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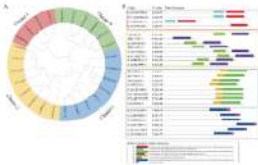
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灵芝C₂H₂转录因子GIZF1的功能分析

孙东伟, 李华君, 王欣杰, 张儒锦, 梁力丹, 史青云, 常思源, 孟丽

菌物学报. 2025, 44(10): 250102.
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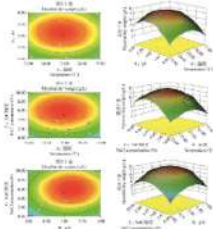


我国节担菌资源及四个种的生物学特性初探

邢汇汶, 杨雅楠, 李佳妮, 张妹, 张永杰

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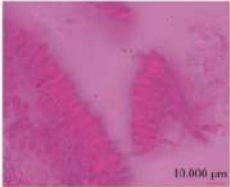


中国西南地区多孔菌目(担子菌门)一个新属

袁琦, 陈琼, 游仕春, 陈雅倩, 周仕丽, 赵长林

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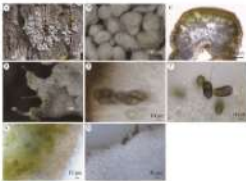


中国蜈蚣衣属*Physcia*地衣一新种

高恺妮, 王思颖, 魏帆, 徐秀琴, 牛东玲

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中国西南地区多孔菌目(担子菌门)一个新属

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摘要: 木腐真菌可以分解木质素、纤维素和半纤维素, 在森林生态系统物质循环中起着不可或缺的作用。本研究基于形态学和分子系统学证据描述并绘制了来自中国西南地区云南省 1 个木腐真菌新属紫韧革菌属 *Porphyrostereum*, 模式种为点状紫韧革菌 *Porphyrostereum punctatum*。该属形态特征为革状担子果, 其子实层体表面光滑有裂纹, 新鲜时奶油色至浅黄色, 干后浅紫粉色或粉紫色, 菌丝系统一体系具锁状联合, 担孢子卵圆形至椭圆形。研究采用最大似然法和贝叶斯推断法对研究标本的 ITS+nLSU nrRNA 基因序列进行系统发育分析, 结果揭示新属紫韧革菌属 *Porphyrostereum* 隶属于 Polyporales, 并形成单一谱系, 且与 *Purpureocorticium* 为近缘类群。

关键词: 分类; 分子系统学; 新种; 云南省

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A new genus of Polyporales (Basidiomycota) from southwest China

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Abstract: Wood-inhabiting fungi can decompose lignin, cellulose and hemicellulose, and play an integral role in the material cycle of forest ecosystems. In this study, a wood-inhabiting polypore collected from

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Yunnan Province, southwest China is introduced as a new genus typified by *Porphyrostereum punctatum*. The new genus *Porphyrostereum* is characterized by corticioid basidiomata with smooth, cream to slightly buff, cracked and becoming purplish pink or pinkish purple hymenial surface, a monomitric hyphal system and generative hyphae bearing clamp connections, and ellipsoid basidiospores. The phylogenetic analyses were performed with maximum likelihood and Bayesian inference methods based on ITS+nLSU nuclear RNA gene regions. Phylogenetic analyses showed that *Porphyrostereum* forms a monophyletic lineage within the order Polyporales in which it is closely related to *Purpureocorticium*.

Keywords: taxonomy; molecular systematics; new species; Yunnan Province

INTRODUCTION

Fungi are well-known as a diverse group of microorganisms, and they play important functional roles in agricultural, ecological and economic perspectives (Dai 2010, 2012; Cui *et al.* 2019; Wu *et al.* 2019, 2020, 2021, 2022; Liu *et al.* 2023c; Dong *et al.* 2024; Ghobad-Nejhad *et al.* 2024; Zhao *et al.* 2024; He *et al.* 2025; Yang X *et al.* 2025; Yang Y *et al.* 2025). Wood-inhabiting fungi are essential to natural ecosystems of organic matter, accelerating rock weathering and responding to plant growth, nutrient cycling, and maintaining plant diversity (Chen *et al.* 2015; Cui *et al.* 2019; Dai *et al.* 2021; Wu *et al.* 2022; Liu *et al.* 2023c; Dong *et al.* 2024; Li *et al.* 2025; Yang X *et al.* 2025; Yang Y *et al.* 2025).

Polyporales is one of the most intensively studied clades of Fungi (Justo *et al.* 2017; Cui *et al.* 2019; Yang *et al.* 2023; Dong *et al.* 2024; Xu *et al.* 2025). Previously, the establishment of families in Polyporales was basically based on phylogenetic analyses and morphological characteristics (Cui *et al.* 2019; Liu *et al.* 2023c). Polyporaceae Fr. ex Corda is the oldest family in Polyporales, which was proposed by Fries (1838) to include all fungi with poroid hymenophores. The Polyporales is a diverse group of Agaricomycetes, not only in molecular sequences but also in morphological characteristics. Moreover, Polyporales include two types of wood decay fungi, white-rot fungi and brown-rot fungi (Binder *et al.* 2013; Justo *et al.* 2017; Liu *et al.* 2023c; Yang Y *et al.* 2025).

In recent years, DNA sequence data have been widely used in the taxonomic studies of polypores and largely contributed to a more natural classification system of Polyporales (Cui *et al.* 2019; Wijayawardene *et al.* 2020, 2022; Hyde *et al.* 2024; Dong *et al.* 2025). Wu *et al.* (2017) established a new genus *Purpureocorticium* close to Jaapiales and Gloeophyllales and the core polyporoid clade based on morphological characteristics and phylogenetic analyses of DNA

sequences inferred from the large subunit nuclear ribosomal RNA gene (LSU nrDNA) and the translation elongation factor 1- α gene (tef1- α). Liu *et al.* (2023c) proposed two new families, Climacocystaceae and Gloeoporellaceae based on the combined sequence datasets of ITS + nLSU + RPB1 and ITS + nLSU + RPB1 + RPB2 + TEF1. Recently, several genera and species with resupinate basidiomata in Polyporales have been described or better defined using morphological and molecular analyses, showing the hidden diversity of this group (Dong *et al.* 2024; Wang *et al.* 2024; Xu *et al.* 2025; Yang Y *et al.* 2025).

During our investigations of wood-inhabiting fungi in Yunnan Province, China, numerous specimens were collected. To clarify the placement and relationships of these specimens, a phylogenetic and taxonomic study of the order Polyporales was carried out based on the ITS and nLSU sequences. The newly collected specimen could not be assigned to any known genus and form a monophyletic lineage within the order Polyporales. Therefore, a new genus, *Porphyrostereum* gen. nov. typified by *P. punctatum* sp. nov., is proposed with descriptions and illustrations based on the morphological characteristics and phylogenetic analyses.

1 MATERIALS AND METHODS

1.1 Morphology studies

Samples were collected from Yunnan Province, China and deposited in the herbarium of the Southwest Forestry University (SWFC), Kunming, Yunnan Province, China. The macromorphologic observation was based on fresh and dried specimens. The color terms in description followed Anonymous and Petersen (Anonymous 1969; Petersen 1996). The micromorphological characteristics were systematically analyzed from the dried specimens, and observed under a light microscope aligned with established methodologies (Dong *et al.* 2024; Yang Y *et al.* 2025). Sections mounted in 5% KOH

and 2% phloxine B dye ($C_{20}H_2Br_4Cl_4Na_2O_5$). Other reagents were also used, including Cotton Blue and Melzer's reagent. Micromorphology observation follows Wu *et al.* (2022).

The following abbreviations were used:

(1) CB = cotton blue, CB- = acyanophilous;

(2) KOH = 5% potassium hydroxide;

(3) IKI = Melzer's reagent, IKI- = both inamyloid and indextrinoid;

(4) W = mean spore width (arithmetic average for all spores);

(5) L = mean spore length (arithmetic average for all spores);

(6) Q = variation in the L/W ratios between the specimens studied;

(7) $n(a/b)$ = number of spores (a) measured from given number (b) of specimens (Guan & Zhao 2021; Wu *et al.* 2022; Wang *et al.* 2023).

1.2 DNA extraction, polymerase chain reaction, and sequencing

The CTAB rapid plant genome extraction kit-DN14 (Aidlab Biotechnologies Co., Ltd.) was used to obtain genomic DNA from the dried specimens according to the manufacturer's instructions. The primer pair of ITS5 and ITS4 (White *et al.* 1990; Zhao *et al.* 2012) was amplified with ITS region. The primer pair LR0R and LR7 was amplified with nuclear LSU region. The PCR was performed following Dong *et al.* (2024) and Yang Y *et al.* (2025). All newly generated sequences were successfully deposited into the National Center for Biotechnology Information (NCBI) GenBank database. All the nucleotide sequences were systematically listed in Table 1.

1.3 Phylogenetic Analyses

The nucleotide sequences were aligned initially by using MAFFT (<https://mafft.cbrc.jp/alignment/server/>) using the "G-INS-I" algorithm and then manually optimized in BioEdit (Hall 1999; Guan & Zhao 2021; Dong *et al.* 2024). The multi-locus sequence dataset aligns firstly and then combine ITS and nLSU sequences with mesquite. To determine the phylogeny, we compiled ITS and LSU sequences matrix, and *Heterobasidion annosum* (Fr.) Bref. was used as outgroup for phylogenetic reconstruction of ITS+nLSU phylogenetic tree (Liu *et al.* 2023c; Fig. 1).

Maximum likelihood (ML), and Bayesian inference (BI) analysis was applied to the combined ITS+nLSU datasets following a previous study (Zhao & Wu 2017; Yang Y *et al.*

2025). The combined dataset was also analyzed using maximum likelihood (ML) in RAXML-HPC2 through the Cipres Science Gateway. Branch support (BS) for ML analysis was determined by 1000 bootstrap replicates (Guan & Zhao 2021; Dong *et al.* 2023b; Wang *et al.* 2024).

MrModeltest 2.3 (Nylander 2004) was used to determine the best-fit evolution model for dataset (ITS+nLSU) for the purposes of Bayesian inference (BI). Bayesian inference was performed using MrBayes3.2.7a with a GTR+I+G model of DNA substitution and a gamma distribution rate variation across sites (Ronquist *et al.* 2012). Four Markov chains were run for 2 runs from random starting trees for 1395 thousand generations for ITS+nLSU (Fig. 1). The first one-fourth of all generations was discarded as burn-in. The majority rule consensus tree of all remaining trees was calculated. Branches exhibiting phylogenetic significance were considered as significantly supported if they received maximum likelihood bootstrap value (BS) > 70%, Bayesian posterior probabilities (BPP) > 0.95 (Dong *et al.* 2024; Yang Y *et al.* 2025).

2 RESULTS

2.1 Molecular phylogeny

The dataset based on ITS+nLSU comprises sequences from 83 fungal specimens representing 82 species. Bayesian analysis and ML analysis resulted in a similar topology as MP analysis with an average standard deviation of split frequencies of 0.009 988 (BI), and the effective sample size (ESS) across the two runs is double the average ESS (avg. ESS) = 386.

2.2 Taxonomy

Porphyrostereum Q. Yuan & C.L. Zhao **gen. nov**

MycoBank: MB858870

Etymology: referring to the purple basidiomata with corticioid hymenophore.

Diagnosis: *Porphyrostereum* Q. Yuan & C.L. Zhao **gen. nov.** differs from other genera in the order Polyporales by its corticioid basidiomata with purplish pink or pinkish purple hymenial surface, a monomitic hyphal system with clamp connection and ellipsoid basidiospores.

Description: Basidiomata resupinate, coriaceous, very hard to separate from substrate. Hymenial surface smooth, cracked, white to cream when

fresh, slightly purplish pink or pinkish purple upon drying. Hyphal system monomitic, generative hyphae with clamp connections, colorless,

thin-walled. Basidia clavate to subclavate, colorless. Basidiospores ellipsoid, colorless, thin-walled, smooth, IKI–, CB–.

Table 1 List of species, specimens, and GenBank accession numbers of sequences used in this study

Species name	Specimen number	GenBank accession number		Country	References
		ITS	LSU		
<i>Abortiporus biennis</i>	Cui 17845	ON417149	ON417197	China	Liu <i>et al.</i> 2023a
<i>Adustoporia sinuosa</i>	Cui 16252	OM039269	OM039169	China	Liu <i>et al.</i> 2023c
<i>Adustoporia xantha</i>	Cui 11544	KR605817	KR605756	China	Han <i>et al.</i> 2016
<i>Antrodia subserpens</i>	Cui 16285	ON417152	ON417201	China	Liu <i>et al.</i> 2023a
<i>Antrodiella stipitata</i>	FD 136	KP135314	KP135197	USA	Floudas & Hibbett 2015
<i>Aurantiporus albidus</i>	Cui 16665	ON682354	ON680806	Australia	Liu <i>et al.</i> 2023c
<i>Bjerkandera adusta</i>	Cui 16670	ON682355	ON680807	Australia	Liu <i>et al.</i> 2023c
<i>Bulbillomyces farinosus</i>	FP 100488 T	KY948802	DQ681201	USA	Justo <i>et al.</i> 2017
<i>Cabalodontia delicate</i>	MCW 564/17	MT849295	MT849295	Brazil	Westphalen <i>et al.</i> 2021
<i>Ceriporiopsis gilvescens</i>	Chen 3340	MZ636936	MZ637099	China	Chen <i>et al.</i> 2021
<i>Cerrena zonata</i>	Cui 16578	ON417153	ON417203	Australia	Liu <i>et al.</i> 2023a
<i>Climacocystis montana</i>	Cui 17124	ON682361	ON680813	China	Liu <i>et al.</i> 2023c
<i>Crustoderma dryinum</i>	FP 105487	KC585320	KC585145	USA	Ortiz-Santana <i>et al.</i> 2013
<i>Cymatoderm aelegans</i>	Dai 17511	ON417155	ON417205	China	Liu <i>et al.</i> 2023a
<i>Dacryobolus gracilis</i>	Dai 14943	MH048972	MH048985	China	Xu <i>et al.</i> 2018
<i>Dacryobolus karstenii</i>	Miettinen 18685	KY948743	KY948900	USA	Justo <i>et al.</i> 2017
<i>Daedalea quercina</i>	Dai 12659	KP171208	KP171230	Finland	Han <i>et al.</i> 2015
<i>Diplomitoporus flavescens</i>	Cui 17419	MW377290	MW377369	China	Liu <i>et al.</i> 2023c
<i>Efibula yunnanensis</i>	Wu 880515-1	MZ636977	GQ470672	China	Chen <i>et al.</i> 2021
<i>Fibroporia ceracea</i>	Cui 16299	MW377293	MW377372	China	Liu <i>et al.</i> 2023c
<i>Fibroporia ceracea</i>	Cui 16300	MW377294	MW377373	China	Liu <i>et al.</i> 2023c
<i>Fomitopsis eucalypticola</i>	Cui 16594	MK852560	MK860110	Australia	Liu <i>et al.</i> 2019
<i>Fragiliporia fragilis</i>	Dai 13561	KJ734262	KJ734266	China	Zhao <i>et al.</i> 2015
<i>Fragiliporia fragilis</i>	Dai 13559	KJ734261	KJ734265	China	Zhao <i>et al.</i> 2015
<i>Gelatoporia subvermispora</i>	Cui 17120	ON417159	ON417209	China	Liu <i>et al.</i> 2023a
<i>Gloeoporellus merulinus</i>	Dai 18735	MW377299	MW377378	Australia	Liu <i>et al.</i> 2023c
<i>Gloeoporellus merulinus</i>	Dai 18782	MW377300	MW377379	Australia	Liu <i>et al.</i> 2023c
<i>Gloeoporus dichrous</i>	Cui 16931	ON682366	ON680818	China	Liu <i>et al.</i> 2023c
<i>Grifola frondosa</i>	Dai 19175	ON417162	ON417212	Canada	Liu <i>et al.</i> 2023a
<i>Grifola frondosa</i>	Dai 19172	ON417161	ON417211	Canada	Liu <i>et al.</i> 2023a
<i>Heterobasidion annosum</i>	Dai 20962	ON417163	ON417213	Belarus	Liu <i>et al.</i> 2023a
<i>Hyphoderma litschaueri</i>	FP 101740	KP135295	KP135219	USA	Floudas & Hibbett 2015
<i>Hyphoderma medioburiense</i>	FD 335	KP135298	KP135220	USA	Floudas & Hibbett 2015
<i>Hypochnicium geogenium</i>	He 6819	OM039282	OM039182	China	Liu <i>et al.</i> 2023c
<i>Hypochnicium punctulatum</i>	FP 101698	KY948827	KY948860	USA	Justo <i>et al.</i> 2017
<i>Irpex flavus</i>	Wu 0705-1	MZ636988	MZ637149	China	Chen <i>et al.</i> 2021
<i>Ischnoderma benzoinum</i>	Cui 17700	ON417165	ON417215	China	Liu <i>et al.</i> 2023a
<i>Ischnoderma benzoinum</i>	Cui 17058	ON417164	ON417214	China	Liu <i>et al.</i> 2023a
<i>Laetiporus montanus</i>	Cui 10011	KF951274	KF951315	China	Song <i>et al.</i> 2014
<i>Laricifomes officinalis</i>	JV 9010/14	KR605822	KR605765	Slovak Republic	Han <i>et al.</i> 2016
<i>Lentoporia carbonica</i>	DAOM F 8281	KC585239	KC585061	Cabada	Ortiz-Santana <i>et al.</i> 2013

(To be continued)

(Table 1 continued)

Species name	Specimen number	GenBank accession number		Country	References
		ITS	LSU		
<i>Leptoporus mollis</i>	RLG 7163	KY948794	MZ637155	USA	Justo <i>et al.</i> 2017
<i>Luteoporia albomarginata</i>	GC 1702-1	LC379003	LC379155	China	Chen <i>et al.</i> 2018
<i>Macrohyporia dictyopora</i>	Dai 18878	OK036736	OK036735	Australia	Liu <i>et al.</i> 2023c
<i>Meripilus giganteus</i>	FP 135344	KP135307	KP135228	UK	Floudas & Hibbett 2015
<i>Metuloidea reniforme</i>	MCW 523/17	MT849302	MT849302	Brazil	Westphalen <i>et al.</i> 2021
<i>Obba rivulosa</i>	Cui 16483	ON417171	ON417221	Vietnam	Liu <i>et al.</i> 2023a
<i>Panus fragilis</i>	HHB 11042	KP135328	KP135233	USA	Floudas & Hibbett 2015
<i>Perenniporia yinggelingsensis</i>	Cui 13627	MH427961	MH427968	China	Liu <i>et al.</i> 2023c
<i>Phaeolus schweinitzii</i>	Dai 8025	KX354457	KX354511	China	Song & Cui 2017
<i>Phaeophlebiopsis caribbeana</i>	HHB 6990	KP135415	KP135243	USA	Floudas & Hibbett 2015
<i>Phanerochaete alnea</i>	FP 151125	KP135177	MZ637181	USA	Floudas & Hibbett 2015
<i>Phanerochaetella angustocystidiata</i>	Wu 9606-39	MZ637020	GQ470638	China	Chen <i>et al.</i> 2021
<i>Phlebia nantahaliensis</i>	HHB 2816	KY948777	KY948852	USA	Justo <i>et al.</i> 2017
<i>Phlebiopsis gigantea</i>	FCUG 1417	MZ637051	AF141634	Norway	Chen <i>et al.</i> 2021
<i>Physisporinus longicystidius</i>	Cui 16630	ON417177	ON417227	Australia	Liu <i>et al.</i> 2023a
<i>Picipes badius</i>	Cui 11136	KU189781	KU189812	China	Zhou <i>et al.</i> 2016
<i>Podoscypha venustula</i>	Cui 16923	ON417181	ON417231	Puerto Rico	Liu <i>et al.</i> 2023a
<i>Polyporus varius</i>	Cui 12249	KU507581	KU507583	China	Zhou <i>et al.</i> 2016
<i>Pseudofibroporia citrinella</i>	Yuan 6181	KU550478	KU550501	China	Chen <i>et al.</i> 2017
<i>Purpureocorticium microsporum</i>	Wu 0806-27	–	MF110292	China	Wu <i>et al.</i> 2017
<i>Purpureocorticium microsporum</i>	Wu 9711-16	–	MF110293	China	Wu <i>et al.</i> 2017
<i>Purpureocorticium</i> sp.	NLB 1389	MT537071	MT537071	Australia	Unpublished
<i>Porphyrostereum punctatum</i>	CLZhao 17713	PV577722	PV577723	China	Present study
<i>Pycnoporellus fulgens</i>	Cui 10033	KX354458	KX354512	China	Song & Cui 2017
<i>Radulodon casearius</i>	HHB 9567	KY948752	KY948871	USA	Justo <i>et al.</i> 2017
<i>Resinoporia sordida</i>	Cui 16469	ON417186	ON417237	Vietnam	Liu <i>et al.</i> 2023a
<i>Rhizochaete sulphurina</i>	HHB 5604	KY273031	GU187610	USA	Nakasone <i>et al.</i> 2017
<i>Rhodofomes roseus</i>	Cui 17081	ON417188	ON417239	China	Liu <i>et al.</i> 2023a
<i>Rhodofomitopsis pseudofeei</i>	Cui 16794	MK461952	MK461956	Australia	Liu <i>et al.</i> 2023c
<i>Rhodonina obliqua</i>	Dai 23436	ON417191	ON417242	China	Liu <i>et al.</i> 2023a
<i>Rickiopora latemarginata</i>	RP 110	KU521770	KU521770	Brazil	Westphalen <i>et al.</i> 2016
<i>Rickiopora latemarginata</i>	RP 58	KU521769	KU521769	Brazil	Westphalen <i>et al.</i> 2016
<i>Rigidoporus</i> sp.	Cui 16859	ON417180	ON417230	Puerto Rico	Liu <i>et al.</i> 2023a
<i>Ryvardenia cretacea</i>	Cui 16732	MW377325	MW377402	Australia	Liu <i>et al.</i> 2023c
<i>Sarcoporia polyspora</i>	Cui 16995	OM039299	OM039199	China	Liu <i>et al.</i> 2023c
<i>Sarcoporia polyspora</i>	Cui 16977	MW377326	MW377403	China	Liu <i>et al.</i> 2023c
<i>Scopuloides rimosa</i>	HHB 15484	KP135352	KP135281	USA	Floudas & Hibbett 2015
<i>Skeletocutis yunnanensis</i>	Dai 15709	KU950434	KU950436	China	Bian <i>et al.</i> 2016
<i>Sparassis crispa</i>	MBUH DORISL	AY218442	AY218404	Germany	Wang <i>et al.</i> 2004
<i>Sparassis radicata</i>	OKM 4756	KC987580	KF053407	USA	Liu <i>et al.</i> 2023c
<i>Steccherinum</i> sp.	Cui 16755	ON682370	ON680822	Australia	Liu <i>et al.</i> 2023c
<i>Trametes cinnabarina</i>	Dai 14386	KX880629	KX880667	China	Liu <i>et al.</i> 2023c
<i>Tyromyces</i> sp.	Cui 16652	ON417196	ON417248	Australia	Liu <i>et al.</i> 2023a
<i>Wolfiporia cocos</i>	CBS 279.55	MW251869	MW251858	USA	Wu <i>et al.</i> 2020
<i>Wolfiporia dilatohypha</i>	CS 635913	KC585400	KC585234	USA	Ortiz-Santana <i>et al.</i> 2013

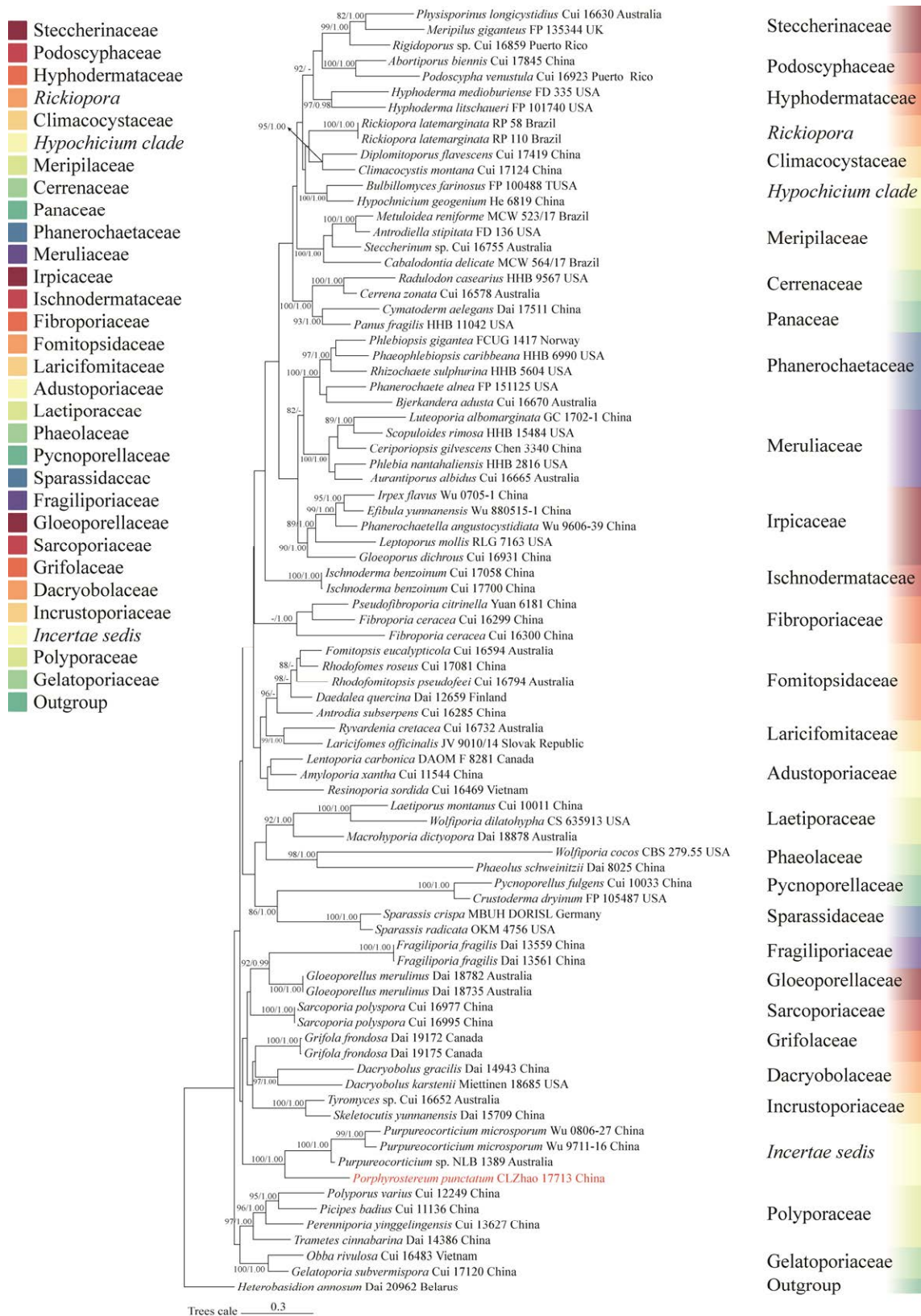


Fig. 1 Phylogeny tree of related species of Polyporales performed by ML analysis based on combined ITS and LSU rDNA sequences. Branches are labeled with maximum likelihood bootstrap values > 70%, and Bayesian posterior probabilities > 0.95, respectively.

Porphyrostereum punctatum Q. Yuan & C.L. Zhao **sp. nov.** Figs. 2, 3, 4

MycoBank: MB858871

Holotype: China. Yunnan Province, Honghe, Pingbian County, Daweishan Nature Reserve, GPS coordinates 28°22'N, 114°4'E, elev. 1 590 m asl., on angiosperm trunk, 1 August 2019, leg. C.L. Zhao, CLZhao 17713 (SWFC).

Etymology: *punctatum* (Lat.), referring to the species having punctate basidiomata.

Diagnosis: It differs from other related species by its corticioid basidiomata, hymenial surface smooth, cracked, white to cream, becoming purplish pink or pinkish purple, a monomitic hyphal system with clamp connections, ellipsoid basidiospores measuring $(3.5\text{--}4.0\text{--}5.0\text{--}5.5) \times 2.5\text{--}3.5\ \mu\text{m}$.

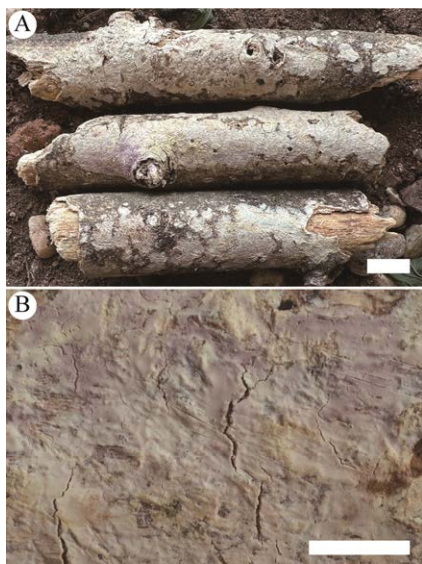


Fig. 2 Basidiomata of *Porphyrostereum punctatum* (holotype, CLZhao 17713). A: Basidiomata on the substrate; B: Macroscopic characteristics of hymenophore. Bars: A= 1 cm; B= 2 mm.

Basidiomata: Annual, resupinate, coriaceous, without odor or taste when fresh, up to 7 cm long, 2 cm wide, less than 1 mm thick. Hymenial surface smooth, white to cream when fresh, becoming slightly purplish pink or pinkish purple upon drying, cracking. Sterile margin narrow, cream, up to 1 mm wide.

Hyphal structure: Hyphal system monomitic, generative hyphae with clamp connections, colorless, thin-walled, unbranched, interwoven, $2.5\text{--}4\ \mu\text{m}$ in diameter, IKI–, CB–; tissues unchanged in KOH.

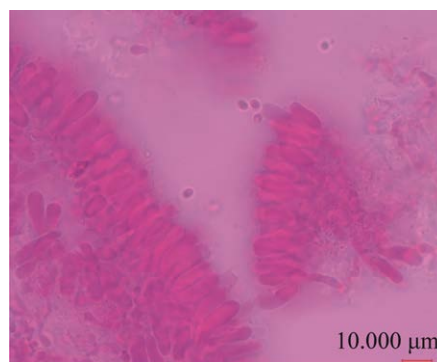


Fig. 3 Sections of hymenia of *Porphyrostereum punctatum* (holotype, CLZhao 17713). 10 × 100 Oil.

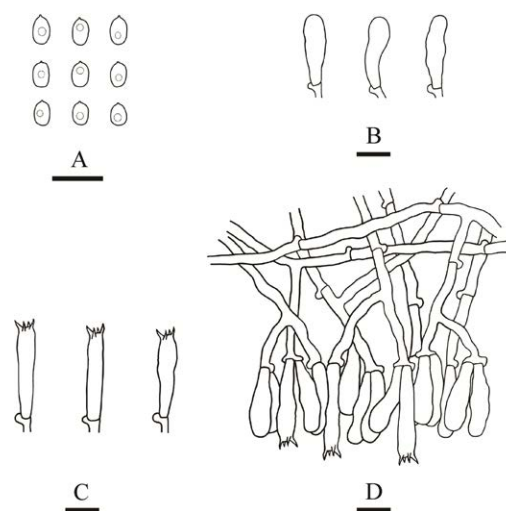


Fig. 4 Microscopic structures of *Porphyrostereum punctatum* (holotype, CLZhao 17713). A: Basidiospores; B: Basidioles; C: Basidia; D: A cross section of hymenium. Bars= 10 μm .

Hymenium: Cystidia lacking. Basidia subclavate, with a basal clamp connection and four sterigmata, $18.5\text{--}27 \times 5\text{--}6\ \mu\text{m}$; basidioles dominating in hymenium, similar to basidia but smaller.

Basidiospores: Ellipsoid, colorless, thin-walled, smooth, containing a guttule, IKI–, CB–, $(3.5\text{--}4.0\text{--}5.0\text{--}5.5) \times 2.5\text{--}3.5\ \mu\text{m}$, $L=4.51\ \mu\text{m}$, $W=3.04\ \mu\text{m}$, $Q=1.48$ ($n=30/1$).

Type of rot: white rot.

3 DISCUSSIONS

The Polyporales is a diverse group of Agaricomycetes, which has received extensive attention and studies (Liu *et al.* 2023c; Yang Y *et al.* 2025). Some mycologists have attempted to adopt ribosomal RNA genes to study the phylogeny of Polyporales, but the results suggest

that it is difficult to resolve all taxonomic groups of Polyporales (Larsson *et al.* 2004; Binder *et al.* 2005; Liu *et al.* 2023c). Subsequently, the protein-coding genes, including RPB1, RPB2, and TEF1, were applied to the phylogenetic study of Polyporales (Matheny *et al.* 2007; Binder *et al.* 2013; Zhao *et al.* 2015; Justo *et al.* 2017; Liu *et al.* 2023c). The present study reveals a genus that forms a monophyletic lineage (100% BS, 1.00 BPP) within the order Polyporales based on the combined ITS and nLSU sequence data (Fig. 1). Therefore, a new genus is proposed here with description and illustrations based on the morphological characteristics and phylogenetic analyses. Phylogenetically, the new genus *Porphyrostereum* forms a monophyletic lineage and is closely related to *Purpureocorticium* (Fig. 1). However, *Purpureocorticium* differs morphologically from *Porphyrostereum* in having membranaceous basidiomata, with a hymenial surface that is turning purple in KOH and utriform basidia (Wu *et*

al. 2017).

Morphologically, *Porphyrostereum* resembles four other corticioid genera in the order Polyporales, viz. *Dacryobolus* Fr., *Hyphoderma* Wallr., *Phlebia* Fr. and *Phanerochaete* P. Karst., However, *Porphyrostereum* differs in having purplish pink or pinkish purple hymenial surface (Table 2).

In recent years, the wood-inhabiting fungi have become an extensively studied group of Basidiomycota in China (Sun *et al.* 2020, 2022; Dai *et al.* 2021; Ji *et al.* 2022; Wu *et al.* 2022; Cui *et al.* 2023; Dong *et al.* 2023a, 2023b; Duan *et al.* 2023; Liu *et al.* 2023a, 2023b, 2023c; Mao *et al.* 2023; Yang *et al.* 2023; Yu *et al.* 2023; Yuan *et al.* 2023; Li *et al.* 2024; Zhang *et al.* 2024; Zhao *et al.* 2024; Zhou *et al.* 2024; Dong *et al.* 2025; Yang Y *et al.* 2025). Up to now, several corticioid genera in Polyporales have been reported and described, but many new taxa remain undiscovered. Extensive collection is still urgently needed.

Table 2 Morphological comparison between *Porphyrostereum* and four similar genera in the order Polyporales

Genus name	Basidiomata	Hymenial surface	Hyphal system	Basidiospores	Cystidia	References
<i>Dacryobolus</i>	Resupinate, adnate, effused, subceraceous	Smooth to odontoid,	Monomitic or dimitic	Allantoid, smooth, thin-walled	Cylindrical or tuber	Maekawa 2021
<i>Hyphoderma</i>	Resupinate, adnate, effused, membranous or ceraceous	Smooth, tuberculate, grandinioid or odontoid	Monomitic	Subglobose, ellipsoid, cylindrical or allantoid, smooth, thin-walled	Present or absent	Maekawa 1994
<i>Phanerochaete</i>	Resupinate, effused, adnate or detachable, pellicular to membranous	Smooth, tuberculate, odontoid or hydroid	Monomitic	Subhyaline, mostly ellipsoid to cylindrical, smooth, thin-walled	Present or absent	Maekawa 2021
<i>Phlebia</i>	Resupinate, effuso-reflexed or dimidiate, cartilaginous, subgelatinous or ceraceous	Smooth, tuberculate, odontoid, phlebioid or merulioid	Monomitic	Ellipsoid to allantoid, smooth, thin-walled	Present or absent	Maekawa 2021
<i>Porphyrostereum</i>	Annual, resupinate, coriaceous	Smooth, white to cream when fresh, slightly purplish pink or pinkish purple upon drying	Monomitic	Ellipsoid, smooth, thin-walled	Absent	Present study

Note: New taxa are in bold.

Author contributions

YUAN Qi: Conducting field surveys and sampling, species identification, thesis conception and initial manuscript drafting; CHEN Qiong, CHEN Yaqian: Field survey and sampling, species identification and data analysis; YOU Shichun, ZHOU Shili: Data analysis and literature search; ZHAO Changlin: Providing guidance on species identification and manuscript writing, species identification, thesis conception, review and editorial oversight.

Declaration of competing interests

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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