

## Molecular phylogeny and morphology reveal a new species of *Radulomyces* (Radulomycetaceae, Agaricales) from Southwestern China



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### Abstract

*Radulomyces tongbiguanensis* sp. nov., discovered in Yunnan Province, southwestern China, is described here as a new species based on its morphology and phylogenetic analysis. *Radulomyces tongbiguanensis* is characterized by its membranaceous basidiomata, which have a smooth hymenial surface and a monomitic hyphal system bearing clamp connections on the generative hyphae, and globose basidiospores measuring  $9.5\text{--}11.5 \times 9\text{--}11\ \mu\text{m}$ . Phylogenetic analyses of the new species were conducted based on internal transcribed spacer (ITS) and large subunit (LSU) ribosomal DNA (rDNA) sequences. The phylogenetic analysis indicated that the new species belongs to the genus *Radulomyces*, and is retrieved grouped with the species *R. zixishanensis*. However, morphologically *R. zixishanensis* differs from *R. tongbiguanensis* by cream to slightly brown basidiomata, narrower basidia ( $28\text{--}43 \times 6.5\text{--}8.5\ \mu\text{m}$  vs.  $28.5\text{--}40 \times 10\text{--}12.5\ \mu\text{m}$ ), and ellipsoid, narrower basidiospores ( $7\text{--}8.8 \times 5.5\text{--}6.8\ \mu\text{m}$  vs.  $9.5\text{--}11.5 \times 9\text{--}11\ \mu\text{m}$ ). A full description, illustrations, and phylogenetic analysis results of the new species are provided.

**Key words:** 1 new species, Biodiversity, Molecular systematics, Taxonomy, Wood-inhabiting fungi, Yunnan Province

### Introduction

Fungi exhibit enormous species diversity in terms of morphological, ecological, and nutritional characteristics (Song *et al.* 2024). Wood-inhabiting fungi play a crucial role in ecosystem processes, particularly in the degradation of wood and the recycling of organic matter (Dong *et al.* 2024).

The corticioid genus *Radulomyces* M.P. Christ., belonging to the family Radulomycetaceae Leal-Dutra *et al.*, was established by Christiansen (1960) with *R. confluens* (Fr.) M.P. Christ. as the type species. The genus is characterized by resupinate, effused, ceraceous, hygrophanous basidiomata; smooth, tuberculate, odontoid to raduloid hymenial surface; a monomitic hyphal system with clamp connections on generative hyphae, hyphal ends frequently present; lacking cystidia; sinuous basidia with abundant oil drops; and slightly thick-walled, smooth or minutely ornamented (spore dimorphism occurs in some species), ellipsoid to globose basidiospores (Christiansen 1960, Bernicchia & Gorjón 2010). Based on the MycoBank database (<http://www.mycobank.org>, accessed on 18 January 2025) and the Index Fungorum (<http://www.indexfungorum.org>, accessed on 18 January 2025), the genus *Radulomyces* has registered 33 specific and infraspecific names are registered under the genus *Radulomyces*, and six have been found from in China (Dong *et al.* 2024, 2025).

The placement of two genera *Aphanobasidium* Jülich and *Radulomyces* was previously located in the family Pterulaceae by the phylogenetic reconstructions of corticioid taxa (Larsson *et al.* 2004, Larsson 2007). Later,

phylogenetically, *Radulomyces* was placed in the family Pterulaceae (Agaricales) and was closely related to *Radulotubus* Y.C. Dai *et al.* and *Aphanobasidium* (Zhao *et al.* 2016). These three genera formed a strongly supported clade related to the *Pterula-Deflexula-Pterulicium-Merulicium-Coronicium* clade based on sequence analyses of ITS+nrLSU (Zhao *et al.* 2016, Wang *et al.* 2018). Based on the phylogenetical and morphological analysis, Leal-Dutra *et al.* (2020) revealed that members of the three genera (i.e., *Aphanobasidium*, *Radulomyces*, and *Radulotubus*) within this major clade were not pteruloid type (i.e., coralloid basidiomes with a dimitic hyphal system) in their morphology and then consequently they proposed the new family, Radulomycetaceae to accommodate them. Recently, based on phylogenetic analyses and morphological characteristics, six *Radulomyces* species have been described in China (Dong *et al.* 2024, 2025).

During investigations on the corticioid fungi in Yunnan Province, southwest China, two specimens of *Radulomyces* were collected. To clarify the taxonomic placement of these specimens, we conducted a phylogenetic and taxonomic study on the genus *Radulomyces*, based on ITS+nrLSU sequences. In this paper, these specimens are identified as a new species of *Radulomyces*. A description, illustrations, and phylogenetic analysis results of the new species are provided.

## Materials and methods

### *Sample collection and herbarium specimen preparation*

The fresh basidiomata were collected from a dead bamboo stem in Dehong, Yunnan Province, southwest China. The samples were photographed *in situ* by a Nikon D7100 camera, and fresh macroscopic details were recorded (Rathnayaka *et al.* 2024). Photographs were recorded. All the photos were focus-stacked using Helicon Focus software. Macroscopic details were recorded and transported to a field station where the basidiomata were dried in an electric food dryer at 40 °C (Hu *et al.* 2022). Once dried, the specimens were sealed in an envelope, placed in zip-lock plastic bags, and labeled (Dong *et al.* 2024). The dried specimens were deposited in the herbarium of the Southwest Forestry University (SWFC), Kunming, Yunnan Province, China.

### *Morphology*

The macromorphological descriptions were based on field notes and photos captured in the field and lab. Petersen (1996) was followed in the use of color terminology. The micromorphological data were obtained from dried specimens observed under a light microscope with a 10× 100 oil immersion objective (Zhao *et al.*, 2023a; Dong *et al.*, 2024). Sections mounted in 5% KOH and 2% phloxine B (C<sub>20</sub>H<sub>2</sub>Br<sub>4</sub>C<sub>14</sub>Na<sub>2</sub>O<sub>5</sub>) and other reagents, including Cotton Blue and Melzer's reagent, were also used to observe micromorphology, following the method described by Wu *et al.* (2022a). To show the variation in spore sizes, 5% of measurements were excluded from each end of the range and shown in parentheses. At least thirty basidiospores from each specimen were measured. Stalks were excluded from basidia measurements, and the hilar appendage was excluded from basidiospore measurements. The following abbreviations are used: KOH = 5% potassium hydroxide water solution, CB– = acyanophilous, CB+ = cyanophilous, IKI– = both inamyloid and non-dextrinoid, L = mean spore length (arithmetic average for all spores), W = mean spore width (arithmetic average for all spores), Q = variation in the L/W ratios between the specimens studied, Q<sub>m</sub> represented the average Q of basidiospores measured ± standard deviation, and n = a/b (number of spores (a) measured from given number (b) of specimens). The new species was registered in the MycoBank database (<http://www.mycobank.org>).

### *Molecular Phylogeny*

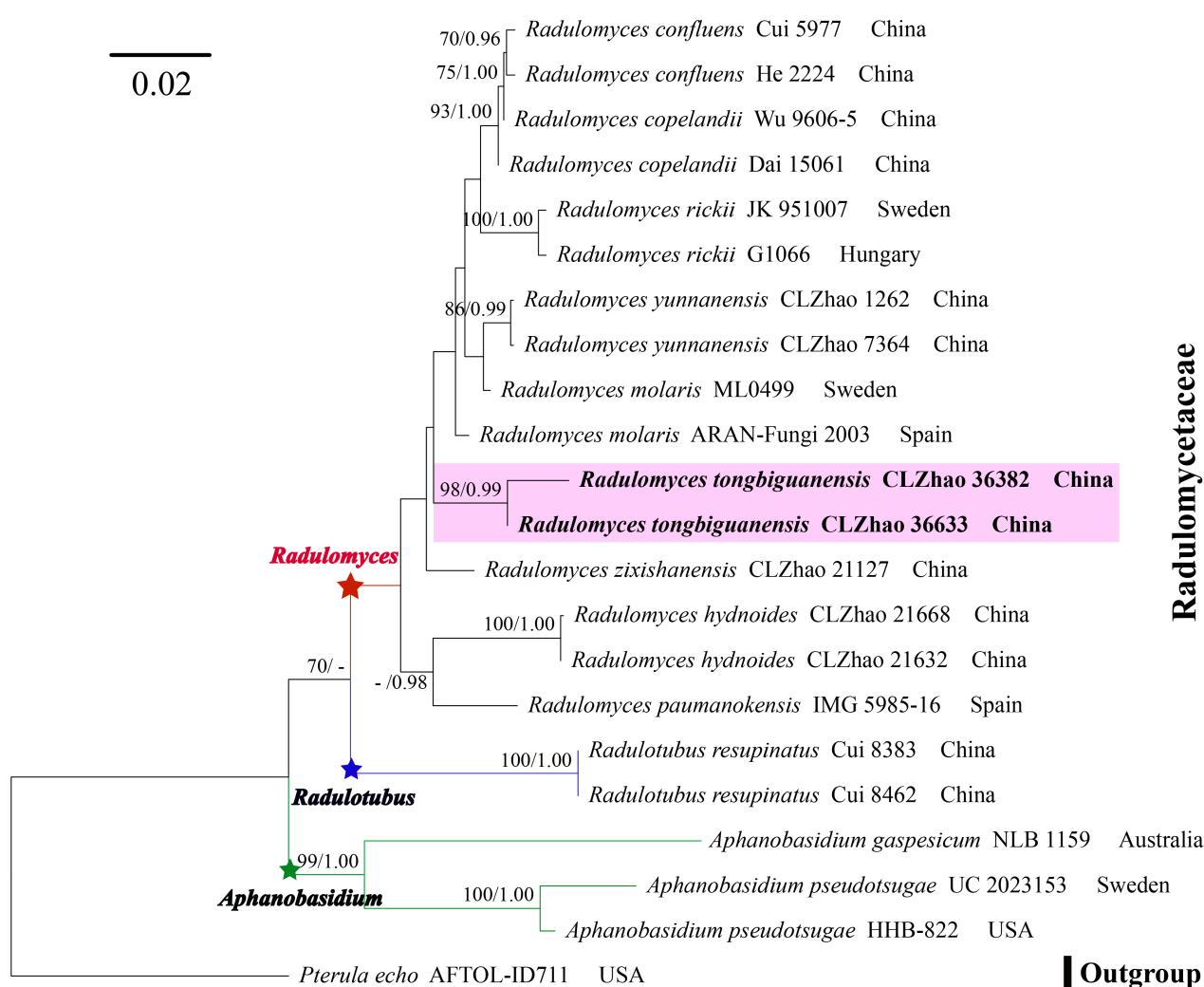
The CTAB rapid plant genome extraction kit-DN14 (Aidlab Biotechnologies Co., Ltd., Beijing, China) was used to obtain genomic DNA from the dried specimens according to the manufacturer's instructions. The nuclear ribosomal internal transcribed spacer (ITS) region was amplified with ITS5 and ITS4 primers (White *et al.* 1990). The nuclear large subunit (nrLSU) region was amplified using the LR0R and LR7 primer pair (Vilgalys & Hester 1990, Rehner & Samuels 1994). The PCR procedure for ITS was as follows: initial denaturation at 95 °C for 3 min, followed by 35 cycles of denaturation at 94 °C for 40 s, annealing at 58 °C for 45 s, and extension at 72 °C for 1 min, and a final extension at 72 °C for 10 min. The PCR procedure for nrLSU was as follows: initial denaturation at 94 °C for 1 min, followed by 35 cycles of denaturation at 94 °C for 30 s, annealing at 48 °C for 1 min, and extension at 72 °C for 1.5 min, and a final extension at 72 °C for 10 min. The PCR products were purified and sequenced at Kunming Tsingke Biological Technology Limited, Yunnan Province, P.R. China. The newly generated sequences were deposited in NCBI GenBank (Table 1).

**TABLE 1.** List of species, specimens, and GenBank accession numbers of sequences used in this study. The new species are in bold.

Species Name	Sample No.	GenBank Accession No.		Country	References
		ITS	nrLSU		
Aphanobasidium gaspeticum	NLB 1159	MT537001	MT524536	Australia	Unpublished
Aphanobasidium pseudotsugae	HHB-822	GU187509	GU187567	USA	Larsson 2007
Aphanobasidium pseudotsugae	UC 2023153	KP814353	AY586696	Sweden	Larsson 2007
Pterula echo	AFTOL-ID711	DQ494693	AY629315	USA	Wang <i>et al.</i> 2018
Radulomyces confluens	Cui 5977	KU535661	KU535669	China	Wang <i>et al.</i> 2018
Radulomyces confluens	He 2224	KU535662	KU535670	China	Wang <i>et al.</i> 2018
Radulomyces copelandii	Dai 15061	KU535664	KU535672	China	Wang <i>et al.</i> 2018
Radulomyces copelandii	Wu 9606-5	KU535663	KU535671	China	Wang <i>et al.</i> 2018
Radulomyces hydroides	CLZhao 21632	OR096184	OR449914	China	Dong <i>et al.</i> 2024
Radulomyces hydroides	CLZhao 21668	OR096185	OR449915	China	Dong <i>et al.</i> 2024
Radulomyces molaris	ARAN-Fungi 2003	—	MT232311	Spain	Olariaga <i>et al.</i> 2020
Radulomyces molaris	ML0499	AY463459	AY586705	Sweden	Larsson <i>et al.</i> 2004
Radulomyces paumanokensis	IMG 5985-16	MG050100	MG050110	Spain	Wang <i>et al.</i> 2018
Radulomyces paumanokensis	LE-BIN 4691	OL764917	—	Russia	Unpublished
Radulomyces rickii	JK 951007	—	AY586706	Sweden	Larsson <i>et al.</i> 2004
Radulomyces rickii	G1066	—	MK278543	Hungary	Varga <i>et al.</i> 2019
<b>Radulomyces tongbiguanensis</b>	<b>CLZhao 36382</b>	<b>PQ771190</b>	—	<b>China</b>	<b>Present study</b>
<b>Radulomyces tongbiguanensis</b>	<b>CLZhao 36633 *</b>	<b>PQ771191</b>	<b>PQ771192</b>	<b>China</b>	<b>Present study</b>
Radulomyces yunnanensis	CLZhao 1262	OR096191	OR449917	China	Dong <i>et al.</i> 2024
Radulomyces yunnanensis	CLZhao 7364	OR096192	OR449918	China	Dong <i>et al.</i> 2024
Radulomyces zixishanensis	CLZhao 21127	ON033887	OR449922	China	Dong <i>et al.</i> 2024
Radulotubus resupinatus	Cui 8383	KU535660	KU535668	China	Zhao <i>et al.</i> 2016
Radulotubus resupinatus	Cui 8462	KU535657	KU535665	China	Zhao <i>et al.</i> 2016

The sequences were aligned using MAFFT version 7 (Katoh *et al.* 2019) with the G-INS-i strategy. The alignment was adjusted manually using AliView version 1.27 (Larsson 2014). The dataset was first aligned, and then the sequences of ITS+nrLSU were combined using Mesquite version 3.51. The combined ITS+nrLSU sequences and ITS datasets were used to infer the position of the new species in the genus *Radulomyces* and related species. Sequences of *Pterula echo* D.J. McLaughlin & E.G. McLaughlin were retrieved from GenBank, and used as outgroup taxa in the ITS+nrLSU analysis (Fig. 1). *Radulotubus resupinatus* Y.C. Dai *et al.* was selected as the outgroup taxon in the ITS analysis (Fig. 2), following the approach of Dong *et al.* (2024).

Maximum Likelihood (ML) and Bayesian Inference (BI) analyses were applied to the combined datasets, following a previous study (Zhou *et al.* 2024). Maximum Likelihood (ML) analysis was performed using RAxML-HPC BlackBox in the CIPRES Science Gateway (<https://www.phylo.org/portal2/login!input.action>, Miller *et al.* 2012) with a GTRCAT model of evolution and 1,000 bootstrap replicates (Felsenstein 1985). jModelTest v2 (Darriba *et al.* 2012) was used to determine the best-fit evolution model for each dataset for the purposes of Bayesian Inference (BI); Bayesian Inference was performed using MrBayes 3.2.7a (Ronquist *et al.* 2012). Four Markov chains were run from random starting trees. Trees were sampled every 1,000 generations. The first 25% of sampled trees were discarded as burn-in, while the remaining trees were used to construct a 50% majority consensus tree and to calculate Bayesian posterior probabilities (BPPs). Branches were considered significantly supported if they received a maximum likelihood bootstrap value (BS) of  $\geq 70\%$  and Bayesian posterior probabilities (BPP) of  $\geq 0.95$ .



**FIGURE 1.** Maximum Likelihood strict consensus tree illustrating the *Radulomyces tongbiguanensis* and related species in the family Radulomycetaceae based on the combined ITS+nrLSU sequences. 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.

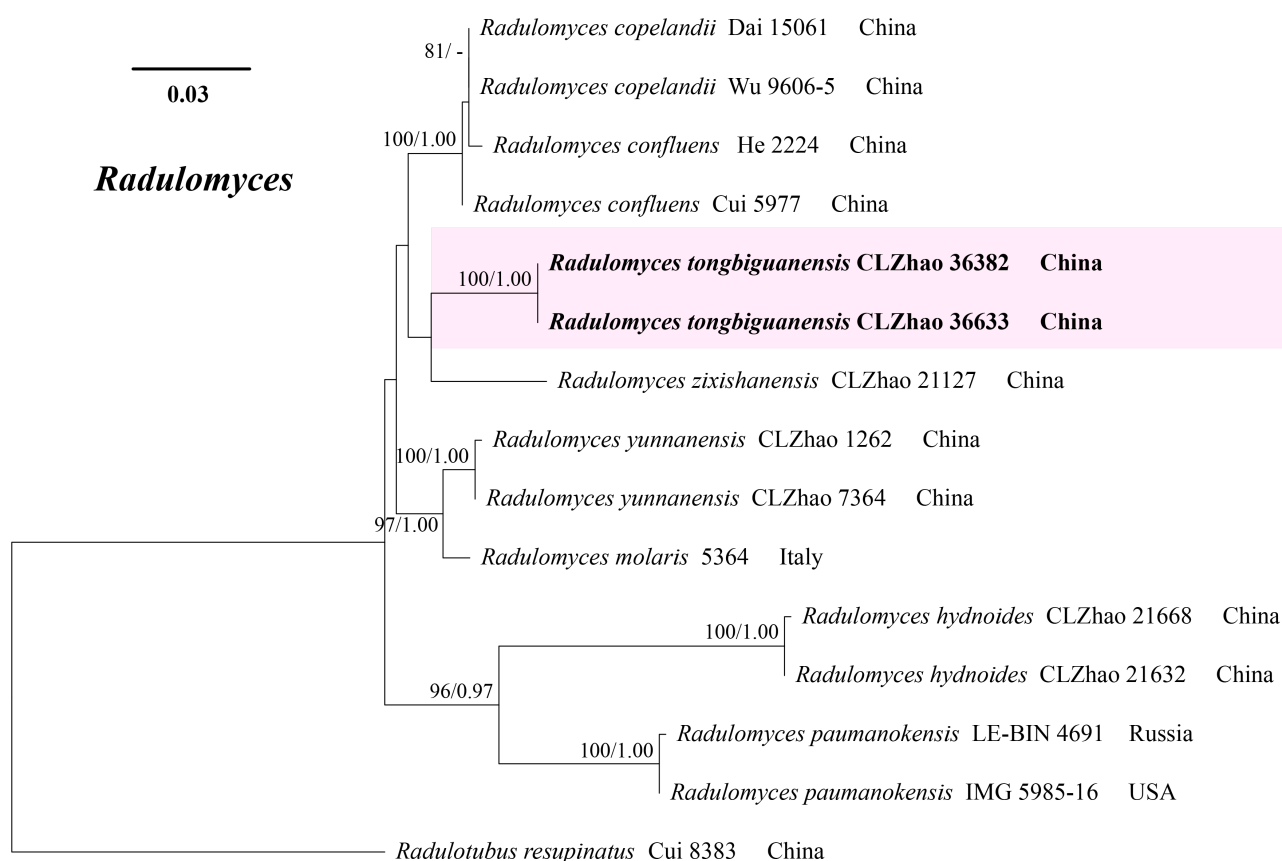
## Results

### Molecular phylogeny

The aligned ITS+nrLSU dataset comprised 22 specimens representing 13 species. Four Markov chains were run for two independent runs from random starting trees, each for 0.8 million generations, using the combined ITS+nrLSU dataset (Fig. 1), with trees and parameters sampled every 1,000 generations. The best model for the ITS+nrLSU dataset, estimated and applied in the Bayesian analysis, was SYM+I+G. Maximum Likelihood (ML) and Bayesian Inference (BI) analysis yielded a similar topology, with an average standard deviation of split frequencies of 0.013291 (BI). The effective sample size (ESS) for Bayesian analysis across the two runs was approximately double the average ESS (avg. ESS) of 579.5.

The aligned ITS dataset comprised 15 specimens representing nine species. Four Markov chains were run for two independent runs from random starting trees, each for 0.3 million generations, using the ITS-only (Fig. 2) data set with trees and parameters sampled every 1000 generations. The best model for the ITS dataset, estimated and applied in the Bayesian analysis, was HKY+G. Maximum Likelihood (ML) and Bayesian Inference (BI) analysis yielded a similar topology, with an average standard deviation of split frequencies of 0.004903 (BI). The effective sample size (ESS) for Bayesian analysis across the two runs was approximately double the average ESS (avg. ESS) of 487.

The phylogram based on the combined ITS+nrLSU sequences (Fig. 1) indicated that the species *Radulomyces tongbiguanensis* was assigned to the genus *Radulomyces*. The topology based on ITS sequences (Fig. 2) revealed that *R. tongbiguanensis* grouped with the species *R. zixishanensis* J.H. Dong & C.L. Zhao.



**FIGURE 2.** Maximum Likelihood strict consensus tree illustrating the *Radulomyces tongbiguanensis* and related species in the genus *Radulomyces* based on the combined ITS sequences. 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

*Radulomyces tongbiguanensis* J.H. Dong & C.L. Zhao, *sp. nov.* Figs. 3–5

MycoBank no.: MB 857049

**Etymology:**—*Tongbiguanensis* (Lat.) refers to the type locality “Tongbiguan Nature Reserve, China”

**Diagnosis:**—Distinguishes it from other species of *Radulomyces* by its membranaceous, cream to straw-colored basidiomata, smooth hymenial surface, a monomitic hyphal system with clamped generative hyphae, and globose basidiospores ( $9.5\text{--}11.5 \times 9\text{--}11\ \mu\text{m}$ ).

**Holotype:**—CHINA. Yunnan Province, Dehong, Tongbiguan Nature Reserve, GPS coordinates  $23^{\circ}38'N$ ,  $97^{\circ}32'E$ , altitude 850 m asl., on a dead bamboo, leg. C.L. Zhao, 29 June 2024, CLZhao 36633 (SWFC!).

**Basidiomata:**—Annual, resupinate, adnate, soft membranaceous, without odor or taste when fresh, becoming coriaceous upon drying, up to 15 cm long, 8 cm wide, 100  $\mu\text{m}$  thick. Hymenial surface smooth, cream to slightly buff when fresh, turning slightly buff to straw upon drying. Sterile margin cream, thinning out, up to 0.5 mm wide.

**Hyphal structure:**—Hyphal system monomitic, generative hyphae with clamp connections, colorless, thin- to thick-walled, branched, interwoven,  $2.5\text{--}4.5\ \mu\text{m}$  in diameter; hyphal ends present in the basidial layer,  $2.5\text{--}3\ \mu\text{m}$  in diameter; IKI–, CB–, tissues unchanged in KOH.

**Hymenium:**—Cystidia and cystidioles absent. Basidia clavate, slightly sinuous or constricted in the middle, with a few granules, four sterigmata, and a basal clamp connection,  $28.5\text{--}40 \times 10\text{--}12.5\ \mu\text{m}$ ; basidioles dominant, similar to basidia in shape, but slightly smaller.

**Basidiospores:**—Globose, slightly thick-walled, smooth, colorless, IKI–, CB+,  $(9.2\text{--})9.5\text{--}11.5(-12) \times (8.5\text{--})9\text{--}11(-11.5)\ \mu\text{m}$ ,  $L = 10.32\ \mu\text{m}$ ,  $W = 9.95\ \mu\text{m}$ ,  $Q = 1.01\text{--}1.10$ ,  $Q_m = 1.04 \pm 0.03$  ( $n = 60/2$ ).

**Additional specimen examined:**—CHINA. Yunnan Province, Dehong, Tongbiguan Nature Reserve, GPS coordinates  $23^{\circ}38'N$ ,  $97^{\circ}32'E$ , altitude 850 m asl., on a dead bamboo, leg. C.L. Zhao, 29 June 2024, CLZhao 36382 (SWFC!).

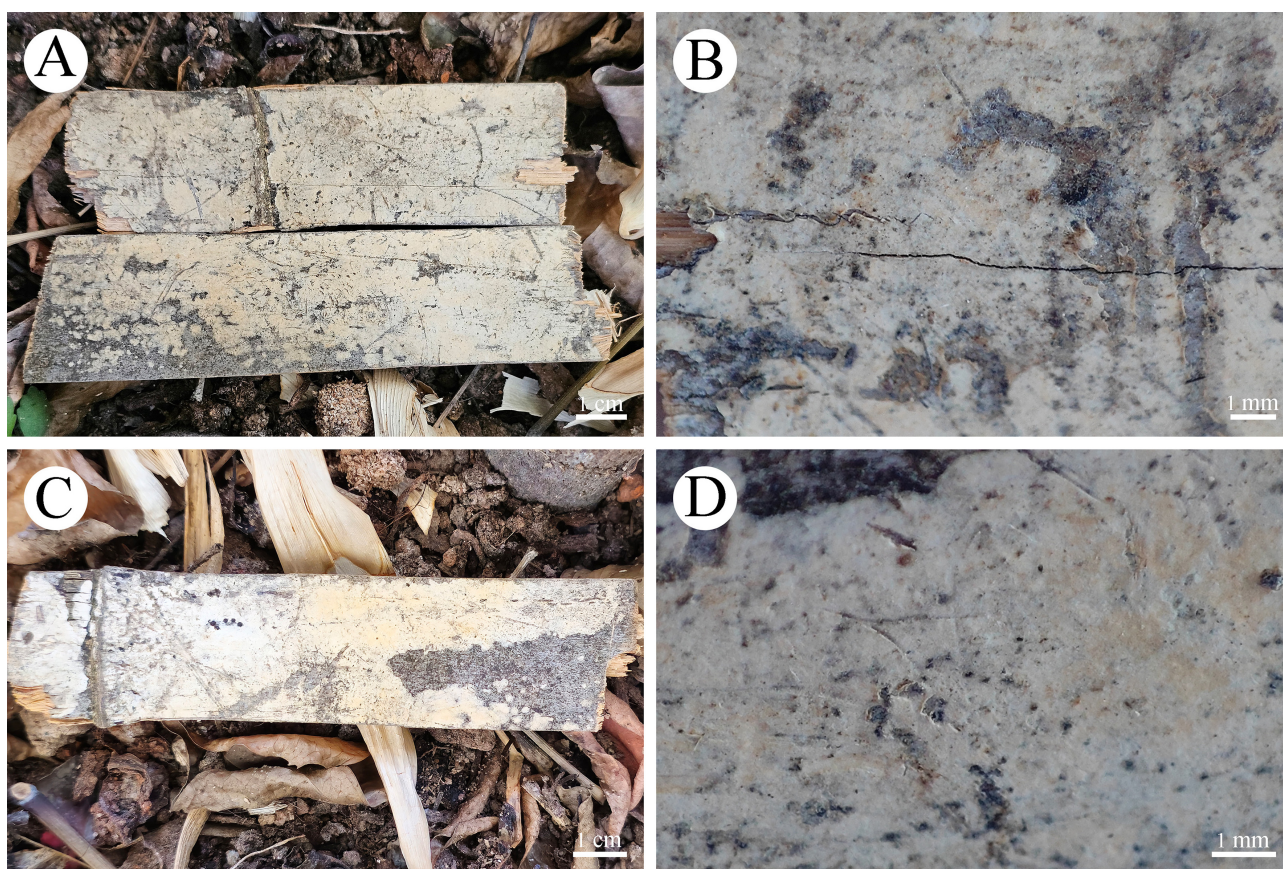
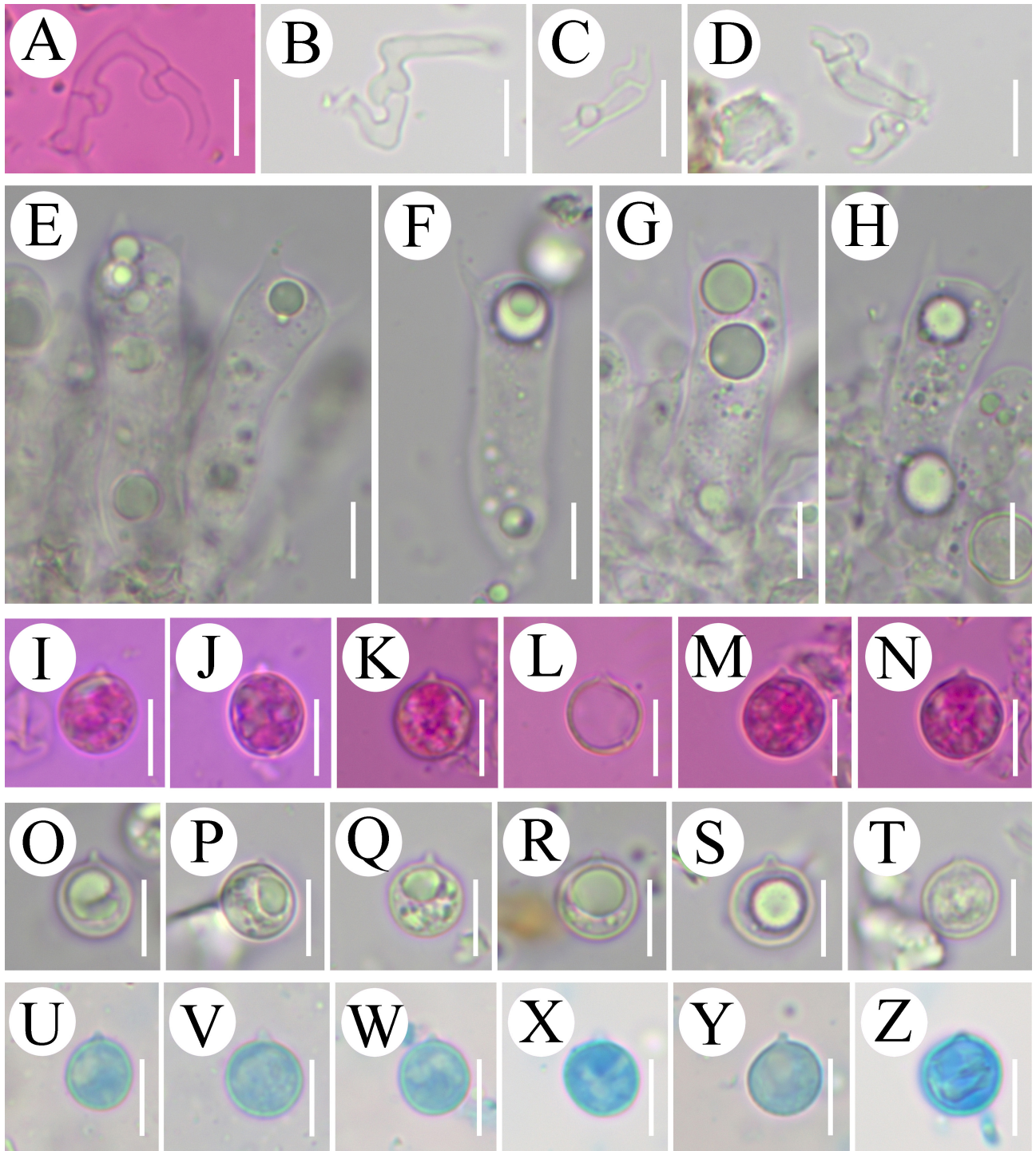
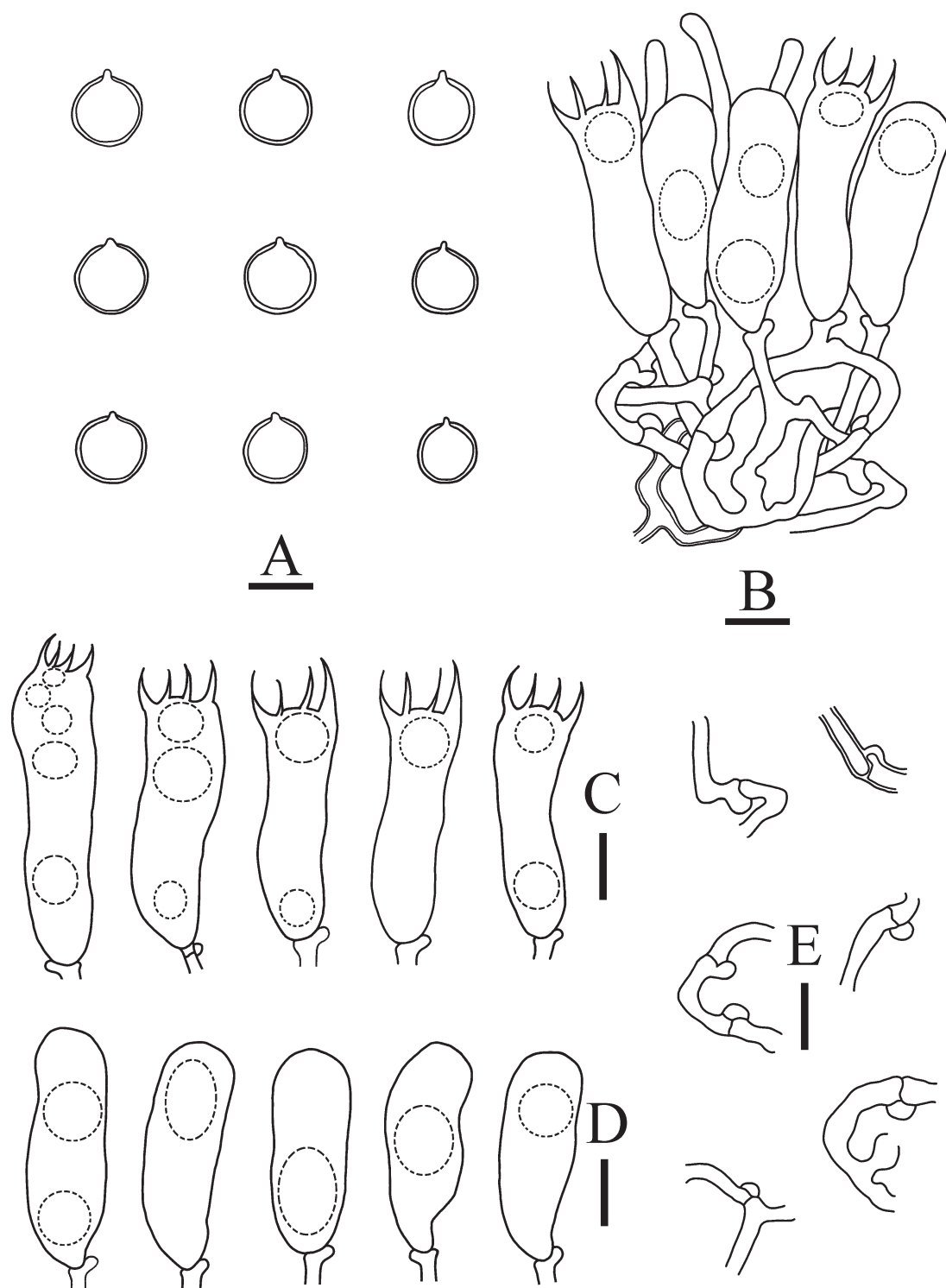


FIGURE 3. Basidiomata of *Radulomyces tongbiguanensis* (A, B) CLZhao 36633 (holotype); (C, D) CLZhao 36382.





**FIGURE 4.** Sections of hymenium of *Radulomyces tongbiguanensis* (holotype, CLZhao 36633). (A–D) Hyphae; (E–H) Basidia; (I–Z) Basidiospores. Scale bars: A–Z = 10 µm.



**FIGURE 5.** Microscopic structures of *Radulomyces tongbiganensis* (holotype, CLZhao 36633). (A) Basidiospores; (B) Part of the vertical section of hymenium; (C) Basidia; (D) Basidioles; (E) Hyphae. Scale bars: A–E = 10  $\mu$ m.



## Discussion

In the present study, a new species, *Radulomyces tongbiguanensis*, is described based on phylogenetic analyses and morphological characteristics.

Phylogenetically, the topology based on ITS and ITS+nrLSU sequences (Fig. 2) revealed that *Radulomyces tongbiguanensis* is grouped with *R. zixishanensis*. However, morphologically, *R. zixishanensis* differs from *R. tongbiguanensis* by cream to slightly brown basidiomata, narrower basidia ( $28\text{--}43 \times 6.5\text{--}8.5\ \mu\text{m}$  vs.  $28.5\text{--}40 \times 10\text{--}12.5\ \mu\text{m}$ ), and ellipsoid, narrower basidiospores ( $7\text{--}8.8 \times 5.5\text{--}6.8\ \mu\text{m}$  vs.  $9.5\text{--}11.5 \times 9\text{--}11\ \mu\text{m}$ , Dong *et al.* 2024)

Morphologically, *Radulomyces tongbiguanensis* resembles *R. copelandii* (Pat.) Hjortstam & Spooner, *R. hydroides*, and *R. paumanokensis* J. Horman *et al.* in having subglobose to globose, slightly thick-walled basidiospores. However, *R. copelandii* differs from *R. tongbiguanensis* due to its white hymenial surface, narrower basidia ( $29\text{--}35 \times 6\text{--}7\ \mu\text{m}$  vs.  $28.5\text{--}40 \times 10\text{--}12.5\ \mu\text{m}$ ), and smaller basidiospores ( $6.4\text{--}7 \times 5.4\text{--}6.2\ \mu\text{m}$  vs.  $9.5\text{--}11.5 \times 9\text{--}11\ \mu\text{m}$ , Ginns & Millman 2011). *Radulomyces hydroides* is distinguished from *R. tongbiguanensis* by its hydroid hymenial surface and smaller basidiospores ( $7.5\text{--}9 \times 7\text{--}8.7\ \mu\text{m}$  vs.  $9.5\text{--}11.5 \times 9\text{--}11\ \mu\text{m}$ , Dong *et al.* 2024). *R. paumanokensis* differentiates from *R. tongbiguanensis* by a hydroid hymenial surface, narrower basidia ( $25\text{--}31 \times 5\text{--}7.5\ \mu\text{m}$  vs.  $28.5\text{--}40 \times 10\text{--}12.5\ \mu\text{m}$ ), and smaller basidiospores ( $5.8\text{--}6.9 \times 5.2\text{--}6.4\ \mu\text{m}$  vs.  $9.5\text{--}11.5 \times 9\text{--}11\ \mu\text{m}$ , Wang *et al.* 2018).

Fungi are closer to humans than to plants and can therefore be considered a strategic biological resource (Ming *et al.* 2023). The application potential of fungi is as important as their natural attributes in recognizing fungi (Liu *et al.* 2024). Climate change and the destruction of natural habitats are also threatening species, and many may become extinct before they are even discovered (Hyde *et al.* 2024b). Studies on the biodiversity of fungi and their applications are important, as they may lead to new products (Hyde *et al.* 2024a). Therefore, it is now urgent to recognize and conserve fungi for future utilization.

The wood-rotting fungi are an extensively studied group of Basidiomycota, which includes several poroid, smooth, grandinoid, odontoid and hydroid basidiomata, and previously many new taxa were described from China (Cui *et al.* 2019, Wu *et al.* 2020, 2022a, b, Wang *et al.* 2021, 2023, 2024, Liu *et al.* 2022, 2023, Mao *et al.* 2023, Zhao *et al.* 2023a, b, 2024, Yuan *et al.* 2023, Dong *et al.* 2024, 2025). Only six species of *Radulomyces* have been found in China (Dong *et al.* 2024, 2025). Therefore, the diversity of *Radulomyces* species remains largely unknown in China, particularly in subtropical and tropical regions. This paper enhances our understanding of fungal diversity in this region, and it is likely that further fieldwork and molecular analyses will reveal additional new taxa.

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