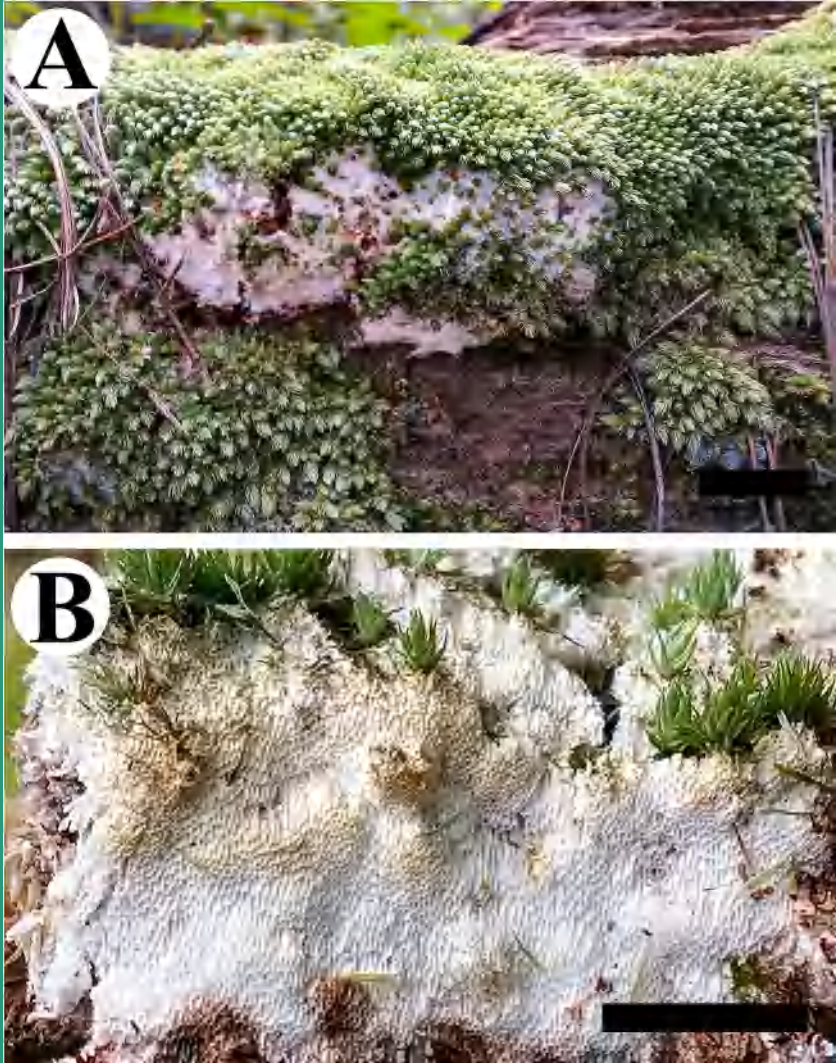


MYCOTAXON

THE INTERNATIONAL JOURNAL OF FUNGAL TAXONOMY & NOMENCLATURE

VOLUME 137 (2)

APRIL–JUNE 2022



Cinereomyces wuliangshanensis sp. nov.

(Luo & Zhao— FIG. 2, p. 215)

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MYCOTAXON

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PUBLICATION DATE FOR VOLUME ONE HUNDRED THIRTY-SEVEN (1)

MYCOTAXON *for* JANUARY–MARCH 2022 (I–XII + 1–172)

was issued on April 28, 2022

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- Anapleurothecium leptospermi* (J.A. Cooper) J.S. Monteiro & R.F. Castañeda
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CORRIGENDA

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- p. 21, line 19 FOR: ADDITIONAL EXAMINATIONS ... *Phaeocollybia* P.
READ: ADDITIONAL EXAMINATIONS ... *P. spadicea*

CORRIGENDA FOR MYCOTAXON 137(2)

Cited below is an omission present in files submitted for PDF conversion in the current issue but not detected by the authors until after the paper had gone to press.

- p. 311, line 23 AFTER THE LAST SENTENCE ADD: *Platismatia* is not closely related with the three other genera included in this study (Divakar et al. 2017).

REVIEWERS — VOLUME ONE HUNDRED THIRTY-SEVEN (2)

The Editors express their appreciation to the following individuals who have, prior to acceptance for publication, reviewed one or more of the papers prepared for this issue.

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FROM THE EDITOR-IN-CHIEF

MYCOTAXON STYLE NUTS AND BOLTS—As this issue goes to press, we are in the process of editing a new set of instructions and manuscript templates to assist authors. In so doing, the supposedly helpful styles formatting of the previous MYCOTAXON template will be eliminated. This past year, although it became obvious that several authors had carefully prepared manuscripts using those styles, their texts arrived at the editorial desk looking nothing like what the authors had intended. There seems to be a growing incompatibility among different computer operating systems and word processing applications that is causing problems. (The fact that one manuscript left Nomenclature Editor Pennycook's computer in perfect Times New Roman but arrived on Editor-in-Chief Norvell's computer displaying several sections written entirely in the Greek alphabet alerted us that there was trouble brewing between Shaun's Times New Roman font family on his PC and Lorelei's Times font family on her Mac.)

Therefore, until we post the 2022 author guides on our MYCOTAXON website, we urge everyone to refer to the sample manuscript or a recent MYCOTAXON publication for formatting suggestions. Use the current blank templates (all of which are sized for the MYCOTAXON-size page) for all the required body-, legend-, and table-text files, but do not apply any built-in 'styles' or introduce your own author-defined character or paragraph styles to your document. Use instead the paragraph formatting menu built into your word-processing application. We hope to have the new guidelines available shortly!

FONT-FAMILY REMINDER—Remember that the only font families permitted in a Mycotaxon manuscript are the serif **TIMES** and san-serif **Arial** families. Authors should begin any manuscripts intended for MYCOTAXON using only those fonts to prevent the sudden and highly dismaying resurrection of an 'alien' font at press time.

NO INTERVENING SPACE IN °C—AN EDITORIAL LABOR-SAVING DEVICE! For several years, we have advised inserting a space between the degree symbol (°) and the temperature abbreviation ('C' or 'F'). Given the number of times scientific papers refer to temperature, it does not seem to make much sense to devote so much room to the lowly space. We feel that the degree symbol is analogous to the percent sign and that neither should be separated from its corresponding abbreviation. During editorial processing, the separate parts

frequently fall on separate lines, requiring valuable editorial time to reunite. Henceforth, we ask all of you to join our Two-Elements-Together-Movement: 20°C and 100%.

The information above might not be of high scientific interest to readers, but your Editor-in-Chief thanks you!

The 2022 April–June MYCOTAXON offers 21 contributions by 89 authors (representing 17 countries) as revised by 38 expert reviewers and the editors.

With 13 titles, the NEW TAXA section proposes TWO new genera (*Andomyces* from Thailand & *Vesiculophora* from Brazil) and 15 species new to science representing *Adustochaete*, *Cinereomyces*, *Corynespora*, *Ellisemia*, *Gangliostilbe*, *Xylodon*, and *Zasmidium* from CHINA; *Anapleurothecium*, *Podosporium*, *Vesiculophora* from BRAZIL; *Andomyces* from THAILAND; *Chaetocapnodium* from MEXICO; *Erysiphe* from IRAN; and *Nephromopsis* and *Passalora* from INDIA. We also offer one new combination in *Anapleurothecium* from Brazil.

The NEW RANGES/HOSTS section contains six titles. New species range extensions are reported for [ascomycetes] *Elaphomyces* for TURKEY; [basidiomycetes] *Anthracoidea* for Russia and *Lactocollybia* for PAKISTAN & ASIA; [myxomycetes] *Diderma*, *Lamproderma*, *Lepidoderma*, *Meriderma*, and *Physarum* for the French and Spanish PYRENEES and *Fuligo* & *Stemonitis* for RUSSIA; AND [zygomycetes] *Coemansia* for BRAZIL & SOUTH AMERICA.

MYCOTAXON 137(2) also provides identification keys to species in all cetrarioid lichen genera (*Cetraria*, *Melanelia*, *Nephromopsis*, *Platismatia*) and species in India as well as to species in *Adustochaete*, *Anapleurothecium*, *Gangliostilbe*, and *Coemansia*. Papers providing conclusions supported by sequence analyses cover five new species representing *Adustochaete*, *Chaetocapnodium*, *Cinereomyces*, *Erysiphe* and *Xylodon* and one range extension in *Lactocollybia*.

We also pleased to announce the posting on our MYCOBIOTA website of two new annotated species lists, which cover 1871 Indian cercosporoid fungi in INDIA and 1619 basidiomycetes collected from Grosseto Province in ITALY. Our issue concludes with book reviews of THE HIDDEN KINGDOM OF FUNGI (Seifert 2022) and THE BOLETES OF CHINA: TYLOPILUS S.L. (Chun & Yang 2021).

Warm regards,

Lorelei L. Norvell (*Editor-in-Chief*)

14 July 2022

2022 MYCOTAXON SUBMISSION PROCEDURE

Prospective MYCOTAXON authors should download the MYCOTAXON 2022 guide, review & submission forms, and MYCOTAXON sample manuscript by clicking the ‘file download page’ link on our INSTRUCTIONS TO AUTHORS page before preparing their manuscript. This page briefly summarizes our ‘4-step’ submission process.

1—PEER REVIEW: Authors first contact peer reviewers (two for journal papers; three for mycobiota/fungae) before sending them formatted text & illustration files and the appropriate 2022 MYCOTAXON journal or mycota reviewer comment form. Experts return revisions & comments to BOTH the *Editor-in-Chief* <editor@mycotaxon.com> and authors. ALL co-authors MUST correct and *proof-read* their files before submitting them to the *Nomenclature Editor*.

2—NOMENCLATURE REVIEW: Authors email all **ERROR-FREE** text, tables, legends, and graphics **in separate files** to the *Nomenclature Editor* <PennycookS@LandcareResearch.co.nz>. Place **first author surname + genus + ‘MYCOTAXON’** on the subject line, and (required) attach a completed SUBMISSION FORM. The Nomenclature Editor will (i) immediately assign the accession number and (ii) after a few weeks return his notes and suggested revisions to the author(s) and *Editor-in-Chief*.

3—FINAL SUBMISSION: All coauthors thoroughly revise and proof-read files to prepare error-free text and images ready for immediate publication. Poorly formatted copy will be rejected or returned for revision. E-mail the final manuscript to the *Editor-in-Chief* <editor@mycotaxon.com>, adding the **accession number** to the message and **all** files, which include a (i) revised 2022 submission form, all (ii) text files and (iii) jpg images, and (iv) FN, IF, or MB identifier verifications for each new name or typification. The *Editor-in-Chief* acknowledges submissions within two weeks of final submission but requests authors to wait at least 14 days before sending a follow-up query (without attachments).

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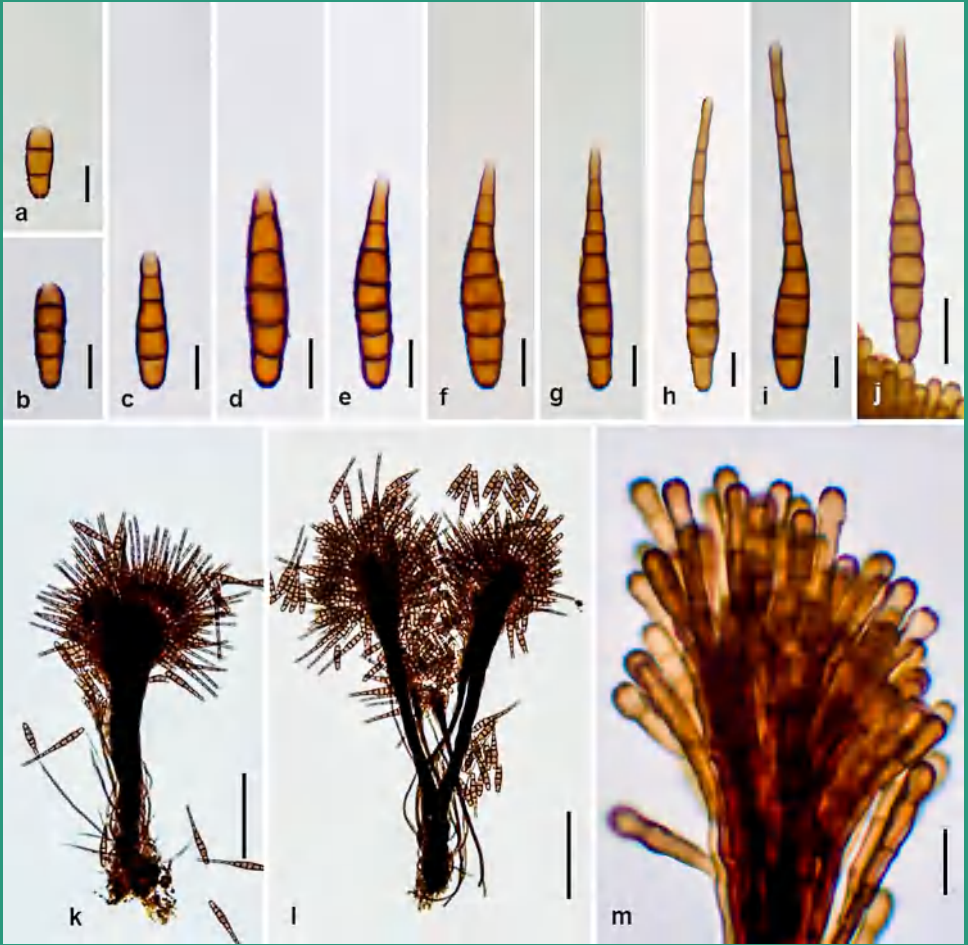
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Podosporium simile sp. nov.
(Monteiro & al.— FIG. 3, p. 234)

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Xylodon flocculosus sp. nov. from Yunnan, China

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ABSTRACT — A new corticioid fungal species, *Xylodon flocculosus*, is described from China based on morphological and ITS+LSU sequence analyses.

KEY WORDS — Honghe county, *Hymenochaetales*, *Schizoporaceae*, taxonomy, wood-rotting fungi

Introduction

The corticioid genus *Xylodon* (Pers.) Gray, with *X. quercinus* (Pers.) Gray as the type, is widespread. Its species are primarily wood decomposers causing white rot of both angiosperms and gymnosperms (Eriksson & Ryvarden 1976, Yurchenko & Wu 2014), although a few *Xylodon* taxa have also been collected on brown rotten spruce stumps, palms or palm tree inflorescences, bamboo, and ferns (Burdall & al. 1981, Langer 1994, Nordén & al. 1999, Kotiranta & Saarenoksa 2000, Boidin & Gilles 2003, Hjortstam & al. 2005, Xiong & al. 2010, Jo & al. 2019). The genus is characterized by resupinate basidiomata with hymenophores that are smooth, tuberculate,

grandinioid, odontoid, coralloid, irpicoid or poroid; a monomitic hyphal system with clamp connections on generative hyphae; cystidia that are bladder-like, bottle-shaped, and capitate to subulate; suburniform basidia; and globose to ellipsoid to cylindrical basidiospores (Gray 1821, Bernicchia & Gorjón 2010). Index Fungorum (<http://www.indexfungorum.org>) lists 192 specific and infraspecific names in *Xylodon*, but currently accepted number of species in the genus is about 90 (Wu 1990, 2000, 2001, 2006; Xiong & al. 2009, 2010; Dai 2011, 2012; Lee & Langer 2012; Yurchenko & al. 2013; Yurchenko & Wu 2014; Zhao & al. 2014; Chen & al. 2016, 2018; Kan & al. 2017a,b; Riebesehl & Langer 2017; Wang & Chen 2017; Shi & al. 2019; Ma & Zhao 2021). About 22 *Xylodon* species have been found and described in China (Wang & Chen 2017, Shi & al. 2019, Ma & Zhao 2021, Wang & al. 2021).

Yurchenko & Wu (2014) placed *Xylodon* in the *Xylodon-Schizopora-Palifer* clade based on nuclear DNA sequence studies of *Hyphodontia* s.l. In their studies based on morphological and molecular analyses Riebesehl & Langer (2017) proposed 16 new *Xylodon* combinations. Riebesehl & al. (2019), who accept 77 species in the genus, synonymised *Palifer* Stalpers & P.K. Buchanan and *Odontopsis* Hjortstam & Ryvarden with *Xylodon*.

We encountered an undescribed taxon during our research on corticioid fungi in southern China. Morphological comparisons and internal transcribed spacer (ITS) and large subunit nuclear ribosomal RNA gene (nLSU) sequence analyses place the fungus in *Xylodon*. The taxon is proposed here as *Xylodon flocculosus*.

Materials & methods

The studied specimens have been deposited at the herbarium of Southwest Forestry University, Kunming, Yunnan Province, P.R. China (SWFC). 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 non-amyloid 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 = number of spores measured/number of specimens.

CTAB rapid plant genome extraction kit-DN14 (Aidlab Biotechnologies Co., Ltd.) was used to obtain genomic DNA from dried specimens, according to the manufacturer's instructions. The ITS region was amplified with primer pairs ITS5

TABLE 1. *Hastodontia*, *Lyomyces*, and *Xylodon* species and sequences used in the phylogenetic analyses.

SPECIES	SAMPLE	GENBANK ACCESSION NO.		REFERENCE
		ITS	LSU	
<i>H. halonata</i>	Mexico	MK575207	MK598738	Yurchenko & al. 2020
<i>H. hastata</i>	KHL14646	MH638232	MH638232	Viner & al. 2018
<i>L. allantosporus</i>	FR-0249548	KY800397	KY795963	Yurchenko & al. 2017
<i>L. mascarensis</i>	KAS-GEL 4833	KY800399	KY795964	Yurchenko & al. 2017
<i>L. organensis</i>	MSK 7247	KY800403	KY795967	Yurchenko & al. 2017
<i>L. orientalis</i>	GEL 3400	DQ340326	DQ340353	Yurchenko & al. 2017
<i>X. apacheriensis</i>	Wu 0910-58	KX857797	KX857822	Chen & al. 2017
<i>X. asper</i>	GEL 3257	EU583424	—	Yurchenko & al. 2020
<i>X. astrocystidiatus</i>	Wu 9211-71	JN129972	JN129973	Yurchenko & Wu 2014
<i>X. australis</i>	CANB869100	MT158715	MT158751	Fernández-López & al. 2020
<i>X. borealis</i>	Spirin 9416	MH317760	MH638259	Viner & al. 2018
<i>X. brevisetus</i>	KHL 12386	DQ873612	DQ873612	Larsson & al. 2006
<i>X. bubalinus</i>	Cui 12888	NR_154097	—	Wang & Chen 2017
<i>X. chinensis</i>	Wu 1407-105	KX857804	KX857811	Chen & al. 2017
<i>X. cystidiatus</i>	FR-0249200	MH880195	MH884896	Riebesehl & al. 2019
<i>X. detriticus</i>	Zibarová 16.05.17	MH320794	—	Viner & al. 2018
<i>X. exilis</i>	MSK-F 7381	MH880196	MH884897	Riebesehl & al. 2019
<i>X. filicinus</i>	FR-0249797	MH880201	MH884901	Riebesehl & al. 2019
<i>X. flocculosus</i>	CLZhao 4544	MW980775	—	Present study
	CLZhao 18342 [T]	MW980776	MW980779	Present study
	CLZhao 18379	MW980777	MW980780	Present study
	CLZhao 18394	MW980778	MW980781	Present study
<i>X. follis</i>	FR-0249814	MH880204	MH884902	Riebesehl & al. 2019
<i>X. hastifer</i>	Ryvarden 19767	KY081801	—	Riebesehl & Langer 2017
<i>X. heterocystidiatus</i>	Wu 9209-27	JX175045	KX857821	Chen & al. 2017
<i>X. hypodontinus</i>	LIP GG-MAR15-127	MH880208	MH884906	Riebesehl & al. 2019
<i>X. kunningensis</i>	CLZhao 755	MK404530	—	Shi & al. 2019
<i>X. lenis</i>	Wu890714-3	KY081802	—	Riebesehl & Langer 2017
<i>X. mollis</i>	Wu 0808-32	JX175043	KX857820	Chen & al. 2017

SPECIES	SAMPLE	GENBANK ACCESSION NO.		REFERENCE
		ITS	LSU	
<i>X. mollissimus</i>	Yuan 4391	KY007518	—	Kan & al. 2017b
<i>X. nesporii</i>	MA:Fungi:79920	MT158717	MT158753	Fernández-López & al. 2020
<i>X. niemelaei</i>	Wu 1010-62	KX857799	KX857817	Chen & al. 2017
<i>X. nongravis</i>	GC 1412-22	KX857801	KX857818	Chen & al. 2017
<i>X. nothofagi</i>	PDD: 91630	GQ411524	—	Fukami & al. 2010
<i>X. ovisporus</i>	SFC20180822-22	MK992859	—	Lupala & al. 2019
<i>X. paradoxus</i>	KAS-JR06	MH880219	—	Riebesehl & al. 2019
<i>X. pseudotropicus</i>	Dai 10768	NR_154066	—	Zhao & al. 2014
<i>X. quercinus</i>	MA:Fungi:84446	MT158719	MT158755	Fernández-López & al. 2020
<i>X. raduloides</i>	KAS-JR26	MH880225	MH884910	Riebesehl & al. 2019
<i>X. reticulatus</i>	GC 1512-1	KX857808	KX857813	Chen & al. 2017
<i>X. rhizomorphus</i>	Dai 12354	KF917544	—	Zhao & al. 2014
<i>X. rimosissimus</i>	Ryberg 021031	DQ873627	—	Larsson & al. 2006
<i>X. serpentiformis</i>	TUB-FO 40688	MH880229	—	Riebesehl & al. 2019
<i>X. spathulatus</i>	MSK-F 12931	MH884914	MH880231	Riebesehl & al. 2019
<i>X. subclavatus</i>	TUB-FO 42167	MH880232	—	Riebesehl & al. 2019
<i>X. subflaviporus</i>	Wu 0809-76	KX857803	KX857815	Chen & al. 2018
<i>X. subtropicus</i>	Wu 9806-105	KX857807	KX857809	Chen & al. 2017
<i>X. verecundus</i>	KHL 12261	DQ873642	—	Larsson & al. 2006

and ITS4 (White & al. 1990), and the nLSU region was amplified with primer pairs LR0R and LR7 (<http://lutzonilab.org/nuclear-ribosomal-dna>). The ITS PCR protocol was: initial denaturation at 95 °C for 3 min; then 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 nLSU PCR protocol was: initial denaturation at 94 °C for 1 min; then 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 directly sequenced at Kunming Tsingke Biological Technology Limited Company. All newly generated sequences were deposited at GenBank (TABLE 1).

Sequencher 4.6 (<https://www.genecodes.com>) was used to edit the DNA sequence. Sequences were aligned using the “G-INS-I” strategy in MAFFT 7 (<https://mafft.cbrc.jp/alignment/server/>) and manually adjusted in BioEdit (Hall 1999). The sequence alignment was deposited in TreeBase (submission ID 28085). The outgroup *Hastodontia halonata* (J. Erikss. & Hjortstam) Hjortstam & Ryvarde

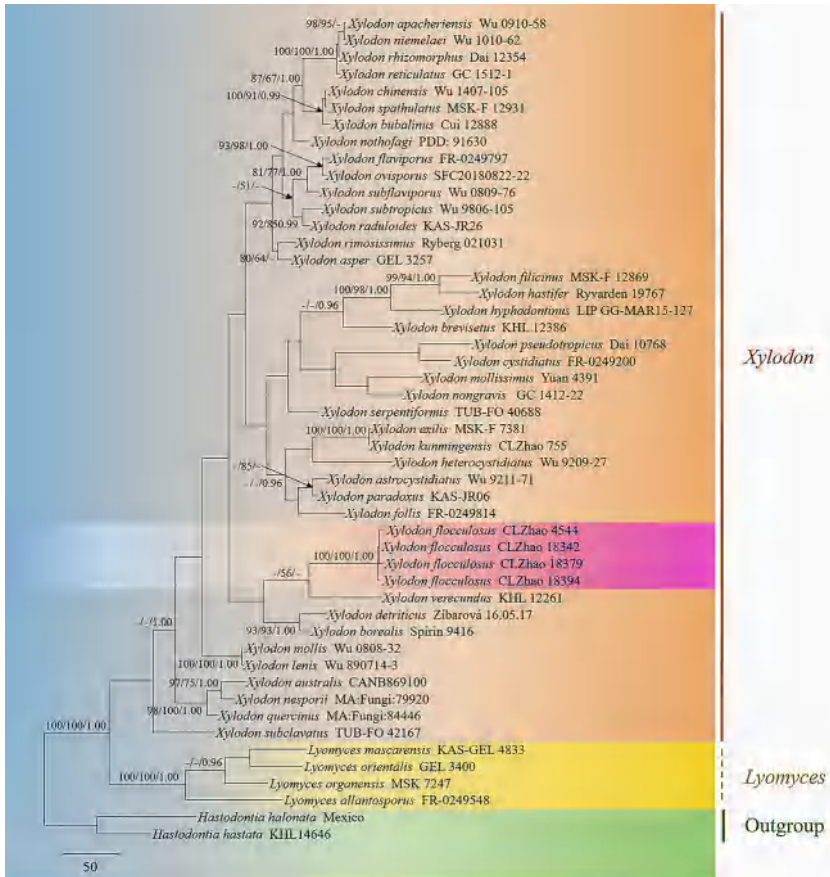


FIG. 1. Maximum parsimony strict consensus tree illustrating the phylogeny of *Xylodon flocculosus* and related species in the residual polyporoid clade, based on ITS+nLSU sequences. Branches are labeled with maximum likelihood bootstrap >70%, parsimony bootstrap proportions >50% and Bayesian posterior probabilities >0.95.

and *H. hastata* (Litsch.) Hjortstam & Ryvarden was used to root the tree in the combined analyses following Shi & al. (2019) (FIG. 1).

Maximum parsimony (MP) analysis was applied to the combined dataset sequences. Approaches to phylogenetic analysis followed Zhao & Wu (2017), and the tree was generated in PAUP* 4.0b10 (Swofford 2002). All characters were equally weighted, and gaps were treated as missing data. Trees were inferred using the heuristic search option with TBR branch swapping and 1000 random sequence additions. Max-trees were set to 5000, branches of zero length were collapsed, and all parsimonious trees were saved. Clade robustness was assessed using a bootstrap

(BT) analysis with 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 MP tree generated. Sequences were also analyzed using Maximum Likelihood (ML) with RAxML-HPC2 through the Cipres Science Gateway (www.phylo.org, Miller & al. 2009). Branch support (BS) for ML analysis was determined by 1000 bootstrap replicate.

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 MrBayes 3.1.2 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 1.4 million generations, with trees sampled every 100 generations. The first one-fourth generations were discarded as burn-in. A majority rule consensus tree was calculated for all remaining trees. Branches were considered as significantly supported if they received a maximum likelihood bootstrap value (BS) >70%, maximum parsimony bootstrap value (BT) >50%, or Bayesian posterior probabilities (BPP) >0.95.

Molecular phylogeny

The combined ITS+nLSU dataset included sequences from 49 fungal specimens representing 46 taxa. The dataset had an aligned length of 2617 characters, of which 960 characters were constant, 208 parsimony-uninformative and 428 parsimony-informative. MP analysis yielded 1 equally parsimonious tree (TL = 2617, CI = 0.380, HI = 0.620, RI = 0.481, RC = 0.183). The best-fit model for ITS+nLSU alignment estimated and applied in the BI was GTR+I+G, lset nst = 6, rates = invgamma; prset statefreqpr = dirichlet (1,1,1,1). BI analysis produced a similar topology with an average standard deviation of split frequencies = 0.009310.

The phylogenetic tree (FIG. 1) inferred from ITS+nLSU sequences includes 46 *Xylodon* species. *Xylodon flocculosus* formed a well-supported distinct lineage and was sister to *X. verecundus* (G. Cunn.) Yurchenko & Riebesehl.

Taxonomy

Xylodon flocculosus C.L. Zhao, sp. nov.

FIGS 2, 3

MB 840651

Differs from *Xylodon verecundus* by its grandinoid hymenial surface and strongly encrusted cystidia.

TYPE: China. Yunnan Province: Honghe, Pingbian County, Daweishan National Nature Reserve, on a fallen angiosperm branch, 3 Aug 2019, CLZhao 18342 (Holotype, SWFC 0018342; GenBank MW980776, MW980779).

ETYMOLOGY: *flocculosus* (Lat.) refers to the flocculent hymenophore of the type specimen.

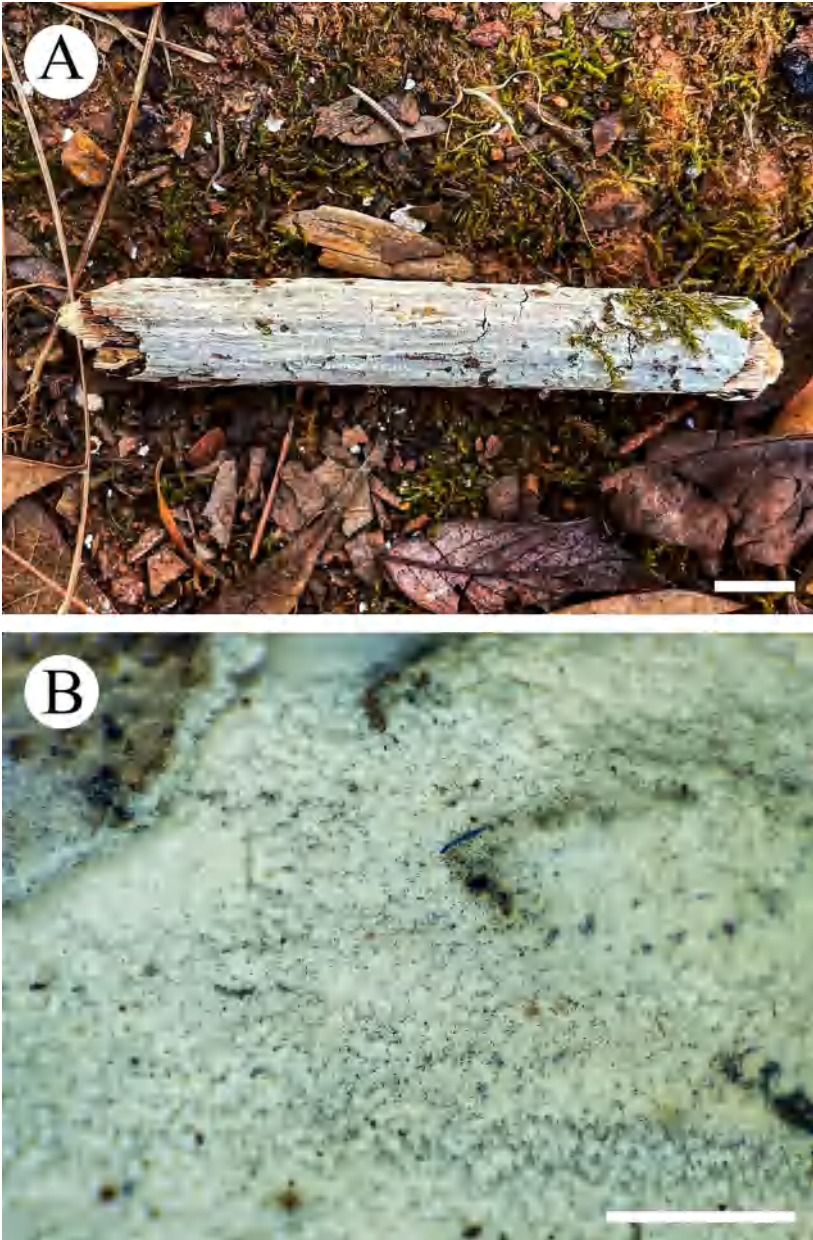


FIG. 2. *Xylodon flocculosus* (holotype, SWFC 0018342).
Basidiomata. Scale bars: A = 1 cm; B = 1 mm.

BASIDIOMATA annual, resupinate, soft, cottony, without odor or taste when fresh, becoming flocculent on drying, $\leq 10 \times 3$ cm (length \times breadth), ≤ 200 μ m thick. Hymenial surface grandinoid, aculei 15–20 per mm, 50–100 μ m long, white to pale buff when fresh, turn to buff upon drying. Margin sterile, white to pale buff, ≤ 1 mm wide.

HYPHAL STRUCTURE monomitic; generative hyphae clamped, hyaline, more or less interwoven, thick-walled, branched, 2–3 μ m in diameter; IKI–, CB–, tissues unchanged in KOH.

HYMENIUM Cystidia numerous in the aculei, strongly encrusted at the obtuse apex, 22–55 \times 2.9–5.6 μ m; cystidioles absent; basidia barrel-shaped, with four sterigmata, basally clamped, slightly constricted in the middle to somewhat sinuous, 11–20 \times 3.3–4.8 μ m; basidioles dominant, in shape similar to basidia, but slightly smaller.

BASIDIOSPORES ellipsoid, hyaline, thick-walled, smooth, IKI–, CB–, (4–)4.2–5.7 (–6) \times 3.1–4.4(–4.6) μ m, L = 4.92 μ m, W = 3.57 μ m, Q = 1.35–1.42 (n = 120/4).

TYPE OF ROT: white rot.

ADDITIONAL SPECIMENS EXAMINED: CHINA. YUNNAN PROVINCE. Puer: JINGDONG COUNTY, Wuliangshan National Nature Reserve, on fallen angiosperm branch, 6 Oct 2017, CLZhao 4544 (SWFC 004544; GenBank MW980775). Honghe: PINGBIAN COUNTY, Daweishan National Nature Reserve, on fallen angiosperm branch, 3 Aug 2019, CLZhao 18379 (SWFC 018379; GenBank MW980777, MW980780) CLZhao 18394 (SWFC 018394; GenBank MW980778, MW980781).

Discussion

Earlier morphological and molecular studies (Yurchenko & Wu 2014, Riebesehl & al. 2019) strongly supported *Xylodon* as an independent genus in the *Xylodon-Schizopora-Palifer* clade. The newly described *X. flocculosus* is nested in *Xylodon* (FIG. 1) based on the combined ITS+nLSU sequence data (BS = 100%, BT = 100%, BPP = 1). The usefulness of the ITS region alone to delimit species in *Xylodon* is approaching its phylogenetic limits. Riebesehl & al. (2019) called for additional genetic markers in *Xylodon*. The present study, based on ITS and nLSU sequences, supports *X. flocculosus* within a distinct, well-supported monophyletic lineage. In ITS phylogenetic tree, *Xylodon flocculosus* was sister to *X. verecundus*. However, morphologically *X. verecundus* differs from *X. flocculosus* in its alutaceous hymenial surface, capitate cystidia, and narrower basidiospores (5 \times 3 μ m; Hjortstam & Ryvar den 1997).

Morphologically, *Xylodon flocculosus* resembles *X. australis* (Berk.) Hjortstam & Ryvar den, *X. rimosissimus* (Peck) Hjortstam & Ryvar den,

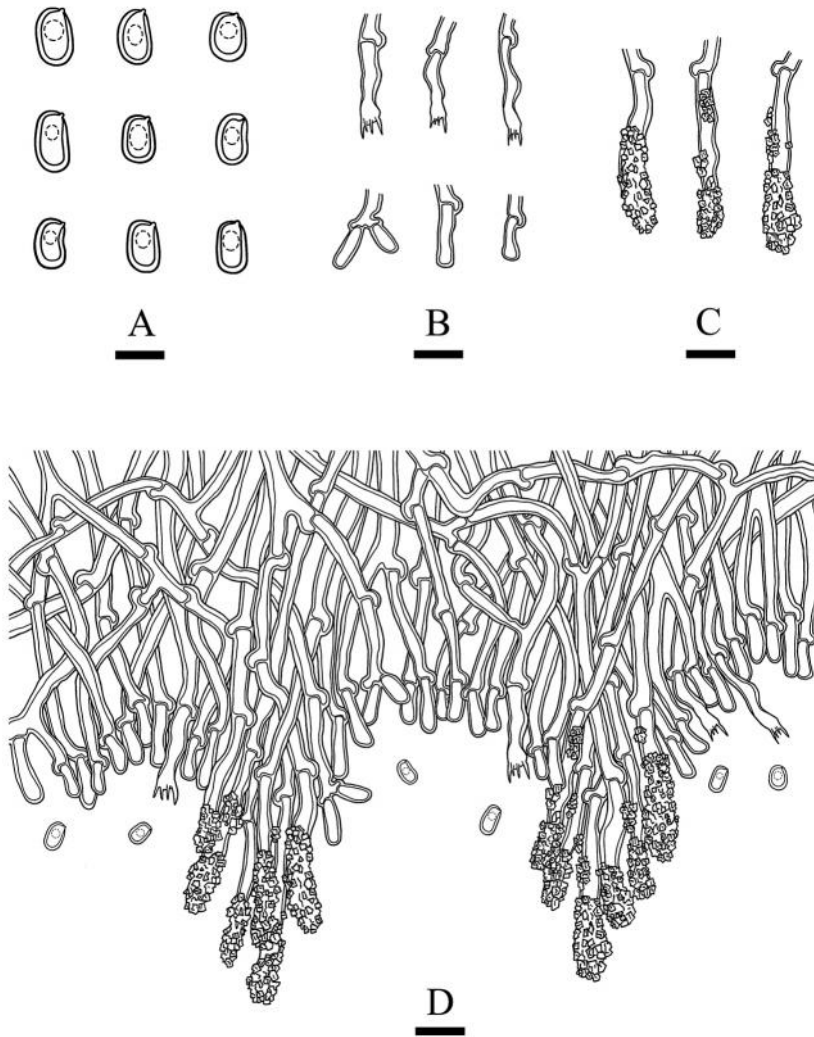


FIG. 3. *Xylodon flocculosus* (holotype, SWFC 0018342).
A. Basidiospores; B. Basidia and basidioles; C. Encrusted cystidia;
D. Section of hymenium. Scale bars: A = 5 μm ; B–D = 10 μm .

and *X. tenellus* Hjortstam & Ryvarden in sharing a grandinoid hymenial surface. *Xylodon australis* differs in having hymenophore cracked into small polygons and larger basidiospores (6–7.5 \times 4–4.5 μm , Riebesehl & al. 2019);

X. rimosissimus is distinguished by its cream to beige, slightly orange hymenial surface and capitate cystidia (Langer 1994); and *X. tenellus* differs in its smaller globose basidiospores ($4\text{--}4.2 \times 4.2\text{--}4.5 \mu\text{m}$, Hjortstam & Ryvarden 2007).

Xylodon fimbriatus (Sheng H. Wu) Hjortstam & Ryvarden, nom. illeg. [= *Lyomyces fimbriatus* (Sheng H. Wu) Riebesehl & Yurchenko (Yurchenko & al. 2020)], *X. papillosus* (Fr.) Riebesehl & al., and *X. subflaviporus* C.C. Chen & Sheng H. Wu also resemble *X. flocculosus* in having strongly encrusted cystidia. However, *X. fimbriatus* is distinguished by its limy-white hymenophore and capitate cystidia (Langer 1994), *X. papillosus* by its smooth or finely odontoid hymenophore (Rattan 1977), and *X. subflaviporus* by its poroid hymenophore with cream to straw-colored hymenial surface and apically encrusted cystidia (Chen & al. 2018).

Xylodon archeri (Berk.) Kuntze, *X. lenis* Hjortstam & Ryvarden, and *X. tuberculatus* (Kotir. & Saaren.) Hjortstam & Ryvarden are also reported with ellipsoid basidiospores. *Xylodon archeri* differs in its coralloid basidiomata with cinnamon-buff or buckthorn brown hymenial surface and presence of the capitate cystidia (Nakasone 2012), *X. lenis* in its pinkish-tinted ochraceous hymenophore and moniliform cystidia (Langer 1994), and *X. tuberculatus* in its smooth to papillose or tuberculate hymenophore and presence of gloeocystidia (Kotiranta & Saarenoksa 2000).

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Literature cited

- Bernicchia A, Gorjón SP. 2010. *Fungi Europaei* 12: *Corticaceae* I. Edizioni Candusso, Lomazzo. 1007 p.
- Boidin J, Gilles G. 2003. *Homobasidiomycètes Aphylophorales* non porés à basides dominantes à 2 (3) stérigmates. Bulletin Trimestriel de la Société Mycologique de France 119: 1–17.
- Burdsall HH, Nakasone KK, Freeman GW. 1981. New species of *Gloeocystidiellum* (*Corticaceae*) from the southeastern United States. Systematic Botany 6: 422–434. <https://doi.org/10.2307/2418453>

- Chen JJ, Zhou LW, Ji XH, Zhao CL. 2016. *Hyphodontia dimitica* and *H. subfebulata* 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>
- Chen CC, Wu SH, Chen CY. 2017. Three new species of *Hyphodontia* s.l. (*Basidiomycota*) with poroid or raduloid hymenophore. *Mycological Progress* 16: 553–564. <https://doi.org/10.1007/s11557-017-1286-0>
- Chen CC, Wu SH, Chen CY. 2018. *Xylodon subflaviporus* sp. nov. (*Hymenochaetales*, *Basidiomycota*) from East Asia. *Mycoscience* 59: 343–352. <https://doi.org/10.1016/j.myc.2017.12.004>
- Dai YC. 2011. A revised checklist of corticioid and hydroid fungi in China for 2010. *Mycoscience* 52: 69–79. <https://doi.org/10.1007/S10267-010-0068-1>
- Dai YC. 2012. Polypore diversity in China with an annotated checklist of Chinese polypores. *Mycoscience* 53: 49–80. <http://doi.org/10.1007/s10267-011-0134-3>
- Eriksson J, Ryvar den L. 1976. The *Corticaceae* of North Europe volume 4, *Hyphodermella-Mycoacia*. Fungiflora, Oslo
- Felsenstein J. 1985. Confidence intervals on phylogenetics: an approach using bootstrap. *Evolution* 39: 783–791. <https://doi.org/10.2307/2408678>
- Fernández-López J, Tellería MT, Dueñas M, Laguna-Castro M, Schlep K, Martín MP. 2020. Linking morphological and molecular sources to disentangle the case of *Xylodon australis*. *Scientific Reports* 10(22004): [14 p.]. <https://doi.org/10.1038/s41598-020-78399-8>
- Fukami T, Dickie IA, Wilkie JP, Paulus BC, Park D, Roberts A, Buchanan PK, Allen RB. 2010. Assembly history dictates ecosystem functioning: evidence from wood decomposer communities. *Ecology Letters* 13: 675–648. <https://doi.org/10.1111/j.1461-0248.2010.01465.x>
- Gray SF. 1821. A natural arrangement of British plants. London: Nabu Press.
- Hall TA. 1999. BioEdit: a user-friendly biological sequence alignment editor and analysis program for Windows 95/98/NT. *Nucleic Acids Symposium Series* 41: 95–98.
- Hjortstam K, Ryvar den L. 1997. Corticioid species (*Basidiomycotina*, *Aphyllphorales*) from Colombia collected by Leif Ryvar den. *Mycotaxon* 64: 229–241.
- Hjortstam K, Ryvar den L. 2007. Studies in corticioid fungi from Venezuela III (*Basidiomycotina*, *Aphyllphorales*). *Synopsis Fungorum* 23: 56–107.
- Hjortstam K, Ryvar den L, Iturriaga T. 2005. Studies in corticioid fungi from Venezuela II (*Basidiomycotina*, *Aphyllphorales*). *Synopsis Fungorum* 20: 42–78.
- Jo JW, Kwag YN, Cho SE, Han SK, Han JG, Oh S, Kim CS. 2019. *Xylodon flaviporus*, a newly recorded macrofungi in Dokdo, South Korea. *Korean Journal of Mycology* 47(3): 241–247. <https://doi.org/10.4489/KJM.20190028>
- Kan YH, Gafforov Y, Li T, Zhou LW. 2017a. *Hyphodontia zhixiangii* sp. nov. (*Schizoporaceae*, *Basidiomycota*) from Uzbekistan. *Phytotaxa* 299: 273–279. <https://doi.org/10.11646/phytotaxa.299.2.12>
- Kan YH, Qin WM, Zhou LW. 2017b. *Hyphodontia mollissima* sp. nov. (*Schizoporaceae*, *Hymenochaetales*) from Hainan, southern China. *Mycoscience*. <https://doi.org/10.1016/j.myc.2017.04.003>
- Kotiranta H, Saarenoksa R. 2000. Three new species of *Hyphodontia* (*Corticaceae*). *Annales Botanici Fennici* 37: 255–278.
- Langer E. 1994. Die Gattung *Hyphodontia* John Eriksson. *Bibliotheca Mycologica* 154. 298 p.
- Larsson KH, Parmasto E, Fischer M, Langer E, Nakasone KK, Redhead SA. 2006. *Hymenochaetales*: a molecular phylogeny for the hymenochaetoid clade. *Mycologia* 98: 926–936. <https://doi.org/10.3852/mycologia.98.6.926>

- Lee IS, Langer E. 2012. New records of *Hyphodontia* species from Taiwan. *Nova Hedwigia* 94: 239–244. <https://doi.org/10.1127/0029-5035/2012/0094-0239>
- Lupala AS, Oh S-Y, Park MS, Kim T, Yoo J-S, Seelan JSS, Lim YW. 2019. Co-occurrence patterns of wood-decaying fungi and ants in dead pines of South Korea. *Journal of Asia-Pacific Entomology* 22: 1154–1160. <https://doi.org/10.1016/j.aspen.2019.10.009>
- Ma X, Zhao CL. 2021. *Xylodon bambusinus* and *X. xinpingsensis* spp. nov. (*Hymenochaetales*) from southern China. *Phytotaxa* 511: 231–247. <https://doi.org/10.11646/phytotaxa.511.3.3>
- Miller MA, Holder MT, Vos R, Midford PE, Liebowitz T, Chan L, Hoover P, Warnow T. 2009. The CIPRES Portals. CIPRES. http://www.phylo.org/sub_sections/portal. 2009-08-04. (Archived by WebCite® at <https://www.webcitation.org/5imQlJeQa>).
- Nakasone KK. 2012. Type studies of corticioid *Hymenomyces* (*Basidiomycota*) with aculei—part II. *Czech Mycology* 64: 23–42. <https://doi.org/10.33585/cmy.64104>
- Nordén B, Appelquist T, Lindahl B, Henningsson M. 1999. Cubic rot fungi – corticioid fungi in highly brown rotted spruce stumps. *Mycologia Helvetica* 10: 13–24.
- Nylander JAA. 2004. MrModeltest v2. Program distributed by the author. Evolutionary Biology Centre, Uppsala University, Uppsala.
- Petersen JH. 1996. Farvekort. The Danish Mycological Society's colour-chart. Foreningen til Svampekundskabens Fremme, Greve.
- Rattan SS. 1977. The resupinate *Aphyllophorales* of the northwestern Himalayas. *Bibliotheca Mycologica* 60. 427 p.
- Riebesehl J, Langer E. 2017. *Hyphodontia* s.l. (*Hymenochaetales*, *Basidiomycota*): 35 new combinations and new keys to all 120 current species. *Mycological Progress* 16: 637–666. <https://doi.org/10.1007/s11557-017-1299-8>
- Riebesehl J, Yurchenko E, Nakasone KK, Langer E. 2019. Phylogenetic and morphological studies in *Xylodon* (*Hymenochaetales*, *Basidiomycota*) with the addition of four new species. *MycKeys* 47: 97–137. <https://doi.org/10.3897/mycokeys.47.31130>
- Ronquist F, Huelsenbeck JP. 2003. MrBayes 3: Bayesian phylogenetic inference under mixed models. *Bioinformatics* 19: 1572–1574. <https://doi.org/10.1093/bioinformatics/btg180>
- Shi ZW, Wang XW, Zhou LW, Zhao CL. 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>
- Swofford DL. 2002. PAUP*: phylogenetic analysis using parsimony (*and other methods). Version 4.0b10. Massachusetts: Sinauer Associates.
- Viner I, Spirin V, Zibarová L, Larsson K-H. 2018. Additions to the taxonomy of *Lagarobasidium* and *Xylodon* (*Hymenochaetales*, *Basidiomycota*). *MycKeys* 41: 65–90. <https://doi.org/10.3897/mycokeys.41.28987>
- Wang M, Chen YY. 2017. Phylogeny and taxonomy of the genus *Hyphodontia* (*Hymenochaetales*, *Basidiomycota*) in China. *Phytotaxa* 309: 45–54. <https://doi.org/10.11646/phytotaxa.309.1.4>
- Wang XW, May TW, Liu SL, Zhou LW. 2021. Towards a natural classification of *Hyphodontia* sensu lato and the trait evolution of basidiocarps within *Hymenochaetales* (*Basidiomycota*). *Journal of Fungi* 7(478): [76 p.]. <https://doi.org/10.3390/jof7060478>
- White TJ, Bruns TD, Lee SB, Taylor JW. 1990. Amplification and direct sequencing of fungal ribosomal RNA genes for phylogenetics. 315–322, in: MA Innis & al. (eds). PCR protocols: a guide to methods and applications. Academic Press, New York. <https://doi.org/10.1016/B978-0-12-372180-8.50042-1>
- Wu SH. 1990. The *Corticiaceae* (*Basidiomycetes*) subfamilies *Phlebioideae*, *Phanerochaetoideae* and *Hyphodermoideae* in Taiwan. *Annales Botanici Fennici* 142. 123 p.

- Wu SH. 2000. Studies on *Schizopora flavipora* s.l., with special emphasis on specimens from Taiwan. *Mycotaxon* 76: 51–66.
- Wu SH. 2001. Three new species of *Hyphodontia* with poroid hymenial surface. *Mycologia* 93: 1019–1025. <https://doi.org/10.2307/3761766>
- Wu SH. 2006. *Hyphodontia tubuliformis*, a new species from Taiwan. *Mycotaxon* 95: 185–188.
- Xiong HX, Dai YC, Wu SH. 2009. Three new species of *Hyphodontia* from Taiwan. *Mycological Progress* 8: 165–169. <https://doi.org/10.1007/s11557-009-0587-3>
- Xiong HX, Dai YC, Wu SH. 2010. Two new species of *Hyphodontia* from China. *Mycologia* 102: 918–922. <https://doi.org/10.3852/09-139>
- Yurchenko E, Xiong HX, Wu SH. 2013. Four new species of *Hyphodontia* (*Xylodon* s.s. Hjortstam & Ryvarde, *Basidiomycota*) from Taiwan. *Nova Hedwigia* 96: 545–558. <https://doi.org/10.1127/0029-5035/2013/0092>
- Yurchenko E, Wu SH. 2014. Three new species of *Hyphodontia* with peg-like hyphal aggregations. *Mycological Progress* 13: 533–545. <https://doi.org/10.1007/s11557-013-0935-1>
- Yurchenko E, Riebesehl J, Langer E. 2017. Clarification of *Lyomyces sambuci* complex with the descriptions of four new species. *Mycological Progress* 16: 865–876. <https://doi.org/10.1007/s11557-017-1321-1>
- Yurchenko E, Riebesehl J, Langer E. 2020. *Fasciodontia* gen. nov. (*Hymenochaetales*, *Basidiomycota*) and the taxonomic status of *Deviodontia*. *Mycological Progress* 19: 171–184. <https://doi.org/10.1007/s11557-019-01554-7>
- Zhao CL, Wu ZQ. 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 CL, Cui BK, Dai YC. 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>