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Article

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Morphological characteristics and phylogenetic analyses reveal *Purpureocorticium niveum sp. nov.* (*Agaricomycetes*, *Basidiomycota*) from southern China

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Abstract

Purpureocorticium niveum sp. nov., discovered in Yunnan Province, southern China, is described here as a new species based on morphology and phylogenetic analyses. *Purpureocorticium niveum* is characterized by its cracking basidiomata with a smooth hymenial surface, a monomitic hyphal system with clamp connections on generative hyphae, and pyriform basidiospores. Phylogenetic analyses of the new species were conducted based on internal transcribed spacer (ITS) and large subunit (LSU) sequences. The phylogenetic analyses revealed that the new species belongs to the genus *Purpureocorticium* and was recovered as a sister species to *P. microsporum*. However, morphologically, *P. microsporum* differs from *P. niveum* by having pinkish purple basidiomata and relatively smaller basidiospores. A full description, illustrations, and phylogenetic analyses results of the new species are provided in this article.

Keywords: Biodiversity, Systematics, Taxonomy, Wood-inhabiting fungi, Yunnan Province

Introduction

Fungi are well known as a diverse group of microorganisms that play important functional roles across agricultural, ecological, and economic contexts (Dai 2012, Wu *et al*. 2020a, Zhao *et al*. 2024, He *et al*. 2025). Wood-inhabiting fungi play a crucial role in ecosystem processes, particularly in the degradation of wood and the recycling of organic matter (Cui *et al*. 2019, Dai *et al*. 2021, Wu *et al*. 2022b, Liu *et al*. 2023a, Dong *et al*. 2024, Chen *et al*. 2025; Li *et al*. 2025, Yang *et al*. 2025a, b). Climate change and the destruction of natural habitats are also threatening species, and many may become extinct before they are even discovered (Hyde *et al*. 2024b). Studies on fungal biodiversity and their applications are important, as they may lead to new products (Hyde *et al*. 2024a). Therefore, it is now urgent to recognize and conserve fungi for future utilization (Chen *et al*. 2025).

The wood inhabiting fungi are an extensively studied group of Basidiomycota, which includes several poroid, smooth, grandinoid, odontioid and hydnoid basidiomata, and previously many new taxa were described from China (Cui *et al* 2019, Wu *et al*. 2020b, 2022a, b, Wang *et al*. 2021, 2023, 2024, Liu *et al*. 2023a, b, Mao *et al*. 2023, Zhao *et al*. 2023a, b, 2024, Yuan *et al*. 2023, Chen *et al*. 2025, Jiang *et al*. 2025, Li *et al*. 2025).

Wood-inhabiting fungal genus *Purpureocorticium* Sheng H. Wu (2017: 17) was established by Wu *et al*. (2017), with *P. microsporum* Sheng H. Wu as the type species. The genus is characterized by resupinate, effused, adnate, membranaceous basidiomata; smooth hymenial surface; a monomitic hyphal system with clamp connections on

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generative hyphae; lacking cystidia; subclavate basidia and ovate-ellipsoid basidiospores (Wu *et al*. 2017). According to the MycoBank database (2025) and the Index Fungorum (2025), the genus *Purpureocorticium* has only one published species, *P. microsporum,* which was discovered in China (Wu *et al*. 2017).

Multiple phylogenetic studies of *Purpureocorticium* were conducted to support the molecular systematics of the wood-inhabiting fungi (Larsson 2007, Wu *et al*. 2017, Yuan *et al*. 2023). Wu *et al*. (2017) described a new genus, *Purpureocorticium*, and a new species, *P. microsporum*, based on morphological characteristics and phylogenetic analyses. However, morphological studies alone are insufficient to determine the taxonomic placement of *Purpureocorticium*, as its main diagnostic features are neither distinctive nor indicative of a clear relationship with known orders or clades within the Agaricomycetes. Additionally, phylogenetic analyses showed that *Purpureocorticium* was closely related to the order *Jaapiales* Manfr. Binder, K.H. Larss. & Hibbett (2010: 102) and *Gloeophyllales* Thorn (2007: 111), as well as to the core polyporoid clade (Wu *et al*. 2017).

During investigations on wood-inhabiting fungi in Yunnan Province, China, a potentially new species was collected. To clarify the taxonomic position of the collected specimen—a wood-inhabiting fungus —phylogenetic analyses based on the nuclear ribosomal internal transcribed spacer (ITS) and nuclear large subunit (nrLSU) sequences, along with morphological studies, were conducted on a single taxon. Based on morphological characteristics and molecular phylogenetic analyses, the new species was described as *P. niveum* and provided with morphological descriptions, illustrations, and a phylogenetic analysis.

Materials and methods

Sample collection and herbarium specimen preparation

The fresh fruiting bodies were collected from Lincang, Lancangjiang Forestry Region, E 100°39′, N 23°21′, elev. 2700 m and Qujing, Cuishan Forest Park, E 103°50′, N 25°30′, elev. 2245 m, in Yunnan Province, Southwestern China. The samples were photographed in situ using a Nikon D7100 camera, and fresh macroscopic details were recorded (Rathnayaka *et al*. 2024). All the photos were focus-stacked using Helicon Focus software. After recording the macroscopic details, the samples were transported to a field station, where the basidiomata were dried in an electric food dryer at 40 °C (Hu *et al*. 2022). Once dried, the specimens were sealed in an envelope, placed in zip-lock plastic bags, and labeled (Dong *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 photographs collected in the field and in the laboratory. Petersen (1996) was followed in the use of color terminology. The micromorphological data were obtained from dried specimens observed under a light microscope with a 10X eyepiece and a 100X oil-immersion objective (Zhao *et al*. 2023a, Dong *et al*. 2024). Sections were mounted in 5% KOH, 2% phloxine B ($C_{20}H_4Br_4CI_2K_2O_5$), and other reagents, including Cotton Blue and Melzer's reagent, were also used to observe micromorphology, following the method described by Wu *et al*. (2022a). To indicate the spore size variation, 5% of measurements were excluded from each end of the range and presented in parentheses. Approximately, thirty basidiospores from each specimen were measured. Sterigmata were excluded from basidium and basidia measurements, and the hilar appendage was excluded from basidiospore measurements, respectively. The following abbreviations are used: KOH = aqueous 5% potassium hydroxide water solution, CB– = acyanophilous, CB+ = cyanophilous, IKI– = both inamyloid and non-dextrinoid, 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. The new species was registered in the MycoBank database (http://www.mycobank.org).

Molecular phylogeny

The CTAB rapid plant genome extraction kit-DN14 (Aidlab Biotechnologies Co., Ltd., Beijing, China) was used to extract genomic DNA from the dried specimens according to the manufacturer's instructions. The ITS region was amplified using the ITS5 and ITS4 primers (White *et al*. 1990). The nrLSU region was amplified using the LR0R and LR7 primer pair (Vilgalys & Hester 1990, Rehner & Samuels 1994). The PCR methods for ITS and nrLSU are consistent with those used by Yang *et al*. (2025b). The PCR products were purified and sequenced at Kunming Tsingke Biological Technology Limited, Yunnan Province, P.R. China. The newly generated sequences were deposited in NCBI GenBank (Table 1).

TABLE 1. A list of species, specimens, and GenBank accession numbers of sequences used in this study. The new species is in bold.

Species name	Sample no.	GenBank accession nos.		Locality	References
		ITS	nrLSU		
Athelia naviculispora	LWZ20200921-21a	NR197530	OR527278	China	Genbank
Calocera cornea	AFTOL-ID 438	AY789083	AY701526	UK	Wu *et al*. (2017)
Columnocystis abietina	KHL12474	EU118619	EU118619	Sweden	Larsson (2007)
Coprinus comatus	AFTOL-ID 626	AY854066	AY635772	USA	Wu *et al*. (2017)
Daedalea quercina	Miettinen 12662	JX109855	JX109855	Finland	Binder *et al*. (2013)
Dentocorticium sulphurellum	FPL11801	-	AF393055	USA	Binder *et al*. (2002)
Diplomitoporus crustulinus	Cui 17475	MW377288	MW377367	China	Liu *et al*. (2023b)
Fomitopsis pinicola	AFTOL-ID 770	AY854083	AY684164	USA	Wu *et al*. (2017)
Ganoderma applanatum	Wei 5787a	KF495001	KF495011	China	Wu *et al*. (2017)
Gelatoporia sp.	CHWC 1506-11	-	MF110287	China	Wu *et al*. (2017)
Gloeophyllum carbonarium	Dai 8884	JX524623	KC782727	China	He *et al*. (2014)
Heliocybe sulcata	IBUG 9930	HM536095	HM536069	Mexico	Garcia-Sandoval *et al*. (2011)
Hydnellum geogenium	PBM 2382	DQ218304	AY631900	Norway	Matheny *et al*. (2007)
Hyphoderma setigerum	He6070	OM100747	OM083980	China	Genbank
Inonotus linteus	MUCL 47139	GU461973	GU462002	Cuba	Amalfi *et al*. (2010)
Jaapia argillacea	CBS:252.74	GU187524	GU187581	Netherlands	Binder *et al*. (2010)
Lactarius lignyotus	AFTOL-ID 681	DQ221107	AY631898	USA	Matheny *et al*. (2007)
Leucogyrophana romellii	CFMR: T-547	GU187529	GU187586	Canada	Binder *et al*. (2010)
Lopharia cinerascens	FP105043sp	JN165019	JN164813	USA	Justo & Hibbett (2011)
Phanerochaete sordida	KHL 12054	EU118653	EU118653	Norway	Larsson (2007)
Phlebiella vaga	KHL 11065	EU118660	EU118661	Sweden	Larsson (2007)
Punctularia strigosozonata	CBS:345.34	MH855559	MH867064	Netherlands	Vu *et al*. 2019
Purpureocorticium microsporum	Wu 0806-27	-	MF110292	China	Wu *et al*. (2017)
Purpureocorticium microsporum	Wu 9711-16	-	MF110293	China	Wu *et al*. (2017)
Purpureocorticium niveum	**CLZhao 22997**	**PQ368636**	–	**China**	**Present study**

...continued on the next page

TABLE 1. (Continued)

Species name	Sample no.	GenBank accession nos.		Locality	References
		ITS	nrLSU		
Purpureocorticium niveum	**CLZhao 22980**	**PQ368635**	**-**	**China**	**Present study**
Purpureocorticium niveum	**CLZhao 26035**	**OR658990**	**PV659480**	**China**	**Present study**
Ramaria rubella	AFTOL-ID 724	AY854078	AY645057	USA	Wu *et al*. (2017)
Rhizochaete filamentosa	HHB-3169	KP135410	KP134818	USA	Floudas & Hibbett (2015)
Steccherinum tenue	BM071615_2	MG663301	MF797692	USA	Genbank
Trametes suaveolens	FP102529sp	JN164966	JN164807	USA	Justo & Hibbett (2011)
Trechispora alnicola	CBS577.83	DQ411529	AY635768	USA	Wu *et al*. (2017)
Tyromyces sp.	X1150	JN710603	JN710603	China	Miettinen *et al*. (2012)
Veluticeps fimbriata	L-10628-Sp	HM536100	HM536083	USA	Garcia-Sandoval *et al*. (2011)

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 first aligned, and then ITS and nrLSU sequences were combined in Mesquite version 3.51. The combined ITS and nrLSU sequences were used to infer the position of the new species within the genus *Purpureocorticium* and related species. Sequences of *Calocera cornea* (Batsch) Fr. were selected as the outgroup taxon in the ITS and nrLSU analyses (Fig. 1), following the approach of Wu *et al*. (2017).

Maximum Likelihood (ML) and Bayesian Inference (BI) analyses were carried out to the combined dataset, following a previous study (Zhou *et al*. 2024). Sequences of *Calocera cornea* (Batsch) Fr. were selected as the outgroup taxon in the ITS and nrLSU analyses (Fig. 1), following the approach of Wu *et al*. (2017). Maximum Likelihood analysis was performed using RAxML-HPC BlackBox implemented on the CIPRES Science Gateway (Miller *et al*. 2012) with a GTRCAT model of evolution and 1,000 bootstrap replicates (Felsenstein 1985). jModelTest v2 (Darriba *et al*. 2012) was used to determine the best-fit evolutionary model for each dataset for Bayesian Inference, which was performed with MrBayes 3.2.7a (Ronquist *et al*. 2012). The best model for the ITS and nrLSU dataset, estimated and applied in the Bayesian analysis, was GTR+I+G. Maximum Likelihood and Bayesian Inference yielded similar topologies, with average standard deviations in split frequencies of 0.009965 (BI). Four Markov chains were run from random starting trees. Trees were sampled every 1,000 generations. 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). Branches were considered significantly supported if they had a maximum likelihood bootstrap value (BS)≥70% and a Bayesian posterior probability (BPP)≥0.95.

Results

Molecular phylogeny

The aligned ITS and nrLSU dataset comprised 34 specimens representing 32 species. Four Markov chains were run for two independent runs from random starting trees, each for 10.5 million generations, using the combined ITS and nrLSU dataset (Fig. 1). The effective sample size (ESS) for Bayesian analysis across the two runs was approximately double the average ESS (avg. ESS) of 10508.

In ITS BLAST results of *Purpureocorticium niveum*, the top two taxa were *Cinereomyces fimbriatus* C.L. Zhao (2020: 459), *Gloeoporellus merulinus* (Berk.) Zmitr. (2018: 6) (Maximum record descriptions: Max score 472; Total score 472; Query cover 97%; E value 4e-128; Ident 81.25%). In nrLSU BLAST results, the two taxa were *Skeletocutis pseudo-odora* L.F. Fan & Jing Si (2017: 8), *Skeletocutis vietnamensis* Rui Du & X.H. Ji (2019: 7) (Maximum record descriptions: Max score 2095; Total score 2095; Query cover 99%; E value 0.0; Ident 94.76%).

The phylogram based on the combined ITS and nrLSU sequences (Fig. 1) revealed that our species, *Purpureocorticium niveum*, is grouped with the genus *Purpureocorticium* and forms a separate lineage sister to *P. microsporum*, with 100% ML and 1.00 BPPs bootstrap support. Thus, we introduce *P. niveum* as a new species, collected from Yunnan Province, China. The new species accessions are in bold (Fig. 1).

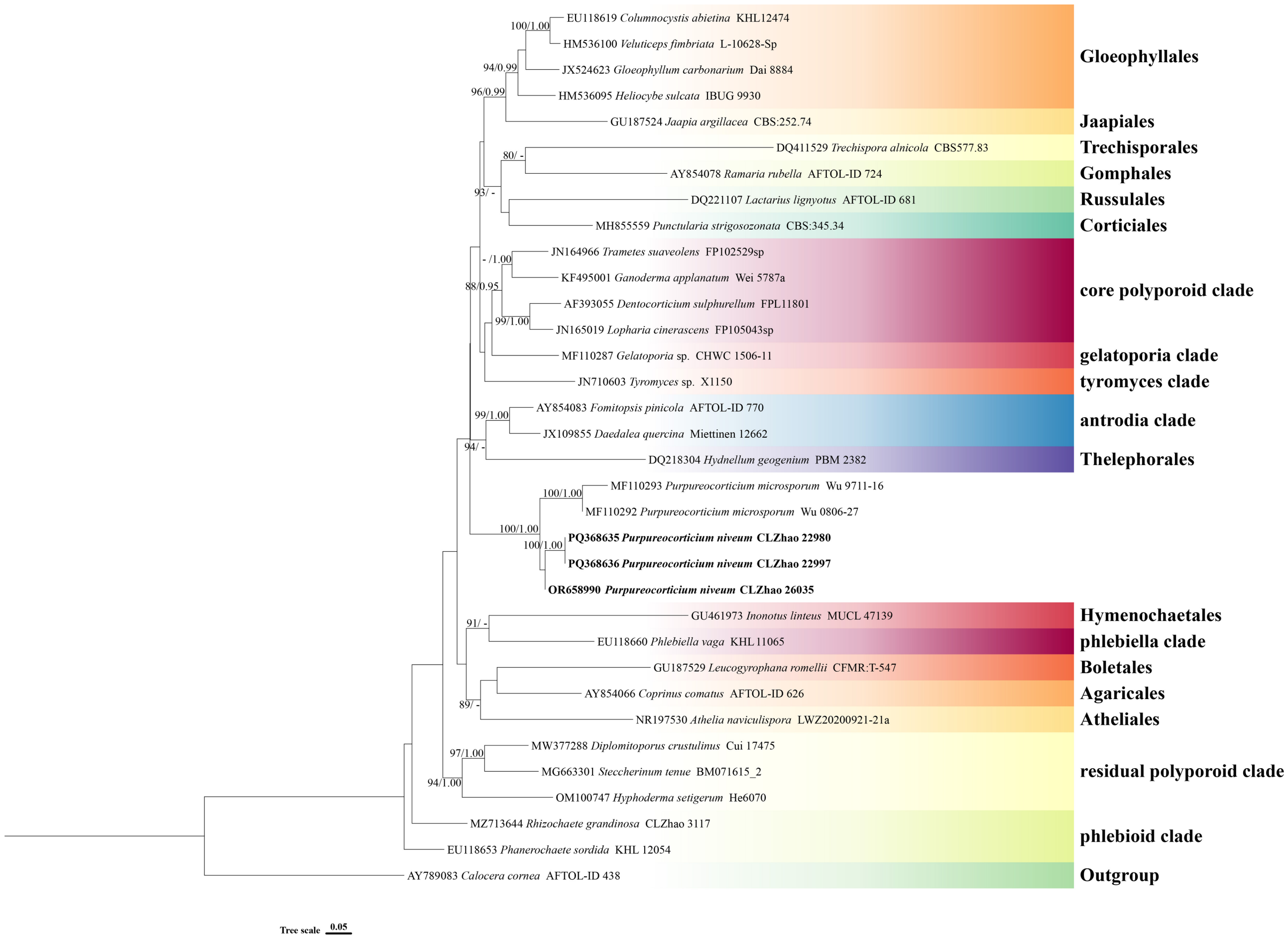

FIGURE 1. Maximum Likelihood strict consensus tree illustrating the phylogeny of *Purpureocorticium* and related species based on the ITS+nrLSU sequence dataset. Branches are labeled with Maximum Likelihood bootstrap values equal to or above 70%, and Bayesian posterior probabilities equal to or above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

Taxonomy

Purpureocorticium niveum Q. Yuan & C.L. Zhao, *sp. nov.* Figs. 2–4

MycoBank no.: MB 859340

***GenBank accession numbers*:—**CLZhao 26035 ITS: OR658990, LSU: PV659480; CLZhao 22980 ITS: PQ368635; CLZhao 22997 ITS: PQ368636.

***Holotype*:—**CHINA, Yunnan Province, Qujing, Cuishan Forest Park, E 103°50′, N 25°30′, elev. 2245 m, on fallen branch of *Pinus* L., 4 November 2022, CLZhao 26035 (SWFCF00026035).

Etymology*:—niveum* (Lat.)—referring to the white hymenial surface of type specimens.

***Basidiomata*:—**Annual, resupinate, adnate, coriaceous, without odor or taste when fresh and drying, up to 3 cm long, 2 cm wide, 50–100 µm thick. Hymenial surface smooth, initially white (60), turning slightly cream (4A2/3) upon drying, cracking. Sterile margin white (60), thinning out, up to 0.5 mm wide.

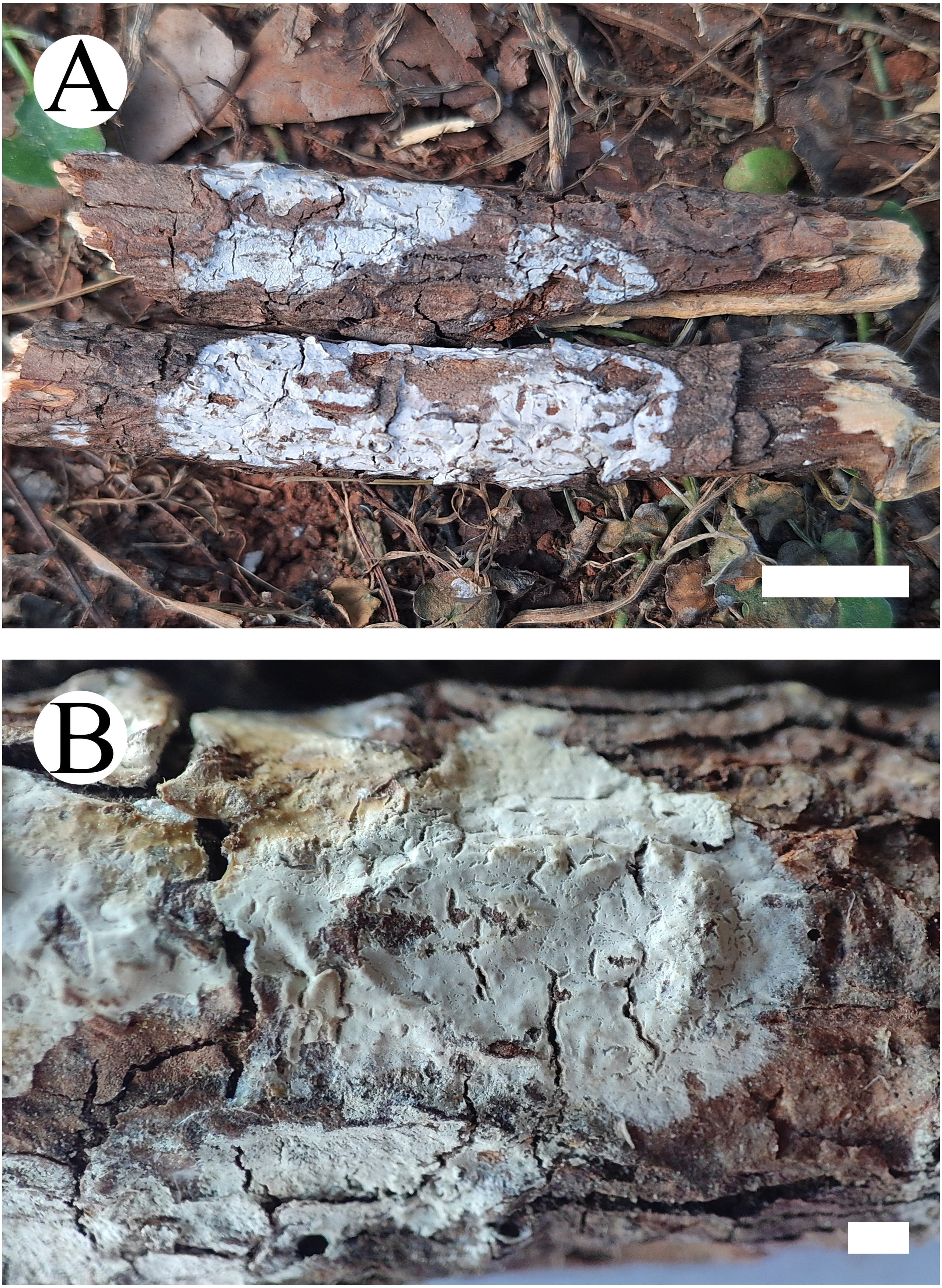

FIGURE 2. Basidiomata of *Purpureocorticium niveum* (holotype). Bars: A = 1 cm, B = 2 mm.

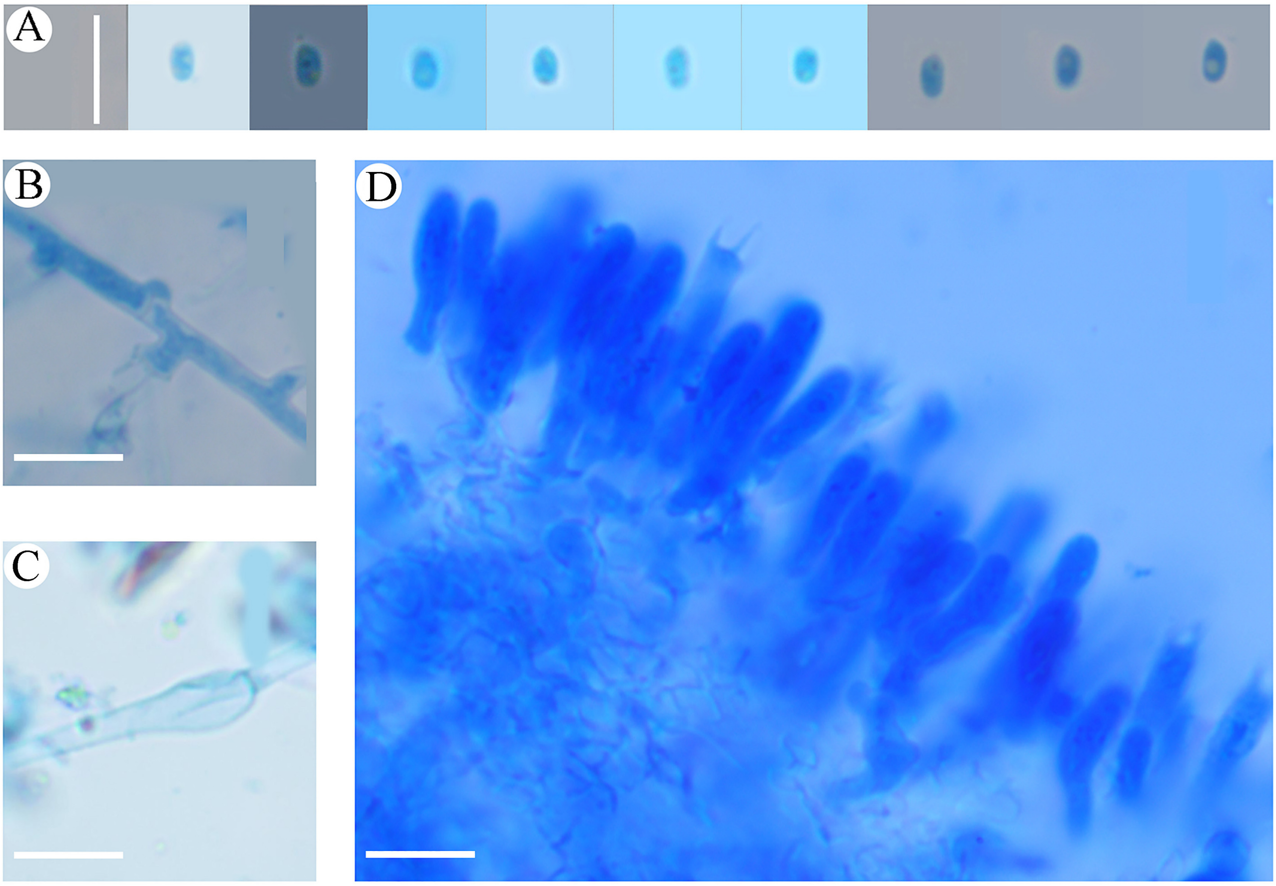

FIGURE 3. Sections of the hymenium of *Purpureocorticium niveum* (holotype, CLZhao 26035). A Basidiospores; (B–C) Hyphae; (D) A cross-section of the hymenium. Scale bars: A–D = 10 µm.

***Hyphal structure*:—**Hyphal system monomitic, generative hyphae with clamp connections, colorless, thin-walled, branched, interwoven, 1.7–2.5 µm in diameter, IKI–, CB–; ampullate hyphae rarely present, 4.5–6.0 µm in diameter, tissues unchanged in KOH.

***Hymenium*:—**Cystidia and cystidioles absent; basidia clavate, slightly sinuous or constricted in the middle, with 4 sterigmata and a basal clamp connection, 18.0–22.5 × 3.0–4.5 µm; basidioles dominant, similar to basidia in shape, but slightly smaller, 10.5–16.5 × 3.0–4.0 µm.

***Spores*:—**Basidiospores pyriform, colorless, smooth, thin-walled, IKI–, CB–, 3.5–4.5 × 2–2.5 µm, L = 3.89 µm, W = 2.28 µm, Q = 1.68–1.73 (n = 60/2).

***Additional specimens examined* (*paratypes*):—**China, Yunnan Province, Lincang, Lancangjiang Forestry Region, E 100°39′, N 23°21′, elev. 2700 m, on a fallen angiosperm branch, 21 July 2022, CLZhao 22997 (SWFCF00022997), CLZhao 22980 (SWFCF00022980).

Discussion

In the present study, a new species, *Purpureocorticium niveum*, is described based on phylogenetic analyses and morphological characteristics. *Purpureocorticium niveum* is characterized by its cracking basidiomata with a smooth hymenial surface, a monomitic hyphal system with clamp connections on generative hyphae, and pyriform basidiospores measuring 3.5–4.5 × 2–2.5 µm.

Phylogenetically, the topology based on ITS+nrLSU sequences (Fig. 1) showed that *P. niveum* is a distinct, well-supported sister clade to *P. microsporum*. Morphologically, *P. niveum* is similar to *P. microsporum* by having a smooth hymenial surface. However, morphologically, *P. microsporum* differs from *P. niveum* with pinkish purple basidiomata and relatively shorter basidiospores (2.8–3.2 × 2–2.2 µm vs. 3.5–4.5 × 2–2.5 µm) (Wu *et al.* 2017).

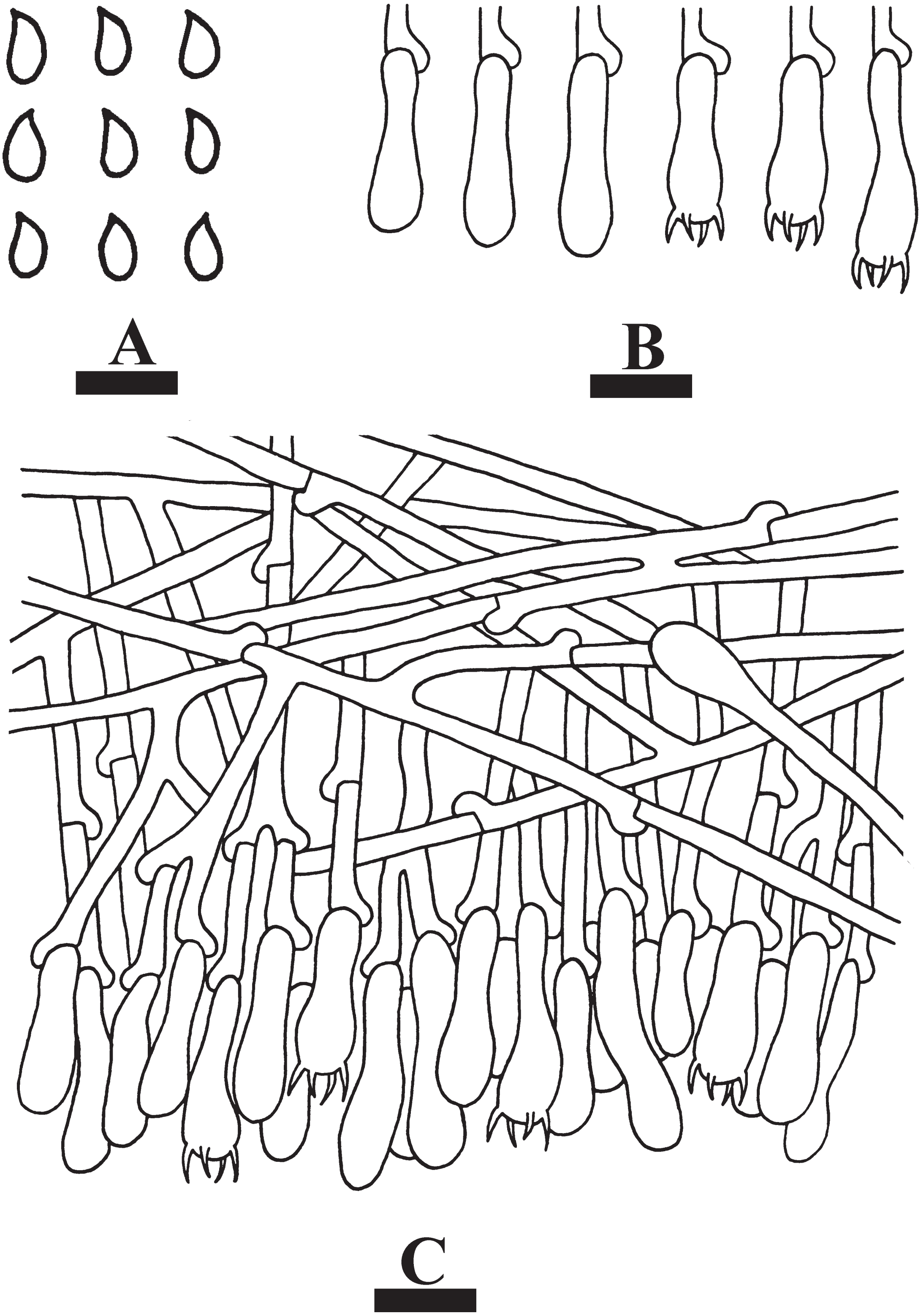

FIGURE 4. Microscopic structures of *Purpureocorticium niveum* (holotype). (A) Basidiospores. (B) Basidia and basidioles. (C) A section of the hymenium. Bars: A–C = 10 µm.

Morphological differences between the new species *Purpureocorticium niveum* and the known species *P. microsporum* are presented in Table 2. The diversity of *Purpureocorticium* species remains largely unknown in China, particularly in subtropical and tropical regions. This paper enhances our understanding of fungal diversity in this region, and further fieldwork and molecular analyses are likely to reveal additional taxa.

TABLE 2. A morphological comparison between the new species (*Purpureocorticium niveum*) and a similar species in the genus *Purpureocorticium*. The new taxon is in bold text.

Species name	Hymenial surface	Hyphae	Cystidia	Basidia	Basidiospores	References
Purpureocorticium microsporum	Smooth/ White, turning purple in KOH	Monomitic/ Thin-walled, 1–6 μm	Absent	Subclavate with a median constriction, or utriform, 13–23 × 3.3–4.3 μm	Ovate-ellipsoid, (2.7–)2.8–3.2(−3.3) × 2–2.2(−2.3) μm	Wu *et al*. (2017)
Purpureocorticium niveum	Smooth or indistinctly colliculose/ cream or brownish	Monomitic/ Thin-walled /Ampullate hyphae rarely present, 1–2.5 μm	Absent	Clavate, 18–22.5 × 3–4.5 μm	Pyriform, 3.5–4.5 × 2.0–2.5 μm	**Present study**

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