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Article



A new corticioid fungus, *Alloexidiopsis sinensis* (Auriculariales, Basidiomycota), in China, evidenced by morphological characteristics and phylogenetic analyses

JUNHONG DONG, ZIRUI GU, YUYUN WANG, YINMEI SHI, CHANGLIN ZHAO

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***Onosma serpentinea* (Boraginaceae), a new serpentine endemic species from the South-West Anatolia, Türkiye**

RIZA BİNZET, TUĞKAN ÖZDÖL, HASAN YILDIRIM

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***Onnia pakistanica* sp. nov., (Hymenochaetaceae, Basidiomycota) from Pakistan**

HUMAIRA BASHIR, SANA JABEEN, AROOJ NASEER, ABDUL NASIR KHALID

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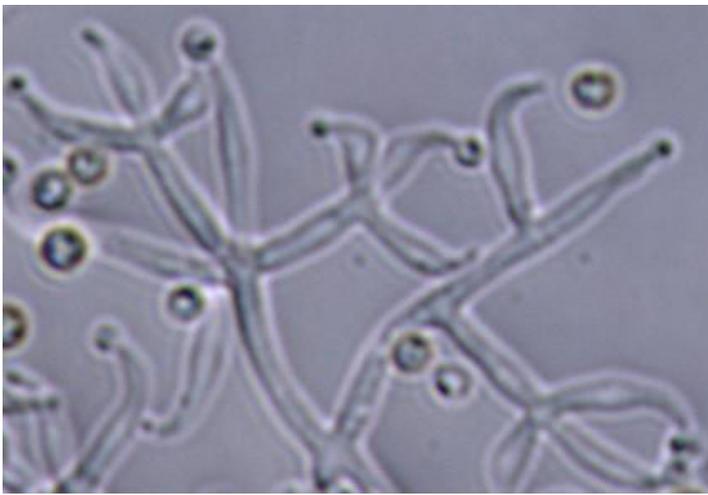
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***Trichoderma changiae* (Hypocreales), a new species isolated from a native orchid in Taiwan**

YU-HUI WEI, SHEAN-SHONG TZEAN, SUNG-YUAN HSIEH

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A new species of *Guatteria* (Annonaceae) from the Andean mountain forest of Colombia

BORIS VILLANUEVA-TAMAYO, NICOLAS PARRA-LIZCANO, JORGE ENRIQUE RIOS-CERVERA

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A new species of *Candolleomyces* (Psathyrellaceae) from Pakistan

ISHTIAQ AHMAD, MUHAMMAD HAQNAWAZ, ABDUL REHMAN NIAZI, ABDUL NASIR KHALID

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***Amana wanyuensis* (Liliaceae), a new species from the Dabieshan Mountains, Anhui Province, China**

XIANGWEN SONG, GUANGYAN LI, WEI WANG, XIANGWEN SONG, TAO XU, XINYI GAO, BANGXING HAN, SHANYONG YI

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Orophea chalermpraiat (Annonaceae; Malmeoideae), a new species from southern Thailand

ANISSARA DAMTHONGDEE, KITHISAK CHANTHAMRONG, SUWANNEE PROMSIRI, BANCHONG TONGSANG, THANI JAISAMUT, CHATTIDA WIYA, AROON SINBUMROONG, TANAWAT CHAOWASKU

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A new corticioid fungus, *Alloexidiopsis sinensis* (Auriculariales, Basidiomycota), in China, evidenced by morphological characteristics and phylogenetic analyses

JUNHONG DONG^{1,3}, ZIRUI GU^{1,4}, YUYUN WANG^{1,5}, YINMEI SHI^{2,6} & CHANGLIN ZHAO^{1,7*}

¹College of Forestry, Southwest Forestry University, Kunming 650224, P.R. China

²Xianggelila Forestry and Grassland Bureau, Diqing, 674499, P.R. China

³✉ fungijunhondong@163.com; <https://orcid.org/0000-0001-8740-0805>

⁴✉ fungiziruig@163.com; <https://orcid.org/0000-0003-1476-9040>

⁵✉ fungiyuyunw@163.com; <https://orcid.org/0009-0007-7011-0327>

⁶✉ 17708878113@163.com; <https://orcid.org/0000-0002-5962-7049>

⁷✉ fungichanglinz@163.com; <https://orcid.org/0000-0002-8668-1075>

*Corresponding author: C.L. Zhao, e-mail: fungichanglinz@163.com

Abstract

Alloexidiopsis sinensis sp. nov. found in Yunnan Province, China, is described here as a new species based on its morphology and phylogeny. *Alloexidiopsis sinensis* is characterized by its membranaceous basidiomata with a grandinoid hymenophore and a monomitic hyphal system bearing generative hyphae with clamp connections and allantoid basidiospores measuring 14.5–23 × 4.5–6.5 µm. Phylogenetic analyses of the new species were based on the internal transcribed spacer (ITS) and large subunit (nLSU) of ribosomal DNA (rDNA) sequences. The phylogenetic analysis indicated that the new species belonged to the genus *Alloexidiopsis*, and was retrieved as a sister to *A. nivea*.

Key words: 1 new species, Molecular systematics, Taxonomy, Wood-inhabiting fungi, Yunnan Province

Introduction

In forest ecosystems, fungi play an essential ecological role in driving carbon cycling in forest soils, mediating the mineral nutrition of plants, and alleviating carbon limitations (Tedersoo *et al.* 2014). The corticioid fungi are a cosmopolitan group and have a rich diversity related to the high diversity of plants growing in boreal, temperate, subtropical, and tropical regions (Gilbertson & Ryvarden 1987, Bernicchia & Gorjón 2010, Dai *et al.* 2015, 2021, Zhao *et al.* 2023).

Contrary to the gelatinous genera, most species in the order Auriculariales Bromhead bear tough, resupinate, and effused to reflexed basidiomata as corticioid and polyporoid fungi (Miettinen *et al.* 2012, Zhou & Dai 2013, Malysheva & Spirin 2017, Liu *et al.* 2022). Species with stereoid basidiocarps are widely distributed in many orders of the Agaricomycetes Doweld, although they are certainly a minority in the order Auriculariales (Malysheva & Spirin 2017). The corticioid genus *Alloexidiopsis* L.W. Zhou & S.L. Liu (2022: 4) belongs to the order Auriculariales, which is characterized by annual, resupinate, effused, adnate basidiomata, smooth or with sterile spines, greyish white to ochraceous hymenophore, a monomitic hyphal structure with clamp connections on generative hyphae, cylindrical to clavate cystidia, presence of abundant hyphidia, ellipsoid to ovoid, septate basidia and with two- to four-celled, cylindrical to broadly cylindrical, slightly curved (allantoid) basidiospores (Liu *et al.* 2022). To date, about five species of *A. australiensis* S.L. Liu, Z.Q. Shen & L.W. Zhou (2022: 4), *A. calcea* (Pers.) L.W. Zhou & S.L. Liu (2022: 6), *A. nivea*, *A. schistacea* L.W. Zhou & S.L. Liu (2022: 9), and *A. yunnanensis* (C.L. Zhao) L.W. Zhou & S.L. Liu (2022: 9) have been accepted in the genus worldwide, based on the MycoBank database (<http://www.mycobank.org>, accessed on 21 February 2024) and the Index Fungorum (<http://www.indexfungorum.org>, accessed on 21 February 2024), of which four have been recorded from China (Guan *et al.* 2020, Li *et al.* 2022, Liu *et al.* 2022).

The corticioid species of the order Auriculariales are traditionally placed in *Eichleriella* Bres. (1903: 115), *Exidiopsis* (Bref.) Möller (195: 82), and *Heterochaete* Pat. (1892: 120) according to morphological characteristics (Burt 1915, Wells 1961, Raitviir & Wells 1966, Wells & Raitviir 1980). Based on both the morphological and phylogenetic

evidences, the genera concepts of *Eichleriella*, *Hirneolina* (Pat.) Bres. (1905: 208) and *Tremellochaete* Raitv. (1964: 29) were revised, and Malysheva & Spirin (2017) proposed that *Heteroradulum* Lloyd ex Spirin & Malysheva (2017: 709) was validated. The genus *Eichleriella* was accepted to be a monophyletic genus, while both genera *Exidiopsis* and *Heterochaete* seemed to be synonymous with a priority of the latter genus (Malysheva & Spirin 2017, Alvarenga *et al.* 2019, Alvarenga & Gibertoni 2021). Studies on the order Auriculariales based on the morphological and phylogenetic studies, supported a monophyletic lineage of *Alloexidiopsis*, in which a new genus *Alloexidiopsis* was reported (Liu *et al.* 2022). Phylogenetically, *Alloexidiopsis* belonged to the family Auriculariaceae Fr. and was closely related to the genera *Crystallodon* Alvarenga (2021: 21), *Metulochaete* Alvarenga (2019: 1082), and *Hirneolina* (Pat.) Bres. (1905: 208) (Liu *et al.* 2022).

During investigations on the corticioid fungi in Yunnan Province, China, many specimens of *Alloexidiopsis* were collected. To clarify the placement and relationships of these specimens, we carried out a phylogenetic and taxonomic study on the genus *Alloexidiopsis* based on the ITS and nLSU sequences. These specimens are identified as an undescribed species of *Alloexidiopsis* and named *Alloexidiopsis sinensis*. Detailed descriptions, illustrations, and phylogenetic analysis results of the new species are provided.

Materials and methods

Sample Collection and Herbarium Specimen Preparation

The fresh fruiting bodies were collected on the trunk of *Quercus* and fallen angiosperm branches which from Chuxiong, Puer, Wenshan, and Yuxi of 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 (Hu *et al.* 2022). Once dried, the specimens were sealed in an envelope and zip-lock plastic bags and labeled (Zhang *et al.* 2024). The dried specimens were deposited in the herbarium of the Southwest Forestry University (SWFC), Kunming, Yunnan Province, China.

Morphology

The macromorphological descriptions were based on field notes and photos captured in the field and lab. The color terminology follows Petersen (1996). The micromorphological data were obtained from the dried specimens after observation under a light microscope with a magnification of 10 × 100 oil (Zhao *et al.* 2023). Sections mounted in 5% KOH and 2% phloxine B (C₂₀H₂Br₄C₁₄Na₂O₅), and other reagents were also used, including Cotton Blue and Melzer's reagent to observe micromorphology following Wu *et al.* (2022). To show the variation in spore sizes, 5% of measurements were excluded from each end of the range and shown in parentheses. At least thirty basidiospores from each specimen were measured. Stalks were excluded from basidia measurements, and the hilar appendage was excluded from basidiospore measurements. 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).

Molecular Phylogeny

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 ITS5 and ITS4 primers (White *et al.* 1990). The nuclear large subunit (nLSU) region was amplified with the LR0R and LR7 primer pair (<http://lutzonilab.org/nuclear-ribosomal-dna/>, accessed on 21 February 2024). 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). The newly generated sequences were deposited in NCBI GenBank (Table 1).

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

Species Name	Sample No.	GenBank Accession No.		References
		ITS	nLSU	
<i>Alloexidiopsis australiensis</i>	LWZ 20180513-22	OM801933	OM801918	Liu <i>et al.</i> 2022
<i>Alloexidiopsis australiensis</i>	LWZ 20180514-18	OM801934	OM801919	Liu <i>et al.</i> 2022
<i>Alloexidiopsis calcea</i>	MW 331	AF291280	AF291326	Weiss & Oberwinkler 2001
<i>Alloexidiopsis calcea</i>	LWZ 20180904-14	OM801935	OM801920	Liu <i>et al.</i> 2022
<i>Alloexidiopsis nivea</i>	CLZhao 11204	MZ352947	MZ352938	Li <i>et al.</i> 2022
<i>Alloexidiopsis nivea</i>	CLZhao 11210	MZ352948	MZ352939	Li <i>et al.</i> 2022
<i>Alloexidiopsis schistacea</i>	LWZ 20200819-21a	OM801939	OM801932	Liu <i>et al.</i> 2022
<i>Alloexidiopsis sinensis</i>	CLZhao 4146	PP377840	PP377833	Present study
<i>Alloexidiopsis sinensis</i>	CLZhao 5171	PP377841	PP377834	Present study
<i>Alloexidiopsis sinensis</i>	CLZhao 5232	PP377842	—	Present study
<i>Alloexidiopsis sinensis</i>	CLZhao 5309	PP377843	PP377835	Present study
<i>Alloexidiopsis sinensis</i>	CLZhao 5316	PP377844	PP377836	Present study
<i>Alloexidiopsis sinensis</i>	CLZhao 5323	PP377845	PP377837	Present study
<i>Alloexidiopsis sinensis</i>	CLZhao 5362	PP377846	—	Present study
<i>Alloexidiopsis sinensis</i>	CLZhao 6775	PP377847	—	Present study
<i>Alloexidiopsis sinensis</i>	CLZhao 6777	PP377848	—	Present study
<i>Alloexidiopsis sinensis</i>	CLZhao 7105	PP377849	PP377838	Present study
<i>Alloexidiopsis sinensis</i>	CLZhao 7292	PP377850	—	Present study
<i>Alloexidiopsis sinensis</i>	CLZhao 7343 *	PP377851	PP377839	Present study
<i>Alloexidiopsis sinensis</i>	CLZhao 8219	PP377852	—	Present study
<i>Alloexidiopsis sinensis</i>	CLZhao 9274	PP377853	—	Present study
<i>Alloexidiopsis sinensis</i>	CLZhao 9283	PP377854	—	Present study
<i>Alloexidiopsis sinensis</i>	CLZhao 16935	PP377855	—	Present study
<i>Alloexidiopsis sinensis</i>	CLZhao 16945	PP377856	—	Present study
<i>Alloexidiopsis sinensis</i>	CLZhao 16947	PP377857	—	Present study
<i>Alloexidiopsis sinensis</i>	CLZhao 16948	PP377858	—	Present study
<i>Alloexidiopsis sinensis</i>	CLZhao 16949	PP377859	—	Present study
<i>Alloexidiopsis sinensis</i>	CLZhao 16964	PP377860	—	Present study
<i>Alloexidiopsis sinensis</i>	CLZhao 17016	PP377861	—	Present study
<i>Alloexidiopsis sinensis</i>	CLZhao 17020	PP377862	—	Present study
<i>Alloexidiopsis sinensis</i>	CLZhao 17064	PP377863	—	Present study
<i>Alloexidiopsis sinensis</i>	CLZhao 17083	PP377864	—	Present study
<i>Alloexidiopsis sinensis</i>	CLZhao 17234	PP377865	—	Present study
<i>Alloexidiopsis yunnanensis</i>	CLZhao 4023	MT215568	MT215564	Guan <i>et al.</i> 2020
<i>Alloexidiopsis yunnanensis</i>	CLZhao 8106	MT215569	MT215565	Guan <i>et al.</i> 2020
<i>Crystallodon subgelatinosum</i>	RC 1609-URM93444	MN475884	MN475888	Alvarenga & Gibertoni 2021
<i>Crystallodon subgelatinosum</i>	TBG BF-18001-URM93445	MN475885	MN475889	Alvarenga & Gibertoni 2021
<i>Heteroradulum kmetii</i>	Ginns 2529	KX262135	KX262183	Malysheva & Spirin 2017
<i>Heteroradulum kmetii</i>	Kmet	KX262124	KX262173	Malysheva & Spirin 2017
<i>Hirneolina hirneoloides</i>	USJ 55480	AF291283	AF291334	Weiss & Oberwinkler 2001
<i>Metulochaete sanctae-catharinae</i>	AM 0678	MK484065	MK480575	Spirin <i>et al.</i> 2019

* is shown type material, holotype.

The sequences were aligned in MAFFT version 7 (Kato *et al.* 2019) using the G-INS-i strategy. The alignment was adjusted manually using AliView version 1.27 (Larsson 2014). The dataset was aligned first, and then the sequences of ITS and nLSU (ITS+nLSU) were combined with Mesquite version 3.5.1. The alignment datasets were deposited in TreeBASE (submission ID 31185). The combined ITS+nLSU sequences and ITS datasets were used to infer the position of the new species in the genus *Alloexidiopsis* and related species. Sequences of *Heteroradulum kmetii* (Bres.) Spirin & Malysheva (2017: 711) was retrieved from GenBank and used as an outgroup in the ITS+nLSU (Fig. 1) and ITS (Fig. 2) analysis.

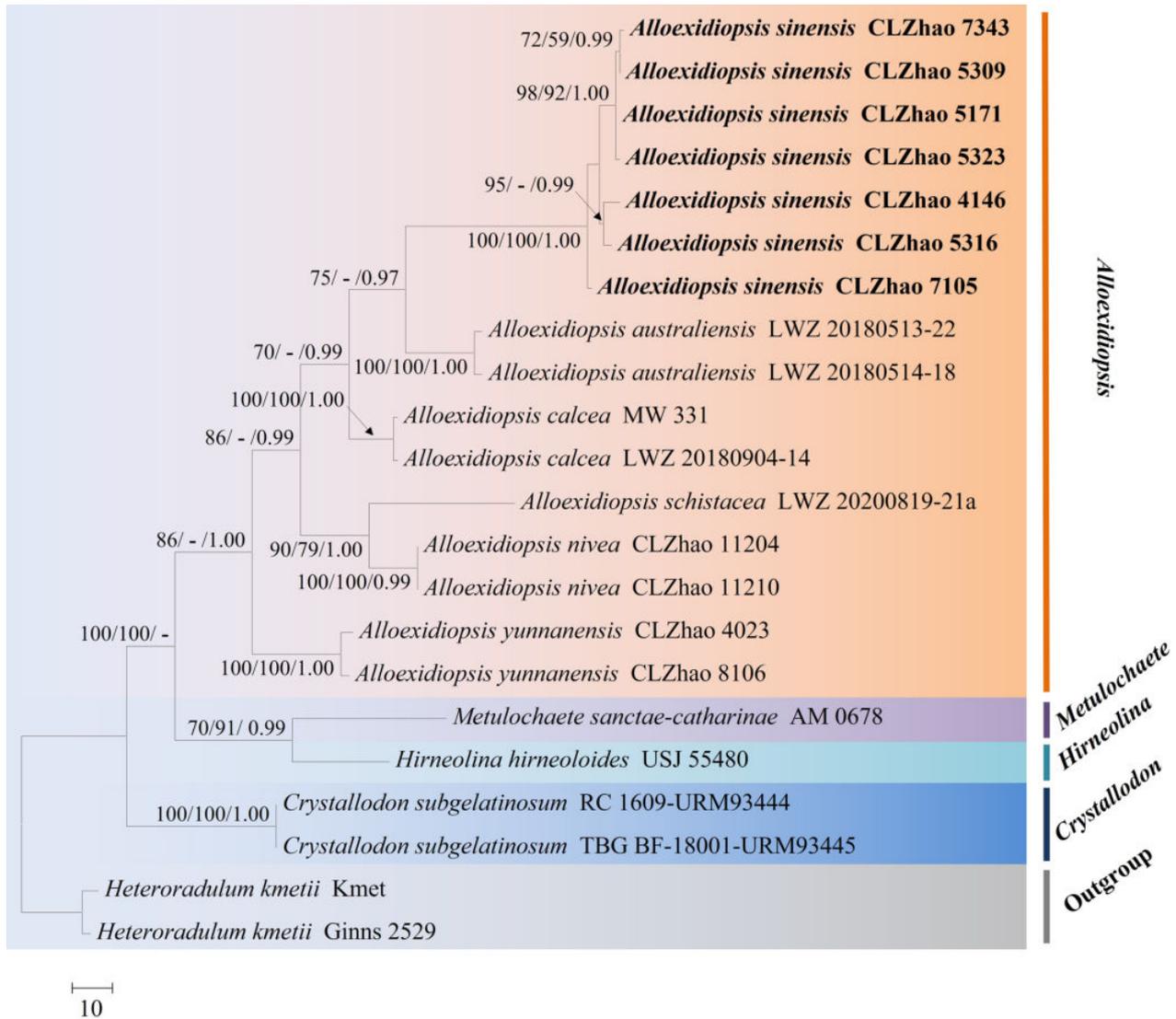


FIGURE 1. Maximum Parsimony strict consensus tree illustrating the *Alloexidiopsis* and related genera based on the combined ITS+nLSU sequences. Branches are labeled with Maximum Likelihood bootstrap values equal to or above 70%, Maximum Parsimony bootstrap values equal to or above 50% and Bayesian posterior probabilities equal to or above 0.95. The new species are in bold.

Maximum parsimony (MP), Maximum Likelihood (ML), and Bayesian Inference (BI) analyses were applied to the combined three 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), consistency index (CI), retention index (RI), rescaled consistency index (RC), and homoplasy index (HI) were calculated for each maximum parsimonious tree generated. The multiple sequence alignment was also analyzed using maximum likelihood (ML) in RAxML-HPC2 (Miller *et al.* 2012). Branch support (BS) for ML analysis was determined by 1000 bootstrap replicates.

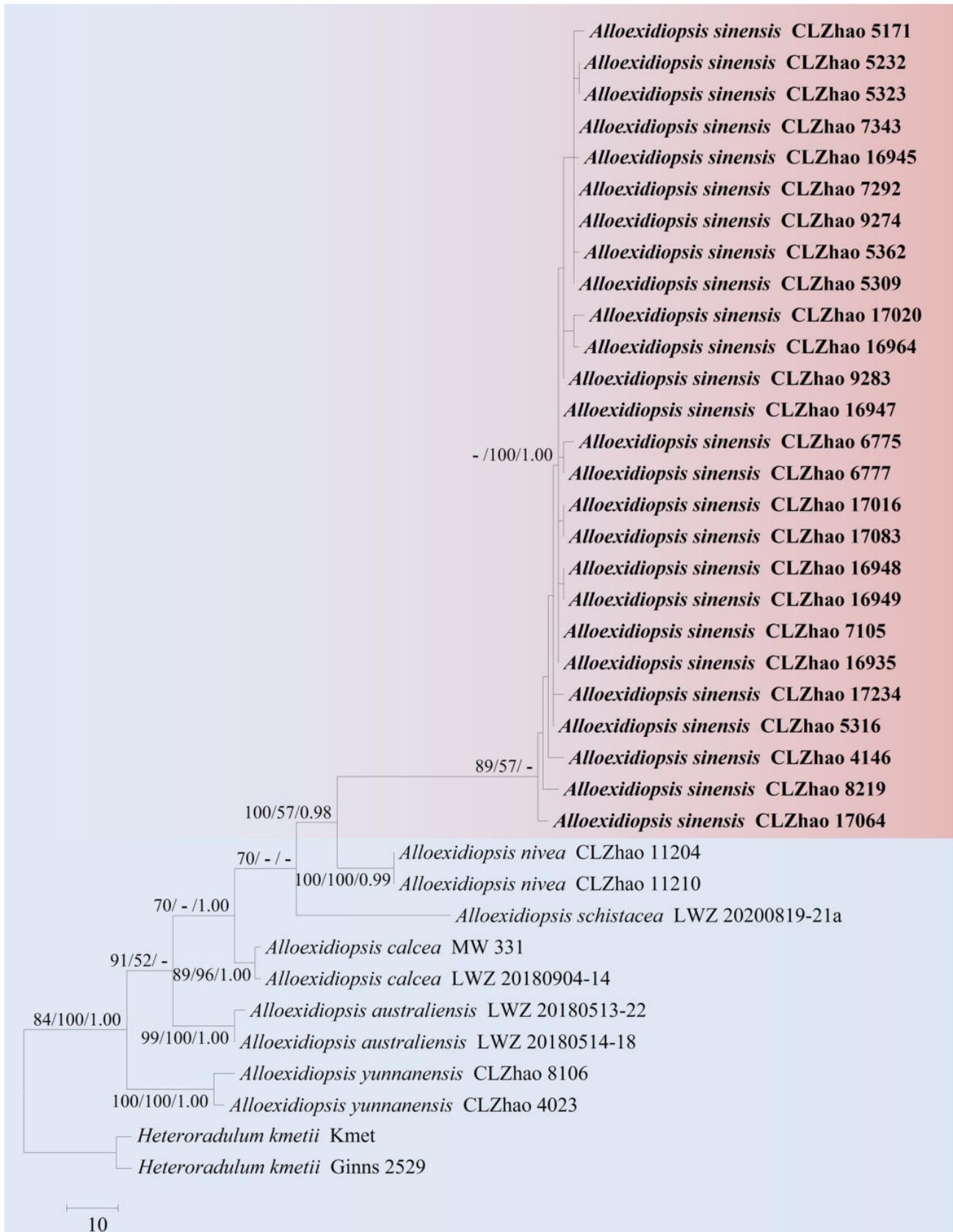


FIGURE 2. Maximum Parsimony strict consensus tree illustrating the phylogeny of the new species *Alloexidiopsis sinensis* and related species in the genus *Alloexidiopsis* based on ITS sequences. Branches are labeled with Maximum Likelihood bootstrap values equal to or above 70%, Maximum Parsimony bootstrap values equal to or above 50% and Bayesian posterior probabilities equal to or above 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 GTR+I+G model of DNA substitution and a gamma distribution rate variation across sites (Ronquist *et al.* 2012). The first one-fourth of all the generations were discarded as burn-ins. The majority-rule consensus tree of all the remaining trees was calculated. Branches were considered significantly supported if they received a maximum likelihood bootstrap value (BS) of $\geq 70\%$, a maximum parsimony bootstrap value (BT) of $\geq 70\%$, or Bayesian posterior probabilities (BPP) of ≥ 0.95 .

Results

Molecular phylogeny

The aligned dataset comprised 22 specimens representing 10 species. Four Markov chains were run for two runs from random starting trees, each for 0.5 million generations for the combined ITS+nLSU (Fig. 1) data set with trees and parameters sampled every 1000 generations. The dataset had an aligned length of 1889 characters, of which 1649 characters are constant, 67 are variable and parsimony uninformative, and 173 are parsimony informative. Maximum parsimony analysis yielded 3 equally parsimonious trees (TL = 466, CI = 0.6438, HI = 0.3562, RI = 0.7784, and RC = 0.5011). The best model for the ITS+nLSU dataset, estimated and applied in the Bayesian analysis, was GTR+I+G (lset nst = 6, rates = invgamma; prset statefreqpr = dirichlet (1,1,1,1)). Both Bayesian analysis and ML analysis resulted in a similar topology to MP analysis with an average standard deviation of split frequencies = 0.004564 (BI), and the effective sample size (ESS) for Bayesian analysis across the two runs is double the average ESS (avg ESS) = 362.

The aligned dataset comprised 37 specimens representing seven species. Four Markov chains were run for two runs from random starting trees, each for 1.5 million generations for the ITS-only (Fig. 2) data set with trees and parameters sampled every 1000 generations. The dataset had an aligned length of 578 characters, of which 429 characters are constant, 34 are variable and parsimony uninformative, and 115 are parsimony informative. Maximum parsimony analysis yielded 418 equally parsimonious trees (TL = 279, CI = 0.6523, HI = 0.3477, RI = 0.8246, and RC = 0.5379). The best model for the ITS dataset, estimated and applied in the Bayesian analysis, was GTR+I+G (lset nst = 6, rates = invgamma; prset statefreqpr = dirichlet (1,1,1,1)). Both Bayesian analysis and ML analysis resulted in a similar topology to MP analysis with an average standard deviation of split frequencies = 0.020675 (BI), and the effective sample size (ESS) for Bayesian analysis across the two runs is double the average ESS (avg ESS) = 178.5.

The phylogram based on the combined ITS+nLSU sequences (Fig. 1) indicated that the species *Alloexidiopsis sinensis* was assigned to the genus *Alloexidiopsis*. The topology based on ITS sequences (Fig. 2), revealed that *A. sinensis* was retrieved as a sister to *A. nivea* (J.J. Li & C.L. Zhao), L.W. Zhou & S.L. Liu (2022: 9).

In addition, the results of BLAST queries in NCBI based on ITS and nLSU separately showed the sequences producing significant alignment descriptions: in ITS blast results, *Alloexidiopsis nivea*, *A. australiensis*, and *Exidia glandulosa* were found as the top ten taxa (Maximum record descriptions: Max score 676; Total score 676; Query cover 98%; E value 0.0; Ident 87.38%). In nLSU blast results, *Alloexidiopsis nivea*, and *A. yunnanensis* were found as the top ten taxa (Maximum record descriptions: Max score 2409; Total score 2409; Query cover 99%; E value 0.0; Ident 98.33%).

Taxonomy

Alloexidiopsis sinensis J.H. Dong & C.L. Zhao, *sp. nov.* Figs. 3, 4, 5

Mycobank no.: MB 852467

Etymology:—*sinensis* (Lat.): referring to the type locality (China).

Diagnosis:—Differs from other species of *Alloexidiopsis* in the yellowish-brown to rose to slightly purple hymenial surface, generative hyphae thin- to thick-walled, allantoid basidiospores (14.5–23 × 4.5–6.5 μm).

Holotype:—CHINA. Yunnan Province, Chxiong, Zixishan National Forest Park, 25°01'N, 101°22'E, elev. 2000 m, on the trunk of *Quercus*, 2 July 2018, CLZhao 7343 (SWFC!).

Basidiomata:—Annual, resupinate, adnate, membranaceous, becoming hard brittle upon drying, very hard to separate from substrate, without odor or taste when fresh, up to 15 cm long, 5 cm wide, 0.2–1 mm thick. Hymenial surface grandinoid, covered by spines, spines 7–10 per mm, up to 0.1 mm long, cream to buff when fresh, turning to yellowish-brown to rose to slightly purple upon drying. Sterile margin distinct, slightly buff, and up to 1 mm wide.

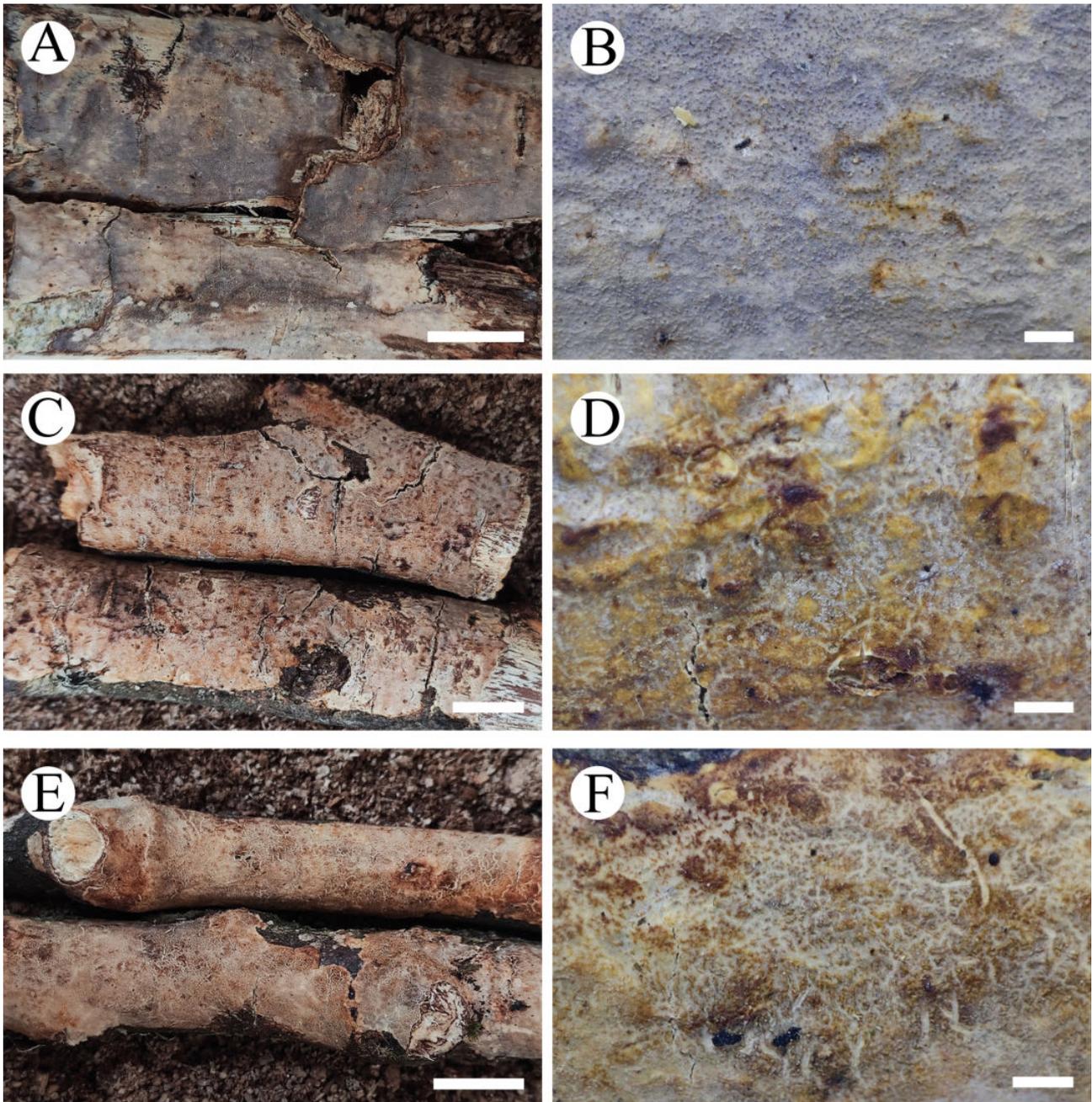


FIGURE 3. Basidiomata of *Alloexidiopsis sinensis* (A, B) CLZhao 7343 (holotype); (C, D) CLZhao 6775; (E, F) CLZhao 16935. Bars: A, C, E= 1 cm; B, D, F= 1 mm.

Hyphal structure:—Hyphal system monomitic, generative hyphae with clamp connections, hyaline, thin- to thick-walled, frequently branched, interwoven, 2–3 μm in diameter; IKI–, CB–, tissues unchanged in KOH.

Hymenium:—Cystidia cylindrical with an obtuse apex, 11.5–15.5 \times 3–5.5 μm , with a clamp connection at the base; cystidioles absent. Hyphidia arising from generative hyphae, nodulose or branched, colorless, thin-walled, 1.5–3.5 μm in diameter. Basidia ellipsoid to ovoid, longitudinally septate, two to four-celled, 16–22 \times 7.5–10 μm ; basidioles dominant, similar to basidia in shape, but slightly smaller.

Basidiospores:—Allantoid, colorless, smooth, thin-walled, with 1–2 oil drops, IKI–, CB–, 14.5–23(–25) \times (4.2–)4.5–6.5(–6.7) μm , L = 18.38 μm , W = 5.38 μm , Q = 3.13–3.15 (n = 210/7).

Type of rot:—White rot.

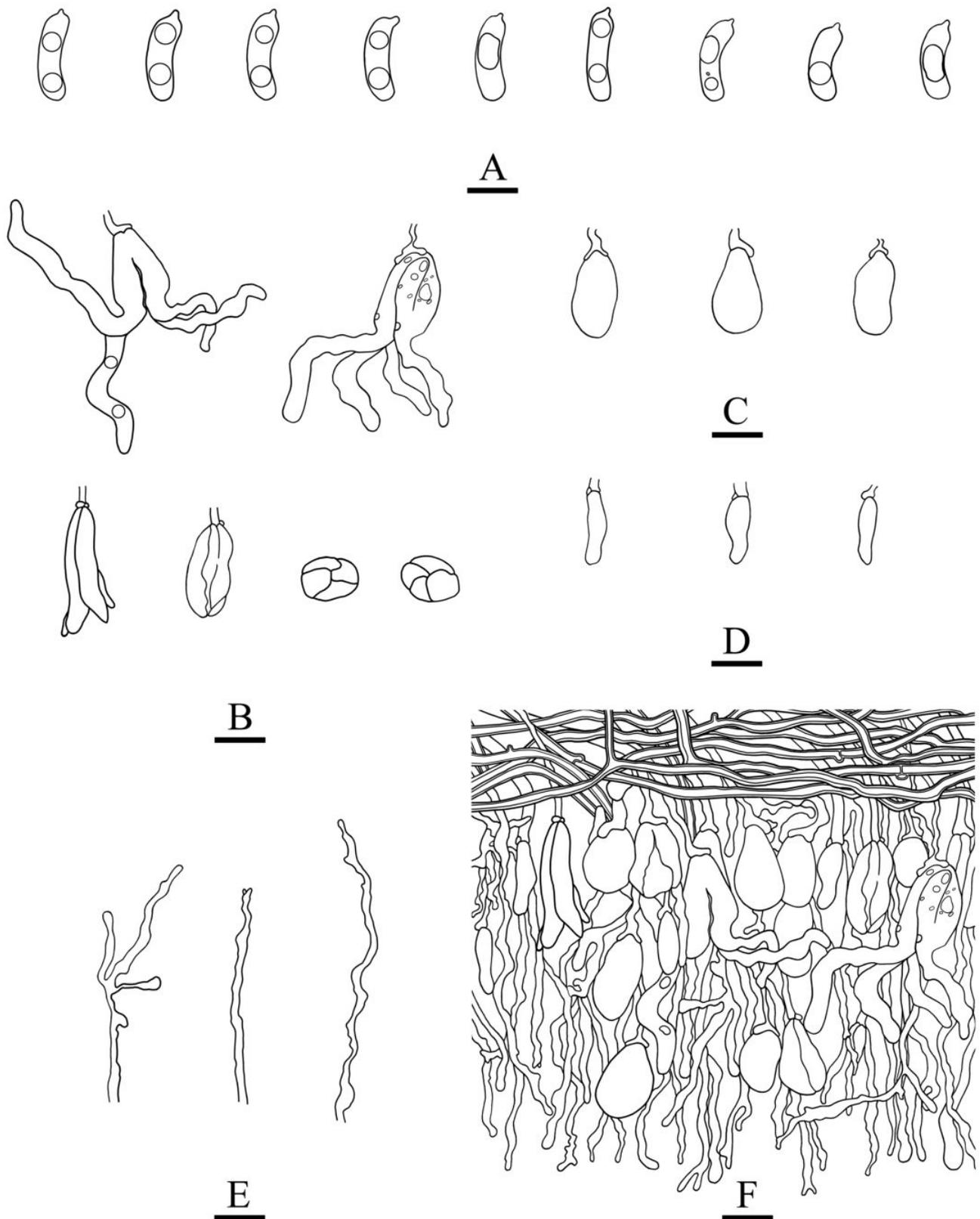


FIGURE 4. Microscopic structures of *Alloexidiopsis sinensis* (holotype, CLZhao 7343). (A) Basidiospores; (B) Basidia; (C) Basidioles; (D) Cystidia; (E) Hyphidia; (F) Part of the vertical section of hymenium. Bars: A–F = 10 μ m.

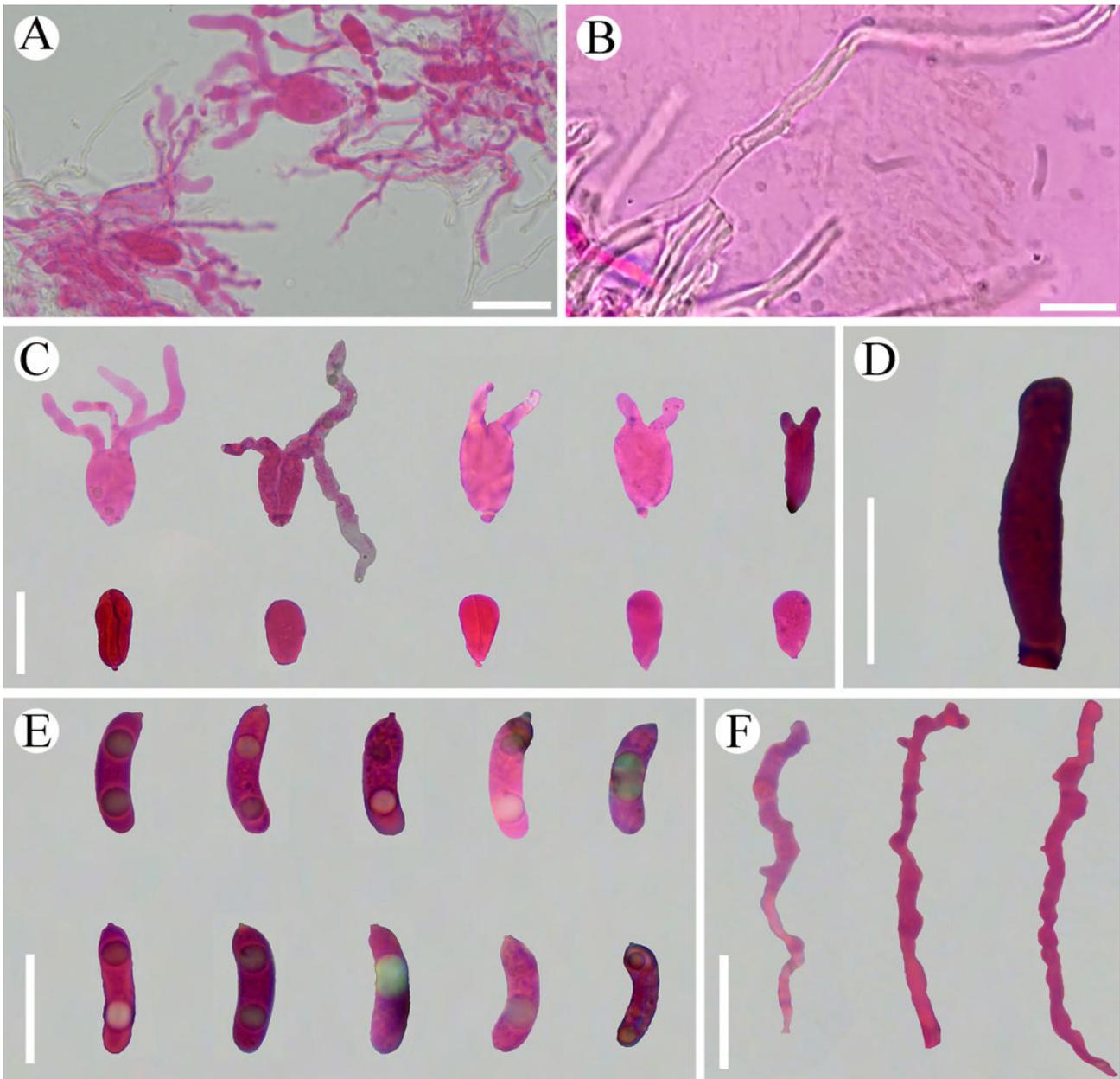


FIGURE 5. Sections of hymenium of *Alloexidiopsis sinensis* (holotype, CLZhao 7343). Scale bars: A, C, E = 20 μm ; B, D, F = 10 μm , 10 \times 100 Oil.

Additional specimens examined:—CHINA. Yunnan Province, Puer, Jingdong County, Wuliangshan National Nature Reserve, 24°22'N, 100°45'E, elev. 2200 m, on the branch fallen of angiosperm, 5 October 2017, CLZhao 4146, 4 January 2019, CLZhao 9274, CLZhao 9283 (SWFC!); Yuxi, Xingping county, Tea Horse Ancient Road Scenic Spot, 22°58'N, 101°05'E, elev. 1500 m, on the branch fallen of angiosperm, 13 January 2018, CLZhao 5171, CLZhao 5232, CLZhao 5309, CLZhao 5316, CLZhao 5323, CLZhao 5362, 21 August 2018, CLZhao 8219 (SWFC!); Chxiong, Zixishan National Forest Park, 25°01'N, 101°22'E, elev. 2000 m, on the branch fallen of angiosperm, 30 June 2018, CLZhao 6775, CLZhao 6777, 1 July 2018, CLZhao 7105, CLZhao 7292(SWFC!); Wenshan, Pingba Town, Wenshan National Nature Reserve, 23°18'N, 104°16'E, elev. 1650 m, on the branch fallen of angiosperm, 28 July 2019, CLZhao 16935, CLZhao 16947, CLZhao 16948, CLZhao 16949, CLZhao 16964, CLZhao 17016, CLZhao 17020, CLZhao 17064, CLZhao 17083, CLZhao 17234 (SWFC!).

Discussion

In the present study, a new species, *A. sinensis* is described based on phylogenetic analyses and morphological characteristics.

Previously, six corticioid genera in the order Auriculariales were phylogenetically studied: *Adustochaete* Alvarenga & K.H. Larss., *Alloexidiopsis*, *Amphistereum* Spirin & Malysheva (2017: 696), *Eichleriella*, *Exidiopsis* and *Sclerotrema* Spirin & Malysheva (2017:712), and to reinstate three previously known genera, e.g., *Heteroradulum*, *Hirneolina* and *Tremellochaete* (Malysheva & Spirin 2017, Alvarenga *et al.* 2019; Alvarenga and Gibertoni 2021, Liu *et al.* 2022). Our result based on the combined ITS+nLSU sequence data (Fig. 1) demonstrated that *A. sinensis* belonged to the genus *Alloexidiopsis*.

Phylogenetically, *A. sinensis* is closely related to *A. nivea* in the ITS based on the phylogeny (Fig. 2). But, morphological characteristics of *A. nivea* differ from *A. sinensis* by having the smooth hymenial surface, unbranched, thin-walled generative hyphae, and shorter basidiospores (6.5–13.5 × 2.7–5.5 μm, Li *et al.* 2022).

Morphologically, *A. sinensis* resembles five similar species in this genus: *A. australiensis*, *A. calcea*, *A. nivea*, *A. schistacea*, and *A. yunnanensis*. Table 2 presents a morphological comparison among *A. sinensis* and five species.

TABLE 2. A morphological comparison between *Alloexidiopsis sinensis* and five similar species in the genus *Alloexidiopsis*.

Species name	Hymenial surface	Hyphae	Cystidia	Basidia	Basidiospores	References
<i>Alloexidiopsis australiensis</i>	Smooth, covered by sterile spines/ Cream to pale orange	Thin-walled, branched	Cylindrical, ventricose; 21.5–24.5 × 9.5–12 μm	Ellipsoid to ovoid, four-celled; 18–21 × 13–18 μm	Cylindrical to broadly cylindrical; 13–25 × 7–11 μm	Liu <i>et al.</i> 2022
<i>Alloexidiopsis calcea</i>	granulose to pruinose/ Grayish white to light ochraceous	Thin-walled, branched	—	Obovate to clavate, two to four-celled; 14–25 × 9.5–15 μm	allantoid to cylindrical, sometimes helicoid; 12–18 × 5–7 μm	Wells 1961
<i>Alloexidiopsis nivea</i>	Smooth/ White to slightly cream	Thin-walled, unbranched	Tubular; 15–34 × 2.5–7 μm	Narrowly ovoid to obconical, two to four-celled; 9–19 × 8–15 μm	Allantoid; 6.5–13.5 × 2.7–5.5 μm	Li <i>et al.</i> 2022
<i>Alloexidiopsis schistacea</i>	Smooth/ Greyish	Thin-walled, branched	Cylindrical; 25–50 × 4–6 μm	Ellipsoid to ovoid, four-celled; 15–20 × 7–10 μm	Cylindrical to broadly cylindrical; 9.5–11 × 4.5–5.5 μm	Liu <i>et al.</i> 2022
<i>Alloexidiopsis sinensis</i>	Grandinoid, covered by spines/ Yellowish-brown to slightly purple	Thin- to thick walled, branched	Cylindrical; 11.5–15.5 × 3–5.5 μm	Ellipsoid to ovoid, two to four-celled; 16–22 × 7.5–10 μm	Allantoid; 14.5–23 × 4.5–6.5 μm	Present study
<i>Alloexidiopsis yunnanensis</i>	Odontoid/ white to smoke grey	Thin-walled, unbranched	Clavate to fusiform; 13–35 × 2–6 μm	Narrowly ovoid to obconical, two to three-celled; 28–41 × 9–14 μm	Cylindrical; 17–24 × 5–8 μm	Guan <i>et al.</i> 2020

The Wood-rotting fungi are an extensively studied group of Basidiomycota, which includes a number of poroid, smooth, grandinoid, odontoid and hydroid basidiomata in China (Wu *et al.* 2020a, b, 2022, Dai *et al.* 2021, Wang *et al.* 2021, Duan *et al.* 2023, Mao *et al.* 2023, Yang *et al.* 2023, 2024, Yuan *et al.* 2023, Zhang *et al.* 2024, Zhou *et al.* 2024). To date, only four species of *Alloexidiopsis* have been recorded in China (Guan *et al.* 2020, Li *et al.* 2022, Liu *et al.* 2022). So, the species diversity of *Alloexidiopsis* is still not well known in China, especially in the subtropical and tropical areas. 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.

Key to the known species of *Alloexidiopsis* worldwide

1. Basidiospores allantoid.....2
1. Basidiospores cylindrical.....3
2. Hymenial surface smooth, basidiospores < 14 µm long..... *Alloexidiopsis nivea*
2. Hymenial surface graninoid, basidiospores > 14 µm long..... *Alloexidiopsis sinensis*
3. Basidia < 28 µm long, cystidia cylindrical.....4
3. Basidia > 28 µm long, cystidia clavate to fusiform..... *Alloexidiopsis yunnanensis*
4. Hymenial surface smooth.....5
4. Hymenial surface granulose to pruinose..... *Alloexidiopsis calcea*
5. Basidiospores > 11 µm long, cystidia < 25 µm long..... *Alloexidiopsis australiensis*
5. Basidiospores < 11 µm long, cystidia > 25 µm long..... *Alloexidiopsis schistacea*

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