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Multigene phylogeny of *Hymenochaetales* (*Basidiomycota*) with two new species from Southwest China

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Abstract

Wood-decaying fungi represent a major group of macrofungi that play critical ecological roles and have considerable economic significance. *Hymenochaetales* (*Agaricomycetes*, *Basidiomycota*) is an important order comprising numerous wood-inhabiting fungal species. In the present study, morphological examination combined with multilocus phylogenetic analyses based on ITS, nLSU, *tef1-α*, and *rpb2* sequences supported the distinctness of two novel species within *Hymenochaetales*, namely *Resinicium albofarinaceum* sp. nov. and *Tubulicrinis sinensis* sp. nov. *Resinicium albofarinaceum* is characterized by its farinaceous basidiomata with a smooth hymenial surface, the presence of two types of cystidia (astrocystidia and halocystidia), and ellipsoid basidiospores measuring 4.3–5.0 × 3.2–3.8 µm. *Tubulicrinis sinensis* is characterized by its farinaceous, fragile basidiomata with a smooth hymenial surface, the presence of lyocystidia in the hymenium, and narrowly cylindrical basidiospores measuring 4.8–5.7 × 1.7–2.3 µm. The phylogenetic analyses indicated that *Resinicium albofarinaceum* formed a separate branch and grouped with *R. yunnanense* and *R. friabile*. *Tubulicrinis sinensis* was sister to *T. calothrix*. The PHI test applied to the ITS and combined datasets revealed no evidence of recombination among phylogenetically related species.

Keywords: Fungal classification · Molecular systematics · New taxa · Wood-decaying fungi · Yunnan Province

Introduction

Hymenochaetales Oberw. is one of the orders mainly composed of wood-inhabiting macrofungi within the class *Agaricomycetes* (*Basidiomycota*), with *Hymenochaete* Lév. as a generic type (Frey et al. 1977). Members of *Hymenochaetales* show diverse basidiomata, including polyporoid, stereoid, corticioid, hydnoid, coralloid, and agaricoid forms (Hibbett et al. 2014; Wang et al. 2026). Ecologically, member of the genus function as important decomposers, pathogens, and mutualists in forest ecosystems. Several taxa within *Hymenochaetales* exhibit a strong host specificity. The host specificity of *Hymenochaetales* can be broadly categorized into four groups: 1) species associated with angiosperms, 2) species associated with gymnosperms, 3) species occurring on both angiosperms and gymnosperms, and 4) species inhabiting bryophytes (Dai 2010; Purahong et al. 2018; Zhao et al. 2025). A comprehensive checklist compiled from the Fungal Names Database and cross-validated against MycoBank, Index Fungorum, and authoritative literature indicates that the order comprises 102 genera across 20 families, with 23 genera remaining incertae sedis (Larsson et al. 2006; Ghobad-Nejhad et al. 2024; Liu et al. 2025).

The genus *Resinicium* was introduced by Parmasto (1968) and is typified by *R. bicolor* (Alb. & Schwein.) Parmasto. It is characterized by resupinate, thin basidiomes with smooth, grandinioid, odontioid or hydnoid hymenophore with white to yellowish hymenial surface, a monomitic hyphal system mainly with clamp connections or with simple septa in few species, the presence of astrocystidia and halocystidia, and thin-walled, smooth, ellipsoid, cylindrical or allantoid basidiospores. *Skvortzovia* Bononi & Hjortstam is quite similar to *Resinicium*, but lacks astrocystidia (Parmasto 1968; Bernicchia and Gorjón 2010). Phylogenetic analyses have indicated that *Resinicium* was not a monophyletic genus (Larsson et al. 2006; Nakasone 2007). Morphological and molecular studies on *Resinicium* s. str. supported two distinct groups as the *Resinicium* s. str. group (*R. bicolor*) and the *Resinicium* s. l. group (*R. furfuraceum* (Bres.)

Parmasto). Morphological research and phylogenetic analyses based on ITS rDNA sequences revealed three major clades within *Resinicium* are; the *Mutabile*-clade, the *Saccharicola*-clade, and the *Bicolor*-clade, with nine species nested in this genus (Gruhn et al. 2017). Cai et al. (2023) examined the genus *Resinicium* s. l. from morphological and phylogenetic perspectives, 12 species were differentiated through ITS-based phylogenetic analysis, and one new species was described.

The genus *Tubulicrinis* Donk, typified by *T. glebulosus* (Fr.) Donk (Donk 1956), is a member of the corticioid fungi, which is characterized by resupinate basidiomata with a firmly adnate, smooth, pruinose to porulose hymenophore; a monomitic hyphal system with clamp connections; projecting, amyloid cystidia and small basidia; and cylindrical to allantoid or globose to ellipsoid, thin-walled, smooth, acyanophilous basidiospores (Donk 1956; Bernicchia and Gorjón 2010; Dong et al. 2024). The research on the molecular phylogeny of the hymenochaetoid clade revealed two *Tubulicrinis* species, *T. gracillimus* (Ellis & Everh. ex D.P. Rogers& H.S. Jacks.) G. Cunn. and *T. subulatus* (Bourdot & Galzin) Donk, formed a monophyletic lineage and were subsequently grouped with the *Coltricia* clade and *Hymenochaetaceae* clade (Larsson et al. 2006). A revised checklist of corticioid and hydnoid fungi in China revealed six recorded *Tubulicrinis* species (Dai 2011). Based on MycoBank entries and Index Fungorum (accessed on 7 May 2026), in total 64 specific and infraspecific names are registered for *Tubulicrinis*, and the actual number of species is 49, of which three new species, viz. *T. incanus* Lu Wang & C.L. Zhao, *T. hongheensis* C.L. Zhao, and *T. tenuis* C.L. Zhao were published from Yunnan Province, China (Wang et al. 2026; Yuan et al. 2026).

During investigations of wood-inhabiting fungi in the Tongbiguan Provincial Nature Reserve, Yunnan Province, China, numerous specimens were collected. The taxonomic placement and phenotypic studies were conducted based on combined ITS, nLSU, *tef1-α*, and *rpb2* sequence data to determine their positions within the order *Hymenochaetales*. Two new species, *Resinicium albofarinaceum* and *Tubulicrinis sinensis*, are described in this study. The Pairwise Homoplasy Index (PHI) analyses were conducted to confirm the new species with related taxa.

Materials and methods

Sample collection and herbarium specimen preparation

Basidiomata were collected from fallen angiosperm branches in Dehong Dai and Jingpo Autonomous Prefecture, Yunnan Province, southwestern China. Samples were photographed *in situ*, and fresh macroscopic characteristics together with relevant field data were recorded (Deng et al. 2025). Photographs were taken using a Vivo X300 camera. Macroscopic features were further examined and documented. The collected basidiomata were dried in an electric food dryer at 40 °C. Dried specimens were sealed in envelopes and zip-lock plastic bags and labeled with voucher numbers (Dong et al. 2025). Voucher specimens were deposited in the herbarium of Southwest Forestry University (SWFC), Kunming, Yunnan Province, China.

Morphological study

Macro-morphological descriptions were based on field notes and photos captured in the field and laboratory. Color descriptions followed Petersen (1996) and were further verified using general CMYK color standards (Deep White Printing Team 2022). Micro-morphological observations were conducted on dried specimens using a light microscope at magnifications of up to 10×100 (Deng et al. 2026). Sections were mounted in 5% KOH and 1% Phloxine B ($C_{20}H_2Br_4Cl_4Na_2O_5$), along with additional reagents such as Cotton Blue and Melzer’s reagent, following the procedures of Dong et al. (2025), to examine micro-morphological features. Basidiospores were measured from sections of the basidiomata; in reporting spore size ranges, the extreme 5% of measurements at both ends were excluded and are indicated in parentheses.

At least 30 basidiospores were measured per specimen. Basidium measurements excluded sterigmata, and basidiospore measurements excluded the hilar appendage. All newly identified species were registered in the MycoBank database (http://www.mycobank.org).

The following abbreviations are used:

KOH = 5% potassium hydroxide water solu tion

CB– = acyanophilous

IKI– = both inamyloid and indextrinoid

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

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

n = a/b (number of spores (a) measured from a given number (b) of specimens)

Q = variation in the L/W ratios between the specimens studied

Qm = the average Q of basidiospores measured ± standard deviation

Molecular phylogenetic studies

Genomic DNA was extracted from dried specimens using the EZNA HP Fungal DNA Kit (Omega Biotechnologies Co., Ltd., Kunming, China) according to the manufacturer's instructions. The extracted DNA was maintained at -20 °C for long-term storage. The ITS, nLSU, *tef1-α* and *rpb2* regions were amplified with the ITS5/ITS4 (White et al. 1990), LR0R/LR7 (Vilgalys and Hester 1990), EF1-983F/EF1-2218R (Rehner and Buckley 2005) and bRPB2-6F/bRPB2-7.1R (Liu et al. 1999) primer pairs, respectively. The accession number of the sequences used in this study is given in Table 1. The PCR products were purified and sequenced at Kunming Tsingke Biological Technology Limited Company (Yunnan Province, China). All newly generated sequences were deposited in NCBI GenBank (https://www.ncbi.nlm.nih.gov/genbank/) (Table 2).

Phylogenetic analyses followed the methods of Deng et al. (2026). Newly generated sequences were initially subjected to BLAST searches in NCBI to identify the most closely related taxa in GenBank (http://blast.ncbi.nlm.nih.gov/), with type specimens or authoritative sequences referenced according to Dong et al. (2024). Additional sequence data were retrieved from GenBank based on recent publications. DNA sequences were aligned using MAFFT version 7 (https://mafft.cbrc.jp/alignment/server/) with the G-INS-i strategy (Katoh et al. 2019), and the alignments were manually adjusted in AliView version 1.27 (Larsson 2014). Subsequently, ITS, nLSU, *tef1-α* and *rpb2* sequences were concatenated using Mesquite version 3.81. Phylogenetic trees were reconstructed based on randomized accelerated Maximum Likelihood (ML) and Bayesian Inference (BI) analyses. The combined dataset was deposited in figshare (DOI: 10.6084/m9.figshare.32305743).

Maximum Likelihood (ML) analysis was performed using the CIPRES Science Gateway (https://www.phylo.org/portal2/login!input.action; Miller et al. 2012) based on the dataset, employing the RAxML-HPC BlackBox tool. The analysis was conducted with the "RAxML halt bootstrapping automatically" option enabled, a maximum runtime of 0.25 h, and the best-scoring tree was obtained through ML search. All other parameters were set to their default values, and statistical support values were estimated using nonparametric bootstrapping with 1,000 replicates. Bayesian Inference (BI) phylogenies were inferred using PhyloSuite v1.2.3 (Zhang et al. 2020; Xiang et al. 2023) with MrBayes v3.2.7a (Ronquist et al. 2012). Branches were considered significantly supported when Maximum Likelihood bootstrap values (BS) were ≥ 70% or Bayesian posterior probabilities (BPP) were ≥ 0.95. Phylogenetic analyses were first conducted using the combined multilocus dataset, followed by separate analyses of individual gene loci.

Phylogenetic trees were visualized and edited using FigTree v1.4.4 (http://tree.bio.ed.ac.uk/software/figtree), and the resulting figures were further refined in Adobe Illustrator CS6 (Adobe Systems, USA). Branches in the consensus tree were considered significantly supported when Maximum Likelihood (ML) bootstrap values were ≥ 70% or Bayesian Inference (BI) posterior probabilities were ≥ 0.95.

Pairwise homoplasy test

The Genealogical Concordance Phylogenetic Species Recognition (GCPSR) analysis was employed to detect significant recombination events. Pairwise homoplasy index (Φw) and the PHI test, implemented in SplitsTree 4, were used to evaluate recombination levels among closely related species (Bruen et al. 2006; Huson and Bryant 2006; Quaedvlieg et al. 2014). The analysis was performed on a single-locus dataset (ITS) of closely related species. A PHI test result below 0.05 ($\Phi w < 0.05$) indicates the presence of significant recombination in the dataset. Split graphs were constructed from the concatenated datasets using the LogDet transformation and splits decomposition options to visualize the relationships among closely related taxa.

Results

Molecular phylogeny

The phylogeny of *Hymenochaetales* based on combined ITS, nLSU, *tef1-α* and *rpb2* sequence data (Fig. 1)

The combined ITS+nLSU+*tef1-α*+*rpb2* dataset (Fig. 1) consisted of 83 sequences representing 76 species across the order *Hymenochaetales*, covering 20 families and 39 genera. *Cerioporus squamosus* (Huds.) Quél. and *Antrodia subserpens* B.K. Cui & Yuan Y. Chen were used as outgroup taxa (Zhang et al. 2025). Eighty-three specimens from the global climate zones were collected from rotten wood. Asia (mainly China) contributed approximately 90% of the specimens. In the phylogenetic tree (Fig. 1), 20 families and 39 genera formed well-separated clades. Our results showed that *Hymenochaetaceae* Donk grouped with *Coltriciaceae* Jülich with strong statistic supports (100% BS, 1.00 BPP; Fig. 1).

The best RAxML tree with a final likelihood value of -60675.920534 is presented. The evolutionary model GTR+GAMMA is applied to all the genes. The matrix contained 2992 distinct alignment patterns, with 58.86% of characters undetermined (gaps). Estimated base frequencies were as follows: A = 0.248384, C = 0.219938, G = 0.274375, T = 0.257303; substitution rates AC = 1.012593, AG = 2.306937, AT = 1.271566, CG = 0.717042, CT = 4.334845, GT = 1.000000; gamma distribution shape parameter $\alpha = 0.408730$.

The best-fit model for the dataset according to BIC: GTR+F+I+G4. Bayesian analysis was performed under the GTR+F+I+G4 model (2 parallel runs, 1,500,000 generations), in which the initial 25% of sampled data were discarded as burn-in. Maximum Likelihood (ML) and Bayesian Inference (BI) analysis yielded a similar topology, with an average standard deviation of split frequencies = 0.006382 (BI), and the effective sample size (ESS) for Bayesian analysis across the two runs is the double of the average ESS (avg. ESS) = 630.5.

The phylogram, based on the combined ITS+nLSU+*tef1-α*+*rpb2* sequences analysis (Fig. 1), showed that the two new species *Resinicium albofarinaceum* and *Tubulicrinis sinensis*, were assigned to the families *Resiniciaceae* and *Tubulicrinaceae* within the order *Hymenochaetales*, respectively.

The phylogeny of *Resinicium* based on ITS sequence data (Fig. 2)

The ITS dataset (Fig. 2) included sequences from 33 fungal specimens representing 14 species. The best RAxML tree with a final likelihood value of -3652.629651 is presented. The evolutionary model GTR+GAMMA is applied to all the genes. The matrix contained 339 distinct alignment patterns, with 23.43% of characters undetermined (gaps). Estimated base frequencies were as follows: A = 0.265202, C = 0.189953, G = 0.203476, T = 0.341368; substitution rates AC = 1.291437, AG = 4.727906, AT = 2.138256, CG = 0.780980, CT = 5.422219, GT = 1.000000; gamma distribution shape parameter α = 0.448616.

The best-fit model for the dataset according to BIC: HKY+F+G4. Bayesian analysis was performed under the HKY+F+G4 model (2 parallel runs, 500000 generations), in which the initial 25% of sampled data were discarded as burn-in. Maximum Likelihood (ML) and Bayesian Inference (BI) analysis yielded a similar topology, with an average standard deviation of split frequencies = 0.009612 (BI), and the effective sample size (ESS) for Bayesian analysis across the two runs is the double of the average ESS (avg. ESS) = 395.

The topology based on ITS sequences (Fig. 2) showed that three specimens of *Resinicium albofarinaceum* formed a separate branch, and grouped with *R. yunnanense* J. Cai & C.L. Zhao, and *R. friabile* Hjortstam & Melo.

The phylogeny of *Tubulicrinis* based on combined ITS and nLSU sequence data (Fig. 3)

The combined ITS and nLSU dataset (Fig. 3) included sequences from 30 fungal specimens representing 21 species. The best RAxML tree with a final likelihood value of -13185.882322 is presented. The evolutionary model GTR+GAMMA is applied to all the genes. The matrix contained 892 distinct alignment patterns, with 40.79% of characters undetermined (gaps). Estimated base frequencies were as follows: A = 0.230926, C = 0.244254, G = 0.288332, T = 0.236488; substitution rates AC = 0.844752, AG = 1.452181, AT = 0.835028, CG = 1.121505, CT = 3.759197, GT = 1.000000; gamma distribution shape parameter α = 0.266887.

The best-fit model for the dataset according to BIC: GTR+F+I+G4. Bayesian analysis was performed under the GTR+F+I+G4 model (2 parallel runs, 2000000 generations), in which the initial 25% of sampled data were discarded as burn-in. Maximum Likelihood (ML) and Bayesian Inference (BI) analysis yielded a similar topology, with an average standard deviation of split frequencies = 0.002223 (BI), and the effective sample size (ESS) for Bayesian analysis across the two runs is the double of the average ESS (avg. ESS) = 1433.5. The phylogenetic tree (Fig. 3), inferred from the combined ITS and nLSU sequences, showed that the new species *Tubulicrinis sinensis* was a sister to *T. calothrix* (Pat.) Donk.

Application of the PHI test to the ITS sequences revealed no recombination among phylogenetically related species. For further confirmation, we performed the PHI test on the combined sequence data (ITS, nLSU, *tef1-α* and *rpb2*), and the results also showed no recombination within phylogenetically related species. No significant recombination events were observed between *Resinicium albofarinaceum* and its phylogenetically closely related species, namely *R. yunnanense* and *R. friabile*. The test results show Φw = 1.00 for ITS data (Fig. 4), Φw = 1.00 for the combined sequence data (Fig. 5), indicating that no recombination is present between the new species and *R. yunnanense* and *R. friabile*. No significant recombination events were observed between *Tubulicrinis sinensis* and its phylogenetically closely related species, namely *T. borealis* J. Erikss., *T. calothrix* and *T. incanus*. The test results show Φw = 0.7661 for ITS data (Fig. 4), Φw = 0.2806 for the combined sequence data (Fig. 5), indicating that no recombination is present between the new species and *T. borealis*, *T. calothrix* and *T. incanus*.

Taxonomy

Resinicium albofarinaceum Qian Q. Jiang & C.L. Zhao, sp. nov.

Chinese name. 白粉末树脂革菌 (bai fen mo shu zhi ge jun)

MycoBank No.: 863663

Figs. 6, 7, 8

Diagnosis: *Resinicium albofarinaceum* is characterized by the smooth hymenial surface, the presence of two types of cystidia (astrocystidia and halocystidia) and ellipsoid basidiospores measuring 4.3–5 × 3.2–3.8 µm.

Holotype: CHINA, Yunnan Province, Dehong Dai and Jingpo Autonomous Prefecture, Ruili City, Tongbiguan Nature Reserve, GPS coordinates 23°41′N, 97°30′E, altitude 950 m asl., on fallen angiosperm branch, leg. C.L. Zhao, 21 November 2024, CLZhao 41345 (SWFC 00041345).

Etymology: *albofarinaceum* (Lat.): referring to the white basidiomata with farinaceous hymenophore of the type specimens.

Basidiomata: Annual, resupinate, closely adnate, thin, farinaceous, without odor or taste when fresh, becoming slightly cracking upon drying, up to 10 cm long, 3 cm wide, 60 µm thick. Hymenial surface smooth, white (C0 M0 Y0 K0) when fresh, white (C0 M0 Y5 K0) upon drying. Sterile margin white (C0 M0 Y0 K0), narrow, up to 1 mm wide.

Hyphal structure: Monomitic, generative hyphae with clamp connections, colorless, thin-walled, branched, interwoven, 1.4–2.8 µm in diameter; IKI–, CB–, tissues unchanged in KOH.

Hymenium: Cystidia of two types: (1) Astrocystidia rare, scattered, colorless, thin-walled, 13–30 × 1.5–4 µm (base 1–2.3 µm in diameter), with an acute or bulbous apex, often developing both terminally and laterally on hyphae; the easily crushed, star-shaped crystals usually free in the hymenium, to 7–24 µm in diameter. (2) Halocystidia numerous, colorless, thin-walled, capitate, 16.7–31 × 7.5–9.5 µm; tapering to 2.5–3 µm diameter at base, the outer layer inflates to a bladder, 10–21.5 µm in diameter, formed a capitate cystidium. Basidia subclavate, with four sterigmata and a basal clamp connection, 11.5–17 × 4.5–6 µm. Basidioles dominant, in shape similar to basidia, but slightly smaller.

Basidiospores: Ellipsoid, colorless, thin-walled, smooth, IKI–, CB–, (4–)4.3–5(–5.2) × (2.5–)3.2–3.8(–4) µm, L = 4.68 µm, W = 3.43 µm, Q = 1.34–1.39, Qm = 1.36 ± 0.07 (n = 90/3).

Type of rot: White rot.

Additional specimens (paratypes) examined: CHINA, Yunnan Province, Dehong Dai and Jingpo Autonomous Prefecture, Ruili City, Tongbiguan Nature Reserve, GPS coordinates 23°41′N, 97°30′E, altitude 950 m asl., on fallen angiosperm branch, leg. C.L. Zhao, 21 November 2024, CLZhao 41425 (SWFC 00041425); 15 January 2025, CLZhao 44282 (SWFC 00044282).

Tubulicrinis sinensis Qian Q. Jiang & C.L. Zhao, sp. nov.

Chinese name. 中国筒毛革菌 (zhong guo tong mao ge jun)

MycoBank No.: 863664

Figs. 9, 10, 11

Diagnosis: *Tubulicrinis sinensis* is characterized by the smooth hymenial surface, the presence of lyocystidia in the hymenium and narrowly cylindrical basidiospores measuring 4.8–5.7 × 1.7–2.3 µm.

Holotype: CHINA, Yunnan Province, Dehong Dai and Jingpo Autonomous Prefecture, Ruili City, Tongbiguan Nature Reserve, GPS coordinates 23°41′N, 97°30′E, altitude 950 m asl., on fallen angiosperm branch, leg. C.L. Zhao, 24 November 2024, CLZhao 42810 (SWFC 00042810).

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

Basidiomata: Annual, resupinate, closely adnate, farinaceous, without odor or taste when fresh, becoming fragile upon drying, up to 8 cm long, 2 cm wide, 100 µm thick. Hymenial surface smooth, white (C0 M0 Y0 K0) when fresh, white (C0 M0 Y0 K0) upon drying. Sterile margin indistinct, white (C0 M0 Y0 K0), narrow, thinning out, up to 0.5 mm wide.

Hyphal structure: Monomitic, generative hyphae with clamp connections, colorless, slightly thick-walled, rarely branched, interwoven, 2–4 µm in diameter; IKI–, CB–, tissues unchanged in KOH.

Hymenium: Lyocystidia numerous, projecting, cylindrical to slightly sinuous, and at times birooted, 50.5–71.2 × 5.5–7.7 µm, projecting above the hymenium; cystidioles absent. Basidia clavate, with 4 sterigmata and a basal clamp connection, 8.4–10.7 × 4–5 µm; basidioles dominant, in shape similar to basidia, but slightly smaller.

Basidiospores: Narrowly cylindrical, colorless, thin-walled, smooth, IKI–, CB–, (4.4–)4.8–5.7(–6) × (1.5–)1.7–2.3 µm, L = 5.26 µm, W = 1.96 µm, Q = 2.63–2.75, Qm = 2.68 ± 0.15 (n = 60/2).

Type of rot: White rot.

Additional specimen (paratype) examined: CHINA, Yunnan Province, Dehong Dai and Jingpo Autonomous Prefecture, Ruili City, Tongbiguan Nature Reserve, GPS coordinates 23°41′N, 97°30′E, altitude 950 m asl., on fallen angiosperm branch, leg. C.L. Zhao, 24 November 2024, CLZhao 48982 (SWFC 00048982).

Discussion

The Dehong Dai and Jingpo Autonomous Prefecture in southwestern China is a global biodiversity hotspot. Its complex topography and diverse ecosystems render it a critical region for mycological research. Recent studies emphasize the necessity of systematic field surveys and taxonomic investigations within these native forests, which act as vital reservoirs of undocumented fungal diversity (Jiang et al. 2025; Zhang et al. 2026). In this study, two new species, *Resinicium albofarinaceum* and *Tubulicrinis sinensis*, are formally described and illustrated based on morphological trails and multilocal phylogenetic analyses.

China's vast territory and climatic heterogeneity harbor an exceptionally high diversity of wood-inhabiting fungi (Dai 2011; Wu et al. 2022). In warm and humid Yunnan, rapid wood decay coupled with continuous substrate renewal creates persistent ecological niches, supporting numerous undescribed fungal species (Ranius et al. 2019; Dong et al. 2025).

Recently, a series of studies on fungal diversity and the ecology of *Basidiomycota* in Dehong, Yunnan Province, has been conducted (Deng et al. 2025; Jiang et al. 2025; Zhang et al. 2026). The region's unique topography and diverse ecosystems are particularly favorable for the occurrence of novel taxa in *Hymenochaetales* (Jiang et al. 2025; Wang et al. 2026). The distribution of wood-inhabiting fungi is closely linked to host plant diversity, which provides essential substrates for colonization (Vainio et al. 2011; Huang et al. 2022; Zhao et al. 2026). In the forests of Dehong, the diversity of potential host plants may promote species diversification within *Hymenochaetales*. However, because most collected specimens were obtained from highly decayed wood, host plant identification remains extremely difficult, resulting in incomplete data on host associations and an overall poor understanding of host specificity in many corticioid fungi (Crous et al. 2016; Cho et al. 2024; Zhao et al. 2025). To meaningfully address host specificity, future studies should systematically investigate the diversity of potential host plants associated with *Hymenochaetales* in Tongbiguan Nature Reserve. This reserve is characterized by dense vegetation and a complete vertical vegetation zonation sequence, encompassing tropical monsoon forests, tropical montane rainforests, south-subtropical monsoon evergreen broad-leaved forests, mid-mountain humid evergreen broad-leaved forests, bamboo forests, shrublands, and grasslands. Within the reserve, angiosperms and gymnosperms are highly diverse, offering a wide array of potential hosts for fungi (Yang and Du 2006; Zhang et al. 2026). Therefore, future studies should carefully document the host tree species associated with each fungal specimen, although the difficulty of identifying host plants from decayed wood remains a major challenge.

Although molecular approaches are widely used in fungal taxonomy and phylogenetics, caution is warranted when species delimitation relies solely on ITS sequence data. The ITS region often provides insufficient resolution for accurate species delimitation, and numerous misidentified or incorrectly annotated sequences remain in the GenBank database (Cho et al.

2023). This limitation is particularly evident in *Resinicium* and *Tubulicrinis*, where current studies still rely predominantly on ITS-based single-locus datasets (Cai et al. 2023; Dai et al. 2025). Therefore, future studies should incorporate multilocus sequence data to improve phylogenetic reconstruction and species delimitation within these two genera. Multilocus datasets can substantially enhance the resolution and reliability of species delimitation in *Resinicium* and *Tubulicrinis*. Similar findings have been reported in studies of wood-inhabiting fungi, where protein-coding loci have provided additional phylogenetically informative characters for resolving species boundaries (Stielow et al. 2015; Cho et al. 2023). Previous phylogenetic studies of *Hymenochaetales* and other wood-inhabiting fungi have likewise demonstrated that multilocus datasets significantly enhance the stability and resolution of phylogenetic relationships among closely related taxa (Cho et al. 2024; Zhao et al. 2025; Wang et al. 2026). Therefore, multilocus phylogenetic analyses are essential for accurate taxonomy and reliable species delimitation in *Hymenochaetales*. Based on the above considerations, in the present study we employed a combination of multilocus phylogenetic analyses and rigorous taxonomic examination to successfully identify and describe two novel species. The two species are characterized by annual basidiomes, occur on angiosperm substrates, and are strongly supported as distinct taxa based on both phylogenetic analyses and morphological characteristics. Through integrated multilocus data and detailed morphological observations, this study provides comprehensive morphological and taxonomic characterization for the two new species. The discovery of these two new species further expands current knowledge of fungal diversity in poorly sampled forests of China and underscores the need for continued taxonomic exploration (Zhao et al. 2026).

Although extensive researches into the phylogenetic relationships within *Hymenochaetales* were carried out for fungal diversity in this area, taxonomic inconsistencies persist as a consequence of taxon sampling and the selection of molecular markers (Binder et al. 2005; Crous et al. 2016; Ghobad-Nejhad et al. 2024). Compiling data from the Fungal Names Database, MycoBank, Index Fungorum and authoritative literature, Zhao et al. (2025) recently compiled a checklist of *Hymenochaetales* recognizing 18 families. *Coltriciaceae* is a monogeneric family containing only the genus *Coltricia* Gray. Although *Coltricia* was previously placed within *Hymenochaetaceae* (Wu et al. 2022; Cho et al. 2024), and it has been accepted as a distinct family by Zhao et al. (2025). In line with previous studies, this study confirms the families *Coltriciaceae* and *Hirschioporaceae* Y.C. Dai, Yuan Yuan & M. Zhou (Wang et al. 2023; Zhou et al. 2023; Zhao et al. 2025; Zhou et al. 2026). Zhao et al. (2025) rejected the families *Chaetoporellaceae* Jülich and *Hyphodontiaceae* X. Wei Wang & L.W. Zhou as independent lineages. Zhou et al. (2026) established two new families within this order: *Pseudotrichaptaceae* M. Zhou, Y.J. Cui, H. Zhao, et al. and *Podocarpioporaceae* M. Zhou, Y.J. Cui, H. Zhao, et al., in which the overall phylogenetic relationships and familial circumscriptions recovered in our study are highly consistent with previous investigations of *Hymenochaetales*. In light of these studies, we constructed a four-gene phylogenetic tree (ITS, nLSU, *tef1-α*, and *rpb2*) covering all 20 families of *Hymenochaetales* (Fig. 1), in which our results confirm the placement of the two new species within *Resiniciaceae* and *Tubulicrinaceae*, respectively. To further clarify the generic placement of the new species, we also constructed phylogenetic trees based on the ITS dataset alone (Fig. 2) and the combined ITS and nLSU dataset (Fig. 3).

The phylogram based on the ITS dataset showed that *Resinicium albofarinaceum* was grouped with *R. friabile* and *R. yunnanense* with supports (95% BS, 1.00 BPP; Fig. 2). Morphologically, *Resinicium friabile* differs from *R. albofarinaceum* by having subceraceous to ceraceous, denticulate to spinose basidiomata and narrower basidiospores (2.8–3 µm vs. 3.2–3.8 µm) (Hjortstam and Melo 1997). *Resinicium yunnanense* is distinguishable from *R. albofarinaceum* by its narrower basidiospores (2.3–3.3 µm vs. 3.2–3.8 µm) and smaller basidia

(7–10 × 3–4.5 µm vs. 11.5–17 × 4.5–6 µm) (Cai et al. 2023). In the combined ITS and nLSU phylogeny (Fig. 3), *Tubulicrinis sinensis* is sister to *T. calothrix*, and together with *T. borealis* and *T. incanus*, they form a single clade. However, *T. calothrix* differs from *T. sinensis* in having longer basidiospores (6–8 µm vs. 4.8–5.7 µm) and longer basidia (12–15 µm vs. 8.4–10.7 µm) (Donk 1956). *Tubulicrinis borealis* can be distinguished from *T. sinensis* by having a reticulate to continuous hymenial surface and subcylindrical to allantoid, longer basidiospores (5.5–6.5 µm vs. 4.8–5.7 µm) (Eriksson et al. 1958). *Tubulicrinis incanus* differs from *T. sinensis* by its larger basidia (17–19 × 6–8 µm vs. 8.4–10.7 × 4–5 µm) and larger basidiospores (8.5–10.5 × 3–4 µm vs. 4.8–5.7 × 1.7–2.3 µm) (Wang et al. 2026).

Morphologically, *Resinicium albofarinaceum* resembles *R. lateastrocystidium* Jia Yu, X.Wei Wang, S.L. Liu & L.W. Zhou, *R. rimulosum* Nakasone and *R. saccharicola* (Burt) Nakasone in the presence of halocystidia and astrocystidia. However, *R. lateastrocystidium* is separated from *R. albofarinaceum* by its straw-yellow to olivaceous buff hymenial surface upon drying (Yu et al. 2021). *Resinicium rimulosum* can be delimited from *R. albofarinaceum* by its narrower basidiospores (2.8–3 µm vs. 3.2–3.8 µm) (Nakasone 2007). *Resinicium saccharicola* is distinct from *R. albofarinaceum* by its longer basidiospores (5.5–6 µm vs. 4.3–5 µm) (Nakasone 2007). A morphological comparison between the new species *Resinicium albofarinaceum* and its closely related species is presented in Table 3. *Tubulicrinis sinensis* resembles *T. hirtellus* (Bourd. & Galz.) John Erikss., *T. orientalis* Parmasto and *T. xantha* C.L. Zhao in having cylindrical basidiospores. However, *T. hirtellus* can be distinguished from *T. sinensis* by its porulose basidiomata and longer basidiospores (7.0–8.5 µm vs. 4.8–5.7 µm) (Hjortstam et al. 1988). *Tubulicrinis orientalis* differs from *T. sinensis* due to its hispidulous basidiomata and longer basidia (11.0–16.0 µm vs. 8.4–10.7 µm) (Parmasto 1967). *Tubulicrinis xantha* differs from *T. sinensis* by its furfuraceous basidiomata, longer lyocystidia (78.0–192.5 µm vs. 50.5–71.5 µm) and narrower basidiospores (1.2–1.6 µm vs. 1.7–2.3 µm) (He et al. 2020).

A morphological comparison between the new species *Tubulicrinis sinensis* and its closely related species is presented in Table 4.

In recent years, the reported species diversity within *Hymenochaetales* has expanded rapidly with the discovery of numerous corticioid taxa (Gruhn et al. 2016; Rosenthal et al. 2017; Ghobad-Nejhad et al. 2024; Jiang et al. 2025; Yuan et al. 2026; Zhou et al. 2026; Zhu et al. 2026). These findings align with broader biogeographic patterns observed in macrofungi, wherein many species remain undescribed and are often confined to fragile and threatened ecosystems (Heilmann-Clausen et al. 2015). In this study, the discovery of two new species within protected natural areas highlights that nature reserves function not only to conserve documented biodiversity but also to facilitate the exploration of novel fungal taxa and the protection of rare fungal resources. Continued exploration will undoubtedly reveal further undocumented taxa, enriching our understanding of this often-overlooked group of fungi.

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Statements and Declarations

Author contributions Conceptualization, CZ; methodology, CZ and QJ; software, CZ, QJ and JL; validation, CZ and QJ; formal analysis, CZ and QJ; investigation, CZ and QJ; resources CZ and QJ; writing—original draft preparation, CZ, QJ, JL, JF, and CP; writing—review and editing, CZ, QJ, and CP; visualization, CZ and QJ; supervision, CZ; project administration, CZ; funding acquisition, CZ. All authors have read and agreed to the published version of the manuscript.

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Data availability Publicly available datasets were analyzed in this study. This data can be found here: [https://www.ncbi.nlm.nih.gov/; https://doi.org/10.6084/m9.figshare.32305743].

Declarations

Ethics approval and consent to participate All authors confirm that no research involving humans or animals was involved in the current study, that there are no issues relating to animal welfare relating to the current study and that they have approval to participate in the current study.

Consent for publication All authors have given explicit consent to the submitted paper and to the inclusion of their data in it.

Competing interests The authors declare no competing interests.

Table

Table 1 Loci, primers, PCR amplification procedures, and references used in this study

Table 2 List of species, specimens and GenBank accession numbers of sequences used in this study

Table 3 Morphological comparison of the new species *Resinicium albofarinaceum* with its closely related species. Newly introduced taxa are indicated in bold black font

Table 4 Morphological comparison of the new species *Tubulicrinis sinensis* with its closely related species. Newly introduced taxa are indicated in bold black font

Figure legends

Figure 1 Maximum likelihood strict consensus tree illustrating the phylogeny of *Resiniciaceae*, *Tubulicrinaceae* and related families in *Hymenochaetales* based on ITS+nLSU+*tef1-α*+*rpb2* sequences. Branches are labeled with Maximum Likelihood bootstrap values ≥ 70%, and Bayesian posterior probabilities ≥ 0.95, respectively. New species are shown in bold, * refers to type material (holotype)

Figure 2 Maximum likelihood strict consensus tree illustrating the *Resinicium albofarinaceum* and related species in the genus *Resinicium* based on ITS sequences. Branches are labeled with Maximum Likelihood bootstrap values ≥ 70%, and Bayesian posterior probabilities ≥ 0.95, respectively. New species are shown in bold, * refers to type material (holotype)

Figure 3 Maximum likelihood strict consensus tree illustrating the *Tubulicrinis sinensis* and related species in the genus *Tubulicrinis* based on the combined ITS and nLSU sequences. Branches are labeled with Maximum Likelihood bootstrap values ≥ 70%, and Bayesian posterior probabilities ≥ 0.95, respectively. New species are shown in bold, * refers to type material (holotype)

Figure 4 Split graphs showing the results of PHI test for the ITS data of two new species and their closely related species using LogDet transformation and splits decomposition. PHI test results with $\Phi w \leq 0.05$ indicate that there is significant recombination within the dataset. The new taxa are in red type. **a** *Resinicium albofarinaceum* and closely related species ($\Phi w = 1.00$). **b** *Tubulicrinis sinensis* and closely related species ($\Phi w = 0.7661$)

Figure 5 Split graphs showing the results of PHI test for the ITS+nLSU+*tef1-α*+*rpb2* data of two new species and their closely related species using LogDet transformation and splits decomposition. PHI test results with $\Phi w \leq 0.05$ indicate that there is significant recombination within the dataset. The new taxa are in red type. **a** *Resinicium albofarinaceum* and closely related species ($\Phi w = 1.00$). **b** *Tubulicrinis sinensis* and closely related species ($\Phi w = 0.2806$)

Figure 6 Basidiomata of *Resinicium albofarinaceum* (CLZhao 41345, holotype)

Figure 7 Sections of hymenium of *Resinicium albofarinaceum* (CLZhao 41345, holotype). **a1–a7** Basidiospores. **b** Basidia and basidioles. **c** Generative hyphae. **d** A section of the hymenium. **e1–e2** Astrocystidia. **f1-f2** Halocystidia. Scale bars: **a–e =** 10 µm; 10×100 oil

Figure 8 Microscopic structures of *Resinicium albofarinaceum* (CLZhao 41345, holotype). **a**

Basidiospores. **b** Basidia and basidioles. **c** Halocystidia. **d** Astrocystidia. **e** A section of the hymenium. Scale bars: **a–e** = 10 µm

Figure 9 Basidiomata of *Tubulicrinis sinensis* (CLZhao 42810, holotype)

Figure 10 Sections of hymenium of *Tubulicrinis sinensis* (CLZhao 42810, holotype). **a1–a10** Basidiospores. **b** Lyocystidia. **c1-c5** Basidia and basidioles. **d** Generative hyphae. Scale bars: **a–d** = 10 µm; 10×100 oil

Figure 11 Microscopic structures of *Tubulicrinis sinensis* (CLZhao 42810, holotype). **a** Basidiospores. **b** Basidia and basidioles. **c** Lyocystidia. **d** A section of the hymenium. Scale bars: **a–d** = 10 µm

Table 1 Loci, primers, PCR amplification procedures, and references used in this study

Name	Abbreviation	Primers	Direction	Sequence (5′-3′)	PCR amplification procedures	References
Internal transcribed spacer region of the rDNA	ITS	ITS5	Forward	GGAAGTAAAAGTCGTAACAAGG	94 °C 3 min; 35 cycles of 94 °C 30s, 56 °C 30 s, 72 °C 1 min; 72 °C 10 min.	White et al. (1990)
		ITS4	Reverse	TCCTCCGCTTATTGATATGC		
Nuclear large subunit ribosomal	nLSU	LR0R	Forward	ACCCGCTGAACTTAAGC	94 °C 1.5 min; 35 cycles of 94 °C 20 s, 48 °C 1.5 min, 72 °C 1.5 min; 72 °C 5 min.	Vilgalys and Hester (1990)
		LR7	Reverse	TACTACCACCAAGATCT		
Translation elongation factor 1-α	*tef1-α*	EF1-983F	Forward	GCYCCYGGHCAYCGTGAYTTYAT	94 °C 1 min; 35 cycles of 94 °C 30 s, 59 °C 1 min, 72 °C 1.5 min; 72 °C 10 min.	Rehner and Buckley (2005)
		EF1-2218R	Reverse	ATGACACCRACRGCRACRGTYTG		
RNA polymerase second largest subunit	*rpb2*	RPB2-6F	Forward	TGGGGYATGGTNTGYCCYGC	94 °C 2 min; 9 cycles of 94 °C 45 s, 60 °C 45 s, 72 °C 1.5 min; 36 cycles of 94 °C 45 s, 53 °C 1 min, 72 °C 1.5 min; 72 °C 10 min.	Liu et al. (1999)
		RPB2-7cR	Reverse	CCCATRGCTTGYTTRCCCAT		

Table 2 List of species, specimens and GenBank accession numbers of sequences used in this study

— indicates data unavailability; * refers to type material (holotype); Newly generated sequences are in bold

Order	Family	Species Name	Sample No.	GenBank Accession No.				Country	References
				ITS	nLSU	*tef1-α*	*rpb2*		
Boletales	*Gyroporaceae*	*Gyroporus castaneus*	JMP 0028	EU819468	EU819468	—	—	USA	Palmer et al. (2008)
Hymenochaetales	*Coltriciaceae*	*Coltricia abieticola*	Cui 10321	KX364785	KX364804	KY693911	KX364876	China	Bian and Dai (2017)
Hymenochaetales	*Coltriciaceae*	*Coltricia wenshanensis*	Dai 15585*	KX364798	KX364818	KY693952	KX364910	China	Bian and Dai (2017)
Hymenochaetales	*Hymenochaetaceae*	*Flaviporellus splitgerberi*	JV 1908/6	MZ484525	MZ437386	—	—	French Guiana	Wu et al. (2022)
Hymenochaetales	*Hymenochaetaceae*	*Fomitiporella vietnamensis*	Dai 18377*	NR_158436	NG_060441	—	—	Vietnam	Zhang et al. (2025)
Hymenochaetales	*Hymenochaetaceae*	*Fomitiporia langloisii*	MUCL 46375	EF429242	EF429225	GU461908	JQ087980	USA	Decock et al. (2007)
Hymenochaetales	*Hymenochaetaceae*	*Fuscoporia torulosa*	CLZhao 18735	PV802412	—	—	—	China	Present study
Hymenochaetales	*Hymenochaetaceae*	*Fuscoporia torulosa*	CLZhao 18788	PV802413	—	—	—	China	Present study
Hymenochaetales	*Hymenochaetaceae*	*Fuscoporia torulosa*	CLZhao 18915	PV802414	—	—	—	China	Present study
Hymenochaetales	*Hymenochaetaceae*	*Fuscoporia torulosa*	CLZhao 18916	PV802415	—	—	—	China	Present study
Hymenochaetales	*Hymenochaetaceae*	*Hymenochaete innexa*	CLZhao 18744	PV802416	—	—	—	China	Present study

Order	Family	Species Name	Sample No.	GenBank Accession No.				Country	References
				ITS	nLSU	*tef1-α*	*rpb2*		
Hymenochaetales	*Hymenochaetaceae*	*Hymenochaete innexa*	CLZhao 18752	PV802417	—	—	—	China	Present study
Hymenochaetales	*Hymenochaetaceae*	*Hymenochaete vitellina*	CLZhao 17846	OR659000	—	—	—	China	Present study
Hymenochaetales	*Hymenochaetaceae*	*Hymenochaete rubiginosa*	He 1049	JQ716407	JQ279667	—	—	China	Zhang et al. (2025)
Hymenochaetales	*Hymenochaetaceae*	*Inonotus henanensis*	Dai 13157*	KP030783	KX832918	—	—	China	Zhang et al. (2025)
Hymenochaetales	*Hymenochaetaceae*	*Meganotus everhartii*	JV 0108/30	MZ484529	MZ437388	—	—	USA	Unpublished
Hymenochaetales	*Hymenochaetaceae*	*Neomensularia duplicata*	LWZ 20150529-4	KX078217	KX078221	—	—	China	Zhang et al. (2025)
Hymenochaetales	*Hymenochaetaceae*	*Neophellinus uncisetus*	MUCL 47061	GU461972	GU462000	GU461938	JQ088021	Argentina	Amalfi et al. (2010)
Hymenochaetales	*Hymenochaetaceae*	*Nothophellinus andinopatagonicus*	JV 1911/20	MZ484532	MZ437391	—	—	Chile	Wu et al. (2022)
Hymenochaetales	*Hymenochaetaceae*	*Perenninotus shoreicola*	Dai 13614	KJ575522	KT749416	—	—	Thailand	Wu et al. (2022)
Hymenochaetales	*Hymenochaetaceae*	*Phylloporia perangusta*	Dai 18139	MH151169	MG738803	MH167413	MH161204	China	Wu et al. (2022)
Hymenochaetales	*Hymenochaetaceae*	*Phellinopsis conchata*	L-7601	KU139188	KU139257	KU139377	KU139315	USA	Brazee (2015)
Hymenochaetales	*Hymenochaetaceae*	*Pseudoinonotus dryadeus*	JV 1907/7	MZ484540	MZ437400	—	—	Czechia	Wu et al. (2022)
Hymenochaetales	*Hymenochaetaceae*	*Porodaedalea pini*	No-6170-T	JX110037	JX110081	JX109993	JX109951	Portugal	Brazee and Lindner (2013)

Order	Family	Species Name	Sample No.	GenBank Accession No.				Country	References
				ITS	nLSU	*tef1-α*	*rpb2*		
Hymenochaetales	*Hymenochaetaceae*	*Sanghuangporus zonatus*	Dai 10841	OP962417	KP030775	—	—	China	Wu et al. (2022)
Hymenochaetales	*Hirschioporaceae*	*Hirschioporus acontextus*	Dai 23793*	OQ449141	OQ449200	OQ831439	—	China	Zhou et al. (2023)
Hymenochaetales	*Hirschioporaceae*	*Hirschioporus tianschanicus*	Dai 19067*	OQ448960	OQ449067	OQ857947	—	China	Zhou et al. (2023)
Hymenochaetales	*Hirschioporaceae*	*Nigrohirschioporus sector*	AS 2707	OQ437344	OQ438025	—	—	Brazil	Zhou et al. (2023)
Hymenochaetales	*Hirschioporaceae*	*Pallidohirschioporus biformis*	Dai 12746	OQ453311	OQ453538	OQ874735	—	USA	Zhou et al. (2023)
Hymenochaetales	*Nigrofomitaceae*	*Nigrofomes melanoporus*	JV 1704/ 39	MF629835	MF629831	—	—	Costa Rica	Zhou et al. (2023)
Hymenochaetales	*Nigrofomitaceae*	*Nigrofomes sinomelanoporus*	Cui 5277	MF629836	MT319398	—	—	China	Zhou et al. (2023)
Hymenochaetales	*Neoantrodiellaceae*	*Neoantrodiella gypsea*	Cui 10372	KT203290	MT319396	—	KT210367	China	Zhou et al. (2023)
Hymenochaetales	*Neoantrodiellaceae*	*Neoantrodiella thujae*	Dai 5065	KT203293	MT319397	—	—	China	Zhou et al. (2023)
Hymenochaetales	*Odonticiaceae*	*Leifia brevispora*	LWZ 20170820-46*	MK343469	MK343473	—	—	China	Zhang et al. (2025)
Hymenochaetales	*Odonticiaceae*	*Odonticium romellii*	KHL s. n. (GB)	DQ873639	DQ873639	—	—	Norway	Larsson et al. (2006)
Hymenochaetales	*Peniophorellaceae*	*Peniophorella aspersa*	CLZhao 18055	PV802477	—	—	—	China	Present study
Hymenochaetales	*Peniophorellaceae*	*Peniophorella aspersa*	CLZhao 18184	PV802478	—	—	—	China	Present study

Order	Family	Species Name	Sample No.	GenBank Accession No.				Country	References
				ITS	**nLSU**	***tef1-α***	***rpb2***		
Hymenochaetales	*Peniophorellaceae*	*Peniophorella aspersa*	CLZhao 18663	PV802479	—	—	—	China	Present study
Hymenochaetales	*Peniophorellaceae*	*Peniophorella aspersa*	CLZhao 18848	PV802480	—	—	—	China	Present study
Hymenochaetales	*Peniophorellaceae*	*Peniophorella cremea*	CLZhao 19034	PV802481	—	—	—	China	Present study
Hymenochaetales	*Peniophorellaceae*	*Peniophorella fissurata*	CLZhao 17871	PV802482	—	—	—	China	Present study
Hymenochaetales	*Peniophorellaceae*	*Peniophorella fissurata*	CLZhao 18247	PV802483	—	—	—	China	Present study
Hymenochaetales	*Peniophorellaceae*	*Peniophorella pertenuis*	CLZhao 18986	PV802484	—	—	—	China	Present study
Hymenochaetales	*Peniophorellaceae*	*Peniophorella praetermissa*	CLZhao 17985	PV802485	—	—	—	China	Present study
Hymenochaetales	*Peniophorellaceae*	*Peniophorella pubera*	LWZ 20210624-16b	ON063687	ON063887	—	—	China	Wang et al. (2023)
Hymenochaetales	*Peniophorellaceae*	*Peniophorella pubera*	CLZhao 18760	PV802486	—	—	—	China	Present study
Hymenochaetales	*Peniophorellaceae*	*Peniophorella pubera*	CLZhao 18822	PV802487	—	—	—	China	Present study
Hymenochaetales	*Peniophorellaceae*	*Peniophorella pubera*	CLZhao 18871	PV802488	—	—	—	China	Present study
Hymenochaetales	*Peniophorellaceae*	*Peniophorella pubera*	CLZhao 18895	PV802489	—	—	—	China	Present study
Hymenochaetales	*Peniophorellaceae*	*Peniophorella reticulata*	F22559*	NR172776	NG073752	—	—	China	Yurchenko et al. (2020b)

Order	Family	Species Name	Sample No.	GenBank Accession No.				Country	References
				ITS	nLSU	*tef1-α*	*rpb2*		
Hymenochaetales	*Peniophorellaceae*	*Peniophorella rude*	CLZhao 19040	PV802490	—	—	—	China	Present study
Hymenochaetales	*Peniophorellaceae*	*Peniophorella rude*	CLZhao 19043	PV802491	—	—	—	China	Present study
Hymenochaetales	*Podocarpioporaceae*	*Podocarpioporus podocarpi*	Dai 21986	OQ449082	OQ449023	OQ785648	—	China	Zhou et al. (2026)
Hymenochaetales	*Podocarpioporaceae*	*Podocarpioporus podocarpi*	Dai 12015	OQ449081	—	—	—	China	Zhou et al. (2026)
Hymenochaetales	*Pseudotrichaptaceae*	*Pseudotrichaptum laricinum*	Dai 19457	OQ449078	OQ449078	—	—	China	Zhou et al. (2026)
Hymenochaetales	*Pseudotrichaptaceae*	*Pseudotrichaptum laricinum*	Dai 23782	OQ449079	OQ449021	—	—	China	Zhou et al. (2026)
Hymenochaetales	*Repetobasidiacea*	*Repetobasidium conicum*	KHL 12338	DQ873647	DQ873647	—	—	USA	Larsson et al. (2006)
Hymenochaetales	*Repetobasidiacea*	*Repetobasidium mirificum*	FP-133558-sp	—	AY293208	—	—	USA	Binder et al. (2005)
Hymenochaetales	*Rigidoporaceae*	*Rigidoporus cuneatus*	Dai 7339	KT203294	KT203315	—	KT210370	China	Cho et al. (2024)
Hymenochaetales	*Rigidoporaceae*	*Rigidoporus juniperinus*	Dai 17100	OQ930261	OQ924537	—	—	Uzbekistan	Cho et al. (2024)
Hymenochaetales	*Rickenellaceae*	*Peniophorella praetermissa*	KHL 13164	DQ873597	DQ873597	—	—	Estonia	Larsson et al. (2006)
Hymenochaetales	*Rickenellaceae*	*Rickenella fibula*	HBK014	MF319082	MF318942	—	MF288866	USA	Cho et al. (2024)
Hymenochaetales	*Rickenellaceae*	*Rickenella minuta*	MES1965	MF319105	MF318963	—	MF288886	Argentina	Cho et al. (2024)

Order	Family	Species Name	Sample No.	GenBank Accession No.				Country	References
				ITS	nLSU	*tef1-α*	*rpb2*		
Hymenochaetales	*Rickenellaceae*	*Skvortzoviella lenis*	LWZ 20180921-17	MW414522	MW414468	—	—	China	Yu et al. (2021)
Hymenochaetales	*Resiniciaceae*	***Resinicium albofarinaceum***	**CLZhao 41345***	**PX890828**	**PX956420**	**PZ301865**	**PZ301331**	**China**	**Present study**
Hymenochaetales	*Resiniciaceae*	***Resinicium albofarinaceum***	**CLZhao 41425**	**PX890829**	**PX956421**	**PZ301866**	**PZ301332**	**China**	**Present study**
Hymenochaetales	*Resiniciaceae*	***Resinicium albofarinaceum***	**CLZhao 44282**	**PX890830**	**PX956422**	**—**	**—**	**China**	**Present study**
Hymenochaetales	*Resiniciaceae*	*Resinicium austroasianum*	LWZ 20171014-3	MW414503	MW414449	—	—	Malaysia	Yu et al. (2021)
Hymenochaetales	*Resiniciaceae*	*Resinicium austroasianum*	LWZ 20180518-2	MW414507	MW414453	—	—	Malaysia	Yu et al. (2021)
Hymenochaetales	*Resiniciaceae*	*Resinicium austroasianum*	LWZ 20180417-5*	MW414504	MW414450	—	—	Malaysia	Yu et al. (2021)
Hymenochaetales	*Resiniciaceae*	*Resinicium bicolor*	O.Miettinen 14049	MF319079	MF319009	—	—	Finland	Yu et al. (2021)
Hymenochaetales	*Resiniciaceae*	*Resinicium bicolor*	TENN57741	AF518763	—	—	—	Germany	Krüger (2002)
Hymenochaetales	*Resiniciaceae*	*Resinicium bicolor*	GEL2071	DQ340321	—	—	—	Germany	Yu et al. (2021)
Hymenochaetales	*Resiniciaceae*	*Resinicium bicolor*	AFTOL-810	DQ218310	AF393061	DQ061277	DQ457635	USA	Cho et al. (2024)
Hymenochaetales	*Resiniciaceae*	*Resinicium confertum*	FP-102863*	DQ826538	—	—	—	USA	Nakasone (2007)
Hymenochaetales	*Resiniciaceae*	*Resinicium friabile*	CBS 126043	MH864058	MH875513	—	—	New Zealand	Vu et al. (2019)

Order	Family	Species Name	Sample No.	GenBank Accession No.				Country	References
				ITS	nLSU	*tef1-α*	*rpb2*		
Hymenochaetales	*Resiniciaceae*	*Resinicium friabile*	LWZ 20210923-23a	ON063692	ON427362	—	—	China	Wang et al. (2023)
Hymenochaetales	*Resiniciaceae*	*Resinicium grandisporum*	GGGUY13-008*	KY995325	—	—	—	French Guiana	Gruhn et al. (2017)
Hymenochaetales	*Resiniciaceae*	*Resinicium grandisporum*	GGGUY13-031	KY995327	—	—	—	French Guiana	Gruhn et al. (2017)
Hymenochaetales	*Resiniciaceae*	*Resinicium lateastrocystidium*	LWZ 20180414-13	MW414508	MW414454	—	—	Malaysia	Yu et al. (2021)
Hymenochaetales	*Resiniciaceae*	*Resinicium lateastrocystidium*	LWZ 20180416-10	MW414510	MW414456	—	—	Malaysia	Yu et al. (2021)
Hymenochaetales	*Resiniciaceae*	*Resinicium lateastrocystidium*	LWZ 20180414-15*	MW414509	MW414455	—	—	Malaysia	Yu et al. (2021)
Hymenochaetales	*Resiniciaceae*	*Resinicium monticola*	FP-150360*	DQ826552	DQ863697	—	—	Jamaica	Nakasone (2007)
Hymenochaetales	*Resiniciaceae*	*Resinicium monticola*	FP-150407	DQ826554	—	—	—	Jamaica	Nakasone (2007)
Hymenochaetales	*Resiniciaceae*	*Resinicium monticola*	FP-150332	DQ826555	—	—	—	Jamaica	Nakasone (2007)
Hymenochaetales	*Resiniciaceae*	*Resinicium mutabile*	FP-102989*	DQ826556	DQ863699	—	—	Puerto Rico	Nakasone (2007)
Hymenochaetales	*Resiniciaceae*	*Resinicium mutabile*	PR-1366	DQ826557	—	—	—	Puerto Rico	Nakasone (2007)
Hymenochaetales	*Resiniciaceae*	*Resinicium rimulosum*	FP-150328*	DQ826546	—	—	—	Jamaica	Nakasone (2007)
Hymenochaetales	*Resiniciaceae*	*Resinicium rimulosum*	KUC20131022-12	KJ668464	KJ668315	—	—	South Korea	Yu et al. (2021)

Order	Family	Species Name	Sample No.	GenBank Accession No.				Country	References
				ITS	nLSU	*tef1-α*	*rpb2*		
Hymenochaetales	*Resiniciaceae*	*Resinicium rimulosum*	CLZhao 17844	PV818519	—	—	—	China	Present study
Hymenochaetales	*Resiniciaceae*	*Resinicium rimulosum*	CLZhao 17847	PV818520	—	—	—	China	Present study
Hymenochaetales	*Resiniciaceae*	*Resinicium rimulosum*	CLZhao 18303	PV818521	—	—	—	China	Present study
Hymenochaetales	*Resiniciaceae*	*Resinicium saccharicola*	GGMAR12-230	KY995328	—	—	—	Martinique	Gruhn et al. (2017)
Hymenochaetales	*Resiniciaceae*	*Resinicium saccharicola*	FP-102754	DQ826547	DQ863691	—	—	Puerto Rico	Nakasone (2007)
Hymenochaetales	*Resiniciaceae*	*Resinicium saccharicola*	FP-102841	DQ826548	—	—	—	Puerto Rico	Nakasone (2007)
Hymenochaetales	*Resiniciaceae*	*Resinicium tenue*	FP-150354*	DQ826539	—	—	—	Jamaica	Nakasone (2007)
Hymenochaetales	*Resiniciaceae*	*Resinicium tenue*	FP-150251	DQ826540	—	—	—	Jamaica	Nakasone (2007)
Hymenochaetales	*Resiniciaceae*	*Resinicium yunnanense*	CLZhao 18543*	MZ810958	—	—	—	China	Cai et al. (2023)
Hymenochaetales	*Resiniciaceae*	*Resinicium yunnanense*	CLZhao 17889	MZ810959	—	—	—	China	Cai et al. (2023)
Hymenochaetales	*Resiniciaceae*	*Resinicium yunnanense*	CLZhao 18543	NR198154	—	—	—	China	Present study
Hymenochaetales	*Resiniciaceae*	*Resinicium yunnanense*	CLZhao 17889	MZ810959	—	—	—	China	Present study
Hymenochaetales	*Schizoporaceae*	*Fasciodontia brasiliensis*	MSK-F 7245a*	MK575201	MK598734	—	—	Brazil	Yurchenko et al. (2020a)

Order	Family	Species Name	Sample No.	GenBank Accession No.				Country	References
				ITS	nLSU	*tef1-α*	*rpb2*		
Hymenochaetales	*Schizoporaceae*	*Fasciodontia bugellensis*	KAS-FD 10705a	MK575203	MK598735	—	—	France	Yurchenko et al. (2020a)
Hymenochaetales	*Schizoporaceae*	*Fasciodontia yunnanensis*	CLZhao 6280	MK811275	MZ146327	—	—	China	Luo and Zhao (2021)
Hymenochaetales	*Schizoporaceae*	*Fibrodontia austrosinensis*	CLZhao 18217	PV802406	—	—	—	China	Present study
Hymenochaetales	*Schizoporaceae*	*Fibrodontia austrosinensis*	CLZhao 18340	PV802407	—	—	—	China	Present study
Hymenochaetales	*Schizoporaceae*	*Fibrodontia austrosinensis*	CLZhao 18393	PV802408	—	—	—	China	Present study
Hymenochaetales	*Schizoporaceae*	*Fibrodontia austrosinensis*	CLZhao 18408	PV802409	—	—	—	China	Present study
Hymenochaetales	*Schizoporaceae*	*Fibrodontia austrosinensis*	CLZhao 18448	PV802410	—	—	—	China	Present study
Hymenochaetales	*Schizoporaceae*	*Fibrodontia austrosinensis*	CLZhao 18467	PV802411	—	—	—	China	Present study
Hymenochaetales	*Schizoporaceae*	*Lyomyces cremeus*	CLZhao 18132	PV802457	—	—	—	China	Present study
Hymenochaetales	*Schizoporaceae*	*Lyomyces cremeus*	CLZhao 18181	PV802458	—	—	—	China	Present study
Hymenochaetales	*Schizoporaceae*	*Lyomyces crustosus*	CLZhao 18102	PV802459	—	—	—	China	Present study
Hymenochaetales	*Schizoporaceae*	*Lyomyces crustosus*	CLZhao 18161	PV802460	—	—	—	China	Present study
Hymenochaetales	*Schizoporaceae*	*Lyomyces crustosus*	CLZhao 18195	PV802461	—	—	—	China	Present study

Order	Family	Species Name	Sample No.	GenBank Accession No.				Country	References
				ITS	nLSU	***tef1-α***	***rpb2***		
Hymenochaetales	*Schizoporaceae*	*Lyomyces crustosus*	CLZhao 18429	PV865550	—	—	—	China	Present study
Hymenochaetales	*Schizoporaceae*	*Lyomyces crustosus*	CLZhao 19049	PV865551	—	—	—	China	Present study
Hymenochaetales	*Schizoporaceae*	*Lyomyces fissuratus*	CLZhao 18368	PV802462	—	—	—	China	Present study
Hymenochaetales	*Schizoporaceae*	*Lyomyces fumosus*	CLZhao 17855	PV802463	—	—	—	China	Present study
Hymenochaetales	*Schizoporaceae*	*Lyomyces leptocystidiatus*	LWZ 20170814-14*	MT319429	MT319163	MT326395	MT326256	China	Wang et al. (2021)
Hymenochaetales	*Schizoporaceae*	*Lyomyces microfasciculatus*	CLZhao 17651	PV802464	—	—	—	China	Present study
Hymenochaetales	*Schizoporaceae*	*Lyomyces microfasciculatus*	CLZhao 17679	PV802465	—	—	—	China	Present study
Hymenochaetales	*Schizoporaceae*	*Lyomyces microfasciculatus*	CLZhao 17735	PV802466	—	—	—	China	Present study
Hymenochaetales	*Schizoporaceae*	*Lyomyces microfasciculatus*	CLZhao 17921	PV802467	—	—	—	China	Present study
Hymenochaetales	*Schizoporaceae*	*Lyomyces microfasciculatus*	CLZhao 18127	PV802468	—	—	—	China	Present study
Hymenochaetales	*Schizoporaceae*	*Lyomyces microfasciculatus*	CLZhao 18447	PV802469	—	—	—	China	Present study
Hymenochaetales	*Schizoporaceae*	*Lyomyces microfasciculatus*	CLZhao 19052	PV802470	—	—	—	China	Present study
Hymenochaetales	*Schizoporaceae*	*Lyomyces orientalis*	CLZhao 18919	PV802471	—	—	—	China	Present study

Order	Family	Species Name	Sample No.	GenBank Accession No.				Country	References
				ITS	nLSU	*tef1-α*	*rpb2*		
Hymenochaetales	*Schizoporaceae*	*Lyomyces orientalis*	CLZhao 18942	PV802472	—	—	—	China	Present study
Hymenochaetales	*Schizoporaceae*	*Lyomyces orientalis*	CLZhao 18979	PV802473	—	—	—	China	Present study
Hymenochaetales	*Schizoporaceae*	*Lyomyces orientalis*	CLZhao 19033	PV802474	—	—	—	China	Present study
Hymenochaetales	*Schizoporaceae*	*Lyomyces orientalis*	CLZhao 19044	PV802475	—	—	—	China	Present study
Hymenochaetales	*Schizoporaceae*	*Lyomyces orientalis*	CLZhao 19053	PV802476	—	—	—	China	Present study
Hymenochaetales	*Schizoporaceae*	*Lyomyces juniperi*	CLZhao 18151	PV865305	—	—	—	China	Present study
Hymenochaetales	*Schizoporaceae*	*Lyomyces sambuci*	LWZ 20180905-1	MT319444	MT319178	—	—	China	Wang et al. (2021)
Hymenochaetales	*Schizoporaceae*	*Xylodon daweishanensis*	CLZhao 18357	OP730715	—	—	—	China	Present study
Hymenochaetales	*Schizoporaceae*	*Xylodon daweishanensis*	CLZhao 18425	OP730716	—	—	—	China	Present study
Hymenochaetales	*Schizoporaceae*	*Xylodon fissilis*	CLZhao 18750	OR096212	—	—	—	China	Present study
Hymenochaetales	*Schizoporaceae*	*Xylodon fissilis*	CLZhao 18740*	OR096211	OR449945	—	OR722809	China	Dong et al. (2024)
Hymenochaetales	*Schizoporaceae*	*Xylodon heterocystidiatus*	CLZhao 17792	PV818524	—	—	—	China	Present study
Hymenochaetales	*Schizoporaceae*	*Xylodon heterocystidiatus*	CLZhao 17960	PV818525	—	—	—	China	Present study

Order	Family	Species Name	Sample No.	GenBank Accession No.				Country	References
				ITS	nLSU	*tef1-α*	*rpb2*		
Hymenochaetales	*Schizoporaceae*	*Xylodon heterocystidiatus*	CLZhao 17982	PV818526	—	—	—	China	Present study
Hymenochaetales	*Schizoporaceae*	*Xylodon heterocystidiatus*	CLZhao 18031	PV818527	—	—	—	China	Present study
Hymenochaetales	*Schizoporaceae*	*Xylodon heterocystidiatus*	CLZhao 18037	PV818528	—	—	—	China	Present study
Hymenochaetales	*Schizoporaceae*	*Xylodon heterocystidiatus*	CLZhao 18038	PV818529	—	—	—	China	Present study
Hymenochaetales	*Schizoporaceae*	*Xylodon heterocystidiatus*	CLZhao 18081	PV818530	—	—	—	China	Present study
Hymenochaetales	*Schizoporaceae*	*Xylodon heterocystidiatus*	CLZhao 18110	PV818531	—	—	—	China	Present study
Hymenochaetales	*Schizoporaceae*	*Xylodon heterocystidiatus*	CLZhao 18135	PV818532	—	—	—	China	Present study
Hymenochaetales	*Schizoporaceae*	*Xylodon heterocystidiatus*	CLZhao 18198	PV818533	—	—	—	China	Present study
Hymenochaetales	*Schizoporaceae*	*Xylodon heterocystidiatus*	CLZhao 18274	PV818534	—	—	—	China	Present study
Hymenochaetales	*Schizoporaceae*	*Xylodon heterocystidiatus*	CLZhao 18280	PV818535	—	—	—	China	Present study
Hymenochaetales	*Schizoporaceae*	*Xylodon heterocystidiatus*	CLZhao 18451	PV818536	—	—	—	China	Present study
Hymenochaetales	*Schizoporaceae*	*Xylodon heterocystidiatus*	CLZhao 18524	PV818537	—	—	—	China	Present study
Hymenochaetales	*Schizoporaceae*	*Xylodon heterocystidiatus*	CLZhao 18540	PV818538	—	—	—	China	Present study

Order	Family	Species Name	Sample No.	GenBank Accession No.				Country	References
				ITS	nLSU	*tef1-α*	*rpb2*		
Hymenochaetales	*Schizoporaceae*	*Xylodon heterocystidiatus*	CLZhao 18672	PV818539	—	—	—	China	Present study
Hymenochaetales	*Schizoporaceae*	*Xylodon hydnoidus*	CLZhao 18239	OR096205	—	—	—	China	Present study
Hymenochaetales	*Schizoporaceae*	*Xylodon laceratus*	CLZhao 18888	PV818540	—	—	—	China	Present study
Hymenochaetales	*Schizoporaceae*	*Xylodon luteodontioides*	CLZhao 18494	PP505422	—	—	—	China	Present study
Hymenochaetales	*Schizoporaceae*	*Xylodon luteodontioides*	CLZhao 17828	PV818541	—	—	—	China	Present study
Hymenochaetales	*Schizoporaceae*	*Xylodon luteodontioides*	CLZhao 17899	PV818542	—	—	—	China	Present study
Hymenochaetales	*Schizoporaceae*	*Xylodon luteodontioides*	CLZhao 18136	PV818543	—	—	—	China	Present study
Hymenochaetales	*Schizoporaceae*	*Xylodon luteodontioides*	CLZhao 18291	PV818544	—	—	—	China	Present study
Hymenochaetales	*Schizoporaceae*	*Xylodon luteodontioides*	CLZhao 18872	PV818545	—	—	—	China	Present study
Hymenochaetales	*Schizoporaceae*	*Xylodon luteodontioides*	CLZhao 18875	PV818546	—	—	—	China	Present study
Hymenochaetales	*Schizoporaceae*	*Xylodon luteodontioides*	CLZhao 18981	PV818547	—	—	—	China	Present study
Hymenochaetales	*Schizoporaceae*	*Xylodon luteodontioides*	CLZhao 19080	PV818548	—	—	—	China	Present study
Hymenochaetales	*Schizoporaceae*	*Xylodon montanus*	CLZhao 18370	PV818549	—	—	—	China	Present study

Order	Family	Species Name	Sample No.	GenBank Accession No.				Country	References
				ITS	nLSU	*tef1-α*	*rpb2*		
Hymenochaetales	*Schizoporaceae*	*Xylodon montanus*	CLZhao 18376	PV818550	—	—	—	China	Present study
Hymenochaetales	*Schizoporaceae*	*Xylodon montanus*	CLZhao 18383	PV818551	—	—	—	China	Present study
Hymenochaetales	*Schizoporaceae*	*Xylodon montanus*	CLZhao 18414	PV818552	—	—	—	China	Present study
Hymenochaetales	*Schizoporaceae*	*Xylodon montanus*	CLZhao 18660	PV818553	—	—	—	China	Present study
Hymenochaetales	*Schizoporaceae*	*Xylodon montanus*	CLZhao 19026	PV818554	—	—	—	China	Present study
Hymenochaetales	*Schizoporaceae*	*Xylodon montanus*	CLZhao 19071	PV818555	—	—	—	China	Present study
Hymenochaetales	*Schizoporaceae*	*Xylodon nesporii*	CLZhao 18042	PV818556	—	—	—	China	Present study
Hymenochaetales	*Schizoporaceae*	*Xylodon nesporii*	CLZhao 19084	PV818557	—	—	—	China	Present study
Hymenochaetales	*Schizoporaceae*	*Xylodon olivaceobubalinus*	CLZhao 25174*	OR167772	OR449948	—	OR722812	China	Dong et al. (2024)
Hymenochaetales	*Schizoporaceae*	*Xylodon quercinus*	Spirin 12030*	OK273841	OK273841	OQ776824	OQ776901	Russia	Viner et al. (2018)
Hymenochaetales	*Schizoporaceae*	*Xylodon reticulatus*	CLZhao 17728	PV818558	—	—	—	China	Present study
Hymenochaetales	*Schizoporaceae*	*Xylodon reticulatus*	CLZhao 18284	PV818559	—	—	—	China	Present study
Hymenochaetales	*Schizoporaceae*	*Xylodon reticulatus*	CLZhao 18298	PV818560	—	—	—	China	Present study

Order	Family	Species Name	Sample No.	GenBank Accession No.				Country	References
				ITS	nLSU	*tef1-α*	*rpb2*		
Hymenochaetales	*Schizoporaceae*	*Xylodon reticulatus*	CLZhao 18779	PV818561	—	—	—	China	Present study
Hymenochaetales	*Schizoporaceae*	*Xylodon reticulatus*	CLZhao 18901	PV818562	—	—	—	China	Present study
Hymenochaetales	*Schizoporaceae*	*Xylodon reticulatus*	CLZhao 18931	PV818563	—	—	—	China	Present study
Hymenochaetales	*Schizoporaceae*	*Xylodon reticulatus*	CLZhao 18934	PV818564	—	—	—	China	Present study
Hymenochaetales	*Schizoporaceae*	*Xylodon reticulatus*	CLZhao 18953	PV818565	—	—	—	China	Present study
Hymenochaetales	*Schizoporaceae*	*Xylodon reticulatus*	CLZhao 18967	PV818566	—	—	—	China	Present study
Hymenochaetales	*Schizoporaceae*	*Xylodon reticulatus*	CLZhao 18990	PV818567	—	—	—	China	Present study
Hymenochaetales	*Schizoporaceae*	*Xylodon rhizomorphus*	CLZhao 18602	PV818568	—	—	—	China	Present study
Hymenochaetales	*Schizoporaceae*	*Xylodon rhizomorphus*	CLZhao 19003	PV818569	—	—	—	China	Present study
Hymenochaetales	*Schizoporaceae*	*Xylodon serpentiformis*	CLZhao 17670	PV818570	—	—	—	China	Present study
Hymenochaetales	*Schizoporaceae*	*Xylodon serpentiformis*	CLZhao 17671	PV818571	—	—	—	China	Present study
Hymenochaetales	*Schizoporaceae*	*Xylodon serpentiformis*	CLZhao 17719	PV818572	—	—	—	China	Present study
Hymenochaetales	*Schizoporaceae*	*Xylodon serpentiformis*	CLZhao 17998	PV818573	—	—	—	China	Present study

Order	Family	Species Name	Sample No.	GenBank Accession No.				Country	References
				ITS	nLSU	*tef1-α*	*rpb2*		
Hymenochaetales	*Schizoporaceae*	*Xylodon serpentiformis*	CLZhao 18317	PV818574	—	—	—	China	Present study
Hymenochaetales	*Schizoporaceae*	*Xylodon serpentiformis*	CLZhao 19066	PV818575	—	—	—	China	Present study
Hymenochaetales	*Schizoporaceae*	*Xylodon wenshanensis*	CLZhao 17803	PV818576	—	—	—	China	Present study
Hymenochaetales	*Schizoporaceae*	*Xylodon wenshanensis*	CLZhao 17944	PV818577	—	—	—	China	Present study
Hymenochaetales	*Schizocorticiaceae*	*Schizocorticium magnosporum*	Wu 1510-34*	MK405351	MK405337	—	—	China	Wu et al. (2021)
Hymenochaetales	*Schizocorticiaceae*	*Schizocorticium mediosporum*	Chen 2456*	MK405359	MK405345	—	—	China	Wu et al. (2021)
Hymenochaetales	*Sideraceae*	*Sidera tibetica*	Dai 23648*	NR_177641	OM974245	—	—	China	Zhang et al. (2025)
Hymenochaetales	*Sideraceae*	*Sidera vesiculosa*	BJFC 025377*	NR_164588	NG066418	—	—	Singapore	Cho et al. (2024)
Hymenochaetales	*Skvortzoviaceae*	*Skvortzovia dabieshanensis*	LWZ 20201012-22*	NR_173964	NG_088189	—	—	China	Yu et al. (2021)
Hymenochaetales	*Skvortzoviaceae*	*Skvortzovia yunnanensis*	CLZhao 16084	MW472754	MW473473	—	ON100725	China	Dong et al. (2021)
Hymenochaetales	*Trichaptaceae*	*Trichaptum abietinum*	CLZhao 17706	PV818522	—	—	—	China	Present study
Hymenochaetales	*Trichaptaceae*	*Trichaptum abietinum*	CLZhao 17710	PV818523	—	—	—	China	Present study

Order	Family	Species Name	Sample No.	GenBank Accession No.				Country	References
				ITS	nLSU	*tef1-α*	*rpb2*		
Hymenochaetales	*Trichaptaceae*	*Trichaptum byssogenum*	Dai 15555	OQ449085	OQ449026	OQ874771	—	China	Cho et al. (2024)
Hymenochaetales	*Trichaptaceae*	*Trichaptum perrottetii*	JV 1908/45	OQ449092	OQ449031	OQ874776	—	French Guiana	Cho et al. (2024)
Hymenochaetales	*Tubulicrinaceae*	*Tubulicrinis accedens*	ACD0414	OL756001	OL742444	—	—	USA	Unpublished
Hymenochaetales	*Tubulicrinaceae*	*Tubulicrinis albobadius*	CLZhao 26202*	PQ523361	PQ523364	—	—	China	Dai et al. (2025)
Hymenochaetales	*Tubulicrinaceae*	*Tubulicrinis albobadius*	CLZhao 26330	PQ523362	PQ523365	—	—	China	Dai et al. (2025)
Hymenochaetales	*Tubulicrinaceae*	*Tubulicrinis australis*	MA Fungi:88838	KX017591	KX017594	—	—	Chile	Crous et al. (2016)
Hymenochaetales	*Tubulicrinaceae*	*Tubulicrinis australis*	MA Fungi:88839*	KX017593	KX017596	—	—	Chile	Crous et al. (2016)
Hymenochaetales	*Tubulicrinaceae*	*Tubulicrinis borealis*	DK14_93	OL436811	—	—	—	USA	Unpublished
Hymenochaetales	*Tubulicrinaceae*	*Tubulicrinis calothrix*	LWZ 20210919-1b	ON063704	ON063904	—	—	China	Wang et al. (2023)
Hymenochaetales	*Tubulicrinaceae*	*Tubulicrinis chaetophorus*	UC2023055	KP814255	—	—	—	USA	Rosenthal et al. (2017)
Hymenochaetales	*Tubulicrinaceae*	*Tubulicrinis chaetophorus*	UC2023059	KP814233	—	—	—	USA	Rosenthal et al. (2017)
Hymenochaetales	*Tubulicrinaceae*	*Tubulicrinis glebulosus*	LWZ 20180903-13	ON063705	ON063905	—	—	China	Wang et al. (2023)

Order	Family	Species Name	Sample No.	GenBank Accession No.				Country	References
				ITS	nLSU	*tef1-α*	*rpb2*		
Hymenochaetales	*Tubulicrinaceae*	*Tubulicrinis globisporus*	KHL 12133 (GB)	DQ873655	DQ873655	—	—	Sweden	Larsson et al. (2006)
Hymenochaetales	*Tubulicrinaceae*	*Tubulicrinis gracillimus*	PDD 95851	HQ533047	—	—	—	New Zealand	Unpublished
Hymenochaetales	*Tubulicrinaceae*	*Tubulicrinis hirtellus*	KHL 11717 (GB)	DQ873657	DQ873657	—	—	Sweden	Larsson et al. (2006)
Hymenochaetales	*Tubulicrinaceae*	*Tubulicrinis hongheensis*	CLZhao 19006*	PV705579	PV705582	—	—	China	Yuan et al. (2026)
Hymenochaetales	*Tubulicrinaceae*	*Tubulicrinis hongheensis*	CLZhao 2574	PV705578	—	—	—	China	Yuan et al. (2026)
Hymenochaetales	*Tubulicrinaceae*	*Tubulicrinis incanus*	HMZhou 407*	PV475576	PV646278	PX692502	—	China	Wang et al. (2026)
Hymenochaetales	*Tubulicrinaceae*	*Tubulicrinis inornatus*	KHL 11763 (GB)	DQ873659	DQ873659	—	—	Sweden	Larsson et al. (2006)
Hymenochaetales	*Tubulicrinaceae*	*Tubulicrinis martinicensis*	GG-MAR12-206*	NR_163282	—	—	—	Martinique	Gruhn et al. (2016)
Hymenochaetales	*Tubulicrinaceae*	*Tubulicrinis pini*	CLZhao 6881*	OR096210	OR449952	OR541911	—	China	Dong et al. (2024)
Hymenochaetales	*Tubulicrinaceae*	*Tubulicrinis pini*	CLZhao 3679	—	OR449951	—	—	China	Dong et al. (2024)
Hymenochaetales	*Tubulicrinaceae*	***Tubulicrinis sinensis***	**CLZhao 42810***	**PX890831**	**PX956423**	—	—	**China**	**Present study**
Hymenochaetales	*Tubulicrinaceae*	***Tubulicrinis sinensis***	**CLZhao 48982**	**PX890832**	—	—	—	**China**	**Present study**
Hymenochaetales	*Tubulicrinaceae*	*Tubulicrinis subulatus*	UC2023072	KP814430	—	—	—	USA	Rosenthal et al. (2017)

Order	Family	Species Name	Sample No.	GenBank Accession No.				Country	References
				ITS	nLSU	***tef1-α***	***rpb2***		
Hymenochaetales	*Tubulicrinaceae*	*Tubulicrinis subulatus*	LWZ 20190914-7	ON063706	ON063906	—	—	China	Wang et al. (2023)
Hymenochaetales	*Tubulicrinaceae*	*Tubulicrinis tenuis*	CLZhao 17221*	PV705580	PV705581	—	—	China	Yuan et al. (2026)
Hymenochaetales	*Tubulicrinaceae*	*Tubulicrinis xantha*	CLZhao 2868*	MT153874	MT153881	—	—	China	He et al. (2020)
Hymenochaetales	*Tubulicrinaceae*	*Tubulicrinis xantha*	CLZhao 2869	MT153875	MT153882	—	—	China	He et al. (2020)
Hymenochaetales	*Tubulicrinaceae*	*Tubulicrinis yunnanensis*	CLZhao 18194	PX049244	—	—	—	China	Present study
Hymenochaetales	*Tubulicrinaceae*	*Tubulicrinis yunnanensis*	CLZhao 3418	MT153879	MT153886	—	—	China	He et al. (2020)
Hymenochaetales	*Tubulicrinaceae*	*Tubulicrinis yunnanensis*	CLZhao 9717*	MT153880	MT153887	—	—	China	He et al. (2020)
Hymenochaetales	*Umbellaceae*	*Umbellus sinensis*	LWZ 20190615-27*	OR242616	OR236212	—	—	China	Wang et al. (2026)
Hymenochaetales	*Umbellaceae*	*Umbellus sinensis*	LWZ 20190615-39	OR242617	OR236213	—	—	China	Wang et al. (2026)
Polyporales	*Fomitopsidaceae*	*Antrodia subserpens*	Dai 13233	KP715309	KT968830	—	KT895889	China	Zhang et al. (2025)
Polyporales	*Polyporaceae*	*Cerioporus squamosus*	Cui 10595	KU189778	KU189809	—	—	China	Zhang et al. (2025)

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Table 3 Morphological comparison of the new species *Resinicium albofarinaceum* with its closely related species. Newly introduced taxa are indicated in bold black font.

Species name	Locality	Basidiomata	Hyphal system	Basidia	Basidiospores	References
Resinicium albofarinaceum	**China**	**Annual, resupinate, closely adnate, thin, smooth, farinaceous, white**	**Monomitic; generative hyphae with clamp connections, colorless, thin-walled**	**Subclavate, with 4 sterigmata, 11.5–17 × 4.5–6 µm**	**Ellipsoid, thin-walled, smooth, 4.3–5 × 3.2–3.8 µm, Q = 1.34–1.39**	**Present study**
Resinicium austroasianum	Malaysia	Annual, resupinate, closely adnate, widely effuse, thin, crustose, grandinioid to odontoid, pale yellow to curry-yellow, usually cracked into polygons	Monomitic; generative hyphae with clamp connections, colorless, thin-walled	Cylindrical, often with a median constriction, 4-sterigmate, 10–20 × 4–6 µm.	Ellipsoid, thin-walled, smooth, 4.5–5.1 × 3.3–4.2 µm, Q = 1.25–1.28	Yu et al. (2021)
Resinicium bicolor	Finland	Resupinate, widely effuse, adnate, thin, subceraceous or ceraceous, rarely soft, farinaceous, smooth, pale yellow, orange-white, greyish orange, pale orange, or brownish orange, with scattered cracks	Monomitic; generative hyphae regularly nodose septate, colorless, thin-walled	Clavate to cylindrical, often with a median constriction, 4-sterigmate, 15–22 × 4.5–6 µm	Cylindrical to narrowly ellipsoid, thin-walled, smooth, 5.5–7.2 × 2.9–3.5 µm, Q = 1.7–2	Yu et al. (2021)

Species name	**Locality**	**Basidiomata**	**Hyphal system**	**Basidia**	**Basidiospores**	**References**
Resinicium confertum	USA	Resupinate, effused, closely appressed, thin to thick, membranous, fragile, minutely odontoid, light orange to greyish orange	Monomitic; generative hyphae regularly nodose septate, colorless, thin-walled	Clavate, with 4 sterigmata, 10–16 × 4–4.5 µm	Ellipsoid, thin-walled, smooth, 5–6 × 3.2–3.5 µm, Q = 1.53	Nakasone (2007)
Resinicium friabile	Brazil	Resupinate, closely adnate, somewhat hard and brittle, hymenium odontoid, pale brown	Monomitic; generative hyphae with clamp connections, colorless, thin-walled or with slight wall thickening	Clavate, with 4 sterigmata, 18–20 × 4–4.5 µm	Broadly ellipsoid, thin-walled, smooth, 4.5–5 × 2.8–3 µm	Hjortstam and Melo (1997)
Resinicium grandisporum	French Guiana	Annual, resupinate, widely effused, adnate, strongly attached, hymenium odontoid, cream to dark yellowish	Monomitic; generative hyphae with clamp connections, colorless, thin-walled	Cylindrical to clavate, with granular content and 4 sterigmata, 19–22 × 6.5–7.5 µm	Ellipsoid, thick-walled, smooth, 8–9.6 × 4.3–5.5 µm, Q = 1.8	Gruhn et al. (2017)
Resinicium lateastrocystidium	Malaysia	Annual, resupinate, closely adnate, widely effuse, thin, farinaceous, grandinioid to odontoid, straw-yellow to olivaceous buff	Monomitic; generative hyphae with clamp connections, colorless, thin-walled	Cylindrical, often with a median constriction, 4-sterigmate, 13–20 × 5–6 µm	Ellipsoid, thin-walled, smooth, 4.1–5 × 2.9–3.9 µm, Q = 1.35–1.36	Yu et al. (2021)

Species name	Locality	Basidiomata	Hyphal system	Basidia	Basidiospores	References
Resinicium monticola	Jamaica	Resupinate, widely effuse, adnate, thin to moderately thick, soft to subceraceous, membranous, tuberculate to papillose, white to pale yellow, with rare cracks	Monomitic; generative hyphae regularly nodose septate, colorless, thin-walled	Cylindrical, often with a median constriction, 4-sterigmate, 16–25 × 5–6 µm	Ellipsoid, sometimes developing a short, narrow peg, thin-walled, smooth, 4.8–5.5 × 2.8–3.2 µm, Q = 1.6–1.7	Nakasone (2007)
Resinicium mutabile	Puerto Rico	Resupinate, widely effuse, adnate, thin, soft to subceraceous, odontoid to spinose, finely porose to farinaceous, mottled greyish orange to light brown, with fine cracks	Monomitic; generative hyphae regularly nodose septate, colorless, thin-walled	Clavate to cylindrical, with a median constriction, 4-sterigmate, 11–16 × 3.5–6 µm	Ellipsoid, thin-walled, smooth, 5–5.5 × 3–3.5 µm, Q = 1.42–1.65	Nakasone (2007)
Resinicium rimulosum	Jamaica	Annual, resupinate, closely appressed, widely effuse, thin, subceraceous, odontoid, white to yellowish white, reticulate to porose with numerous cracks	Monomitic; generative hyphae regularly nodose septate, colorless, thin-walled	Clavate to cylindrical, with a median constriction, 4-sterigmate, 11–22 × 4–5 µm	Ellipsoid, thin-walled, smooth, 4–4.8 × 2.8–3 µm, Q = 1.5	Nakasone (2007)

Species name	Locality	Basidiomata	Hyphal system	Basidia	Basidiospores	References
Resinicium saccharicola	Puerto Rico	Resupinate, closely adnate, thin, smooth to finely farinaceous or grandinioid, aculeate, white to yellowish grey	Monomitic; generative hyphae with simple septa and rare clamp connections, colorless, thin-walled	Short cylindrical, with 4 sterigmata, 11-20 × 4-7 µm	Ellipsoid, thin-walled, smooth, 5.5–6 × 3.5–4 µm	Nakasone (2007)
Resinicium tenue	Jamaica	Resupinate, widely effuse, adnate, thin, soft to subceraceous, odontoid to grandinioid, white to yellowish white or greyish brown, with scattered cracks	Monomitic; generative hyphae with simple septa and rare clamp connections, colorless, thin-walled	Clavate, sometimes with a short, narrow stalk, with 4 sterigmata, 16-20 × 4.5-5 µm	Ellipsoid, thin-walled, smooth, 5–6 × 3.5–4 µm, Q = 1.4–1.47	Nakasone (2007)
Resinicium yunnanense	China	Annual, resupinate, farinaceous, smooth to irregular poroid, buff to cinnamon-buff	Monomitic; generative hyphae with clamp connections, colorless, thin-walled	Clavate, with 4 sterigmata, 7-10 × 3-4.5 µm	Ellipsoid, thin-walled, smooth, 3.7–5 × 2.3–3.3 µm, Q = 1.54–1.65	Cai et al. (2023)

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Table 4 Morphological comparison of the new species *Tubulicrinis sinensis* with its closely related species. Newly introduced taxa are indicated in bold black font.

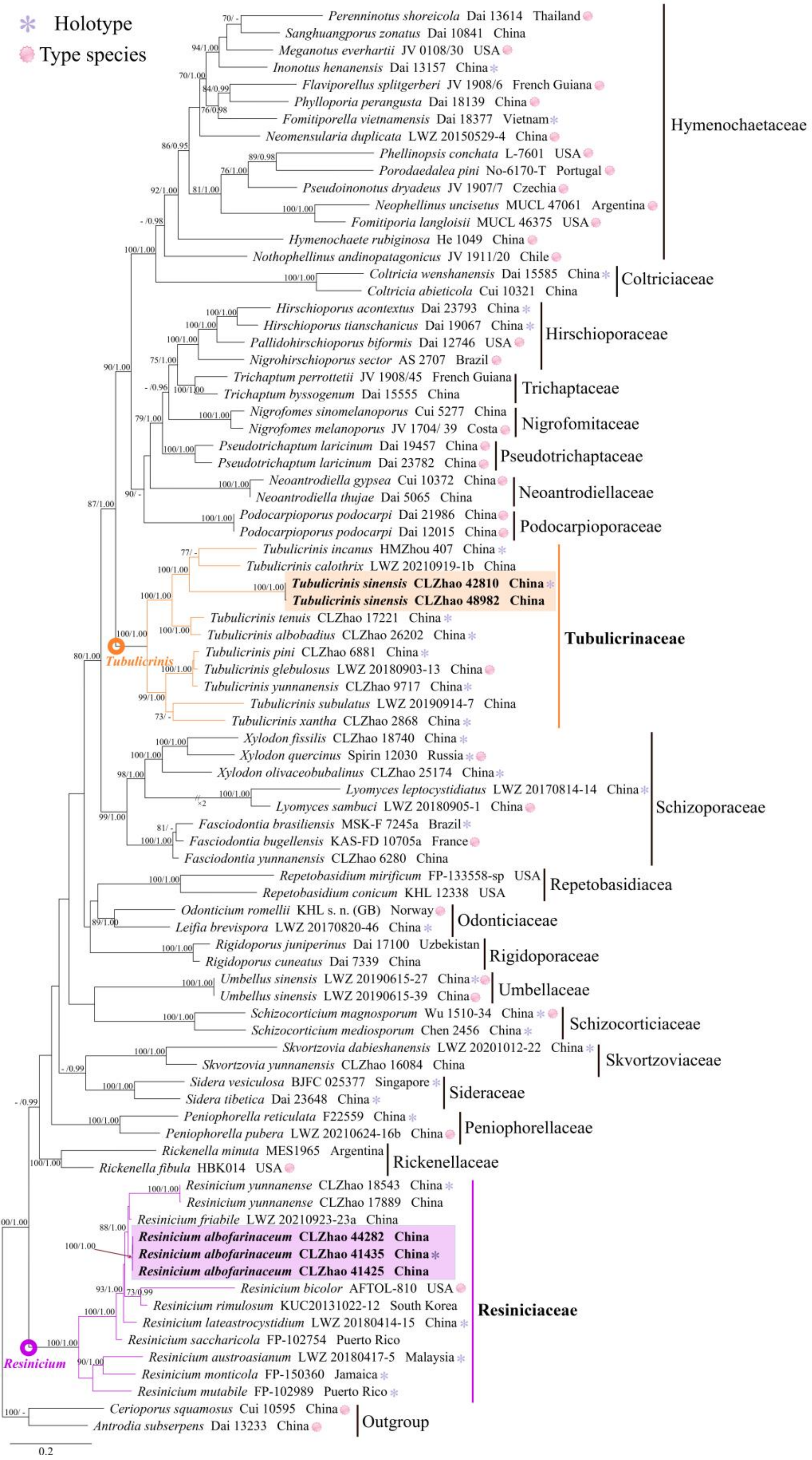
Species name	Locality	Basidiomata	Hyphal system	Basidia	Basidiospores	References
Tubulicrinis accedens	USA	Resupinate, effused, thin, smooth, white	Monomitic; generative hyphae with clamp connections, colorless, thin-walled	Subclavate to conical, with 4 sterigmata, 10–15 × 3.5–4.5 µm	Ellipsoid to broadly ellipsoid, thin-walled, smooth, 4–5 × 2.5–3.4 µm	Donk (1956)
Tubulicrinis albobadius	China	Annual, resupinate, adnate, thin, arachnoid, white to gray	Monomitic; generative hyphae with clamp connections, colorless, thick-walled	Barrel-shaped, with 4 sterigmata, 9.5–14 × 4–5 µm	Cylindrical to allantoid, thin-walled, smooth, with one or two guttate, 4–6 × 1.5–2.2 µm, Q = 2.55–2.77	Dai et al. (2025)
Tubulicrinis australis	Chile	Annual, resupinate, loosely adnate, effuse, thin, furfuraceous, porose-reticulate to tuberculate, white to cream	Monomitic; generative hyphae with clamp connections, colorless, thick-walled	Subclaviform, with 4 sterigmata, 9.5–14 × 4–5 µm	Narrowly ellipsoid, thin-walled, smooth, guttulate, 6–7.5 × 3–3.5 µm	Crous et al. (2016)
Tubulicrinis borealis	USA	Annual, resupinate, adnate, effuse, thin, smooth, reticulate to continuous, white	Monomitic; generative hyphae with clamp connections, colorless, thin- to thick-walled	Subclavate, slightly thick-walled at the basal part, with 4 sterigmata, 8–13 × 4–5 µm	Subcylindrical to allantoid, thin-walled, smooth, 5.5–6.5 × 2–2.5 µm	Eriksson (1958)

Species name	Locality	Basidiomata	Hyphal system	Basidia	Basidiospores	References
Tubulicrinis calothrix	Tunisia	Resupinate, adnate, effused, thin later thicker, smooth, farinose, reticulate or continuous, withish to pale yellow or ochraceous	Monomitic; generative hyphae with clamp connections, colorless, thin- to slightly thick-walled	Subclavate, slightly thick-walled at the basal part, with 4 sterigmata, 12–15 × 4–5 µm	Allantoid, thin-walled, smooth, 6–8 × 1.5–2 µm	Donk (1956)
Tubulicrinis chaetophorus	USA	Resupinate, effused, smooth and formed by discontinuous patches, grayish to pale ochraceous	Monomitic; generative hyphae with clamp connections, colorless, thin- to thick-walled	Cylindrical, with 4 sterigmata, 15–20 × 4.5–5 µm	Narrowly ellipsoid, thin-walled, smooth, 5.5–6.5 × 3–3.5 µm	Donk (1956)
Tubulicrinis glebulosus	Denmark	Resupinate, effused, mostly thick, smooth, floccose to granular, rimose, whitish to pale ochraceous	Monomitic; generative hyphae with clamp connections, colorless, thin- to thick-walled	Subclavate, with a median constriction, 4 sterigmata, 20–25 × 4–5 µm	Suballantoid, thin-walled, smooth, 6–9 × 1.5–2.25 µm	Donk (1956)
Tubulicrinis globisporus	Sweden	Resupinate, effused, very thin, smooth, porulose and discontinuous, whitish to greyish white	Monomitic; generative hyphae with clamp connections, colorless, thin-walled or with slight wall thickening	Subclavate, basally with slight wall thickening, forming rather loose clusters, with 4 sterigmata, 10–15 × 5–7 µm	Obliquely globose, thin-walled, smooth, 4.0-5.0 µm in diam	Hjortstam and Larsson (1978)

Species name	Locality	Basidiomata	Hyphal system	Basidia	Basidiospores	References
Tubulicrinis gracillimus	New Zealand	Resupinate, effuse, thick, minutely flocculose or granular, pale yellowish white	Monomitic; generative hyphae with clamp connections, colorless, thin- to slightly thick-walled	Narrowly clavate, slightly thick-walled at the basal part, with 4 sterigmata, 20–27 × 4–5 µm	Allantoid, thin-walled, smooth, 6.5–8 × 1.5–2 µm	Maekawa (2021)
Tubulicrinis hirtellus	Sweden	Resupinate, thin, porulose, whitish or pale to sordidly ochraceous	Monomitic; generative hyphae with clamp connections, colorless, thin-walled	Subclavate, with 4 sterigmata, 13–18 × 4–4.5 µm	Cylindrical or subfusiform, thin-walled, smooth, 7–8.5 × 2–2.5 µm	Hjortstam et al. (1988)
Tubulicrinis hongheensis	China	Annual, resupinate, adnate, cracked, coriaceous, cream to pale yellow	Monomitic; generative hyphae with clamp connections, colorless, thin to thick-walled	Clavate, with 4 sterigmata, 7.5–14.5 × 4–7 µm	Broadly ellipsoid, thin-walled, smooth, 3.6–4.1 × 3–3.5 µm, Q = 1.19–1.22	Yuan et al. (2026)
Tubulicrinis incanus	China	Annual, resupinate, closely adnate, smooth, farinaceous, white to cream	Monomitic; generative hyphae with clamp connections, colorless, thin-walled	Clavate, with 4 sterigmata, 17–19 × 6–8 µm	Cylindrical, thin-walled, smooth, with oil drops, 8.5–10.5 × 3–4 µm, Q = 2.58	Wang et al. (2026)
Tubulicrinis inornatus	Sweden	Annual, resupinate, adnate, effused, thin, smooth, reticulate to porulose, grayish white to pale yellowish white	Monomitic; generative hyphae with clamp connections, colorless, thin- to slightly thick-walled	Subclavate to cylindrical, slightly constricted, with 4 sterigmata, 12–15 × 4–5 µm	Ovate to ellipsoid, thin-walled, smooth, 4–5 × 2.5–3.5 µm	Donk (1956)

Species name	Locality	Basidiomata	Hyphal system	Basidia	Basidiospores	References
Tubulicrinis martinicensis	Martinique	Annual, effused, adnate, strongly attached to the wood, thin, furfuraceous, yellow to buff, cracked	Monomitic; generative hyphae with clamp connections, colorless, thin-walled	Short clavate, with 4 sterigmata, 9–12 × 3.5–4 µm	Subcylindrical to suballantoid, multiguttulate, thin-walled, smooth, 5.6–7 × 1.9–2.6 µm, Q = 2.9	Gruhn et al. (2016)
Tubulicrinis orientalis	Russia	Annual, resupinate, adnate, effused, smooth, hispidulous under the lens, pale cream to "Primrose"	Monomitic; generative hyphae with clamp connections, colorless, thin-to slightly thick-walled	Narrowly clavate, with 4 sterigmata, 11–16 × 3.5–4 µm	Cylindrical to suballantoid, thin-walled, smooth, 5–6 × 1.5–2 µm	Parmasto (1967)
Tubulicrinis pini	China	Annual, resupinate, adnate, thin, smooth, coriaceous, white to slightly buff	Monomitic; generative hyphae with clamp connections, colorless, thin-walled	Clavate, with 4 sterigmata, 11–14.5 × 4.5–5.5 µm	Cylindrical to allantoid, thin-walled, smooth, 5–6 × 1.8–2.3 µm, Q = 2.43–2.51	Dong et al. (2024)
Tubulicrinis sinensis	**China**	**Annual, resupinate, closely adnate, smooth, farinaceous, white**	**Monomitic; generative hyphae with clamp connections, colorless, slightly thick-walled**	**Clavate, with 4 sterigmata, 8.4–10.7 × 4–5 µm**	**Narrowly cylindrical, thin-walled, smooth, 4.8–5.7 × 1.7–2.3 µm, Q = 2.63–2.75**	**Present study**

Species name	Locality	Basidiomata	Hyphal system	Basidia	Basidiospores	References
Tubulicrinis subulatus	USA	Resupinate, adnate, thick in maturity, smooth and continuous but cracking in irregular pieces, strongly pilose, white to cream	Monomitic; generative hyphae with clamp connections, colorless, thin- to thick-walled	Subclavate, with 4 sterigmata, 15–18 × 3.5–4.5 µm	Allantoid, thin-walled, smooth, 6–8 × 1.5–2 µm	Donk (1956)
Tubulicrinis tenuis	China	Annual, resupinate, adnate, smooth, pruinose, white to pale yellow	Monomitic; generative hyphae with clamp connections, colorless, thin to slightly thick-walled	Barreled, with 4 sterigmata, 7–9.5 × 3.8–4.5 µm	Cylindrical to allantoid, thin-walled, smooth, with one or two guttate, 4.5–5.5 × 1.5–2 µm, Q = 2.75	Yuan et al. (2026)
Tubulicrinis xantha	China	Annual, resupinate, adnate, thin, smooth, cracked, furfuraceous, yellow to buff	Monomitic; generative hyphae with clamp connections, colorless, thin-walled	Clavate, with 4 sterigmata, 8–14.5 × 2.5–3.5 µm	Cylindrical to allantoid, thin-walled, smooth, 5.3–6.3 × 1.2–1.6 µm, Q = 3.94–4.12	He et al. (2020)
Tubulicrinis yunnanensis	China	Annual, resupinate, adnate, thin, smooth, pruinose, primrose to olivaceous buff	Monomitic; generative hyphae with clamp connections, colorless, thin-walled	Clavate, with 4 sterigmata, 8.5–20.5 × 2.5–4.5 µm	Cylindrical, thin-walled, smooth, multiguttulate, 4.2–6.2 × 1.2–2 µm, Q = 2.9–3.59	He et al. (2020)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Phylloporia perangusta Dai 18139 China
Fomitiporella vietnamensis Dai 18377 Vietnam
Neomensularia duplicata LWZ 20150529-4 China
Phellinopsis conchata L-7601 USA
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Podocarpioporus podocarpi Dai 21986 China
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Xylodon quercinus Spirin 12030 Russia
Xylodon olivaceobubalinus CLZhao 25174 China
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Lyomyces sambuci LWZ 20180905-1 China
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Fasciodontia brasiliensis MSK-F 7245a Brazil
Fasciodontia bugellensis KAS-FD 10705a France
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Leifia brevispora LWZ 20170820-46 China
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Rigidoporus cuneatus Dai 7339 China
Rigidoporaceae
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Resinicium monticola FP-150360 Jamaica
Resinicium mutabile FP-102989 Puerto Rico
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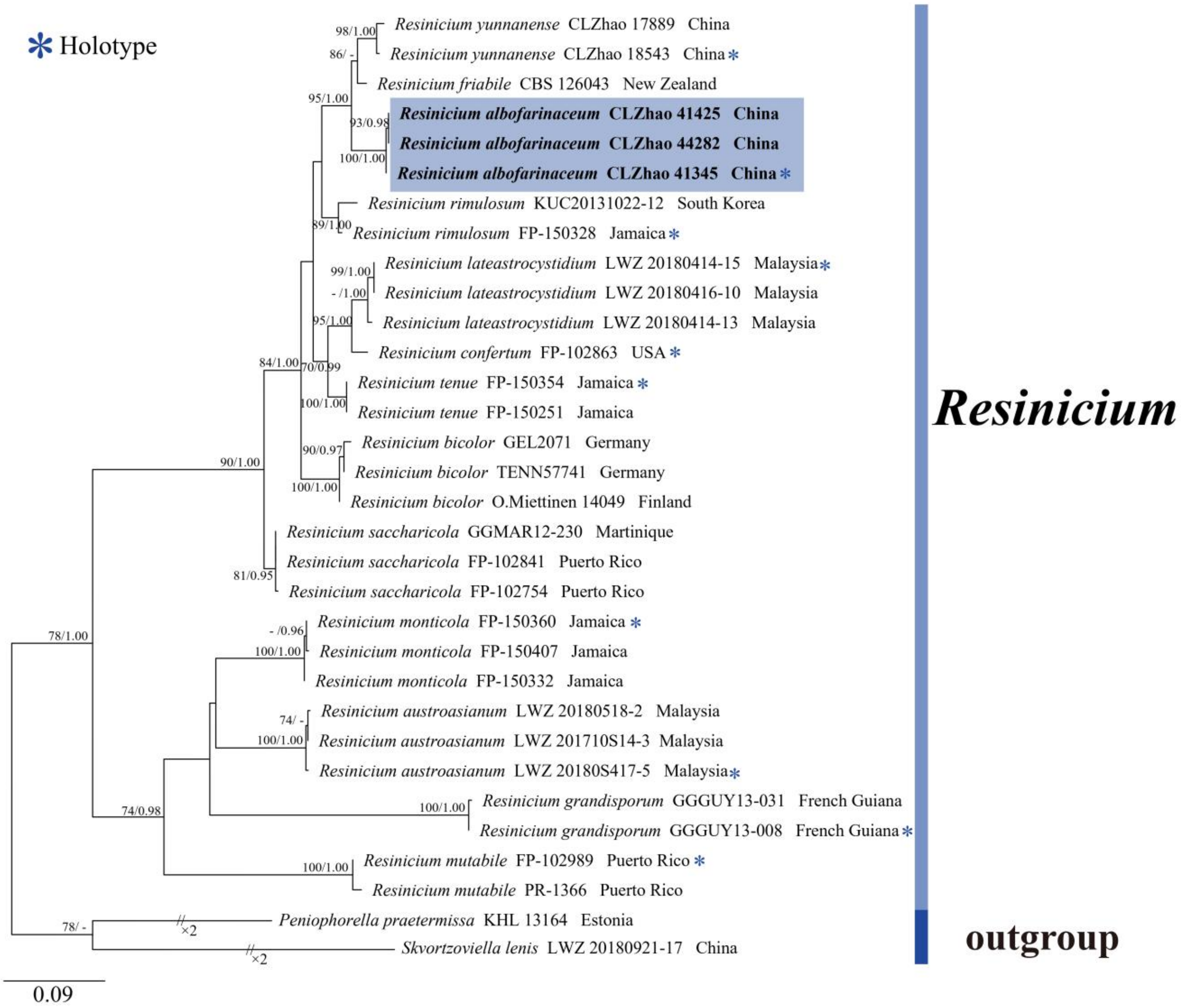
Outgroup
0.2

Fig. 1

4



✻ Holotype
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86/ -
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Resinicium friabile CBS 126043 New Zealand
95/1.00
93/0.98
Resinicium albofarinaceum CLZhao 41425 China
Resinicium albofarinaceum CLZhao 44282 China
100/1.00
Resinicium albofarinaceum CLZhao 41345 China ✻
Resinicium rimulosum KUC20131022-12 South Korea
89/1.00
Resinicium rimulosum FP-150328 Jamaica ✻
99/1.00
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95/1.00
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Resinicium confertum FP-102863 USA ✻
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Resinicium tenue FP-150354 Jamaica ✻
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78/ -
×2
Peniophorella praetermissa KHL 13164 Estonia
×2
Skvortzoviella lenis LWZ 20180921-17 China
Resinicium
outgroup
0.09

Fig. 2

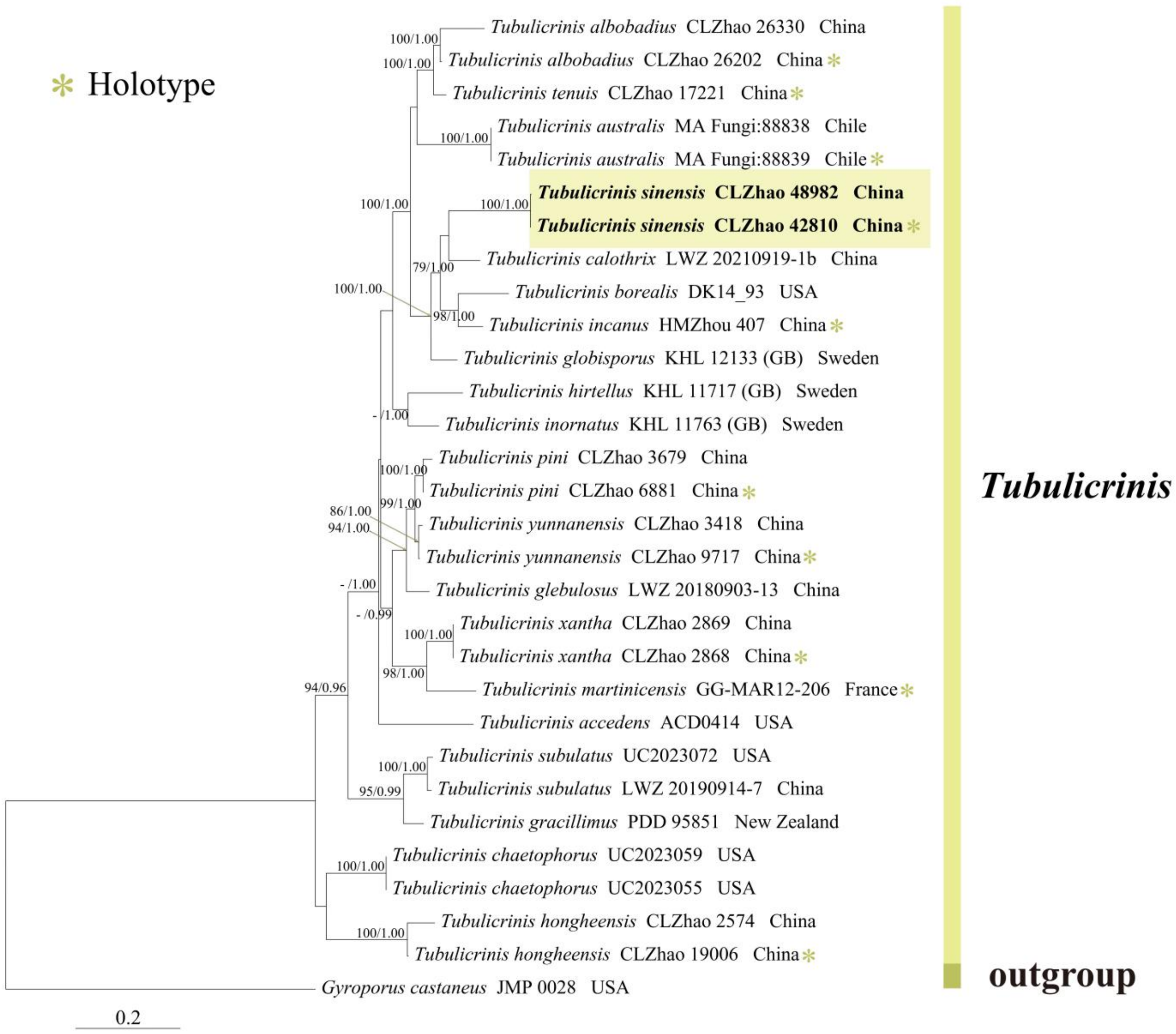
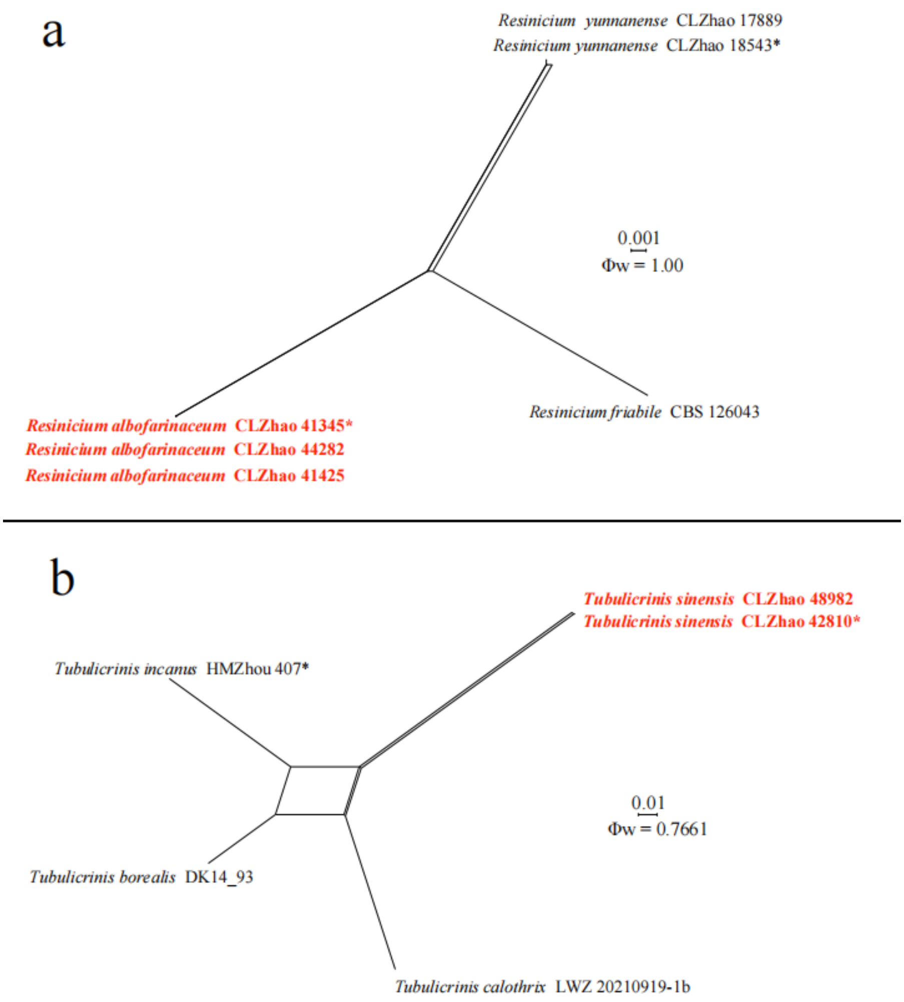

* Holotype
100/1.00
Tubulicrinis albobadius CLZhao 26330 China
100/1.00
Tubulicrinis albobadius CLZhao 26202 China *
Tubulicrinis tenuis CLZhao 17221 China *
100/1.00
Tubulicrinis australis MA Fungi:88838 Chile
Tubulicrinis australis MA Fungi:88839 Chile *
100/1.00
100/1.00
Tubulicrinis sinensis CLZhao 48982 China
Tubulicrinis sinensis CLZhao 42810 China *
79/1.00
Tubulicrinis calothrix LWZ 20210919-1b China
100/1.00
Tubulicrinis borealis DK14_93 USA
98/1.00
Tubulicrinis incanus HMZhou 407 China *
Tubulicrinis globisporus KHL 12133 (GB) Sweden
Tubulicrinis hirtellus KHL 11717 (GB) Sweden
- /1.00
Tubulicrinis inornatus KHL 11763 (GB) Sweden
Tubulicrinis pini CLZhao 3679 China
100/1.00
Tubulicrinis pini CLZhao 6881 China *
99/1.00
86/1.00
94/1.00
Tubulicrinis yunnanensis CLZhao 3418 China
Tubulicrinis yunnanensis CLZhao 9717 China *
- /1.00
Tubulicrinis glebulosus LWZ 20180903-13 China
- /0.99
Tubulicrinis xantha CLZhao 2869 China
100/1.00
Tubulicrinis xantha CLZhao 2868 China *
98/1.00
Tubulicrinis martinicensis GG-MAR12-206 France *
94/0.96
Tubulicrinis accedens ACD0414 USA
Tubulicrinis subulatus UC2023072 USA
100/1.00
95/0.99
Tubulicrinis subulatus LWZ 20190914-7 China
Tubulicrinis gracillimus PDD 95851 New Zealand
Tubulicrinis chaetophorus UC2023059 USA
100/1.00
Tubulicrinis chaetophorus UC2023055 USA
Tubulicrinis hongheensis CLZhao 2574 China
100/1.00
Tubulicrinis hongheensis CLZhao 19006 China *
Gyroporus castaneus JMP 0028 USA
0.2
Tubulicrinis
outgroup

Fig. 3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Resinicium yunnanense CLZhao 17889
Resinicium yunnanense CLZhao 18543*
0.001
Φw = 1.00
Resinicium friabile CBS 126043
Resinicium albofarinaceum CLZhao 41345*
Resinicium albofarinaceum CLZhao 44282
Resinicium albofarinaceum CLZhao 41425
b
Tubulicrinis sinensis CLZhao 48982
Tubulicrinis sinensis CLZhao 42810*
Tubulicrinis incanus HMZhou 407*
0.01
Φw = 0.7661
Tubulicrinis borealis DK14_93
Tubulicrinis calothrix LWZ 20210919-1b

Fig. 4

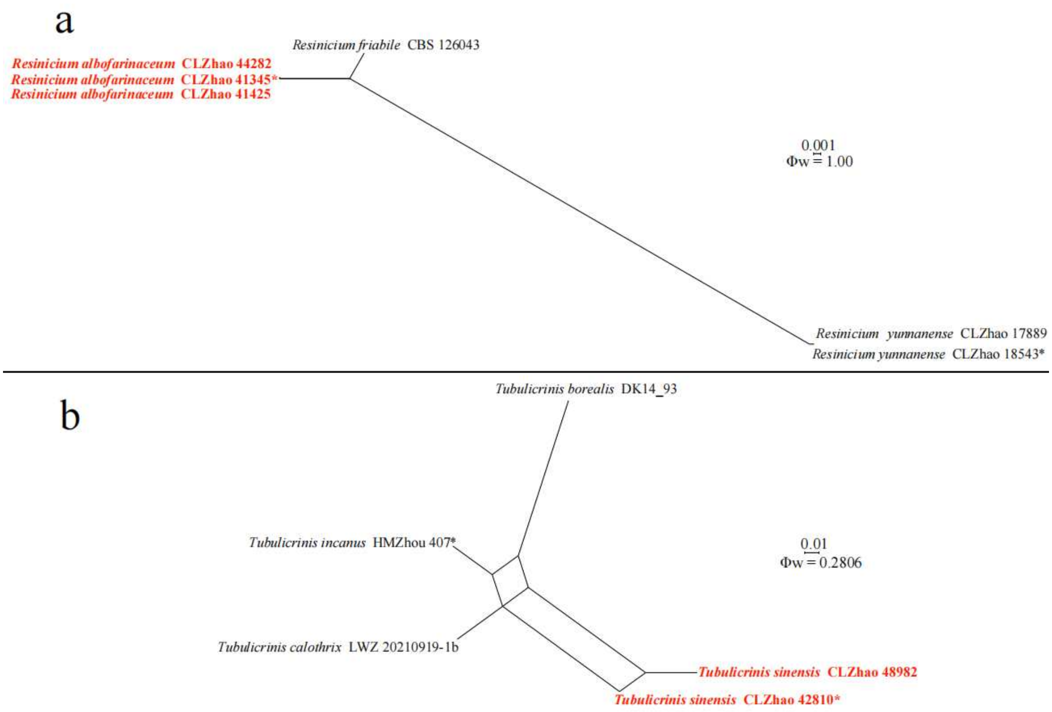
a
Resinicium friabile CBS 126043
Resinicium albofarinaceum CLZhao 44282
Resinicium albofarinaceum CLZhao 41345*
Resinicium albofarinaceum CLZhao 41425
0.001
Φw = 1.00
Resinicium yunnanense CLZhao 17889
Resinicium yunnanense CLZhao 18543*
b
Tubulicrinis borealis DK14_93
Tubulicrinis incanus HMZhou 407*
0.01
Φw = 0.2806
Tubulicrinis calothrix LWZ 20210919-1b
Tubulicrinis sinensis CLZhao 48982
Tubulicrinis sinensis CLZhao 42810*

Fig. 5

Fig. 6

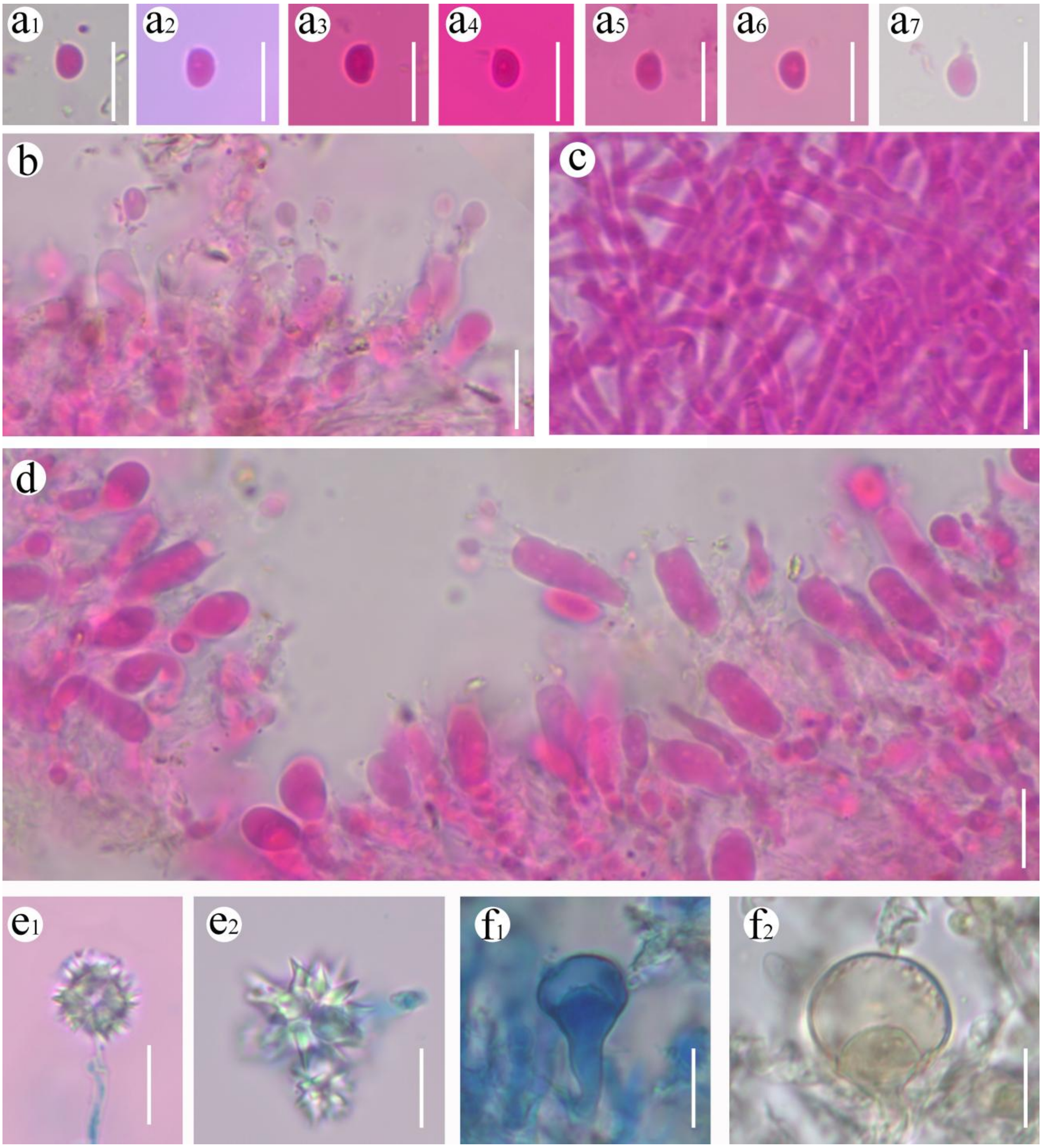

Fig. 7

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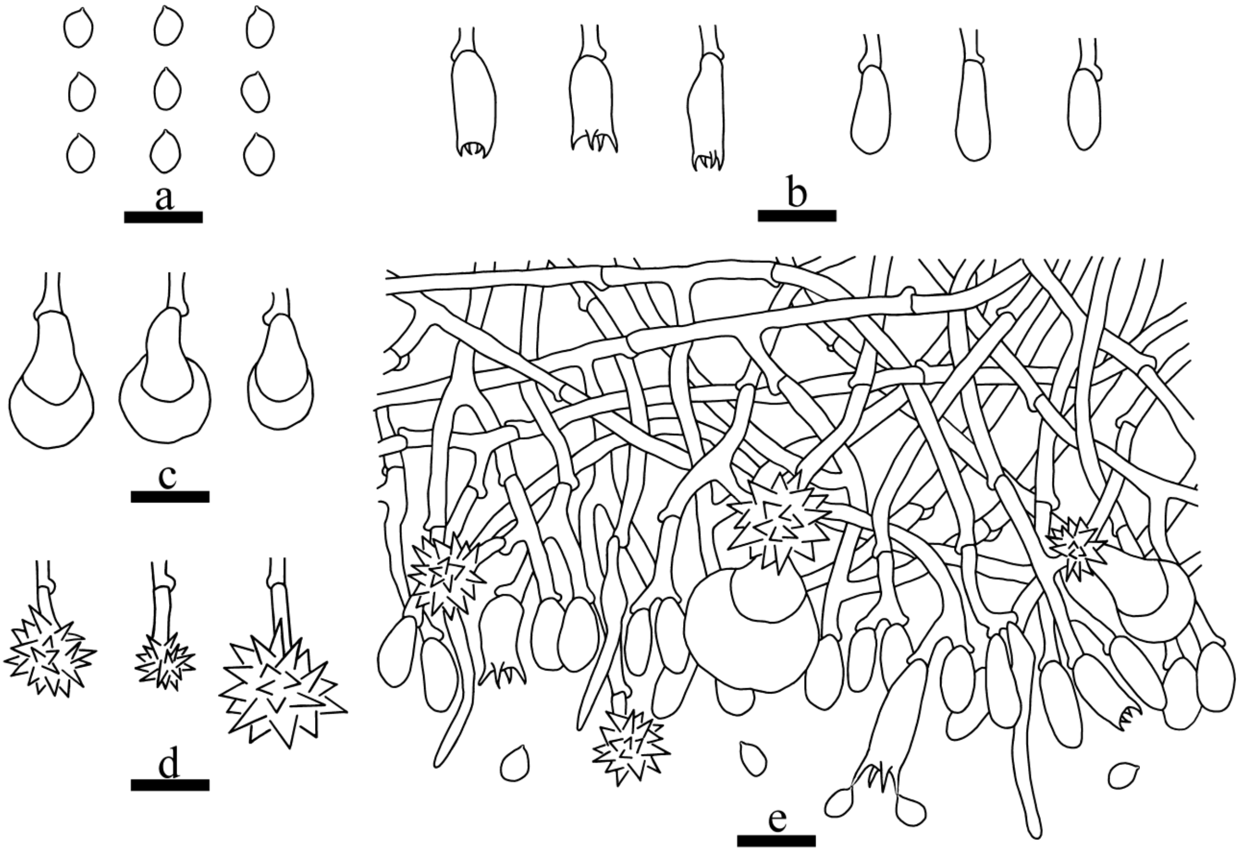

Fig. 8

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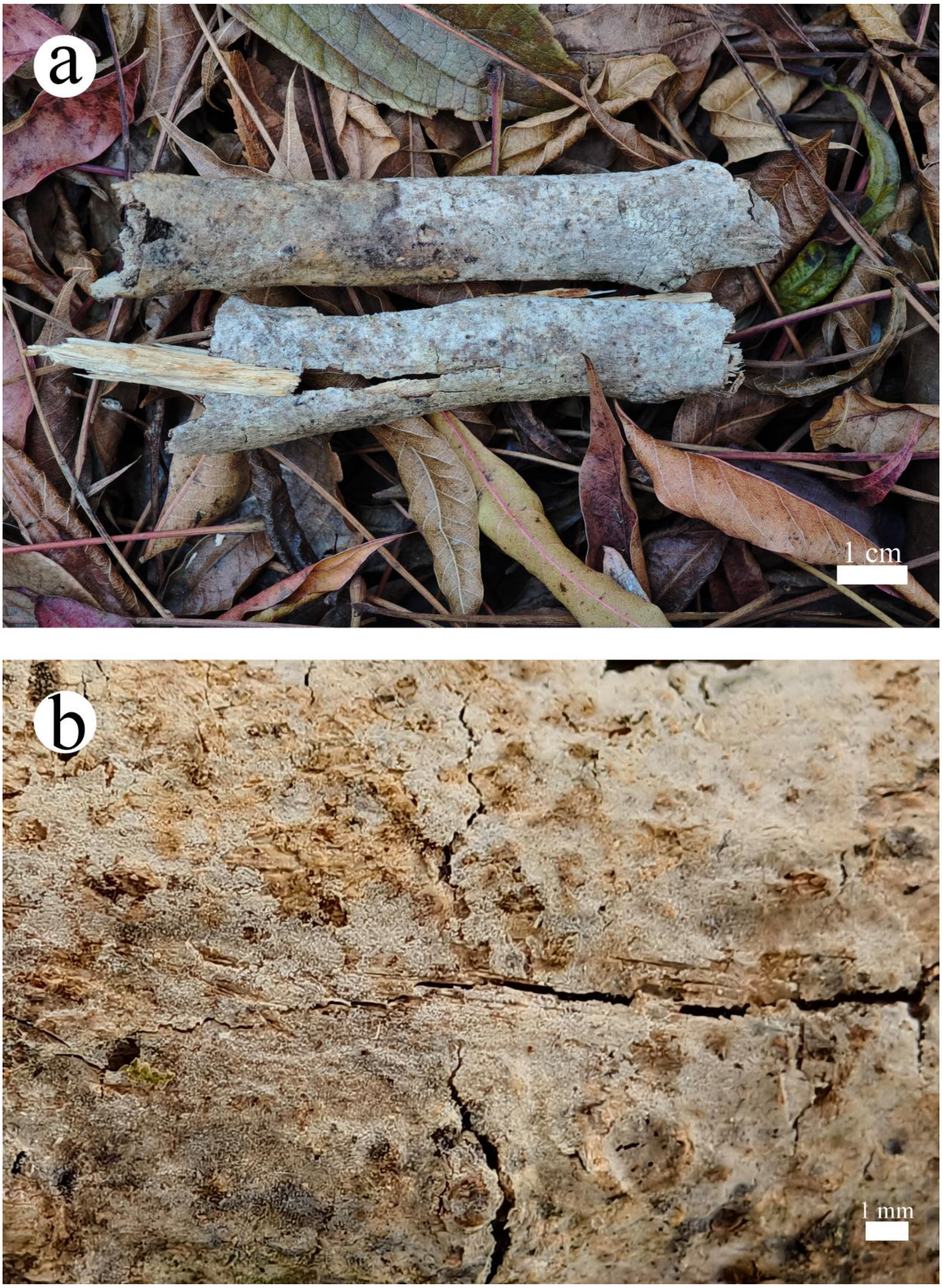

Fig. 9

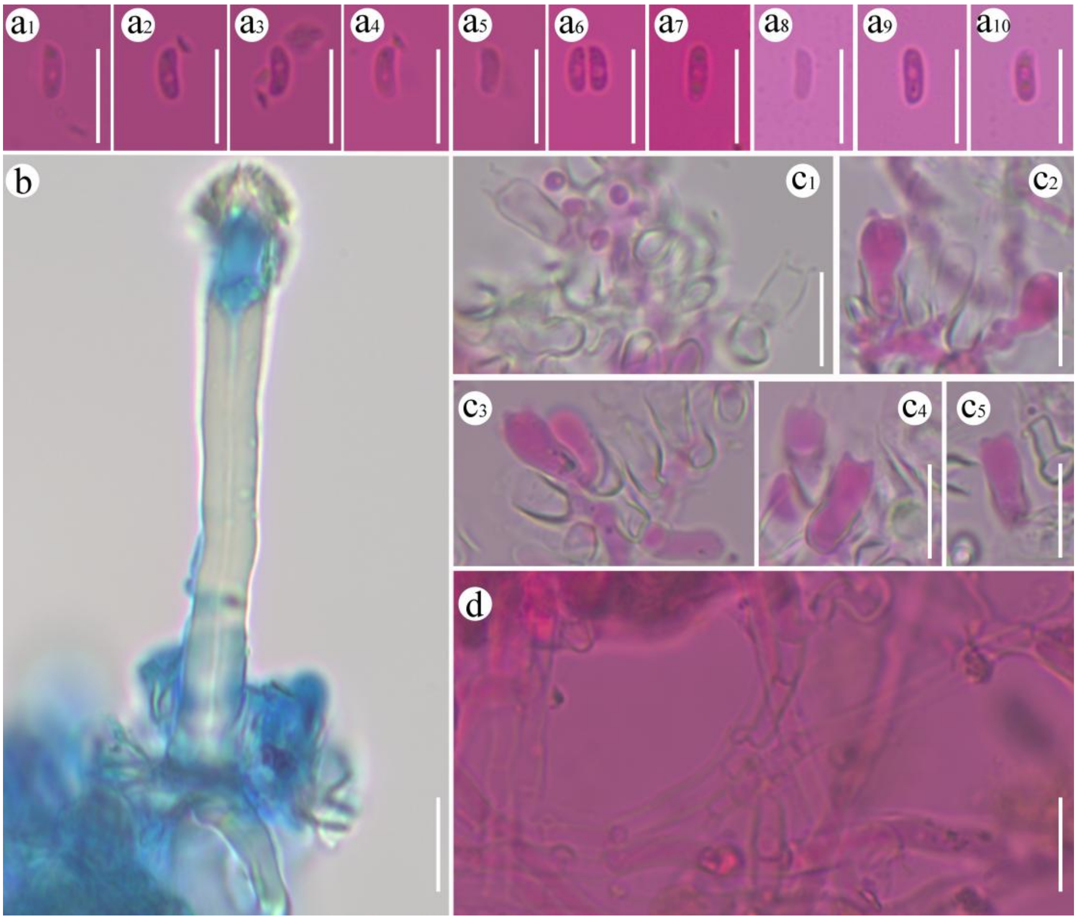

Fig. 10

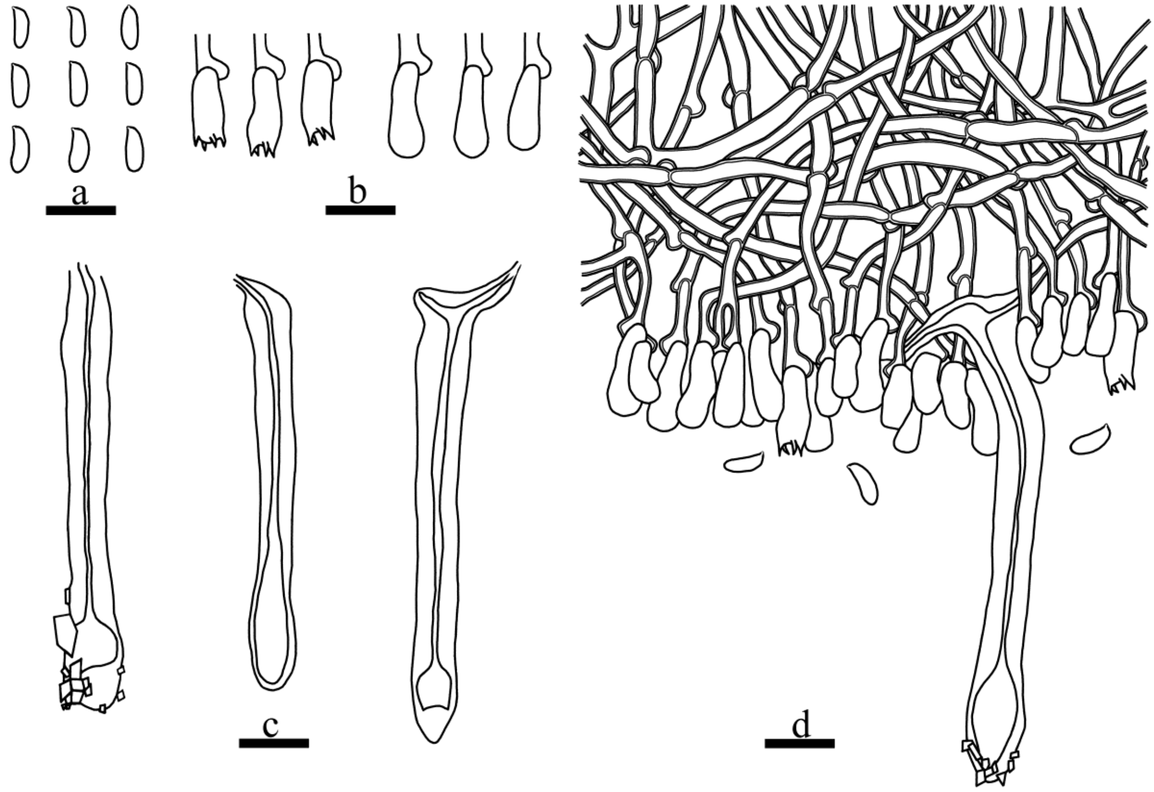

Fig. 11