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Two new species of *Trichoderma* from (Hypocreaceae, Hypocreales) Jilin Province, China

YU WANG, TOLGOR BAI

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Multigene phylogeny and morphology reveal a new species of *Apiospora* from the sclerotium of *Papiliomyces longiclavatus*

HUI CHEN, YINGZI HE, DEJIANG TANG, YAO WANG

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Erysimum nasturtioides (Brassicaceae): a local endemic to the massif Kallar and Sabzkuh rediscovered after 154 years

AMIN ZERAATKAR, HAMZEH ALI SHIRMAZI

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Morphological characteristics and phylogenetic analysis reveal a new species *Punctulariopsis tenuis* (Punctulariaceae, Basidiomycota) from southwestern China

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Abstract

Punctulariopsis is an important group of corticioid fungi, with only seven species currently recognized in the genus. Although recent studies have clarified the classification of *Punctulariopsis* by combining phylogenetic analyses and morphological evidence, the species diversity of *Punctulariopsis* in the high-elevation forests of Yunnan Province, China, remains insufficiently explored. In this study, the detailed morphological observations and phylogenetic analyses based on the internal transcribed spacers (ITS) and the large subunit (LSU) of the nuclear ribosomal DNA (rDNA) revealed a new species, *P. tenuis* sp. nov. This species is characterized by hard, coriaceous basidiomata with a smooth hymenial surface, a monomitic hyphal system, and broadly ellipsoid basidiospores measuring $6.5\text{--}8.5 \times 4.5\text{--}6.5\ \mu\text{m}$. The phylogenetic analysis revealed that the new species was nested within *Punctulariopsis* in Punctulariaceae and constituted an independent lineage (100% BS, 1.00 BPP) closely related to *P. asiana*. A description, micrograph, and results of the phylogenetic analysis of the new species are provided.

Key words: molecular systematics, new species, taxonomy, Yunnan Province

Introduction

Corticioid fungi represent a highly diverse group of microorganisms that play essential roles in forest ecosystems (Dai *et al.* 2021, Hibbett *et al.* 2025, Song *et al.* 2025, Zhao *et al.* 2025). They are key drivers of wood decomposition, producing lignocellulosic enzymes capable of degrading lignin, cellulose and hemicellulose (Wang *et al.* 2013, Tedersoo *et al.* 2014, Schoutteten *et al.* 2024, Case *et al.* 2025, Zhao *et al.* 2026).

These fungi constitute a large and distinctive group within Basidiomycota and are widespread worldwide, exhibiting particularly high diversity in tropical and subtropical regions (Dai *et al.* 2004, Ghobad-Nejhad *et al.* 2010, Dai 2011, Muhammad *et al.* 2025, Yang *et al.* 2025, Yuan *et al.* 2026, Zhou *et al.* 2026). As non-poroid and resupinate fungi, they form a phylogenetically diverse group, typically characterized by relatively simple fruiting body morphology (Wang *et al.* 2024, Liu *et al.* 2025, Muhammad *et al.* 2025). Corticioid lineages occur across all major clades of Agaricomycotina (Binder *et al.* 2005, Ghobad-Nejhad *et al.* 2021), and the resupinate habit is widely regarded as the primordial form of basidiomycete fruiting bodies (Hibbett & Binder 2002). Species of corticioid fungi exhibit notable

ecological and nutritional heterogeneity, with lineages inhabiting various substrata as lichenicolous, saprophytic, and plant pathogenic (Lawrey *et al.* 2008, Rungjindamai *et al.* 2008, Yuan *et al.* 2023). Within Corticiales, the family Punctulariaceae Donk accommodates corticioid species with simple, resupinate basidiomata on angiosperm wood (Donk 1964). Members of Punctulariaceae are characterized by ellipsoid, inamyloid basidiospores and the presence of dendrohyphidia (Ghobad-Nejhad *et al.* 2010). Currently, Punctulariaceae comprises three genera: *Punctularia* Pat., *Dendrocorticium* M.J. Larsen & Gilb., and *Punctulariopsis* Ghob.-Nejh (Ariyawansa *et al.* 2015, Muhammad *et al.* 2025).

The genus *Punctulariopsis* (Punctulariaceae, Corticiales) was recognized in 2010 and typified by *P. subglobispora* (Hallenb. & Hjortstam) Ghob.-Nejh. (2010: 1529) (Ghobad-Nejhad *et al.* 2010). The genus is characterized by resupinate, strictly adnate basidiomata having reddish to ochraceous in color; the hymenial surface smooth when fresh, subgelatinous, becoming corneous upon drying; the hyphal system monomitric with generative hyphae bearing clamp connections; basidia elongate, large, clavate to flexuous, bearing four sterigmata and a basal clamp, and the absence of cystidia; dendrohyphidia smooth or irregularly encrusted and sparingly branched; basidiospores smooth, broadly ellipsoid, thick-walled, and contain granular contents (Ghobad-Nejhad *et al.* 2010). According to MycoBank (<http://www.mycobank.org>, accessed on 4 June 2026) and the Index Fungorum (<http://www.indexfungorum.org>, accessed on 4 June 2026), *Punctulariopsis* currently includes seven species, viz. *P. asiana* Yang Yang & C.L. Zhao (2025: 277), *P. cremeoalbida* (M.J. Larsen & Nakasone) Ghob.-Nejh. (2015: 224), *P. efibulata* (M.J. Larsen & Nakasone) Ghob.-Nejh. (2015: 224), *P. fissurata* A. Muhammad & C.L. Zhao (2025: 347), *P. obducens* (Hjortstam & Ryvarden) Ghob.-Nejh. (2010: 1529), *P. subglobispora* (Hallenb. & Hjortstam) Ghob.-Nejh. (2010: 1529), and *P. yunnanensis* A. Muhammad & C.L. Zhao (2024: 63) (Ghobad-Nejhad *et al.* 2010, Ariyawansa *et al.* 2015, Muhammad *et al.* 2024, 2025, Yang *et al.* 2025).

Fungal systematics has undergone a fundamental change with the implementation of DNA sequencing technology (Wu *et al.* 2022, Dissanayake *et al.* 2024; Crous *et al.* 2025). Based on ITS+LSU phylogenetic analyses, three genera *Dendrocorticium*, *Punctulariopsis*, and *Punctularia* were described in Punctulariaceae (Ghobad-Nejhad *et al.* 2010). Based on ITS+LSU phylogenetic analyses, a new genus, *Punctulariopsis* was proposed, and the species *Vuilleminia obducens* Hjortstam & Ryvarden (2010: 59) and *V. subglobispora* Hallenb. & Hjortstam (2010: 59) were transferred to this new genus as *P. obducens* and *P. subglobispora*, respectively (Ghobad-Nejhad *et al.* 2010). In recent years, the species diversity of the resupinate *Punctulariopsis* has been described or better defined through morphological and molecular analyses, revealing the hidden diversity of this group (Ghobad-Nejhad *et al.* 2010, Ariyawansa *et al.* 2015, Muhammad *et al.* 2024, 2025, Yang *et al.* 2025). Recent research shows that *Punctulariopsis* is a small fungal genus with only seven species recognized to date, and many remain undiscovered.

During investigations on corticioid fungi in the Yunnan Province, China, many specimens were collected. To clarify the placement and relationships of these specimens, we conducted a phylogenetic and taxonomic study based on ITS+LSU sequences. These specimens are identified as a previously undescribed species of *Punctulariopsis* and named as *P. tenuis*. The description, illustration, and phylogenetic analysis results of the new species are provided.

Materials and methods

Sample collection and herbarium specimen preparation

The fresh fruiting bodies were collected on a fallen angiosperm branch from Puer, Yunnan Province, China. The samples were photographed *in situ*, and fresh macroscopic details and collection data were recorded (Rathnayaka *et al.* 2025). Photographs were captured with a Nikon D7100. All the photos were focus-stacked using Helicon Focus software. Macroscopic details were recorded and transported to a field station, where the fruit body was dried on an electronic food dryer at 45 °C (Dong *et al.* 2025). Once dried, the specimens were sealed in envelopes and zip-lock plastic bags and labelled (Yang *et al.* 2025). The dried specimens were deposited in the Herbarium of the Southwest Forestry University (SWFC), Kunming, Yunnan Province, China.

Morphological observations

The macro-morphological descriptions were based on field notes and photos taken in the field and in the laboratory. Petersen (1996) was followed for the color terminology. The micro-morphological data were obtained from dried

specimens observed under a light microscope at 1000× oil immersion objective (Zhao *et al.* 2023, Dong *et al.* 2025). Sections were mounted in 5% KOH and 1% phloxine B (C₂₀H₂Br₄Cl₄Na₂O₃), as well as Cotton Blue and Melzer’s reagent were used where necessary to observe micromorphology following the method of Yang *et al.* (2025). To present the variations of spore sizes, 5% of measurements were excluded from each end of the range and shown in parentheses. A minimum of thirty basidiospores from each specimen was measured. Stalks were excluded from basidia measurements, and the hilar appendage was excluded from basidiospores measurements. The MycoBank numbers were registered in the MycoBank database (<http://www.mycobank.org>).

- The following abbreviations are used:
- CB = Cotton Blue
 - CB+ = cyanophilous
 - CB– = acyanophilous
 - IKI = Melzer’s reagent
 - IKI– = both inamyloid and non-dextrinoid
 - KOH = 5% potassium hydroxide water solution
 - 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 the given number (b) of specimens)
 - Q = variation in the L/W ratios between the specimens studied

Molecular phylogeny

CTAB rapid fungi genome extraction kit-DN14 (Aidlab Biotechnologies Co., Ltd, Beijing) was used to obtain genomic DNA from dried specimens, according to the manufacturer’s instructions. The gene fragments employed in this study are detailed in Table 1.

TABLE 1. Genes/loci, respective primers and references used in the study.

Genes/loci	Primers	Sequence (5'-3')	Annealing temperature (°C)	References
ITS	ITS5	GGA AGT AAA AGT CGT AAC AAG G	55°C	White <i>et al.</i> (1990)
	ITS4	TCC TCC GCT TAT TGA TAT GC		
LSU	LR0R	ACC CGC TGA ACT TAA GC	48°C	Vilgalys & Hester (1990)
	LR7	TAC TAC CAC CAA GAT CT		

The PCR protocol for ITS was as follows: initial denaturation at 95 °C for 3 min, followed by 35 cycles at 94 °C for 40 s, and 58 °C for 40 s. The PCR protocol for LSU was as follows: initial denaturation at 94 °C for 1 min, followed by 35 cycles at 94 °C for 30 s, 48 °C for LSU for 1 min, and 72 °C for 1.5 min, and a final extension of 72 °C for 10 min (Dong *et al.* 2025). The PCR products were purified and sequenced at Kunming Tsingke Biological Technology Limited Company, Kunming, Yunnan Province, P.R. China. All newly generated sequences were deposited in GenBank (Table 2).

TABLE 2. List of species, specimens, and GenBank accession number of sequences used in this study.

Species Name	Sample No.	GenBank Accession No.		Country	References
		ITS	LSU		
<i>Dentocorticium bicolor</i>	He2772	MF626354	MF626378	China	Liu <i>et al.</i> (2018)
<i>Dentocorticium bicolor</i>	He2757	MF626355	MF626379	China	Liu <i>et al.</i> (2018)
<i>Dentocorticium portoricense</i>	He2161	MF626356	MF626380	USA	Liu <i>et al.</i> (2018)
<i>Dentocorticium portoricense</i>	He2202	MF626357	MF626381	USA	Liu <i>et al.</i> (2018)
<i>Dentocorticium sulphurellum</i>	DLL2011-016	KJ140542	-	USA	Brazee <i>et al.</i> (2014)
<i>Dentocorticium sulphurellum</i>	FP11801	JN165018	-	USA	Justo & Hibbett (2011)

.....continued on the next page

TABLE 2. (Continued)

Species Name	Sample No.	GenBank Accession No.		Country	References
		ITS	LSU		
<i>Dentocorticium taiwanianum</i>	He4615	MF626362	MF626386	China	Liu <i>et al.</i> (2018)
<i>Dentocorticium taiwanianum</i>	He3777	-	MF626388	China	Liu <i>et al.</i> (2018)
<i>Dentocorticium ussuricum</i>	CLZhao 16063	MW582752	-	China	Yang <i>et al.</i> (2025)
<i>Dentocorticium ussuricum</i>	He3278	MF626358	MF626382	China	Liu <i>et al.</i> (2018)
<i>Gloeophyllum abietinum</i>	P254	-	AJ583431	Germany	Ghobad-Nejhad & Ginns (2012)
<i>Gloeophyllum sepiarium</i>	FP 125002-T	-	AY333806	China	Moreth & Schmidt (2005)
<i>Punctularia bambusicola</i>	CLZhao 4133	MW559982	MW559984	China	Guan <i>et al.</i> (2021)
<i>Punctularia strigosozonata</i>	CBS 345.34	MH855559	MH867064	Netherlands	Vu <i>et al.</i> (2019)
<i>Punctularia strigosozonata</i>	BHI-F586b	MH558554	-	USA	Haelewaters <i>et al.</i> (2018)
<i>Punctularia subhepatica</i>	He 5695	MW507075	MW507015	China	Yang <i>et al.</i> (2025)
<i>Punctularia subhepatica</i>	He 4436	MW507074	MW507014	China	Yang <i>et al.</i> (2025)
<i>Punctulariopsis asiana</i>	CLZhao 27375	PP819726	-	China	Yang <i>et al.</i> 2025
<i>Punctulariopsis asiana</i>	CLZhao 27479	PP819727	-	China	Yang <i>et al.</i> 2025
<i>Punctulariopsis cremeoalbida</i>	Burdsall 9616	KR494275	-	USA	Ariyawansa <i>et al.</i> (2015)
<i>Punctulariopsis efibulata</i>	Burdsall 8824	KR494276	-	USA	Ariyawansa <i>et al.</i> (2015)
<i>Punctulariopsis efibulata</i>	He 2027	MW507077	-	China	Ariyawansa <i>et al.</i> (2015)
<i>Punctulariopsis fissurata</i>	CLZhao 27503	PQ062039	PQ109091	China	Muhammad <i>et al.</i> (2025)
<i>Punctulariopsis fissurata</i>	CLZhao 27439	PQ062037	PQ109089	China	Muhammad <i>et al.</i> (2025)
<i>Punctulariopsis obducens</i>	MG70	HM046918	-	Ethiopia	Ghobad-Nejhad <i>et al.</i> (2010)
<i>Punctulariopsis tenuis</i>	CLZhao 46076	PX921936	PZ072266	China	Present study
<i>Punctulariopsis tenuis</i>	CLZhao 46123	PX921937	PZ072267	China	Present study
<i>Punctulariopsis tenuis</i>	CLZhao 46186	PX921938	PZ072268	China	Present study
<i>Punctulariopsis tenuis</i>	CLZhao 46190	PX921939	PZ072269	China	Present study
<i>Punctulariopsis tenuis</i>	CLZhao 46229	PX921940	PZ072270	China	Present study
<i>Punctulariopsis subglobispora</i>	GB: Hallenberg 12761	NR_119827	-	Argentina	Ariyawansa <i>et al.</i> (2015)
<i>Punctulariopsis subglobispora</i>	FCUG 2535	HM046917	HM046932	Argentina	Ghobad-Nejhad <i>et al.</i> (2010)
<i>Punctulariopsis yunnanensis</i>	CLZhao 21443	PP425905	PP572972	China	Muhammad <i>et al.</i> (2024)
<i>Punctulariopsis yunnanensis</i>	CLZhao 21561	PP425906	PP572970	China	Muhammad <i>et al.</i> (2024)

Phylogenetic analyses followed the methods in Dissanayake *et al.* (2020). Newly generated sequence data were initially subjected to a BLAST search in NCBI to obtain the most probable closely related taxa in the GenBank (<http://blast.ncbi.nlm.nih.gov/>). Sequence data were retrieved from GenBank based on recent publications (<https://www.ncbi.nlm.nih.gov/nucleotide/>). The sequences were aligned using MAFFT version 7 (Kato *et al.* 2019) with the G-INS-I strategy. The alignment was adjusted manually using AliView version 1.27 (Larsson 2014). The dataset was initially aligned and later, ITS and nrLSU sequences were combined using Mesquite version 3.51. FASTA data file formats were converted to PHYLIP and NEXUS formats using the online tool available on the ALTER website (<http://sing.ei.uvigo.es/ALTER/>, Glez-Peña *et al.* 2010). Phylogenetic trees were constructed based on randomized accelerated Maximum Likelihood (ML) and Bayesian Inference (BI) analyses.

Maximum Likelihood analyses were performed using the CIPRES Science Gateway (<https://www.phylo.org/portal2/login!input.action>, Miller *et al.* 2012) based on the dataset using the RAxML-HPC BlackBox tool, with

RAxML halt bootstrapping automatically, 0.25 for maximum hours and obtaining the best tree using ML search. Other parameters in ML analysis used default settings, and statistical support values were obtained using nonparametric bootstrapping with 1000 replicates. Bayesian inference (BI) analysis was performed on the same dataset using MrBayes v3.2.7a (Ronquist *et al.* 2012). The best substitution model for the dataset was selected using ModelFinder v2.2.0 (Kalyaanamoorthy *et al.* 2017) with the Bayesian Information Criterion, and the model was used for Bayesian analysis. Four Markov chains were run from random starting trees. Trees were sampled every 1,000th generation. The first 25% of sampled trees were discarded as burn-in, while the remaining trees were used to construct a 50% majority consensus tree and to calculate Bayesian posterior probabilities (BPPs).

Phylogenetic trees were visualized and adjusted using FigTree v1.4.4 (<http://tree.bio.ed.ac.uk/software/figtree>), and the exports were edited using Adobe Illustrator CS6 software (Adobe Systems, USA). Branches of the consensus tree that received bootstrap support for Maximum Likelihood (ML) equal to or above 70%, and Bayesian Inference (BI) equal to or above 0.95, respectively.

Results

Molecular phylogeny

The combined ITS+LSU dataset (Figure 1) included sequences from 34 fungal specimens representing 18 species, and *Gloeophyllum abietinum* (Bull.) P. Karst. and *G. sepiarium* (Wulfen) P. Karst. were retrieved as the outgroup taxa (Yang *et al.* 2025). For Bayesian Inference (BI) analysis, a total of four Markov chains were run for two independent runs from random starting trees, each with 0.55 million generations for the ITS+LSU dataset, with trees and parameters sampled every 1000 generations, with an average standard deviation of split frequencies = 0.009331 (BI) and an effective sample size (ESS) average ESS (avg. ESS) = 476.5. ModelFinder v2.2.0 (Kalyaanamoorthy *et al.* 2017) was used to select the best-fit model using the BIC criterion. The best model for the combined ITS+LSU dataset, as estimated and applied in the Bayesian analysis, was GTR+I+G. Maximum Likelihood (ML) and Bayesian Inference (BI) analyses yielded similar topologies.

Phylogenetic analyses based on a combined ITS+LSU dataset (Figure 1) revealed that the new species, *Punctulariopsis tenuis*, was nested within the genus *Punctulariopsis* in Punctulariaceae and showed that the new species constituted an independent lineage (100% BS, 1.00 BPP) closely related to *P. asiana*.

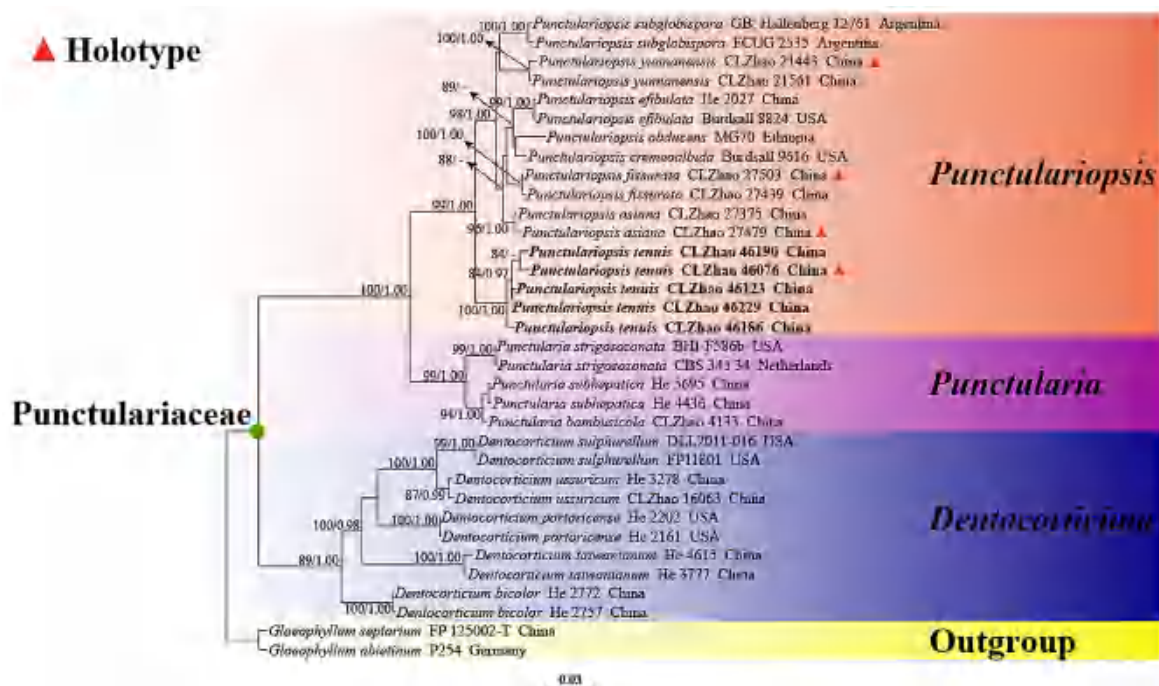


FIGURE 1. Maximum Likelihood tree illustrating the phylogeny of *Punctulariopsis* and related genera in Punctulariaceae, based on the ITS+LSU sequence dataset. Branches are labeled with Maximum Likelihood bootstrap values equal to or above 70%, and Bayesian posterior probabilities equal to or above 0.95.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

Taxonomy

Punctulariopsis tenuis Q. Yuan & C.L. Zhao, *sp. nov.* Figs. 2–4

Etymology:—*Tenuis* (Lat.) refers to the thin basidiomata of the type specimen.

MycoBank No.: MB862690



FIGURE 2. Basidiomata of *Punctulariopsis tenuis*. (A–B) CLZhao 46076 (holotype); (C–D) CLZhao 46123; (E–F) CLZhao 46186; (G–H) CLZhao 46190; (I–J) CLZhao 46229.

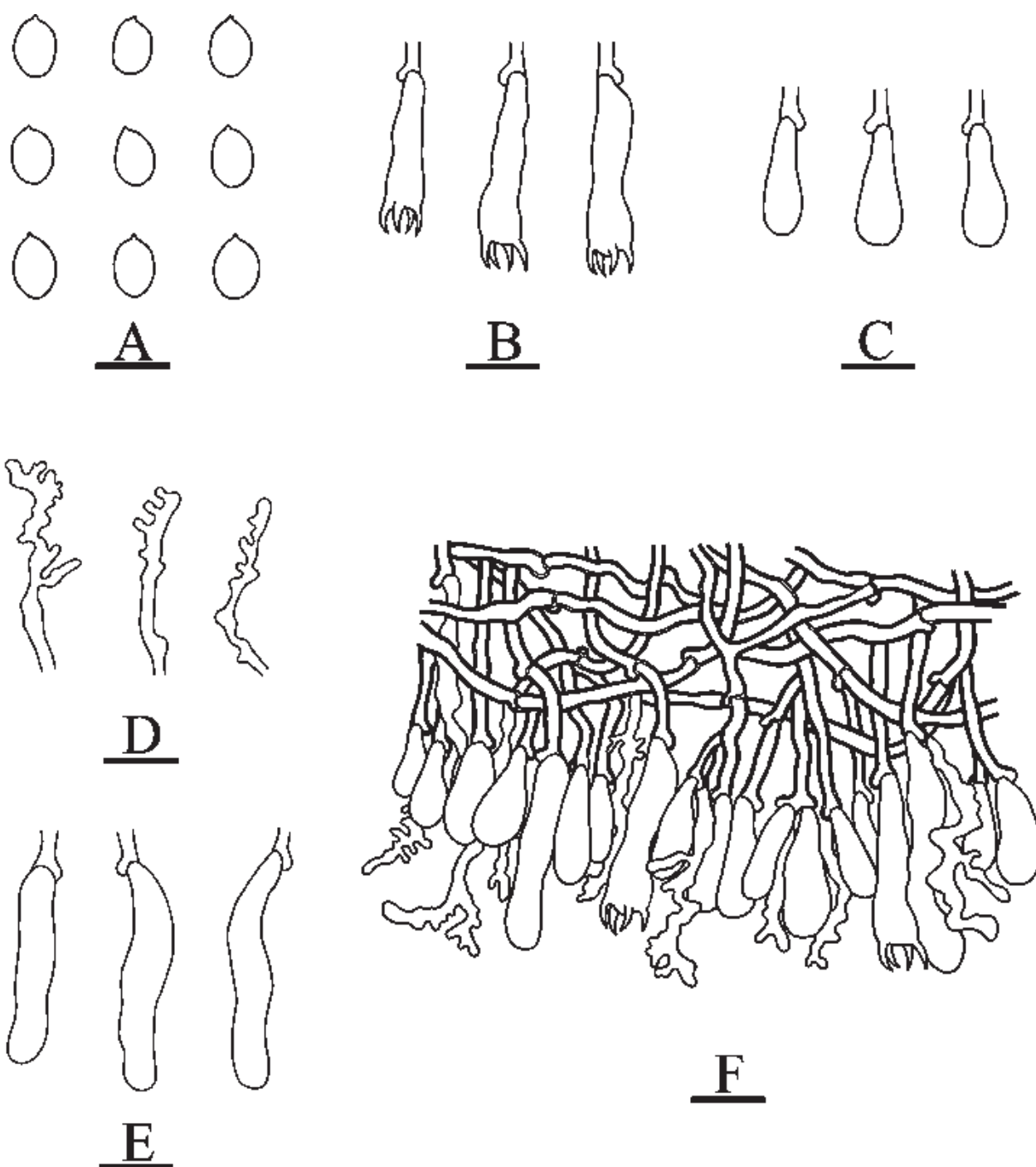


FIGURE 3. Microscopic structures of *Punctulariopsis tenuis* (CLZhao 46076, holotype). (A) Basidiospores; (B) Basidia; (C) Basidioles. (D) Hyphidia; (E) Cystidia; (F) Part of the vertical section of the hymenium. Scale bars: A–F = 10 μ m.

Holotype:—CHINA. Yunnan Province, Puer, Jinggu County, Xiaoheijiang Original Forest Park, GPS coordinates 23°38' N, 100°94' E, elevation 2420 m asl., on a fallen angiosperm branch, leg. C.L. Zhao, 19 August 2025, CLZhao 46076 (SWFC 00046076).

Basidiomata:—Annual, resupinate, hard coriaceous, thin, without odor or taste when fresh, up to 12 cm long, 2 cm wide, and 150 μ m thick at the center. Hymenial surface smooth, cream when fresh, turning to cream to slightly brown upon drying. Sterile margin narrow, cream, up to 1 mm.

Hyphal structure:—Hyphal system monomitic; generative hyphae with clamp connections, colorless, slightly thick-walled, with a wide lumen, smooth, flexuous, interwoven, 1.5–2.5 μ m in diameter, IKI–, CB–; tissues unchanged in KOH.

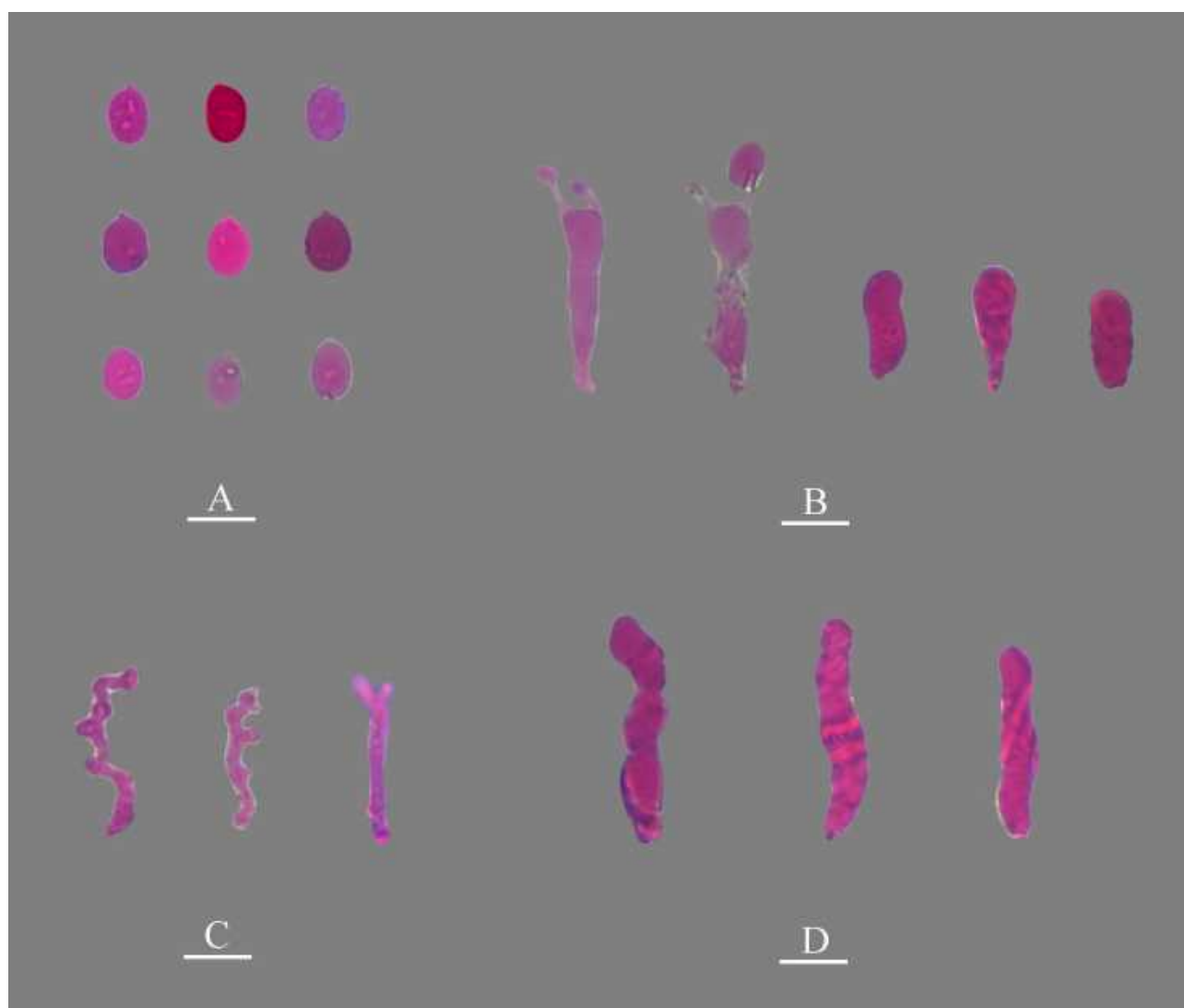


FIGURE 4. Microscopic structures of *Punctulariopsis tenuis* (CLZhao 46076, holotype). (A) Basidiospores; (B) Basidia and basidioles; (C) Cystidia; (D) Hyphidia. All structures were mounted in 5% KOH and stained with 1% phloxine B. Scale bars: A–D = 10 μ m; 10 $\times$ 100 Oil.

Hymenium:—Cystidia subclavate, colorless, thin-walled, mostly embedded, $26\text{--}33.5 \times 5\text{--}6.5$ μ m. Dendrohyphidia colorless, thin-walled. Basidia clavate, with four sterigmata and a basal clamp connection, $15\text{--}24 \times 4.5\text{--}6.5$ μ m. Basidioles dominant, similar to basidia in shape, but slightly smaller.

Basidiospores:—Broadly ellipsoid, colorless, thin-walled, smooth, IKI–, CB–, $(6\text{--})6.5\text{--}8.5(9) \times (4\text{--})4.5\text{--}6.5$ μ m, $L = 7.33$ μ m, $W = 5.35$ μ m, $Q = 1.36\text{--}1.37$ ($n = 60/2$).

Additional specimens examined (paratypes):—CHINA. Yunnan Province, Puer, Jinggu County, Xiaoheijiang Original Forest Park, GPS coordinates $23^{\circ}38' \text{N}$, $100^{\circ}94' \text{E}$, elevation 2420 m asl., on a fallen angiosperm branch, leg. C.L. Zhao, 19 August 2025, CLZhao 46123 (SWFC 00046123), CLZhao 46186 (SWFC 00046186), CLZhao 46190 (SWFC 00046190), and CLZhao 46229 (SWFC 00046229).

Discussion

Wood-inhabiting fungi play essential roles in ecosystem functioning, which have substantial economic values, and are of considerable importance in scientific researches (Dai 2021, Dong *et al.* 2024, Ghobad-Nejhad *et al.* 2024, Case *et al.* 2025, Wu *et al.* 2026). To date, only eight species (including the new species) have been described in *Punctulariopsis*, four of which are distributed in China (Ghobad-Nejhad *et al.* 2010, Muhammad *et al.* 2024, 2025, Yang *et al.* 2025),

indicating that the global species diversity of the genus remains poorly understood. In the present study, *P. tenuis* sp. nov. is described based on integrative evidence from morphology and phylogenetic analyses. This study enriches our knowledge of fungal diversity in southwestern China, and it is highly probable that additional taxa will be uncovered through continued fieldwork and molecular analyses.

Morphologically, *Punctulariopsis tenuis* resembles *P. fissurata*, *P. subglobispora* and *P. yunnanensis* in having a smooth hymenial surface. However, *P. fissurata* differs from *P. tenuis* by both bigger basidia ($85\text{--}109 \times 10\text{--}11.5\ \mu\text{m}$ vs. $15\text{--}24 \times 4.5\text{--}6.5\ \mu\text{m}$) and basidiospores ($13\text{--}15.5 \times 8.5\text{--}11.5\ \mu\text{m}$ vs. $6.5\text{--}8.5 \times 4.5\text{--}6.5\ \mu\text{m}$, Muhammad *et al.* 2025). *P. subglobispora* is distinguished from *P. tenuis* by its light ochraceous with a slight reddish tint hymenial surface and bigger basidiospores ($14.5\text{--}16 \times 9.5\text{--}12\ \mu\text{m}$ vs. $6.5\text{--}8.5 \times 4.5\text{--}6.5\ \mu\text{m}$, Ghobad-Nejhad *et al.* 2010). *P. yunnanensis* differs from *P. tenuis* by its gelatinous basidiomata and cream to pinkish buff to salmon hymenial surface (Muhammad *et al.* 2024).

Phylogenetically, the analyses of the combined ITS+LSU dataset (Figure 1) revealed that *Punctulariopsis tenuis* forms a single lineage within *Punctulariopsis* and is closely related to *P. asiana*, with strong support (100% BS, 1.00 BPP). However, *P. asiana* is distinguished from *P. tenuis* by its membranous basidiomata and narrower basidiospores ($7\text{--}12.5 \times 2\text{--}3\ \mu\text{m}$ vs. $6.5\text{--}8.5 \times 4.5\text{--}6.5\ \mu\text{m}$, Yang *et al.* 2025).

Species of *Punctulariopsis* serve important ecological functions as wood-inhabiting fungi within forest ecosystems. This genus demonstrates a marked preference for angiosperms. The newly described species, *P. tenuis*, as well as other recognized taxa, are exclusively associated with angiosperms. For example, *P. cremeoalbida* and *P. efibulata* are found on *Vitis* sp. and *Vaccinium* sp., respectively, whereas *P. fissurata*, *P. subglobispora*, and *P. yunnanensis* colonize fallen branches, logs, or bark of various angiosperms. In terms of geographic distribution, *Punctulariopsis* species have been documented in China, the United States, Argentina, and Ethiopia (Ghobad-Nejhad *et al.* 2010, Muhammad *et al.* 2024, 2025, Yang *et al.* 2025). Notably, four species have been reported from China, suggesting that this country possesses one of the highest levels of species diversity for this genus.

Fungi are evolutionarily closer to humans than to plants and may therefore be regarded as a strategic biological resource (Tedersoo *et al.* 2014, Wijesinghe *et al.* 2025). In addition to their ecological roles, the potential of fungi for application is increasingly recognized as an important component of fungal research and biodiversity assessment (Si *et al.* 2011, 2019, Case *et al.* 2025). However, climate change and habitat loss are accelerating biodiversity decline, and many species may disappear before they are discovered and documented (Hyde *et al.* 2024). Continued efforts to inventory fungal diversity and explore fungal applications are thus urgent and may facilitate the discovery of novel bioresources and products (Hyde *et al.* 2024).

In conclusion, the discovery and description of *Punctulariopsis tenuis* further enrich our understanding of species diversity within Corticiales. Continued fieldwork combined with integrative morphological and molecular approaches will undoubtedly reveal additional undescribed wood-inhabiting fungal taxa.

Key to the known species of *Punctulariopsis* worldwide

1	Generative hyphae thin-walled.....	2
1	Generative hyphae thick-walled.....	5
2	Generative hyphae with clamp connections.....	3
2	Generative hyphae with simple septa.....	<i>P. efibulata</i>
3	Basidiospores < 3 μm wide.....	<i>P. asiana</i>
3	Basidiospores > 3 μm wide.....	4
4	Hymenial surface cream, basidiospores broadly ellipsoid.....	<i>P. cremeoalbida</i>
4	Hymenial surface pale brown with a somewhat violet tint, basidiospores subglobose.....	<i>P. obducens</i>
5	Cystidia absent.....	6
5	Cystidia present.....	<i>P. tenuis</i>
6	Basidiospores < 13 μm long.....	<i>P. yunnanensis</i>
6	Basidiospores > 13 μm long.....	7
7	Hymenial surface slightly brown to yellowish brown.....	<i>P. fissurata</i>
7	Hymenial surface light ochraceous with a slight reddish tint.....	<i>P. subglobispora</i>

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