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Morphological characteristics and phylogenetic analyses reveal *Ceraceocium vitreum gen. et sp. nov.* (Auriculariales, Basidiomycota) from southwestern China

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Abstract

Wood-inhabiting fungi represent a highly diverse group of macrofungi that play essential roles in forest ecosystems, they are considered as the "key player" in wood decomposition, because of their ability to produce lignocellulosic enzymes breaking down lignin, cellulose and hemicellulose. In the present study, a new wood-inhabiting fungal genus, *Ceraceocium gen. nov.*, and a new species, *C. vitreum sp. nov.*, found from southwestern China, are proposed based on a combination of morphological characteristics and molecular evidence. The new genus *Ceraceocium* is characterized by gelatinous basidiomata with smooth hymenial surface, a monomitic hyphal system and generative hyphae bearing clamp connections, and broadly ellipsoid basidiospores. Sequences of the internal transcribed spacers (ITS) and the large subunit (nrLSU) of the nuclear ribosomal DNA (rDNA) markers of the studied samples were generated. Phylogenetic analyses were conducted using Maximum Likelihood (ML) and Bayesian Inference (BI) methods. Phylogenetic analyses based on combined ITS+nrLSU datasets indicated that *Ceraceocium vitreum* gen. et sp. formed a distinct monophyletic lineage within the order Auriculariales.

Key words: Biodiversity, new genus, taxonomy, Yunnan Province

Introduction

Wood-inhabiting fungi occur in nearly all terrestrial ecosystems and have been reported from diverse habitats, including air, marine environments, exposed rock surfaces, soils and all tissues of land plants (Tedersoo *et al*. 2014, Case *et al*. 2025, Crous *et al*. 2025). They are a highly diverse group of eukaryotic organisms that play crucial roles in various biological processes (Wang *et al*. 2013, Dai *et al*. 2021, Hibbett *et al*. 2025, Wijesinghe *et al*. 2025, Zhao *et al*. 2025, 2026).

The order Auriculariales Bromhead (1840: 2) is mainly composed of wood-inhabiting fungi within Agaricomycetes Doweld (Basidiomycota) (Wells 1964, Weiss & Oberwinkler 2001, Alvarenga *et al*. 2015, Spirin *et al*. 2025). The type genus *Auricularia* Bull. includes several economically important edible and medicinal species (Wu *et al*. 2019, 2026, Yuan *et al*. 2019), together with other gelatinous genera such as *Exidia* Fr. (1822: 2), *Guepinia* Fr. (1825: 92) and *Pseudohydnum* P. Karst. (1868: 9) (Liu *et al*. 2022, Zhou *et al*. 2023). Consequently, research interest in the species diversity of gelatinous genera has increased significantly in recent years (Malysheva *et al*. 2018, Spirin *et al*. 2019b, Tohtirjap *et al*. 2023, Zeng *et al*. 2026, Zhang *et al*. 2026, Zhuang *et al*. 2026).

Currently, molecular phylogenetic analyses based on multiple genes play a vital role in the taxonomy of Auriculariales, particularly within Auriculariaceae Fr. (1836: 530), not only for the delineation of novel species but also for revising the classification of previously unclassified taxa (Weiss & Oberwinkler 2001, Malysheva *et al*. 2018,

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Wu *et al*. 2015). Weiss & Oberwinkler (2001) constructed phylogenetic relationships in Auriculariales and related groups based on nrLSU sequences, which proposed that this order Auriculariales was a polyphyletic and the family Sebacinaceae K. Wells & Oberw. (1982: 74) was confirmed as a monophyletic group, which appeared distant from other taxa ascribed to the Auriculariales (Weiss & Oberwinkler 2001). Wells *et al*. (2004) based on nrLSU sequences accepted Auriculariaceae and Hyaloriaceae Lindau (1897: 1), and considered Exidiaceae R.T. Moore (1978: 70) as a synonym of Auriculariaceae. Furthermore, based on the combined ITS+nrLSU sequence dataset, *Exidia* species were also classified into Auriculariaceae by several researches (Zhou & Dai 2013, Yuan *et al*. 2018, Spirin *et al*. 2019a, b, He *et al*. 2024). Hyaloriaceae was rarely mentioned and even abandoned (He *et al*. 2024). However, based on ITS+nrLSU phylogenetic analyses, Weiss & Oberwinkler (2001) concluded, the phylogenetic clade included *Myxarium* Wallr. (1833: 2) species and *Hyaloria pilacre* Möller (1895: 8) was distant from other core taxa of Auriculariaceae (Weiss & Oberwinkler 2001, Yuan *et al*. 2018, Spirin *et al*. 2018). Tohtirjap *et al*. (2023) reached the same conclusion through combined ITS+nrLSU phylogenetic analyses. Therefore, the family was accepted by some researchers (Wells *et al*. 2004, Tohtirjap *et al*. 2023). Currently, two families, Auriculariaceae and Hyaloriaceae, are accepted in the order (He *et al*. 2024, Spirin *et al*. 2025). In recent years, the species diversity of the resupinate Auriculariales have been described or better defined using morphological and molecular analyses and the results showed the hidden diversity of this group and several gelatinous genera, for example, *Crystallodon* Alvarenga (2021: 42), *Gelacantha* Malysheva & Spirin (2019: 27), *Metulochaete* R.L.M. Alavarenga (2019: 18), and *Tremellochaete* Raitv. (1964: 13), which have been established and described, based on the morphological and phylogenetic studies (Malysheva & Spirin 2017, Spirin *et al*. 2019a, b, Alvarenga & Gibertoni 2021). However, a considerable number of species within this order remain undiscovered.

During investigations of wood-inhabiting fungi on the Yunnan-Guizhou Plateau, China, numerous specimens were collected. To clarify the placement and relationships of these specimens, we carried out a phylogenetic and taxonomic study of the order Auriculariales based on the ITS and nrLSU sequences. The newly collected specimens could not be assigned to any known genera and formed a distinct monophyletic lineage within the order Auriculariales. Therefore, a new genus, *Ceraceocium gen. nov.* with the type species *C. vitreum sp. nov.*, are proposed with descriptions and illustrations based on the morphological characteristics and phylogenetic analysis.

Materials and methods

Sample collection and herbarium specimen preparation

The fresh fruiting bodies were collected on fallen angiosperm branch from Dehong Autonomous Prefecture, Yunnan Province, China. The samples were photographed in situ and fresh macroscopic details were recorded. Photographs were recorded by a Nikon D7100 camera. All the photos were focus-stacked using Helicon Focus software. Macroscopic details were recorded and transported to a field station where the fruit body was dried on an electronic food dryer at 45 °C (Dong *et al*. 2025b). Once dried, the specimens were sealed in an envelope and zip-lock plastic bags and labelled (Yang *et al*. 2025). The dried specimens were deposited in the Herbarium of the Southwest Forestry University (SWFC), Kunming, Yunnan Province, China.

Morphology

The macro-morphological descriptions were based on field notes and photos captured in the field and laboratory. Petersen (1996) was followed for the color terminology. The micro-morphological data were obtained from dried specimens observed using a light microscope with a magnification of 1000× oil (Wu *et al*. 2022, Zhao *et al*. 2023, Dong *et al*. 2025b). Sections were mounted in 5% KOH and 1% phloxine B ($C_{20}H_2Br_4Cl_4Na_2O_5$), as well as Cotton Blue and Melzer's reagent were used where necessary to observe micromorphology following the method of Yang *et al*. (2025). To present the variations of spore sizes, 5% of measurements were excluded from each end of the range and shown in parentheses. A minimum of thirty basidiospores from each specimen was measured. Stalks were excluded from basidia measurements, and the hilar appendage was excluded from basidiospores measurements. The MycoBank numbers were registered in the MycoBank database (http://www.mycobank.org).

The following abbreviations are used:

CB = Cotton Blue

CB– = acyanophilous
IKI = Melzer's reagent
IKI– = both inamyloid and non-dextrinoid
KOH = 5% potassium hydroxide water solution
L = mean spore length (arithmetic average for all spores)
W = mean spore width (arithmetic average for all spores)
n = a/b (number of spores (a) measured from the given number (b) of specimens)
Q = variation in the L/W ratios between the specimens studied

Molecular phylogeny

CTAB rapid fungi genome extraction kit-DN14 (Aidlab Biotechnologies Co., Ltd, Beijing) was used to obtain genomic DNA from dried specimens, according to the manufacturer's instructions. The gene fragments employed in this study are detailed in Table 1.

The PCR protocol for ITS was as follows: initial denaturation at 95 °C for 3 min, followed by 35 cycles at 94 °C for 40 s, and 58 °C for 40 s. The PCR protocol for nrLSU was as follows: initial denaturation at 94 °C for 1 min, followed by 35 cycles at 94 °C for 30 s, 48 °C for nrLSU for 1 min, and 72 °C for 1.5 min, and a final extension of 72 °C for 10 min (Deng *et al*. 2026). The PCR products were purified and sequenced at Kunming Tsingke Biological Technology Limited Company, Kunming, Yunnan Province, P.R. China. All newly generated sequences were deposited in GenBank (Table 2).

Phylogenetic analyses followed the methods in Dissanayake *et al*. (2020). Newly generated sequence data were initially subjected to a BLAST search in NCBI to obtain the most probable closely related taxa in the GenBank (http://blast.ncbi.nlm.nih.gov/). Sequence data were retrieved from GenBank based on recent publications (https://www.ncbi.nlm.nih.gov/nuccore/). The sequences were aligned using MAFFT version 7 (Katoh *et al*. 2019) with the G-INS-I strategy. The alignment was adjusted manually using AliView version 1.27 (Larsson 2014). The dataset was initially aligned and later, ITS and nrLSU sequences were combined using Mesquite version 3.51. FASTA data file formats were converted to PHYLIP and NEXUS formats using the online tool available on the ALTER website (http://sing.ei.uvigo.es/ALTER/, Glez-Peña *et al*. 2010). Phylogenetic trees were constructed based on randomized accelerated Maximum Likelihood (ML) and Bayesian Inference (BI) analyses.

Maximum Likelihood analyses were performed using the CIPRES Science Gateway (https://www.phylo.org/portal2/login!input.action; Miller *et al*. 2012) based on the dataset using the RAxML-HPC BlackBox tool, with setting RAxML halt bootstrapping automatically and 0.25 for maximum hours and obtaining the best tree using ML search. Other parameters in ML analysis used default settings, and statistical support values were obtained using nonparametric bootstrapping with 1000 replicates. Bayesian inference (BI) analysis was performed on the same dataset using MrBayes v3.2.7a (Ronquist *et al*. 2012). The best substitution model for the dataset was selected by ModelFinder v2.2.0 (Kalyaanamoorthy *et al*. 2017) using a Bayesian Information criterion, and the model was used for Bayesian analysis. Four Markov chains were run from random starting trees. Trees were sampled every 1000th generation. The first 25% of sampled trees were discarded as burn-in, while the remaining trees were used to construct a 50% majority consensus tree and to calculate Bayesian posterior probabilities (BPPs).

Phylogenetic trees were visualized and adjusted using FigTree v1.4.4 (http://tree.bio.ed.ac.uk/software/figtree), and the exports were edited using Adobe Illustrator CS6 software (Adobe Systems, USA). Branches of the consensus tree that received bootstrap support for Maximum Likelihood (ML) equal to or above 70%, and Bayesian Inference (BI) equal to or above 0.95, respectively.

TABLE 1. Genes/loci, respective primers and references used in the study.

Genes/loci	Primers	Sequence (5'-3')	Annealing temperature (°C)	References
ITS	ITS5	GGA AGT AAA AGT CGT AAC AAG G	55°C	White *et al*. (1990)
	ITS4	TCC TCC GCT TAT TGA TAT GC		
nrLSU	LR0R	ACC CGC TGA ACT TAA GC	48°C	Vilgalys & Hester (1990)
	LR7	TAC TAC CAC CAA GAT CT		

TABLE 2. A list of species, specimens, and GenBank accession number of sequences used in this study.

Species Name	Sample No.	GenBank Accession No.		Country	References
		ITS	nrLSU		
Adustochaete nivea	RLMA 531	MN165954	MN165989	Brazil	Alvarenga *et al*. (2019)
Adustochaete rava	KHL 15526	MK391517	MK391526	Brazil	Alvarenga *et al*. (2019)
Alloexidiopsis australiensis	LWZ 20180514-18	OM801934	OM801919	China	Liu *et al*. (2022)
Alloexidiopsis schistacea	LWZ 20200819-21a	OM801939	OM801932	China	Liu *et al*. (2022)
Amphistereum leveilleanum	FP-106715	KX262119	KX262168	USA	Malysheva & Spirin (2017)
Amphistereum schrenkii	HHB 8476	KX262130	KX262178	USA	Malysheva & Spirin (2017)
Aporpium caryae	WD 2207	AB871751	AB871730	Japan	Sotome *et al*. (2014)
Auricularia heimuer	Xiaoheimao	KM396781	KM396834	China	Wang *et al*. (2023)
Auricularia mesenterica	Kytovuori-89-333	KP729284	KP729302	Estonia	Wu *et al*. (2021)
Basidiodendron luteogriseum	KHL 16022	MT040881	MT040861	Brazil	Spirin *et al*. (2020)
Basidiodendron trachysporum	VS 11886	MW152419	MW136128	Russia	Spirin *et al*. (2021)
Bourdotia galzinii	MiettinenX3067	MG757511	MG757511	Spain	Malysheva *et al*. (2018)
Ceraceocium vitreum	**CLZhao 41901**	**PX628486**	**PX724311**	**China**	**Present study**
Ceraceocium vitreum	**CLZhao 50616**	**PX628487**	—	**China**	**Present study**
Crystallodon subgelatinosum	RC1609	MN475884	MN475888	Brazil	Alvarenga & Gibertoni (2021)
Ductifera pululahuana	KW 1733	—	AF291315	USA	Weiss & Oberwinkler (2001)
Eichleriella alliciens	HHB 7194	KX262120	KX262169	USA	Malysheva & Spirin (2017)
Eichleriella alpina	He 20120916-1	MH178245	MH178268	China	Li *et al*. (2023)
Elmerina cladophora	X1902	MG757509	MG757509	Indonesia	Malysheva *et al*. (2018)
Endoperplexa dartmorica	VS 11781	MT235621	MT235602	Norway	Spirin *et al*. (2025)
Exidia glandulosa	Dai 21232	MT663362	MT664781	China	Wu *et al*. (2020)
Exidia pithya	MW 313	AF291275	AF291321	Germany	Weiss & Oberwinkler (2001)
Exidiopsis effusa	Miettinen 19136	KX262145	KX262193	Finland	Tohtirjap *et al*. (2023)
Gelacantha pura	LE 254018	MK098882	MK098930	Russia	Spirin *et al*. (2019a)
Grammatus labyrinthinus	Yuan 1600	KM379139	KM379140	China	Alvarenga *et al*. (2019)
Grammatus semis	OM10618	KX262146	KX262194	China	Malysheva & Spirin (2017)
Guepinia montana	Yang 6743	OR822233	OR803013	China	Cui *et al*. (2024)
Helicomyxa everhartioides	TNM	—	AY640107	China	Kirschner and Chen (2004)
Heteroacanthella acanthophysa	ID 7083-C1	MW586897	—	—	Unpublished
Heterochaete andina	Lagerheim	—	KX262187	Ecuador	Malysheva & Spirin (2017)
Heterocorticium bambusicola	He4604	MH178260	MH178284	China	Li *et al*. (2023)
Heterocorticium latisporum	He20120923-20	MH178261	MH178285	China	Li *et al*. (2023)
Heteroradulum adnatum	LR 23453	KX262116	KX262165	Mexico	Malysheva & Spirin (2017)
Heteroradulum kmetii	VS 6466	KX262104	KX262152	Russia	Malysheva & Spirin (2017)
Hyalodon antui	Niemelä 6389	MG735416	MG735424	China	Spirin *et al*. (2019b)
Hyalodon piceicola	Spirin 11063	MG735415	MG735423	Russia	Spirin *et al*. (2019b)
Hyaloria pilacre	TI 2768	—	AF291338	Venezuela	Weiss & Oberwinkler (2001)
Hydrophana sphaerospora	VS 11622	MK098884	MK098932	Norway	Spirin *et al*. (2019a)
Hydrophana sphaerospora	VS 11133	MK098883	MK098931	Norway	Spirin *et al*. (2019a)
Metulochaete sanctae-catharinae	AM 0678	MK484065	MK480575	Russia	Spirin *et al*. (2019b)
Mycostilla vermiformis	Spirin 11330	MG735417	MG735425	Russia	Spirin *et al*. (2019b)
Myxariellum concinnum	VS 8393c	MK098885	MK098933	USA	Spirin *et al*. (2019a)
Myxarium nucleatum	Spirin 10013	KY801879	KY801906	Norway	Spirin *et al*. (2018)
Nigrochaete bambusicola	CLZhao 11314	PQ571173	PQ571168	China	Dong *et al*. (2025a)

.....continued on the next page

TABLE 2. (Continued)

Species Name	Sample No.	GenBank Accession No.		Country	References
		ITS	nrLSU		
Nigrochaete bambusicola	CLZhao 11307	PQ571172	PQ571167	China	Dong *et al*. (2025a)
Nodulochaete fssurata	CLZhao 27533	PQ166573	PQ166565	China	Dong *et al*. (2025c)
Nodulochaete punctata	CLZhao 22803	PQ166569	PQ166561	China	Dong *et al*. (2025c)
Ofella glaira	VS 11809	MK098920	MK098964	Norway	Spirin *et al*. (2019a)
Oliveonia fibrillosa	Spirin 8257	MT235628	MT235607	USA	Spirin *et al*. (2025)
Ovipoculum album	HKAS57058	—	GU292813	China	Kirschner *et al*. (2010)
Porpopycnis lubae	R. Kirschner *et al*. 2745 (M)	—	HQ914244	Panama	Kirschner *et al*. (2012)
Proterochaete adusta	VS 9021	MK391520	MK391528	Canada	Alvarenga *et al*. (2019)
Protoacia delicata	VS 4615	MK098923	MK098967	Russia	Spirin *et al*. (2019a)
Protodaedalea hispida	Spirin 5139	MG757510	MG757510	Finland	Spirin *et al*. (2019b)
Protodontia africana	AS 171126/1104	MK098978	MK098973	Russia	Spirin *et al*. (2019a)
Protohydnum cartilagineum	SP 467240	MG735419	MG735426	Russia	Spirin *et al*. (2019b)
Protomerulius brasiliensis	LR 19735	—	AF291359	Argentina	Weiss & Oberwinkler (2001)
Protomerulius substuppeus	O 19171	JX134482	JQ764649	China	Zhou & Dai (2013)
Pseudohydnum gelatinosum	AFTOL ID1875	DQ520094	DQ520094	Germany	Lutzoni *et al*. (2004)
Psilochaete multifora	VS 11596	MK484066	MK480576	Norway	Spirin *et al*. (2019b)
Punctochaete murina	CLZhao 32118	PP819689	PP819701	China	Dong *et al*. (2025d)
Renatobasidium notabile	VS 11118	MT235654	MT353648	Norway	—
Sclerotrema griseobrunnea	VS 7674	KX262140	KX262188	Russia	Malysheva & Spirin (2017)
Sebacina incrustans	MW 573	DQ520095	—	Germany	Spirin *et al*. (2025)
Stypella papillata	KHL 11751	EU118672	—	Finland	Larsson (2007)
Stypellopsis farlowii	KHL 12337	MG857095	MG857099	Russia	Spirin *et al*. (2019c)
Stypellopsis hyperborea	J Norden 9751	MG857097	MG857101	Russia	Spirin *et al*. (2019c)
Tremellochaete atlantica	URM90199	MG594381	MG594383	Brazil	Alvarenga *et al*. (2019)

Results

Phylogenetic analyses

The combined ITS+nrLSU dataset (Fig. 1) included sequences from 68 fungal specimens representing 65 species, and *Sebacina incrustans* (Pers.) Tul. & C. Tul. (1871: 15) was retrieved as the outgroup (Spirin *et al*. 2025). For Bayesian Inference (BI) analysis, a total of four Markov chains were run for two independent runs from random starting trees, each with 5.08 million generations for the ITS+nrLSU dataset, with trees and parameters sampled every 1000 generations, with an average standard deviation of split frequencies = 0.009946 (BI) and an effective sample size (ESS) average ESS (avg. ESS) = 2060.5. ModelFinder v2.2.0 (Kalyaanamoorthy *et al*. 2017) was used to select the best-fit model based on the BIC criterion. The best model for the combined ITS+nrLSU dataset estimated and applied in the Bayesian analysis was GTR+I+G. Maximum Likelihood (ML) and Bayesian Inference (BI) analyses yielded similar topologies.

Phylogenetic analysis of combined ITS and nrLSU sequences showed that the new genus *Ceraceocium gen. nov.* formed a supported monophyletic lineage (BS = 100%, BPP = 1.00) within Auriculariales, closely related to *Auricularia*, *Heteroacanthella* Oberw. and *Oliveonia* Donk (Fig. 1).

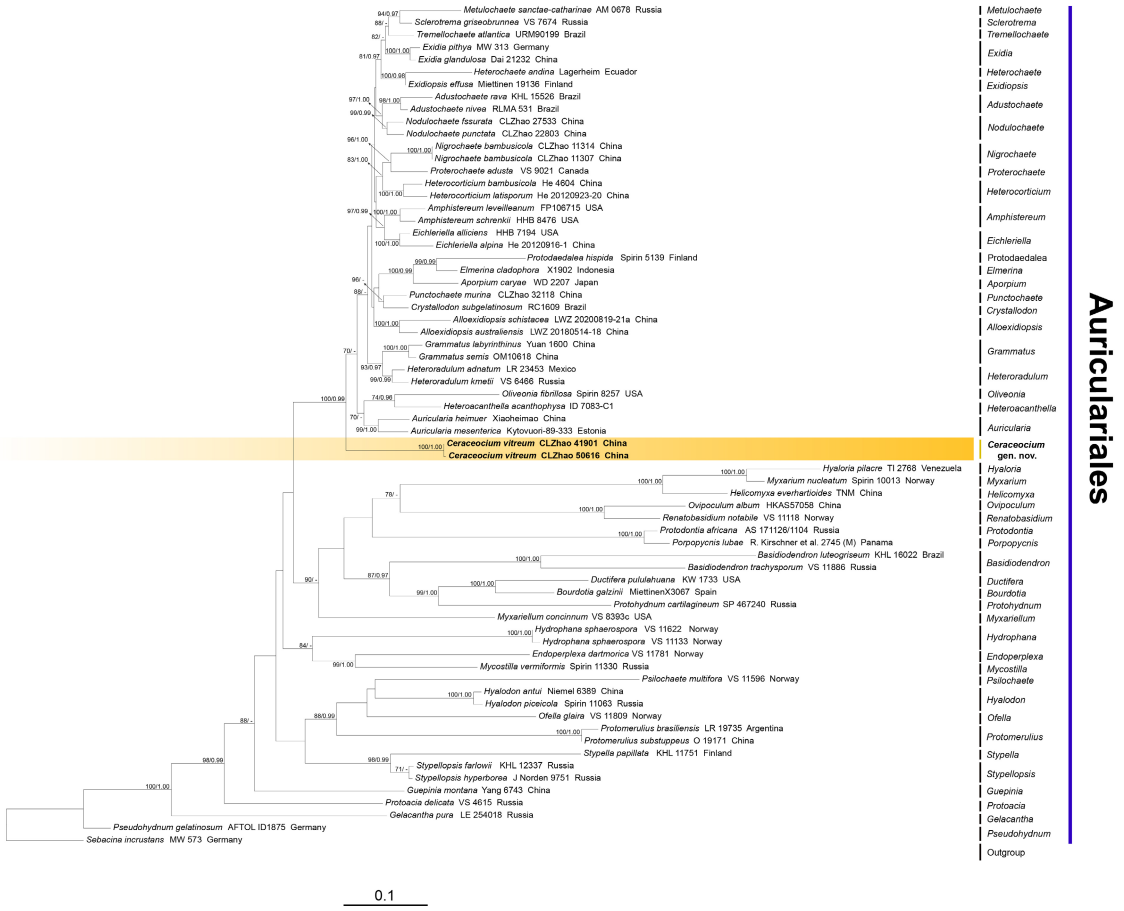

FIGURE 1. Maximum Likelihood tree illustrating the phylogeny of *Ceraceocium gen. nov.* and related genera in the order Auriculariales, based on the ITS+nrLSU sequence dataset. Branches are labeled with Maximum Likelihood bootstrap values equal to or above 70%, and Bayesian posterior probabilities equal to or above 0.95. The new species are in bold.

Taxonomy

Ceraceocium Q. Yuan & C.L. Zhao, *gen. nov.*
MycoBank No.: MB863345

Etymology*:—Ceraceocium* (Lat.): Referring to the ceraceous basidiomata of the type specimen.

***Description*:—**Basidiomata annual, resupinate, adnate, gelatinous, without odor or taste when fresh, becoming ceraceous upon drying. Hymenial surface smooth, black to brown when fresh, turning to brown to purple-red upon drying. Hyphal system monomitic; generative hyphae with clamp connections, colorless, thin walled, smooth. Cystidia subclavate, thin-walled, smooth. Basidia ellipsoid to ovoid, longitudinally septate, two- to four-celled. Basidiospores ellipsoid to subglobose, colorless, thin-walled, smooth, usually with oil drops.

Ceraceocium vitreum Q. Yuan & C.L. Zhao. *gen. et sp. nov*. Figs. 2–4.
MycoBank No.: MB863348

***Holotype*:—**CHINA, Yunnan Province, Dehong, Ruili City, Tongbiguan Provincial Nature Reserve, GPS coordinates 24°11′ N, 97°31′ E, elevation 1945 m asl., on fallen angiosperm branch, 22 November 2024, CLZhao 41901 (SWFC 00041901).

FIGURE 2. Basidiomata of *Ceraceocium vitreum* (CLZhao 41901, holotype). Scale bars: A=1 cm; B=2 mm.

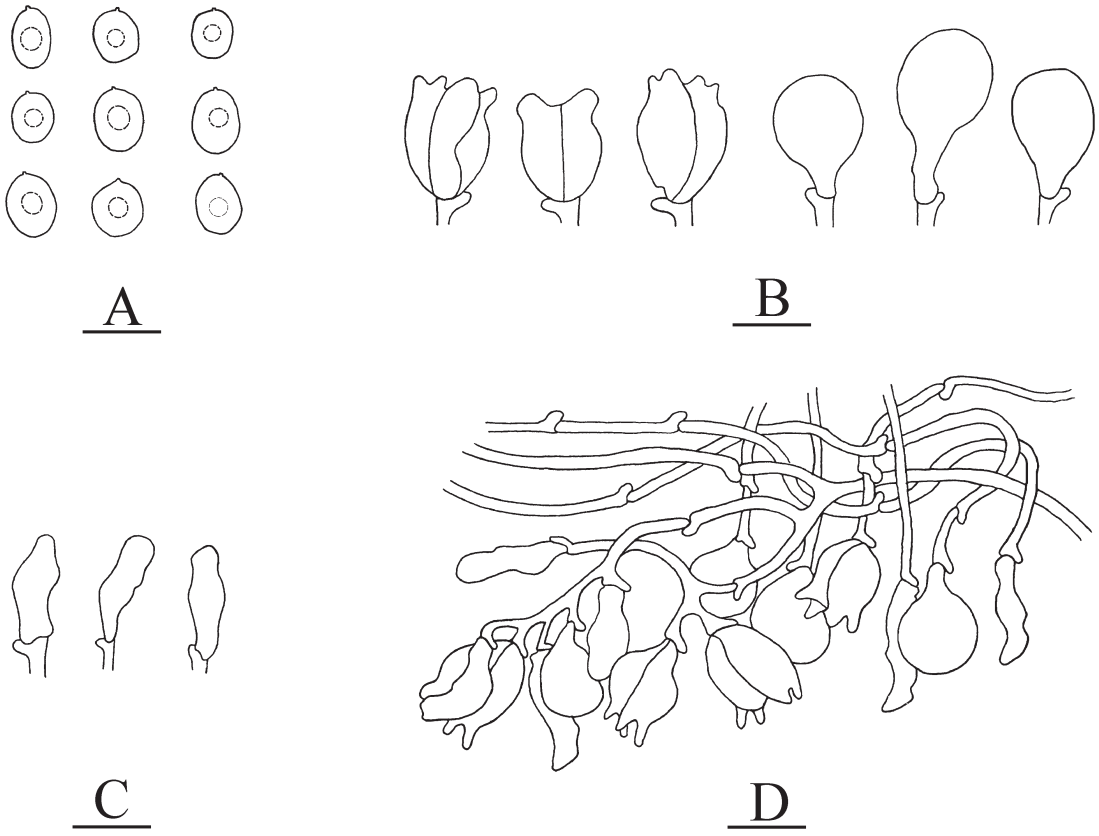

FIGURE 3. Microscopic structures of *Ceraceocium vitreum* (CLZhao 41901, holotype). (A) Basidiospores; (B) Basidia and basidioles; (C) Cystidioles; (D) A section of hymenium. Scale bars: A–D = 10 µm.

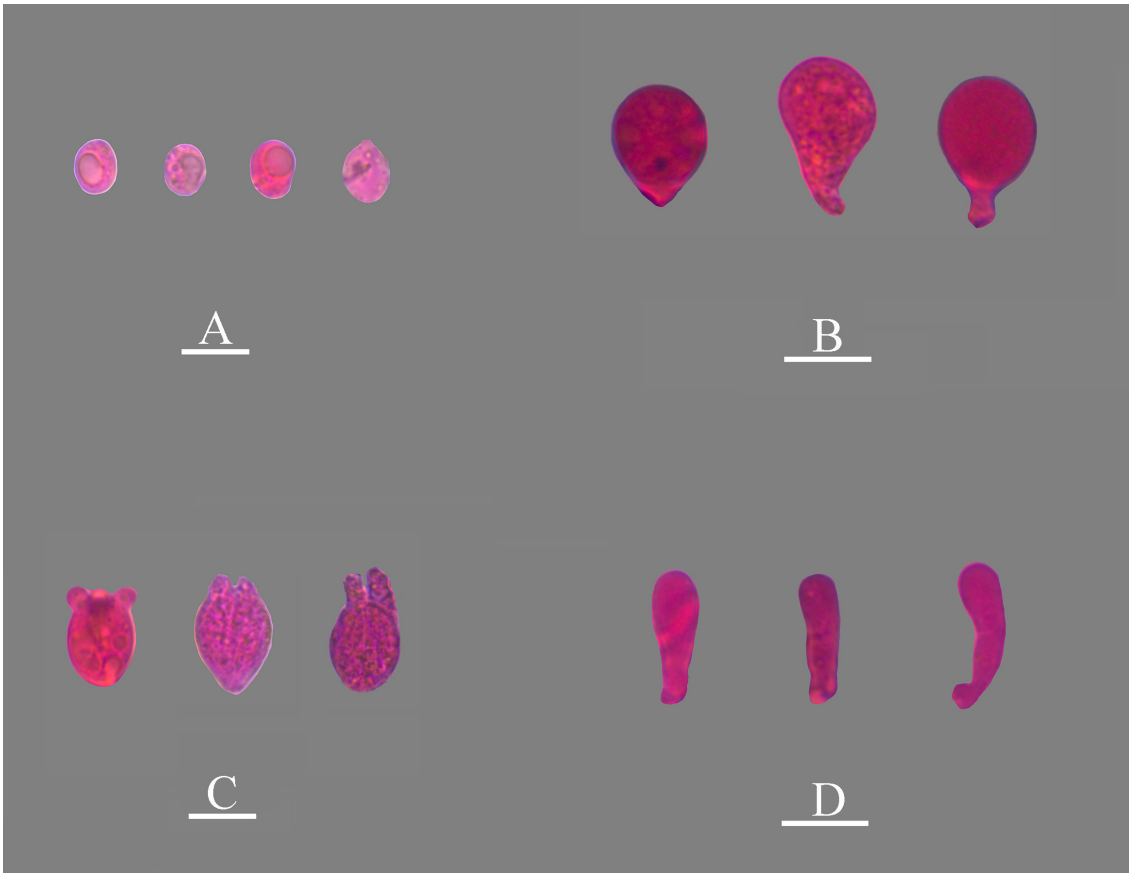

FIGURE 4. Microscopic structures of *Ceraceocium vitreum* (CLZhao 41901, holotype). (A) Basidiospores; (B) Basidioles; (C) Basidia; (D) Cystidioles. Scale bars: A–D = 10 µm; 10 × 100 Oil.

***Etymology*:**—*Vitreum* (Lat.). Referring to the slightly transparent hymenial surface of the type specimen.

***Basidiomata*:**—Annual, resupinate, adnate, gelatinous, without odor or taste when fresh, becoming ceraceous upon drying, up to 5.5 cm long, 2 cm wide, and 150 µm thick at center. Hymenial surface smooth, grayish violet brown to vinaceous gray when fresh, turning to brown to purple-red upon drying. Sterile margin narrow, brown, up to 1 mm.

***Hyphal structure*:**—Monomitic, generative hyphae with clamp connections, colorless, thin-walled, smooth, interwoven, 1.5–2.5 µm in diameter, IKI–, CB–; tissues unchanged in KOH.

***Hymenium*:**—Cystidia absent, cystidioles present, subclavate, thin-walled, smooth, 9–15.5 × 4–7 µm. Basidia ellipsoid to ovoid, longitudinally septate, two- to four-celled, 12.5–14.5 × 10–11.5 µm. Basidioles dominant, similar to basidia in shape, but slightly smaller.

***Basidiospores*:**—Broadly ellipsoid, colorless, thin-walled, smooth, usually with oil drops, IKI–, CB–, 5–8(–9) × 4.5–6.5(–7) µm, L = 6.51 µm, W = 5.62 µm, Q = 1.15–1.22 (n = 60/2).

***GenBank accession numbers:*—**CLZhao 41901 ITS: PX628486, nrLSU: PX724311; CLZhao 46100 ITS: PZ628949, nrLSU: PZ628951; CLZhao 50616 ITS: PX628487; CLZhao 50719 ITS: PZ628950, nrLSU: PZ628952.

***Additional specimen* (*paratype*) *examined*:**—CHINA, Yunnan Province, Puer, Jinggu County, Xiaoheijiang Original Forest Park, GPS coordinates 23°18′ N, 100°87′ E, elevation 2360 m asl., on fallen angiosperm branch, 19 August 2025, CLZhao 46100 (SWFC 00046100); GPS coordinates 23°45′ N, 100°22′ E, elevation 2510 m asl., on fallen angiosperm branch, 23 August 2025, CLZhao 50719 (SWFC 00050719); Dehong, Ruili City, Tongbiguan Provincial Nature Reserve, GPS coordinates 24°38′ N, 97°61′ E, elevation 2030 m asl., on fallen angiosperm branch, 27 November 2024, CLZhao 50616 (SWFC 00050616).

Discussion

The order Auriculariales represents a highly diverse clade, encompassing numerous corticioid, poroid, and hydnoid genera. In addition, several genera within this order are characterized by gelatinous basidiomata, including *Auricularia*, *Exidia*, *Exidiopsis*, *Metulochaete*, and others (Wells & Raitviir 1977, Malysheva & Spirin 2017, Spirin *et al*. 2018, Alvarenga *et al*. 2019, Wu *et al*. 2021, Jiang *et al.* 2025). Within this gelatinous group, however, several lineages remain poorly resolved, and additional diversity is likely to be uncovered. In the present study a new gelatinous genus *Ceraceocium gen. nov.* is proposed with *C. vitreum sp. nov.* as its type species based on morphological and phylogenetic evidence.

Morphologically, the new genus *Ceraceocium* resembles *Bourdotia*, *Exidia* Fr., *Exidiopsis* (Bref.) Möller, *Hyalodon* V. Malysheva & Spirin MycoBank and *Metulochaete* because of the gelatinous basidiomata. However, the latter four genera are distinguished molecularly and clustered apart from *Ceraceocium*. A morphological comparison between *Ceraceocium* and its related gelatinous genera in Auriculariales is presented in Table 3.

Phylogenetically, the new genus *Ceraceocium* forms a monophyletic lineage and is closely related to *Auricularia*, *Heteroacanthella* Oberw. and *Oliveonia* Donk in the ITS+nrLSU analyses based on the phylogeny tree (Fig. 1). However, *Auricularia* differs from *Ceraceocium* in having transversely three-septate basidia and allantoid basidiospores (Lowy 1951). *Heteroacanthella* can be distinguished from *Ceraceocium* by its grey hymenophore and larger basidiospores (10–16 × 8.5–13 µm vs. 5–8 × 4.5–6.5 µm) (Zamora *et al*. 2014). *Oliveonia* differs from *Ceraceocium* in having greyish to white hymenophore and narrower basidia (5–14 × 4–10 µm vs. 12.5–14.5 × 10–11.5 µm) (Eriksson *et al*. 1978, Spirin *et al*. 2025).

Fungi represent one of the most diverse groups of organisms on Earth and play a crucial role in ecosystem processes and functions (Dai *et al*. 2004, 2011, Acharya *et al*. 2017, Hyde *et al*. 2020, Yuan *et al.* 2021; Zhou *et al.* 2023, Case *et al*. 2025, Crous *et al*. 2025, Su *et al*. 2026, Wang *et al*. 2026, Tarafder *et al*. 2025a, 2026). Advances in DNA sequencing techniques have revolutionized the studies of fungal taxonomy and diversity, with approximately 150,000 species formally described to date (Hyde 2020). Wood-inhabiting fungi are an extensively studied group of Basidiomycota, which includes a number of poroid, smooth, grandinioid, odontioid, hydnoid and lamellate hymenophores in China (Tarafder *et al*. 2018, 2023, 2025b, Zhang *et al*. 2023, Wang *et al*. 2025). In the past several years, many gelatinous species have been reported and described in the order Auriculariales (Wells & Raitviir 1977, Malysheva & Spirin 2017, Spirin *et al*. 2018, Alvarenga *et al*. 2019, Wu *et al*. 2021, Jiang *et al.* 2025, Spirin *et al*. 2025). Nevertheless, the gelatinous diversity of Auriculariales remains insufficiently known, particularly in subtropical and tropical regions of China. This paper enriches our knowledge of the fungal diversity in this area. We anticipate

that more undescribed gelatinous taxa will be discovered throughout China after extensive collection combined with morphological and molecular analyses.

TABLE 3. Morphological comparison between *Ceraceocium* Q. Yuan & C.L. Zhao *gen. nov.* and related gelatinous genera in Auriculariales. Newly introduced taxon is indicated in bold black font.

Species name	Basidiomata	Cystidia	Basidia	Basidiospores	References
Bourdotia	Waxy gelatinous	Gloeocystidia	Obovate, pyriform, or petiolate	Ovoid and adaxially depressed to cylindrical	Wells & Raitviir 1975
Ceraceocium	Gelatinous, becoming ceraceous upon drying	Subclavate	Ellipsoid to ovoid	Ellipsoid to subglobose	**Present study**
Exidia	Gelatinous	Absent	Ellipsoid to subglobose	Cylindrical to allantoid	Tohtirjap *et al*. 2023
Exidiopsis	Corticioid to ceraceous or subgelatinous	Absent	Ovoid to ellipsoid	Ellipsoid to broadly ellipsoid; 5–6 × 4–4.5 µm	Wells & Raitviir 1977
Hyalodon	Gelatinous	Absent	Ovoid to globose	Broadly ellipsoid to subglobose	Malysheva *et al*. 2018
Metulochaete	Gelatinous to waxy-arid	Metuloid, covering hymenial spines	Ovoid	Allantoid, straight to slightly curved	Spirin *et al*. 2019b

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