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Adustochaete sinensis (Auriculariales, Basidiomycota): a new species from Yunnan, Southwest China, based on morphology and phylogeny

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Abstract

Adustochaete is a small genus of wood-inhabiting basidiomycetes, currently comprising only six described species. A recent study has clarified the classification of this genus by combining phylogenetic analyses and morphological characteristics. However, the species diversity of *Adustochaete* in the high-altitude forests of Yunnan Province, China, has not been systematically studied. In the present study, detailed morphological characteristics and combined multi-locus phylogenetic analyses based on the internal transcribed spacers (ITS) and the large subunit (nrLSU) of the nuclear ribosomal DNA (rDNA) revealed a new species in *Adustochaete*, *viz. A. sinensis*. Comprehensive descriptions, micrographs, and phylogenetic analysis results are provided. The present study enriches the species diversity of Auriculariales in China, which should help protect and sustainably use fungal natural resources.

Key words: Biodiversity, molecular systematics, taxonomy, Yunnan Province

Introduction

Wood-inhabiting fungi play essential roles in ecosystems, which have significant economic value, and are of considerable importance in scientific research (Dai *et al*. 2021; Bhunjun *et al.* 2024; Schoutteten *et al*. 2024; Case *et al*. 2025).

Auriculariales is a highly diverse order with gelatinous, poroid, lamellate, corticoid and hydnoid basidiomes; transversely or longitudinally septate, cylindrical to clavate or subglobose to ovoid basidia; cystidia and hyphidia present or absent; and ovoid, subglobose, oblong-ellipsoid, cylindrical, or allantoid, thin-walled basidiospores (Malysheva *et al*. 2018; Yuan *et al*. 2018; Alvarenga *et al*. 2019; Spirin *et al*. 2025; Zhang *et al*. 2026; Zhaung *et al*. 2026). Most known species of Auriculariales are saprotrophs on wood, causing a white rot (Tohtirjap *et al*. 2023). Furthermore, some species in Auriculariales are important edible and medicinal mushrooms, e.g., *Auricularia heimuer* F. Wu, B.K. Cui & Y.C. Dai (2014: 186) and *A. cornea* Ehrenb. (1820: 91) are widely cultivated in China (Wu *et al*. 2021, 2026). Therefore, interest in species diversity in Auriculariales has increased significantly in recent years.

The genus *Adustochaete* Alvarenga & K.H. Larss. (2019: 97) was erected by Alvarenga and Larsson in 2019 by type species *A. rava* Alvarenga & K.H. Larss (2019: 97) (Alvarenga *et al*. 2019). It is characterized by the resupinate basidiomata, spiny or tuberculate hymenophore, a monomitic hyphal structure with clamp connections on generative hyphae, present cystidia and hyphidia, ellipsoid-ovoid to obconical basidia, cylindrical to broadly cylindrical, straight or curved basidiospores (Alvarenga *et al*. 2019). Based on the MycoBank (http://www.mycobank.org, accessed on 5

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February 2026) and Index Fungorum (http://www.indexfungorum.org, accessed on 5 February 2026), six species are currently recognized in *Adustochaete* (Alvarenga *et al*. 2019; Li & Zhao 2022; Dong *et al*. 2024).

Fungal systematics has undergone a fundamental change with the implementation of DNA sequencing technology (Crous *et al*. 2025). Multi-gene molecular phylogenetic analyses play a vital role in the taxonomy of Auriculariales, particularly within Auriculariaceae, not only for delimiting novel species, but also for revising the classification of previously unresolved taxa (Weiss & Oberwinkler 2001; Malysheva *et al*. 2018). The phylogenetic relationships in Auriculariales and related groups based on nrLSU sequences suggested that Auriculariales is polyphyletic, and the family Sebacinaceae was confirmed as a monophyletic group, which appeared distant from other taxa ascribed to Auriculariales (Weiss & Oberwinkler 2001). Wells *et al*. (2004) based on nrLSU sequences reconsidered that Auriculariaceae and Hyaloriaceae, and considered Exidiaceae as a synonym of Auriculariaceae. Furthermore, based on the combined ITS+nrLSU sequence dataset, several researchers classified *Exidia* species in Auriculariaceae (Yuan *et al.* 2018; Spirin *et al.* 2019a, b). Hyaloriaceae was rarely mentioned and even abandoned (He *et al*. 2024). However, based on ITS+nrLSU phylogenetic analyses, the phylogenetic clade included *Myxarium* species and *Hyaloria pilacre*, which was distant from other core taxa of Auriculariaceae (Weiss & Oberwinkler 2001). Tohtirjap *et al*. (2023) reached the same conclusion that *Myxarium* and *Hyaloria* do not belong to the core Auriculariaceae and instead form an independent lineage, through combined ITS+nrLSU phylogenetic analyses. Therefore, this family was accepted by some researchers based on morphological and molecular phylogenetic evidences (Wells *et al*. 2004; Tohtirjap *et al*. 2023). Currently, two families, Auriculariaceae and Hyaloriaceae, are accepted in this order (He *et al*. 2024; Spirin *et al*. 2025). In recent years, the species diversity of the resupinate Auriculariales has been described or better defined using morphological and molecular analyses and the results showed the hidden diversity of this group and several corticioid genera (Weiss & Oberwinkler 2001; Dong *et al*. 2024). Based on ITS+nrLSU phylogenetic analyses, Alvarenga *et al*. (2019) established the new genus *Adustochaete*, with *A*. *rava* designated as the type species. Based on combined ITS and nrLSU phylogenetic analyses, Dong *et al*. (2024) introduced two new species in *Adustochaete*, viz. *A. albomarginata* J.H. Dong & C.L. Zhao (2024: 108) and *A. punctata* J.H. Dong & C.L. Zhao (2024: 108).

During investigations on wood-inhabiting fungi in Yunnan Province, China, several specimens were collected. To clarify the placement and relationships of these wood-inhabiting fungal specimens, we conducted a phylogenetic and taxonomic study based on ITS+nrLSU sequences. This taxon is identified as a previously undescribed species of *Adustochaete* and named *A. sinensis*. A description, illustrations, and phylogenetic analysis of the new species are provided. Additionally, the Pairwise Homoplasy Index (PHI) analysis was performed to assess potential recombination among the new species and closely related taxa.

Materials and methods

Sample collection and herbarium specimen preparation

The fresh fruiting bodies were collected on the dead bamboo from Dehong Dai and Jingpo Autonomous Prefecture, Yunnan Province, China. The samples were photographed in situ, and fresh macroscopic details were recorded (Rathnayaka *et al*. 2025). Photographs were captured with a Nikon D7100. 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 collected in the field and in the laboratory. Petersen (1996) was followed for the color terminology. The micro-morphological data were obtained from dried specimens observed under a light microscope at 1000× oil magnification (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+ = cyanophilous
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.

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		

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 1 min, 72 °C for 1.5 min, and a final extension of 72 °C for 10 min. (Dong *et al*. 2025b). 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).

TABLE 2. 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 albomarginata	CLZhao 22774	PP852049	PP849033	China	Dong *et al*. (2024)
Adustochaete interrupta	LR 23435	MK391518	MK391527	Brazil	Alvarenga *et al*. (2019)
Adustochaete nivea	RLMA 531	MN165954	MN165989	Brazil	Alvarenga *et al*. (2019)
Adustochaete punctata	CLZhao 29669	PP852050	-	China	Dong *et al*. (2024)
Adustochaete punctata	CLZhao 29671	PP852051	PP852057	China	Dong *et al*. (2024)
Adustochaete punctata	CLZhao 29675	PP852052	PP849035	China	Dong *et al*. (2024)
Adustochaete punctata	CLZhao 29685	PP852052	PP849036	China	Dong *et al*. (2024)
Adustochaete punctata	CLZhao 29686	PP852054	PP849037	China	Dong *et al*. (2024)

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TABLE 2. (Continued)

Species Name	Sample No.	GenBank Accession No.		Country	References
		ITS	nrLSU		
Adustochaete punctata	CLZhao 29706	PP852055	-	China	Dong *et al*. (2024)
Adustochaete punctata	CLZhao 29710	PP852056	PP849038	China	Dong *et al*. (2024)
Adustochaete punctata	CLZhao 29711	PP852057	PP849039	China	Dong *et al*. (2024)
Adustochaete rava	RC 841	MK391516	-	Brazil	Alvarenga *et al*. (2019)
Adustochaete rava	KHL 15526	MK391517	MK391526	Brazil	Alvarenga *et al*. (2019)
Adustochaete sinensis	**CLZhao 44399**	**PX890276**	**PX899182**	**China**	**Present study**
Adustochaete sinensis	**CLZhao 48983**	**PX890277**	**PX899183**	**China**	**Present study**
Adustochaete yunnanensis	CLZhao 8212	MZ911964	MZ950629	China	Li & Zhao (2022)
Adustochaete yunnanensis	CLZhao 4671	MZ911965	-	China	Li & Zhao (2022)
Adustochaete yunnanensis	CLZhao 4401	MZ911966	MZ950630	China	Li & Zhao (2022)
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	Otto MiettinenX3067	MG757511	MG757511	Spain	Malysheva *et al*. (2018)
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)

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TABLE 2. (Continued)

Species Name	Sample No.	GenBank Accession No.		Country	References
		ITS	nrLSU		
Grammatus semis	OM10618	KX262146	KX262194	China	Malysheva & Spirin (2017)
Guepinia montana	Yang6743	OR822233	OR803013	China	Cui *et al*. (2024)
Helicomyxa everhartioides	TNM	-	AY640107	China	Kirschner & Chen (2004)
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)
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)
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	Ryv. 19735	-	AF291359	Argentina	Weiss & Oberwinkler (2001)
Protomerulius substuppeus	O 19171	JX134482	JQ764649	China	Zhou & Dai (2013)

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TABLE 2. (Continued)

Species Name	Sample No.	GenBank Accession No.		Country	References
		ITS	nrLSU		
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)
Sistotrema brinkmannii	isolate 236	JX535169	JX535170	Netherlands	Alvarenga & Gibertoni (2021)
Stypella papillata	KHL 11751	EU118672	-	Finland	Larsson (2007)
Stypellopsis farlowii	Larsson 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)

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 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 1,000 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 using ModelFinder v2.2.0 (Kalyaanamoorthy *et al.* 2017) with the Bayesian Information Criterion, and the model was used for Bayesian analysis. Four Markov chains were run from random starting trees. Trees were sampled every 1,000th 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 0.9, respectively.

Results

Molecular phylogeny

The combined ITS+nrLSU dataset (Figure 1) included sequences from 66 fungal specimens representing 63 species, and *Sistotrema brinkmannii* (Bres.) J. Erikss. was retrieved as the outgroup taxon (Dong *et al*. 2025b). For Bayesian Inference (BI) analysis, a total of four Markov chains were run for two independent runs from random starting trees, each with 1.225 million generations for the ITS+nrLSU dataset, with trees and parameters sampled every 1,000 generations, with an average standard deviation of split frequencies = 0.009904 (BI) and an effective sample size (ESS) average ESS (avg. ESS) = 536. ModelFinder v2.2.0 (Kalyaanamoorthy *et al*. 2017) was used to select the best-fit model using the BIC criterion. The best model for the combined ITS+nrLSU dataset, as estimated and applied in the Bayesian analysis, was GTR+I+G. Maximum Likelihood (ML) and Bayesian Inference (BI) analyses yielded similar topologies.

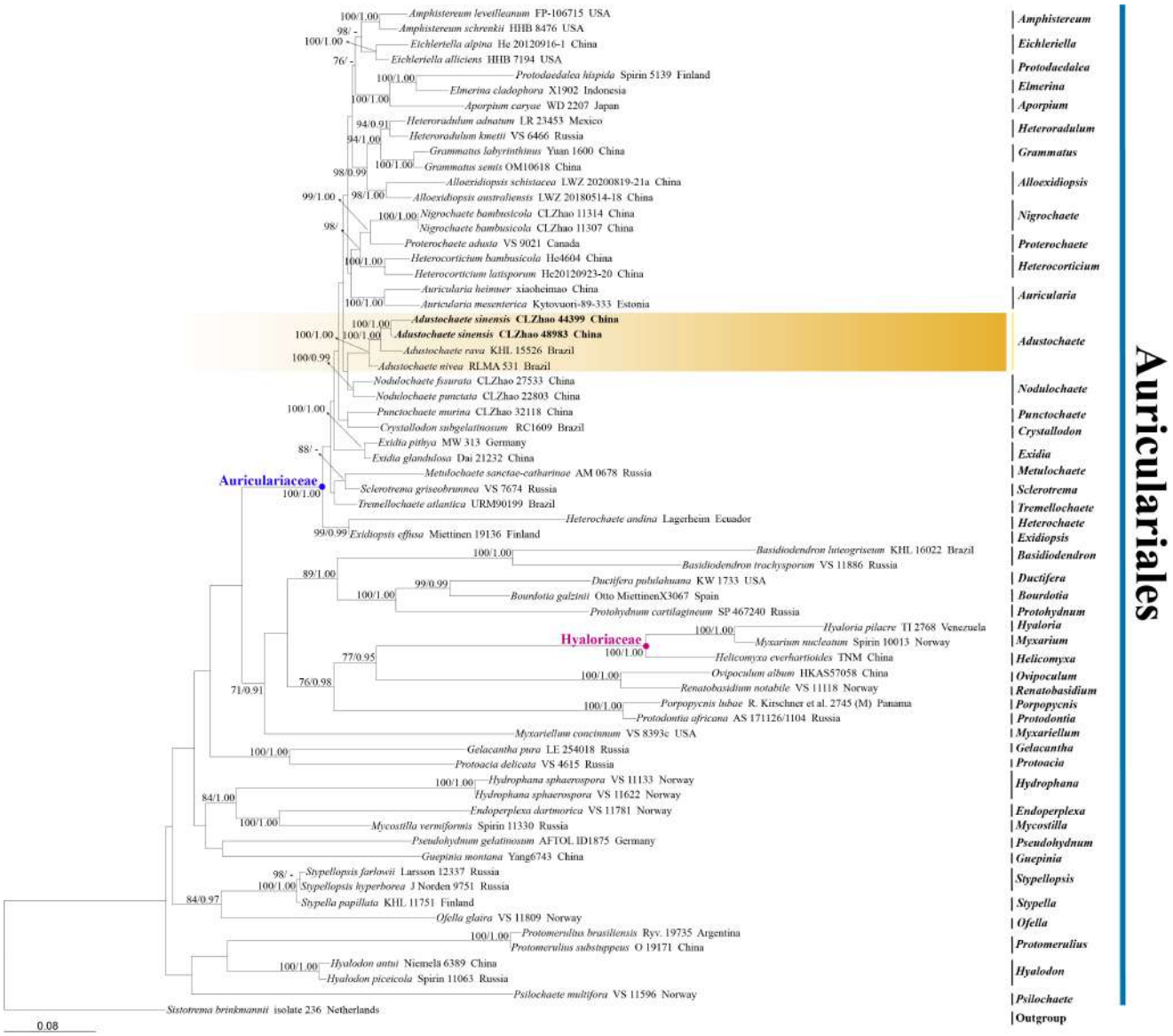

FIGURE 1. Maximum Likelihood tree illustrating the phylogeny of *Adustochaete* and related genera in the order Auriculariales, based on the ITS+nrLSU sequence dataset. Branches are labeled with Maximum Likelihood bootstrap values equal to or above 70%, and Bayesian posterior probabilities equal to or above 0.9. The new species is in bold.

The ITS+nrLSU data (Figure 2) included sequences from 19 fungal specimens representing 8 species. Sequences of *Amphistereum leveilleanum* (Berk. & M.A. Curtis) Spirin & Malysheva were retrieved from GenBank and used as the outgroup (Dong *et al*. 2024). For Bayesian Inference (BI) analysis, a total of four Markov chains were run for two independent runs from random starting trees, each with 0.7 million generations for the ITS+nrLSU dataset, with trees and parameters sampled every 1,000 generations, with an average standard deviation of split frequencies = 0.006490 (BI) and an effective sample size (ESS) average ESS (avg. ESS) = 591.5. ModelFinder v2.2.0 (Kalyaanamoorthy *et al*. 2017) was used to select the best-fit model using the BIC criterion. The best model for the ITS data estimated and applied in the Bayesian analysis was GTR+I+G. Maximum Likelihood (ML) and Bayesian Inference (BI) analyses yielded similar topologies.

Phylogenetic analyses based on the combined ITS+nrLSU dataset (Figure 1) revealed that the new species, *Adustochaete sinensis*, is nested within the genus *Adustochaete* in Auriculariales. In the ITS+nrLSU-based phylogeny (Figure 2), *A. sinensis* constituted an independent lineage (100% BS, 1.00 BPP) closely related to *A. punctaca* and *A. rara*.

Application of the PHI test to the concatenated tree-locus sequences (ITS, nrLSU) revealed no recombination level within phylogenetically related species. No significant recombination events were observed between *Adustochaete sinensis* and phylogenetically closely related species with *A. nivea*, *A. punctaca*, and *A. rara* (Figure 3). The test results

show Φw = 1.0 for the combined sequence data and that no recombination is present in this new species with *A. nivea*, *A. punctaca*, and *A. rara*.

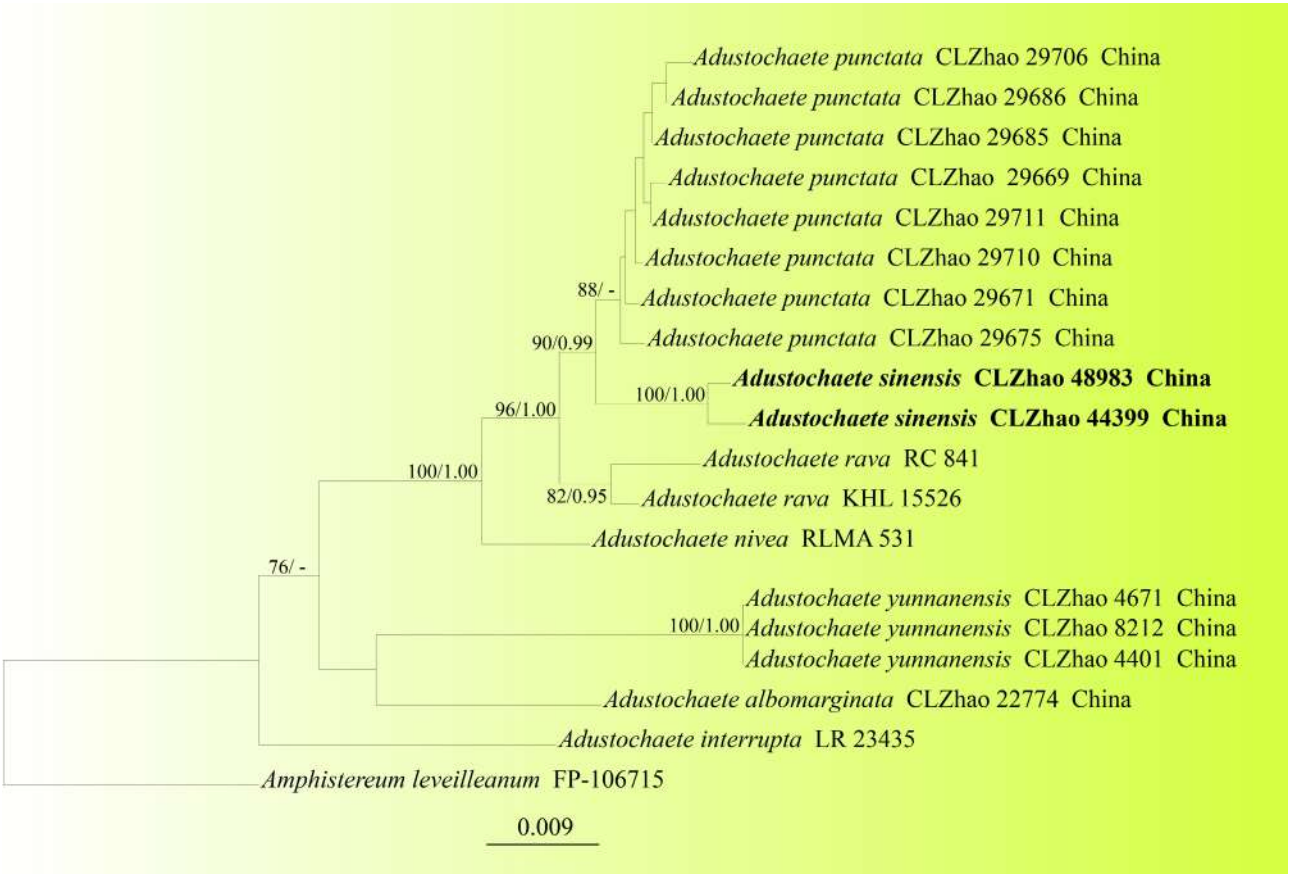

FIGURE 2. Maximum Likelihood tree illustrating the phylogeny of the three new species and related species in the genus *Adustochaete*, based on the ITS+nrLSU sequence dataset. Branches are labeled with Maximum Likelihood bootstrap values equal to or above 70%, and Bayesian posterior probabilities equal to or above 0.9. The new species is in bold.

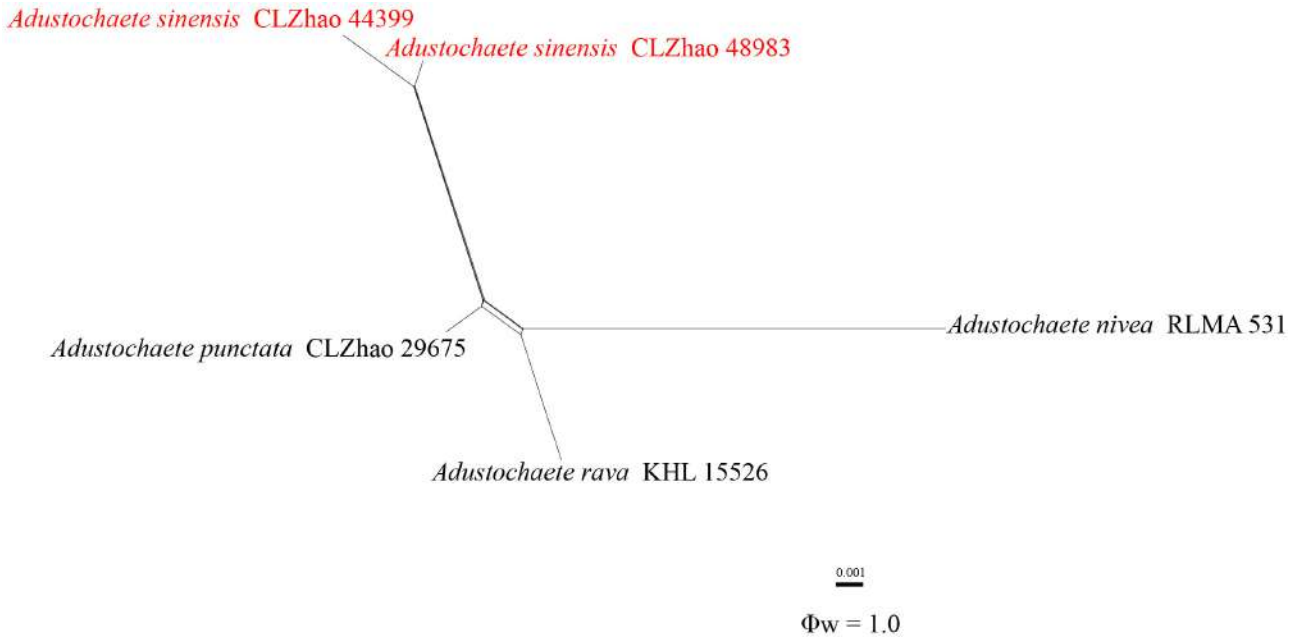

FIGURE 3. Pairwise homoplasy index (PHI) test results for *Adustochaete sinensis* and closely related species using the LogDet transformation and split decomposition. PHI test results (Φw = 1.0; Φw ≤ 0.05) indicate no significant recombination within the dataset. The new taxon is in red.

Taxonomy

Adustochaete sinensis Q. Yuan & C.L. Zhao, *sp. nov.* Figs. 4,5,6
MycoBank: MB 862050

***Etymology*:** *Sinensis* (Lat.) refers to the type locality, China.

***Holotype*:** China, Yunnan Province, Dehong, Ruili City, Tongbiguan Provincial Nature Reserve, GPS coordinates 24°03′ N, 97°42′ E, elevation 1980 m asl., on fallen angiosperm branch, leg. C.L. Zhao, 15 January 2025, CLZhao 44399 (SWFC 00044399).

FIGURE 4. Basidiomata of *Adustochaete sinensis* (CLZhao 44399, holotype).

***Basidiomata*:** Annual, resupinate, membranaceous, thin, closely adnate, without odor or taste when fresh, becoming coriaceous upon drying, up to 10.5 cm long, 1 cm wide, 100 µm thick. Hymenial surface smooth, white when fresh, turning to cream upon drying. Sterile margin narrow, white to cream, up to 1 mm.

***Hyphal system*:** 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 fusiform, colorless, thin-walled, with an acute or obtuse apex, occasionally sinuous in the basal, 20–31 × 5.5–8 µm. Hyphidia arising from generative hyphae, nodulose, rarely branched, colorless, thin-walled, 2–5 µm in diameter. Basidia subellipsoid to ovoid, longitudinally septate, two- to four-celled, 11–15.5 × 8.5–10.5 µm. Basidioles dominant, similar to basidia in shape, but slightly smaller.

***Basidiospores*:** Allantoid, colorless, thin-walled, smooth, IKI–, CB–, (9.5–)10.5–13 × 4.5–5.5(–6) µm, L = 11.5 µm, W = 5.03 µm, Q = 2.28–2.31 (n = 60/2).

***Additional specimens examined* (*paratype*).** China, Yunnan Province, Dehong, Ruili City, Tongbiguan Provincial Nature Reserve, GPS coordinates 24°03′ N, 97°42′ E, elevation 1980 m asl., on fallen angiosperm branch, leg. C.L. Zhao, 15 January 2025, CLZhao 48983 (SWFC 00048983).

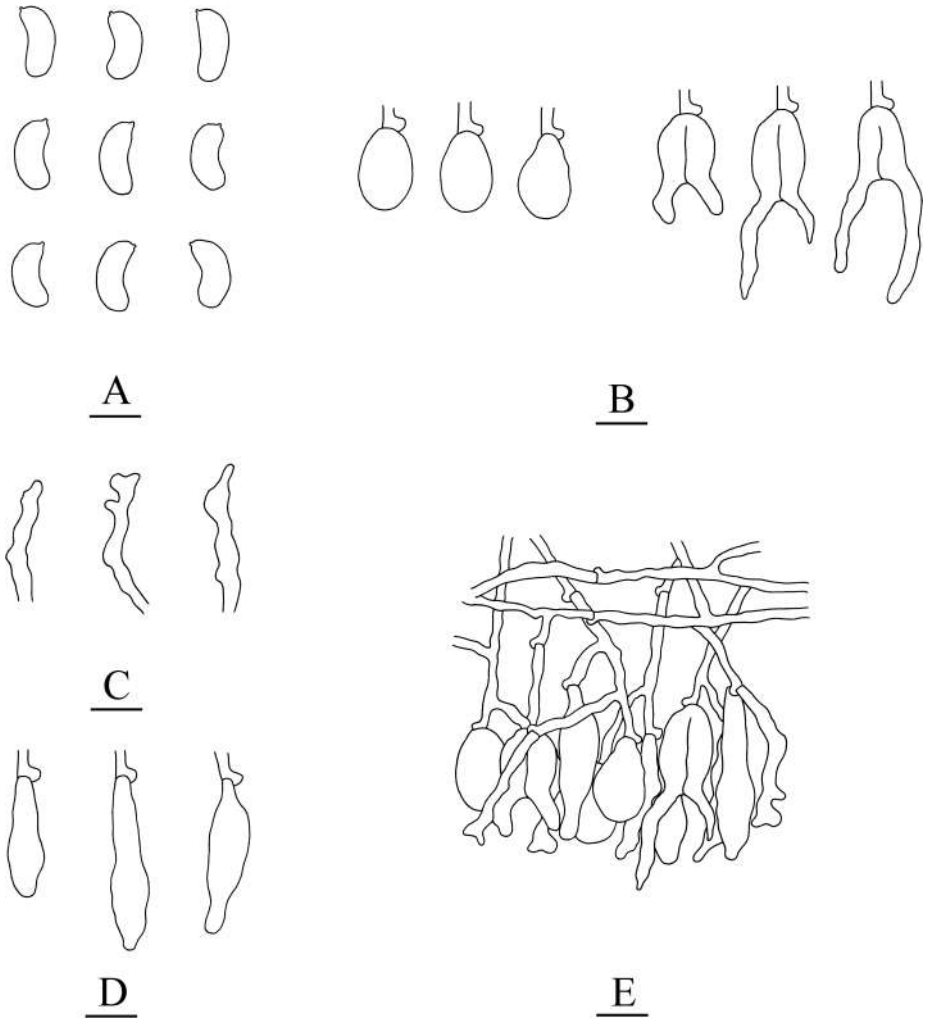

FIGURE 5. Microscopic structures of *Adustochaete sinensis* (CLZhao 44399, holotype): (A) basidiospores. (B) basidioles and basidia. (C) hyphidia. (D) cystidia. (E) a vertical section of hymenium. Scale bars: 10 μm (A–E).

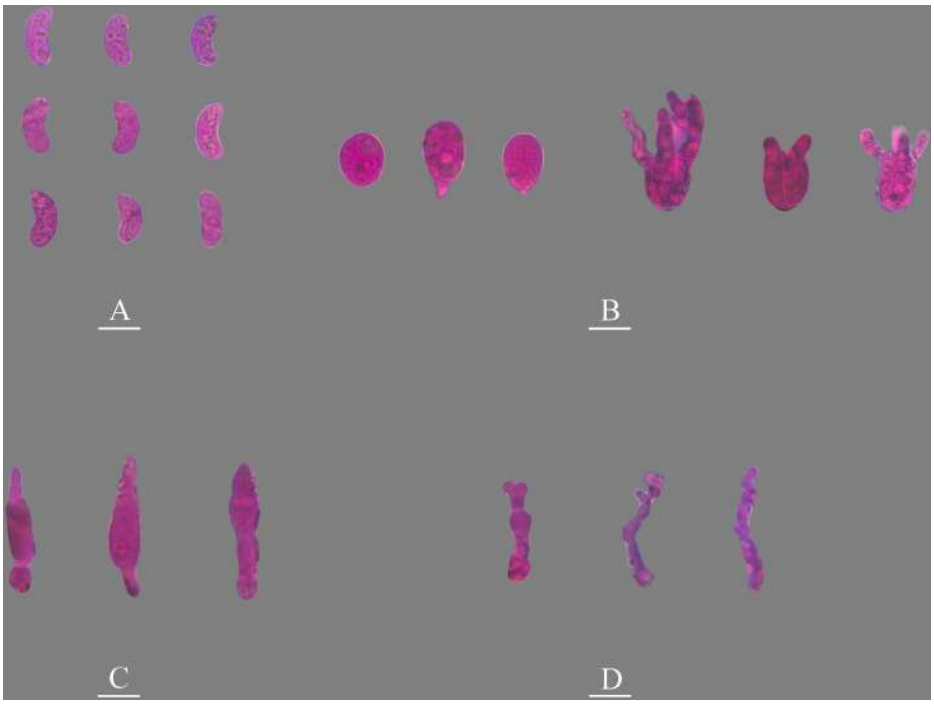

FIGURE 6. Microscopic structures of *Adustochaete sinensis* (CLZhao 44399, holotype): (A) basidiospores; (B) basidioles and basidia; (C) cystidia; (D) hyphidia. Scale bars: 10 μm (A–D); 10 × 100 Oil.

Discussion

Wood-rotting fungi have been extensively studied, especially in China, recently, which includes a number of poroid, smooth, grandinoid, odontioid, and hydnoid basidiomata in China (Zhang *et al*. 2023; Zhou *et al*. 2023, 2026; Wang *et al*. 2024; Muhammad *et al*. 2025; Zhang *et al*. 2025). To date, only six species of the genus *Adustochaete* have been found (Alvarenga *et al*. 2019; Dong *et al*. 2024). In the present study, the new species *Adustochaete sinensis* is described based on the phylogenetic analyses and morphological characteristics. Thus, the species diversity of *Adustochaete* remains poorly known in China. This paper enriches our knowledge of fungal diversity in this area, and likely, more new taxa will be found with further fieldwork and molecular analyses.

Morphologically, the new species *Adustochaete sinensis* resembles the related morphological species of the genus. A morphological comparison among this new *Austrochaete* species and six similar species is presented in Table 3.

TABLE 3. A morphological comparison between the new species *Adustochaete sinensis* and six similar species in the genus *Adustochaete*. Newly introduced taxa are indicated in bold black font.

Species name	Hymenial surface	Hyphae	Cystidia	Basidia	Basidiospores	References
Adustochaete albomarginata	Smooth/Cream to buff	Thin-walled, unbranched	Subclavate to fusiform; 23.5–48.5 × 10–13.5 µm	Ellipsoid to ovoid, two- to four-celled; 17–24.5 × 11–16.5 µm	Subcylindrical to allantoid; 12–17.5 × 6.5–9 µm	Dong *et al*. (2024)
Adustochaete interrupta	Smooth/ Light ochraceous-grey to brownish	Thin-walled	Clavate to fusiform; 45–96 × 6–13.5 µm	Narrowly ovoid to obconical, four celled; 15.1–24 × 9.1–11.8 µm	Broadly cylindrical; 11.3–14.3 × 5.7–6.2 µm	Alvarenga *et al*. (2019)
Adustochaete nivea	Sharp-tipped spines/ White	Thin-walled	-	Narrowly ovoid to obconical, four-celled; 14.9–16.2 × 9.7–10.1 µm	Cylindrical; 10.2–13.6 × 4.6–5.9 µm	Hyde *et al*. (2020)
Adustochaete punctata	Smooth/Punctate, white to cream	Thin-walled, unbranched	Subcylindrical to clavate; 15.5–23.5 × 5.5–7.5 µm	Ellipsoid to ovoid, two to four-celled; 17–25 × 16.5–21 µm	Subcylindrical to allantoid; 13.5–18 × 6–8.2 µm	Dong *et al*. (2024)
Adustochaete rava	Sharp-tipped spines/ Pale to dark grey	Thin-walled	Clavate to fusiform; 27–52 × 4–8 µm	Narrowly ovoid to obconical, four celled; 10.8–15.2× 7.3–10 µm	Cylindrical; 10.2–13.7 × 3.8–4.7 µm	Alvarenga *et al*. (2019)
Adustochaete sinensis	Smooth/Cream	Thin-walled	Fusiform; 20–31 × 5.5–8 µm	Subellipsoid to ovoid; two to four-celled; 11–15.5 × 8.5–10.5 µm	Allantoid; 10.5–13 × 4.5–5.5 µm	**Present study**
Adustochaete yunnanensis	Grandinioid/Dark greyish to brownish	Thin-walled, branched	Clavate to fusiform; 17.5–24.5 × 3.5–5.8 µm	Narrowly ovoid to obconical, four celled; 25–47.5 × 8.5–14 µm	Narrow cylindrical to allantoid; 12–20 × 5–7 µm	Li & Zhao (2022)

Phylogenetically, analyses based on the combined ITS+nrLSU dataset (Figure 1), it revealed that *Adustochaete sinensis* was firmly nested within the genus *Adustochaete* in Auriculariales. In the ITS+nrLSU-based phylogeny focusing on *Adustochaete* (Figure 2), *A. sinensis* constituted an independent lineage (100% BS, 1.00 BPP) closely related to *A. punctaca* and *A. rara*. However, *A. punctaca* differs from *A. sinensis* by its punctate basidiomata and smaller basidiospores (13.5–18 × 6–8.2 µm vs. 10.5–13 × 4.5–5.5 µm) (Dong *et al*. 2024). *Adustochaete rara* can be distinguished from *A. sinensis* by its hymenial surface with sharp-tipped spines and narrower basidiospores (10.2–13.7 × 3.8–4.7 µm vs. 10.5–13 × 4.5–5.5 µm) (Alvarenga *et al*. 2019).

Fungi represent one of the most diverse groups of organisms on Earth and play an essential role in ecosystem processes and functions (Dai *et al*. 2021; Case *et al*. 2025; Wijesinghe *et al*. 2025). In the past several years, many corticioid species have been reported and described in the order Auriculariales (Wells and Bandoni 2001; Miettinen *et al*. 2012; Hibbett *et al*. 2014; Malysheva and Spirin 2017; Alvarenga *et al*. 2019; Spirin *et al*. 2019a, b, 2025; Tohtirjap *et al*. 2023). Nevertheless, the fungal diversity of Auriculariales inhabiting wood remains insufficiently explored, particularly in subtropical and tropical regions of China.

In conclusion, the discovery and description of *Adustochaete sinensis* further enrich our understanding of species diversity within Auriculariales. Continued fieldwork combined with integrative morphological and molecular approaches will undoubtedly reveal additional undescribed wood-inhabiting fungal taxa.

Key to the known species of *Adustochaete* worldwide

1 Hymenial surface smooth 2
- Hymenial surface hydnoid or grandinioid 5
2 Basidia > 16.5 µm wide ..... *A. punctata*
- Basidia < 16.5 µm wide 3
3 Basidiospores > 6.5 µm wide ..... *A. albomarginata*
- Basidiospores < 6.5 µm wide 4
4 Hymenial surface light ochraceous-grey to brownish, basidiospores cylindrical ..... *A. interrupta*
- Hymenial surface cream, basidiospores allantoid ..... *A. sinensis*
5 Cystidia absent ..... *A. nivea*
- Cystidia present 6
6 Basidia > 25 µm long ..... *A. yunnanensis*
- Basidia < 25 µm long ..... *A. rava*

Disclosure statement

No potential conflict of interest was reported by the author(s).

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