



Two new wood-inhabiting fungal species (Polyporales, Basidiomycota) from Yunnan Province, China

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Abstract

Wood-inhabiting fungi are a cosmopolitan fungal group worldwide. Two new wood-inhabiting fungal species, *Rhodoantrodia purpurascens* and *Steccherinum wumengshanense* are proposed based on a combination of the morphological features and molecular evidence. *Rhodoantrodia purpurascens* is characterized by the corky basidiomata with a pale lilac to lavender pore surface, a dimitic hyphal system with clamped generative hyphae, and broadly ellipsoid basidiospores. *Steccherinum wumengshanense* is characterized by the corticoid basidiomata having a white to cream hymenial surface, a monomitic hyphal system with clamp generative hyphae, and ellipsoid basidiospores. Full descriptions, photo plates and phylogenetic analysis results of the new species are provided.

Keywords: Biodiversity; Molecular systematics; Multi-genes; New taxa

Introduction

Fungi comprise an under described, a poorly documented clade of eukaryotes that have immense ecological and economic impacts, and the fungi exist in ecosystems mainly on soil, water, air, or tissues of other organisms (Hibbett *et al.* 2016). Wood-inhabiting fungi are a cosmopolitan fungal group with a rich diversity in boreal, temperate, subtropical, and tropical vegetation, in which they degrade hard-to-digest substrates, such as lignin and cellulose that push the sustainable ecosystem cycle (Tedersoo *et al.* 2014, James *et al.* 2020, Liu *et al.* 2023a). Polyporales is one of the most intensively studied clades of fungi (Justo *et al.* 2017). As major wood-inhabiting fungi, the species in Polyporales are of interest to both fungal ecologists and applied scientists (Justo *et al.* 2017). The species diversity, taxonomy, and phylogeny of Polyporales have been intensively studied in recent years, and the number of taxa has dramatically increased (Justo *et al.* 2017, Liu *et al.* 2023a, c). In previous research work, Polyporales contained about 1,800 species, 216 genera, and 13 families (Kirk *et al.* 2008), while the latest research showed that about 2,500 species, 285 genera, and 18 families were included in Polyporales (He *et al.* 2019).

The genus *Rhodoantrodia* B.K. Cui, Y.Y. Chen & Shun Liu (2022: 59) is a member of the family Fomitopsidaceae (Polyporales, Basidiomycota), typified by *R. tropica* B.K. Cui, Y.Y. Chen & Shun Liu (2022: 59) (Liu *et al.* 2023a). Based on the Index Fungorum (www.indexfungorum.org; accessed on 20 March 2024), the genus *Rhodoantrodia* has three specific and registered names accepted worldwide (Liu *et al.* 2023a, b). The genus *Steccherinum* Gray. (1821: 651) is the core genus of the family Steccherinaceae (Polyporales, Basidiomycota), typified by *S. ochraceum* (Pers. ex J.F. Gmel.) Gray. (1821: 651) (Liu *et al.* 2023d). Based on the Index Fungorum (www.indexfungorum.org; accessed on 20 March 2024), the genus *Steccherinum* has 122 specific and registered names, and currently, 84 species have been accepted worldwide (Dong *et al.* 2022, 2023, Liu *et al.* 2023d).

DNA sequencing and phylogenetic techniques have been widely used in the systematic study of Polyporales,

which presented a phylogenetic and phylogenomic overview of the Polyporales and listed 40 validly published and legitimate family names since the 21st century (Binder *et al.* 2005, 2013, Larsson *et al.* 2007, Miettinen *et al.* 2012, James *et al.* 2020, Liu *et al.* 2023a). Seven gene loci (ITS, nLSU, nSSU, mtSSU, TEF1, RPB1, and RPB2) were used to reconstruct phylogenetic trees and revealed that the genus *Rhodoantrodia* included three new species, *R. subtropica* B.K. Cui & Shun Liu, *R. tropica* (B.K. Cui) B.K. Cui, Y.Y. Chen & Shun Liu and *R. yunnanensis* (M.L. Han & Q. An) B.K. Cui & Shun Liu (Liu *et al.* 2023a, b).

Molecular phylogeny has provided increased knowledge concerning the evolution of *Steccherinum* (Miettinen *et al.* 2016). The study revealed that the phylogeny of the poroid and hydroid genera *Antrodiella* Ryvarden & I. Johans., *Junghuhnia* Corda and *Steccherinum* (Polyporales, Basidiomycota) grouped together and *Steccherinum* was shown to contain both hydroid and poroid species (Miettinen *et al.* 2012). The genus *Steccherinum* is the largest genus in the family Steccherinaceae with a worldwide distribution (Dong *et al.* 2022, 2023), and recently based on results of molecular phylogenetic analyses, some *Steccherinum* species have been transferred to other genera (Westphalen *et al.* 2021, Liu *et al.* 2023c).

During the surveys of wood-inhabiting fungi, we collected two species from the order Polyporales in southwestern China, which were inconsistent with any known species of wood-inhabiting fungi. We presented the morphological characteristics and multi-gene molecular analyses with ITS and nLSU DNA markers that supported the taxonomy and phylogeny of *Rhodoantrodia* and *Steccherinum*.

Materials and methods

Sample Collection and Herbarium Specimen Preparation

Fresh fruiting bodies of fungi growing on angiosperm branches were collected from Qujing and Zhaotong of Yunnan Province, P.R. China. The samples were photographed *in situ* and fresh macroscopic details were recorded. Photographs were recorded using a Jianeng 80D camera (Tokyo, Japan). Specimens were dried in an electric food dehydrator at 45 °C (Hu *et al.* 2022). Once dried, the specimens were sealed in an envelope and zip-lock plastic bags and labeled (Zhao *et al.* 2023). The dried specimens were deposited in the herbarium of the Southwest Forestry University (SWFC), Kunming, Yunnan Province, China.

Morphology

The macromorphological descriptions were based on field notes and photos captured in the field and lab. The color terminology follows Petersen (1996). The micromorphological data were obtained from the dried specimens observed under a Nikon Eclipse E100 light microscope following Zhao & Wu (2017). The following abbreviations are used: KOH = 5% potassium hydroxide water solution, CB- = acyanophilous, IKI- = both inamyloid and indextrinoid, L = mean spore length (arithmetic average for all spores), W = mean spore width (arithmetic average for all spores), Q = variation in the L/W ratios between the specimens studied, and n = a/b (number of spores (a) measured from given number (b) of specimens).

DNA Extraction and Sequencing

The CTAB rapid plant genome extraction kit-DN14 (Aidlab Biotechnologies Co., Ltd., Beijing, China) was used to obtain genomic DNA from the dried specimens according to the manufacturer's instructions. The nuclear ribosomal of the internal transcribed spacer (ITS) region was amplified with the primer pair ITS5/ITS4 (White *et al.* 1990), the nuclear large subunit (nLSU) region with the primer pair LR0R/LR7 (Vilgalys & Hester 1990). The PCR procedure for ITS was as follows: initial denaturation at 95 °C for 3 min, followed by 35 cycles at 94 °C for 40 s, 58 °C for 45 s, and 72 °C for 1 min, and a final extension of 72 °C for 10 min. The PCR procedure for nLSU was as follows: initial denaturation at 94 °C for 1 min, followed by 35 cycles at 94 °C for 30 s, 48 °C for 1 min, and 72 °C for 1.5 min, and a final extension of 72 °C for 10 min. The PCR products were purified and sequenced at Kunming Tsingke Biological Technology Limited Company (Yunnan Province, P.R. China). All newly generated sequences were deposited in GenBank (Table 1).

TABLE 1. Names, sample numbers, references, and corresponding GenBank accession numbers of sequences used in this study.

Species Name	Sample No.	GenBank Accession No.		References
		ITS	nLSU	
<i>Antella americana</i>	Larsson 11949	JN710509		Cao <i>et al.</i> 2021
<i>A. chinensis</i>	Dai 9019	JX110844	KC485542	Yuan 2013
<i>A. niemelaei</i>	Renvall 3218	AF126876		Cao <i>et al.</i> 2021
<i>A. tibetica</i>	Dai 23334	OM855604		Du <i>et al.</i> 2022
<i>Anthoporia albobrunnea</i>	S 4665	KY948808	KY948880	Justo <i>et al.</i> 2017
<i>Antrodia bambusicola</i>	Cui 11280	MG787579	MG787620	Chen 2018
<i>A. heteromorpha</i>	Dai 12755	KP715306	KP715322	Chen & Cui 2016
<i>A. serpens</i>	Dai 7465	KR605813	KR605752	Liu <i>et al.</i> 2023a
<i>Antrodiella onychoides</i>	Miettinen X2312	JN710517		Miettinen <i>et al.</i> 2012
<i>A. pallescens</i>	Miettinen X1080	JN710518		Miettinen <i>et al.</i> 2012
<i>A. romellii</i>	X154	JN710520		Miettinen <i>et al.</i> 2012
<i>A. semisupina</i>	X242	JN710521		Miettinen <i>et al.</i> 2012
<i>Atraporiella neotropica</i>	Miettinen X1021	HQ659221		Cao <i>et al.</i> 2021
<i>A. yunnanensis</i>	CLZhao 604	MF962482	MF962485	Wu <i>et al.</i> 2017
<i>Brunneoporus cyclopis</i>	Miettinen 9166	KU866249	MG787627	Wang <i>et al.</i> 2021
<i>B. malicola</i>	Cui 7258	MG787586	MG787631	Chen 2018
<i>B. minuta</i>	Spirin 3477	KU866250	MG787633	Liu <i>et al.</i> 2023a
<i>Buglossoporus eucalypticola</i>	Dai 13660	KR605808	KR605747	Han <i>et al.</i> 2016
<i>B. pulvinus</i>	CBS 858.72	DQ491419	MH872316	Kim <i>et al.</i> 2007
<i>B. quercinus</i>	JV 0906/15-J	KR605800	KR605739	Han <i>et al.</i> 2016
<i>Butyrea japonica</i>	10202	JN710556		Cao <i>et al.</i> 2021
<i>B. luteoalba</i>	FP-105786	KP135320	KP135226	Dong <i>et al.</i> 2022
<i>Cartilosoma ramentacea</i>	Cui 16256	OK045506	OK045512	Liu <i>et al.</i> 2023a
<i>C. renehenticii</i>	PRM 944766	MK558725		Zíbarová <i>et al.</i> 2019
<i>Climacocystis borealis</i>	KHL 13318	JN710527		Cao <i>et al.</i> 2021
<i>Daedalea circularis</i>	Cui 10134	JQ314352	KP171221	Han <i>et al.</i> 2016
<i>D. quercina</i>	Dai 12152	KP171207	KP171229	Liu <i>et al.</i> 2023a
<i>Daedalella micropora</i>	Dai 18509	MW377286	MW377365	Liu <i>et al.</i> 2023a
<i>Elaphroporia ailaoshanensis</i>	CLZhao 596	MG231572	MG748855	Wu <i>et al.</i> 2018
<i>E. ailaoshanensis</i>	CLZhao 597	MG231847	MG748856	Wu <i>et al.</i> 2018
<i>Etheirodon fimbriatum</i>	KHL 11905	JN710530		Cao <i>et al.</i> 2021
<i>E. purpureum</i>	MCW 642/18	MT849301		Westphalen <i>et al.</i> 2021
<i>Flavidoporia pulvinascens</i>	Cui 10441	MG787590	MG787636	Chen 2018
<i>Flaviporus brownii</i>	MCW 362/12	KY175008		Liu <i>et al.</i> 2019
<i>F. liebmannii</i>	X 249	JN710539		Cao <i>et al.</i> 2021
<i>F. tenuis</i>	MCW 442/13	KY175001		Liu <i>et al.</i> 2019
<i>Fomitopsis abieticola</i>	Cui 10532	MN148230	OL621246	Liu <i>et al.</i> 2021
<i>F. ginkgonis</i>	Cui 17170	MK852563	MK860114	Liu <i>et al.</i> 2019
<i>F. pinicola</i>	LT 319	KF169652		Haight <i>et al.</i> 2019
<i>Fragifomes niveomarginatus</i>	Cui 10108	KR605778	KR605717	Han <i>et al.</i> 2016
<i>Frantisekia mentschulensis</i>	BRNM 710170	FJ496670		Dong <i>et al.</i> 2022
<i>F. fissiliformis</i>	CBS 435.72	MH860521	MH872232	Dong <i>et al.</i> 2022
<i>F. ussuri</i>	Wei 3081	KC485527	KC485545	Yuan 2014
<i>Heterobasidion annosum</i>	Dai 20962	ON417163	ON417213	Liu <i>et al.</i> 2023a

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TABLE 1. (Continued)

Species Name	Sample No.	GenBank Accession No.		References
		ITS	nLSU	
<i>Junghuhnia crustacea</i>	X 262	JN710553		Wang <i>et al.</i> 2021
<i>J. delicata</i>	MCW 564/17	MT849295		Du <i>et al.</i> 2022
<i>J. pseudocrustacea</i>	Yuan 6160	MF139551		Yuan <i>et al.</i> 2018
<i>Loweomyces fractipes</i>	X 1149	JN710570		Cao <i>et al.</i> 2021
<i>L. spissus</i>	MCW 488/14	KX378869		Cao <i>et al.</i> 2021
<i>L. tomentosus</i>	MCW 366/12	KX378870		Cao <i>et al.</i> 2021
<i>L. wynneae</i>	X 1215	JN710604		Cao <i>et al.</i> 2021
<i>Melanoporia nigra</i>	FP-90888	KC585357	KC585186	Liu <i>et al.</i> 2023a
<i>M. tropica</i>	Cui 16444	MW377306	MW377384	Liu <i>et al.</i> 2023a
<i>Metuloidea cinnamomea</i>	X 1228	KU926963		Cao <i>et al.</i> 2021
<i>M. fragrans</i>	LE 295277	KC858281		Cao <i>et al.</i> 2021
<i>M. murashkinskyi</i>	X 449	JN710588		Cao <i>et al.</i> 2021
<i>M. reniformis</i>	MCW 542/17	MT849303		Westphalen <i>et al.</i> 2021
<i>Mycorrhaphium adustum</i>	KHL12255	JN710573		Miettinen <i>et al.</i> 2012
<i>M. hispidum</i>	MCW 363/12	MH475306		Cao <i>et al.</i> 2021
<i>M. subadustum</i>	Dai 10173	KC485537	KC485554	Cao <i>et al.</i> 2021
<i>Neoantrodia angusta</i>	Cui 17068	ON417166	ON417216	Liu <i>et al.</i> 2023a
<i>N. primaeva</i>	Dai 11156	MG787598	MG787645	Chen 2018
<i>N. serialis</i>	JV 1509/5	KT995120	KT995143	Spirin <i>et al.</i> 2017
<i>Neolentiporus maculatissimus</i>	CIEFAP 92	JX090121		Chen 2018
<i>N. tropicus</i>	Cui 13915	MW377308	MW377386	Liu <i>et al.</i> 2023a
<i>Nigroporus vinosus</i>	KaiR 116	MT110231		Piepenbring <i>et al.</i> 2020
<i>N. vinosus</i>	MQN 015	AB811861		Hai <i>et al.</i> 2014
<i>Niveoporofomes globosporus</i>	M.C. Aime 3413	KC017760	KC017762	Ryvarden <i>et al.</i> 2014
<i>N. oboensis</i>	MUCL 53518	OM366266	OM366267	Decock <i>et al.</i> 2022
<i>N. spraguei</i>	Cui 8969	KR605785	KR605724	Han <i>et al.</i> 2016
<i>Pseudoantrodia monomitica</i>	Dai 10828	MG787601	MG787648	Liu <i>et al.</i> 2023a
<i>Pseudofomitopsis microcarpa</i>	Cui 16404	MW377316	MW377394	Liu <i>et al.</i> 2023a
<i>Rhodoantrodia purpurascens</i>	CLZhao 26267	OR658991	OR999390	Present study
<i>R. subtropica</i>	Cui 18021	OQ476259		Liu <i>et al.</i> 2023d
<i>R. subtropica</i>	Dai 19798	OQ476260		Liu <i>et al.</i> 2023d
<i>R. tropica</i>	Dai 13428	MG787605	MG787652	Chen 2018
<i>R. tropica</i>	Dai 13434	MG817481	MG817479	Chen 2018
<i>R. yunnanensis</i>	CL Zhao 4566	MT497887	MT497885	Han <i>et al.</i> 2020
<i>R. yunnanensis</i>	Han 1157	MT497886	MT497884	Han <i>et al.</i> 2020
<i>Rhodofomes cajanderi</i>	Cui 9888	KC507156	KC507166	Han & Cui 2015
<i>R. incarnatus</i>	Cui 10348	KC844848	KC844853	Han & Cui 2015
<i>R. roseus</i>	Cui 17081	ON417188	ON417239	Liu <i>et al.</i> 2023a
<i>Rhodofomitopsis feei</i>	Ryvarden 37603	KC844850	KC844855	Han & Cui 2015
<i>R. pseudofeei</i>	Cui 16794	MK461952	MK461956	Liu <i>et al.</i> 2023a
<i>Rubellofomes cystidiatus</i>	Cui 5481	KF937288	KF937291	Han <i>et al.</i> 2016
<i>R. minutisporus</i>	Rajchenberg 10661	KR605777	KR605716	Han <i>et al.</i> 2016
<i>Steccherinum austrosinense</i>	Dai 17540	MN871755	MN877768	Du <i>et al.</i> 2022
<i>S. autumnale</i>	Spirin 2957	JN710549		Liu & Dai 2021

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TABLE 1. (Continued)

Species Name	Sample No.	GenBank Accession No.		References
		ITS	nLSU	
<i>S. bourdotii</i>	Saarenoksa 10195	JN710584		Miettinen <i>et al.</i> 2012
<i>S. ciliolatum</i>	Ryvarden 47033	JN710585		Miettinen <i>et al.</i> 2012
<i>S. collabens</i>	KHL 11848	JN710552		Liu & Dai 2021
<i>S. fimbriatellum</i>	Miettinen 2091	JN710555		Miettinen <i>et al.</i> 2012
<i>S. formosanum</i>	TFRI 652	EU232184	EU232268	Liu & Dai 2021
<i>S. fragile</i>	Dai 19972	MW364629	MW364627	Liu & Dai 2021
<i>S. hirsutum</i>	CLZhao 4222	MW290040	MW290054	Dong <i>et al.</i> 2022
<i>S. incrustans</i>	Dai 19442	ON182084	ON182087	Liu <i>et al.</i> 2023c
<i>S. juniperi</i>	Dai 23931	OP956077	OP956031	Liu <i>et al.</i> 2023c
<i>S. larssonii</i>	MCW 593/17	MT849306		Westphalen <i>et al.</i> 2021
<i>S. meridionalis</i>	MR 10466	KY174994		Liu <i>et al.</i> 2019
<i>S. neonitidum</i>	MCW 371/12	KY174990		Liu <i>et al.</i> 2019
<i>S. nitidum</i>	KHL 11903	JN710560		Westphalen <i>et al.</i> 2021
<i>S. ochraceum</i>	KHL 11902	JN710590		Westphalen <i>et al.</i> 2021
<i>S. polycystidiferum</i>	RP 140	KY174996		Liu <i>et al.</i> 2019
<i>S. pseudozilingianum</i>	Kulju 1004	JN710561		Lin & Dai 2021
<i>S. puerense</i>	CLZhao 3644	MW682342	MW682338	Wu <i>et al.</i> 2021
<i>S. punctatum</i>	CLZhao 9181	OP799401	OP799375	Dong <i>et al.</i> 2023
<i>S. rubigimaculatum</i>	CLZhao 4069	MW682343	MW682339	Wu <i>et al.</i> 2021
<i>S. straminellum</i>	KHL 13849	JN710597		Cao <i>et al.</i> 2021
<i>S. subcollabens</i>	Dai 19344	MN871758	MN877771	Liu & Dai 2021
<i>S. subtropicum</i>	CLZhao 11059	OP799390	OP799377	Dong <i>et al.</i> 2023
<i>S. tenue</i>	5356	JN710598		Liu & Dai 2021
<i>S. tenuispinum</i>	X453	JN710600		Miettinen <i>et al.</i> 2012
<i>S. undigerum</i>	MCW 472/13	KY174987		Liu <i>et al.</i> 2019
<i>S. wumengshanense</i>	CLZhao 23586	OR658995	OR999392	Present study
<i>S. yunnanense</i>	CLZhao 1445	MW290042	MW290056	Dong <i>et al.</i> 2022
<i>Subantrodia juniperina</i>	SRM 403	KC585285	KC585109	Xu <i>et al.</i> 2020
<i>S. uzbekistanica</i>	Dai 17104	KX958182	KX958186	Liu <i>et al.</i> 2023a
<i>Trullella dentipora</i>	X 200	JN710512		Cao <i>et al.</i> 2021
<i>T. duracina</i>	MCW 410/13	MH475309		Cao <i>et al.</i> 2021
<i>Ungulidaedalea fragilis</i>	Cui 10919	KF937286	KF937290	Han <i>et al.</i> 2016
<i>Xanthoporus syringae</i>	Jeppson 2264	JN710607		Cao <i>et al.</i> 2021

The sequences were aligned in MAFFT version 7 using the G-INS-i strategy (Katoh *et al.* 2019). The alignment was adjusted manually using AliView version 1.27 (Larsson 2014). The sequence alignments were deposited in TreeBase (ID 31262). The combined ITS and nLSU sequences were used to infer the position of the two new species in the genus *Rhodoantrodia* and *Steccherinum* and related species. (1) *Heterobasidion annosum* (Fr.) Bref. was assigned as an outgroup to root trees in the ITS+nLSU analysis (Figure 1) (Liu *et al.* 2023a); (2) *Climacocystis borealis* (Fr.) Kotl. & Pouzar was assigned as an outgroup to root trees following the ITS+nLSU analysis (Figure 2) (Cao *et al.* 2021).

Maximum parsimony (MP), Maximum Likelihood (ML), and Bayesian Inference (BI) analyses were applied to the combined datasets following a previous study (Zhao & Wu 2017), and the tree construction procedure was performed in PAUP* version 4.0b10 (Swofford 2002). All 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 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 maximum parsimonious tree generated. The multiple sequence alignment was also analyzed using maximum likelihood (ML) in RAxML-HPC2 (Miller *et al.* 2012). Branch support (BS) for ML analysis was determined by 1000 bootstrap replicates.

MrModeltest 2.3 (Nylander 2004) was used to determine the best-fit evolution model for each dataset for Bayesian inference (BI), which was performed using MrBayes 3.2.7a with a GTR+I+G model of DNA substitution and a gamma distribution rate variation across sites (Ronquist *et al.* 2012). Four Markov chains were run twice from a random starting tree for 4 million generations of the datasets (Figure 1), and for 0.8 million generations of the datasets (Figure 2), and the tree was sampled every 1000 generations. The first one-fourth of all generations were discarded as burn-in. The majority rule consensus tree of all remaining trees was calculated. Branches were considered as significantly supported if they received a maximum likelihood bootstrap value (BS) $\geq 70\%$, maximum parsimony bootstrap value (BT) $\geq 70\%$, or Bayesian posterior probabilities (BPP) ≥ 0.95 .

Results

Phylogenetic analyses

The datasets based on ITS+nLSU (Figure 1) comprise sequences from 47 fungal specimens representing 45 species. The datasets had an aligned length of 2165 characters, of which 1442 characters are constant, 252 are variable and parsimony-uninformative, and 471 are parsimony-informative. Maximum parsimony analysis yielded 1 equally parsimonious tree (TL = 2794, CI = 0.3944, HI = 0.6056, RI = 0.4364, RC = 0.1721). Bayesian analysis and ML analysis resulted in a similar topology as MP analysis with an average standard deviation of split frequencies of 0.006424 (BI), and the effective sample size (ESS) across the two runs is double the average ESS (avg ESS) = 844.5. The phylogenetic tree (Figure 1) inferred from ITS and nLSU sequences revealed that *Rhodoantrodia purpurascens* grouped into the genus *Rhodoantrodia* (Fomitopsidaceae), in which it was retrieved as a sister to *R. yunnanensis* (M.L. Han & Q. An) B.K. Cui & Shun Liu. The datasets based on ITS+nLSU (Figure 2) comprise sequences from 70 fungal specimens representing 68 species. The datasets had an aligned length of 2379 characters, of which 1485 characters are constant, 267 are variable and parsimony-uninformative, and 627 are parsimony-informative. Maximum parsimony analysis yielded 32 equally parsimonious trees (TL = 4341, CI = 0.3439, HI = 0.6561, RI = 0.5196, RC = 0.1787). Bayesian analysis and ML analysis resulted in a similar topology as MP analysis with an average standard deviation of split frequencies of 0.009403 (BI), and the effective sample size (ESS) across the two runs is double the average ESS (avg ESS) = 126. The phylogenetic tree (Figure 2) inferred from ITS and nLSU sequences revealed that *Steccherinum wumengshanense* grouped into the genus *Steccherinum* and clustered into the family Steccherinaceae, in which it was retrieved as a sister to *S. yunnanense* Y.X. Wu & C.L. Zhao.

Taxonomy

Rhodoantrodia purpurascens L. Wang & C.L. Zhao, *sp. nov.* Figs. 3 and 4.

Mycobank no.: 851549

Etymology:—*purpurascens* (Lat.): refers to the purple hymenial surface.

Holotype:—CHINA. Yunnan Province: Qujing, Qilin District, Cuishan Forest Park, GPS coordinates: 25°55' N, 103°69' E, altitude: 2245 m asl., on the fallen branch of angiosperm, leg. C.L. Zhao, 24 November 2022, C.L. Zhao 26267 (SWFC!).

Basidiomata:—Annual, resupinate, easy to separate from substrate, corky, and up to 8 cm long, 3 cm wide, and 4.5 mm thick. Pore surface pale lilac (54D) to lavender (18/19A4) when fresh, become greyish purple (98B) when dry; pores round, 2–3 per mm, dissepiments thin, entire. Sterile margin very narrow, greyish purple (98B), up to 0.5 mm. Subiculum cream (4A2/3), corky, up to 1 mm thick. Tubes thin, greyish purple (98B), corky, up to 3.5 mm long.

Hyphal system:—Dimitic; generative hyphae with clamp connections, hyaline, slightly encrusted with crystals, thick-walled, branched, interwoven, 2.5–3 μm in diameter, IKI–, CB–, tissues unchanged in KOH; skeletal hyphae colorless, thick-walled with a narrow lumen to subsolid, unbranched, straight to flexuous, 3–3.5 μm in diameter, IKI–, CB–; tissues unchanged in KOH.

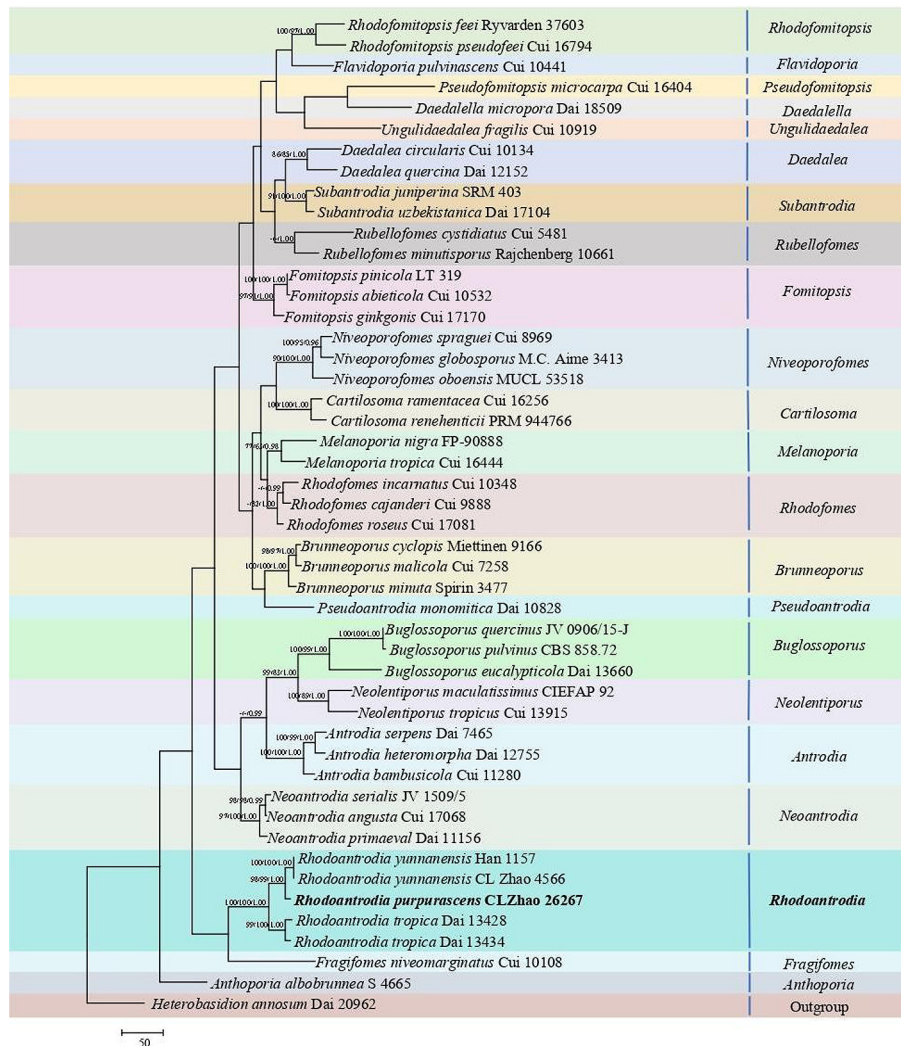


FIGURE 1. Maximum parsimony strict consensus tree illustrating the phylogeny of the new species and related species in *Rhodoantrodia* within Fomitopsidaceae based on ITS+nLSU sequences. The branch is labeled with a maximum likelihood lead value greater than 70%, a reduced lead value greater than 50% and a Bayesian posterior probability greater than 0.95. The new species are in bold.

Hymenium:—Cystidia absent; cystidioles fusoid, colorless, thin-walled, 17.5–25.5 × 2–3.5 µm. Basidia clavate to subcylindrical, hyaline, thin-walled, with a basal clamp connection and four sterigmata, 21.5–24.5 × 4.5–5.2 µm; basidioles dominant, in shape similar to basidia, but slightly smaller.

Spores:—Basidiospores ellipsoid, hyaline, thin-walled, smooth, IKI–, CB–, 5.5–7.5(–8) × 3–4 µm, L = 6.43 µm, W = 3.44 µm, Q = 1.87 (n = 30/1).

Steccherinum wumengshanense L. Wang & C.L. Zhao, *sp. nov.* Figs. 5 and 6.
Mycobank no.: 851550.

Etymology:—*wumengshanens* (Lat.): refers to the locality (Wumengshan National Natural Reserve) of the type specimen.

Holotype:—CHINA. Yunnan Province: Zhaotong, Yiliang County, Luozehe Town, Lijiaping Village, GPS coordinates: 27°29' N, 103°55' E, altitude: 1900 m asl., on the fallen branch of angiosperm, leg. C.L. Zhao, 24 August 2022, C.L. Zhao 23586 (SWFC!).

Basidiomata:—Annual, resupinate, adnate, corticoid, up to 3 cm long, 2 cm wide, and 1 mm thick. Hymenial surface grandinoid, white when fresh, turning to white to cream (4A2/3) upon drying, aculei 5–8 per mm, the length of aculei up to 0.1 mm. Sterile margin narrow, cream (4A2/3), up to 0.5 mm wide.

Hyphal system:—Monomitic; generative hyphae with clamp connections, colorless, thin-walled, frequently branched, interwoven, 2.5–4 µm in diameter; IKI–, CB–, tissues unchanged in KOH.

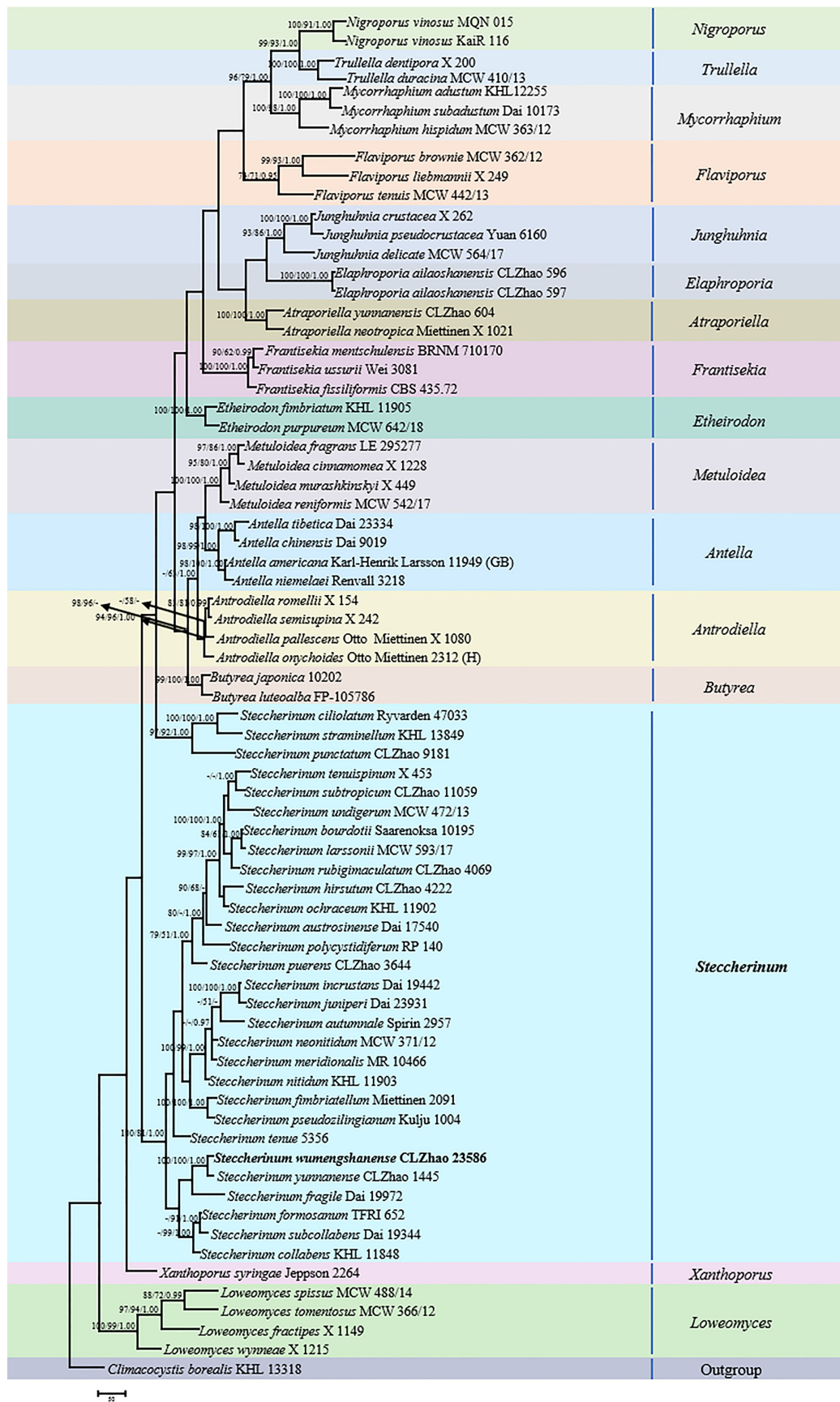


FIGURE 2. Maximum parsimony strict consensus tree illustrating the phylogeny of the new species and related species in *Steccherinum* within Steccherinaceae based on ITS+nLSU sequences. The branch is labeled with a maximum likelihood lead value greater than 70%, a reduced lead value greater than 50% and a Bayesian posterior probability greater than 0.95. The new species are in bold.



FIGURE 3. *Rhodoantrodia purpurascens* (holotype, C.L. Zhao 26267): basidiomata on the substrate (A), macroscopic characteristics of hymenophore (B). Bars: (A) = 1 cm and (B) = 1 mm.

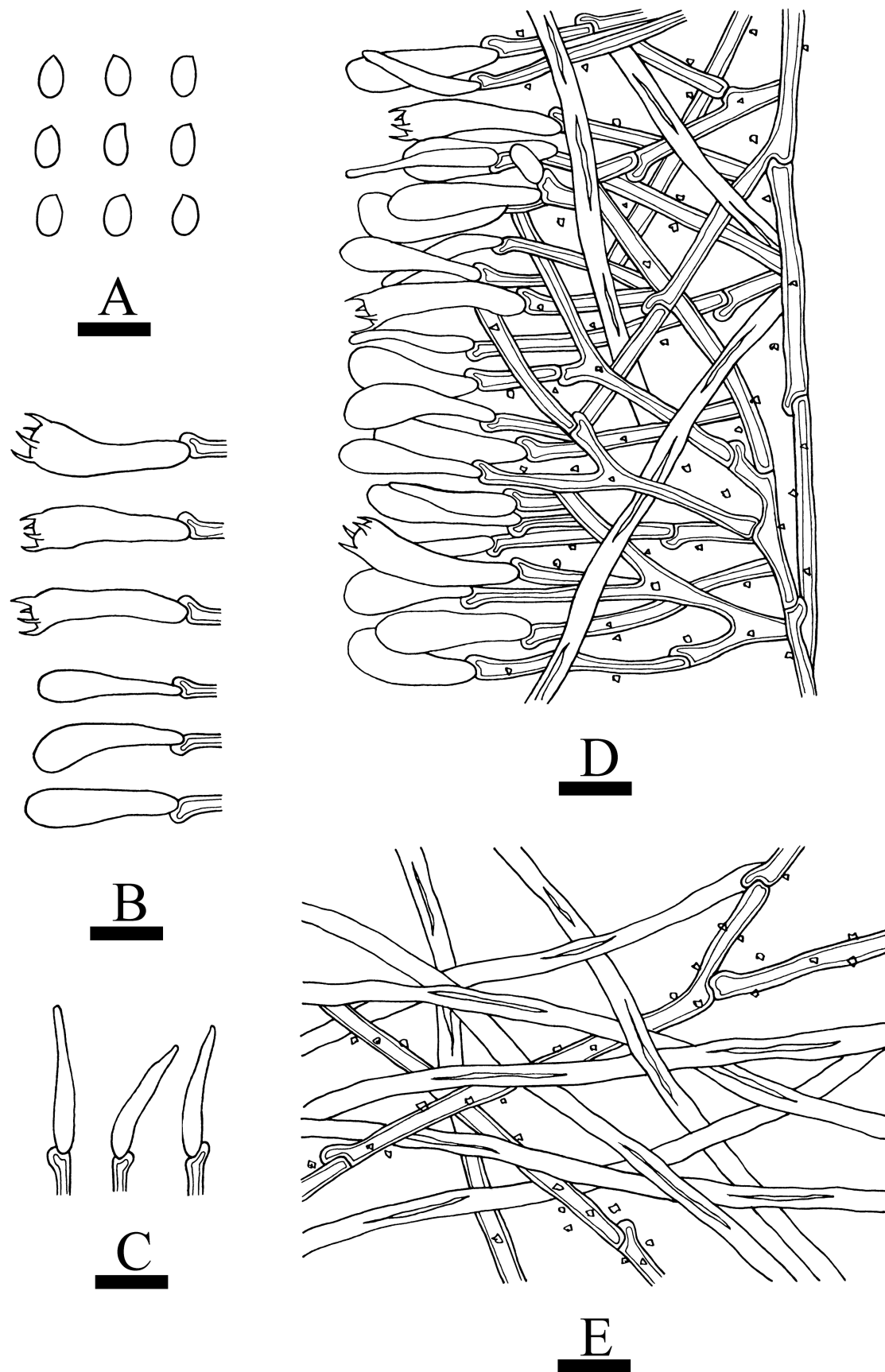


FIGURE 4. Microscopic structures of *Rhodoantrodia purpurascens* (holotype, C.L. Zhao 26267): basidiospores (A), basidia and basidioles (B), cystidia (C), a section of the hymenium (D), hyphae from context (E). Bars: (A–E) = 10 μ m.

Hymenium:—Skeletocystidia numerous, subclavate to cylindrical, colorless, thin-walled, strongly encrusted in the surface and almost entirely, $75\text{--}97 \times 10\text{--}12 \mu\text{m}$; cystidioles absent. Basidia subclavate to barrel, hyaline, thin-walled, with a basal clamp connection and four sterigmata, $15\text{--}18 \times 5\text{--}6.5 \mu\text{m}$; basidioles dominant, in shape similar to basidia, but slightly smaller.

Spores:—Basidiospores ellipsoid to subglobose, hyaline, thin-walled, smooth, IKI–, CB–, $(4\text{--})4.5\text{--}6(\text{--}6.5) \times 3\text{--}4.5 \mu\text{m}$, $L = 5.16 \mu\text{m}$, $W = 3.69 \mu\text{m}$, $Q = 1.40$ ($n = 30/1$).

Discussion

The species diversity, taxonomy, and phylogeny of the phlebioid clade in Polyporales were intensively studied recently by many researchers, and a large number of new taxa from East Asia were described (Dai *et al.* 2015, Justo *et al.* 2017, Hawksworth & Lücking 2017, Chen *et al.* 2021, Liu *et al.* 2023a, b).

Based on the recent research work, the keys to *Rhodoantrodia* and *Steccherinum* species in China were given (Han *et al.* 2020, Liu & Dai 2021, Westphalen *et al.* 2021, Wu *et al.* 2021, Dong *et al.* 2022, 2023, Liu *et al.* 2023a, c). The research about the genus *Rhodoantrodia* showed that it formed a single lineage, and was distant from *Antrodia*, so the mycologist proposed the genus *Rhodoantrodia* as a new genus based on phylogenetic analyses and morphological characteristics (Liu *et al.* 2023a). In our study, four species of *Rhodoantrodia* formed a single lineage in the Fomitopsidaceae, including *Rhodoantrodia purpurascens*, *R. subtropica*, *R. tropica* and *R. yunnanensis*. In the phylogenetic tree (Figure 1), *Rhodoantrodia purpurascens* is closely related to *R. yunnanensis*. However, *R. yunnanensis* is distinct from *R. purpurascens* by having a greyish blue to vinaceous pore surface and longer cylindrical basidiospores ($7\text{--}9.9 \times 2.5\text{--}3.1 \mu\text{m}$) (Han *et al.* 2020, Liu *et al.* 2023a).

In the present study, the new species *Steccherinum wumengshanense* clustered into the genus *Steccherinum* based on phylogenetic analyses and morphological characters. In the phylogenetic tree (Figure 2), *Steccherinum wumengshanense* is retrieved as a sister species to *S. yunnanense* Y.X. Wu & C.L. Zhao (Dong *et al.* 2022). However, *S. yunnanense* can be distinguished from *S. wumengshanense* by its smaller skeletocystidia ($14\text{--}31 \times 3.5\text{--}6 \mu\text{m}$) and shorter basidia ($10.5\text{--}15 \times 5\text{--}6 \mu\text{m}$) (Dong *et al.* 2022).

Morphologically, *Rhodoantrodia tropica* and *R. subtropica* are similar to *R. purpurascens* by having the corky hymenophore and hyaline, thick-walled with a wide to narrow lumen skeletal hyphae (Han *et al.* 2020, Liu *et al.* 2023a, b). However, *R. tropica* differs in *R. purpurascens* by its greyish to pinkish buff pore surface, larger angular pores (3–4 per mm) and longer cylindrical to subfusiform basidiospores ($8.3\text{--}10 \times 2.5\text{--}3 \mu\text{m}$) (Cui 2013, Liu *et al.* 2023a); *R. subtropica* is distinguished from *R. purpurascens* by its larger angular pores (3–4 per mm) and longer cylindrical to subfusiform basidiospores ($7\text{--}8.4 \times 2.6\text{--}3.3 \mu\text{m}$) (Liu *et al.* 2023b). *Steccherinum fragile* Z.B. Liu & Y.C. Dai, *S. hirsutum* Y.X. Wu & C.L. Zhao, *S. incrustans* Z.B. Liu, Y.C. Dai & Jing Si and *S. punctatum* J.H. Dong & C.L. Zhao are similar to *S. wumengshanense* by having the ellipsoid basidiospores (Liu & Cui 2021, Dong *et al.* 2022, 2023, Liu *et al.* 2023c). However, *S. fragile* is distinguished from *S. wumengshanens* by having the salmon to peach pore surface and smaller clavate basidia ($13\text{--}14 \times 4\text{--}4.5 \mu\text{m}$) (Liu & Cui 2021); *S. hirsutum* is distinguished from *S. wumengshanens* by having the stipitate, scarlet to red basidiomata and larger conical aculei (2–4 per mm) (Dong *et al.* 2022); *S. incrustans* differs from *S. wumengshanens* by having buff yellow to clay buff pore surface and smaller skeletocystidia ($15\text{--}35 \times 5\text{--}10 \mu\text{m}$) (Dong *et al.* 2023); *S. punctatum* is separated from *S. wumengshanens* by having the shorter skeletocystidia ($36\text{--}47 \times 7.5\text{--}12 \mu\text{m}$) and longer basidia ($23\text{--}27 \times 5.5\text{--}7.5 \mu\text{m}$) (Liu *et al.* 2023c).

Wood-inhabiting fungi are an extensively studied group of Basidiomycota (Dai *et al.* 2015, Justo *et al.* 2017, Zhao *et al.* 2017, 2023, Xu *et al.* 2020, Liu *et al.* 2023a, b, Wang & Cai 2023). During the investigations of wood-inhabiting fungi, more and more samples of Polyporales were collected in tropical and subtropical regions of Eastern Asia (Zhao *et al.* 2017, Han *et al.* 2020, Gu & Zhao 2021, Wang & Zhao 2022, Dong *et al.* 2022, 2023, Li *et al.* 2023a, b, Duan *et al.* 2023, Yang *et al.* 2023, Yuan *et al.* 2023, Zhang *et al.* 2024). We believe that more species of Polyporales will be found in the oriental realm since wood-inhabiting fungi are a cosmopolitan group and they are rich in this area (Tedersoo *et al.* 2014, Dai *et al.* 2015, Hibbett *et al.* 2016, Guan & Zhao 2017, James *et al.* 2020, Wu *et al.* 2020, Zhou *et al.* 2021, Luo & Zhao 2023, Zhao *et al.* 2023, Wang & Cai 2023, Yang *et al.* 2023) and it is very possible that the same phenomenon occurs for *Rhodoantrodia* and *Steccherinum*.

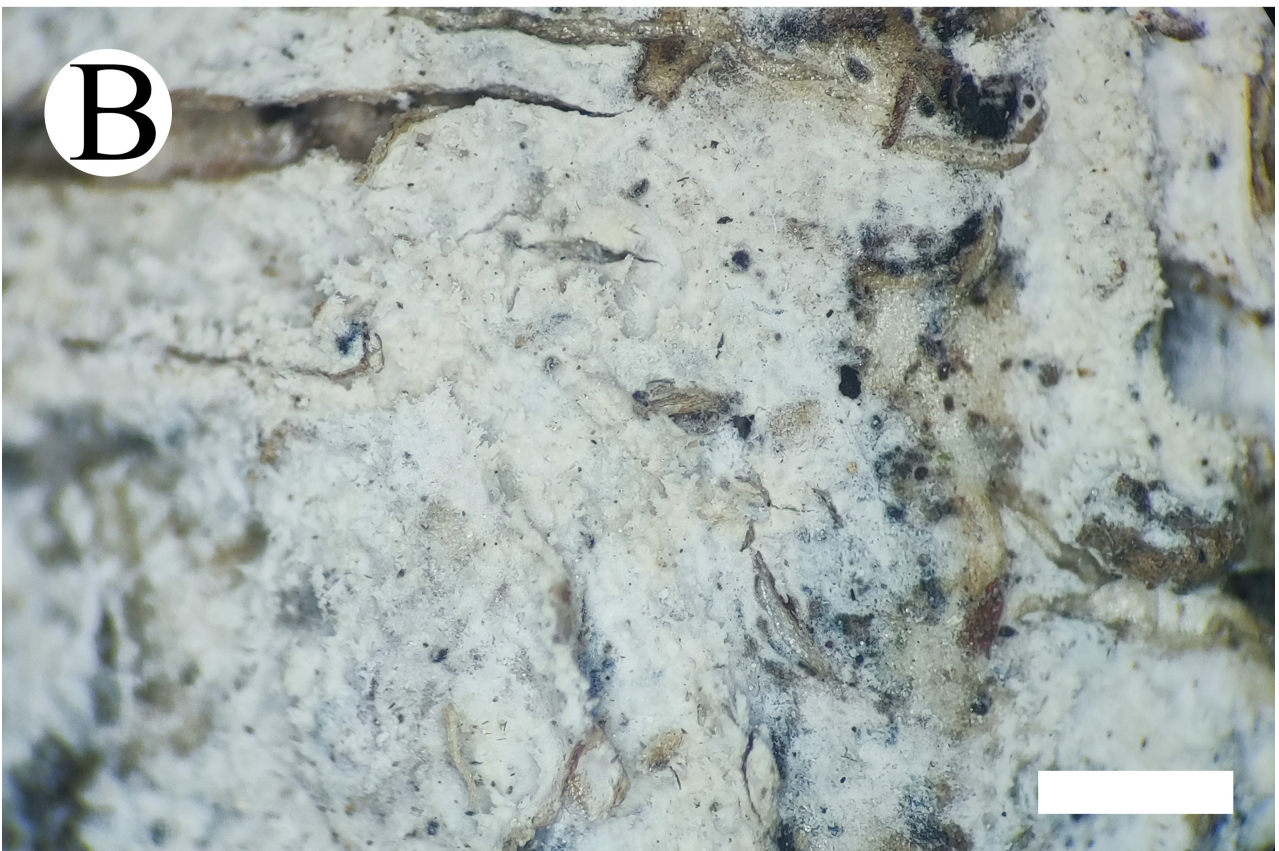


FIGURE 5. *Steccherinum wumengshanense* (holotype, C.L. Zhao 23586): basidiomata on the substrate (A), macroscopic characteristics of hymenophore (B). Bars: (A) = 1 cm and (B) = 1 mm.

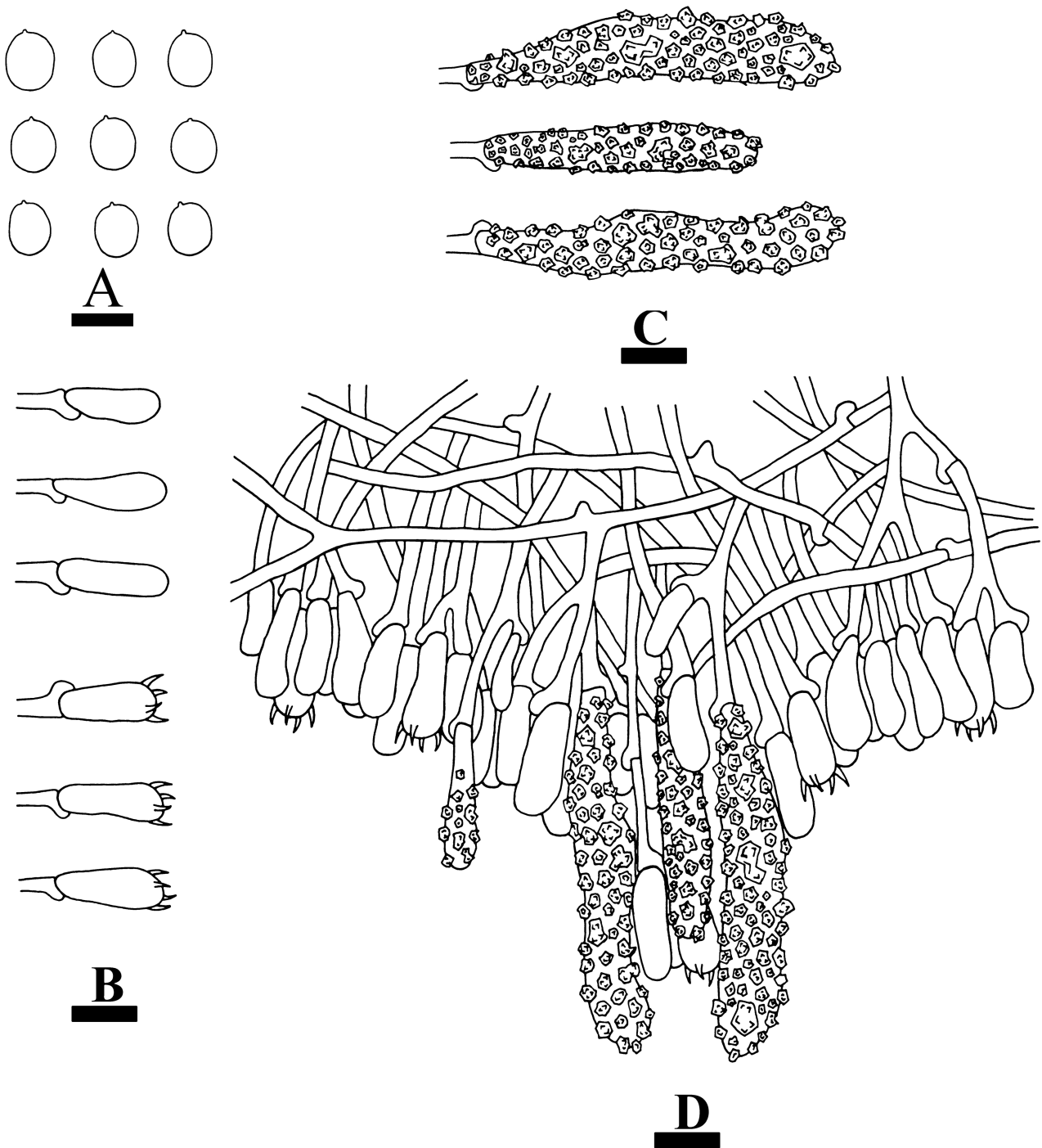


FIGURE 6. Microscopic structures of *Steccherinum wumengshanense* (holotype, C.L. Zhao 23586): basidiospores (A), basidia and basidioles (B), cystidia (C), a section of the hymenium (D). Bars: A= 5 μ m, (B–D) = 10 μ m.

Acknowledgements

The research was supported by the National Natural Science Foundation of China (Project No. 32170004, U2102220), the High-level Talents Program of Yunnan Province (YNQR-QNRC-2018-111), the Research Project of Yunnan Key Laboratory of *Gastrodia* and Fungal Symbiotic Biology (TMKF2023A03), and the Yunnan Province College Students Innovation and Entrepreneurship Training Program (Project no. s202310677034).

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