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#### OCTOBER-DECEMBER 2019



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

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#### Lorelei L. Norvell

editor@mycotaxon.com Pacific Northwest Mycology Service 6720 NW Skyline Boulevard Portland, Oregon 97229-1309 USA

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#### 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.

M. Catherine Aime D. Jayarama Bhat Lu-Sen Bian Marcela Eugenia da Silva Cáceres Rafael F. Castañeda-Ruiz Vagner G. Cortez Cvetomir M. Denchev Shouyu Guo Tom Hsiang Shah Hussain Sevda Kirbağ Klaus Kalb Paul M. Kirk John C. Landolt De-Wei Li José G. Marmolejo Tom May Eric H.C. McKenzie

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## Nomenclatural 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 Türkekul, and Dr. Shaun Pennycook for their helpful comments and careful review.

READ: The author would like to thank Yüzüncü Yıl Üniversity, Coordination of Scientific Research Projects for financial support (2010-FED-B031 and FYL-2016-5213) and Prof. Dr. Ertuğrul Sesli, Prof. Dr. İbrahim Türkekul, and Dr. Shaun Pennycook for their helpful comments and careful review.

#### 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.

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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)

MYCOTAXON for JULY–SEPTEMBER 2019 (I–XIV + 423–590) was issued on October 2, 2019

#### 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—NOMENCLATURAL 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.

The PDF proof and bibliographic & nomenclatural index entries are sent to all coauthors for final inspection. After PDF processing, the *Editor-in-Chief* corrects ONLY PDF editorial/conversion and index entry errors; corrections of all other errors are listed in the ERRATA of a subsequent issue for no charge. Authors will pay fees for mycobiota uploads, optional open access, and correction of major author errors to the *Business Manager* <subscriptions@mycotaxon.com> at this time.

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

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

TAI-MIN XU<sup>1,2</sup>, XIANG-FU LIU<sup>3</sup>, YU-HUI CHEN<sup>2</sup>, CHANG-LIN ZHAO<sup>1,3\*</sup>

 <sup>1</sup>Yunnan Provincial Innovation Team on Kapok Fiber Industrial Plantation;
 <sup>2</sup>College of Life Sciences; <sup>3</sup>College of Biodiversity Conservation: Southwest Forestry University, Kunming 650224, P.R. China

\* Correspondence to: fungichanglinz@163.com

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.		DEPENDING
		ITS	LSU	References
Abortiporus biennis	TFRI 274	EU232187	EU232235	Larsson 2007
Antrodiella americana	Gothenburg 3161	JN710509	JN710509	Miettinen & al. 2012
A. semisupina	FCUG 960	EU232182	EU232266	Binder & al. 2005
Antrodiella sp.	X 418	JN710523	JN710523	Miettinen & al. 2012
Climacocystis borealis	KH 13318	JQ031126	JQ031126	Binder & al. 2013
Diplomitoporus flavescens	X 84	FN907908	_	Miettinen & al. 2012
Elaphroporia ailaoshanensis	CLZhao 595	MG231568	MG231568	Wu & al. 2018
	CLZhao 596	MG231572	MG231572	Wu & al. 2018
Flabellophora sp.	X340	JN710534	JN710534	Miettinen & al. 2012
Flaviporus brownii	X 1216	JN710537	JN710537	Miettinen & al. 2012
F. liebmannii	X 251	JN710541	JN710541	Miettinen & al. 2012
	X 249	JN710539	JN710539	Miettinen & al. 2012
	X 666	JN710540	JN710540	Miettinen & al. 2012
Frantisekia mentschulensis	BRNM 710170	FJ496728	_	Tomšovský & al. 2010
	1377	JN710544	JN710544	Miettinen & al. 2012
Hypochnicium bombycinum	MA 15305	FN552537	_	Binder & al. 2013
H. lyndoniae	NL 041031	JX124704	JX124704	Binder & al. 2005
Irpex lacteus	CBS 431.48	MH856423	MH867969	Vu & al. 2019
	DO 421/951208	JX109852	JX109852	Binder & al. 2013
Ischnoderma benzoinum	KHL 12099	JX109841	JX109841	Binder & al. 2013
I. resinosum	FD-328	KP135303	KP135225	Floudas & Hibbett 2015
Junghuhnia crustacea	X 1127	JN710554	JN710554	Miettinen & al. 2012
	X 262	JN710553	JN710553	Miettinen & al. 2012
J. micropora	Spirin 2652	JN710559	JN710559	Miettinen & al. 2012
Loweomyces fractipes	X 1149	JN710570	JN710570	Miettinen et al. 2012
	X 1253	JN710569	JN710569	Miettinen & al. 2012
	X 1250	JN710568	JN710568	Miettinen & al. 2012
Mycorrhaphium adustum	8024	JN710573	JN710573	Miettinen & al. 2012
	Dai 10173	KC485537	KC485554	_

Nigroporus vinosus	X 839	N710576	N710576	Miettinen & al. (012
	8182	JN710728	JN710728	Miettinen & al. 2012
	BHS2008-100	JX109857	JX109857	Binder & al. 2013
Panus conchatus	X 1234	JN710579	JN710579	Miettinen & al. 2012
P. strigellus	INPA 243940	JQ955725	JQ955732	Binder & al. 2013
Physisporinus sanguinolentus	BRNM 699576	FJ496671	FJ496725	Tomšovský & al. 2010
P. vitreus	3163	JN710580	JN710580	Miettinen & al. 2012
	KHL11959	JQ031129	JQ031129	Sjökvist & al. 2012
	CBS 486.72	MH860538	MH872244	Vu & al. 2019
Podoscypha venustula	CBS 65684	JN649367	JN649367	Binder & al. 2013
Pseudolagarobasidium acaciicola	CBS 115543	DQ517883	_	Miettinen & Rajchenberg 2012
	CBS 115544	DQ517882	_	Miettinen & Rajchenberg 2012
P. belizense	CFMR DLC 04-31	JQ070173	_	Miettinen & Rajchenberg 2012
				, ,
Rhomboidia wuliangshanensis	CLZhao 4406 [T]	MK860715	MK860710	Present study
Rhomboidia wuliangshanensis	CLZhao 4406 [T] CLZhao 4411	MK860715 MK860716	MK860710 MK860711	Present study Present study
Rhomboidia wuliangshanensis Skeletocutis novae-zelandiae	CLZhao 4406 [T] CLZhao 4411 Ryvarden 38641	MK860715 MK860716 JN710582	MK860710 MK860711 JN710582	Present study Present study Miettinen & al. 2012
Rhomboidia wuliangshanensis Skeletocutis novae-zelandiae Spongipellis spumeus	CLZhao 4406 [T] CLZhao 4411 Ryvarden 38641 PRM 891931	MK860715 MK860716 JN710582 HQ728287	MK860710 MK860711 JN710582 HQ729021	Present study Present study Miettinen & al. 2012 Tomšovský & al. 2010
Rhomboidia wuliangshanensis Skeletocutis novae-zelandiae Spongipellis spumeus	CLZhao 4406 [T] CLZhao 4411 Ryvarden 38641 PRM 891931 BRNM 712630	MK860715 MK860716 JN710582 HQ728287 HQ728288	MK860710 MK860711 JN710582 HQ729021 HQ728288	Present study Present study Miettinen & al. 2012 Tomšovský & al. 2010 Tomšovský & al. 2010
Rhomboidia wuliangshanensis Skeletocutis novae-zelandiae Spongipellis spumeus	CLZhao 4406 [T] CLZhao 4411 Ryvarden 38641 PRM 891931 BRNM 712630 BRNM 734877	MK860715 MK860716 JN710582 HQ728287 HQ728288 HQ728283	MK860710 MK860711 JN710582 HQ729021 HQ728288 HQ728283	Present study Present study Miettinen & al. 2012 Tomšovský & al. 2010 Tomšovský & al. 2010
Rhomboidia wuliangshanensis Skeletocutis novae-zelandiae Spongipellis spumeus Steccherinum fimbriatum	CLZhao 4406 [T] CLZhao 4411 Ryvarden 38641 PRM 891931 BRNM 712630 BRNM 734877 KHL 11905	MK860715 MK860716 JN710582 HQ728287 HQ728288 HQ728283 EU118668	MK860710 MK860711 JN710582 HQ729021 HQ728288 HQ728283 EU118668	Present study Present study Miettinen & al. 2012 Tomšovský & al. 2010 Tomšovský & al. 2010 Tomšovský & al. 2010
Rhomboidia wuliangshanensis Skeletocutis novae-zelandiae Spongipellis spumeus Steccherinum fimbriatum S. ochraceum	CLZhao 4406 [T] CLZhao 4411 Ryvarden 38641 PRM 891931 BRNM 712630 BRNM 734877 KHL 11905 Ryberg s.n.	MK860715 MK860716 JN710582 HQ728287 HQ728288 HQ728283 EU118668 EU118669	MK860710 MK860711 JN710582 HQ729021 HQ728288 HQ728283 EU118668 EU118668	Present study Present study Miettinen & al. 2012 Tomšovský & al. 2010 Tomšovský & al. 2010 Tomšovský & al. 2010 Tomšovský & al. 2010 Larsson 2007
Rhomboidia wuliangshanensis Skeletocutis novae-zelandiae Spongipellis spumeus Steccherinum fimbriatum S. ochraceum	CLZhao 4406 [T] CLZhao 4411 Ryvarden 38641 PRM 891931 BRNM 712630 BRNM 734877 KHL 11905 Ryberg s.n. KHL 11902	MK860715 MK860716 JN710582 HQ728287 HQ728288 HQ728283 EU118668 EU118669 JQ031130	MK860710 MK860711 JN710582 HQ729021 HQ728288 HQ728283 EU118668 EU118670 JQ031130	Present study Present study Miettinen & al. 2012 Tomšovský & al. 2010 Tomšovský & al. 2010 Tomšovský & al. 2010 Larsson 2007 Sjökvist & al. 2012
Rhomboidia wuliangshanensis Skeletocutis novae-zelandiae Spongipellis spumeus Steccherinum fimbriatum S. ochraceum Trullella dentipora	CLZhao 4406 [T] CLZhao 4411 Ryvarden 38641 PRM 891931 BRNM 712630 BRNM 734877 KHL 11905 Ryberg s.n. KHL 11902 X 200	MK860715 MK860716 JN710582 HQ728287 HQ728288 HQ728283 EU118668 EU118669 JQ031130 JN710512	MK860710 MK860711 JN710582 HQ729021 HQ728288 HQ728283 EU118668 EU118668 EU118670 JQ031130 JN710512	Present study Present study Miettinen & al. 2012 Tomšovský & al. 2010 Tomšovský & al. 2010 Tomšovský & al. 2010 Larsson 2007 Sjökvist & al. 2012 Miettinen & al. 2012
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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 ml 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 LROR 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 (Katoh & 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)  $\geq$ 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.



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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 wuliangshanensisC.L. Zhao, sp. nov.FIGS 2, 3MB 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 sequencebased 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:  $a = 5 \mu m$ ;  $b-f = 10 \mu m$ .

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 spathulate 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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