

MYCOTAXON

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VOLUME 134 (4)

OCTOBER–DECEMBER 2019



Rhomboidia wuliangshanensis gen. & sp. nov.
(Xu & al.— Fig. 2, p. 657)

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MYCOTAXON

VOLUME ONE HUNDRED THIRTY-FOUR (4) — TABLE OF CONTENTS

134-4: TABLE OF CONTENTS, NOMENCLATRURAL UPDATES, PEERS, EDITORIALS

<i>Reviewers</i>	vi
<i>Nomenclatural novelties & typifications</i>	vii
<i>Corrigenda</i>	viii
<i>From the Editor</i>	ix
<i>2020 submission procedure</i>	xi

RESEARCH ARTICLES

<i>Urocystis cumminsii</i> sp. nov., a smut fungus on <i>Themidaceae</i> from Arizona	KYRYLL G. SAVCHENKO, SYLENA R. HARPER, LORI M. CARRIS, LISA A. CASTLEBURY 591
<i>Leucoagaricus brunneus</i> sp. nov. from Khyber Pakhtunkhwa, Pakistan	ZIA ULLAH, SANA JABEEN, MUHAMMAD FAISAL, HABIB AHMAD, ABDUL NASIR KHALID 601
Dictyostelids from Jilin Province, China 3: new <i>Cavenderia</i> and <i>Dictyostelium</i> records	PU LIU, SHUNHANG ZHANG, ZHUANG LI*, YUE ZOU, XUEPING KANG, YU LI 613
Records of <i>Aureobasidium harposporum</i> , <i>Sarcophoma miribelii</i> , and <i>Stigmina dothideoides</i> from Turkey	MAKBULE ERDOĞDU, MERVE ULUKAPI, ALI IHSAN KARAYEL, ZEKIYE SULUDERE 619
<i>Bactrodesmium pulcherrimum</i> sp. nov. from Ecuador	FERNANDO ESPINOZA, DAYNET SOSA, LIZETTE SERRANO, ADELA QUEVEDO, FREDDY MAGDAMA, MARCOS VERA, SIMÓN PÉREZ-MARTINEZ, ELAINE MALOSSO, RAFAEL F. CASTAÑEDA-RUIZ 627
<i>Dendrographium multiseptatum</i> sp. nov. from China	LI-GUO MA, YUE-LI ZHANG, BO ZHANG, KAI QI, CHANG-SONG LI, JUN-SHAN QI 633
<i>Haematomma pluriseptatum</i> sp. nov. from China	CONGCONG MIAO, RONG TANG, LINLIN DONG, ZHAOJIE REN, ZUNTIAN ZHAO 637
New records of <i>Didymium inconspicuum</i> , <i>D. karstensis</i> , and <i>D. rugulosporum</i> from China	CHAOFENG YUAN, SHU LI, WAN WANG, SHUWEI WEI, QI WANG, YU LI 643

- Rhomboidia wuliangshanensis* gen. & sp. nov.
from southwestern China
TAI-MIN XU, XIANG-FU LIU, YU-HUI CHEN, CHANG-LIN ZHAO 649
- Filsoniana lhasanensis* sp. nov. from Tibet, China
XUE-MEI WEN, HURNISA SHAHIDIN, ABDULLA ABBAS 663
- Sarcopodium flocculentum*, the correct name for *S. macalpinei*
SHAUN R. PENNYCOOK & PAUL M. KIRK) 677
- Pteridicolous ascomycetes from a cloud forest in eastern Mexico
ROSARIO MEDEL-ORTIZ, YAJAIRA BAEZA,
FRANCISCO G. LOREA-HERNÁNDEZ 681
- First sexual morph record of *Sarcopodium vanillae*
NAPALAI CHAIWAN, SAJEWA S.N. MAHARACHCHIKUMBURA,
DHANUSHKA N. WANASINGHE, MINGKWAN DOILOM,
RUVISHIKA JAYAWARDENA, KEVIN D. HYDE 707
- Notes on rust fungi in China 7. *Aecidium caulophylli* life cycle
inferred from phylogenetic evidence and renamed as
Puccinia caulophylli comb. nov. JING-XIN JI, ZHUANG LI,
YU LI, MAKOTO KAKISHIMA 719
- Exserticlava aquatica* sp. nov., a microfungus
from the Brazilian Amazon LUANA TEIXEIRA DO CARMO,
DIOGO CARELI DOS SANTOS, CAROLINA RIBEIRO SILVA,
SHEILA MIRANDA LEÃO FERREIRA, THAMARA ARÃO FELETTI,
LUÍS FERNANDO PASCHOLATI GUSMÃO 731
- MYCOBIOTA (FUNGA) NEW TO THE MYCOTAXON WEBSITE
- Ascomycota* (lichenized and non-lichenized) on *Syagrus coronata*
in the Caatinga biome: new and interesting records
for Brazil and South America (SUMMARY)
MAIARA A.L. DOS SANTOS, NILO G. S. FORTES,
TÁSSIO E. F. SILVA, NADJA S. VITÓRIA 737
- Checklist of Bolivian *Agaricales*. 1:
Species with dark and pink spore prints (SUMMARY)
E. MELGAREJO-ESTRADA, M.E. SUÁREZ,
D. ROCABADO, O. MAILLARD, B.E. LECHNER 739

REVIEWERS — VOLUME ONE HUNDRED THIRTY-FOUR (4)

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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NOMENCLATRURAL NOVELTIES AND TYPIFICATIONS
PROPOSED IN MYCOTAXON 134(4)

- Bactrodesmium pulcherrimum* R.F. Castañeda, F. Espinoza & D. Sosa
[MB 830569], p. 629
- Dendrographium multiseptatum* L.G. Ma & J.S. Qi
[MB 832847], p. 634
- Exserticlava aquatica* L.T. Carmo, C.R. Silva, Careli, S.M. Leão, Feletti
& Gusmão [MB 831391], p. 732
- Filsoniana lhasanensis* X.M. Wen, Shahidin & A. Abbas
[FN 570592], p. 669
- Haematomma pluriseptatum* R. Tang
[MB 830618], p. 638
- Leucoagaricus brunneus* Z. Ullah, Jabeen & Khalid
[MB 827985], p. 603
- Puccinia caulophylli* (Kom.) Jing X. Ji & Kakish.
[MB 830631; epitypified: MBT 386779], p. 726
- Rhomboidia* C.L. Zhao
[MB 833318], p.654
- Rhomboidia wuliangshanensis* C.L. Zhao
[MB 833320], p. 656
- Urocystis cumminsii* Savchenko, Carris & Castl.
[MB 830145], p. 595

CORRIGENDA

VOLUME 134-1

p.174, ACKNOWLEDGMENTS

FOR: The author would like to thank Prof. Dr. Ertuğrul Sesli, Prof. Dr. İbrahim Türkekel, and Dr. Shaun Pennycook for their helpful comments and careful review.

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MYCOTAXON 134-3

p. vii, line 21 FOR: *Marthamyces culmigenus* (Ellis & Everh.) P.R. Johnst.

READ: *Marthamyces culmigenus* (Ellis & **Langl.**) P.R. Johnst.

p.496, lines 3-5

FOR: *Marthamyces culmigenus* (Ellis & Everh.) P.R. Johnst., comb. nov.

IF 556322

≡ *Naemacyclus culmigenus* Ellis & Everh.,

Proc. Acad. Nat. Sci. Philadelphia 45: 151, 1893.

READ: *Marthamyces culmigenus* (Ellis & **Langl.**) P.R. Johnst., comb. nov.

IF 556322

≡ *Naemacyclus culmigenus* Ellis & **Langl.**, in Ellis & Everhart,

Proc. Acad. Nat. Sci. Philadelphia 45: 151, 1893.

[Semi-bold fonts used above to flag corrected terms.]

CORRIGENDA IN CURRENT ISSUE (134-4)

Cited below are mistakes or oversights present in approved input files not detected by authors until after PDF conversion.

p. 613: Pu Liu and fellow coauthors wish to acknowledge the contributions made to “Dictyostelids from Jilin Province, China 3: new *Cavenderia* and *Dictyostelium* records” (MYCOTAXON 134: 613–618) by Prof. Zhuang Li (Shandong Provincial Key Laboratory for Biology of Vegetable Diseases and Insect Pests, College of Plant Protection, Shandong Agricultural University, Tai’an 271018, China). The author sequence originally intended should read “Pu Liu, Shunhang Zhang, Zhuang Li, Yue Zou, Xueping Kang, Yu Li.”

p.669, line 26 FOR: MK43983

READ: MK439830

FROM THE EDITOR-IN-CHIEF

DEADLINES, MYCOTAXON & NOMENCLATURE—The most onerous task your esteemed *Editor-in-Chief* faces is bringing the year-end issue in ‘on time.’ A glance at our publication history suggests that during her tenure, she has failed miserably. Since 2004, she has met only three of her sixteen December deadlines: New Year’s Eve 2004, Boxing Day 2007, 30 December 2009. Given this deplorable 37% success rate, it is no surprise that, once again, an October–December MYCOTAXON will appear in January. (It could be worse: after adopting electronic submission and new software, we released the last 2005 volume on 11 MAY 2006!)

Reasons/excuses for delays are myriad: time-consuming nomenclatural revision and editorial repair of sloppily prepared submissions (on the misplaced notion that it is quicker for us to do authors’ work for them), outside research commitments, severe health problems, uncontrollable press delays. Nonetheless, this year we were convinced that MYCOTAXON 134(4) would be ready for delivery well before 2020.

What we did NOT anticipate was the small number of research papers submitted. With several authors not sending us their final papers after their 2019 nomenclatural review, we waited until December 27 before deciding to release the issue with only 140 pages (the smallest issue EVER since 1974) rather than waiting for final submissions that have yet to appear. Frustrating, because removal of required page charges produced a flood of 138 accessions during 2019.

What makes the year-end release date so important to MYCOTAXON? With nomenclatural priority date-based, the date of publication is dictated by the actual release date and not what is displayed on the cover. That means that taxonomic names published in periodicals must cite both the actual date of publication and the ‘nominal’ date printed in the issue, e.g., following the order, *Haematomma pluriseptatum* R. Tang, Mycotaxon 134: 638 (2020) but indexed as “Miao, C, Tang R, Dong L, Ren Z, Zhao Z. 2020 (‘2019’). *Haematomma pluriseptatum* sp. nov. from China. Mycotaxon 134: 637–641. <https://doi.org/10.5248/134.637> ” Much less confusing and infinitely more restful to have only ONE date to cite!

MYCOTAXON 134(4) presents 15 papers by 81 authors (representing 15 countries) as revised by 34 expert reviewers and the editors.

The 2019 October–December MYCOTAXON proposes one new genus (*Rhomboidia* from China) and eight new species representing *Bactrodesmium* from ECUADOR; *Dendrographium*, *Filsoniana*, *Haematomma*, and *Rhomboidia* from CHINA; *Exserticlava* from BRAZIL; *Leucoagaricus* from PAKISTAN; and *Urocystis* from the U.S.A. We also offer a new combination in *Puccinia* and epitypification for *Puccinia caulophylli*.

New species range extensions are reported for [ascomycetes] *Aureobasidium*, *Sarcophoma*, *Stigmina* in TURKEY and new records and hosts of fern-associated ascos in eastern MEXICO and [myxomycetes] *Cavenderia*, *Dictyostelium*, and *Didymium* in CHINA.

Two papers on *Sarcopodium* [1] explain why *S. flocculentum* is the correct name for *S. macalpinei* and [2] discuss the first sexual morph recorded for *S. vanillae* in Thailand. Another paper treats the full life cycle for the rust *Puccinia* (\equiv *Aecidium*) *caulophylli*.

Our small year-end issue closes with the announcements of two mycobiota [recently posted on www.mycotaxon.com] covering [1] new records of ascomycetes on *Syagrus coronata* in Brazil's Caatinga biome and [2] dark- and pink-spored agarics in Bolivia.

Wishing us all health, happiness, illumination, and PEACE in 2020,

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

8 January 2020

PUBLICATION DATE FOR VOLUME ONE HUNDRED THIRTY-FOUR (3)

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2020 MYCOTAXON SUBMISSION PROCEDURE

Prospective MYCOTAXON authors should download the MYCOTAXON 2020 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 2020 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 & illustration 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 2020 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).

4—FINAL EDITORIAL REVIEW & PUBLICATION: The *Editor-in-Chief* conducts a final grammatical and scientific review and returns her editorial revisions to all expert reviewers and coauthors for final author approval. Author-approved files are placed in the publication queue.

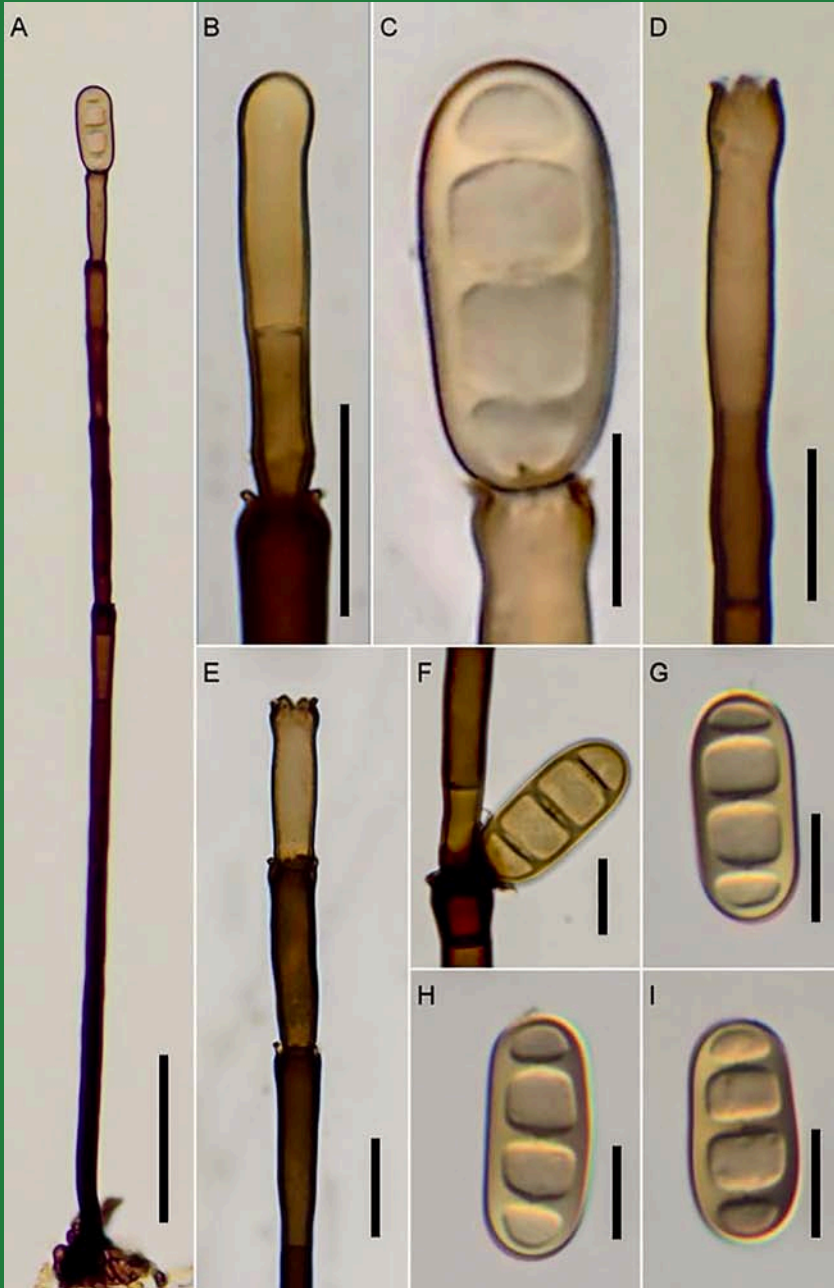
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Exserticlava aquatica sp. nov.
(Carmo & al.— Pl at E 1, p. 733)

***Rhomboidia wuliangshanensis* gen. & sp. nov. from southwestern China**

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ABSTRACT—A new, white-rot, poroid, wood-inhabiting fungal genus, *Rhomboidia*, typified by *R. wuliangshanensis*, is proposed based on morphological and molecular evidence. Collected from subtropical Yunnan Province in southwest China, *Rhomboidia* is characterized by annual, stipitate basidiomes with rhomboid pileus, a monomitic hyphal system with thick-walled generative hyphae bearing clamp connections, and broadly ellipsoid basidiospores with thin, hyaline, smooth walls. Phylogenetic analyses of ITS and LSU nuclear RNA gene regions showed that *Rhomboidia* is in *Steccherinaceae* and formed as distinct, monophyletic lineage within a subclade that includes *Nigroporus*, *Trullella*, and *Flabellophora*.

KEY WORDS—*Polyporales*, residual polyporoid clade, taxonomy, wood-rotting fungi

Introduction

Polyporales Gäum. is one of the most intensively studied groups of fungi with many species of interest to fungal ecologists and applied scientists (Justo & al. 2017). Species of wood-inhabiting fungi in *Polyporales* are important as saprobes and pathogens in forest ecosystems and in their application in biomedical engineering and biodegradation systems (Dai & al. 2009, Levin & al. 2016). With roughly 1800 described species, *Polyporales* comprise about 1.5% of all known species of Fungi (Kirk & al. 2008). Currently, there are 46 genomes of polyporalean taxa available from the Joint Genome Institute MycoCosm portal (Grigoriev & al. 2013).

TABLE 1. Species and sequences used in the phylogenetic analyses

SPECIES	SAMPLE	GENBANK ACCESSION NO.		REFERENCES
		ITS	LSU	
<i>Abortiporus biennis</i>	TFRI 274	EU232187	EU232235	Larsson 2007
<i>Antrodiella americana</i>	Gothenburg 3161	JN710509	JN710509	Miettinen & al. 2012
<i>A. semisupina</i>	FCUG 960	EU232182	EU232266	Binder & al. 2005
<i>Antrodiella</i> sp.	X 418	JN710523	JN710523	Miettinen & al. 2012
<i>Climacocystis borealis</i>	KH 13318	JQ031126	JQ031126	Binder & al. 2013
<i>Diplomitoporus flavescens</i>	X 84	FN907908	—	Miettinen & al. 2012
<i>Elaphroporia ailaoshanensis</i>	CLZhao 595	MG231568	MG231568	Wu & al. 2018
	CLZhao 596	MG231572	MG231572	Wu & al. 2018
<i>Flabellophora</i> sp.	X340	JN710534	JN710534	Miettinen & al. 2012
<i>Flaviporus brownii</i>	X 1216	JN710537	JN710537	Miettinen & al. 2012
<i>F. liebmannii</i>	X 251	JN710541	JN710541	Miettinen & al. 2012
	X 249	JN710539	JN710539	Miettinen & al. 2012
	X 666	JN710540	JN710540	Miettinen & al. 2012
<i>Frantisekia mentschulensis</i>	BRNM 710170	FJ496728	—	Tomšovský & al. 2010
	1377	JN710544	JN710544	Miettinen & al. 2012
<i>Hypochnicium bombycinum</i>	MA 15305	FN552537	—	Binder & al. 2013
<i>H. lyndoniae</i>	NL 041031	JX124704	JX124704	Binder & al. 2005
<i>Irpex lacteus</i>	CBS 431.48	MH856423	MH867969	Vu & al. 2019
	DO 421/951208	JX109852	JX109852	Binder & al. 2013
<i>Ischnoderma benzoinum</i>	KHL 12099	JX109841	JX109841	Binder & al. 2013
<i>I. resinorum</i>	FD-328	KP135303	KP135225	Floudas & Hibbett 2015
<i>Junghuhnia crustacea</i>	X 1127	JN710554	JN710554	Miettinen & al. 2012
	X 262	JN710553	JN710553	Miettinen & al. 2012
<i>J. micropora</i>	Spirin 2652	JN710559	JN710559	Miettinen & al. 2012
<i>Loweomyces fractipes</i>	X 1149	JN710570	JN710570	Miettinen et al. 2012
	X 1253	JN710569	JN710569	Miettinen & al. 2012
	X 1250	JN710568	JN710568	Miettinen & al. 2012
<i>Mycorrhaphium adustum</i>	8024	JN710573	JN710573	Miettinen & al. 2012
	Dai 10173	KC485537	KC485554	—

<i>Nigroporus vinosus</i>	X 839	N710576	N710576	Miettinen & al. (012
	8182	JN710728	JN710728	Miettinen & al. 2012
	BHS2008-100	JX109857	JX109857	Binder & al. 2013
<i>Panus conchatus</i>	X 1234	JN710579	JN710579	Miettinen & al. 2012
<i>P. strigellus</i>	INPA 243940	JQ955725	JQ955732	Binder & al. 2013
<i>Physisporinus sanguinolentus</i>	BRNM 699576	FJ496671	FJ496725	Tomšovský & al. 2010
<i>P. vitreus</i>	3163	JN710580	JN710580	Miettinen & al. 2012
	KHL11959	JQ031129	JQ031129	Sjökvist & al. 2012
	CBS 486.72	MH860538	MH872244	Vu & al. 2019
<i>Podoscypha venustula</i>	CBS 65684	JN649367	JN649367	Binder & al. 2013
<i>Pseudolagarobasidium acaciicola</i>	CBS 115543	DQ517883	—	Miettinen & Rajchenberg 2012
	CBS 115544	DQ517882	—	Miettinen & Rajchenberg 2012
<i>P. belizense</i>	CFMR DLC 04-31	JQ070173	—	Miettinen & Rajchenberg 2012
<i>Rhomboidia wuliangshanensis</i>	CLZhao 4406 [T]	MK860715	MK860710	Present study
	CLZhao 4411	MK860716	MK860711	Present study
<i>Skeletocutis novae-zelandiae</i>	Ryvarden 38641	JN710582	JN710582	Miettinen & al. 2012
<i>Spongipellis spumeus</i>	PRM 891931	HQ728287	HQ729021	Tomšovský & al. 2010
	BRNM 712630	HQ728288	HQ728288	Tomšovský & al. 2010
	BRNM 734877	HQ728283	HQ728283	Tomšovský & al. 2010
<i>Steccherinum fimbriatum</i>	KHL 11905	EU118668	EU118668	Tomšovský & al. 2010
<i>S. ochraceum</i>	Ryberg s.n.	EU118669	EU118670	Larsson 2007
	KHL 11902	JQ031130	JQ031130	Sjökvist & al. 2012
<i>Trullella dentipora</i>	X 200	JN710512	JN710512	Miettinen & al. 2012
<i>T. duracina</i>	X 290	JN710513	JN710513	Miettinen & al. 2012
<i>T. polyporoides</i>	X 510	JN710602	JN710602	Miettinen & al. 2012
<i>Xanthoporus syringae</i>	X 339	JN710606	JN710606	Miettinen & al. 2012
	Cui 2177	DQ789395	—	Miettinen & al. 2012
	Gothenburg 1488	JN710607	JN710607	Miettinen & al. 2012

Systematics of the *Polyporales* has benefitted from numerous molecular phylogenetic studies (e.g., Binder & al. 2005, 2013; Larsson 2007; Miettinen & al. 2012; Dai & al. 2015; Choi & Kim 2017). *Steccherinaceae* Parmasto, one of 18 families recognized in *Polyporales* (Justo & al. 2017), has been included in several molecular studies (e.g., Binder & al. 2005, 2013; Miettinen & al. 2012; Miettinen & Ryvarden 2016; Justo & al. 2017; Westphalen & al. 2018). Miettinen & al. (2012) published a multigene, molecular phylogenetic study of *Steccherinum* and allied taxa that clearly delineated *Steccherinaceae*. They uncovered surprising morphological diversity and plasticity in this family, requiring revision of generic concepts and 15 new genera to accommodate existing and new species. Subsequently, Miettinen & Ryvarden (2016) introduced five new genera, revised one genus, and described two new species that had been identified earlier by Miettinen & al. (2012). Justo & al. (2017), who revised family-level classification in *Polyporales*, confirmed *Steccherinaceae* as a distinct lineage in *Polyporales* that grouped with *Cerrenaceae* Miettinen & al. and *Panaceae* Miettinen & al. In a morphological and molecular study of Neotropical taxa of *Junghuhnia* and *Steccherinum*, Westphalen & al. (2018) uncovered a new genus and several new species and reclassified four taxa.

Cosmopolitan in distribution, *Steccherinaceae* has a rich diversity because it is found in boreal, temperate, subtropical, and tropical ecosystems (Núñez & Ryvarden 2001, Dai 2012, Ryvarden & Melo 2014, Dai & al. 2015, Zhou & al. 2016). Many new species in *Polyporales* have been described from southern, subtropical China (e.g., Li & Cui 2010, Zhao & Wu 2017, Zhao & Ma 2019). Recently, we collected an undescribed taxon from Yunnan Province that could not be assigned to any described genus. We present morphological and molecular phylogenetic evidence that support the recognition of a new monotypic genus in *Steccherinaceae*—*Rhomboidia*, typified by *R. wuliangshanensis*.

Materials & methods

The specimens studied are deposited at the herbarium of Southwest Forestry University, Kunming, China (SWFC). Macromorphological descriptions are based on field notes. Special colour terms follow Petersen (1996). Micromorphological data were obtained from the dried specimens and observed under a light microscope following Dai (2010). The following abbreviations are used: KOH = 5% potassium hydroxide; CB = cotton blue; CB- = acyanophilous; IKI = Melzer's reagent; IKI- = 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 = a/b) = number of spores (a) from number of specimens (b).

HiPure Fungal DNA Mini Kit II was used to obtain genomic DNA from dried specimens, according to the manufacturer's instructions with some modifications. A small piece (about 30 mg) of dried fungal material was ground to powder with liquid nitrogen. The powder was transferred to a 1.5 ml centrifuge tube, suspended in 0.4 ml of lysis buffer, and incubated in a 65 °C water bath for 60 min. After that, 0.4 ml phenol-chloroform (24:1) was added to each tube and the suspension was shaken vigorously. After centrifugation at 13,000 rpm for 5 min, 0.3 ml supernatant was transferred to a new tube and mixed with 0.45 ml binding buffer. The mixture was then transferred to an adsorbing column (AC) for centrifugation at 13,000 rpm for 0.5 min. Then, 0.5 ml inhibitor removal fluid was added in AC for a centrifugation at 12,000 rpm for 0.5 min. After washing twice with 0.5 ml washing buffer, the AC was transferred to a clean centrifuge tube, and 100 µl elution buffer was added to the middle of adsorbed film to elute the genomic DNA. The internal transcribed spacer region (ITS) was amplified with primer pairs ITS5 and ITS4 (White & al. 1990). The nuclear large subunit region (LSU) was amplified with primer pairs LR0R and LR7 (https://sites.duke.edu/vilgalyslab/rdna_primers_for_fungi/). The PCR procedure for ITS was: initial denaturation at 95 °C for 3 min, followed by 35 cycles of 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 LSU was: initial denaturation at 94 °C for 1 min, followed by 35 cycles of 94 °C for 30 s, 48 °C 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 was used to edit the DNA sequence. Sequences were aligned in MAFFT 6 (Katoch & Toh 2008, <http://mafft.cbrc.jp/alignment/server/>) using the "G-INS-I" strategy and manually adjusted in BioEdit (Hall 1999). The sequence alignment was deposited in TreeBase (submission ID 24216). *Xanthoporus syringae* (Parmasto) Audet obtained from GenBank was used as an outgroup to root trees following Miettinen & al. (2012) in the ITS+LSU analyses (FIG. 1).

The ITS+LSU sequences were analyzed phylogenetically using maximum parsimony, maximum likelihood, and Bayesian inference methods. Maximum parsimony (MP) analyses followed Zhao & Wu (2017), and tree construction was performed in PAUP* version 4.0b10 (Swofford 2002). All characters were equally weighted and gaps were treated as missing data. Trees were inferred using the heuristic search option with TBR branch swapping and 1000 random sequence additions. Max-trees was set to 5000, branches of zero length were collapsed and all parsimonious trees were saved. Clade robustness was assessed using bootstrap (BP) analysis with 1000 replicates (Felsenstein 1985). Tree statistics tree length (TL), consistency index (CI), retention index (RI), rescaled consistency index (RC), and homoplasy index (HI) were calculated for each Maximum Parsimonious Tree generated. Sequences were 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 replicates.

MrModeltest 2.3 (Posada & Crandall 1998; Nylander 2004) was used to determine the best-fit evolution model for data set for Bayesian inference (BI). Bayesian inference was calculated with MrBayes_3.1.2 using a general time reversible (GTR+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 4 million generations (ITS+LSU) in Fig. 1 and trees were sampled every 100 generations. The first 25% of the generations were discarded as burn-in. A majority rule consensus tree of all remaining trees was calculated. Branches that received bootstrap support for maximum likelihood (BS) $\geq 75\%$, maximum parsimony (BP) $\geq 75\%$, and Bayesian posterior probabilities (BPP) ≥ 0.95 were considered significantly supported.

Molecular phylogenetic results

The ITS+LSU (FIG. 1) dataset comprised sequences from 55 fungal specimens representing 34 taxa, including the outgroup taxon. The dataset had an aligned length of 2296 of which 1395 were constant, 201 parsimony-uninformative, and 700 parsimony-informative. MP analysis yielded two equally parsimonious trees (TL = 3897, CI = 0.376, HI = 0.624, RI = 0.627, RC = 0.236). The best-fit model for ITS+LSU alignment estimated and applied in the BI was GTR+I+G, lset nst = 6, rates = invgamma; prset statefreqpr = dirichlet (1,1,1,1). BI resulted in a similar topology with an average standard deviation of split frequencies equal to 0.006862.

Rhomboidia wuliangshanensis forms a monophyletic lineage with strong support (BS = 100%, BP = 100%, BPP = 1) and is sister to the *Nigroporus-Trullella* clade (FIG. 1).

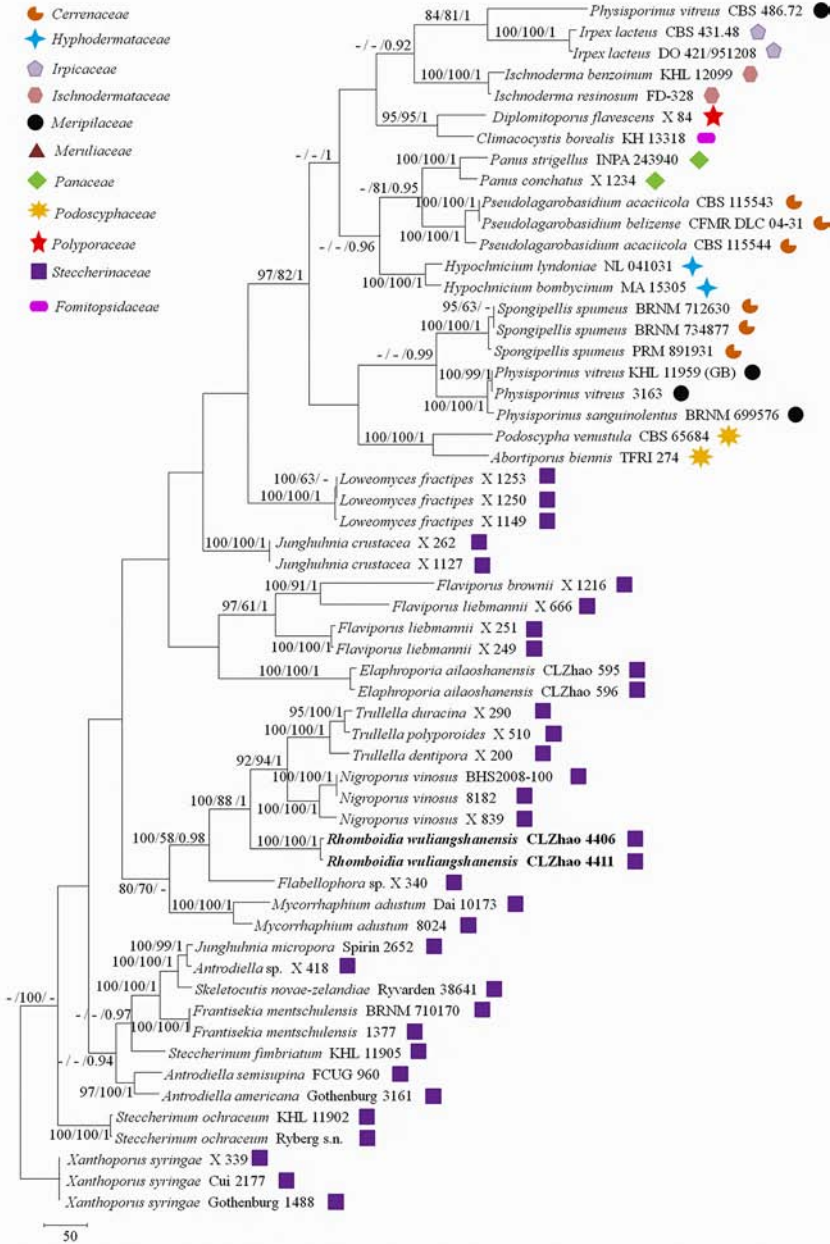
Taxonomy

Rhomboidia C.L. Zhao, *gen. nov.*

MB 833318

Differs from *Nigroporus* and *Trullella* by its stipitate to substipitate basidiomata, its orange-brown to reddish brown surface, and its monomitic hyphal system in both context and trama.

FIG. 1. Maximum parsimony strict consensus tree illustrating the phylogeny of *Rhomboidia wuliangshanensis* 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.



TYPE SPECIES: *Rhomboidia wuliangshanensis* C.L. Zhao

ETYMOLOGY: *Rhomboidia* (Lat.): referring to the rhomboid pileus of the basidiocarp with the poroid hymenophore.

BASIDIOMATA annual, stipitate. Pileus rhomboid, arising from a multiple branched stipe. Pores angular, small, dissepiments thin, entire. Hyphal system monomitic; generative hyphae thick-walled bearing clamp connections, IKI–, CB–; tissues unchanged in KOH. Cystidia absent, fusoid cystidioles numerous; hyphal ends numerous. Basidia barrel-shaped to clavate. Basidiospores broadly ellipsoid, hyaline, thin-walled, smooth, IKI–, CB–.

TYPE OF ROT: white rot.

Rhomboidia wuliangshanensis C.L. Zhao, sp. nov.

FIGS 2, 3

MB 833320

Differs from *Nigroporus vinosus* by its stipitate to substipitate basidiomata and monomitic hyphal structure.

TYPE: China. Yunnan Province: Puer, Jingdong County, Wuliangshan National Nature Reserve, on angiosperm trunk, 6 Oct 2017, CLZhao 4406 (Holotype, SWFC 0004406; GenBank MK860715, MK860710).

ETYMOLOGY: The specific epithet *wuliangshanensis* (Lat.) refers to the type locality, Wuliangshan.

BASIDIOMATA annual, stipitate to substipitate. Pileus rhomboid, arising from a multiple branched stipe, edges curling slightly inward, 3.5 cm from the base to margin, 4 cm wide, up to 3 mm thick; pileus surface radially striate, slightly brown to orange brown when fresh, drying brown to reddish; the margin acute, entire. Pore surface white when fresh, cream to buff upon drying. Pores angular, 7–9 per mm, dissepiments thin, entire. Context corky, white, thin, up to 0.5 mm thick. Tubes concolorous with pore surface, corky, up to 2.5 mm long.

-TYPE OF ROT: white rot.

ADDITIONAL SPECIMEN EXAMINED: CHINA. YUNNAN PROVINCE. Puer: Jingdong County, Wuliangshan National Nature Reserve, on angiosperm trunk, 6 Oct 2017, CLZhao 4411 (SWFC 004411; GenBank MK860716, MK860711).

Discussion

Rhomboidia is supported as a new genus by phylogenetic analyses and morphological characters. It is embedded in *Steccherinaceae* with strong support. Phylogenetically, *Rhomboidia* is closely related to *Flabellophora* G. Cunn., *Nigroporus* Murrill, and *Trullella* Zmitr. based on ITS+LSU nuclear RNA gene analyses (FIG. 1), which is similar to the previous multigene sequence-based study (Miettinen & al. 2012). The genera closely related to *Rhomboidia*

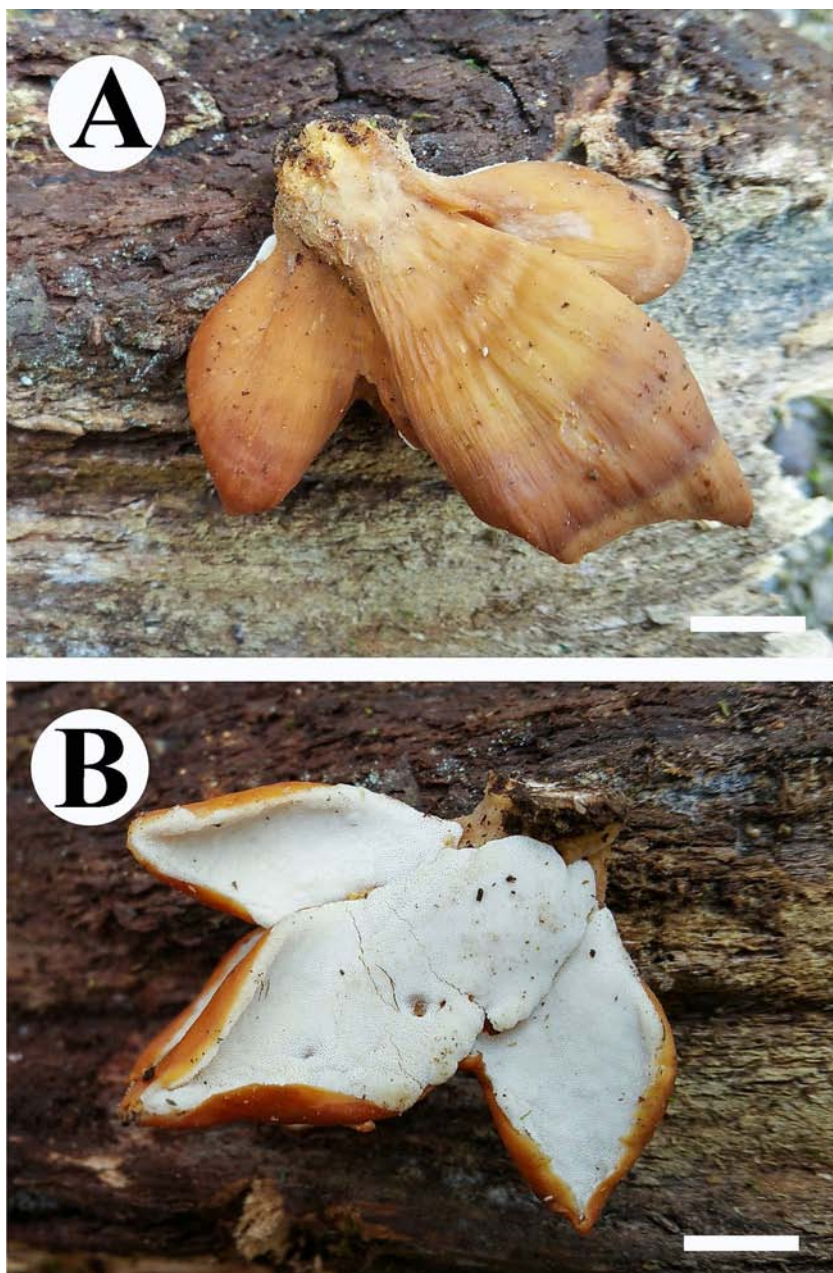


FIG. 2. *Rhomboidia wuliangshanensis* (holotype, SWFC 0004406). Scale bars = 5 mm.

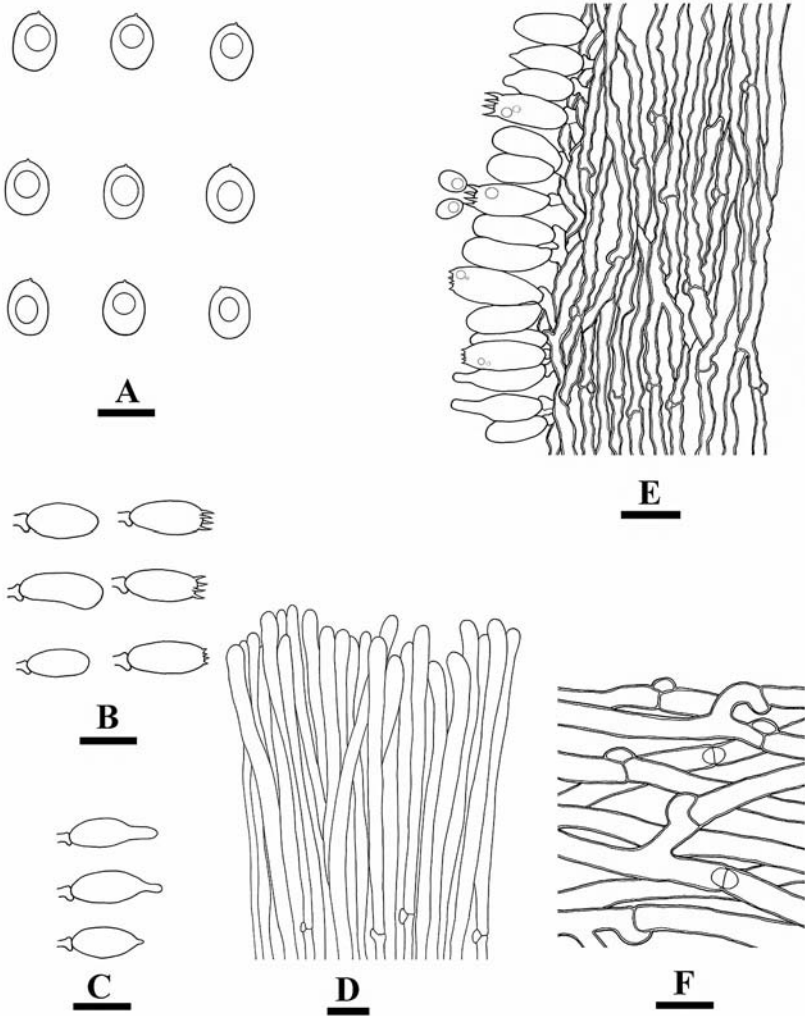


FIG. 3. *Rhomboidia wuliangshanensis* (drawn from the holotype, SWFC 0004406). A. Basidiospores; B. Basidia and basidioles; C. Cystidioles; D. Hyphal ends; E. Hyphae from trama; F. Hyphae from subiculum. Scale bars: a = 5 μm ; b–f = 10 μm .

are easily separated morphologically: In *Flabellophora* basidiomata arise from a submerged pseudosclerotium and develop unilateral pilei with a crust and a coriaceous context (Núñez & Ryvarden 2001). *Nigroporus* differs from *Rhomboidia* by developing resupinate to pileate basidiocarps with vinaceous brown to pink or violet pore surface and a dimitic hyphal system (Gilbertson & Ryvarden 1987). In *Trullella* basidiomata are spatulate and light-coloured, with a monomitic hyphal system in the context but dimitic in the trama (Miettinen & al. 2012, Zmitrovich 2018).

Rhomboidia resembles other stipitate genera in *Polyporales* such as *Abortiporus* Murrill, *Jahnoporus* Nuss, and *Polyporus* P. Micheli ex Adans. *Abortiporus*, however, has a duplex structure and thick-walled basidiospores (Núñez & Ryvarden 2001). *Jahnoporus* is characterized by large spindle-shaped basidiospores (Gilbertson & Ryvarden 1987), and *Polyporus* has a dimitic hyphal system (Bernicchia & Gorjón 2010).

Polypores are extensively studied and well-known in North America (Gilbertson & Ryvarden 1987, Zhou & al. 2016) and Eurasia (Núñez & Ryvarden 2001, Bernicchia & Gorjón 2010, Dai 2012, Ryvarden & Melo 2014, Dai & al. 2015), but Chinese polypore diversity is still being explored, especially in subtropical and tropical areas. *Rhomboidia wuliangshanensis* was collected from Yunnan Province, where many new taxa in *Polyporales* and *Hymenochaetales* have been described (e.g., Li & Cui 2010, He & Li 2011, Yu & al. 2013, Yang & He 2014, Zhao & Wu 2017, Zhao & Ma 2019). We anticipate that additional, undescribed polypore taxa will be discovered throughout China after extensive collections are analyzed both morphologically and molecularly.

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