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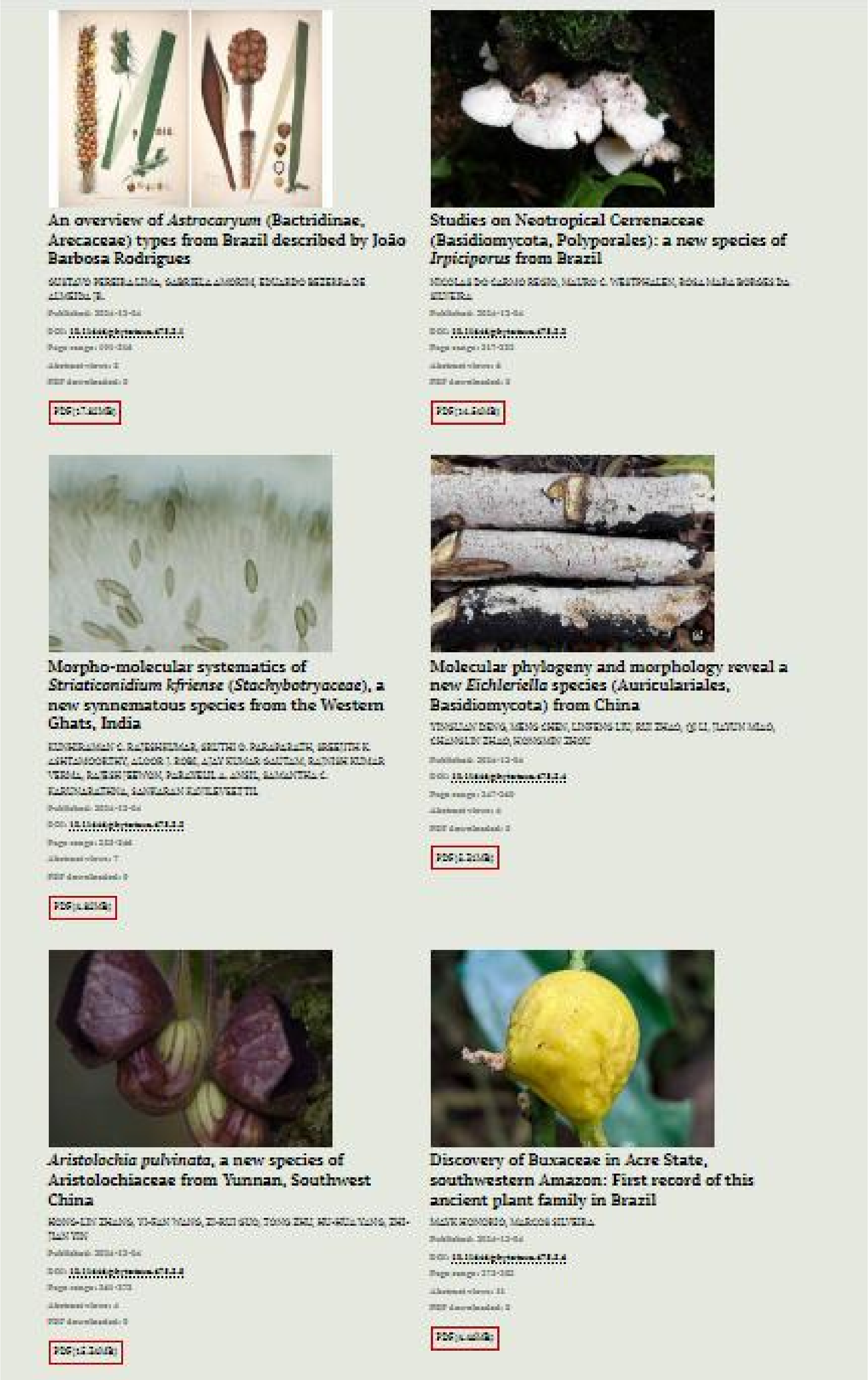

An overview of *Astrocaryum* (Bactridinae, Arecaceae) types from Brazil described by João Barbosa Rodrigues

GUSTAVO PEREIRA LIMA, GABRIELA AMORIM, EDUARDO BEZERRA DE ALMEIDA JR.

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Studies on Neotropical Cerrenaceae (Basidiomycota, Polyporales): a new species of *Irpiciporus* from Brazil

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Morpho-molecular systematics of *Striaticonidium kfriense* (*Stachybotryaceae*), a new synnematous species from the Western Ghats, India

KUNHIRAMAN C. RAJESHKUMAR, SRUTHI O. PARAPARATH, SREEJITH K. ASHTAMOORTHY, ALOOR J. ROSE, AJAY KUMAR GAUTAM, RAJNISH KUMAR VERMA, RAJESH JEEWON, [illegible] A. ANSIL, SAMANTHA C. KARUNARATHNA, SANKARAN [illegible]

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Molecular phylogeny and morphology reveal a new *Eichleriella* species (Auriculariales, Basidiomycota) from China

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***Aristolochia pulvinata*, a new species of Aristolochiaceae from Yunnan, Southwest China**

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[illegible], MARCOS SILVEIRA

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Molecular phylogeny and morphology reveal a new *Eichleriella* species (Auriculariales, Basidiomycota) from China

YINGLIAN DENG[1,4], MENG CHEN[1,5], LINFENG LIU[1,6], RUI ZHAO[1,7], QI LI[1,8], JIAYUN MIAO[2,9], CHANGLIN ZHAO[1,3,10]*& HONGMIN ZHOU[1,11]*

[1] *College of Forestry, Southwest Forestry University, Kunming 650224, P.R. China*
[2] *Yunnan Senhao Fungus Development Corporation Limited Company, Zhaotong, 657000, China*
[3] *Yunnan Key Laboratory of Gastrodia and Fungal Symbiotic Biology, Zhaotong University, Zhaotong 657000, P.R. China*
[4] *fungiyingliand@163.com; https://orcid.org/0000-0002-8220-508X*
[5] *fungilmengchen@163.com; https://orcid.org/0009-0005-9916-8704*
[6] *fungillinfeng@163.com; https://orcid.org/0009-0003-4058-301X*
[7] *fungilruizhao@163.com; https://orcid.org/0009-0005-8445-8223*
[8] *fungiqili@163.com; https://orcid.org/0009-0007-4990-9273*
[9] *youyisidejin@sina.cn*
[10] *fungichanglinz@163.com; https://orcid.org/0000-0002-8668-1075*
[11] *hongminzhou@foxmail.com; https://orcid.org/0000-0002-0724-5815*
**Corresponding author: C.L. Zhao, fungichanglinz@163.com; H.M. Zhou, hongminzhou@foxmail.com*

Abstract

A new wood-inhabiting fungus *Eichleriella yunnanensis* is proposed based on a combination of the morphological features and molecular evidence. *Eichleriella yunnanensis* is characterized by the buff to clay-pink hymenial surface, a monomitic hyphal system with thin- to thick walled generative hyphae having the clamp connections, and thin-walled, subglobose to subclavate basidia with longitudinally septate, and thin-walled, curved-cylindrical to allantoid basidiospores. The phylogenetic tree inferred from ITS+nLSU sequences revealed that the new species was nested into the family Auriculariaceae within the order Auriculariales, in which it was closely related to the species *E. discolor* and *E. xinpingensis.* On the basis of ITS sequences indicated that the new species was nested into the genus *Eichleriella*, and also grouped with the clade comprising *E. discolor* and *E. xinpingensis*.

Key words: Biodiversity, Classification, Molecular systematics, Wood-inhabiting fungi, Yunnan province

Introduction

Auriculariales is a fungal order being mainly composed of wood-inhabiting macrofungi in Agaricomycetes and Basidiomycota (Hibbett *et al.* 2007). The family Auriculariaceae accounts for most of the species in the Auriculariales, and all species in the family are wood-inhabiting fungi with gelatinous, crustaceous, or woody basidiomes (Wells *et al.* 2004, McLaughlin & Spatafora 2014, Bandara *et al.* 2015, Ye *et al.* 2020, Wang & Thorn 2021, Wu *et al.* 2021). Corticioid and stereoid taxa are numerous in Auriculariaceae and typically classified in three main genera, *Eichleriella* Bres., *Exidiopsis* (Bref.) A. Møller, and *Heterochaete* Pat. (Bodman 1952, Wells 1961, Wells & Raitviir 1980, Malysheva & Spirin 2017, Li *et al.* 2023).

The genus *Eichleriella* Bres. (1903: 115) (Auriculariaceae, Auriculariales) was erected in 1903 and typified by *E. incarnata* Bres. (1903: 115), which is characterised by annual or short-living perennial, leathery to ceraceous basidiomata with smooth, pale coloured hymenophore (in some species covered by spines), monomitic to dimitic hyphal structure with clamped genitive hyphae, cystidia often present, longitudinally septate basidia with 2- or 4-celled, and hyaline, cylindrical to narrowly cylindrical basidiospores (Bresadola 1903, Malysheva & Spirin 2017). According to Index Fungorum (www.indexfungorum.org; accessed on 11 June 2024), the genus *Eichleriella* has 31 specific and registered names with 21 species been accepted worldwide (Bresadola 1903, Roberts 2008, Malysheva & Spirin 2017, Liu *et al.* 2019, Wang *et al.* 2022, Li *et al.* 2023).

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The classification and phylogeny of Auriculariales revealed that *Eichleriella* clustered with *Amphistereum* Spirin & Malysheva (Weiß & Oberwinkler 2001, Malysheva & Spirin 2017, Li *et al.* 2023). Malysheva & Spirin (2017) showed that the generic types of *Heterochaete* and *Exidiopsis*, *H. andina* Pat. & Lagerh. and *E. effusa* (Bref. ex Sacc.) A. Møller, respectively, were placed together in a well-supported lineage, and other species of *Heterochaete* were nested within the *Eichleriella* s.s. and *Heteroradulum* Lloyd ex Spirin & Malysheva clades. They reintroduced *Heteroradulum* to accommodate *Eichleriella* and related species that are distantly related to *Eichleriella* s.s. (Bodman 1952, Wells 1961, Wells & Raitviir 1980, Malysheva & Spirin 2017, Li *et al.* 2022). Recently, *Eichleriella aculeobasidiata* Hui Wang, Dong Qiong Wang, C.L. Zhao (2022: 326) was described as a new species from southern China and formed a monophyletic lineage with strong support, and showed that *E. aculeobasidiata* grouped with a clade comprised of *E. xinpingensis* C.L. Zhao (2019: 249) and *E. tenuicula* (Lév.) Spirin & Malysheva (2017: 709) (Wang *et al.* 2022). Phylogenetic analyses on concatenated ITS and 28S rDNA sequences of the Auriculariaceae reported that the five new *Eichleriella alpina* S.H. He, T. Nie & Yue Li (2023: 11), *E. bambusicola* S.H. He, T. Nie & Yue Li (2023: 12), *E. delicata* (Bres.) S.H. He & Nakasone (2023: 14), *E. discolor* (Berk. & Broome) S.H. He & Nakasone (2023: 14) and *E. sinensis* (Teng) S.H. He & Nakasone (2023: 16), in which *Heterochaete sinensis* Teng (1936: 530), *H. delicata* Bres. (1912: 77) and *Kneiffia discolor* Berk. & Broome (1873: 62) were moved to *Eichleriella* based on morphological evidence and DNA analyses (Li *et al.* 2023).

During the surveys of the wood-inhabiting fungi, we collected a new species of *Eichleriella* from Yunnan Province, China, which was not consistent with any known species. We presented the morphological characteristics and multi-genes molecular analyses with ITS and nLSU DNA markers that supported the taxonomy and phylogenetic position of the new species.

Materials and methods

Morphological studies

Fresh fruiting bodies of fungi growing on angiosperm branches were collected from Zhaotong of Yunnan Province, P.R. China. Specimens were dried in an electric food dehydrator at 40 °C, then sealed and stored in an envelope bag and deposited in the herbarium of the Southwest Forestry University (SWFC), Kunming, Yunnan Province, P.R. China. The macromorphological descriptions were based on field notes and photos captured in the field and lab. Color terms follow Petersen (1996) and Kornerup & Wanscher (1967). The micromorphological data were obtained from the dried specimens when observed under a light microscope following Zhao *et al.* (2023). The following abbreviations were used: KOH = 5% potassium hydroxide water solution, CB = Cotton Blue, CB- = acyanophilous, IKI = Melzer's reagent, IKI- = both inamyloid and indextrinoid, L = mean spores length (arithmetic average for all spores), W = mean spores 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 a given number (b) of specimens), Qm = the average of Q (arithmetic average for all spores).

Molecular procedures and phylogenetic analyses

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 (Zhao *et al.* 2023). 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 of the newly generated sequences were deposited in GenBank (Table 1).

TABLE 1. List of species, specimens and GenBank accession numbers of sequences used in this study.

Species	Specimen No.	Locality	GenBank Accession No.		Reference
			ITS	LSU	
Adustochaete nivea	RLMA 531	Brazil	MN165954	MN165989	Hyde *et al.* 2020
Adustochaete rava	KHL15526	Brazil	MK391517	MK391526	Alvarenga *et al.* 2019
Alloexidiopsis australiensis	LWZ 20180513-22	Australia	OM801933	OM801918	Liu *et al.* 2022
Alloexidiopsis nivea	CLZhao 16280	China	MZ352941	MZ352933	Li *et al.* 2022
Alloexidiopsis schistacea	LWZ 20200819-21a	China	OM801939	OM801932	Liu *et al.* 2022
Alloexidiopsis yunnanensis	CLZhao 9132	China	MT215570	MT215566	Guan *et al.* 2020
Amphistereum leveilleanum	FP-106715	USA	KX262119	KX262168	Malysheva & Spirin 2017
Amphistereum schrenkii	HHB 8476	USA	KX262130	KX262178	Malysheva & Spirin 2017
Auricularia mesenterica	FO 25132	Germany	AF291271	AF291292	Weiß & Oberwinkler 2001
Auricularia mesenterica	TUFC12805	Japan	AB915192	AB915191	Sotome *et al.* 2014
Auricularia polytricha	TUFC12920	Japan	AB871752	AB871733	Sotome *et al.* 2014
Eichleriella aculeobasidiata	CLZhao 4422	China	MZ416783	-	Wang *et al.* 2022
Eichleriella alliciens	He 4055b	Thailand	MH178244	-	Li *et al.* 2023
Eichleriella alliciens	HHB 7194	USA	KX262120	KX262169	Malysheva & Spirin 2017
Eichleriella alpina	He 20120916-1 *	China	MH178245	MH178268	Li *et al.* 2023
Eichleriella bactriana	TAAM 104431	Uzbekistan	KX262138	KX262186	Malysheva & Spirin 2017
Eichleriella bambusicola	Dai 6391	China	MH178246	-	Li *et al.* 2023
Eichleriella bambusicola	He 4168	China	MH178247	MH178270	Li *et al.* 2023
Eichleriella crocata	He 2969	China	MH178248	MH178271	Li *et al.* 2023
Eichleriella crocata	TAAM 101077	Russia	KX262100	KX262147	Malysheva & Spirin 2017
Eichleriella delicata	FP-140099	Australia	MH178249	MH178272	Li *et al.* 2023
Eichleriella delicata	He 3469	China	MH178250	MH178273	Li *et al.* 2023
Eichleriella desertorum	LR 49350	Namibia	KX262142	KX262190	Malysheva & Spirin 2017
Eichleriella discolor	He 4584	China	MH178252	MH178275	Li *et al.* 2023
Eichleriella discolor	He 4763	China	MH178253	MH178276	Li *et al.* 2023
Eichleriella flavida	LR 49412	UK	KX262137	KX262185	Malysheva & Spirin 2017
Eichleriella leucophaea	LE 303261	Russia	KX262111	KX262161	Malysheva & Spirin 2017
Eichleriella macrospora	He 2189	USA	MH178251	MH178274	Li *et al.* 2023
Eichleriella ochracea	SP467242	Brazil	MK391514	-	Alvarenga *et al.* 2019
Eichleriella sicca	OM 17349	USA	KX262143	KX262191	Malysheva & Spirin 2017
Eichleriella sinensis	He 4196	China	MH178254	MH178277	Li *et al.* 2023
Eichleriella sinensis	He 5057	China	MH178255	MH178278	Li *et al.* 2023
Eichleriella tenuicula	He 3483	China	MH178256	MH178279	Li *et al.* 2023
Eichleriella tenuicula	LR 17599	Thailand	KX262141	KX262189	Malysheva & Spirin 2017
Eichleriella xinpingensis	CLZhao 836	China	MK560879	MK560883	Liu *et al.* 2019
Eichleriella xinpingensis	CLZhao 842	China	MK560880	MK560884	Liu *et al.* 2019
Eichleriella yunnanensis	**CLZhao 31317***	**China**	**PP889850**	**PP897009**	**present study**
Eichleriella yunnanensis	**CLZhao 31325**	**China**	**PP889851**		**present study**
Eichleriella yunnanensis	**CLZhao 31350**	**China**	**PP889852**	**PP897010**	**present study**
Eichleriella yunnanensis	**CLZhao 31354**	**China**	**PP889853**	**PP897011**	**present study**
Eichleriella yunnanensis	**CLZhao 31364**	**China**	**PP889854**	**PP897012**	**present study**
Eichleriella yunnanensis	**CLZhao 31369**	**China**	**PP889855**		**present study**
Eichleriella yunnanensis	**CLZhao 31372**	**China**	**PP889856**		**present study**

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TABLE 1. (Continued)

Species	Specimen No.	Locality	GenBank Accession No.		Reference
			ITS	LSU	
Eichleriella yunnanensis	**CLZhao 31376**	**China**	**PP889857**		**present study**
Eichleriella yunnanensis	**CLZhao 31437**	**China**	**PP889858**	**PP897013**	**present study**
Eichleriella yunnanensis	**CLZhao 31440**	**China**	**PP889859**	**PP897014**	**present study**
Eichleriella yunnanensis	**CLZhao 31441**	**China**	**PP889860**	**PP897015**	**present study**
Eichleriella yunnanensis	**CLZhao 31456**	**China**	**PP889861**	**PP897016**	**present study**
Eichleriella yunnanensis	**CLZhao 31479**	**China**	**PP889862**	**PP897017**	**present study**
Eichleriella yunnanensis	**CLZhao 31496**	**China**	**PP889863**		**present study**
Eichleriella yunnanensis	**CLZhao 31514**	**China**	**PP889864**	**PP897018**	**present study**
Eichleriella yunnanensis	**CLZhao 31525**	**China**	**PP889865**	**PP897019**	**present study**
Eichleriella yunnanensis	**CLZhao 31527**	**China**	**PP889866**	**PP897020**	**present study**
Eichleriella yunnanensis	**CLZhao 31537**	**China**	**PP889867**	**PP897021**	**present study**
Eichleriella yunnanensis	**CLZhao 31545**	**China**	**PP889868**		**present study**
Eichleriella yunnanensis	**CLZhao 31550**	**China**	**PP889869**	**PP897022**	**present study**
Eichleriella yunnanensis	**CLZhao 31554**	**China**	**PP889870**	**PP897023**	**present study**
Eichleriella yunnanensis	**CLZhao 31556**	**China**	**PP889871**		**present study**
Eichleriella yunnanensis	**CLZhao 31560**	**China**	**PP889872**		**present study**
Eichleriella yunnanensis	**CLZhao 31563**	**China**	**PP889873**		**present study**
Eichleriella yunnanensis	**CLZhao 31606**	**China**	**PP889874**		**present study**
Eichleriella yunnanensis	**CLZhao 31628**	**China**	**PP889875**		**present study**
Eichleriella yunnanensis	**CLZhao 31681**	**China**	**PP889876**		**present study**
Eichleriella yunnanensis	**CLZhao 31688**	**China**	**PP889877**		**present study**
Eichleriella yunnanensis	**CLZhao 31854**	**China**	**PP889878**		**present study**
Eichleriella yunnanensis	**CLZhao 31870**	**China**	**PP889879**		**present study**
Eichleriella yunnanensis	**CLZhao 31872**	**China**	**PP889880**		**present study**
Eichleriella yunnanensis	**CLZhao 31875**	**China**	**PP889881**	**PP897024**	**present study**
Eichleriella yunnanensis	**CLZhao 31929**	**China**	**PP889882**		**present study**
Eichleriella yunnanensis	**CLZhao 31940**	**China**	**PP889883**		**present study**
Eichleriella yunnanensis	**CLZhao 31943**	**China**	**PP889884**		**present study**
Eichleriella yunnanensis	**CLZhao 31963**	**China**	**PP889885**	**PP897025**	**present study**
Eichleriella yunnanensis	**CLZhao 32002**	**China**	**PP889886**		**present study**
Eichleriella yunnanensis	**CLZhao 32461**	**China**	**PP889887**	**PP897026**	**present study**
Eichleriella yunnanensis	**CLZhao 32743**	**China**	**PP889888**	**PP897027**	**present study**
Eichleriella yunnanensis	**CLZhao 32762**	**China**	**PP889889**		**present study**
Eichleriella yunnanensis	**CLZhao 32797**	**China**	**PP889890**		**present study**
Eichleriella yunnanensis	**CLZhao 32845**	**China**	**PP889891**	**PP897028**	**present study**
Eichleriella yunnanensis	**CLZhao 33416**	**China**	**PP889892**		**present study**
Eichleriella yunnanensis	**CLZhao 33431**	**China**	**PP889893**		**present study**
Eichleriella yunnanensis	**CLZhao 33486**	**China**	**PP889894**		**present study**
Elmerina caryae	WD2207	Japan	AB871751	AB871730	Sotome *et al.* 2014
Elmerina cladophora	OM X1902	Indonesia	MG757509	MG757509	Spirin *et al.* 2019
Elmerina sclerodontia	OM X3269	Malaysia	MG757512	MG757512	Spirin *et al.* 2019
Exidia glandulosa	TUFC34008	Japan	AB871761	AB871742	Sotome *et al.* 2014
Exidia pithya	MW 313	Germany	AF291275	AF291321	Weiß & Oberwinkler 2001

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TABLE 1. (Continued)

Species	Specimen No.	Locality	GenBank Accession No.		Reference
			ITS	LSU	
Heterocorticium bambusicola	He 4236 *	China	MH178259	MH178283	Li *et al.* 2023
Heterocorticium bambusicola	He 4604	China	MH178260	MH178284	Li *et al.* 2023
Heterocorticium latisporum	He 20120923-20 *	China	MH178261	MH178285	Li *et al.* 2023
Heteroradulum adnatum	LR 23453	Mexico	KX262116	KX262165	Malysheva & Spirin 2017
Heteroradulum australiense	LWZ 20180512-25	Australia	MZ325255	MZ310425	Li *et al.* 2022
Heteroradulum australiense	LWZ 20180515-26	Australia	MZ325256	MZ310426	Li *et al.* 2022
Heteroradulum deglubens	LE 38182	Sweden	KX262112	KX262162	Malysheva & Spirin 2017
Heteroradulum kmetii	He 4915	China	MH178262	MH178286	Li *et al.* 2023
Heteroradulum kmetii	Kmet	Slovakia	KX262124	KX262173	Malysheva & Spirin 2017
Heteroradulum labyrinthinum	He 5431	China	OQ341430	OQ341434	Li *et al.* 2023
Heteroradulum labyrinthinum	He 5439	China	OQ341431	OQ341435	Li *et al.* 2023
Heteroradulum maolanense	He 4773 *	China	MH178263	MH178287	Li *et al.* 2023
Heteroradulum maolanense	He 4786	China	MH178264	MH178288	Li *et al.* 2023
Heteroradulum mussooriense	Dai 17193	China	MH178265	MH178289	Li *et al.* 2023
Heteroradulum mussooriense	He 2756	China	MH178266	MH178290	Li *et al.* 2023
Metulochaete sanctae-catharinae	AM 0678	Brazil	MK484065	MK480575	Spirin *et al.* 2019
Proterochaete adusta	CN OM10519	China	MK391519	-	Alvarenga *et al.* 2019
Proterochaete adusta	VS9021	Canada	MK391520	MK391528	Alvarenga *et al.* 2019
Protoacia delicata	VS 4615	Russia	MK098923	MK098967	Spirin *et al.* 2019a
Protoacia delicata	VS 7824	Russia	MK098922	MK098966	Spirin *et al.* 2019a
Protodaedalea foliacea	Yuan 5691	China	JQ764666	JQ764644	Zhou & Dai 2013
Protodaedalea hispida	WD 548	Japan	AB871768	AB871749	Sotome *et al.* 2014
Sclerotrema griseobrunneum	TN 2722	Canada	KX262144	KX262192	Malysheva & Spirin 2017
Sclerotrema griseobrunneum	VS 7674	Russia	KX262140	KX262188	Malysheva & Spirin 2017
Tremellochaete atlantica	URM90199	Brazil	MG594381	MG594383	Phookamsak *et al.* 2019
Tremellochaete cilliata	SP467241	Brazil	MK391523	MK391529	Alvarenga *et al.* 2019

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). Two specimens of *Protoacia delicata* Spirin & Malysheva (2019: 19) sequences were assigned as outgroups to root trees in the ITS+nLSU analysis (Figure 1). Sequences of *Amphistereum leveilleanum* (Berk. & M.A. Curtis) Spirin & Malysheva (2017: 697) and *A. schrenkii* (Burt) Spirin & Malysheva (2017: 698) retrieved from GenBank were used as outgroups in the ITS analysis (Figure 2, Li *et al.* 2023).

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 of the characters were equally weighted, and gaps were treated as missing data. Using the heuristic search option with TBR branch swapping and 1000 random sequence additions, trees were inferred. 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), the consistency index (CI), the retention index (RI), the rescaled consistency index (RC), and the 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 data set for Bayesian Inference (BI), which was calculated with MrBayes 3.2.7a with a general time reversible 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 2 million generations of the datasets (Figure 1) and for 1 million generations of the datasets (Figure 2) with trees and parameters sampled every 1,000 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) >70%, maximum parsimony bootstrap value (BT) >70% or Bayesian posterior probabilities (BPP) >0.95.

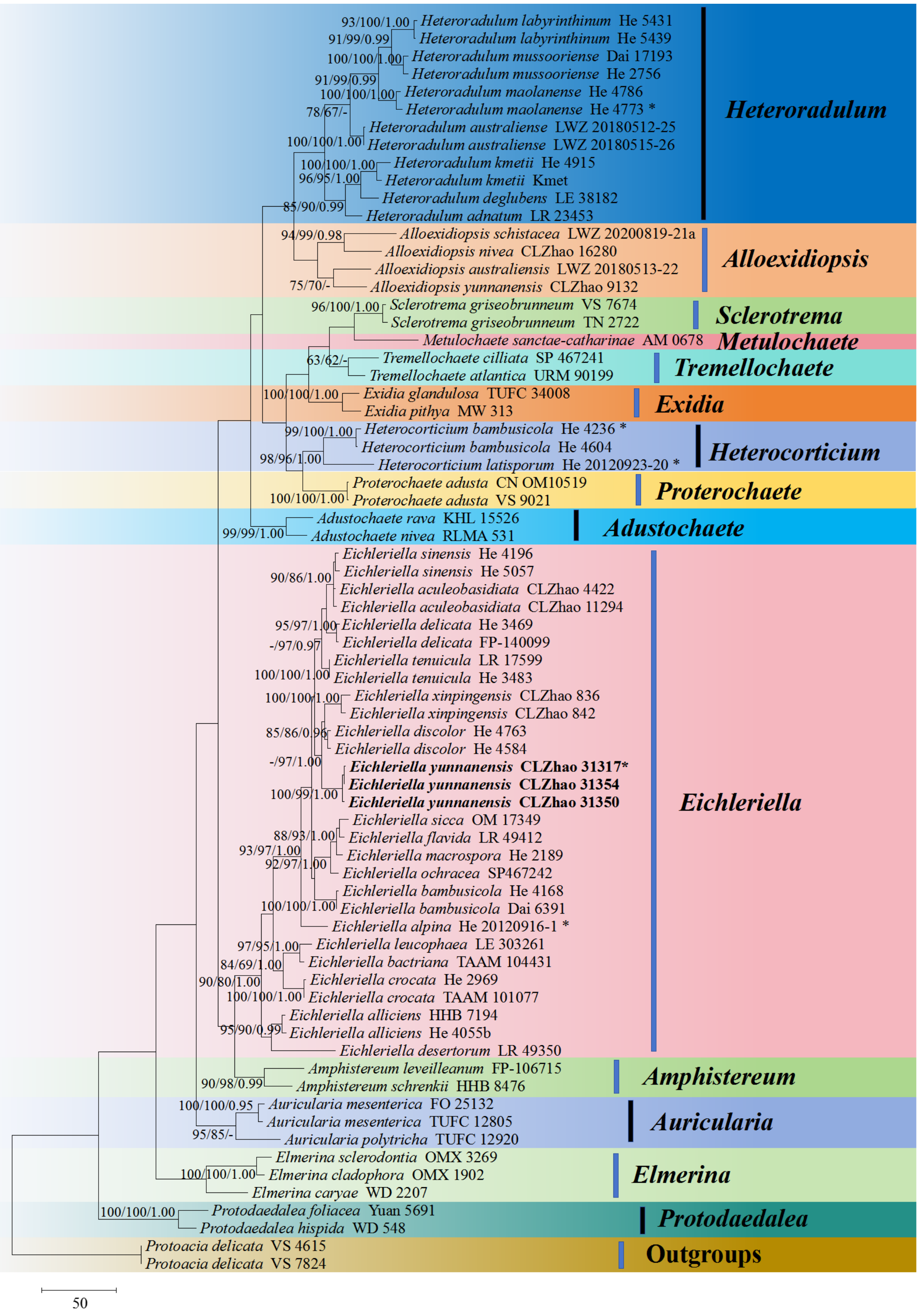

FIGURE 1. Maximum parsimony strict consensus tree illustrating the phylogeny of two new species and related species in Auriculariaceae within Auriculariales based on ITS+nLSU sequences. The branch is labeled with a maximum likelihood lead value greater than 70%, a reduced lead value greater than 50%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

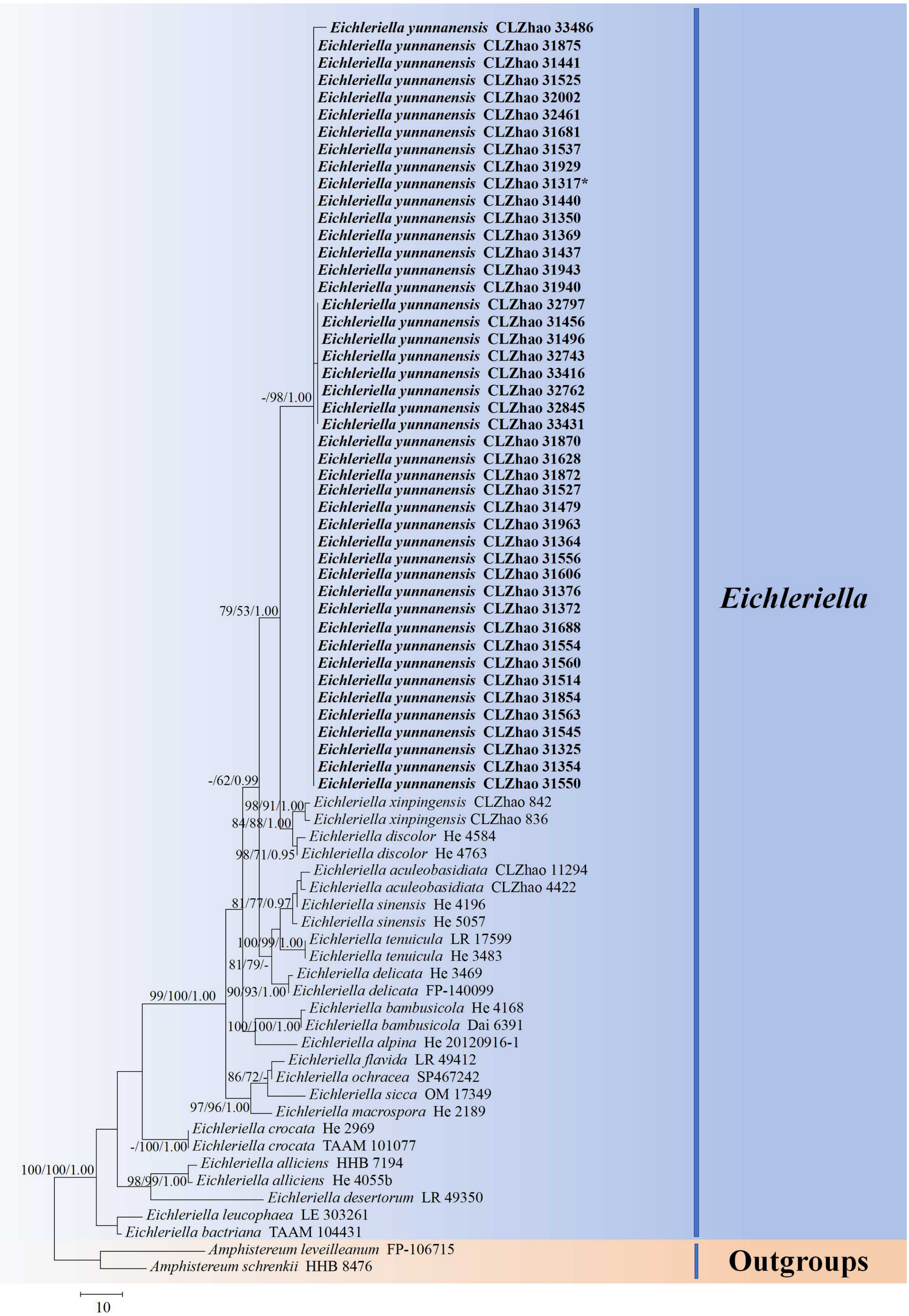

FIGURE 2. Maximum parsimony strict consensus tree illustrating the phylogeny of the new species and related species in *Eichleriella* based on ITS sequences. The branch is labeled with a maximum likelihood lead value greater than 70%, a reduced lead value greater than 50% and a Bayesian posterior probability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

Results

Phylogenetic analyses

The dataset based on ITS+nLSU (Figure 1) comprises sequences from 71 fungal specimens representing 50 species. The dataset had an aligned length of 1959 characters, of which 1447 characters are constant, 107 are variable and parsimony-uninformative, and 405 are parsimony-informative. Maximum parsimony analysis yielded 2 equally parsimonious trees (TL = 1820, CI = 0.4093, HI = 0.5907, RI = 0.6750, RC = 0.2763). The best model for the ITS+nLSU dataset estimated and applied in the Bayesian analysis was TIM2ef+I+G. Bayesian analysis and ML analysis resulted in a similar topology as MP analysis with an average standard deviation of split frequencies of 0.008370 (BI), and the effective sample size (ESS) across the two runs is double the average ESS (avg ESS) = 215. The phylogenetic tree inferred from ITS+nLSU sequences revealed that *Eichleriella yunnanensis* was nested into the family Auriculariaceae within the order Auriculariales, in which it was closely related to the species *E. discolor* and *E. xinpingensis.*

The dataset based on ITS (Figure 2) comprises sequences from 73 fungal specimens representing 20 species. The dataset had an aligned length of 549 characters, of which 413 characters are constant, 49 are variable and parsimony-uninformative, and 87 are parsimony-informative. Maximum parsimony analysis yielded 2 equally parsimonious trees (TL = 281, CI = 0.6335, HI = 0.3665, RI = 0.8286, RC = 0.5249). The best model for the ITS+nLSU dataset estimated and applied in the Bayesian analysis was TIM2ef+I+G. Bayesian analysis and ML analysis resulted in a similar topology as MP analysis with an average standard deviation of split frequencies of 0.008652 (BI), and the effective sample size (ESS) across the two runs is double the average ESS (avg ESS) = 127. On the basis of ITS sequences indicated that the new species nested into the genus *Eichleriella*, in which *Eichleriella yunnanensis* grouped with the clade comprising *E. discolor* and *E. xinpingensis*.

Taxonomy

Eichleriella yunnanensis Y.L. Deng & C.L. Zhao, *sp. nov.* Figs. 3 and 4
MycoBank no.: MB 854309

Etymology:—*yunnanensis* (Lat.): referring to the locality (Yunnan Province) of the new species.

Holotype:—CHINA. Yunnan Province, Zhaotong, Wumengshan National Natural Reserve, 27°51′N, 104°22′E, elev. 2300 m, on the fallen branch of angiosperm, 25 August 2023, CLZhao 31317 (SWFC).

Basidiomata:—Annual, resupinate, ceraceous, without odor or taste when fresh, becoming hard brittle upon drying, very hard to separate from substrate, first as small circular to orbicular colonies, later confluent, up to 18 cm long, 4 cm wide, 100–300 µm thick. Hymenial surface grandinioid, cream (4A2/3) to flesh-pink (8A3/9A4) when fresh, turning to buff (4A4) to clay-pink (6B/C4) upon drying. Sterile margin thin, slightly cream, up to 1 mm.

Hyphal structure:—Hyphal system monomitic, generative hyphae with clamp connections, colorless, thin- to thick walled, interwoven, 1.5–4 µm in diameter; IKI-, CB-, tissues unchanged in KOH.

Hymenium:—Cystidia and cystidioles absent. Dendrohyphidia arising from generative hyphae, nodulose or branched, colorless, thin-walled, 1–3.5 µm in diameter. Basidia subglobose to subclavate, longitudinally septate, two to four-celled, thin-walled, 10–35 × 6–10 µm, with oil drops; basidioles subglobose, similar to basidia in shape, but slightly smaller.

Spores:—Basidiospores curved-cylindrical to allantoid, hyaline, smooth, thin-walled, with 1–2 oil drops, IKI-, CB-, (6.5–)7.5–11.5(–12) × (3–)3.5–5(–6) µm, L = 9.53 µm, W = 4.06 µm, Q = 2.04–2.69 (n = 300/10).

Type of rot:—White rot

Additional specimens examined (paratypes):—CHINA. Yunnan Province, Zhaotong, Wumengshan National Natural Reserve, 27°51′N, 104°22′E, elev. 2300 m, on the branch fallen of angiosperm, 25 August 2023, CLZhao 31325, CLZhao 31350, CLZhao 31354, CLZhao 31364, CLZhao 31369, CLZhao 31372, CLZhao 31376, CLZhao 31437, CLZhao 31440, CLZhao 31441, CLZhao 31456, CLZhao 31479, CLZhao 31496, CLZhao 31514, CLZhao 31525, CLZhao 31527, CLZhao 31537, CLZhao 31545, CLZhao 31550, CLZhao 31554, CLZhao 31556, CLZhao 31560, CLZhao 31563 (SWFC); 26 August 2023, CLZhao 31606, CLZhao 31628, CLZhao 31681, CLZhao 31688 (SWFC), 27 August 2023, CLZhao 31854, CLZhao 31870, CLZhao 31872, CLZhao 31875, CLZhao 31929, CLZhao 31943, CLZhao 32002 (SWFC); on the stump of angiosperm, 27 August 2023, CLZhao 31940, CLZhao 31963 (SWFC); on the trunk of angiosperm, 28 June 2023, CLZhao 32461 (SWFC); on the branch fallen of angiosperm, 29

August 2023, CLZhao 32743, CLZhao 32762, and CLZhao 32845 (SWFC); on the trunk of angiosperm, 29 June 2023, CLZhao 32797 (SWFC); on the branch fallen of angiosperm, 20 September 2023, CLZhao 33416, CLZhao 33431, and CLZhao 33486 (SWFC).

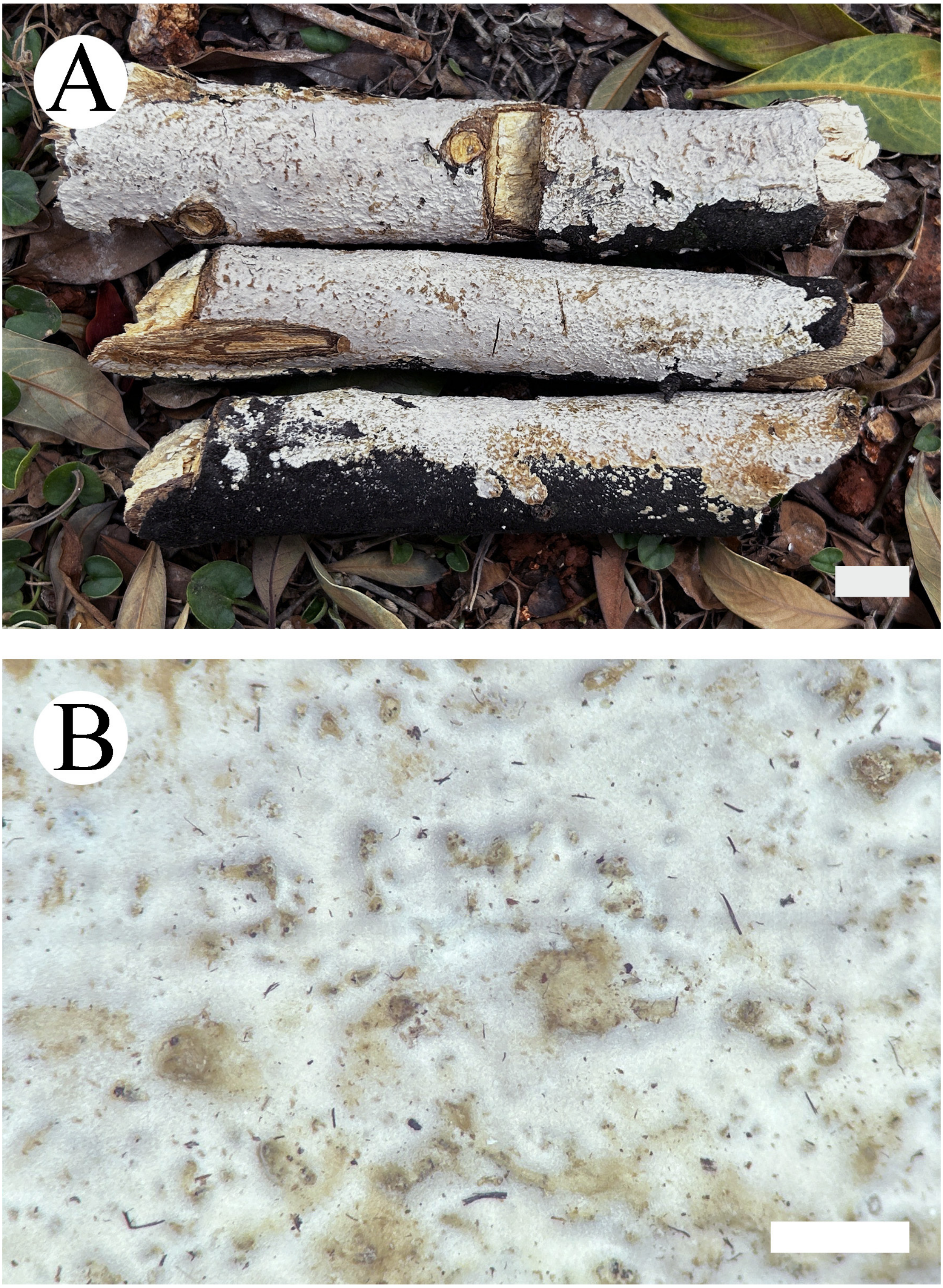

FIGURE 3. *Eichleriella yunnanensis* (holotype, CLZhao 31317): basidiomata on the substrate (A), macroscopic characteristics of hymenophore (B). Bars: (A) = 1 cm and (B) = 1 mm.

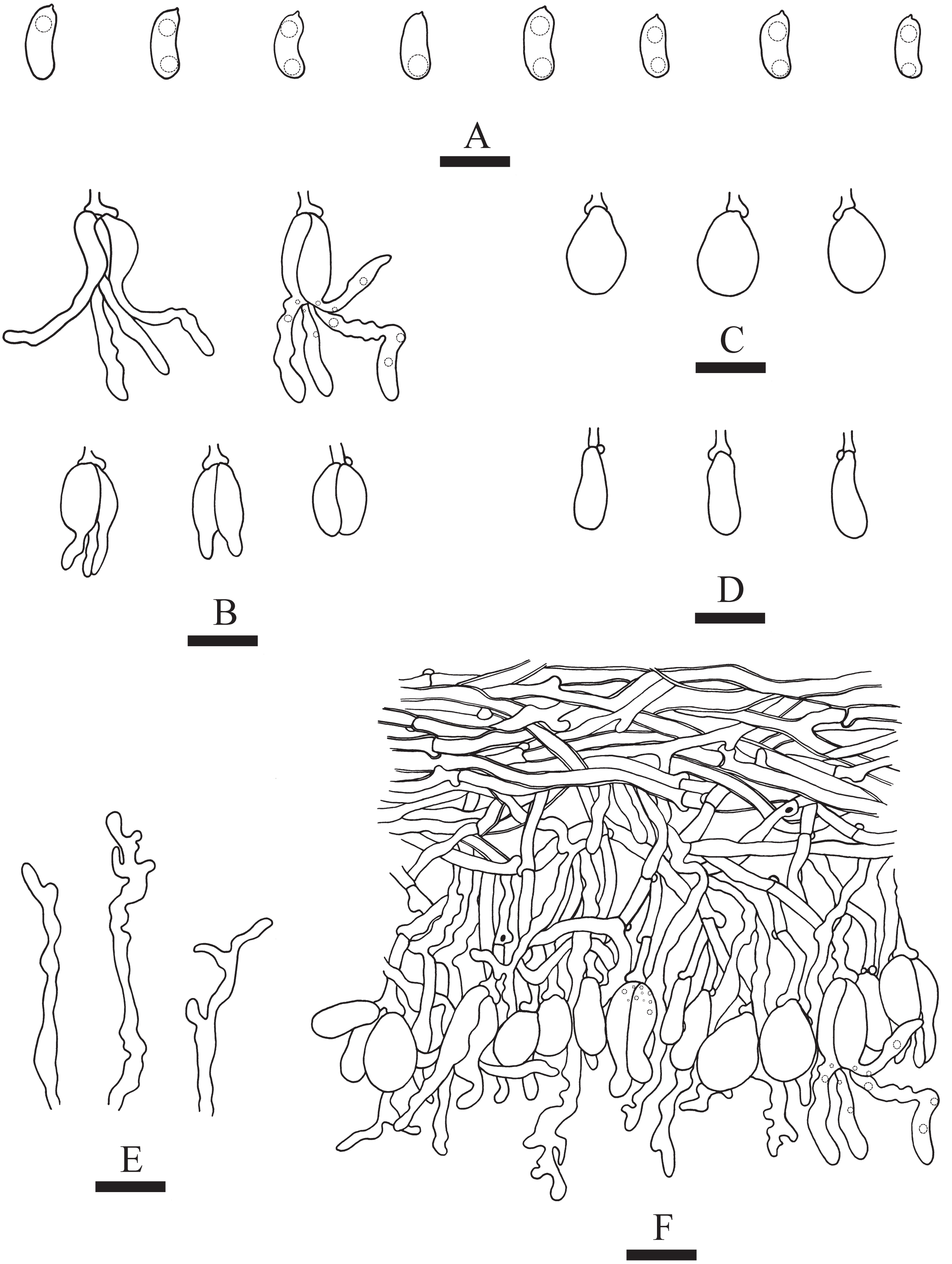

FIGURE 4. Microscopic structures of *Eichleriella yunnanensis* (holotype, CLZhao 31317): basidiospores (A), basidia (B), basidioles (C), cystidia (D), hyphidia (E), a section of the hymenium (F). Bars: A–F= 10 µm.

Notes:—The phylogenetic tree (Figures 1 and 2) inferred from ITS and nLSU sequences revealed that *Eichleriella yunnanensis* was nested into the genus *Eichleriella* s.s. within the family Auriculariaceae, in which *E. yunnanensis* formed a monophyletic lineage, and it was then grouped closely with two taxa *E. discolor* and *E. xinpingensis* from China. However, *E. discolor* can be delimited from *E. yunnanensis* by having spiny-to-velutinous from hyphal pegs, with smooth areas between pegs, hymenial surface first yellowish white (4A2), pale yellow (4A3), orange white (5A2), pale orange (5A3), light orange (5A4), then darkening to greyish orange (5B3), brownish orange (5C5), yellowish brown (5D4), thin-walled generative hyphae, ellipsoid to ovoid basidia, and larger cylindrical basidiospores (11–13.5 × 5–6 µm), often ventrally depressed (Li *et al.* 2023). The species *E. xinpingensis* can be distinguished from *E. yunnanensis* by its flesh-pink to clay-pink to vinaceous hymenial surface covered by blunt-pointed spines, narrowly ovoid to obconical basidia with two celled, and broadly cylindrical basidiospores (Liu *et al.* 2019).

Furthermore, *Eichleriella yunnanensis* resembles *E. aculeobasidiata* and *E. xinpingensis* in sharing cylindrical to allantoid basidiospores. Howerver, *E. aculeobasidiata* can be distinguished from *E. yunnanensis* by having dimitic hyphal system with clamped generative hyphae, and larger allantoid basidiospores (9–13.5 × 4.5–7.5 µm, Wang *et al*. 2022). The taxa *E. xinpingensis* differs from the new species by its blunt-pointed spines hymenial surface, dimitic hyphal system (Liu *et al*. 2019).

Eichleriella yunnanensis shares similarities with *Heterocorticium bambusicola* S.H. He, T. Nie & Yue Li (2023: 7) and *H. latisporum* S.H. He, T. Nie & Yue Li (2023: 10) in sharing monomitic hyphal system with clamped generative hyphae. However, morphologically, *Heterocorticium bambusicola* differs from *E. yunnanensis* by its wider ovoid to subglobose basidia with four-celled, without enucleate stalk (13–20 × 9–11 µm), and larger cylindrical basidiospores with a distinct apiculus (10–14 × 5–6 µm, Li *et al*. 2023); *H. latisporum* can be different from *E. yunnanensis* by having wider ovoid to subglobose, longitudinally septate basidia with four–celled (16–22 × 11–15 µm), and capable of germinating by repetition, broadly ellipsoid-to-ovoid basidiospores with a distinct apiculus (11–13 × 8–9 µm, Li *et al*. 2023). In addition, the new speices resembles *Heteroradulum maolanense* S.H. He, T. Nie & Yue Li (2023: 18) and *H. yunnanense* C.L. Zhao (2020: 57) in sharing cylindrical to allantoid basidiospores. However, *H. maolanense* differs from *Eichleriella yunnanensis* by its odontoid, irpicoid to subporoid from hyphal pegs hymenophore, monomitic-to-subdimitic hyphal system, longitudinally septate, ovoid to subglobose basidia with four-celled (18–25 × 10–15 µm), and capable of germinating by repetition, larger basidiospores with an apiculus (12–15 × 6–7.5 µm, Li *et al*. 2023). *H. yunnanense* can be different from *E. yunnanensis* by having odontoid hymenial surface, longitudinally septate and narrowly ovoid to obconical basidia with two to three-celled (28–41 × 9–14 µm), and larger basidiospores (17–24 × 5–8 µm, Guan *et al*. 2020).

Discussion

In the present study, a new species, *Eichleriella yunnanensis* is described based on phylogenetic analyses and morphological characters.

On phylogenetic trees, the genera *Eichleriella* and *Amphistereum* formed a clade, which are otherwise morphologically very similar. The hyphal structure differentiates *Eichleriella* from *Amphistereum* spp., pronounced a dimitic structure, and smooth hymenium surface differ *Amphistereum* from *Eichleriella* (the sole dimitic representative of the latter genus) (Weiss & Oberwinkler 2001, Malysheva & Spirin 2017, Li *et al.* 2023). Up to now, the genus *Amphistereum* only has been accepted two species, *A. leveilleanum* (Berk. & M.A. Curtis) Spirin & Malysheva (2017: 697) and *A. schrenkii* (Burt) Spirin & Malysheva (2017: 698). However, *A. leveilleanum* can be clearly different from *Eichleriella yunnanensis* by its perennial cupulate-orbicular, hard leathery basidiocarps with pink to pale ochraceous to azonate hymenial surface, dimitic hyphal system and larger cylindrical basidiospores, measuring as 12–16 × 5–6 µm (Malysheva & Spirin 2017). The species *A. schrenkii* can be separated from the new species by having cupulate-orbicular, leathery basidiocarps with pale brown, azonate, densely hirsute abhymenial surface, dimitic hyphal structure with clamp connections, and larger broadly cylindrical basidiospores, measuring as 11.8–14.3 × 6.0–7.1 µm (Malysheva & Spirin 2017). In the Auriculariaceae tree (Figure 1), 14 distinct lineages corresponding to 14 known genera, in which the lineages representing *Eichleriella* was strongly supported as monophyletic genera and grouped closely with *Amphistereum*, and the new species *E. yunnanensis* of the genus *Eichleriella*, was recognized and formed a distinct lineage with strong support values.

The estimation of fungal species ranges from 1 million to 11 million, depending on the criteria employed by various researchers (Hyde *et al.* 2020). The researches of fungal species numbers are still ongoing, and the value of fungi is, however, indisputable with both beneficial and negative impacts (Hyde *et al.* 2023). Our focusing on the species *Eichleriella yunnanensis* is new to science, which enrich the fungal diversity, and both taxa were found in

Yunnan Province, southwest China, which is a hotspot for biodiversity, and more new taxa have been discovered in here by mycologists in the recent years (Dong *et al.* 2023, Yang *et al.* 2023, Yuan *et al.* 2023, Zhang *et al.* 2024).

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