Phytotaxa 674 (1): 001–017
https://www.mapress.com/pt/
Copyright © 2024 Magnolia Press

Article

ISSN 1179-3155 (print edition)
PHYTOTAXA
ISSN 1179-3163 (online edition)

https://doi.org/10.11646/phytotaxa.674.1.1

Morphological and molecular identification of two new wood-inhabiting macrofungi (Basidiomycota) from Yunnan-Guizhou Plateau, China

HONG-MIN ZHOU[1,2,3], XIN YANG[2,4], YU-YUN WANG[2,5] & CHANG-LIN ZHAO[1,2,6*]
[1]*The Key Laboratory of Forest Resources Conservation and Utilization in the Southwest Mountains of China Ministry of Education, Key Laboratory of National Forestry and Grassland Administration on Biodiversity Conservation in Southwest China, Yunnan Provincial Key Laboratory for Conservation and Utilization of In-forest Resource, Southwest Forestry University, Kunming 650224, P.R. China*
[2]*College of Forest, Southwest Forestry University, Kunming 650224, P.R. China*
[3] *zhouhongmin@swfu.edu.cn; https://orcid.org/0000-0002-0724-5815*
[4] *fungixiny@163.com; https://orcid.org/0009-0009-7755-0581*
[5] *fungiyuyunw@163.com; https://orcid.org/0009-0007-7011-0327*
[6] *fungichanglinz@163.com; https://orcid.org/0000-0002-8668-1075*
**Corresponding author: fungichanglinz@163.com*

Abstract

Two new species of wood-inhabiting fungi viz. *Luteoporia flavula* and *Xylodon subpunctus* are described from the Yunnan-Guizhou Plateau in southwestern China. *Luteoporia flavula* is characterized by annual basidiomata with an odontioid and lemon-chrome hymenophore, a monomitic hyphal structure with clamped generative hyphae, subuliform cystidia, and oblong-ellipsoid basidiospores (4–5.2 × 2.3–3.2 µm). The phylogenetic analysis based on ITS sequences indicated that Luteoporia flavula formed a single lineage and was nested within the genus *Luteoporia*. *Xylodon subpunctus* is characterized by annual basidiomata with a coriaceous and buff hymenophore, a monomitic hyphal structure with clamped generative hyphae, capitate and fusiform cystidia, ellipsoid to ovoid basidiospores measuring 5.5–7.2 × 2.5–3.6 µm. *Xylodon subpunctus* is clustered into the genus *Xylodon*, in the family Schizoporaceae, with *Hyphodontia*, *Lyomyces*, and *Schizopora*. Descriptions, illustrations, and phylogenetic analysis results of two new species are provided.

Key words: 2 new species, Diversity, ITS sequence, Macrofungi, Molecular systematics

Introduction

In fungal taxonomy, the morphology of basidiomata, such as gilled, poroid, toothed, and coralloid, has traditionally served as a fundamental classification criterion (Fries 1874, Sun *et al*. 2022), known for its practical application (Lloyd 1925, Dai & Yuan 2007, Zhao *et al*. 2016, Wu *et al*. 2021, 2022, Chen & Hu 2022, Wang *et al.* 2023, 2024). However, the emergence of molecular systematic research revealed conflicts, revealing that taxa with different basidiomata types were clustered together in the same lineages (Binder & Hibbett 2002, Liu *et al*. 2023). Therefore, the prevailing approach in fungal taxonomy research now emphasizes an integrated consideration of morphology and phylogeny.

Luteoporia (2016: 37) F. Wu, Jia J. Chen & S.H. He, was established by Wu *et al*. (2016) with *L. albomarginata* F. Wu, Jia J. Chen & S.H. He as the type species. *Luteoporia* is characterized by the resupinate, ceraceous basidiomata, poroid or odontioid to hydnoid hymenophore featuring a distinctive yellow hymenial surface that turns pink, reddish, or purple when treated with KOH. The genus exhibits a monomitic hyphal system with generative hyphae bearing clamp connections, and hyaline, smooth basidiospores (Wu *et al*. 2016, Liu & Yuan 2020, Zhao *et al*. 2023a). Previously, four species have been recognized in the genus: *L. citriniporia* Z.B. Liu & Yuan Yuan (2020: 36), *L. lutea* (G. Cunn.) C.C. Chen & Sheng H. Wu (2021: 427), *L. albomarginata* F. Wu, Jia J. Chen & S.H. He (2016: 37), and *L. straminea* C.L. Zhao (2023: 19), while *L. citriniporia* is exclusively found in Europe (Liu & Yuan 2020), *L. lutea* occurs in Oceania (Cunningham 1959), and the latter two species were originally described in southwest China (Wu *et al*. 2016, Liu & Yuan 2020).

Xylodon (Pers.) Gray (1821: 649), established in 1821, was typified by *X. quercinus* (Pers.) (1821: 649) (Bernicchia & Gorjón 2010), within the order Hymenochaetales. The genus is characterized by resupinate or effuse basidiomata,

Accepted by Samantha C. Karunarathna: 7 Nov. 2024; published: 26 Nov. 2024

a monomitic or a dimitic hyphal system with clamped generative hyphae; different types of cystidia, uniform or suburniform basidia, and cylindrical, ellipsoid to globose basidiospores (Gray 1821, Bernicchia & Gorjón 2010, Cho *et al.* 2021). Initially, species of *Xylodon* exhibited similarities with *Hyphodontia* J. Erikss. (1958: 101), such as odontioid and poroid hymenophores (Larsson *et al*. 2006). Recent phylogenetic analyses of *Xylodon* have revealed that this genus comprises many species exhibiting such both hymenophores (Hjortstam & Ryvarden 2009, Yurchenko *et al*. 2024). The genus *Xylodon* is distributed across various habitats worldwide, spanning the temperate, tropical, and subtropical regions (Langer 1994, Riebesehl *et al*. 2019; Zhao *et al.* 2024). A number of *Xylodon* species have been reported in China (Cho *et al*. 2021, Qu *et al*. 2022, Qu & Zhao 2022, Yurchenko *et al*. 2024, Zhang *et al*. 2024).

Two distinct fungi samples were collected during a survey of the wood-inhabiting fungi in the Yunnan-Guizhou Plateau of China. Morphological and phylogenetic analyses conducted in this study revealed that these two species are distinct from all the known species of wood-inhabiting macrofungi and are introduced as *Luteoporia flavula sp. nov.* and *Xylodon subpunctus sp. nov.*

Material and methods

Morphological studies

Samples were collected from the Guizhou Province of China, and important collection information was recorded (Rathnayaka *et al.* 2024). Specimens were dried in an electric food dehydrator at 35 °C (Hu *et al.* 2022), and then deposited in the herbarium of the Southwest Forestry University (SWFC), Kunming, Yunnan Province, China. The macro-morphology was based on fresh and dried specimens. The colour terms in the description followed Anonymous (1969) and Petersen (1996). Micro-morphology was studied at magnifications 1000 ×, using a Nikon Eclipse 80i microscope with phase contrast illumination. The Melzer's reagent, Cotton Blue, and 5% KOH were used in the study. Drawings were made with the aid of a drawing tube. In the text these abbreviations were used: IKI = Melzer's reagent, IKI− = non-dextrinoid and non-amyloid, IKI+ = amyloid, KOH = 5% potassium hydroxide, CB = Cotton Blue, CB− = acyanophilous, L = mean basidiospores length (arithmetic average of all basidiospores), W = mean basidiospores width (arithmetic average of all basidiospores), Q = variation in the L/W ratios between the specimens studied, n = number of basidiospores measured from number of specimens.

DNA Extraction, Polymerase Chain Reaction, and Sequencing

Genomic DNA was extracted from dried basidiomata using a cetyltrimethylammonium bromide rapid plant genome extraction kit (Aidlab Biotechnologies Co., Ltd., Beijing) according to the manufacturer's instructions with some modifications (Dai *et al*. 2010, Zhao *et al*. 2023a). ITS sequences were analyzed to determine the taxonomic status of *Luteoporia* and *Xylodon*. PCR was performed following Zhou *et al*. (2023). All newly generated sequences were deposited in the GenBank database. All the sequence information is listed in Table 1.

Phylogenetic Analyses

We compiled two ITS sequence data sets to determine the phylogeny: *Meripilus giganteus* (Pers.) P. Karst. (1882: 33) and *Corticium roseum* Pers. (1794: 111) were used as outgroups for *Luteoporia* and *Xylodon* analyses, respectively. The sequences were initially aligned using MAFFT (https://mafft.cbrc.jp/alignment/server/) using the "G-INS-I" strategy and then manually optimized in BioEdit (Hall 1999). ModelFinder (Kalyaanamoorthy *et al*. 2017) was used to select the best-fit model using the AIC criterion. The best-fit model was selected according to AIC: GTR+I+G4.

ML analysis was conducted through the Cipres Science Gateway (https://www.phylo.org/portal2/login!input.action). BI was performed using MrBayes (Ronquist & Huelsenbeck 2003) with two independent runs, performing 2,000,000 and 9,000,000 replicates each for the concatenated respectively and the ITS datasets, sampling one tree every 1,000 generations. The first 25% of the sampled trees were discarded as burn-in, and the remaining trees were used to reconstruct a majority rule consensus and calculate the BPP of the clades. Branches of the consensus tree that received bootstrap support for ML greater than or equal to 75%, bayesian posterior probabilities more than 0.95, respectively.

TABLE 1 Names, voucher numbers, and corresponding GenBank accession numbers of the taxa used in the phylogenetic analysis of this study.

Species name	Species voucher	ITS
Climacodon septentrionalis	AFTOL-767	AY854082
Climacodon septentrionalis	FP-72067	KP135345
Corticium roseum	CBS 104.52	MH856944
Crustodontia chrysocreas	HHB-6333-sp	KP135358
Crustodontia nigrodontea	CLZhao 2729	MT896823
Fasciodontia brasiliensis	MSK-F 7245a	MK575201
Fasciodontia bugellensis	KAS-FD 10705a	MK575203
Geesterania carneola	MCW 388/12	KY174999
Geesterania carneola	SP 446193	NR 158508
Hydnophlebia acanthocystis	FP 150571	KY948767
Hydnophlebia canariensis	MA-Fungi 86619	KF483009
Hydnophlebia caspica	CUG 3159	HQ153410
Hydnophlebia chrysorhiza	FD-282	KP135338
Hydnophlebia fimbriata	Dai 11672	KJ698633
Hydnophlebia fissurata	CLZhao 2900	MW732402
Hydnophlebia gorgonea	MA-Fungi 86642	KF483031
Hydnophlebia omnivora	KKN-112-sp	KP135334
Hyphodontia alutaria	GEL 3183	DQ340318
Hyphodontia arguta	KHL 11938	EU118632
Hyphodontia pachyspora	LWZ 20170908-5	MT319426
Hyphodontia pallidula	KAS-GEL 2097	DQ340317
Hyphodontia zhixiangii	LWZ 20180903-5	MT319423
Kneiffiella barba-jovis	KHL 11730	DQ873609
Kneiffiella barba-jovis	KHL 11730	DQ873609
Kneiffiella eucalypticola	LWZ 20180515-9	MT319411
Kneiffiella palmae	KAS-GEL 3456	DQ340333
Kneiffiella subalutacea	GEL 2196	DQ340341
Luteochaete subglobosa	CLZhao 3475	MK881897

......continued on the next page

TABLE 1 (Continued)

Species name	Species voucher	ITS
Luteochaete subglobosa	Wu 870918	MZ636996
Luteoporia albomarginata	Dai 15229	KU598873
Luteoporia albomarginata	GC 1702-1	LC379003
Luteoporia citriniporia	Dai 19507	MT872218
Luteoporia flavum	CLZhao 31241	OR681873
Luteoporia flavum	CLZhao 31243	OR681874
Luteoporia flavum	CLZhao 31245	OR681875
Luteoporia lutea	GC 1409-1	MZ636998
Luteoporia straminea	CLZhao 18947	MW732407
Luteoporia straminea	CLZhao 5794	OM897115
Lyomyces bambusinus	CLZhao 4831	MN945968
Lyomyces fimbriatus	Wu 911204-4	MK575210
Lyomyces mascarensis	KAS-GEL 4833	NG_060351
Lyomyces orientalis	LWZ 20170909-7	MT326529
Lyomyces sambuci	KAS-JR7	KY800402
Meripilus giganteus	FP 135344 Sp	KP135307
Merulius fuscotuberculata	CLZhao 10227	MT020759
Merulius hydnoidea	HHB-1993-sp	KY948778
Merulius livida	FBCC 1283	LN611123
Merulius nantahaliensis	HHB-2816-sp	KY948777
Merulius sinensis	CLZhao 2562	MW732401
Merulius tomentopileata	CLZhao 10274	MT020771
Merulius tremellosus	CBS 217.56	MH857589
Mycoacia aurea	FCUG 2767	HQ153409
Mycoacia aurea	RLG 5075sp	KY948759
Mycoacia fuscoatra	HHB-10782-sp	KP135365
Mycoacia fuscoatra	OMC 1380	KY948754
Mycoacia gilvescens	Chen 3340	MZ636936

......*continued on the next page*

TABLE 1 (Continued)

Species name	Species voucher	ITS
Mycoacia gilvescens	Yuan 2752	KF845953
Mycoacia gilvescens	Chen 156	MZ636935
Mycoacia gilvescens	BRNM 710166	FJ496684
Mycoacia kunmingensis	CLZhao 153	KX081073
Mycoacia kunmingensis	CLZhao 152	KX081072
Mycoacia livida	FP-135416-sp	KP135309
Mycoacia nothofagi	HHB-4273-sp	KP135369
Mycoacia nothofagi	HHB-6906-sp	KP135368
Mycoacia subfascicularis	Chen 3873	MZ637007
Mycoacia subfascicularis	Wu 1004	MZ637008
Mycoacia tuberculata	MG 128	HQ153425
Mycoacia tuberculata	FCUG 3186	HQ153418
Mycoaciella bispora	EL 1399	AY463446
Mycoaciella brunneospina	CLZhao 15876	MW732404
Pappia fssilis	BRNM 699803	HQ728292
Phlebia acerina	FD-301	KP135378
Phlebia floridensis	HHB-9905-sp	KP135383
Phlebia griseoflavescens	MR-4310	KY948797
Phlebia leptospermi	CBS 126031	MH863894
Phlebia ochraceofulva	FBCC 360	LN611117
Phlebia radiata	CBS 285.56	MH857642
Phlebia rhododendri	CLZhao 6168	MW732400
Phlebia rufa	CBS 213.47	MH856224
Phlebicolorata alboaurantia	Cui 4136	KF845955
Phlebicolorata brevispora	FBCC 1463	LN611135
Phlebicolorata crocea	Miettinen 16483	KY948745
Phlebicolorata pseudoplacenta	Miettinen 18997	KY948744

......continued on the next page

TABLE 1 (Continued)

Species name	Species voucher	ITS
Phlebicolorata rosea	Dai 13573	KJ698635
Phlebiporia bubalina	Dai 9798	KY131842
Pseudophlebia mayanensis	JV 1504/128	KT156706
Pseudophlebia semisupina	Cui 10222	KF845956
Pseudophlebia setulosa	HHB-6891-sp	KP135382
Sarcodontia crocea	OMC 1488	KY948798
Sarcodontia crocea	BRNM 721609	KX831470
Scopuloides allantoidea	GC 1602-11	MZ637080
Scopuloides dimorpha	FP-102935	KP135353
Scopuloides hydnoides	FP-150473	KP135355
Scopuloides rimosa	HHB-7042-sp	KP135350
Xylodon acuminatus	Larsson 16029	ON197552
Xylodon acystidiatus	LWZ 20180514-9	MT319474
Xylodon afromontanus	H 7006811	OQ645463
Xylodon angustisporus	Ryvarden 50691b	OK273831
Xylodon apacheriensis	Canfield 180	KY081800
Xylodon asiaticus	CLZhao 10368	OM959479
Xylodon asperus	Spirin 11923	OK273838
Xylodon astrocystidiatus	TMN F24764	NR154054
Xylodon attenuatus	Spirin 8775	MH324476
Xylodon australis	LWZ 20180509-8	MT319503
Xylodon bambusinus	CLZhao 11310	MW394660
Xylodon borealis	JS26064	AY463429
Xylodon brevisetus	JS17863	AY463428
Xylodon crystalliger	KUN 2312	NR166242
Xylodon cymosus	Miettinen 19606	ON197554
Xylodon cystidiatus	FR-0249200	MH880195
Xylodon damansaraensis	LWZ 20180417-23	MT319499

......*continued on the next page*

TABLE 1 (Continued)

Species name	Species voucher	ITS
Xylodon daweishanensis	CLZhao 18357	OP730715
Xylodon detriticus	Zíbarová 30.10.17	MH320793
Xylodon dissiliens	Ryvarden 44817	OK273856
Xylodon echinatus	H 7200350	OQ645464
Xylodon filicinus	MSK F 12869	MH880199
Xylodon fissuratus	CLZhao 9407	OP730714
Xylodon flaviporus	FR-0249797	MH880201
Xylodon flocculosus	CLZhao 18342	MW980776
Xylodon follis	FR-0249814	MH880204
Xylodon gloeocystidiifer	BLS M-5232	OQ645467
Xylodon gossypinus	CLZhao 8375	MZ663804
Xylodon grandineus	CLZhao 6425	OM338090
Xylodon hastifer	K (M) 172400	NR166558
Xylodon heterocystidiatus	Wei 17-314	MT731753
Xylodon hjortstamii	Gorjón 3187	ON188816
Xylodon hyphodontinus	KAS-GEL9222	MH880205
Xylodon jacobaeus	MA-Fungi91340	MH430073
Xylodon kunmingensis	TUB-FO 42565	MH880198
Xylodon laceratus	CLZhao 9892	OL619258
Xylodon lagenicystidiatus	LWZ20180513-16	MT319634
Xylodon lanatus	CFMR FP-101864-A	OQ645474
Xylodon lenis	Wu 890714-3	KY081802
Xylodon macrosporus	CLZhao 10226	MZ663809
Xylodon magallanesii	MA-Fungi 90397	MT158729
Xylodon mantiqueirensis	SP467059	OQ645478
Xylodon mollissimus	LWZ 20160318-3	KY007517
Xylodon montanus	CLZhao 8179	OL619260
Xylodon neotropicus	SP 467096	OQ645479

......*continued on the next page*

TABLE 1 (Continued)

Species name	Species voucher	ITS
Xylodon nesporii	LWZ 20180921-35	MT319655
Xylodon niemelaei	LWZ 20150707-13	MT319630
Xylodon nongravis	GC 1412-22	KX857801
Xylodon nothofagi	ICMP 13842	AF145583
Xylodon ovisporus	LWZ 20170815-31	MT319666
Xylodon papillosus	CBS 114.71	MH860026
Xylodon paradoxus	Dai 14983	MT319519
Xylodon patagonicus	ICMP 13832	AF145581
Xylodon pruinosus	Spirin 2877	MH332700
Xylodon pruniaceus	Ryvarden 11251	OK273828
Xylodon pseudolanatus	FP-150922	MH880220
Xylodon pseudotropicus	Dai 10768	KF917543
Xylodon puerensis	CLZhao 8142	OP730720
Xylodon punctus	CLZhao 17908	OM338093
Xylodon punctus	CLZhao 17691	OM338092
Xylodon punctus	CLZhao 17908	OM338093
Xylodon punctus	CLZhao 17916	OM338094
Xylodon quercinus	Spirin 12030	OK273841
Xylodon raduloides	FCUG 2433	AF145570
Xylodon ramicida	Spirin 7664	NR138013
Xylodon reticulatus	GC 1512.1	KX857808
Xylodon reticulatus	Wu 1109-178	KX857805
Xylodon reticulatus	GC 1512.1	KX857808
Xylodon rhizomorphus	Dai 12367	NR_154067
Xylodon rhododendricola	LWZ 20180513-9	MT319621
Xylodon rimosissimus	Ryberg 21031	DQ873627
Xylodon serpentiformis	LWZ 20170816-15	MT319673
Xylodon sinensis	CLZhao 9197	MZ663810

......continued on the next page

TABLE 1 (Continued)

Species name	Species voucher	ITS
Xylodon sinensis	CLZhao 11120	OK560885
Xylodon spathulatus	LWZ 20180804-10	MT319646
Xylodon subclavatus	TUB-FO 42167	MH880232
Xylodon subflaviporus	TNM F29958	NR184880
Xylodon submucronatus	Renvall 1602	OK273830
Xylodon subpunctus	CLZhao 6165	PP537958
Xylodon subpunctus	CLZhao 31242	PP537957
Xylodon subserpentiformis	LWZ 20180512-16	MT319486
Xylodon subtilissimus	Spirin 12228	ON188818
Xylodon subtropicus	LWZ 20180510-24	MT319541
Xylodon taiwanianus	CBS 125875	MH864080
Xylodon tropicus	CLZhao 3351	OL619261
Xylodon ussuriensis	KUN 1989	NR166241
Xylodon verecundus	KHL 12261	DQ873642
Xylodon victoriensis	LWZ 20180510-29	MT319487
Xylodon wenshanensis	CLZhao 15729	OM338097
Xylodon xinpingensis	CLZhao 9147	MW394657
Xylodon yarraensis	LWZ 20180510-5	MT319639
Xylodon yunnanensis	LWZ 20180922-47	MT319660

Results

The combined ITS dataset of *Luteoporia* included sequences from 77 specimens (Table 1). The dataset had an aligned length of 944 characters, of which 412 were constant, 132 were variable but parsimony uninformative, and 400 were parsimony informative. Bayesian and ML analyses resulted in a similar topology, with an average standard deviation of split frequencies of 0.008741 (BI).

The combined ITS dataset of *Xylodon* included sequences from 108 specimens (Table 1). The dataset had an aligned length of 875 characters, of which 346 were constant, 108 were variable but parsimony uninformative, and 421 were parsimony-informative. Bayesian analysis and ML analysis resulted in a similar topology.

The phylogeny (Fig. 1) inferred from ITS sequences demonstrated 58 species. The new species *Luteoporia flavula* clusters in the family Meruliaceae clade and groups with *Geesterania* Westphalen (2018: 134) and *Phlebiporia* Jia J. Chen, B.K. Cui & Y.C. Dai (2014: 568). In the phylogenetic trees, the species of *Luteoporia* cluster together with a high support value (0.96/96). The new species, *L. flavula* forms a sister group to the other two species, *L. lutea* and *L. straminea*, with the same morphological characteristics of the odontioid hymenophore, while the two species, *L. albomarginata* and *L. citriniporia* with the poroid hymenophore receive strong support (Fig. 1).

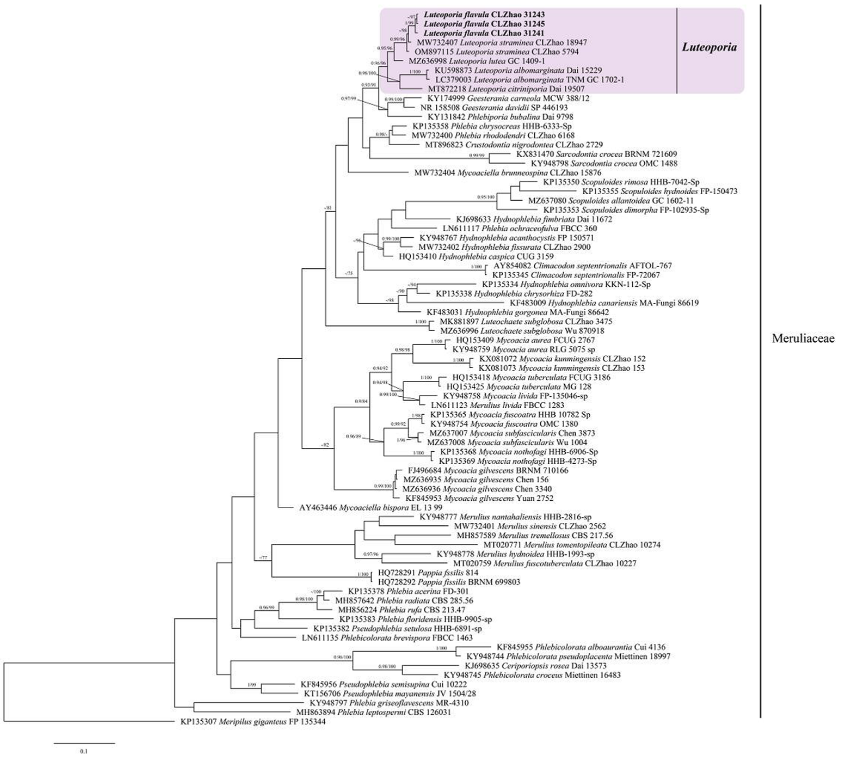

FIGURE 1. Phylogeny of *Luteoporia flavula* (in bold) and related species by ML analysis based on combined ITS rDNA sequences. Branches are labeled with maximum likelihood bootstrap equal to or higher than 75%, and Bayesian posterior probabilities equal to or higher than 0.95, respectively.

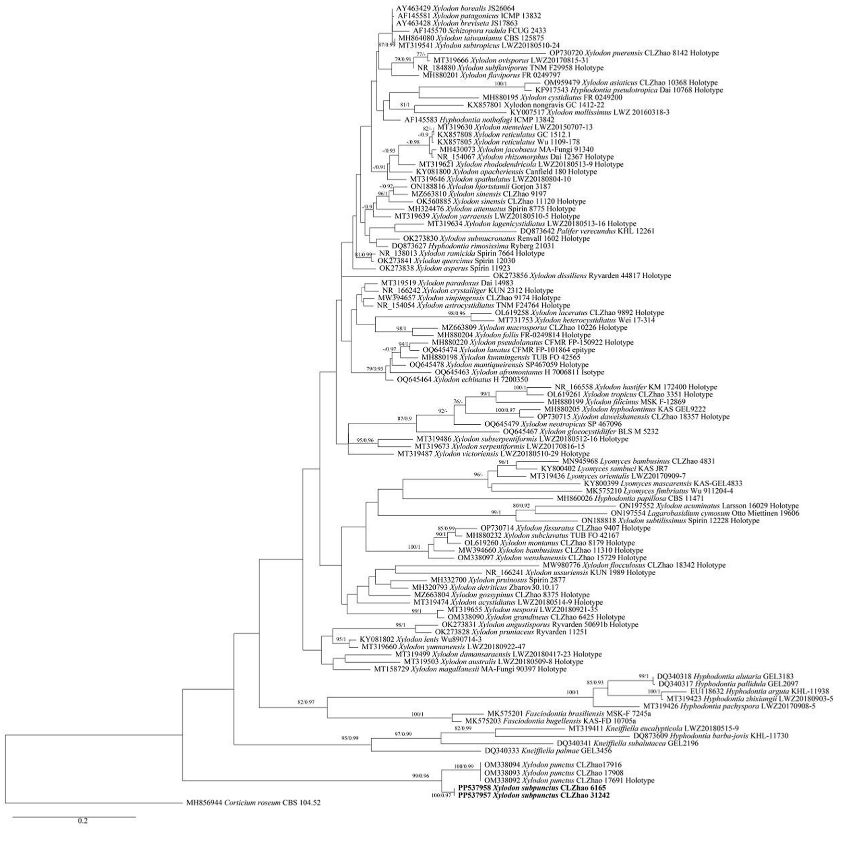

FIGURE 2. Phylogeny of *Xylodon subpunctus* (in bold) and related species by ML analysis based on combined ITS rDNA sequences. Branches are labeled with maximum likelihood bootstrap equal to or higher than 75%, and Bayesian posterior probabilities equal to or higher than 0.95, respectively.

The phylogeny (Fig. 2) inferred from ITS sequences demonstrates 105 species. The new species *Xylodon subpunctus* clusters in the family Schizoporaceae clade, groups with *Schizopora* Velen., *Hyphodontia*, and *Lyomyces* P. Karst. In the phylogenetical tree, the new species *X. subpunctus* forms a sister group with *X. punctus* K.Y. Luo & C.L. Zhao (2022: 9) outside the core *Xylodon* clade.

Taxonomy

Luteoporia flavula C.L. Zhao & H.M. Zhou, *sp. nov*. Figs. 3, 4.
MycoBank: MB 850569

***Diagnosis*:**—It is characterized by the purple tissue in KOH, in contrast to the reddish colouration of *L. straminea*.

***Etymology*:**—*Flavula* (Lat.) refers to the lemon-chrome hymenial surface when fresh.

***Holotype*:**—CHINA. Guizhou Province, Guiyang, Qianlingshan Forest Park, on an angiosperm trunk, 25 August 2023, CLZhao 31245 (SWFC F0031245).

FIGURE 3. Basidiomata of *Luteoporia flavula* (A, C) CLZhao 31245; (B, D) CLZhao 31241.

***Basidiomata*:**—Annual, resupinate, ceraceous, without odor or taste when fresh, becoming hard upon drying, up to 1 cm long, 1.2 cm wide, 200–250 µm thick when dry. Hymenophore odontioid, lemon-chrome when fresh, curry-yellow upon drying, tissue becoming purple in KOH. Sterile margin, narrow, and light lemon.

***Hyphal structure*:**—Monomitic, generative hyphae with clamp connections, hyaline, thin- to thick-walled, IKI-, CB-. Subicular hyphae unbranched, 2.5–4 µm in diam; subhymenial hyphae unbranched, 2–4 µm in diam; numerous yellow to yellowish brown gelatinous substances present among subhymenium. Hymenial cystidia subuliform, hyaline, thick-walled, 15.5–30 × 3.8–5.7 µm, cystidioles absent; basidia 4-celled, clavate, with a basal clamp connection, 24–29 × 4–5.2 µm. Basidiospores oblong ellipsoid, hyaline, thin-walled, smooth, occasionally with guttules, IKI-, CB-, (3.4–)4–5.2(–5.5) × (2.2–)2.3–3.2(–3.4) µm, L = 4.56 µm, W = 2.74 µm, Q = 1.63–1.71 (n = 90/3).

***Additional specimens examined (paratypes)*:**—CHINA. Guizhou Province, Guiyang, Qianlingshan Forest Park, on an angiosperm trunk, 25 August 2023, CLZhao 31241 (SWFC F0031241), CLZhao 31243 (SWFC F0031243).

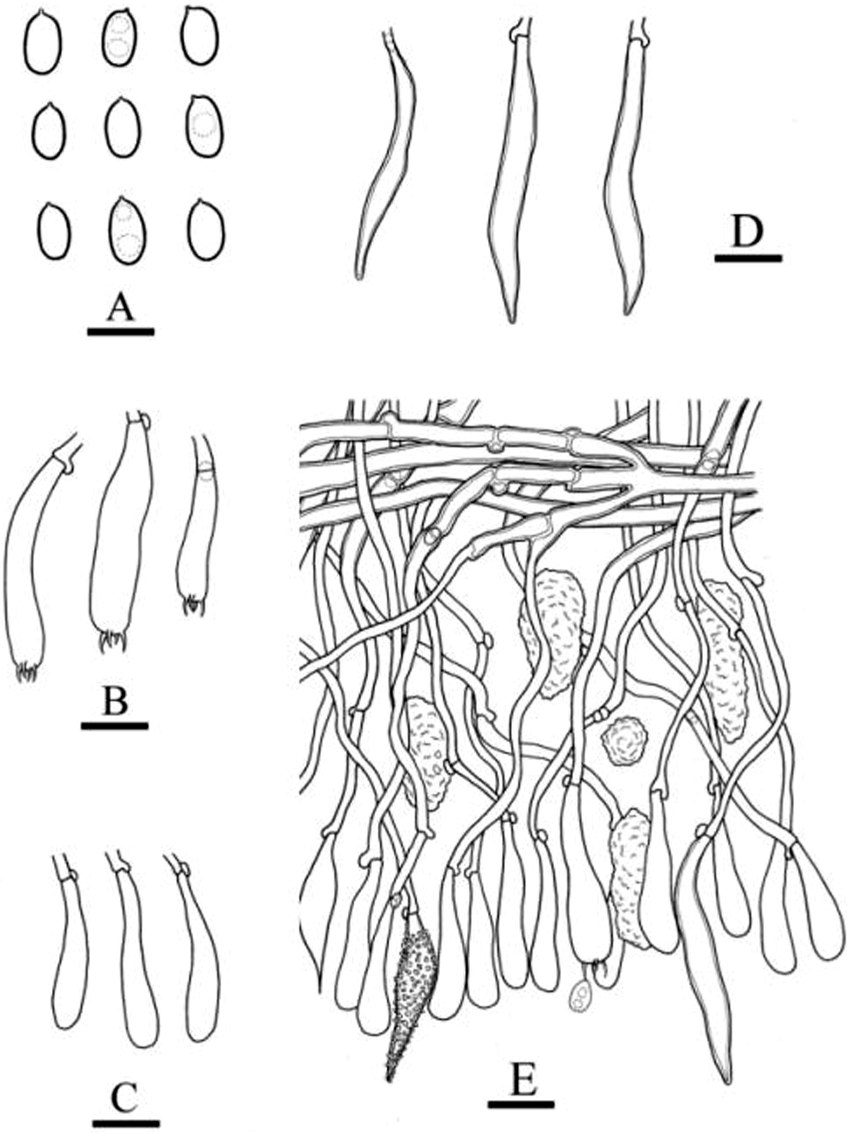

FIGURE 4. Microscopic structures of *Luteoporia flavula* (CLZhao 31245, holotype). (A) Basidiospores; (B) Basidia; (C) Basidioles; (D) Cystidia; (E) A section of hymenium. Scale bars: A = 5 µm; B–E = 10 µm.

Xylodon subpunctus C.L. Zhao & H.M. Zhou, *sp*. *nov*. Fig. 5.
MycoBank: MB 853205

***Diagnosis*:—**It differs from *Xylodon punctus* by smaller basidiospores (2–4 × 1.5–2.5 µm vs. 5.5–7.2 × 2.5–3.6 µm).

Etymology*:—Subpunctus* (Lat.) refers to the similarity of the species to *Xylodon punctus.*

***Holotype*:—**CHINA. Guizhou Province, Guiyang, Qianlingshan Forest Park, on a fallen angiosperm branch, 25 August 2023, CLZhao 31242 (SWFC F0031242).

***Basidiomata*:—**Basidiomata annual, resupinate, without odor and taste, coriaceous when fresh, hard coriaceous upon drying, up to 4 cm long, 2 cm wide, 20–50 µm thick. Hymenial surface farinaceous, buff when dry, cracking. Sterile margin indistinct.

***Hyphal system*:—**Monomitic, generative hyphae with clamp connections, hyaline, thin-walled, frequently branched, interwoven, IKI-, CB-, 1.8–4.4 µm in diameter; tissues unchanged in KOH; subhymenial hyphae densely covered by larger, irregular crystals; a basal layer of hyphae regularly arranged.

***Hymenium*:—**Cystidia of two types: (1) capitate cystidia occasional, hyaline, thin-walled, slightly constricted at the neck, with a globose tip, 27–34.2 × 3–3.5 µm; (2) fusiform cystidia frequent, hyaline, thin-walled, 20.3–26.8 × 5.3–6.4 µm; basidia 4-celled, barreled to clavate, with a basal clamp connection, 10–17.4 × 2–5.2 µm.

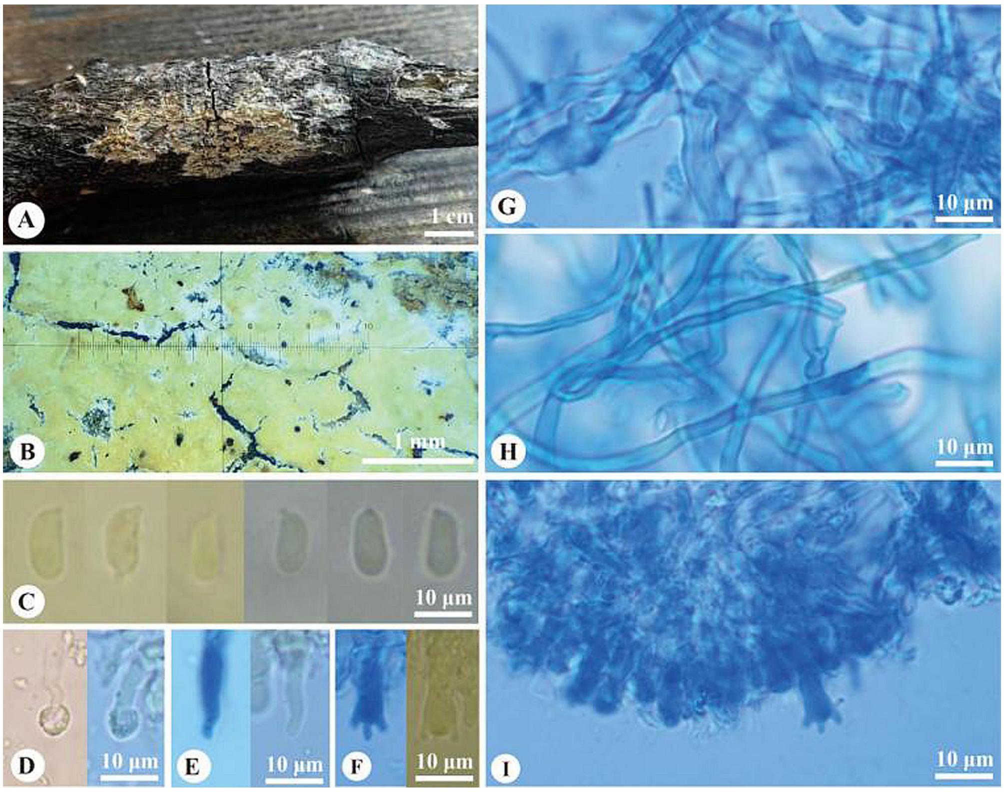

FIGURE 5. Basidiomata and microscopic structures of *Xylodon subpunctus* (holotype, CLZhao 31242). A–B. Basidiomata; C. Basidiospores; D. Capitate cystidia; E. Cystidia; F. Basidia; G. Subhymenial hyphae; H. Hymenial hyphae; I. A section of hymenium.

***Spores*:**—Basidiospores ellipsoid to ovoid, hyaline, thin-walled, smooth, IKI-, CB-, (5.3–)5.5–7.2(–7.4) × (2.6–)2.5–3.6(–4.5) µm, L = 6.33 µm, W = 3.00 µm, Q = 2.08–2.13 (n = 60/2).

***Additional specimen examined (paratype)*:**—CHINA. Yunnan Province, Puer, Zhenyuan County, Damo Mountain, on a fallen angiosperm branch, 16 January 2018, CLZhao 6165 (SWFC).

Discussion

The phylogenetic analysis reveals that *Luteoporia* is monophyletic with high support (Fig. 1), which is consistent with previous studies (Wu *et al*. 2016, Liu & Yuan 2020, Chen *et al*. 2021, Zhao *et al*. 2023a). The hymenophores of *L. albomarginata* and *L. citriniporia* are poroid and hydnoid in *L. lutea*, *L. straminea*, and *L. flavula*.

Phylogenetically, *Luteoporia flavula* groups with *L. albomarginata*, *L. citriniporia*, *L. lutea*, and *L. straminea*. Morphologically, *L. albomarginata* and *L. citriniporia* differ from *L. flavula* in their poroid hymenophores. In addition, *L. lutea* is distinguished from *L. flavula* by the longer basidiospores (5–6 µm vs. 4–4.6 µm), shorter basidia (16–24 µm vs. 24–29 µm), and it occurs in New Zealand (Chen *et al*. 2021). *Luteoporia straminea* and *L. flavula* are found in Yunnan Province of China, with a similar yellow, odontioid hymenophore and the same shape and size basidiospores. At the same time, the latter has smaller basidia (17.5–24.1 × 2.7–4.2 µm vs. 24–29 × 4–5.2 µm), and the tissue of *L. straminea* becomes reddish in KOH, but purple in *L. flavula* (Zhao *et al*. 2023a).

Luteoporia flavula resembles *Phanerochaetella leptoderma* (Sheng H. Wu) C.C. Chen & Sheng H. Wu (2021: 417) by having similar yellowish and ceraceous basidiomata, but the latter has longer basidiospores (6–7.2 µm vs. 4–5.2 µm, Chen *et al*. 2021).

The phenomenon of taxa with different basidiomata types clustering in the same lineage has been observed in numerous studies: Mucoromycota (Zhao *et al*. 2023b), Auriculariales (Zhou & Dai 2013, Wu *et al*. 2021), Agaricales (Zhang *et al*. 2023), Hymenochaetales (Zhao *et al*. 2014, Chen *et al*. 2016, Guan *et al*. 2020, Wu *et al*. 2022, Zhou *et al*. 2023), Albatrellaceae (Albee-Scott 2007, Smith *et al*. 2013) and Polyporales (Dai 2012, Zhao & Wu 2017, Cui *et al*. 2019, Ma & Zhao 2019, Huan & Zhao 2020, Wang *et al*. 2021, Zhao *et al*. 2021, Mao *et al*. 2023). In our study, species exhibiting poroid or odontioid-to-hydnoid hymenophore were grouped within *Luteoporia*, indicating that hymenophore characteristics may not always be consistent with phylogenetic analysis results (Table 2).

Xylodon is a widely recognized genus in diverse biomes with abundant woody plant debris worldwide. Recent phylogenies conducted by Luo *et al*. (2022) and Qu *et al*. (2022) expanded our understanding of *Xylodon* and its four related families, comprising six genera. Our novel taxonomic analysis using the ITS dataset revealed that *X. subpunctus* and *X. punctus* are grouped within the same subclade outside the core clade of *Xylodon*. Given the available data, we classified them as *Xylodon* species for the time being, pending further examination and phylogenetic analysis of additional material.

Nineteen species of *Xylodon* have been identified in Yunnan Province (Luo *et al*. 2022, Qu & Zhao 2022, Qu *et al*. 2022, Zhang *et al*. 2024). Among these, *X. subpunctus* shows a closer phylogenetic relationship with *X. punctus*, but *X. punctus* has smaller basidiospores (2–4 × 1.5–2.5 µm vs. 5.5–7.2 × 2.5–3.6 µm). Two species, *X. kunmingensis* L.W. Zhou & C.L. Zhao and *X. rhizomorphus* (C.L. Zhao, B.K. Cui & Y.C. Dai) Riebesehl, Yurch. & Langer, are readily confused with *X. subpunctus.* However, *X. kunmingensis* is characterized by the adnate and cream basidiomata (Shi *et al*. 2019); while *X. rhizomorphus* is characterized by rhizomorphic basidiomata with a poroid hymenophore and wider basidiospores (3.7–4.1 µm vs. 2.5–3.6 µm, Zhao *et al*. 2014).

Previously, species in *Luteoporia* and *Xylodon* were reported as saprophytic, and our two new species have the same ecology as the other species in these two genera (Yuan *et al.* 2023). The other functions of the two new species are unknown so far.

The Yunnan-Guizhou Plateau, with its important virgin forests, is a unique and vital habitat for a variety of wood-decaying fungi, including poroid, gilled, clavarioid, and Jelly hymenophore species (Dai 2012; Zhao &Wu 2017, Zhou *et al.* 2023, Wang *et al.* 2024). However, the diversity of corticoid fungi in this region is poorly understood, highlighting the urgent need for further research. Recent discoveries of new species in China, identified through a combination of morphology and phylogeny (Yuan *et al.* 2023, Zhao *et al.* 2023a, Dong *et al.* 2024), underscore the potential for exciting new findings. The application of advanced techniques, such as molecular phylogeny and omics, offers a promising avenue for future research in mycology.

Author contribution

All authors contributed to the concept and design of the study. ZHM, ZCL, and YX performed material preparation and data collection. ZHM and ZCL performed phylogenetic analysis, and ZHM and WYY did drawings. ZHM and YX wrote the first draft of the manuscript. ZCL commented on previous versions of the manuscript. All authors read and approved the final manuscript.

Acknowledgements

The research was supported by the National Natural Science Foundation of China (Project No. 32170004, 3246006, U2102220), the Scientific Research Fund of Yunnan Provincial Department of Education (2024J0668), the Forestry Innovation Programs of Southwest Forestry University (Grant No: LXXK-2023M07) and the High-level Talents Program of Yunnan Province (Project No. YNQR-QNRC-2018-111).

Declarations

Those authors declare no competing interests.

References

Albee-Scott, S. (2007) The phylogenetic placement of the Leucogastrales, including *Mycolevis siccigleba* (Cribbeaceae), in the Albatrellaceae using morphological and molecular data. *Mycological Research* 111: 653–662. https://doi.org/10.1016/j.mycres.2007.03.020

Anonymous. (1969) *Flora of British fungi. colour identification chart.* Her Majesty's Stationery Office: London, UK.

Bernicchia, A. & Gorjón, S.P. (2010) *Fungi Europaei 12.* Corticiaceae s.l. Edizioni Candusso, Alassio. 1008 pp.

Binder, M. & Hibbett, D.S. (2002) Higher-level phylogenetic relationships of Homobasidiomycetes (mushroom-forming fungi) inferred from four rDNA region. *Molecular Phylogenetics and Evolution* 22: 76–90.
https://doi.org/10.1006/mpev.2001.1043

Chen, C.C., Chen, C.Y. & Wu, S.H. (2021) Species diversity, taxonomy and multi-gene phylogeny of phlebioid clade (Phanerochaetaceae, Irpicaceae, Meruliaceae) of Polyporales. *Fungal Diversity* 111: 337–442.
https://doi.org/10.1007/s13225-021-00490-w

Chen, J.B. & Hu, G.R. (2022) The lichen family Physciaceae (Ascomycota) in China VII. Five species new to China. *Mycosystema* 41: 155–159.
https://doi.org/10.13346/j.mycosystema.210159

Chen, J.J., Zhou, L.W., Ji, X.H. & Zhao, C.L. (2016) *Hyphodontia dimitica* and *H. Subefibulata* spp. nov. (Schizoporaceae, Hymenochaetales) from southern China based on morphological and molecular characters. *Phytotaxa* 269: 1–13.
https://doi.org/10.11646/phytotaxa.269.1.1

Cho, Y., Kim, J.S., Dai, Y.C., Gafforov, Y. & Lim, Y.W. (2021) Taxonomic evaluation of *Xylodon* (Hymenochaetales, Basidiomycota) in Korea and sequence verification of the corresponding species in GenBank. *Peer J* 9: e12625.
https://doi.org/10.7717/peerj.12625

Cui, B.K., Li, H.J., Ji, X., Zhou, J.L., Song, J., Si, J., Yang, Z.L. & Dai, Y.C. (2019) Species diversity, taxonomy and phylogeny of Polyporaceae (Basidiomycota) in China. *Fungal Diversity* 97: 137–392.
https://doi.org/10.1007/s13225-019-00427-4

Cunningham, G.H. (1959) Hydnaceae of New Zealand. II. The genus *Odontia*. *Transactions and Proceedings of the Royal Society of New Zealand* 86: 65–103.

Dai, Y.C. (2010) Hymenochaetaceae (Basidiomycota) in China. *Fungal Diversity* 45: 131–343.
https://doi.org/10.1007/s13225-010-0066-9

Dai, Y.C. (2012) Polypore diversity in China with an annotated checklist of Chinese polypores. *Mycoscience* 53: 49–80.
https://doi.org/10.1007/s10267-011-0134-3

Dai, Y.C. & Yuan, H.S. (2007) Type studies on polypores described by G. Y. Zheng and Z. S. Bi. from southern China. *Sydowia* 59: 25–31.
https://doi.org/10.1002/yea.1500

Dong, J.H., Li, Q., Yuan, Q., Luo, Y.X., Zhang, X.C., Dai, Y.F., Zhou, Q., Liu, X.F., Deng, Y.L., Zhou, H.M., Muhammad, A. & Zhao, C.L. (2024) Species diversity, taxonomy, molecular systematics and divergence time of wood-inhabiting fungi in Yunnan-Guizhou Plateau, Asia. *Mycosphere* 15: 1110–1293.
https://doi.org/10.5943/mycosphere/15/1/10

Fries, E.M. (1874) *Hymenomycetes Europaei.* Upsaliae, E. Berling, Uppsala.

Gray, S.F. (1821) *A natural arrangement of British plants,* vol. 1. Baldwin, Cradock, and Joy, London, 824 pp.

Guan, Q.X., Zhao, T.J. & Zhao, C.L. (2020) Morphological characters and phylogenetic analyses reveal two new species of *Peniophorella* from southern China. *Mycological Progress* 19: 397–404.
https://doi.org/10.1007/s11557-020-01568-6

Hall, T.A. (1999) Bioedit: a user-friendly biological sequence alignment editor and analysis program for windows 95/98/NT. *Nucleic Acids Symposium Series* 41: 95–98.
https://doi.org/10.1021/bk-1999-0734.ch008

Hjortstam, K. & Ryvarden, L. (2009) A checklist of names in *Hyphodontia* sensu stricto-sensu lato and *Schizopora* with new combinations in *Lagarobasidium*, *Lyomyces*, *Kneiffiella*, *Schizopora*, and *Xylodon*. *Synopsis Fungorum* 26: 33–55.

Huang, R.X. & Zhao, C.L. (2020) Three new species of *Phlebia* (Polyporales, Basidiomycota) based on the evidence from morphology and DNA sequence data. *Mycological Progress* 19: 753–767.
https://doi.org/10.1007/s11557-020-01591-7

Kalyaanamoorthy, S., Min, B., Wong, T., von Haeseler, A. & Jermiin, L. (2017) ModelFinder: fast model selection for accurate phylogenetic estimates. *Nature Methods* 14: 587–589.
https://doi.org/10.1038/nmeth.4285

Karsten, P.A. (1882) Rysslands, Finlans och den Skandinaviska halföns Hattsvampar. *Bidrag till Kännedom av Finlands Natur och Folk* 37: 1–257.

Larsson, K.H., Parmasto, E., Fischer, M., Langer, E., Nakasone, K.K. & Redhead, S.A. (2006) Hymenochaetales: a molecular phylogeny for the hymenochaetoid clade. *Mycologia* 98 (6): 926–936.
https://doi.org/10.3852/mycologia.98.6.926

Langer, E. (1994) Die gattung *Hyphodontia* john eriksson. *Bibliotheca Mycologica* 154: 1–298.

Liu, S., Chen, Y.Y., Sun, Y.F., He, X.L., Song, C.G., Si, J., Liu, D.M., Gates, G. & Cui, B.K. (2023) Systematic classification and phylogenetic relationships of the brown-rot fungi within the Polyporales. *Fungal Diversity* 118: 1–94. https://doi.org/10.1007/s13225-022-00511-2

Liu, Z.B. & Yuan, Y. (2020) *Luteoporia citriniporia* sp. nov. (Polyporales, Basidiomycota), evidenced by morphological characters and phylogenetic analysis. *Phytotaxa* 461: 31–39. https://doi.org/10.11646/phytotaxa.461.1.4

Lloyd, C.G. (1925) Mycological notes 75. *Mycological Writings* 7: 1349–1364

Luo, K.Y., Chen, Z.Y. & Zhao, C.L. (2022) Phylogenetic and taxonomic analyses of three new wood-inhabiting fungi of *Xylodon* (Basidiomycota) in a forest ecological system. *Journal of Fungi* 8: 405. https://doi.org/10.3390/jof8040405

Ma, X. & Zhao, C.L. (2019) *Crepatura ellipsospora* gen. et sp. nov. in Phanerochaetaceae (Polyporales, Basidiomycota) bearing a tuberculate hymenial surface. *Mycological Progress* 18: 785–793. https://doi.org/10.1007/s11557-019-01488-0

Mao, W.L., Wu, Y.D., Liu, H.G., Yuan, Y. & Dai, Y.C. (2023) A contribution to *Porogramme* (Polyporaceae, Agaricomycetes) and related genera. *IMA Fungus* 14: 5. https://doi.org/10.1186/s43008-023-00110-z

Petersen, J.H. (1996) *Farvekort. The danish mycological society´s colour-chart.* Foreningen til Svampekundskabens Fremme: Greve, Italy.

Qu, M.H., Wang, D.Q. & Zhao, C.L. (2022) A phylogenetic and taxonomic study on *Xylodon* (Hymenochaetales): focusing on three new *Xylodon* species from Southern China. *Journal of Fungi* 8: 35. https://doi.org/10.3390/jof8010035

Qu, M.H. & Zhao, C.L. (2022) *Xylodon flocculosus* sp. nov. from Yunnan, China. *Mycotaxon* 137: 189–201. https://doi.org/10.5248/137.189

Riebesehl, J., Yurchenko, E., Nakasone, K.K. & Langer, E. (2019) Phylogenetic and morphological studies in *Xylodon* (Hymenochaetales, Basidiomycota) with the addition of four new species. *MycoKeys* 47: 97–137. https://doi.org/10.3897/mycokeys.47.31130

Ronquist, F. & Huelsenbeck, J.P. (2003) MrBayes 3: bayesian phylogenetic inference under mixed models. *Bioinformatics* 19: 1572–1574. https://doi.org/10.1093/bioinformatics/btg180

Shi, Z.W., Wang, X.W., Zhou, L.W. & Zhao, C.L. (2019) *Xylodon kunmingensis* sp. nov. (Hymenochaetales, Basidiomycota) from southern China. *Mycoscience* 60 (3): 184–188. https://doi.org/10.1016/j.myc.2019.02.002.

Smith, M., Schell, K., Castellano, M., Trappe, M. & Trappe, J. (2013) The enigmatic truffle *Fevansia aurantiaca* is an ectomycorrhizal member of the *Albatrellus* lineage. *Mycorrhiza* 23: 663–668. https://doi.org/10.1007/s00572-013-0502-2

Sun, Y.F., Xing, J.H., He, X.L., Wu, D.M., Song, C.G., Liu, S., Vlasák, J., Gates, G., Gibertoni, T.B. & Cui, B.K. (2022) Species diversity, systematic revision and molecular phylogeny of Ganodermataceae (Polyporales, Basidiomycota) with an emphasis on Chinese collections. *Studies in Mycology* 101: 287–415. https://doi.org/10.3114/sim.2022.101.05

Wang, C.G., Zhao, H., Liu, H.G., Zeng, GY, Yuan, Y. & Dai, Y.C. (2023) A multi-gene phylogeny clarifies species diversity, taxonomy, and divergence times of *Ceriporia* and other related genera in Irpicaceae (Polyporales, Basidiomycota). *Mycosphere* 14 (1): 1665–1729. https://doi.org/10.5943/mycosphere/17/1/9

Wang, C.G., Dai, Y.C., Kout, J., Gates, G.M., Liu, H.G., Yuan, Y. & Vlasák, J. (2024) Multi-gene phylogeny and taxonomy of *Physisporinus* (Polyporales, Basidiomycota). *Mycosphere* 15: 1455–1521. https://doi.org/10.47371/mycosci.2023.09.002

Wang, Y.R., Wu, Y.D., Vlasák J, Yuan, Y. & Dai, Y.C. (2021) Phylogenetic analysis demonstrating four new species in *Megasporoporia* sensu lato (Polyporales, Basidiomycota). *Mycosphere* 12: 1012–1037. https://doi.org/10.5943/mycosphere/12/1/11

Wu, F., Tohtirjap, A., Fan, L.F., Zhou, L.W., Alvarenga, R.L.M., Gibertoni, T.B. & Dai, Y.C. (2021) Global diversity and updated phylogeny of *Auricularia* (Auriculariales, Basidiomycota). *Journal of Fungi* 7: 933. https://doi.org/10.3390/jof7110933

Wu, F., Yuan, Y., Chen, J.J. & He, S.H. (2016) *Luteoporia albomarginata* gen. et sp. nov. (Meruliaceae, Basidiomycota) from tropical China. *Phytotaxa* 263 (1): 31–41. https://doi.org/10.11646/phytotaxa.263.1.3

Wu, F., Zhou, L.W., Vlasák, J. & Dai, Y.C. (2022) Global diversity and systematics of Hymenochaetaceae with poroid hymenophore. *Fungal Diversity* 113: 1–192.
https://doi.org/10.1007/s13225-021-00496-4

Yuan, Y., Bian, L.S., Wu, Y.D., Chen, J.J., Wu, F., Liu, H.G., Zeng, G.Y. & Dai, Y.C. (2023) Species diversity of pathogenic wood-rotting fungi (Agaricomycetes, Basidiomycota) in China. *Mycology* 14: 204–226.
https://doi.org/10.1080/21501203.2023.2238779

Yurchenko, E., Riebesehl, J., Viner, I., Motato-Vásquez, V. & Miettinen, O. (2024) *Xylodon lanatus* complex and other additions to *Xylodon*. *Mycological Progress* 23: 9.
https://doi.org/10.1007/s11557-024-01947-3

Zhang, Q.Y., Liu, H.G., Papp, V., Zhou, M., Dai, Y.C. & Yuan, Y. (2023) New insights into the classification and evolution of *Favolaschia* (Agaricales, Basidiomycota) and its potential distribution, with descriptions of eight new species. *Mycosphere* 14: 777–814.
https://doi.org/10.5943/mycosphere/14/1/10

Zhang, X.C., Li, Y.C., Wang, Y.Y., Xu, Z., Zhao, C.L. & Zhou, H.M. (2024) *Xylodon asiaticus* (Hymenochaetales, Basidiomycota), a new species of corticioid fungus from southern China. *Phytotaxa* 634 (1): 1–15.
https://doi.org/10.11646/phytotaxa.634.1.1

Zhao, C.L., Cui, B.K. & Dai, Y.C. (2014) Morphological and molecular identification of two new species of *Hyphodontia* (Schizoporaceae, Hymenochaetales) from southern China. *Cryptogamie Mycologie* 35: 87–97.
https://doi.org/10.7872/crym.v35.iss1.2014.87

Zhao, C.L., Qu, M.H., Huang, R.X. & Karunarathna, S. (2023a) Multi-gene phylogeny and taxonomy of the wood-rotting fungal genus *Phlebia* sensu lato (Polyporales, Basidiomycota). *Journal of Fungi* 9: 320.
https://doi.org/10.3390/jof9030320

Zhao, C.L., Wu, F. & Dai, Y.C. (2016) *Leifiporia rhizomorpha* gen. et sp. nov. and *L. eucalypti* comb. nov. in Polyporaceae (Basidiomycota). *Mycological Progress* 15: 799–809.
https://doi.org/10.1007/s11557-016-1210-z

Zhao, C.L. & Wu, Z.Q. (2017) *Ceriporiopsis kunmingensis* sp. nov. (Polyporales, Basidiomycota) evidenced by morphological characters and phylogenetic analysis. *Mycological Progress* 16: 93–100.
https://doi.org/10.1007/s11557-016-1259-8

Zhao, H., Nie, Y., Zong, T.K., Wang, K.L., M.L., Cui, Y.J., Tohtirjap, A., Chen, J.J., Zhao, CL, Wu, F., Cui, B.K., Yuan, Y., Dai, Y.C. & Liu, X.Y. (2023b) Species diversity, updated classification and divergence times of the phylum Mucoromycota. *Fungal Diversity* 123: 49–157.
https://doi.org/10.1007/s13225-023-00525-4

Zhao, H., Wu, Y.D., Yang, Z.R., Liu, H.G., Wu, F., Dai, Y.C. & Yuan, Y. (2024) Polypore and a comparison with temperate and boreal regions of the Northern Hemisphere. *Forest Ecosystem* 11: 100200.
https://doi.org/10.1016/j.fecs.2024.100200

Zhao, Y.N., He, S.H., Nakasone, K., Liyanage, W., Chen, C.C., Liu, S.L., Ma, H.X. & Huang, M.R. (2021) Global phylogeny and taxonomy of the wood-decaying fungal genus *Phlebiopsis* (Polyporales, Basidiomycota). *Frontiers in Microbiology* 12: 622460.
https://doi.org/10.3389/fmicb.2021.622460

Zhou, L.W. & Dai, Y.C. (2013) Phylogeny and taxonomy of poroid and lamellate genera in the Auriculariales (Basidiomycota). *Mycologia* 105: 1219–1230.
https://doi.org/10.3852/12-212

Zhou, M., Dai, Y.C., Vlasák, J., Liu, H.G. & Yuan, Y. (2023) Updated systematics of *Trichaptum* s.l. (Hymenochaetales, Basidiomycota). *Mycosphere* 14: 815–917.
https://doi.org/10.5943/mycosphere/14/1/1