

Molecular phylogeny and morphology reveal a new species of *Exidia* (Auriculariaceae, Auriculariales) from Yunnan Province, China

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Abstract

In this study, *Exidia punctata* is described and illustrated as a novel species based on morphological characteristics and phylogenetic analyses of internal transcribed spacer (ITS) regions and the large subunit (nLSU) of nuclear ribosomal RNA genes. The species is characterized by smooth, membranaceous, cushion-shaped basidiomata with white to cream hymenial surface, and narrowly cylindrical to allantoid basidiospores ($13\text{--}15.5 \times 5\text{--}6.5 \mu\text{m}$). The phylogenetic tree inferred from ITS+nLSU sequences revealed that the new species was nested into the genus *Exidia* within the family Auriculariaceae, in which it grouped with the clade comprising *E. glandulosa*, *E. pithya*, *E. reflexa* and *E. subglandulosa*.

Key words: Biodiversity, corticioid fungi, molecular systematic, taxonomy

Introduction

Species in the family Auriculariaceae (Auriculariales) include important edible and medicinal mushrooms, and all species in the family are wood-inhabiting fungi with gelatinous, crustaceous, or woody basidiomata (Wu *et al.* 2014, 2015; Deng *et al.* 2024b; Dong *et al.* 2024b; He *et al.* 2024). *Exidia sensu lato* is a genus of wood-inhabiting fungi that grows on dead woody plants and is best known in the temperate regions of America, Asia and Europe (Spirin *et al.* 2018; Wu *et al.* 2020; Ye *et al.* 2020; Wang & Thorn 2021; Bian *et al.* 2023; Tohtirjap *et al.* 2023; Sun *et al.* 2023; Yuan *et al.* 2023; Jiang *et al.* 2024; Zhu *et al.* 2024). At present, there are about 10 species of *Exidia sensu lato* distributed in China, viz., *E. glandulosa* (Bull.) Fr., *E. nigricans* (With.) P. Roberts, *E. recisa* (Ditmar) Fr., *E. repanda* Fr., *E. saccharina* Fr., *E. thurettiana* (Lév.) Fr., *E. truncata* Fr., *E. umbrinella* Bres., *E. uvapassa* Lloyd, *E. yadongensis* F. Wu, Qi Zhao, Zhu L. Yang & Y.C. Dai, which improved knowledge of *Exidia sensu lato* across the world (Wu *et al.* 2015, 2022; Ye *et al.* 2020; Wang & Thorn 2021; Tohtirjap *et al.* 2023).

The genus *Exidia* Fr. was proposed by Fries (Fries 1822) and typified by *Exidia glandulosa* (Bull.) Fr., which is characterized by gelatinous basidiomata, ellipsoid to subglobose, longitudinally cruciate septate, 4-celled basidia, cylindrical to allantoid basidiospores, and the ability to cause white rot in woody plants (Spirin *et al.* 2018; Wu *et al.* 2020; Ye *et al.* 2020; Wang & Thorn 2021; Tohtirjap *et al.* 2023). Based on the MycoBank database (<http://www.mycobank.org>, accessed on 7 February 2025) and the Index Fungorum (<http://www.indexfungorum.org>, accessed on

7 February 2025), the genus *Exidia* has 183 specific and registered names with 96 species been accepted worldwide (Wang & Thorn 2021; Tohtirjap *et al.* 2023).

During the last five years, based on multigene phylogenies several species have been described and proposed in the genus *Exidia*, the species *E. qinghaiensis* S.R. Wang & Thorn, *E. reflexa* F. Wu, L.F. Fan & S.Y. Ye, *E. subglandulosa* F. Wu, L.F. Fan & S.Y. Ye and *E. yadongensis* were discovered in China (Wu *et al.* 2020; Ye *et al.* 2020; Wang & Thorn 2021; Tohtirjap *et al.* 2023). In addition, *E. yadongensis* is also an edible and medicinal mushroom with high economic value in Xizang, Southwestern China (Chen *et al.* 2019; Wu *et al.* 2020; He *et al.* 2024).

During the surveys of the wood-inhabiting fungi, we found species of *Exidia*, and it is not consistent with any known species. After morphological characteristics and multi-genes molecular analyses with ITS+nLSU DNA markers that it is a new species, and described here.

Materials and methods

Sample Collection and Herbarium Specimen Preparation

Fresh fruit bodies of fungi growing on angiosperm branches were collected from Lincang and Zhaotong of Yunnan Province, P.R. China. The samples were photographed *in situ* and fresh macroscopic details were recorded. Photographs were taken using a Canon 80D camera (Tokyo, Japan). Specimens were dried in an electric food dehydrator at 45 °C, then 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 derived from comprehensive macroscopic features documented during the specimen collection. The color terminology follows *Farvekort. The Danish Mycological Society's Colour-Chart* (Petersen 1996). The micromorphological data were obtained from the dried specimens observed under a Nikon Eclipse E100 light microscope (Japan) 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, PCR amplification 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).

Molecular Phylogeny

Additional sequences were downloaded from GenBank (Table 1). These sequences were compared with the GenBank database using the Basic Local Alignment Search Tool (BLAST), and available sequences of species in the genus containing ex-type or representative sequences were downloaded from GenBank following previous publications (Spirin *et al.* 2018; Wu *et al.* 2020; Ye *et al.* 2020; Wang & Thorn 2021; Tohtirjap *et al.* 2023; Yuan *et al.* 2023; Dong

et al. 2024a, b). The sequences were aligned in MAFFT version 7 using the G-INS-i strategy (Kato *et al.* 2019). The alignment was adjusted manually using AliView version 1.27 (Larsson 2014). The dataset was aligned and the ITS and nLSU sequences were combined using Mesquite version 3.51. (1) *Sistotrema brinkmannii* (Bres.) J. Erikss. was assigned as an outgroup to root trees in the ITS+nLSU analysis (Figure 1) (Alvarenga & Gibertoni 2021); (2) *Alloexidiopsis nivea* (J.J. Li & C.L. Zhao) L.W. Zhou & S.L. Liu was assigned as an outgroup to root trees following the ITS+nLSU analysis (Figure 2) (Dong *et al.* 2024a).

TABLE 1. Names, voucher numbers, references, & corresponding GenBank accession numbers of the taxa used in the phylogenetic analyses. [* Indicates type materials; — indicates sequence unavailability].

Taxa	Voucher no.	Locality	GenBank accession no.		References
			ITS	nLSU	
<i>Alloexidiopsis australiensis</i>	LWZ 20180514-18	China	OM801934	OM801919	Liu <i>et al.</i> 2022
<i>Alloexidiopsis calcea</i>	LWZ 20180904-14	China	OM801935	OM801920	Liu <i>et al.</i> 2022
<i>Alloexidiopsis grandinea</i>	CLZhao 33798*	China	PP852058	—	Dong <i>et al.</i> 2024b
<i>Alloexidiopsis nivea</i>	CLZhao 11210	China	MZ352948	MZ352939	Li <i>et al.</i> 2022
<i>Alloexidiopsis xantha</i>	CLZhao 25093*	China	PP852060	PP849040	Dong <i>et al.</i> 2024b
<i>Alloexidiopsis yunnanensis</i>	CLZhao 8106	China	MT215569	MT215565	Guan <i>et al.</i> 2020
<i>Amphistereum leveilleianum</i>	FP-106715	USA	KX262119	KX262168	Malysheva & Spirin 2017
<i>Amphistereum schrenkii</i>	HHB 8476	USA	KX262130	KX262178	Malysheva & Spirin 2017
<i>Aporpium caryae</i>	Miettinen 14774	Finland	JX044145	—	Miettinen <i>et al.</i> 2012
<i>Aporpium caryae</i>	WD 2207	Japan	AB871751	AB871730	Sotome <i>et al.</i> 2014
<i>Auricularia auricula-judae</i>	JT 04	UK	KT152099	KT152115	Tohtirjap <i>et al.</i> 2023
<i>Auricularia cornea</i>	Dai 13621	China	MZ618936	MZ669905	Tohtirjap <i>et al.</i> 2023
<i>Auricularia mesenterica</i>	FO 25132	Germany	AF291271	AF291292	Weiß & Oberwinkler 2001
<i>Auricularia polytricha</i>	TUFC 12920	Japan	AB871752	AB871733	Sotome <i>et al.</i> 2014
<i>Auricularia tibetica</i>	Dai 13336	China	MZ618943	MZ669915	Tohtirjap <i>et al.</i> 2023
<i>Eichleriella alliciens</i>	HHB 7194	USA	KX262120	KX262169	Malysheva & Spirin 2017
<i>Eichleriella crocata</i>	TAAM 101077	Russia	KX262100	KX262147	Malysheva & Spirin 2017
<i>Eichleriella flavida</i>	LR 49412	UK	KX262137	KX262185	Malysheva & Spirin 2017
<i>Eichleriella sinensis</i>	He4196	China	MH178254	MH178277	Li <i>et al.</i> 2023
<i>Eichleriella xinpingensis</i>	CLZhao 836	China	MK560879	MK560883	Liu <i>et al.</i> 2019
<i>Elmerina cladophora</i>	Miettinen 14314	Indonesia	MG757509	MG757509	Malysheva <i>et al.</i> 2018
<i>Elmerina sclerodontia</i>	Miettinen 16431	Malaysia	MG757512	MG757512	Malysheva <i>et al.</i> 2018
<i>Exidia candida</i>	VS 3921	Russia	KY801867	KY801892	Spirin <i>et al.</i> 2018
<i>Exidia candida</i>	VS 8588	USA	KY801870	KY801895	Spirin <i>et al.</i> 2018
<i>Exidia crenata</i>	Dai 19464	Canada	MT663359	MT664778	Wu <i>et al.</i> 2020
<i>Exidia crenata</i>	Wu 26	Canada	MT663361	MT664780	Wu <i>et al.</i> 2020
<i>Exidia glandulosa</i>	MW 355	Germany	AF291273	AF291319	Weiß & Oberwinkler 2001
<i>Exidia glandulosa</i>	TUFC34008	Japan	AB871761	AB871742	Wu <i>et al.</i> 2020
<i>Exidia pithya</i>	MW 313	Germany	AF291275	AF291321	Weiß & Oberwinkler 2001

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TABLE 1. (Continued)

Taxa	Voucher no.	Locality	GenBank accession no.		References
			ITS	nLSU	
<i>Exidia punctata</i>	CLZhao 25823*	China	PQ783835	PQ783845	Present study
<i>Exidia punctata</i>	CLZhao 33767	China	PQ783836	PQ783846	Present study
<i>Exidia qinghaiensis</i>	HMAS 156328*	China	NR172805	MW353409	Wang & Thorn 2021
<i>Exidia qinghaiensis</i>	HMAS 156376	China	—	MW353408	Wang & Thorn 2021
<i>Exidia recisa</i>	MW 315	Germany	AF291276	AF291322	Weiß & Oberwinkler 2001
<i>Exidia recisa</i>	SL 180317	Finland	MT663365	MT664783	Tohtirjap <i>et al.</i> 2023
<i>Exidia reflexa</i>	Dai 20833	China	MN850386	MN850362	Tohtirjap <i>et al.</i> 2023
<i>Exidia reflexa</i>	Dai 20861	China	MN850388	MN850364	Tohtirjap <i>et al.</i> 2023
<i>Exidia repanda</i>	LY BR 7046	France	MT663367	MT664784	Wu <i>et al.</i> 2020
<i>Exidia saccharina</i>	Dai 15848	China	OP605366	OP605350	Tohtirjap <i>et al.</i> 2023
<i>Exidia saccharina</i>	Dai 15890	China	OP605367	OP605351	Tohtirjap <i>et al.</i> 2023
<i>Exidia subglandulosa</i>	Wu 270	China	MN850381	MN850357	Wu <i>et al.</i> 2020
<i>Exidia subglandulosa</i>	Wu 272	China	MN850383	MN850359	Tohtirjap <i>et al.</i> 2023
<i>Exidia subsaccharina</i>	Dai 22187*	France	OP605371	OP605355	Tohtirjap <i>et al.</i> 2023
<i>Exidia subsaccharina</i>	Dai 22195	France	OP605370	OP605354	Tohtirjap <i>et al.</i> 2023
<i>Exidia thurettiana</i>	MW 373	Germany	AF291278	AF291324	Weiß & Oberwinkler 2001
<i>Exidia thurettiana</i>	VS 9999	Finland	KY801878	KY801905	Spirin <i>et al.</i> 2018
<i>Exidia truncata</i>	Dai 21231	Finland	MT663369	MT664785	Wu <i>et al.</i> 2020
<i>Exidia truncata</i>	MW 365	Germany	AF291279	AF291325	Weiß & Oberwinkler 2001
<i>Exidia uvapassa</i>	TUFC 34007	Japan	AB871863	AB871744	Wu <i>et al.</i> 2020
<i>Exidia yadongensis</i>	Dai 17209	China	MT663370	MT664786	Wu <i>et al.</i> 2020
<i>Exidia yadongensis</i>	Dai 17212	China	MT663373	MT664789	Wu <i>et al.</i> 2020
<i>Exidiopsis effusa</i>	OM 19136	Finland	KX262145	KX262193	Malysheva & Spirin 2017
<i>Heteroradulum australiense</i>	LWZ 20180512-25*	Australia	MZ325255	MZ310425	Malysheva & Spirin 2017
<i>Heteroradulum deglubens</i>	LE 38182	Sweden	KX262112	KX262162	Malysheva & Spirin 2017
<i>Heteroradulum kmetii</i>	He 4915	China	MH178262	MH178286	Li <i>et al.</i> 2023
<i>Heteroradulum labyrinthinum</i>	Yuan 1600*	China	KM379139	KM379140	Yuan <i>et al.</i> 2018
<i>Heteroradulum mussooriense</i>	Dai 17193	China	MH178265	MH178289	Li <i>et al.</i> 2023
<i>Protodaedalea hispida</i>	WD 548	Japan	AB871768	AB871749	Sotome <i>et al.</i> 2014
<i>Sclerotrema griseobrunneum</i>	TN 2722	Canada	KX262144	KX262192	Malysheva & Spirin 2017
<i>Sclerotrema griseobrunneum</i>	VS 7674	Russia	KX262140	KX262188	Malysheva & Spirin 2017
<i>Sistotrema brinkmannii</i>	236	Netherlands	JX535169	JX535170	Alvarenga & Gibertoni 2021
<i>Tremellochaete atlantica</i>	URM90199	Brazil	MG594381	MG594383	Tohtirjap <i>et al.</i> 2023
<i>Tremellochaete ciliata</i>	SP467241	Brazil	MK391523	MK391529	Alvarenga <i>et al.</i> 2019
<i>Tremellochaete japonica</i>	LE 303446	Russia	KX262110	KX262160	Malysheva & Spirin 2017

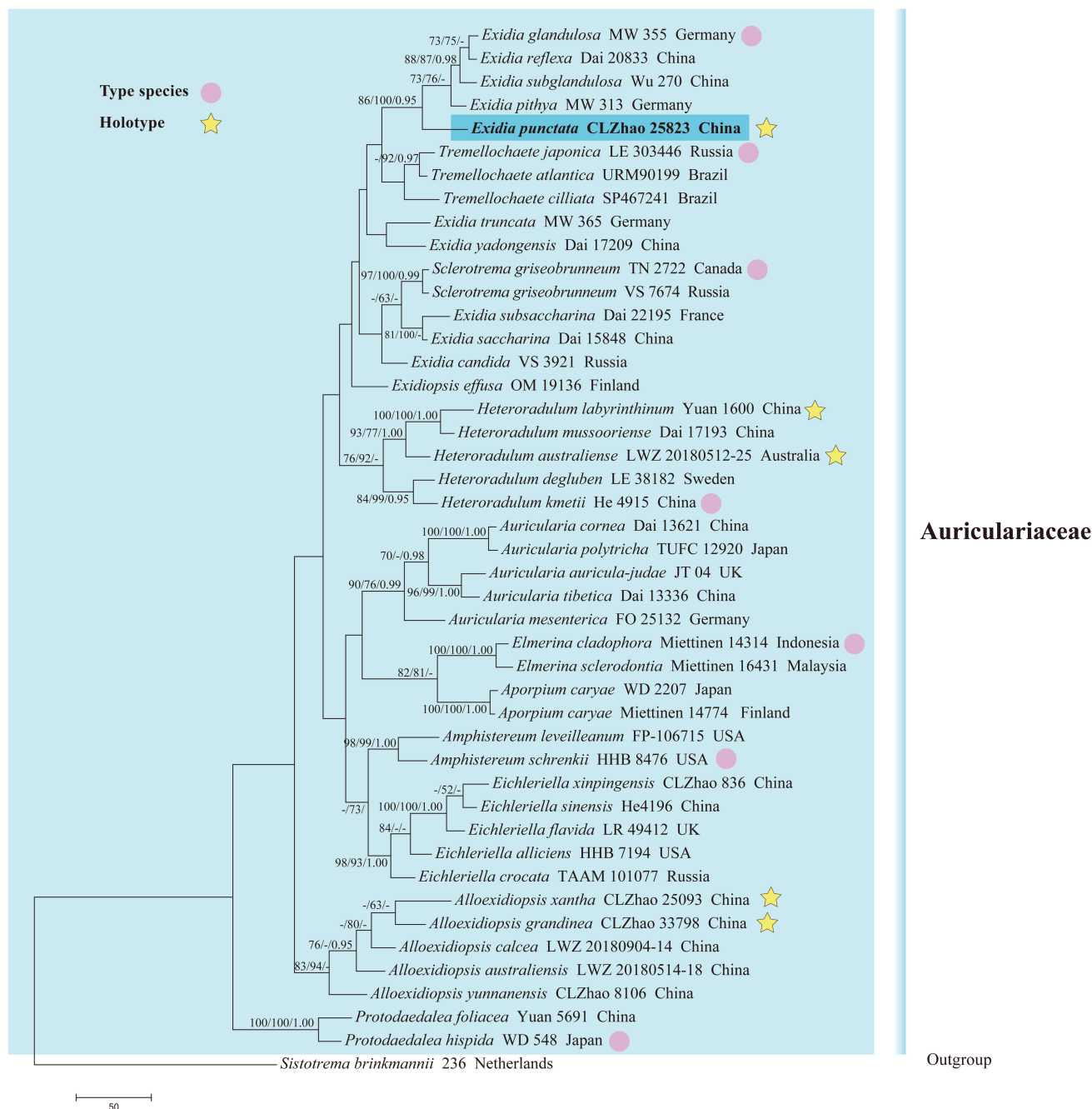


FIGURE 1. Maximum parsimony strict consensus tree illustrating the phylogeny of *Exidia* and related genus in the family Auriculariaceae, based on ITS+nLSU sequences; branches are labeled with maximum likelihood bootstrap value $\geq 70\%$, parsimony bootstrap value $\geq 50\%$ and Bayesian posterior probabilities ≥ 0.95 .

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-HP2 (Miller et al. 2012). Branch support (BS) for ML analysis was determined by 1000 bootstrap replicates.

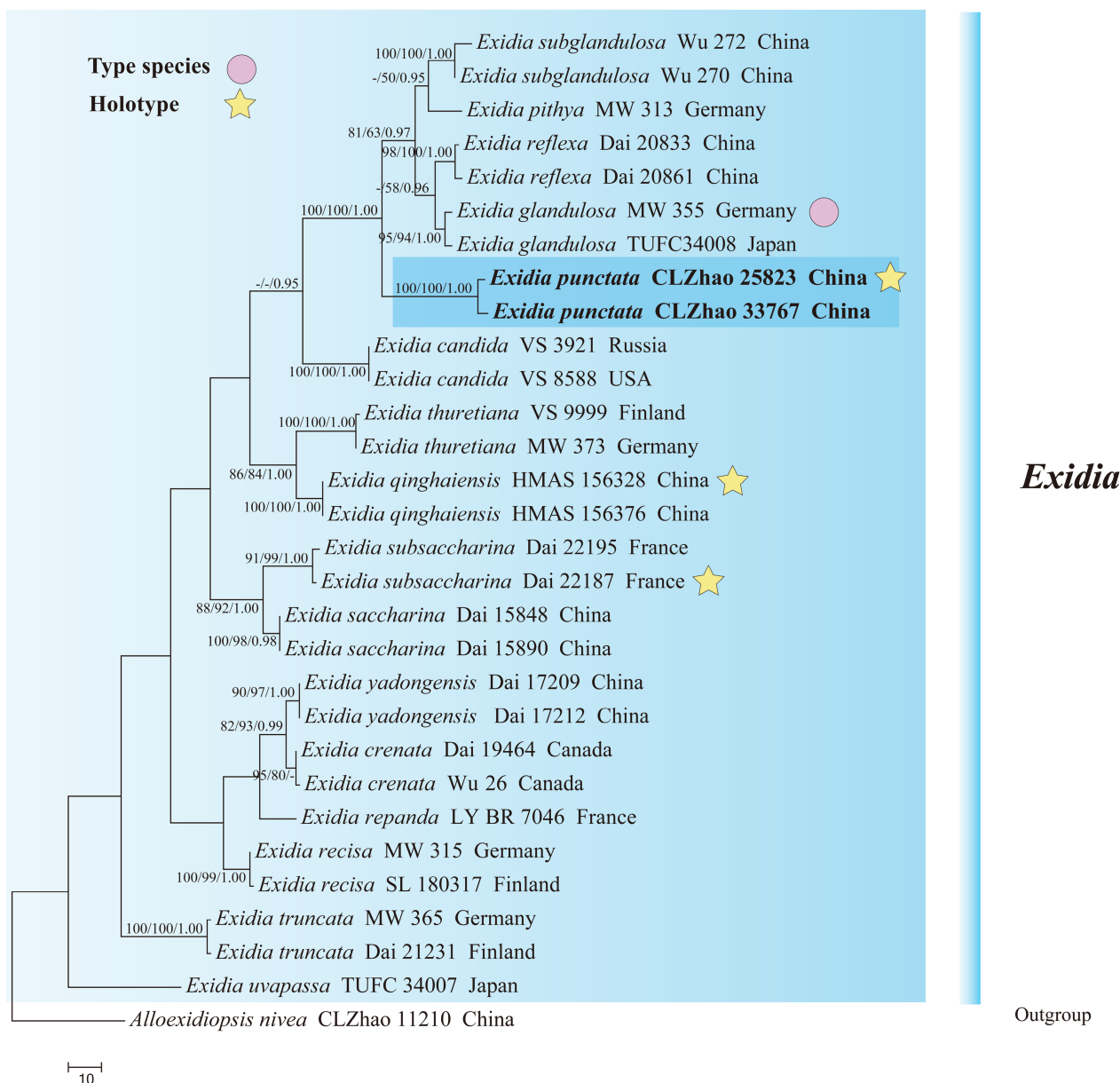


FIGURE 2. Maximum parsimony strict consensus tree illustrating the phylogeny of *Exidia punctata* and related species in the genus *Exidia*, based on ITS+nLSU sequences; branches are labeled with maximum likelihood bootstrap value $\geq 70\%$, parsimony bootstrap value $\geq 50\%$ and Bayesian posterior probabilities ≥ 0.95 .

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 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 0.8 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 burnin. 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) $\geq 50\%$, or Bayesian posterior probabilities (BPP) ≥ 0.95 .

Results

Phylogenetic analyses

The datasets based on ITS+nLSU (Figure 1) comprise sequences from 45 fungal specimens representing 44 species. The datasets had an aligned length of 2056 characters, of which 1460 characters are constant, 246 are variable and parsimony-uninformative, and 350 are parsimony-informative. Maximum parsimony analysis yielded 1 equally parsimonious tree (TL = 1884, CI = 0.4549, HI = 0.5451, RI = 0.5169, RC = 0.2351). Bayesian analysis and ML analysis resulted in a similar topology as MP analysis with an average standard deviation of split frequencies of 0.032178 (BI), and the effective sample size (ESS) across the two runs is double the average ESS (avg ESS) = 341.5. The phylogenetic tree (Figure 1) inferred from ITS and nLSU sequences revealed that the new taxon *Exidia punctata* grouped into the genus *Exidia* and clustered into the family Auriculariaceae (Auriculariales), in which it grouped with the clade comprising *E. glandulosa*, *E. pithya* (Alb. & Schwein.) Fr., *E. reflexa* and *E. subglandulosa*.

Maximum parsimony strict consensus tree illustrating the phylogeny of *Exidia* and related genus in the family Auriculariaceae, based on ITS+nLSU sequences; branches are labeled with maximum likelihood bootstrap value $\geq 70\%$, parsimony bootstrap value $\geq 50\%$ and Bayesian posterior probabilities ≥ 0.95 .

The datasets based on ITS+nLSU (Figure 2) comprise sequences from 30 fungal specimens representing 17 species. The datasets had an aligned length of 1952 characters, of which 1729 characters are constant, 49 are variable and parsimony-uninformative, and 147 are parsimony-informative. Maximum parsimony analysis yielded 32 equally parsimonious trees (TL = 507, CI = 0.5365, HI = 0.4635, RI = 0.7420, RC = 0.3981). Bayesian analysis and ML analysis resulted in a similar topology as MP analysis with an average standard deviation of split frequencies of 0.006210 (BI), and the effective sample size (ESS) across the two runs is double the average ESS (avg ESS) = 193.5. The phylogenetic tree (Figure 2) inferred from ITS and nLSU sequences revealed that *Exidia punctata* grouped into the genus *Exidia*, in which it grouped with the clade comprising *E. glandulosa*, *E. pithya* (Alb. & Schwein.) Fr., *E. reflexa* and *E. subglandulosa*.

Maximum parsimony strict consensus tree illustrating the phylogeny of *Exidia punctata* and related species in the genus *Exidia*, based on ITS+nLSU sequences; branches are labeled with maximum likelihood bootstrap value $\geq 70\%$, parsimony bootstrap value $\geq 50\%$ and Bayesian posterior probabilities ≥ 0.95 .

Taxonomy

Exidia punctata L. Wang & C.L. Zhao, *sp. nov.* FIGS. 3–5

Mycobank no.: 856963

Diagnosis: Differs from other *Exidia* species by the smooth hymenophore with white to cream hymenial surface, monomitic hyphal system with clamped generative hyphae and allantoid basidiospores ($13\text{--}15.5 \times 5\text{--}6.5\ \mu\text{m}$).

Typification: CHINA. Yunnan Province: Lincang, Fengqing County, Yaojie, Xingyuan, GPS coordinates: $24^{\circ}15' \text{N}$, $99^{\circ}55' \text{E}$, altitude: 1600 m asl., on the fallen angiosperm branch, leg. C.L. Zhao, 23 October 2022, CLZhao 25823 (SWFC!).

Etymology: *punctata* (Lat.): refers to the species having dotted basidiomata.

Basidiomata: Annual, resupinate, closely adnate, membranaceous when dry, without odor or taste when fresh, up to 5 cm long, 3 cm wide, and $400\ \mu\text{m}$ thick. Hymenophore smooth, white (60) when fresh, white (60) to cream (4A2/3) upon drying. Sterile margin narrow, cream (4A2/3), up to 1 mm.

Hyphal system: Monomitic; generative hyphae with clamp connections, colorless, thin- to thick-walled, smooth, rarely branched, interwoven, $1\text{--}3\ \mu\text{m}$ in diameter; IKI–, CB–; tissues unchanged in KOH.

Hymenium: Cystidia and cystidioles absent. Basidia narrowly ovoid to ellipsoid, longitudinally septate, four-celled, with a basal clamp septum and four sterigmata ($2\text{--}20 \times 2\text{--}4\ \mu\text{m}$), $18.5\text{--}20 \times 9\text{--}11.5\ \mu\text{m}$; basidioles numerous, in shape similar to basidia but smaller, $18\text{--}19.5 \times 9\text{--}10\ \mu\text{m}$.

Spores: Basidiospores allantoid, with a distinct apiculus, colorless, thin-walled, smooth, usually with one or more oil drops, IKI–, CB–, $13\text{--}15.5\text{--}(17) \times 5\text{--}6.5\text{--}(7)\ \mu\text{m}$, $L = 14.18\ \mu\text{m}$, $W = 5.69\ \mu\text{m}$, $Q = 2.19\text{--}2.49$ ($n = 60/2$).

Additional specimen examined (paratype)—CHINA. Yunnan Province: Zhaotong, Wumengshan National Nature Reserve, GPS coordinates: $27^{\circ}46' \text{N}$, $104^{\circ}15' \text{E}$, altitude: 1900 m asl., on the fallen angiosperm branch, leg. C.L. Zhao, 21 September 2023, CLZhao 33767 (SWFC!).



FIGURE 3. Basidiomata of *Exidia punctata* (holotype CLZhao 25823). Scale bars: 1 cm (A); 1 mm (B).

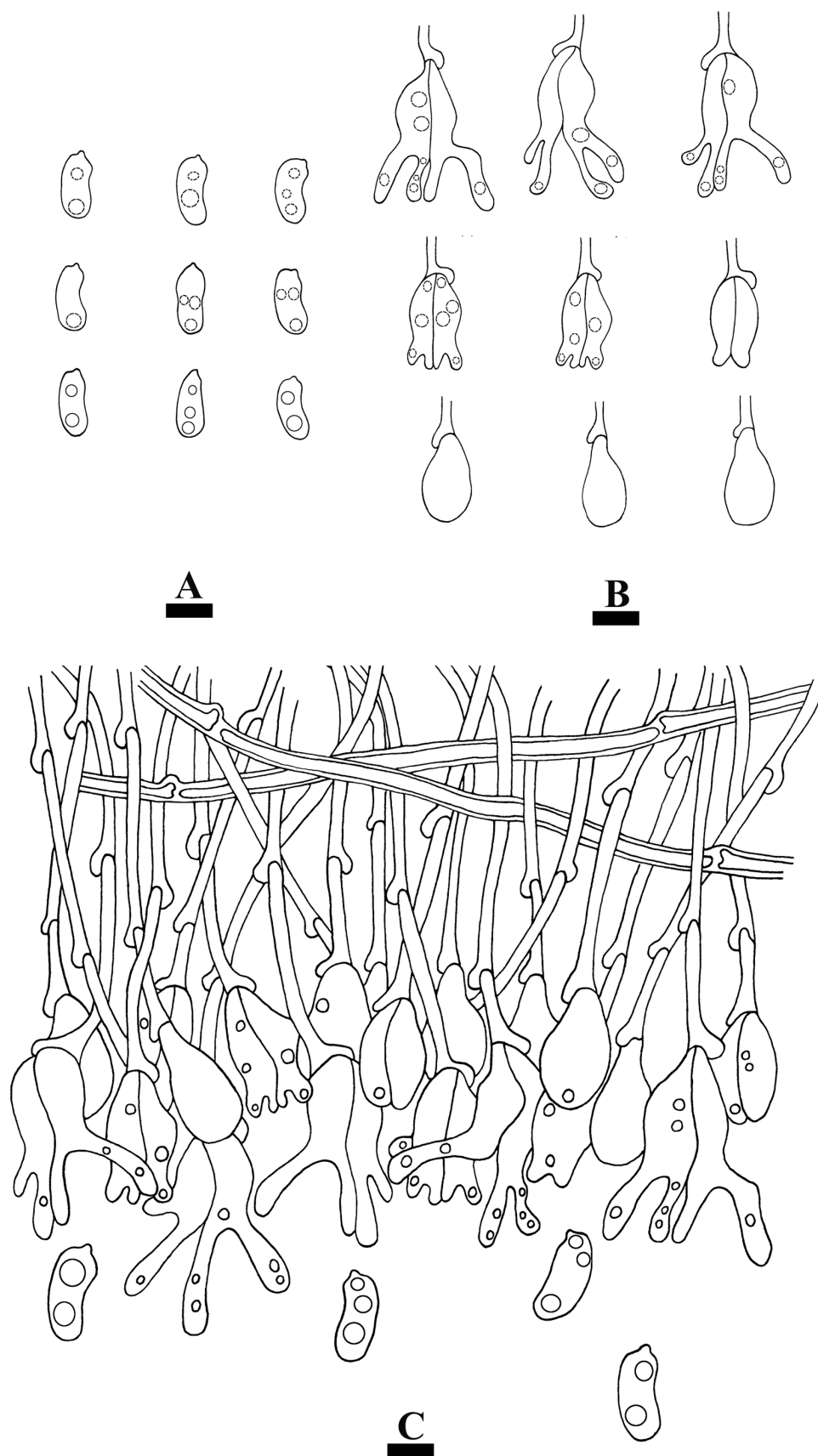


FIGURE 4. Microscopic structures of *Exidia punctata* (holotype CLZhao 25823): (A) basidiospores; (B) basidia and basidioles; (C) a section of the hymenium. Scale bars: 10 μ m (A–C).

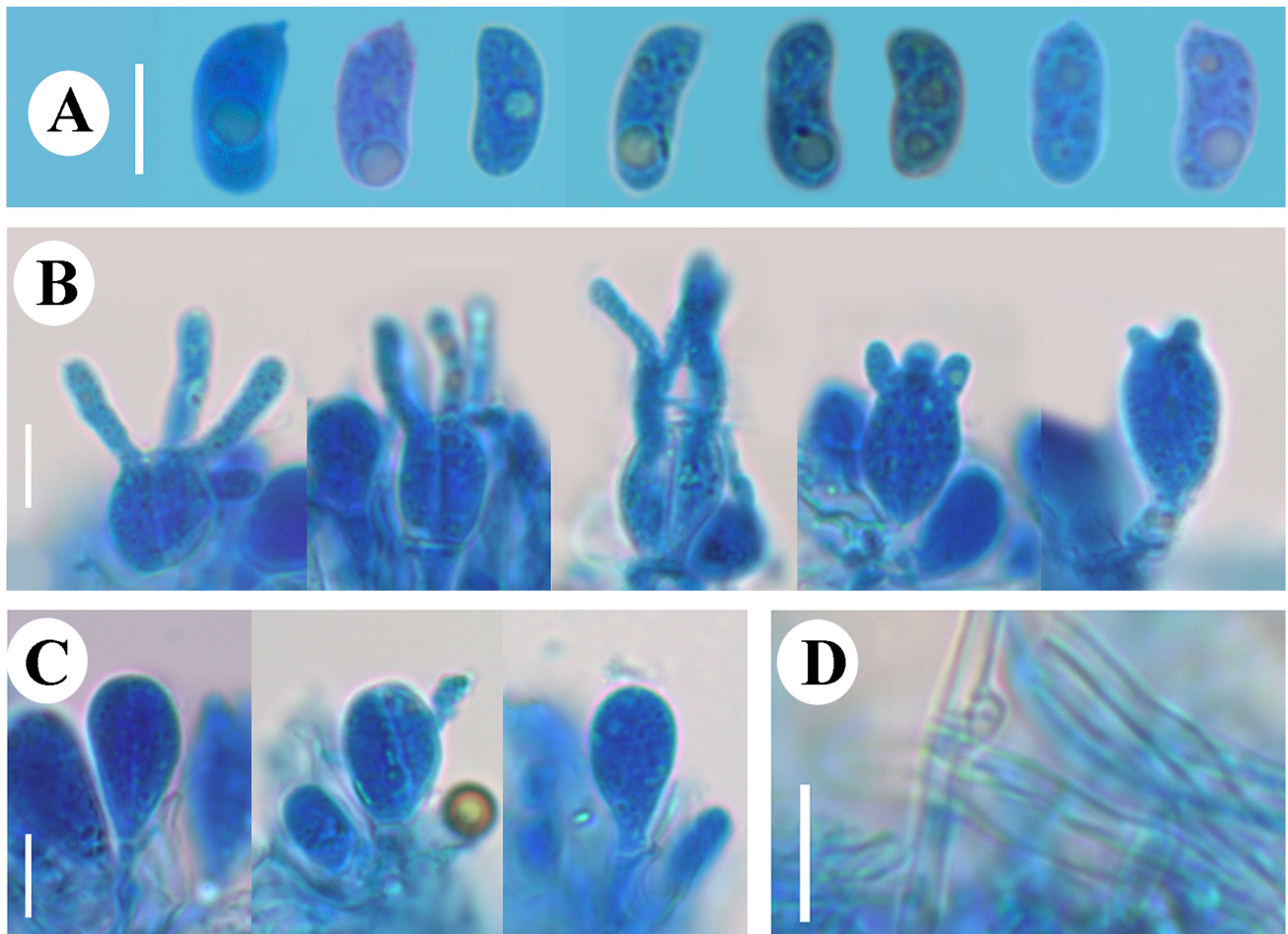


FIGURE 5. Microscopic structures of *Exidia punctata* (holotype CLZhao 25823): (A) basidiospores; (B) basidia; (C) basidioles; (D) a section of context. Scale bars: 10 µm (A–D); 10 × 100 Oil.

Discussion

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

The phylogenetic tree inferred from ITS+nLSU sequences revealed that the new species *Exidia punctata* was nested into the genus *Exidia* within the family Auriculariaceae, in which it grouped with a clade comprising *E. glandulosa*, *E. pithya*, *E. reflexa* and *E. subglandulosa*.

Morphologically, a comparison of morphological characteristics of *E. glandulosa*, *E. pithya*, *E. reflexa* and *E. subglandulosa* is provided in Table 2. The species *E. punctata* is morphologically similar to others species by having allantoid basidiospores. However, *E. punctata* has white to cream, cushion-shaped basidiomata, whereas *E. glandulosa* and *E. subglandulosa* have basidiomata which are not cushion-shaped; *E. pithya* and *E. reflexa* are usually having dark gray to black effused-reflexed basidiomata (Malysheva 2012; Ye *et al.* 2020).

The genus *Exidia* was less studied, but it has received attention in recent years, because of its edible species and medicinal values (Spirin *et al.* 2018; Wu *et al.* 2020; Ye *et al.* 2020; Wang & Thorn 2021; Tohtirjap *et al.* 2023; He *et al.* 2024). We are focusing on taxonomy and phylogeny of wood rotting fungi, in which *Exidia punctata* is new to science, which enriches the fungal diversity, and the taxa was found in Yunnan Province, southwest China, and this area is a hotspot for biodiversity. It also helping the scientific community and professionals in the field of mycology and biodiversity conservation to further explore and utilize these resources.

TABLE 2. Morphological characteristics used for distinguishing the clade comprising *E. reflexa*, *E. glandulosa*, *E. pithya*, *E. punctata* and *E. subglandulosa*.

Species name	Basidiomata	Basidia	Basidiospores	Habitat	Distribution	References
<i>E. reflexa</i>	Effused-reflexed	Subglobose to ovoid (9.6–11.7 × 7.6–9.5 µm)	Allantoid (9–10 × 2–2.5 µm)	Hardwood	Asia	Ye <i>et al.</i> 2020
<i>E. glandulosa</i>	Effused	Ellipsoid to ovoid (12–14 × 8–10 µm)	Allantoid (10.4–14 × 3.2–4.5 µm)	Hardwood	Europe, America, Asia	Malysheva 2012 Ye <i>et al.</i> 2020
<i>E. pithya</i>	Effused	Ellipsoid to ovoid (9.6–11.7 × 7.6–9.5 µm)	Allantoid (9–10 × 2–2.5 µm)	Conifer wood	Europe, America	Malysheva 2012 Ye <i>et al.</i> 2020
<i>E. punctata</i>	Effused	Narrowly ovoid to ellipsoid (18.5–20 × 9–11.5 µm)	Allantoid (13–15.5 × 5–6.5 µm)	Hardwood	Asia	Present study
<i>E. subglandulosa</i>	Gelatinous	Subglobose to ovoid (12–14.6 × 8.7–10.8 µm)	Allantoid (14.2–16.8 × 3.2–4.6 µm)	Hardwood	Asia	Ye <i>et al.</i> 2020

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