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Taxonomy and Phylogeny of Amylocorticiales (Basidiomycota): Two New Genera, Six New Species, and Four New Combinations

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Abstract

Amylocorticiales forms a well-supported clade within Agaricomycetes, Basidiomycota, and most of the species have resupinate basidiomes and cause brown rot on wood. It is one of the smallest orders of the basidiomycetes, with the species diversity and phylogeny being understudied. In the present study, we conduct phylogenetic analyses based on the concatenated ITS + nLSU sequence dataset of the order with an emphasis on the samples from southern China. As a result, ten new lineages were found. Combined with the morphological evidence, two new genera and six new species are described and illustrated, and four new combinations are proposed. *Amylophanerochaete hainanense* gen. et sp. nov. is closely related to *Serpulomyces* but differs in having smooth hymenophores with rhizomorphs and narrowly cylindrical to slightly sigmoid amyloid basidiospores. The new genus *Pseudoathelia* is proposed to accommodate *Leptosporomyces linzhiense* and *Athelia septentrionalis*, two athelioid species. Four new species, viz. *Amylocorticium athelioides*, *A. bisporum*, *A. guangxiense*, and *A. luteolum*, collected from southern China, formed distinct lineages within the *Amylocorticium* clade. *Serpulomyces borealis*, the only species of the genus, is proven to be a species complex, while one new species, *S. subborealis*, and two new combinations, *S. rhizomorphus* and *S. yunnanensis*, transferred from *Ceraceomyces*, are found in the lineage. An identification key to all the known genera is provided.

Keywords: brown rot; corticioid fungi; molecular phylogenetics; new species; wood-decaying fungi

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1. Introduction

Amylocorticiales is a recently described small order with about just over 70 species [1]. Morphologically, there is no distinct synapomorphic character for the order, but most species have resupinate corticioid basidiomes with smooth, merulioid, or poroid hymenophores, a monomitic hyphal system with loosely interwoven nodose-septate generative hyphae, absence of cystidia, and smooth basidiospores with an amyloid reaction in Melzer's reagent [2]. Ecologically, most species are saprotrophic, causing a brown or white rot on wood, whereas *Agroathelia rolfsii* (Sacc.) Redhead & Mullineux is a serious

soilborne pathogen infecting many plant species [3]. Phylogenetically, few studies have been carried out, and the generic position of some lineages has not been resolved since the foundation of the order. Recently, Yuan et al. [4] described a new monotypic genus from China, *Amyloceraceomyces* S.H. He, and Redhead & Mullineux established the new genus *Agroathelia* to accommodate *Athelia rolfsii* (Sacc.) C.C. Tu & Kimbr [5]. Eleven genera are recognized in the order. *Agroathelia*, *Amyloceraceomyces* S.H. He, *Amylocorticiellum* Spirin & Zmitr., *Amylocorticium* Pouzar, *Anomoloma* Niemelä & K.H. Larss., *Anomoporia* Pouzar, *Ceraceomyces* Jülich, Willdenowia, *Irpicodon* Pouzar, *Plicaturopsis* D.A. Reid, *Podoserpula* D.A. Reid, and *Serpulomyces* Spirin & Zmitr. [4,6–13]. The genera *Irpicodon* and *Plicaturopsis* were synonymized with and recombined into the genus *Plicatura* Peck. Morphological similarities and close evolutionary relationships justify the taxonomic revision [14].

Although several new taxa have been added to the order in recent years [15–22], it still seems that the species diversity of the order is not sufficiently studied and recognized when compared to other orders in Basidiomycota dominated by wood-inhabiting fungi, such as Polyporales, Hymenochaetales, and Russulales [23–28]. It is also possible that some cryptic species were overlooked because those taxa in Amylocorticiales have small resupinate corticioid basidiomes, which are usually ignored by mycologists when collecting specimens. Meanwhile, some cryptic species were not discovered because of insufficient sequencing of specimens. In order to investigate the species diversity and resolve the phylogenetic positions of some recently described species of the order, we carried out an intensive taxonomic and molecular phylogenetic study by focusing on samples from China. The results show that Amylocorticiales has two new genera, six new species, and four new combinations. This study belongs to the study series of species diversity, taxonomy, and phylogeny of corticioid fungi in China.

2. Materials and Methods

2.1. Specimen Collection

Specimens were collected in nature reserves or forest parks of different types of forests in China by the authors during rainy seasons, usually from June to October. Specimens of new species were collected from Sichuan, Yunnan, Hainan Provinces, Guanxi Autonomous Region, and Taiwan from 2016 to 2024. In situ photographs of specimens were captured using a Canon EOS 70D camera (Canon Corporation, Tokyo, Japan). Fresh specimens were dried with a portable dryer (Evermat, Tampere, Finland; 40–50 °C). Dried specimens were placed in a freezer at minus 40 °C for two weeks to kill insects and their eggs before proceeding with morphological and molecular studies. Voucher specimens were deposited at the herbaria of Beijing Forestry University, Beijing, China (BJFC), Southwest Forestry University (SWFC), Kunming, Yunnan Province, China, and the National Museum of Natural History (BJM). Detailed information on the collection localities and GPS coordinates of the studied specimens of new taxa is provided in Table 1.

Table 1. Detailed information on the studied specimens of new taxa, including specific collection localities and GPS coordinates.

Name	Voucher Number	Collection Localities	GPS Coordinates
Amylocorticium athelioides	He4624b	China, Taiwan, Nantou County, Nandongyan Mountains	24° 03′ N, 121° 08′ E
Amylocorticium bisporum	He9235	China, Sichuan Province, Jiulong County, Wuxuhai Scenic Area	29° 10′ N, 101° 23′ E

Table 1. *Cont.*

Name	Voucher Number	Collection Localities	GPS Coordinates
Amylocorticium guangxiense	Dai27527	China, Guangxi Autonomous Region, Shangsi County, Shiwandashan National Forest Park	21° 53′ N, 107° 54′ E
Amylocorticium guangxiense	Dai32929	China, Guangxi Autonomous Region, Shangsi County, Shiwandashan National Forest Park	21° 53′ N, 107° 54′ E
Amylocorticium luteolum	Yuan1414	China, Yunnan Province, Binchuan County, Jizhu Mountains Scenic Spot	25° 56′ N, 100° 23′ E
Amylocorticium luteolum	Yuan1577	China, Sichuan Province, Yanyuan County, Lugu Lake Scenic Spot	27° 44′ N, 100° 49′ E
Amylophanerochaete hainanense	He7950	China, Hainan Province, Ledong County, Jianfengling Nature Reserve	18° 23′ N, 108° 46′ E
Pseudoathelia linzhiense	CLZhao31183	China, Xizang Autonomous Region, Linzhi, Sejilashan Forest Park	29° 64′ N, 94° 71′ E
Pseudoathelia linzhiense	CLZhao31174	China, Xizang Autonomous Region, Linzhi, Sejilashan Forest Park	29° 64′ N, 94° 71′ E
Serpulomyces rhizomorphus	CLZhao31188	China, Xizang Autonomous Region, Linzhi, Sejilashan Forest Park	29° 64′ N, 94° 71′ E
Serpulomyces rhizomorphus	CLZhao31197	China, Xizang Autonomous Region, Linzhi, Sejilashan Forest Park	29° 64′ N, 94° 71′ E
Serpulomyces subborealis	Yuan1428	China, Yunnan Province, Binchuan County, Jizhu Mountains Scenic Spot	25° 56′ N, 100° 23′ E
Serpulomyces yunnanensis	CLZhao18992	China, Yunnan Province, Honghe, Pingbian County, Daiweishan National Nature Reserve	22° 57′ N, 103° 42′ E
Serpulomyces yunnanensis	CLZhao19070	China, Yunnan Province, Honghe, Pingbian County, Daiweishan National Nature Reserve	22° 57′ N, 103° 42′ E

2.2. Morphological Studies

Macro-morphological features, including the color, odor, size, hymenophore, and margin of basidiomes, were observed and recorded. Thin, freehand sections from dried basidiomes were mounted in 3% (*w*/*v*) aqueous potassium hydroxide (KOH) and 1% (*w*/*v*) aqueous phloxine. The amyloidity and cyanophily of basidiospores were determined using Melzer's reagent (IKI) and 1% (*w*/*v*) cotton blue in 60% (*w*/*v*) lactic acid (CB), respectively. A Nikon Eclipse 80i microscope (Nikon Corporation, Tokyo, Japan) was used for microscopic examinations at magnifications up to 1000×. Microscopic structures were drawn using a drawing tube. The following abbreviations are used: IKI− = neither amyloid nor dextrinoid, CB− = acyanophilous, L = mean spore length, W = mean spore width, Q = L/W ratio, n (a/b) = number of spores (a) measured from the number of specimens (b). Color codes and names follow Kornerup and Wanscher [29].

2.3. DNA Extraction and Sequencing

The extraction of total genomic DNA from dried specimens was performed using a CTAB plant genomic DNA extraction kit, DN14 (Aidlab Biotechnologies Co., Ltd., Beijing, China), according to the manufacturer's instructions. The ITS region and the D1–D2 region of the nucleic ribosomal LSU (nrLSU) were amplified by the Polymerase Chain Reaction (PCR) using the primer pairs ITS5/ITS4 and LR0R/LR7 [30,31]. The PCR procedures followed Zhang et al. [32]. The PCR products were purified and sequenced at the Beijing Liuhe BGI Co., Ltd. with the same primers using the Sanger method on an ABI 3730XL sequencer (Thermo Fisher Scientific, Waltham, MA, USA). Newly generated sequences were deposited

in GenBank (https://www.ncbi.nlm.nih.gov/, Table 2). BioEdit v.7.0.5.3 [33] and Geneious Basic v.11.1.15 [34] were used to review the chromatograms and for sequence concatenation.

2.4. Phylogenetic Analyses

The concatenated ITS-nrLSU sequence dataset of the Amylocorticiales was subjected to phylogenetic analyses with ingroup and outgroup taxa sampling, as consulted with [1] (Table 2). Sequences of ITS and nrLSU were aligned separately using MAFFT v.74 (http://mafft.cbrc.jp/alignment/server/ accessed on 1 November 2025) [35] with the G-INS-I iterative refinement algorithm and optimized manually in BioEdit v.7.0.5.3. The separate alignments were then concatenated using Mesquite v.3.5.1 [36]. The final alignments and the topologies were deposited in TreeBase (http://treebase.org/treebase-web/home.html, submission ID: 32405). Maximum likelihood (ML) analyses and Bayesian inference (BI) were carried out by using RAxML v.8.2.10 [37] and MrBayes 3.2.6 [38], respectively. The best-fit substitution model was estimated with ModelFinder, which is integrated into the PhyloSuite v1.2.3. soft package [39]. For Bayesian analysis, four Markov chains were run for 40,000,000 generations for the dataset until the split deviation frequency value was lower than 0.01.

Table 2. Taxa information and GenBank accession numbers of the sequences used in this study. New taxa are in bold with type specimens indicated with an asterisk (*).

Name	Voucher Number	Country	ITS	nrLSU	Reference
Agroathelia rolfsii	ATCC 201126	Argentina	AF499018	AF499019	—
Agroathelia rolfsii	AFTOL-ID 664	USA	—	AY635773	—
Amyloathelia crassiuscula	GB/K169-796	Sweden	DQ144610	DQ144610	—
Amyloceraceomyces angustisporus	He2819	China	MK520871	—	[2]
Amyloceraceomyces angustisporus	He2824	China	MK520872	MK491337	[2]
Amyloceraceomyces angustisporus	He2844	China	MK520873	MK491338	[2]
Amylocorticiales sp.	UC2022802	USA	KP814164	—	[40]
Amylocorticiellum molle	BAFCcult4706	Argentina	MW370510	MW368666	[41]
Amylocorticiellum subillaqueatum	K(M):165142	USA	MZ159402	—	—
Amylocorticium athelioides	**He4624b ***	**China**	**—**	**MK491342**	**This study**
Amylocorticium bisporum	**He9235 ***	**China**	**PV185712**	**PV211327**	**This study**
Amylocorticium canadense	MO414701	USA	OK346339	—	—
Amylocorticium cebennense	He3074	China	PV185711	—	This study
Amylocorticium cebennense	CFMR: HHB-2808	USA	GU187505	GU187561	[1]
Amylocorticium cebennense	JS24813	Sweden	—	AY586627	[42]
Amylocorticium ellipsosporum	He4457	China	MK520876	MK491341	[2]
Amylocorticium indicum	He3748	China	MK520875	MK491340	[2]
Amylocorticium indicum	He5357	China	MK520874	MK491339	[2]
Amylocorticium guangxiense	**Dai27527**	**China**	**PX614364**	**—**	**This study**
Amylocorticium guangxiense	**Dai32929 ***	**China**	**PX614365**	**—**	**This study**
Amylocorticium luteolum	**Yuan1414 ***	**China**	**PX614366**	**PX491137**	**This study**
Amylocorticium luteolum	**Yuan1577**	**China**	**PX614367**	**PX491138**	**This study**
Amylocorticium subincarnatum	AS95	Sweden	—	AY586628	[42]
Amylocorticium subsulphureum	CFMR: HHB-13817	USA	GU187506	GU187562	[1]
Amylophanerochaete hainanense	**He7950 ***	**China**	**PV185713**	**PV211328**	**This study**
Amyloxenasma allantosporum	SREF408	Poland	MN660833	—	[43]
Amyloxenasma allantosporum	SREF166	Poland	MN660447	—	[43]
Anomoloma albolutescens	LYBR5671	China	ON053465	ON038410	[22]
Anomoloma albolutescens	CFMR: L-6088	USA	GU187507	GU187563	[1]
Anomoloma denticulatum	Dai23150	USA	NR185681	NG228934	[22]
Anomoloma eurasiaticum	Dai22860	China	NR185680	NG228933	[22]
Anomoloma flavissimum	Cui12188	China	KT954956	KT954971	[18]

Table 2. *Cont.*

Name	Voucher Number	Country	ITS	nrLSU	Reference
Anomoloma flavissimum	Dai2968a	China	KT954952	KT954966	[18]
Anomoloma luteoalbum	LWZ20210918-39a	China	ON897828	ON885290	[44]
Anomoloma luteoalbum	Cui8686	China	KT954962	KT954976	[18]
Anomoloma myceliosum	JV0509/117	China	OM914151	—	[22]
Anomoloma myceliosum	CFMR: MJL-4413	USA	GU187500	GU187559	[1]
Anomoloma rhizosum	Cui9717	China	KT954958	KT954972	[18]
Anomoloma rhizosum	Cui10589	China	KT954959	KT954973	[18]
Anomoloma submyceliosum	Dai7402	China	KT954963	KT954977	[18]
Anomoporia bombycina	CFMR: L-6240	USA	GU187508	GU187564	[1]
Anomoporia kamtschatica	KHL11072	Sweden	—	AY586630	[42]
Anomoporia kamtschatica	GB/M Edman K426	Sweden	—	DQ144615	—
Anomoporia vesiculosa	Dai22795	China	ON413718	ON413720	—
Ceraceomyces atlanticus	URM85888	Brazil	KX685875	NG060427	[15]
Ceraceomyces tessulatus	KHL16429	Sweden	KU518951	—	—
Ceraceomyces tessulatus	KHL8474	Sweden	—	AY586642	[42]
Ceraceomyces tessulatus	He3008	China	PV185714	PV211329	This study
Irpicodon pendulus	LWZ 20210925-8b	China	ON897889	ON885348	[44]
Jaapia argillacea	CBS 252.74	USA	NR119766	NG042523	[1]
Jaapia ochroleuca	KHL 8433	Sweden	EU118637	EU118637	[45]
Phlebiella sp.	GEL4684	Germany	—	AJ406516	[46]
Plicaturopsis crispa	HMAS293434	China	OR237017	—	—
Plicaturopsis crispa	CFMR: DLL2011-011	USA	KJ140537	—	[47]
Podoserpula ailaoshanensis	ZJL2015015	China	NR158915	NG060161	[22]
Podoserpula aliweni	SGO170081	Chile	MN970529	—	[16]
Podoserpula pusio	MEL2297270	Chile	MN970540	—	[16]
Podoserpula pusio	PDD81253	Chile	MN970537	—	[16]
Podoserpula pusio	H. Lepp 329 ACT	USA	GU187555	—	[1]
Pseudoathelia linzhiense	**CLZhao31183** *	**China**	**NR198738**	**PP862918**	**[20]**
Pseudoathelia linzhiense	**CLZhao31174**	**China**	**PP399152**	**PP862922**	**[20]**
Pseudoathelia septentrionalis	**UC2023047**	**USA**	**KP814348**	**—**	**[40]**
Pseudoathelia septentrionalis	**GB0090937**	**Sweden**	**—**	**LR694181**	**—**
Serpulomyces borealis	He20120911-12	China	—	MK491344	—
Serpulomyces borealis	KHL 8432	Sweden	EU118610	EU118610	[45]
'Serpulomyces borealis'	UC2023227	USA	KP814487	—	[40]
'Serpulomyces borealis'	CFMR: L-8014	USA	GU187512	GU187570	[1]
Serpulomyces rhizomorphus	**CLZhao31188** *	**China**	**NR198737**	**NG244072**	**[20]**
Serpulomyces rhizomorphus	**CLZhao31197**	**China**	**PP399150**	**PP862916**	**[20]**
Serpulomyces subborealis	**Yuan1428** *	**China**	**PX614368**	**—**	**This study**
Serpulomyces yunnanensis	**CLZhao18992**	**China**	**OQ132519**	**OQ147003**	**[19]**
Serpulomyces yunnanensis	**CLZhao19070** *	**China**	**NR198731**	**NG243202**	**[19]**

3. Results

3.1. Phylogenetic Analyses

The Amylocorticiales dataset contained 62 ITS and 52 nrLSU sequences from 72 samples representing 70 ingroup taxa and the outgroup (Table 1). The dataset had an aligned length of 1734 characters. PhyloSuite suggested GTR+F+I+G4 as the best-fit model of nucleotide evolution. The average standard deviations of split frequencies of BI were 0.005911 at the end of the runs. The ML and BI analyses resulted in almost identical tree topologies. The ML tree is shown in Figure 1 with likelihood bootstrap values (≥70%, first) and Bayesian posterior probabilities (≥ 0.95, second) labeled along the branches.

In the tree, twelve generic lineages including ten known genera, viz. *Agroathelia*, *Amyloceraceomyces*, *Amylocorticiellum*, *Amylocorticium*, *Anomoloma*, *Anomoporia*, *Ceraceomyces*, *Plicatura*, *Podoserpula*, and *Serpulomyces*, and two new genera, *Amylophanerochaete* and

Pseudoathelia, were recovered. The monotypic new genus *Amylophanerochaete* is close to *Serpulomyces*, but their relationship was not well supported by the ML analyses (55/0.95). *Pseudoathelia linzhiense* and *P. septentrionalis*, transferred from *Leptosporomyces* (a member of Atheliales), formed a distinct lineage sister to *Ceraceomyces*. The *Serpulomyces* lineage contains a new species, *S. subborealis*, two new combinations, *S. rhizomorphus* and *S. yunnanensis* from *Ceraceomyces*, and the type species, *S. borealis*. It seems that *S. borealis* is a species complex, since two sequences named as this species (UC2023227 and CFMR: L-8014 from the USA) formed distinct lineages independent of the core *S. borealis*. The four new species of *Amylocorticium*—*A. athelioides*, *A. bisporum*, *A. guangxiense*, and *A. luteolum*—were nested within the *Amylocorticium* lineage and distinct from each other and known species.

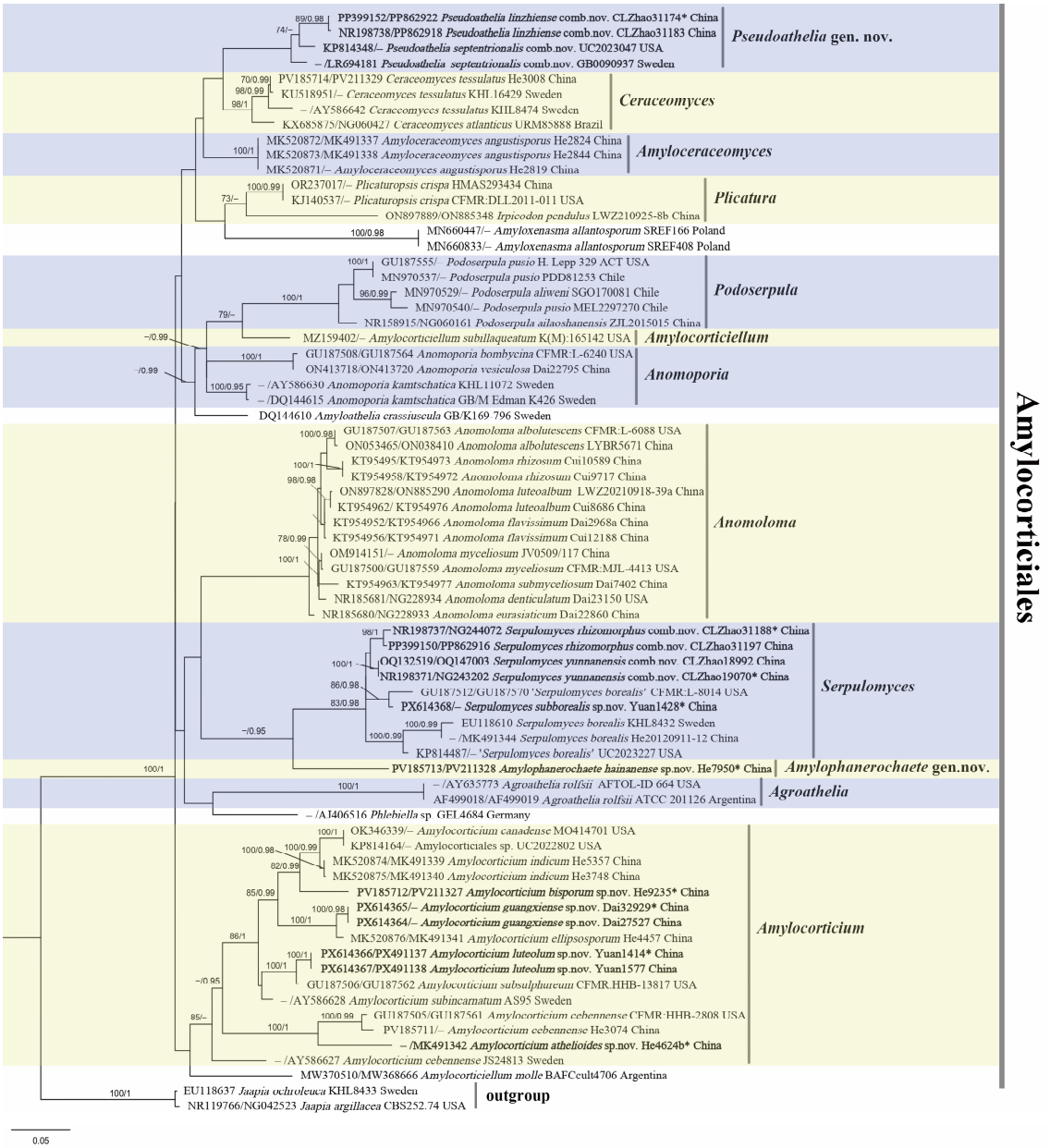


Figure 1. Phylogeny of Amylocorticiales generated by ML analyses based on combined ITS-nrLSU sequences. Branches are labeled with likelihood bootstrap values (≥70%, left) and Bayesian posterior probabilities (≥0.95, right). New species and new combinations are indicated in bold with type specimens indicated with an asterisk (*).

3.2. Taxonomy

Amylophanerochaete Y.Q. Liu & S.H. He, **gen. nov.**

MycoBank number: MB861519.

Type—*Amylophanerochaete hainanense* Y.Q. Liu & S.H. He.

Etymology—"*Amylo-*": amyloid, refers to the amyloidity of the basidiospores; "*-phanerochaete*": *Phanerochaete* P. Karst., a common corticioid genus of Polyporales, Basidiomycota, refers to the basidiome similarity of the two genera.

Description—Basidiomes annual, resupinate, widely effused, pellicular to membranaceous, readily separable from the substrate. Hymenophore smooth, white to cream, turning black in KOH, sparsely cracked when dry; margin fimbriate, byssoid or indistinct, white; rhizomorphs present, distinct, white. Hyphal system monomitic; generative hyphae with clamp connections, colorless, thin- to slightly thick-walled with a wide lumen, smooth, interwoven. Cystidia absent. Basidia clavate, with four sterigmata and a basal clamp connection. Basidiospores narrowly cylindrical to slightly sigmoid, colorless, thin-walled, smooth, amyloid, CB−. Rot type undetermined.

Notes—*Amylophanerochaete* is characterized by the pellicular to membranaceous basidiomes with rhizomorphs, a monomitic hyphal system, and narrowly cylindrical to slightly sigmoid basidiospores (Q = 10) with amyloid reactions in Melzer's reagent. Morphologically, the new genus is similar to *Amyloceraceomyces* S.H. He, which differs by having basidiomes without rhizomorphs and distinctly shorter basidiospores [4]. *Amylophanerochaete* shares similar basidiomes with some species of *Phanerochaete*, which is a member of Polyporales, and has mostly simple-septate generative hyphae and inamyloid basidiospores [2]. In the phylogenetic tree, *Amylophanerochaete* is sister to *Serpulomyces* (Zmitr.), which usually has merulioid hymenophores and inamyloid basidiospores [6].

Amylophanerochaete hainanense Y.Q. Liu & S.H. He, **sp. nov.**

Figure 2: Basidioma and microscopic structures of *Amylophanerochaete hainanense*.

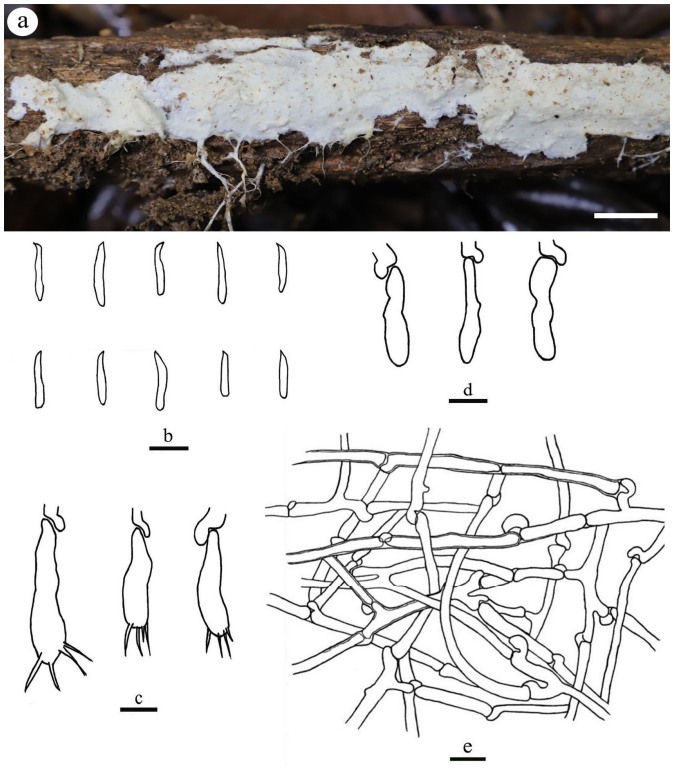


Figure 2. *Amylophanerochaete hainanense*. He 7950 (BJFC 040137, holotype). Scale bars: (**a**) = 1 cm; (**b**–**e**) = 10 μm. (**a**) Basidiomes; (**b**) basidiospores; (**c**) basidia; (**d**) basidioles; (**e**) generative hyphae from subiculum.

MycoBank number: MB861520.

Type—China, Hainan Province, Ledong County, Jianfengling Nature Reserve, 18°23′ N, 108°46′ E, on dead angiosperm branch, 14 May 2023, S.H. He, He 7950 (BJFC 040137, holotype; isotype: BJM).

Etymology—"*hainanense*" refers to the type locality in Hainan Province, southern China.

Description—Basidiocarp annual, resupinate, widely effused, pellicular to membranaceous, readily separable from the substrate, without odor or taste when fresh, up to 10 cm long, 3 cm wide, 0.2 mm thick. Hymenophore smooth, white, yellowish-white to pale yellow [4A (1–3)], turning black in KOH, sparsely cracked after dry; margin thinning out, fimbriate, byssoid or indistinct, concolorous with the hymenophoral surface; rhizomorphs present, distinct, white, unchanged in KOH. Hyphal system monomitic; generative hyphae with clamp connections, colorless, thin- to slightly thick-walled with a wide lumen, smooth, moderately branched, frequently septate, loosely interwoven, 2–2.5 μm diam. Cystidia and cystidioles are absent. Basidia clavate, with four sterigmata and a basal clamp connection, colorless, thin-walled, smooth, 19–31 × (3−) 4–7 μm; sterigmata up to 6 μm long. Basidioles dominant, similar to basidia in shape but slightly smaller, (15.5−) 17.5–27 × (3.5−) 4–5.5 μm. Basidiospores narrowly cylindrical to slightly sigmoid, with an apiculus, colorless, thin-walled, smooth, amyloid in Melzer's reagent, CB−, 9.2–14.3 × (0.7−) 1–1.5 μm, L = 12.1 μm, W = 1.2 μm, Q = 10.08 (*n* = 30/1).

Notes—Known only from the holotype collection, from Jianfengling Nature Reserve, on a dead angiosperm branch, the most striking characters of the species are the white, pellicular to membranaceous basidiomes with distinct rhizomorphs and the slim basidiospores with an amyloid reaction. Among the corticioid fungi, some species of *Tubulicrinis* Donk and *Subulicystidium* Parmasto also have long and narrow but inamyloid basidiospores, but they have distinct characteristic cystidia and belong to different orders [2]. Superficially, the species resembles *Phanerochaete* because of the white-to-cream, membranaceous basidiomes, but the absence of cystidia and amyloid basidiospores indicates its identity in Amylocorticiales. In the aligned ITS region, *Amylophanerochaete hainanense* differs from *Serpulomyces borealis* (UC2023227) by 103 nucleotide base pairs and from *Agroathelia rolfsii* (ATCC 201126) by 131 base pairs, confirming its phylogenetic distinctiveness.

Pseudoathelia Y.Q. Liu & S.H. He, **gen. nov.**

MycoBank number: MB861521.

Type species—*Pseudoathelia septentrionalis* (J. Erikss.) Y.Q. Liu & S.H. He

Etymology—"*Pseudo-*": false; "*-athelia*": *Athelia* Pers., an old and common corticioid genus, refers to the similarity to *Athelia* in morphology but represents a different genus.

Description—Basidiomes annual, resupinate, broadly effused, loosely adnate, athelioid, thin. Hymenial surface smooth, reticulate or continuous under the lens, grayish white to yellowish cream, unchanged in KOH; margin fimbriate, indeterminate, white. Hyphal system monomitic; generative hyphae with clamp connections, colorless, thin-walled or slightly thick-walled at base, smooth or slightly encrusted, loosely interwoven. Cystidia absent. Basidia clavate, with four sterigmata and a basal clamp connection, colorless, thin-walled, smooth. Basidiospores oblong ellipsoid, subcylindrical or subfusiform, colorless, thin-walled, smooth, IKI−, CB−. Causing a white rot.

Notes—Our phylogenetic analyses demonstrated that *Leptosporomyces linzhiense* and *L. septentrionalis* represent a new clade within the Amylocorticiales, and are transferred to the new genus *Pseudoathelia*. *Pseudoathelia* is characterized by the athelioid basidiomes, nodose-septate hyphae, and non-amyloid basidiospores. Morphologically, *Pseudoathelia* belongs to the *Athelia s*.l. group that includes many taxa with simple and similar macro- and microscopic structures. In the phylogenetic tree, *Pseudoathelia* is sister to *Ceraceomyces*, but differs in having well-developed basidiomes and subhymenia. *Agroathelia* Redhead &

Mullineux also has athelioid basidiomes but differs in growing on crops, and is phylogenetically distantly related. Thus, the following two new combinations were proposed.

Pseudoathelia septentrionalis (J. Erikss.) Y.Q. Liu & S.H. He, **comb. nov.**

MycoBank number: MB861522.

≡*Athelia septentrionalis* J. Erikss., Symb. Bot. Upsal. 16(no. 1): 88 (1958).

≡*Fibulomyces septentrionalis* (J. Erikss.) Jülich, Willdenowia, Beih. 7: 187 (1972).

≡*Leptosporomyces septentrionalis* (J. Erikss.) Krieglst., Z. Mykol. 57(1): 53 (1991).

The species is widely distributed in the northern hemisphere and was shown to belong to Amylocorticiales in previous studies [1,48,49]. See Bernicchia & Gorjón 2010 [2], Maekawa 2021 [50] for detailed descriptions and illustrations.

Pseudoathelia linzhiense (C.L. Zhao and H.M. Zhou) Y.Q. Liu & S.H. He, **comb. nov.**

MycoBank number: MB861523.

≡*Leptosporomyces linzhiensis* C.L. Zhao & H.M. Zhou, in Zhou, Zhang, Li, Wu & Zhao, MycoKeys 106: 215 (2024).

This species was recently described from Xizang Autonomous Region, southwestern China [20]. In their phylogenetic tree, *Leptosporomyces linzhiense*, *L. septentrionalis*, and two species of *Amylocorticium* formed a clade sister to other species of *Leptosporomyces* and related taxa that belong to Atheliales.

Specimen examined—China, Xizang Autonomous Region, Linzhi, Sejilashan Forest Park, 29°64′ N, 94°71′ E, elev. 3848 m, on fallen trunk of *Abies*, 2 August 2023, CLZhao 31,174 & 31,183 (SWFC).

Amylocorticium athelioides Y.Q. Liu & S.H. He, **sp. nov.**

MycoBank number: MB861524.

Figure 3: Basidiomata and microscopic structures of *Amylocorticium athelioides*.

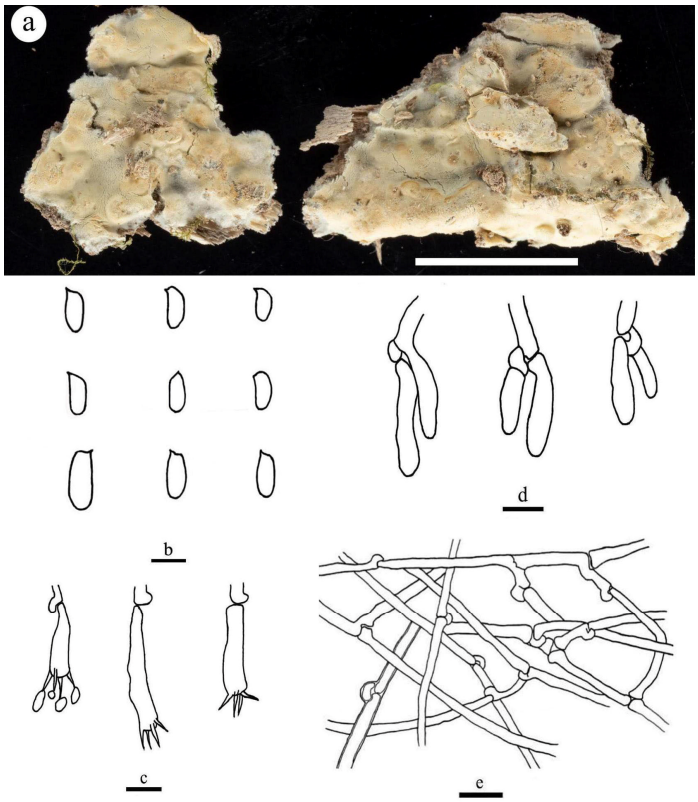


Figure 3. *Amylocorticium athelioides*. He 4624b (BJFC 024067, holotype). Scale bars: (**a**) = 1 cm; (**b**) = 5 μm; (**c**–**e**) = 10 μm. (**a**) Basidiomes; (**b**) basidiospores; (**c**) basidia; (**d**) basidioles; (**e**) generative hyphae from subiculum.

Type—China, Taiwan, Nantou County, Nandongyan Mountains, 24°03′ N, 121°08′ E, on fallen angiosperm trunk, 7 December 2016, S.H. He, He 4624b (BJFC 024067, holotype; isotype: BJM).

Etymology—"*athelioides*" refers to the athelioid basidiomes.

Description—Basidiomes annual, resupinate, effused, adnate, athelioid to pellicular, separable, without odor or taste when fresh, up to 0.3 mm thick. Hymenophore smooth, white, yellowish-white, pale yellow to light yellow [4A (1–4)], turning black in KOH, partly cracked upon drying; margin thinning out, fimbriate, white or concolorous with the hymenophoral surface. Hyphal system monomitic, generative hyphae with clamp connections, colorless, thin- to slightly thick-walled, moderately branched, frequently septate, loosely interwoven, 3–3.5 μm diam. Cystidia and cystidioles are absent. Basidia clavate, with four sterigmata and a basal clamp connection, colorless, thin-walled, smooth, 17.5–26 × 3–5.5 μm; basidioles dominant, similar to basidia in shape but slightly smaller. Basidiospores ellipsoid to oblong ellipsoid, with an apiculus, colorless, thin-walled, smooth, with an amyloid reaction in Melzer's reagent, CB−, (4−) 4.5–6 (−6.5) × 1.5–2 (−2.5) μm, L = 5.3 μm, W = 1.9 μm, Q = 2.8 (*n* = 30/1).

Notes—*Amylocorticium athelioides* is characterized by the cream to light yellow athelioid basidiomes and its occurrence on angiosperm trees in the subtropical area. In the phylogenetic tree, *A. athelioides* is closely related to *A. cebennense* (Bourdot) Pouzar, which differs in having white basidiomes, slightly longer basidiospores (6.5–7.5 μm), and a temperate distribution [2,7]. In the aligned LSU region, *Amylocorticium athelioides* differs from *A. cebennense* (CFMR: HHB-2808) by 49 nucleotide base pairs, providing molecular evidence for its separation from closely related taxa.

Amylocorticium bisporum Y.Q. Liu & S.H. He, **sp. nov.**

MycoBank number: MB861525.

Figure 4: Basidioma and microscopic structures of *Amylocorticium bisporum*.

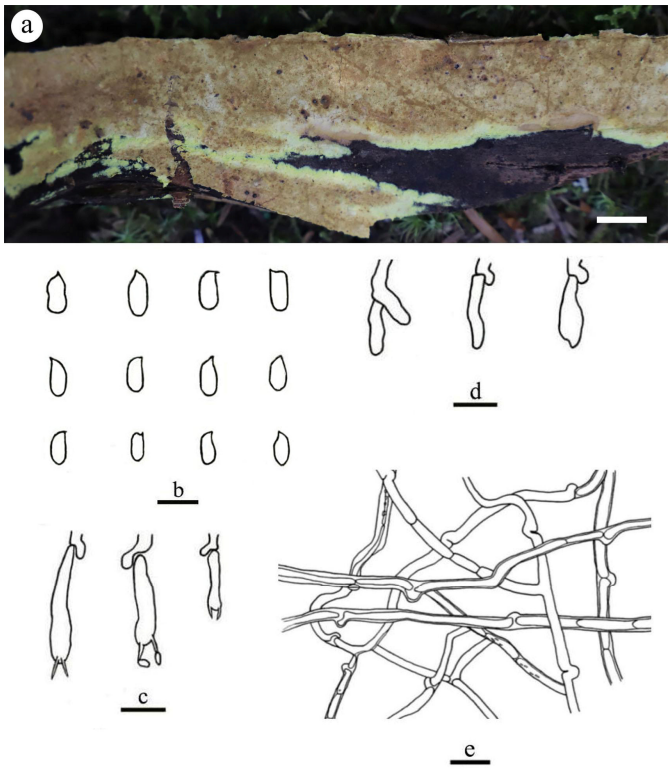


Figure 4. *Amylocorticium bisporum*. He 9235 (BJFC 045577, holotype). Scale bars: (**a**) = 1 cm; (**b**) = 5 μm; (**c**–**e**) = 10 μm. (**a**) Basidiomes; (**b**) basidiospores; (**c**) basidia; (**d**) basidioles; (**e**) generative hyphae from subiculum.

Type—China, Sichuan Province, Jiulong County, Wuxuhai Scenic Area, 29°10′ N, 101°23′ E, on fallen trunk of *Picea*, 26 August 2024, S.H. He, He 9235 (BJFC 045577, holotype; isotype: BJM).

Etymology—"*bisporum*" refers to basidia with two basidiospores.

Description—Basidiomes annual, resupinate, broadly effused, adnate, separable, without odor or taste when fresh, up to 30 cm long, 8 cm wide, 0.5 mm thick. Hymenophore smooth, light orange [5A (4–5)], brownish-orange [5C (4–6)] to light brown [5D (4–5)], turning black in KOH, not cracked; margin thinning out, pale yellow [3A (3–4)], distinct, up to 0.5 cm wide. Subhymenium thickening with new hymenial elements growing from old ones, stratified, with a moderately dense texture, with hyphae densely interwoven, with scattered crystals. Hyphal system monomitic; generative hyphae with clamp connections, secondary simple septa occasionally present, thin- to thick-walled, moderately branched, frequently septate, 3–4 μm in diam. Cystidia and cystidioles are absent. Basidia clavate, with two sterigmata and a basal clamp connection, colorless, thin-walled, smooth, (13.5−) 15–21 (−24.5) × (2–) 3–4 (−5.5) μm; basidioles dominant, similar to basidia in shape but slightly smaller. Basidiospores ellipsoid to oblong ellipsoid, with an apiculus, colorless, thin-walled, smooth, with an amyloid reaction in Melzer's reagent, CB−, (2−) 3.5–4.5 (−5.5) × (1−) 1.5–2.5 (−3) μm, L = 4.1 μm, W = 1.8 μm, Q = 2.28 (*n* = 30/1).

Notes—*Amylocorticium bisporum* is characterized by having broadly effused, well-developed basidiomes, a stratified hymenium, and basidia with two sterigmata. In the phylogenetic tree, *A. bisporum* is sister to *A. indicum* K.S. Thind & S.S. Rattan and *A. canadense* (Burt) J. Erikss. & Weresub., which are widely distributed in temperate or boreal areas [2,50,51]; obviously, they share different habits. Morphologically, *A. indicum* and *A. canadense* are similar to *A. bisporum* by sharing the same basidiomes, but differ in having basidia with four sterigmata. Moreover, *A. canadense* has longer cylindrical basidiospores (4–6 μm) than *A. bisporum* [2]. In the aligned ITS region, *Amylocorticium bisporum* differs from *A. indicum* (He3748) by 50 nucleotide base pairs and from *A. guangxiense* (Dai32929) by 77 base pairs, indicating clear molecular divergence from its allies.

Amylocorticium guangxiense Y.Q. Liu, Y.C. Dai & S.H. He, **sp. nov.**

MycoBank number: MB861526.

Figure 5: Basidioma and microscopic structures of *Amylocorticium guangxiense.*

Type—China, Guangxi Autonomous Region, Shangsi County, Shiwandashan National Forest Park, 21°53′ N, 107°54′ E, on fallen branch of *Pinus*, 4 September 2024, Y.C. Dai, Dai 32,929 (BJFC 053188).

Etymology—"*guangxiense*" refers to the type locality in Guangxi Autonomous Region, southern China.

Description—Basidiomes annual, resupinate, effused, loosely adnate, pellicular to membranaceous, separable from the substrate, without odor or taste when fresh, up to 8 cm long, 2 cm wide, 0.2 mm thick. Hymenophore smooth, white (3A1), pale yellow to pastel yellow [3A (3–4)], sparsely cracked after drying, turning black in KOH; margin thinning out, indetermined, concolorous with hymenophoral surface. Hyphal system monomitic; generative hyphae with clamp connections, colorless, thin-walled, smooth, moderately branched, frequently septate, loosely interwoven, 3–4 μm in diam. Cystidia and cystidioles are absent. Basidia clavate, with four sterigmata and a basal clamp connection, colorless, thin-walled, smooth, 17.5–21.5 (−22) × (3−) 3.5–4 μm. Basidioles are dominant, similar to basidia in shape but slightly smaller. Basidiospores oblong ellipsoid to cylindrical, colorless, thin-walled, smooth, with an amyloid reaction in Melzer's reagent, CB−, 4–5.5 × 1.5–2.5 μm, L = 4.7 μm, W = 2 μm, Q = 2.34 (*n* = 60/2).

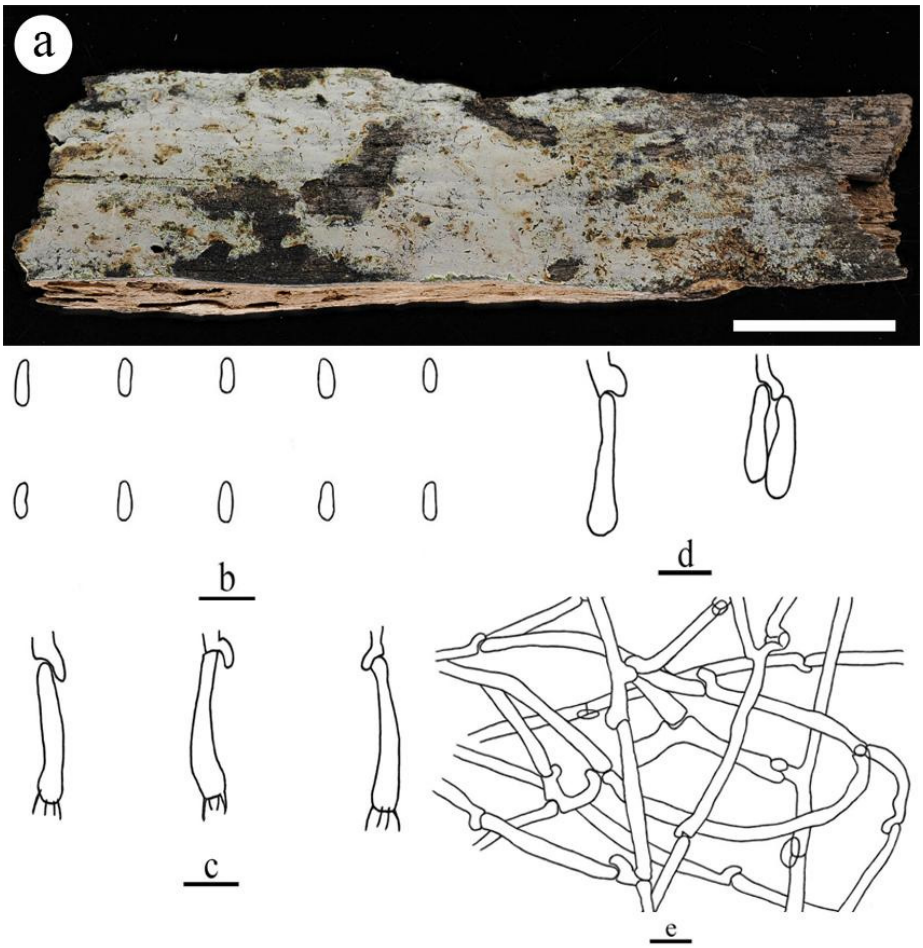


Figure 5. *Amylocorticium guangxiense*. Dai 32,929 (BJFC 053188, holotype). Scale bars: (**a**) = 1 cm; (**b**–**e**) = 10 μm. (**a**) Basidiomes; (**b**) basidiospores; (**c**) basidia; (**d**) basidioles; (**e**) generative hyphae from subiculum.

Additional specimens examined (paratype)—China, Guangxi Autonomous Region, Shangsi County, Shiwandashan National Forest Park, on rotten wood of *Pinus*, 27 May 2024, Y.C. Dai, Dai 27,527 (BJFC 047787).

Notes—*Amylocorticium guangxiense* is characterized by a white-to-cream hymenophore, short oblong ellipsoid to cylindrical basidiospores, and grows on *Pinus* in subtropical areas. In the phylogenetic tree, *A. guangxiense* is closely related to *A. ellipsosporum* S.H. He, which differs in having ellipsoid basidiospores (3.5–4.5 × 2–2.5 μm) and growing on *Tsuga chinensis var. tchekiangenesis* [4]. *Amylocorticium cebennense* is similar to *A. guangxiense* by sharing the white-to-cream basidiomes but differs in having allantoid basidiospores measuring 6–7.5 × 1.7–2 μm and a northern temperate distribution on both gymnosperms and angiosperms [50,52]. In the aligned ITS region, *Amylocorticium guangxiense* (Dai27527) differs from *A. ellipsosporum* (He4457) by 45 nucleotide base pairs, supporting its recognition as a separate species.

Amylocorticium luteolum Y.Q. Liu, Yuan Yuan & S.H. He, **sp. nov.**

MycoBank number: MB861527.

Figure 6: Basidiomata and microscopic structures of *Amylocorticium luteolum*.

Type—China, Yunnan Province, Binchuan County, Jizhu Mountains Scenic Spot, 25°56′ N, 100°23′ E, on fallen branch of *Pinus yunnanensis*, 17 July 2024, Yuan 1414 (BJFC 053827).

Etymology—"*luteolum*": yellow, refers to the color of hymenophores.

Description—Basidiomes annual, resupinate, broadly effused, adnate, separable from the substrate, membranaceous, without odor or taste when fresh, up to 7 cm long,

2 cm wide, 0.2 mm thick. Hymenophore smooth, pale yellow (1A3), light yellow [1A (4–5)] to greenish-yellow [1A (6–7)], turning black in KOH; margin thinning out, fimbriate, indetermined, slightly paler or concolorous with hymenophoral surface. Hyphal system monomitic; generative hyphae with clamp connections, colorless, thin- to slightly-thick-walled, smooth, moderately branched and septate, loosely interwoven, 3–4 μm in diam. Cystidia and cystidioles are absent. Basidia clavate, with four sterigmata and a basal clamp connection, colorless, thin-walled, smooth, 17–22 × 4–5 μm; basidioles dominant, similar to basidia in shape but slightly smaller. Basidiospores oblong ellipsoid, with an apiculus, occasionally two to four in groups, colorless, thin-walled, smooth, with an amyloid reaction in Melzer's reagent, CB−, 4.5–6 (−6.5) × 2–2.5 μm, L = 5.3 μm, W = 2.2 μm, Q = 2.4 (*n* = 60/2).

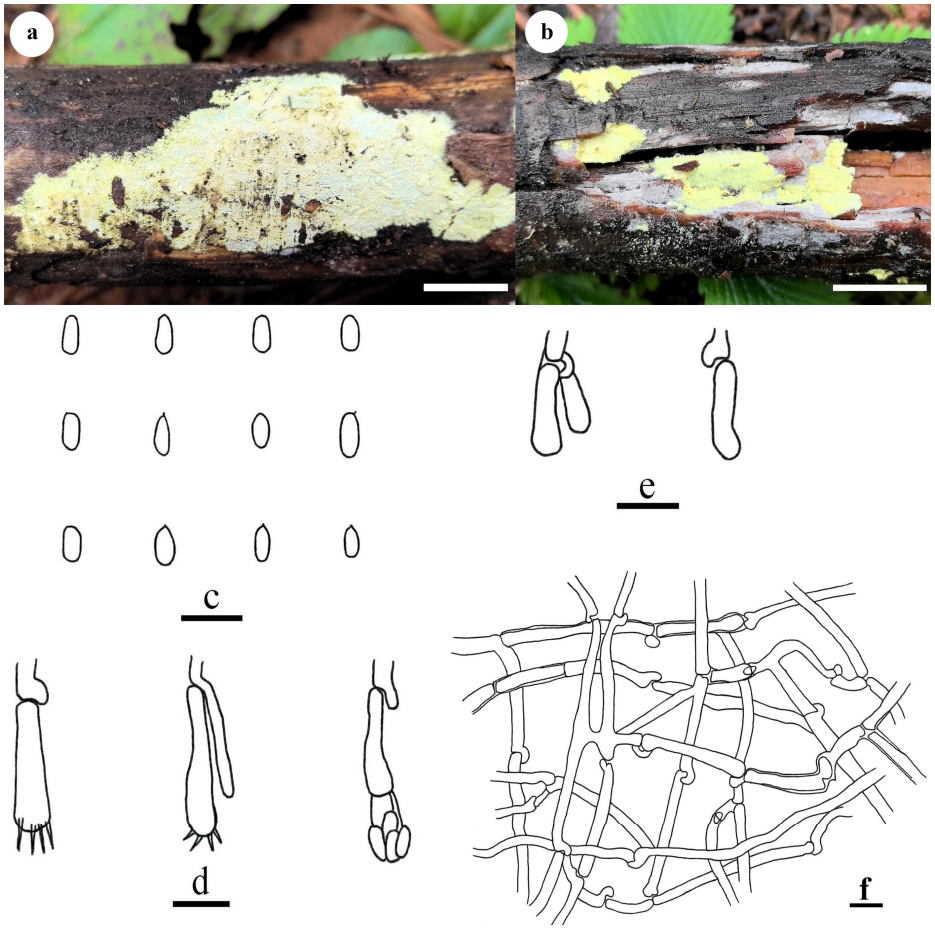


Figure 6. *Amylocorticium luteolum*. (**a**,**c**–**f**) Yuan 1414 (BJFC 053827, holotype); (**b**) Yuan 1577 (BJFC 053990, paratype). Scale bars: (**a**,**b**) = 1 cm; (**c**–**f**) = 10 μm. (**a**,**b**) Basidiomes; (**c**) basidiospores; (**d**) basidia; (**e**) basidioles; (**f**) generative hyphae from subiculum.

Additional specimen examined (paratype)—China, Sichuan Province, Yanyuan County, Lugu Lake Scenic Spot, on fallen branch of *Pinus yunnanensis*, 21 July 2024, Yuan 1577 (BJFC 053990).

Notes—*Amylocorticium luteolum* is characterized by the brightly yellow basidiomes and its occurrence on rotten woods of *Pinus yunnanensis* in southwestern China. In the phylogenetic tree, *A. luteolum* is closely related to *A. subsulphureum* (P. Karst.) Pouzar, which differs in having slightly longer basidiospores (6–7 μm) and a wide distribution in the Northern Hemisphere [2,51]. In the aligned ITS region, *Amylocorticium luteolum* (Yuan1414 and Yuan1577) exhibits clear genetic divergence from its closely related species *A. subsulphureum* (CFMR: HHB-13817). Specifically, Yuan1414 differs by 23 nucleotide base pairs, while Yuan1577 differs by 21 nucleotide base pairs from the latter. Combined with

morphological distinctions, this level of genetic divergence adequately supports *A. luteolum* as a distinct species.

Serpulomyces subborealis Y.Q. Liu, Yuan Yuan & S.H. He, **sp. nov.**

MycoBank number: MB861528.

Figure 7: Basidiomata and microscopic structures of *Serpulomyces subborealis.*

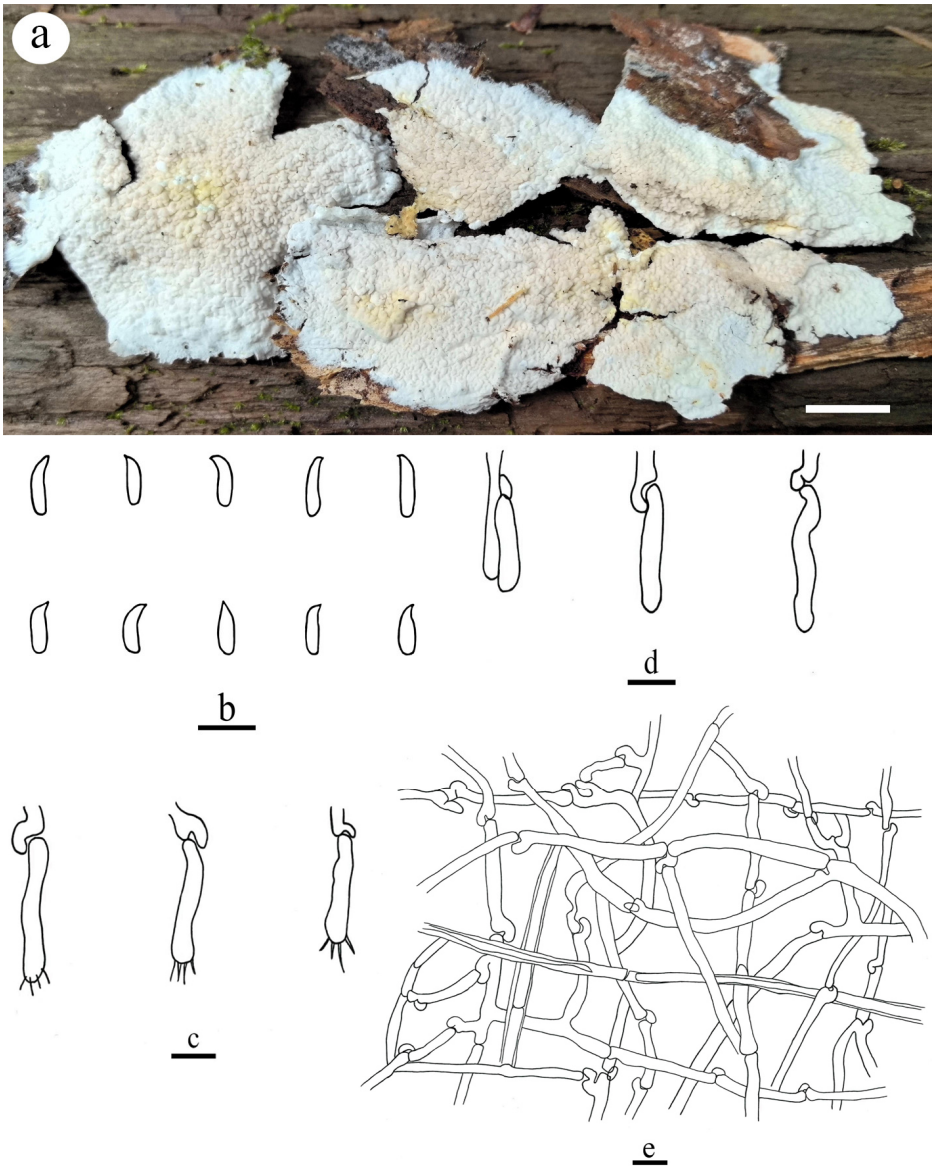


Figure 7. *Serpulomyces subborealis*. Yuan 1428 (BJFC 053841, holotype). Scale bars: (**a**) = 1 cm; (**b**–**e**) = 10 μm. (**a**) Basidiomes; (**b**) basidiospores; (**c**) basidia; (**d**) basidioles; (**e**) generative hyphae from subiculum.

Type—China, Yunnan Province, Binchuan County, Jizhu Mountains Scenic Spot, 25°56′ N, 100°23′ E, on rotten wood of *Pinus yunnanensis*, 17 July 2024, Yuan 1428 (BJFC 053841, holotype).

Etymology—"*subborealis*" refers to morphological similarity and close relationship in phylogeny with *Serpulomyces borealis* (Romell) Zmitr.

Description—Basidiomes annual, resupinate, broadly effused, loosely adnate, easily separable from the substrate, membranaceous, without odor or taste when fresh, up to 11 cm long, 5 cm wide, 0.3 mm thick. Hymenophore merulioid, white (4A1), pale yellow [4A (2–3)] to light yellow [4A (4–5)] when fresh, becoming more or less smooth, pale orange (5A3) to light orange [5A (4–5)] after dry, turning black in KOH; margin

thinning out, fimbriate, white (5A1). Hyphal system monomitic; generative hyphae with clamp connections, colorless, thin- to slightly thick-walled, smooth, moderately branched, frequently septate, loosely interwoven, 3.5–5 µm in diam. Cystidia and cystidioles are absent. Basidia clavate, with four sterigmata and a basal clamp connection, colorless, thin-walled, smooth, (17−) 18–22.5 × (3.5–) 4.5–5 (−6) µm; basidioles dominant, similar to basidia in shape, but slightly smaller. Basidiospores cylindrical to allantoid, with an apiculus, occasionally two to four in groups, colorless, thin-walled, smooth, IKI−, CB−, (5−) 5.5–6.5 (–7) × 1.5–2 µm, L = 5.97 µm, W = 1.67 µm, Q = 3.57 (*n* = 30/1).

Notes—*Serpulomyces subborealis* is characterized by broadly effused basidiomes with a merulioid hymenophore, cylindrical to allantoid basidiospores negative in Melzer's reagent, and its occurrence on the decorticated trunk of *Pinus yunnanensis*. It seems that *S. borealis* is a species complex, since three distinct lineages can be recognized based on the available sequences (Figure 1). We treat the lineage of two samples, KHL 8432 from Sweden and He 20120911-12 from southwestern China as *S. borealis* s.s., while the identities of the two other samples (CFMR: L-8014 and UC2023227) from WA need to be further studied. In previous studies [2,53,54], *S. borealis* was recorded growing on both angiosperm and gymnosperm trees, causing a white or brown rot. This situation is abnormal for a species from the modern view of taxonomy. Moreover, Nakasone [54] found that the cultural characteristics of the isolate of *S. borealis* CFMR: L-8014 were distinctly different from those of the other two isolates of the species. Morphologically, *S. subborealis* differs from *S. borealis* s.s. by having shorter basidiospores (5.5–6.5 µm vs. 6–8 µm) and growing on *Pinus yunnanensis* [2]. In the aligned ITS region, *Serpulomyces subborealis* differs from *S. rhizomorphus* (CLZhao31188) by 54 nucleotide base pairs, from *S. yunnanensis* (CLZhao18992) by 50 base pairs, and from '*S. borealis*' (CFMR: L-8014) by 29 base pairs. These consistent genetic divergences support its status as a distinct species.

Serpulomyces rhizomorphus (C.L. Zhao & H.M. Zhou) Y.Q. Liu & S.H. He, **comb. nov.**

MycoBank number: MB861529.

≡*Ceraceomyces rhizomorphus* C.L. Zhao & H.M. Zhou, in Zhou, Zhang, Li, Wu & Zhao, MycoKeys 106: 211 (2024).

Notes—*Ceraceomyces rhizomorphus* was recently described from Xizang Autonomous Region on *Abies*. Our phylogenetic analysis showed that it was nested within the *Serpulomyces* lineage in Amylocorticiales. See Zhou et al. [20] for detailed descriptions and illustrations.

Specimens examined—China, Xizang Autonomous Region, Linzhi, Sejilashan National Forest Park, 29°64′ N, 94°71′ E, elev. 3848 m, on the fallen branch of *Abies*, 2 August 2023, CLZhao 31,154 & 31,188 (SWFC).

Serpulomyces yunnanensis (Qi Yuan & C.L. Zhao) Y.Q. Liu & S.H. He, **comb. nov.**

MycoBank number: MB861530.

≡*Ceraceomyces yunnanensis* Qi Yuan & C.L. Zhao, in Yuan, Luo, Zhang & Zhao, Phytotaxa 592(3): 186 (2023).

Notes—In our phylogenetic tree of Amylocorticiales (Figure 1), *C. yunnanensis* was nested within the *Serpulomyces* lineage rather than *Ceraceomyces*. Thus, we propose this combination. See Yuan et al. [4] for detailed descriptions and illustrations.

Specimens examined—China, Yunnan Province, Honghe, Pingbian County, Daiweishan National Nature Reserve, E 103°42′, N 22°57′, elev. 2100 m, on the fallen branch of an angiosperm, 9 June 2020, CLZhao 18,992 & 19,070 (SWFC).

A key to the known genera in Amylocorticiales

1. Basidiomes with pilei superimposed on a stipe.....*Podoserpula*
1. Basidiomes single pileate or resupinate.....2
2. Basidiomes pileate; hymenophore plicate, hydnoid, lamellate.....*Plicatura* (*Irpicodon*, *Plicaturopsis*)
2. Basidiomes resupinate; hymenophore porioid, smooth, merulioid.....3
3. Hymenophore porioid.....4
3. Hymenophore non-porioid.....5
4. Causing a white rot.....*Anomoloma*
4. Causing a brown rot.....*Anomoporia*
5. Basidiospores with an amyloid reaction.....6
5. Basidiospores without an amyloid reaction.....10
6. Basidia plural.....*Amyloxenasma*
6. Basidia terminal.....7
7. Basidiospores thick-walled.....*Amylocorticiellum*
7. Basidiospores thin-walled.....8
8. Basidiomes with rhizomorphs.....*Amylophanerochaete*
8. Basidia without rhizomorphs.....9
9. On angiosperm wood, causing a white rot.....*Amyloceraceomyces*
9. Mostly on gymnosperm wood, causing a brown rot.....*Amylocorticium*
10. Causing wilt or blight of trees, forming sclerotia.....*Agroathelia*
10. Causing a rot on wood, without sclerotia.....11
11. Hymenophore merulioid.....*Serpulomyces*
11. Hymenophore smooth.....12
12. Basidiomes athelioid; basidiospores oblong ellipsoid to cylindrical.....*Pseudoathelia*
12. Basidiomes membranaceous, well-developed; basidiospores obliquely ellipsoid to pip-shaped.....*Ceraceomyces*

4. Discussion

The Amylocorticiales is a small order dominated by the wood-decaying fungi with corticioid basidiomes. Many species are locally distributed, and specimens are infrequently collected during investigations. However, as already shown in previous studies [1,4,16,21], our results demonstrated that the phylogenetic divergences at the generic and specific levels are extremely high within the order. In the present study, *Ceraceomyces* s.l. is proven to be polyphyletic, and *Serpulomyces borealis* is a species complex. Two new generic clades and six new species lineages were found based on specimens from southern China. Meanwhile, there are still some lineages that have not been named because of the lack of evidence and specimen materials. It is difficult to find enough morphological differences between some distinct lineages, since their macro- and microscopical structures are really simple. In addition, our study found that the host may play an important role in species discrimination.

Compared to other orders of Basidiomycota, such as Agaricales, Hymenochaetales, and Polyporales, the Amylocorticiales have not been sufficiently studied in the past [23–27,29]. In the future, more studies should be carried out in order to explore the species diversity and rebuild a more natural and reasonable system of Basidiomycota. It can be imagined that more new lineages will be found as more samples are collected and sequenced. Future investigations should focus on biodiversity hotspots and gymnosperm hosts.

Author Contributions: Conceptualization, Y.-Q.L.; methodology, Y.-Q.L. and Y.L.; software, Y.-Q.L.; validation, Y.-Q.L., J.Y. and S.-H.H.; formal analysis, Y.-Q.L. and S.-H.H.; investigation, Y.-Q.L., S.-Y.H., Y.Y., S.L., N.Y. and S.-H.H.; resources, M.-R.H., N.Y. and S.-H.H.; data curation, Y.-Q.L.; writing—original draft preparation, Y.-Q.L.; writing—review and editing, Y.-Q.L., J.Y. and S.-H.H.; visualization, Y.-Q.L.; supervision, S.-H.H.; project administration, S.-H.H.; funding acquisition, S.-H.H. All authors have read and agreed to the published version of the manuscript.

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Conflicts of Interest: The authors declare no conflicts of interest.

References

1. Binder, M.; Larsson, K.H.; Matheny, P.B.; Hibbett, D.S. Amylocorticiales ord. nov. and Jaapiales ord. nov.: Early diverging clades of agaricomycetidae dominated by corticioid forms. *Mycologia* **2010**, *102*, 865–880. [CrossRef]
2. Bernicchia, A.; Gorjón, S.P. *Corticiaceae s.l. Fungi Europaei*; Candusso: Puglia, Italia, 2010; Volume 12.
3. Mordue, J.E.M. CMI descriptions of pathogenic fungi and bacteria No. 961. *Mycopathologia* **1988**, *103*, 167–186. [CrossRef]
4. Yuan, H.S.; Lu, X.; Dai, Y.C.; Hyde, K.D.; Kan, Y.-H.; Kušan, I.; He, S.-H.; Liu, N.-G.; Sarma, V.V.; Zhao, C.-L.; et al. Fungal diversity notes 1277–1386: Taxonomic and phylogenetic contributions to fungal taxa. *Fungal Divers.* **2020**, *104*, 1–266. [CrossRef]
5. Redhead, S.A.; Mullineux, S.T. *Nomenclatural Novelties*; Index Fungorum: London, UK, 2023; Volume 554, p. 1.
6. Zmitrovich, I.V.; Spirin, W.A. A contribution to the taxonomy of corticioid fungi. II. Genera *Serpula*, *Serpulomyces* gen. nov., *Amylocorticiellum* gen. nov. *Mikol. I Fitopatol.* **2002**, *36*, 11–26.
7. Pouzar, Z. New genera of higher fungi III. *Česká Mykol.* **1959**, *13*, 10–19.
8. Niemelä, T.; Larsson, K.H. *Anomoloma*, a new genus separated from *Anomoporia* on the basis of decay type and nuclear rDNA sequence data. *Mycotaxon* **2007**, *100*, 305–317. [CrossRef]
9. Pouzar, Z. Studies in the taxomomy of the Polypores I. *Česká Mykol.* **1966**, *20*, 171–177. [CrossRef]
10. Jülich, W. *Monographie der Athelieae (Corticiaceae, Basidiomycetes)*; Willdenowia Beiheft; Botanischer Garten u. Museum: Berlin, Germany, 1972; Volume 7, pp. 1–283.
11. Pouzar, Z. Studies in the taxonomy of polypores II. *Folia Geobot. Phytotaxon.* **1966**, *1*, 356–375. [CrossRef]
12. Reid, D.A. Fungi Venezuelani: VI. (New or interesting records of Australasian Basidiomycetes: IV). *Podoserpula* Reid: A new genus based on *Craterellus pusio* Berk. (C. multiplex Cooke & Massee). *Kew Bull.* **1963**, *16*, 437–445. [CrossRef]
13. Reid, D.A. Notes on some fungi of Michigan-I. Cyphellaceae. *Persoonia* **1964**, *3*, 97–154.
14. Palla, B.; Dima, B.; Papp, V. Less is better than more: Reassessing the monotypic nature of Irpicodon (Amylocorticiaceae, Basidiomycota). *Plant Fungal Syst.* **2024**, *69*, 177–185. [CrossRef]
15. Chikowski, R.; Larsson, K.H.; Gibertoni, T. *Ceraceomyces atlanticus* (Amylocorticiales, Basidiomycota), a new species from the Atlantic Rain Forest, Brazil. *Phytotaxa* **2017**, *296*, 73. [CrossRef]
16. Garnica, S.; Sandoval-Leiva, P.; Riess, K. Phylogenetic relationships in the genus *Podoserpula* and description of *P. aliweni*, a new species from Chile. *Mycologia* **2021**, *113*, 1110–1121. [CrossRef] [PubMed]
17. Cooper, J.A. *Nomenclatural Novelties*; Index Fungorum: London, UK, 2023; Volume 531, pp. 1–4.
18. Song, J.; Liu, X.Y.; Wang, M.; Cui, B.K. Phylogeny and taxonomy of the genus *Anomoloma* (Amylocorticiales, Basidiomycota). *Mycol. Prog.* **2016**, *15*, 11. [CrossRef]
19. Yuan, Q.; Luo, K.Y.; Zhang, Y.; Zhao, C.L. Morphological characteristics and phylogenetic analyses revealed three new wood-inhabiting fungi (Agaricomycetes, Basidiomycota) in Southern China. *Phytotaxa* **2023**, *592*, 179–195. [CrossRef]
20. Zhou, H.M.; Zhang, X.C.; Li, J.T.; Wu, F.; Zhao, C.L. Morphological characteristics and phylogenetic analyses revealed four new wood inhabiting fungi (Agaricomycetes, Basidiomycota) in Xizang Autonomous Region, China. *MycoKeys* **2024**, *106*, 201–224. [CrossRef]
21. Zhou, J.L.; Chen, H.; Cui, B.K. *Podoserpula ailaoshanensis* sp. nov. (Amylocorticiales, Basidiomycota) from China based on morphological and sequence analyses. *Mycoscience* **2016**, *57*, 295–301. [CrossRef]

22. Zhou, M.; Vlasák, J.; Ghobad-Nejhad, M.; Lim, Y.W.; Dai, Y.C. Taxonomy and an Updated Phylogeny of *Anomoloma* (Amylocorticiales, Basidiomycota). *Forests* **2022**, *13*, 713. [CrossRef]
23. Han, M.L.; Chen, Y.; Shen, L.L.; Song, J.; Vlasák, J.; Dai, Y.C.; Cui, B.K. Taxonomy and phylogeny of the brown-rot fungi: Fomitopsis and its related genera. *Fungal Divers.* **2016**, *80*, 343–373. [CrossRef]
24. Liu, S.; Chen, Y.; Sun, Y.F.; He, X.L.; Song, C.G.; Si, J.; Liu, D.M.; Gates, G.; Cui, B.K. Systematic classification and phylogenetic relationships of the brown-rot fungi within the Polyporales. *Fungal Divers.* **2022**, *118*, 1–94. [CrossRef]
25. Wu, F.; Zhou, L.W.; Vlasák, J.; Dai, Y.C. Global Diversity and Systematics of Hymenochaetaceae with Poroid Hymenophore. *Fungal Divers.* **2022**, *113*, 1–192. [CrossRef]
26. Liu, Z.B.; Yuan, Y.; Dai, Y.C.; Liu, H.G.; Vlasák, J.; Zeng, G.Y.; He, S.H.; Wu, F. Global diversity and systematics of Hymenochaetaceae with non-poroid hymenophore. *Fungal Divers.* **2025**, *131*, 1–97. [CrossRef]
27. Xu, Y.L.; Tian, Y.; He, S.H. Taxonomy and Phylogeny of *Peniophora* Sensu Lato (Russulales, Basidiomycota). *Fungi* **2023**, *9*, 93. [CrossRef] [PubMed]
28. Kornerup, A.; Wanscher, J.H. *Methuen Handbook of Colour*, 3rd ed.; E. Methuen and Co., Ltd.: London, UK, 1978.
29. Wu, F.; Yuan, Y.; Chen, J.J.; Cui, B.K.; Dai, Y.C. Terrestriporiaceae fam. nov., a new family of Russulales (Basidiomycota). *Mycosphere* **2020**, *11*, 2755–2766. [CrossRef]
30. White, T.J.; Bruns, T.; Lee, S.; Taylor, J. Amplification and direct sequencing of fungal ribosomal RNA genes for phylogenetics. In *PCR Protocols: A Guide to Methods and Applications*; Innis, M.A., Gelfand, D.H., Sninsky, J.J., White, T.J., Eds.; Academic Press: San Diego, CA, USA, 1990; pp. 315–322. [CrossRef]
31. Hopple, J.S.; Vilgalys, R. Phylogenetic relationships in the mushroom genus *Coprinus* and dark-spored allies based on sequence data from the nuclear gene coding for the large ribosomal subunit RNA: Divergent domains, outgroups, and monophyly. *Mol. Phylogenetics Evol.* **1999**, *13*, 1–19. [CrossRef]
32. Zhang, Y.P.; Li, Y.; Nakasone, K.K.; He, S.H. *Stratocorticium sinensis* gen. et sp. nov. and *Cericium gloeocystidiatum* sp. nov. (Cyphellaceae, Agaricales) from East Asia. *Fungi* **2024**, *10*, 722. [CrossRef]
33. Hall, T.A. Bioedit: A user-friendly biological sequence alignment editor and analysis program for Windows 95/98/NT. *Nucleic Acids Symp. Ser.* **1999**, *41*, 95–98.
34. Kearse, M.; Moir, R.; Wilson, A.; Stones-Havas, S.; Cheung, M.; Sturrock, S.; Buxton, S.; Cooper, A.; Markowitz, S.; Duran, C.; et al. Geneious Basic: An integrated and extendable desktop software platform for the organization and analysis of sequence data. *Bioinformatics* **2012**, *28*, 1647–1649. [CrossRef]
35. Katoh, K.; Rozewicki, J.; Yamada, K.D. MAFFT online service: Multiple sequence alignment, interactive sequence choice and visualization. *Brief. Bioinform.* **2019**, *20*, 1160–1166. [CrossRef]
36. Maddison, W.P.; Maddison, D.R. *Mesquite: A Modular System for Evolutionary Analysis*; Version 3.5.1; Mesquite Software, Inc.: Austin, TX, USA, 2018. Available online: http://www.mesquiteproject.org (accessed on 30 August 2025).
37. Stamatakis, A. RAxML version 8: A tool for phylogenetic analysis and post-analysis of large phylogenies. *Bioinformatics* **2014**, *30*, 1312–1313. [CrossRef]
38. Ronquist, F.; Teslenko, M.; van der Mark, P.; Ayres, D.L.; Darling, A.; Hőhna, S.; Larget, B.; Liu, L.; Suchard, M.A.; Huelsenbeck, J.P. MrBayes 3.2: Efficient Bayesian phylogenetic inference and model choice across a large model space. *Syst. Biol.* **2012**, *61*, 539–542. [CrossRef] [PubMed]
39. Xiang, C.Y.; Gao, F.; Jakovlić, I.; Lei, H.P.; Hu, Y.; Zhang, H.; Zou, H.; Wang, G.T.; Zhang, D. Using PhyloSuite for molecular phylogeny and tree-based analyses. *iMeta* **2023**, *2*, e87. [CrossRef] [PubMed]
40. Rosenthal, L.M.; Larsson, K.H.; Branco, S.; Chung, J.A.; Glassman, S.I.; Liao, H.L.; Peay, K.G.; Smith, D.P.; Talbot, J.M.; Taylor, J.W.; et al. Survey of corticioid fungi in North American pinaceous forests reveals hyperdiversity, underpopulated sequence databases, and species that are potentially ectomycorrhizal. *Mycologia* **2017**, *109*, 115–127. [CrossRef] [PubMed]
41. Gaiser, R.F.; Robles, C.A.; Kobashigawa, J.M.; Pereira, S.; Skronski, N.; Carmarán, C.C. Mycobiota associated to Casa Moneta Museum wood, South Orkney Islands, Antarctica. *Polar Biol.* **2021**, *44*, 1817–1831. [CrossRef]
42. Larsson, K.H.; Larsson, E.; Kõljalg, U. High phylogenetic diversity among corticioid homobasidiomycetes. *Mycol. Res.* **2004**, *108*, 983–1002. [CrossRef]
43. Maunoury, L.S.; Deveau, A.; Moreno, M.; Todesco, F.; Belmondo, S.; Murat, C.; Courty, P.E.; Jąkalski, M.; Selosse, M.A. Two ectomycorrhizal truffles, *Tuber melanosporum* and *T. aestivum*, endophytically colonise roots of non-ectomycorrhizal plants in natural environments. *New Phytol.* **2020**, *225*, 2542–2556. [CrossRef]
44. Liu, X.Y.; Liu, S.L.; Wei, H.W.; Wang, X.W.; Yu, J.; Shen, S.; Zhou, L.W. Preliminary species diversity and community phylogenetics of wood-inhabiting basidiomycetous fungi in the Dabie Mountains, Central China reveal unexpected richness. *IMA Fungus* **2023**, *14*, 23. [CrossRef]
45. Larsson, K.H. Re-thinking the classification of corticioid fungi. *Mycol. Res.* **2007**, *111*, 1040–1063. [CrossRef]
46. Langer, E. Phylogeny of non-gilled and gilled basidiomycetes—DNA sequence inference, ultrastructure and comparative morphology. *Persoonia* **2001**, *18*, 1–208.

47. Brazee, N.J.; Lindner, D.L.; D'Amato, A.W.; Fraver, S.; Forrester, J.A.; Mladenoff, D.J. Disturbance and diversity of wood-inhabiting fungi: Effects of canopy gaps and downed woody debris. *Biodivers Conserv.* **2014**, *23*, 2155–2172. [CrossRef]
48. Eriksson, J. Studies in the Heterobasidiomycetes and Homobasidiomycetes—Aphyllophorales of Muddus National Park in North Sweden. In *Symbolae Botanicae Upsalienses*; University of Uppsala: Uppsala, Sweden, 1958; Volume 16, pp. 1–172.
49. Krieglsteiner, G.J. 1991: Über neue, seltene, kritische Makromyzeten in Westdeutschland (ehemalige BR Deutschland, Mitteleuropa). XIII. Porlinge, Korallen-, Rinden- und Gallertpilze. *Z. Mykol.* **2023**, *57*, 17–54.
50. Maekawa, N. Taxonomy of corticioid fungi in Japan: Present status and future prospects. *Mycoscience* **2021**, *62*, 345–355. [CrossRef]
51. Gilbertson, R.L.; Lindsey, J.P. North American species of *Amylocorticium* (Aphyllophorales, Corticiaceae), a genus of brown rot fungi. *Mem. N. Y. Bot. Gard.* **1989**, *49*, 138–146.
52. Hjortstam, K.; Ryvarden, L. Notes on Corticiaceae (Basidiomycetes) V. *Mycotaxon* **1979**, *10*, 201–209. [CrossRef]
53. Ginns, J. Merulius: S.s. and s.l., taxonomic disposition and identification of species. *Can. J. Bot.* **1976**, *54*, 100–167. [CrossRef]
54. Nakasone, K.K. *Cultural Studies and Identification of Wood-Inhabiting Corticiaceae and Selected Hymenomycetes from North America*; Mycologia Memoirs; New York Botanical Garden: New York, NY, USA, 1990; Volume 15, pp. 1–412.

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