i>et al.</i> 2020
<i>F. bugellensis</i>	KASFD 10705a	France	MK575203	MK598735	Yurchenko <i>et al.</i> 2020
<i>Hastodontia halonata</i>	HHB 17058	Mexico	MK575207	MK598738	Yurchenko <i>et al.</i> 2020
<i>Hymenochaete cinnamomea</i>	He 2074	China	KU975460	KU975500	Unpublished
<i>Hym. rubiginosa</i>	He 1049	China	JQ716407	JQ279667	He <i>et al.</i> 2013
<i>Hyphodontia alutaria</i>	GEL 3183	Germany	DQ340318	DQ340373	Unpublished
<i>Hyp. arguta</i>	KHL 11938	Sweden	EU118632	EU118633	Larsson 2007
<i>Hyp. pachyspora</i>	LWZ 20170908-5*	China	MT319426	MT319160	Luo <i>et al.</i> 2022
<i>Hyp. pallidula</i>	KASGEL 2097	Germany	DQ340317	DQ340372	Unpublished
<i>Hyp. zhixiangii</i>	LWZ 20180903-5	China	MT319423	MT319158	Luo <i>et al.</i> 2022
<i>Kneiffiella barba-jovis</i>	KHL 11730	Sweden	DQ873609	DQ873610	Riebesehl <i>et al.</i> 2019
<i>K. eucalypticola</i>	LWZ 20180515-9	Australia	MT319411	MT319143	Luo <i>et al.</i> 2022
<i>K. palmae</i>	KASGEL 3456	China	DQ340333	DQ340369	Yurchenko <i>et al.</i> 2020
<i>K. subalutacea</i>	GEL 2196	Norway	DQ340341	DQ340362	Yurchenko <i>et al.</i> 2020
<i>Lyomyces allantosporus</i>	FR 0249548*	Réunion	KY800397	KY795963	Yurchenko <i>et al.</i> 2017
<i>L. bambusinus</i>	CLZhao 4831*	China	MN945968	MW264919	Chen & Zhao 2020
<i>L. fimbriatus</i>	Wu 911204-4	China	MK575210	MK598740	Yurchenko <i>et al.</i> 2020
<i>L. mascarensis</i>	KASGEL 4833*	Réunion	KY800399	KY795964	Yurchenko <i>et al.</i> 2020
<i>L. orientalis</i>	LWZ 20170909-7	China	MT319436	MT319170	Luo <i>et al.</i> 2022
<i>L. sambuci</i>	KASJR 7	Germany	KY800402	KY795966	Yurchenko <i>et al.</i> 2017
<i>Xylodon acystidiatus</i>	LWZ 20180514-9*	Australia	MT319474	MT319211	Luo <i>et al.</i> 2022
<i>X. apacheriensis</i>	Wu 0910-58	China	KX857797	KX857822	Chen <i>et al.</i> 2017
<i>X. asiaticus</i>	CLZhao 2282	China	OM959481	OM967416	Present study
<i>X. asiaticus</i>	CLZhao 10368*	China	OM959479	OM967417	Present study
<i>X. asiaticus</i>	CLZhao 10430	China	OM959480	OM967418	Present study
<i>X. asiaticus</i>	CLZhao 11531	China	OM959471	-	Present study

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TABLE 1. (Continued)

Species name	Specimen number	Country	GenBank accession number		References
			ITS	nLSU	
<i>X. asper</i>	KHL 8530	Sweden	AY463427	AY586675	Larsson <i>et al.</i> 2004
<i>X. astrocystidiatus</i>	Wu 9211-71	China	JN129972	JN129973	Yurchenko & Wu 2014
<i>X. attenuatus</i>	Spirin 8775*	USA	MH324476	-	Viner <i>et al.</i> 2018
<i>X. australis</i>	LWZ 20180509-8	China	MT319503	-	Luo <i>et al.</i> 2022
<i>X. bambusinus</i>	CLZhao 9174	China	MW394657	MW394650	Ma & Zhao 2021
<i>X. borealis</i>	JS 26064	Norway	AY463429	AY586677	Larsson <i>et al.</i> 2004
<i>X. brevisetus</i>	JS 17863	Norway	AY463428	AY586676	Larsson <i>et al.</i> 2004
<i>X. crystalliger</i>	LWZ 20170816-33	China	MT319521	MT319269	Luo <i>et al.</i> 2022
<i>X. cystidiatus</i>	FR 0249200	Réunion	MH880195	MH884896	Riebesehl <i>et al.</i> 2019
<i>X. damansaraensis</i>	LWZ 20180417-23	Malaysia	MT319499	-	Luo <i>et al.</i> 2022
<i>X. dawweishanensis</i>	CLZhao 18357*	China	OP730715	-	Guan <i>et al.</i> 2023
<i>X. detriticus</i>	Zibarová 30.10.17	Czech Republic	MH320793	MH651372	Viner <i>et al.</i> 2018
<i>X. exilis</i>	TUBFO 42565*	China	MH880198	MH884898	Riebesehl <i>et al.</i> 2019
<i>X. filicinus</i>	MSKF 12869*	China	MH880199	NG067836	Riebesehl <i>et al.</i> 2019
<i>X. flaviporus</i>	FR-0249797	Réunion	MH880201	MH884901	Riebesehl <i>et al.</i> 2019
<i>X. fissuratus</i>	CLZhao 9407*	China	OP730714	-	Guan <i>et al.</i> 2023
<i>X. follis</i>	FR-0249814*	Réunion	MH880204	MH884902	Riebesehl <i>et al.</i> 2019
<i>X. grandineus</i>	CLZhao 6425*	China	OM338090	-	Luo <i>et al.</i> 2022
<i>X. gossypinus</i>	CLZhao 4465	China	MZ663803	MZ663812	Luo <i>et al.</i> 2021
<i>X. hastifer</i>	K(M) 172400*	USA	NR166558	-	Riebesehl <i>et al.</i> 2017
<i>X. heterocystidiatus</i>	LWZ20180921-19	Australia	MT319676	MT319266	Luo <i>et al.</i> 2022
<i>X. heterocystidiatus</i>	Wei 17-314	China	MT731753	MT731754	Unpublished
<i>X. hyphodontinus</i>	KASGEL 9222	Kenya	MH880205	MH884903	Riebesehl <i>et al.</i> 2019
<i>X. kunmingensis</i>	CLZhao 230	China	MK404528	-	Shi <i>et al.</i> 2019
<i>X. laceratus</i>	CLZhao 9892*	China	OL619258	OL619266	Qu <i>et al.</i> 2022
<i>X. lagenicystidiatus</i>	LWZ 20180513-16*	Australia	MT319634	MT319368	Luo <i>et al.</i> 2022
<i>X. lenis</i>	Wu 890714-3	China	KY081802	-	Riebesehl <i>et al.</i> 2017
<i>X. macrosporus</i>	CLZhao 10226*	China	MZ663809	MZ663817	Luo <i>et al.</i> 2021
<i>X. mollissimus</i>	LWZ 20160318-3*	China	KY007517	MT319347	Luo <i>et al.</i> 2022
<i>X. montanus</i>	CLZhao 8179*	China	OL619260	OL619268	Qu <i>et al.</i> 2022
<i>X. nesporii</i>	LWZ 20180921-35	China	MT319655	MT319238	Luo <i>et al.</i> 2022
<i>X. niemelaei</i>	LWZ 20150707-13	China	MT319630	MT319365	Luo <i>et al.</i> 2022
<i>X. nongravis</i>	GC 1412-22	China	KX857801	KX857818	Chen <i>et al.</i> 2017
<i>X. nothofagi</i>	ICMP 13842	China	AF145583	-	Paulus <i>et al.</i> 2000
<i>X. ovisporus</i>	LWZ 20170815-31	China	MT319666	MT319346	Luo <i>et al.</i> 2022
<i>X. papillosus</i>	CBS 114.71	Netherlands	MH860026	-	Vu <i>et al.</i> 2019
<i>X. paradoxus</i>	Dai 14983	China	MT319519	MT319267	Luo <i>et al.</i> 2022
<i>X. puerensis</i>	CLZhao 8142*	China	OP730720	-	Guan <i>et al.</i> 2023
<i>X. pruinus</i>	Spirin 2877	Estonia	MH332700	-	Viner <i>et al.</i> 2018
<i>X. pseudolanatus</i>	FP 150922*	Belize	MH880220	NG067837	Riebesehl <i>et al.</i> 2019
<i>X. pseudotropicus</i>	Dai 16167	China	MT319509	MT319255	Luo <i>et al.</i> 2022
<i>X. punctus</i>	CLZhao 17691*	China	OM338092	-	Luo <i>et al.</i> 2022
<i>X. punctus</i>	CLZhao 17908	China	OM338093	-	Luo <i>et al.</i> 2022
<i>X. quercinus</i>	KHL 11076	Sweden	KT361633	AY586678	Larsson <i>et al.</i> 2004

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TABLE 1. (Continued)

Species name	Specimen number	Country	GenBank accession number		References
			ITS	nLSU	
<i>X. ramicida</i>	Spirin 7664*	USA	NR138013	-	Unpublished
<i>X. rhododendricola</i>	LWZ 20180513-9	Australia	MT319621	MT319357	Luo <i>et al.</i> 2022
<i>X. rimosissimus</i>	Ryberg 021031	Sweden	DQ873627	DQ873628	Larsson <i>et al.</i> 2006
<i>X. serpentiformis</i>	LWZ 20170816-15	China	MT319673	MT319218	Luo <i>et al.</i> 2022
<i>X. sinensis</i>	CLZhao 9197	China	MZ663810	MZ663818	Luo <i>et al.</i> 2021
<i>X. spathulatus</i>	LWZ 20180804-10	China	MT319646	MT319354	Luo <i>et al.</i> 2022
<i>X. subclavatus</i>	TUBFO 42167	China	MH880232	-	Riebesehl <i>et al.</i> 2019
<i>X. subflaviporus</i>	Wu 0809-76	China	KX857803	KX857815	Chen <i>et al.</i> 2017
<i>X. subserpentiformis</i>	LWZ 20180512-16	Australia	MT319486	MT319226	Luo <i>et al.</i> 2022
<i>X. subtropicus</i>	LWZ 20180510-24	China	MT319541	MT319308	Luo <i>et al.</i> 2022
<i>X. taiwanianus</i>	CBS 125875	Netherlands	MH864080	MH875537	Vu <i>et al.</i> 2019
<i>X. tropicus</i>	CLZhao 3351*	China	OL619261	OL619269	Qu <i>et al.</i> 2022
<i>X. ussuriensis</i>	KUN 1989*	USA	NR166241	-	Unpublished
<i>X. verecundus</i>	KHL 12261	Sweden	DQ873642	DQ873643	Larsson <i>et al.</i> 2006
<i>X. victoriensis</i>	LWZ 20180510-29	Australia	MT319487	MT319228	Luo <i>et al.</i> 2022
<i>X. wenshanensis</i>	CLZhao 15729*	China	OM338097	-	Luo <i>et al.</i> 2022
<i>X. xinpingensis</i>	CLZhao 11224	China	MW394662	MW394654	Ma & Zhao 2021
<i>X. yarraensis</i>	LWZ 20180510-5	Australia	MT319639	MT319378	Luo <i>et al.</i> 2022
<i>X. yunnanensis</i>	LWZ 20180922-47	China	MT319660	-	Luo <i>et al.</i> 2022

* Indicates type material (holotype).

The sequences were aligned in MAFFT version 7 (Katoh *et al.* 2019) using the G-INS-i strategy. The alignment was adjusted manually using AliView version 1.27 (Larsson 2014). The dataset was aligned first, and then the sequences of ITS and nLSU were combined with Mesquite version 3.51. The alignment datasets were deposited in TreeBASE (submission ID 30797). The combined ITS and nLSU sequences and ITS datasets were used to infer the position of the new species in the genus *Xylodon* and related species. Sequences of *Hymenochaete cinnamomea* (Pers.) Bres. (1897: 110) and *H. rubiginosa* (Dicks.) Lév. (1846: 150) retrieved from GenBank were used as an outgroup in the combined ITS and nLSU analysis. Sequences of *Lyomyces mascarensis* Riebesehl, Yurch. & Langer (2017: 870) and *Lyomyces sambuci* (Pers.) P. Karst. (1882: 153) retrieved from GenBank were used as an outgroup in the ITS analysis (Fig. 2) (Qu *et al.* 2022).

Maximum parsimony (MP), Maximum Likelihood (ML), and Bayesian Inference (BI) analyses were applied to the combined datasets following a previous study (Zhao & Wu 2017), and the tree construction procedure was performed in PAUP* version 4.0b10 (Swofford 2002). All of the characters were equally weighted, and gaps were treated as missing data. Using the heuristic search option with TBR branch swapping and 1000 random sequence additions, trees were inferred. 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 (Felsenstein 1985). Descriptive tree statistics, tree length (TL), the consistency index (CI), the retention index (RI), the rescaled consistency index (RC), and the homoplasy index (HI) were calculated for each maximum parsimonious tree generated. The multiple sequence alignment was also analyzed using maximum likelihood (ML) in RAxML-HPC2 (Miller *et al.* 2012). 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 dataset for Bayesian inference (BI), which was performed using MrBayes 3.2.7a with a GTR+I+G model of DNA substitution and a gamma distribution rate variation across sites (Ronquist *et al.* 2012). A total of 4 Markov chains were run for 2 runs from random starting trees for 5 million generations for the combined ITS and nLSU sequences and 3 million generations for ITS sequences with trees and parameters sampled every 1000 generations. The first one-fourth of all the generations were discarded as burn-ins. The majority-rule consensus tree of all the remaining trees was calculated. Branches were considered significantly supported if they received a maximum likelihood bootstrap value (BS) of >70%, a maximum parsimony bootstrap value (BT) of >70%, or Bayesian posterior probabilities (BPP) of >0.95.

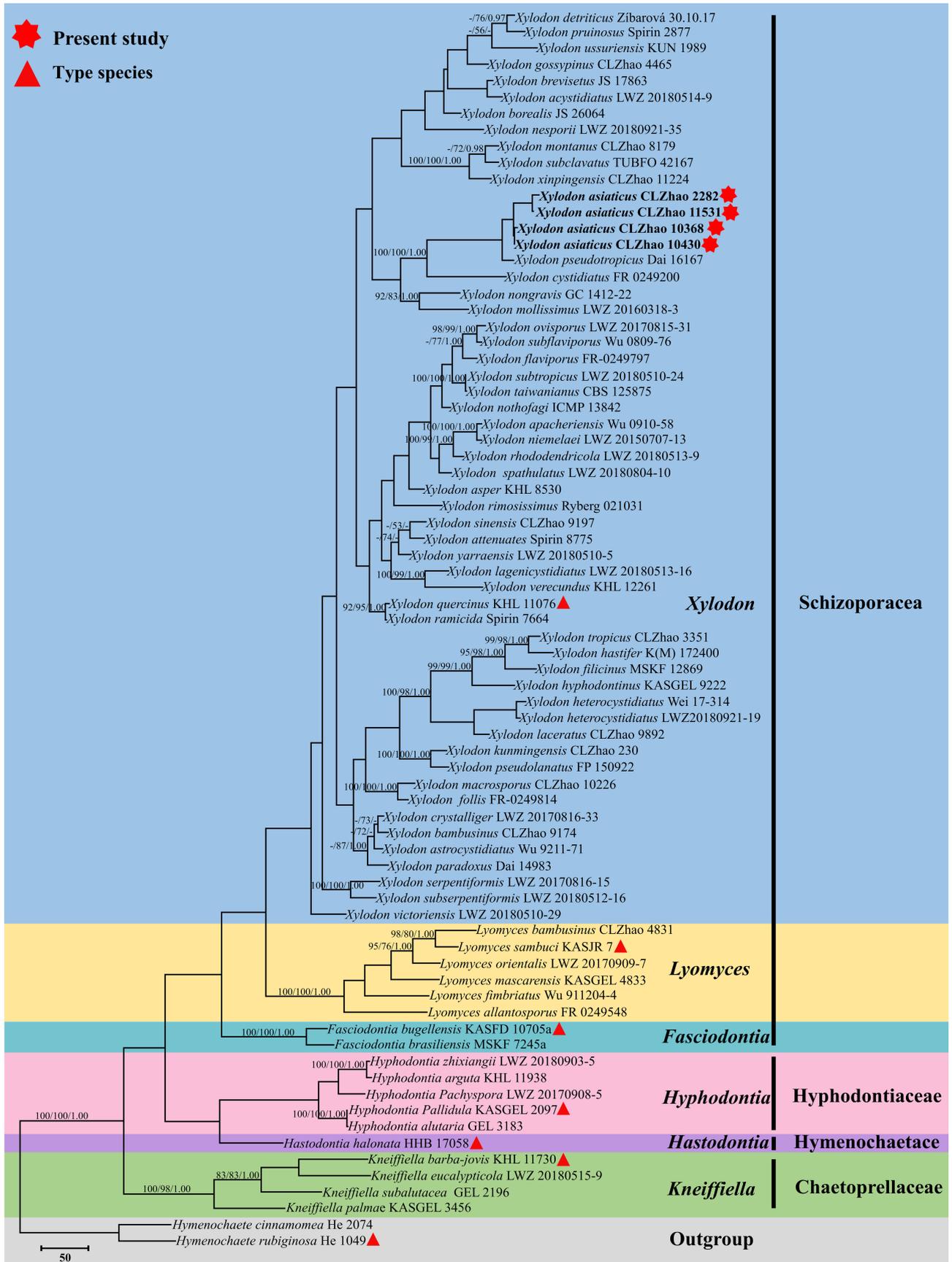


FIGURE 1. Maximum Parsimony strict consensus tree illustrating the *Xylodon* and related genera in the order Hymenochaetales based on the combined ITS and nLSU sequences. Branches are labeled with Maximum Likelihood bootstrap values equal to or above 70%, Maximum Parsimony bootstrap values equal to or above 50% and Bayesian posterior probabilities equal to or above 0.95. The new species are in bold.



FIGURE 2. Maximum Parsimony strict consensus tree illustrating the phylogeny of the new species *Xylodon asiaticus* and related species in *Xylodon* based on ITS sequences. Branches are labeled with Maximum Likelihood bootstrap values equal to or above 70%, Maximum Parsimony bootstrap values equal to or above 50% and Bayesian posterior probabilities equal to or above 0.95.

Results

Phylogenetic analyses

The combined ITS and nLSU dataset (Fig. 1) included sequences from 76 fungal specimens representing 72 species.

A total of 4 Markov chains were run for 2 runs from random starting trees for 5 million generations for ITS and nLSU dataset with trees and parameters sampled every 1000 generations. The dataset had an aligned length of 2257 characters, of which 1294 characters are constant, 292 are variable and parsimony uninformative, and 671 are parsimony informative. Maximum parsimony analysis yielded 6 equally parsimonious trees (TL = 4514, CI = 0.3476, HI = 0.6524, RI = 0.5753, and RC = 0.2000). The best model for the combined ITS and nLSU dataset estimated and applied in the Bayesian analysis was GTR+I+G. Bayesian analysis and ML analysis resulted in a similar topology to MP analysis with an average standard deviation of split frequencies = 0.015070 (BI), and the effective sample size (ESS) average ESS (avg ESS) = 781.5. The phylogram based on the ITS and nLSU rRNA sequences (Fig. 1) includes six genera within Schizoporaceae (Hymenochaetales), which are *Fasciodontia*, *Hastodontia*, *Hyphodontia*, *Kneiffiella*, *Lyomyces*, and *Xylodon*, in which the new species grouped within the genera *Xylodon*.

The ITS-only dataset (Fig. 2) included sequences from 71 fungal specimens representing 54 species. A total of 4 Markov chains were run for 2 runs from random starting trees for 8 million generations for ITS and nLSU dataset with trees and parameters sampled every 1000 generations. The dataset had an aligned length of 694 characters, of which 278 characters are constant, 82 are variable and parsimony uninformative, and 334 are parsimony informative. Maximum parsimony analysis yielded 100 equally parsimonious trees (TL = 2636, CI = 0.2735, HI = 0.7265, RI = 0.4351, and RC = 0.1190). The best model for the ITS dataset estimated and applied in the Bayesian analysis was GTR+I+G. Bayesian analysis and ML analysis resulted in a similar topology to the MP analysis with an average standard deviation of split frequencies = 0.037405 (BI), and the effective sample size (ESS) of the average ESS (avg ESS) = 268. The topology based on ITS sequences (Fig. 2), revealed that *X. asiaticus* was retrieved as a sister to *X. pseudotropicus* (C.L. Zhao, B.K. Cui & Y.C. Dai) Riebesehl, Yurch. & Langer, in Riebesehl & Langer.

Taxonomy

Xylodon asiaticus X.C. Zhang & C.L. Zhao, *sp. nov.* Figs. 3, 4
MycoBank no.: MB 850228

Etymology:—*asiaticus* (Lat.): referring to the provenance (Asian) of the type specimen.

Diagnosis:—It differs from other *Xylodon* species by its buff to ochraceous and hynoid hymenial surface, a monomitic hyphal system with clamped generative hyphae and ellipsoid to subcylindrical basidiospores measuring (3.7)4–5.2(–6) × (2.5–)2.8–3.5(–4) μm.

Holotype:—CHINA. Yunnan Province, Dali, Nanjian County, Lingbaoshan National Forest Park, 24°46'58"N, 100°30'46"E, elev. 2523 m, on fallen angiosperm branch, 10 January 2019, leg. C.L. Zhao, CLZhao 10368 (SWFC!), GenBank No. (ITS OM959479; nLSU OM967417).

Basidiomata:—Annual, resupinate, adnate, coriaceous, very hard to separate from substrate, without odor or taste when fresh, up to 15 cm long, 2 cm wide, less than 1 mm thick. Hymenial surface hydroid, aculei 4–6 per mm, up to 0.5 mm long, buff when fresh, turning to buff to ochraceous upon drying. Sterile margin distinct, slightly buff, up to 1 mm wide.

Hyphal structure:—Hyphal system monomitic, generative hyphae with clamp connections, colorless, thin-walled, branched, interwoven, 2–3.5 μm in diameter; IKI–, CB–, tissues unchanged in KOH.

Hymenium:—Cystidia and cystidioles absent. Basidia barrelled to subcylindrical, with 4 sterigmata and a basal clamp connection, 11.5–20 × 4–5 μm; basidioles dominant, similar to basidia in shape, but slightly smaller.

Basidiospores:—Ellipsoid to subcylindrical, colorless, smooth, thin-walled, with 1–2 oil drops, IKI–, CB–, (3.7)4–5.2(–6) × (2.5–)2.8–3.5(–4) μm, L = 4.72 μm, W = 2.97 μm, Q = 1.59–1.91 (n = 120/4).

Type of rot:—White rot.

Additional specimens examined:—CHINA. Yunnan Province, Yuxi, Xiping County, Mopanshan National Forestry Park, 23°55'48"N, 101°59'22"E, elev. 2150 m, on the trunk of *Quercus semecarpifolia*, 19 August 2017, leg. C.L. Zhao, CLZhao 2282 (SWFC!), GenBank No. (ITS OM959481; nLSU OM967416); Dali, Nanjian County, Lingbaoshan National Forest Park, 24°46'58"N, 100°30'46"E, elev. 2522 m, on fallen angiosperm branch, 10 January 2019, leg. C.L. Zhao, CLZhao 10430 (SWFC!), GenBank No. (ITS OM959480; nLSU OM967418); Wenshan, Xichou County, Pingzhai Forestry Farm, 23°26'27"N, 104°40'48"E, elev. 1500 m, on fallen angiosperm branch, 18 January 2019, leg. C.L. Zhao, CLZhao 11531 (SWFC!), GenBank No. (ITS OM959471).



FIGURE 3. Basidiomata of *Xylodon asiaticus* A. The front of the basidiomata; B. A section of hymenophore. Bars: A= 1 cm; B= 1 mm. (holotype).

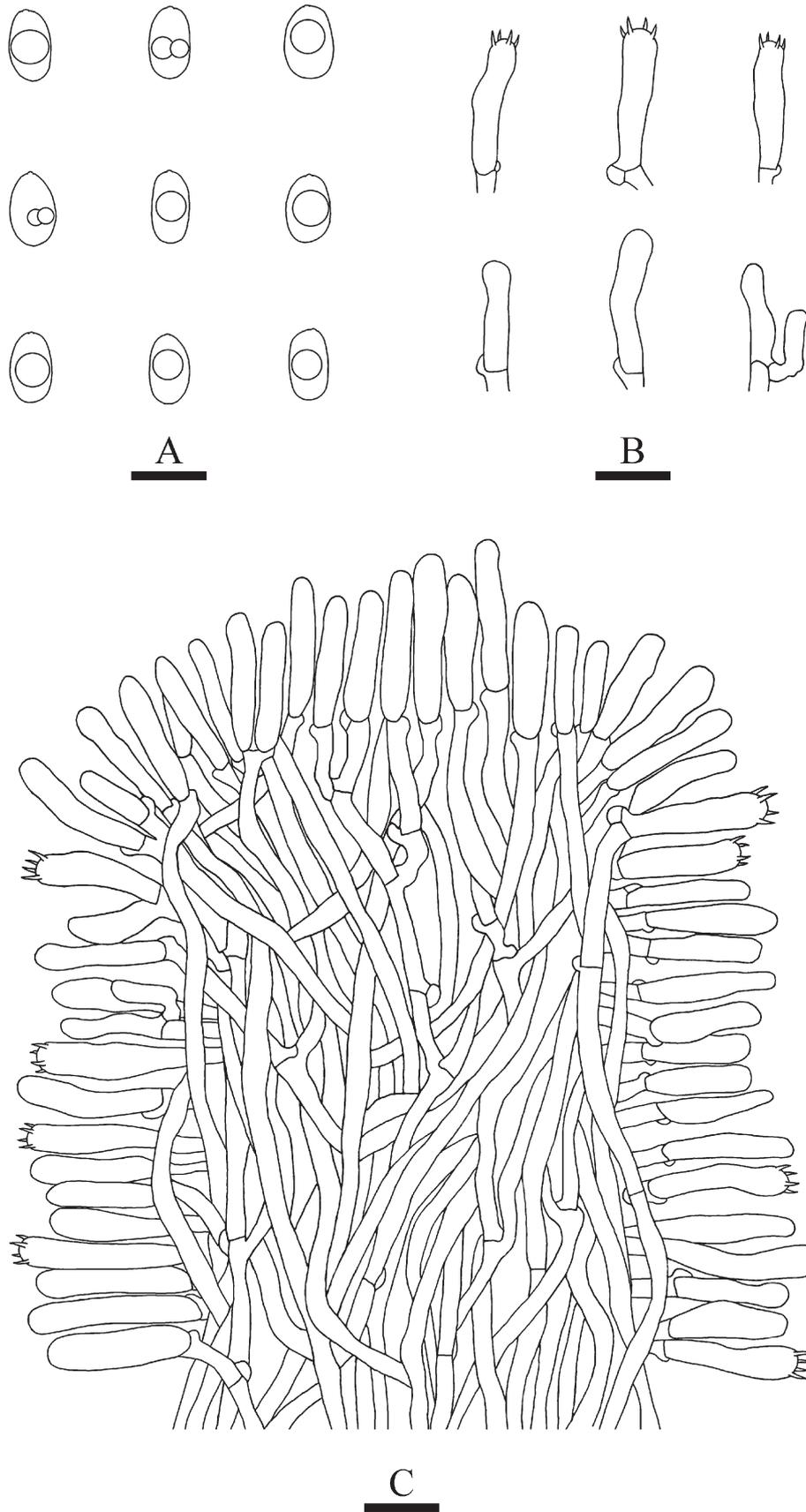


FIGURE 4. Microscopic structures of *Xylodon asiaticus* (drawn from the holotype). A. Basidiospores; B. Basidia and basidioles; C. Part of the vertical section of hymenium. Bars: A= 5 μ m; B–D= 10 μ m.

Notes:—Morphologically, *Xylodon asiaticus* resembles *X. asper* (Fr.) Hjortstam & Ryvarden. (2009: 34), *X. australis* (Berk.) Hjortstam & Ryvarden. (2007: 98) and *X. tenuicystidius* (Hjortstam & Ryvarden) Hjortstam & Ryvarden. (2009: 41) in having ellipsoid or cylindrical basidiospores. However, *X. asper* can be delimited from *X. asiaticus* by its odontoid hymenial surface and longer basidia (20–25 × 4–5 µm, Hjortstam & Ryvarden 2009); *X. australis* is distinguished from *X. asiaticus* by its grandinoid hymenial surface and larger basidiospores (6–7.5 × 4–4.5 µm, Hjortstam & Ryvarden 2007); *X. tenuicystidius* differs from *X. asiaticus* by its tuberculate hymenial surface and longer basidia (20–25 × 3–4 µm, Hjortstam & Ryvarden 2009).

Discussion

In the present study, one new species, *Xylodon asiaticus* is described based on phylogenetic analyses and morphological characteristics.

Phylogenetically, the *Xylodon* and related genera located in *Hyphodontia* s.l. of the Hymenochaetales, on the basis of the combined datasets of ITS, nLSU, and mt-SSU regions, and seven families, Chaetoporellaceae Jülich, Coltriciaceae Jülich, Hymenochaetaceae Donk, Neoantrodiaellaceae Y.C. Dai, B.K. Cui, Jia J. Chen & H.S. Yuan, Nigrofomitaceae Jülich, Oxyporaceae Zmitr. & Malysheva, and Schizoporaceae, were monophyletic lineages nested in Hymenochaetales, in which *Xylodon*, *Schizopora Palifer*, *Lyomyces*, and *Rogersella* grouped into *Hyphodontia* s.l. as independent genera (Luo *et al.* 2022).

In our study, the phylogenetic research inferred from ITS sequences (Fig. 2), revealed that the new species grouped into genus *Xylodon*: the new species *X. asiaticus* was sister to *X. pseudotropicus* (C.L. Zhao, B.K. Cui & Y.C. Dai) Riebesehl, Yurch. & Langer, in Riebesehl & Langer. (2017: 649), and then grouped with the clade composing *X. papillosus* (Fr.) Riebesehl, Yurch. & Langer, in Riebesehl & Langer. (2017: 648), and *X. punctus* K.Y. Luo & C.L. Zhao, in Luo, Chen & Zhao (2022: 9). However, morphologically, *X. pseudotropicus* differs from *X. asiaticus* by its poroid hymenial surface and oblong-ellipsoid basidiospores (Zhao *et al.* 2014); *X. papillosus* differs from *X. asiaticus* by its grandinoid hymenial surface and narrower basidia (15 × 3.5–4 µm, Yurchenko & Wu 2016); *X. punctus* is distinguished from *X. asiaticus* by its smooth hymenial surface, and smaller basidiospores (2–4 × 1.5–2.5 µm, Luo *et al.* 2022).

The macromorphology of the basidiomata and hymenophore construction do not reflect monophyletic groups based on a higher-level phylogenetic classification of polypores (Miettinen *et al.* 2016). The current phylogeny (Fig. 2) shows that the morphological characteristics do not follow the phylogenetic relationship of different taxa in *Xylodon* based on the ITS datasets. Morphologically, *X. asiaticus* resembles *X. asper* (Fr.) Hjortstam & Ryvarden. (2009: 34), *X. australis* (Berk.) Hjortstam & Ryvarden. (2007: 98) and *X. tenuicystidius* (Hjortstam & Ryvarden) Hjortstam & Ryvarden. (2009: 41) in having ellipsoid or cylindrical basidiospores. However, *X. asper* can be delimited from *X. asiaticus* by its odontoid hymenial surface and longer basidia (20–25 × 4–5 µm, Hjortstam & Ryvarden 2009); *X. australis* is distinguished from *X. asiaticus* by its grandinoid hymenial surface and larger basidiospores (6–7.5 × 4–4.5 µm, Hjortstam & Ryvarden 2007); *X. tenuicystidius* is distinguished from *X. asiaticus* by its tuberculate hymenial surface and longer basidia (20–25 × 3–4 µm, Hjortstam & Ryvarden 2009).

The corticioid fungi is a large characteristic group of Basidiomycota, which includes a number of species with poroid, smooth, grandinoid, odontoid and hydroid basidiomata in China (Wu *et al.* 2020, 2022, Dai *et al.* 2021, Duan *et al.* 2023, Yang *et al.* 2023, Yuan *et al.* 2023). To date, the accepted species of *Xylodon* is about 103, and thirty-nine species of *Xylodon* have been recorded in China (Gafforov *et al.* 2017, Riebesehl & Langer 2017, Viner *et al.* 2018, Riebesehl *et al.* 2019, Shi *et al.* 2019, Yurchenko *et al.* 2020, Luo *et al.* 2021, Ma & Zhao 2021, Qu *et al.* 2022, Guan *et al.* 2023), but the deep study of *Xylodon* is still not well known in China, especially in the subtropical and tropical areas. This paper enriches our knowledge of fungal diversity in this area, and it is likely that more new taxa will be found with further fieldwork and molecular analyses.

Acknowledgements

The research was supported by the National Natural Science Foundation of China (Project nos. 32170004 and 32160063), the High-level Talents Program of Yunnan Province (Project no. YNQR-QNRC-2018-111), the Research Project of Yunnan Key Laboratory of Gastrodia and Fungal Symbiotic Biology (Project no. TMKF2023A03) and the Yunnan Province College Students Innovation and Entrepreneurship Training Program (Project no. s202310677028).

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