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Efibula cremea sp. nov. (Irpicaceae, Polyporales), a coriaceous fungus from Yunnan Province, China

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Abstract

A new species, *Efibula cremea*, found in Yunnan Province, China, is described and illustrated based on morphological and phylogenetic analyses. *Efibula cremea* is characterized by its coriaceous basidiomata with a grandinioid hymenial surface, a monomitic hyphal system with generative hyphae bearing simple-septate, and ellipsoid basidiospores measuring 4.7–5.7 × 3.3–4 µm. Sequences of ITS and nLSU of the studied samples were generated, and phylogenetic analysis was performed with Maximum Likelihood, Maximum Parsimony, and Bayesian Inference methods. The phylogenetic analysis indicated that the new species belongs to the genus *Efibula* and is grouped with the taxa *E. daweishanensis*, *E. grandinosa*, and *E. shenghuae*. A description, illustrations, and phylogenetic analysis results of the new species are provided. The discovery of this species not only contributes to the diversity of *Efibula* in subtropical Asia but also provides further clarification of its phylogenetic relationships.

Key words: Morphology, New taxon, Polyporales, Taxonomy, Wood-inhabiting fungi

Introduction

The fungal kingdom is more than one billion years old and comprises millions of species of remarkable morphological diversity, ranging from macroscopic mushrooms to microscopic unicellular yeasts (Case *et al.* 2025). These eukaryotic organisms exhibit tremendous genomic and phenotypic plasticity, and this adaptive evolutionary potential has made them central to Earth's ecosystems (Case *et al.* 2025). Fungi secrete a spectacular array of bioactive chemical compounds and enzymes, which play crucial roles in the biosphere, from digesting organic matter and recycling nutrients from dead plant and animal tissues to mediating intimate and mutually beneficial associations with the roots of almost all land plants (Case *et al.* 2025). In the ecosystem, wood-inhabiting fungi are found in living trees, dead standing trees, fallen decorticated trunks, fallen trunks and branches, stumps as well as manufactured wood products (Dai 2010, Cui *et al.* 2019, Wu *et al.* 2022, Yuan *et al.* 2023), in which these fungi secrete various enzymes that effectively degrade cellulose, hemicellulose and lignin into simple inorganic substances, and consequently play an important role in forest ecosystems as an important group of decomposers (Dai *et al.* 2011, 2021, Yang *et al.* 2023, Li *et al.* 2024, Yang *et al.* 2025).

The genus *Efibula* Sheng H. Wu (1990: 21) was introduced by Wu (1990) and typified by *E. tropica* Sheng H. Wu (1990: 21). The genus is characterized by resupinate basidiomata with smooth hymenophore, compact subiculum; a monomitic hyphal system, generative hyphae with simple septa, and a lack of cystidia; basidia cylindrical to clavate, and hyaline, thin-walled, smooth, ellipsoid to oblong, acyanophilous basidiospores (Wu 1990). Based on the MycoBank database (http://www.mycobank.org, accessed on 25 August 2025) and the Index Fungorum (http://www.indexfungorum.org, accessed on 25 August 2025), the genus *Efibula* has a registry of 31 specific and infraspecific names, of which approximately 27species of *Efibula* are currently accepted.

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A phylogenetic study revising the family-level classification within the order Polyporales showed that both species *E. clarkii* Floudas & Hibbett (2015: 710) and *E. gracilis* Floudas & Hibbett (2015: 711) grouped into the genus *Efibula* within the family Irpicaceae (Justo *et al.* 2017, Wang *et al.* 2023). During their investigation of corticoid fungi in southern China, Ma *et al.* (2020) reconstructed the phylogenetic tree of *Efibula*, revealing relationships among species of this genus. Phylogenetic analyses of multiple genes revealed that the genus *Efibula* was paraphyletic, but insufficient morphological evidence supported the recognition of separate genera (Chen *et al.* 2021). Subsequently, further research identified four distinct subclades within *Efibula* and recovered a well-supported clade comprising *Phanerochaete allantospora* Burds. & Gilb. (1974: 780), *Leptoporus mollis* (Pers.) Quél. (1886: 175), and several species from the genus *Ceriporia* Donk (1933: 170) and *Candelabrochaete* Boidin (1970: 24) (Li *et al.* 2022). Using ITS, nLSU, and TEF1 sequences, which play crucial roles in the biosphere, from digesting organic matter and recycling nutrients from dead plant and animal tissues to mediating introduced the taxonomy and phylogeny of taxa within *Efibula* from China.

Recently, we found a coriaceous taxon in Yunnan Province, China. Morphological and molecular phylogenetic evidence supported the recognition of the new species within *Efibula*, based on internal transcribed spacer (ITS) regions and the large subunit nuclear ribosomal RNA gene (nLSU). Detailed descriptions, illustrations, and phylogenetic analysis results for the new species are provided.

Materials and methods

Sample collection and herbarium specimen preparation

Fresh basidiomata of the wood-inhabiting fungi growing on angiosperm branches were collected from a broad-leaf forest in Zhaotong, Yunnan Province, China. The samples were photographed *in situ* using a Jianeng 80D camera, collection details were recorded (Rathnayaka *et al.* 2025), and the samples were taken to the laboratory, where fresh macroscopic details were recorded. All the photos taken in the field were focus stacked using Helicon Focus software. Specimens were dried in an electric food dehydrator at 40 °C (Hu *et al.* 2022), then sealed in an envelope and deposited in the herbarium of Southwest Forestry University (SWFC), Kunming, Yunnan Province, China.

Morphology

The macromorphological descriptions were based on field notes and photos taken in the field and in the lab. Petersen (1996) was followed for the color terminology. The micromorphological data were obtained from the dried specimens using a light microscope with a 1000× magnification using a 100× oil immersion objective with a 10× ocular lens (Zhao *et al.* 2023, Dong *et al*. 2024), in which the measurements (e.g., spore sizes) did not change in water, CB, IKI, and KOH. The following abbreviations are used: KOH = 5% potassium hydroxide water solution, CB = Cotton Blue, CB– = acyanophilous, IKI = Melzer's Reagent, IKI– = both inamyloid and indextrinoid, L = mean spore length (average for all spores), W = mean spore width (average for all spores), Q = variation in the L/W ratios between the specimens studied and n = a/b (number of spores (a) measured from given number (b) of specimens). The MycoBank number will be registered in the MycoBank database (http://www.mycobank.org).

Molecular Phylogeny

The CTAB rapid fungal genome extraction HiPure Fungal DNA Mini Kit II (Meiji Biotechnologies Co. Ltd., Guangzhou) was used to extract genomic DNA from dried specimens according to the manufacturer's instructions. The ITS region was amplified with the primer pair ITS5 and ITS4 (White *et al.* 1990), and the nLSU region with primer pair LR0R and LR7 (Vilgalys & Hester 1990, Hopple 1994). The PCR cycling procedure for ITS was as follows: an initial denaturation at 95 °C for 3 min, followed by 35 cycles at 94 °C for 40 s, 58 °C for 45 s, and 72 °C for 1 min, and a final extension at 72 °C for 10 min (Shen *et al.* 2019). The PCR procedure for nLSU was as follows: an initial denaturation at 94 °C for 1 min, followed by 35 cycles at 94 °C for 30 s, 48 °C for 1 min, and 72 °C for 1.5 min, and a final extension at 72 °C for 10 min. The PCR products were purified and directly sequenced at the Kunming Tsingke Biological Technology Ltd. Co. (Yunnan, P.R. China). All newly generated sequences were deposited in GenBank (Table 1).

TABLE 1. A list of species, specimens, and GenBank accession numbers of sequences used in this study. The new species is in bold.

Species name	Sample no.	GenBank accessions no.		Country	References
		ITS	LSU		
Byssomerulius corium	FP-102382	KP135007	KP135230	USA	Justo *et al.* 2017
Byssomerulius corium	Wu 1708-327	LC427007	LC427031	China	Chen *et al.* 2020
Ceriporia reticulata	CBS 462.50	MH856710	MH868228	France	Vu *et al.* 2019
Ceriporia reticulata	RLG-11354-Sp	KP135041	KP135204	USA	Justo *et al.* 2017
Efibula americana	FP-102165	KP135016	KP135256	USA	Floudas & Hibbett 2015
Efibula americana	HHB-8468	KP135012	–	USA	Floudas & Hibbett 2015
Efibula daweishanensis	CLZhao 18946	OR094488	–	China	Dong *et al.* 2024
Efibula daweishanensis	CLZhao 19002	OR094489	OR449958	China	Dong *et al.* 2024
Efibula gracilis	FD-455	KP135027	MZ637116	USA	Chen *et al.* 2021
Efibula gracilis	FP-102052	KP135028	–	China	Floudas & Hibbett 2015
Efibula grandinosa	He 6312	MZ422509	MZ422480	China	Li *et al.* 2022
Efibula hainanensis	He 6004	MW580949	MW580939	China	Li *et al.* 2022
Efibula hainanensis	Chen 1284	ON117184	–	China	Li *et al.* 2022
Efibula intertexta	Wu 1707-93	MZ636953	MZ637117	China	Chen *et al.* 2021
Efibula intertexta	Wu 1707-96	MZ636954	MZ637118	China	Chen *et al.* 2021
Efibula matsuensis	Chen 1510	MZ636955	–	China	Chen *et al.* 2021
Efibula matsuensis	Wu 1011-19	MZ636957	MZ637120	China	Chen *et al.* 2021
Efibula cremea	**Clzhao 19248**	**PV759508**	**PV857759**	**China**	**Present study**
Efibula cremea	**Clzhao 19298**	**PV759509**	**PV857760**	**China**	**Present study**
Efibula shenghuae	He 3384	MZ422508	MZ422479	China	Li *et al.* 2022
Efibula subglobispora	Chen 1716	MZ636962	MZ637124	China	Chen *et al.* 2021
Efibula subglobispora	GC 1604-13	MZ636963	MZ637125	China	Chen *et al.* 2021
Efibula tropica	WEI 18-149	MZ636967	MZ637129	China	Chen *et al.* 2021
Efibula tropica	Wu 0809-8	MZ636968	MZ637130	China	Chen *et al.* 2021
Efibula tuberculata	Wu 0711-148	MZ636969	MZ637131	Finland	Chen *et al.* 2021
Efibula tuberculata	Wu 1005-55	MZ636970	MZ637132	Finland	Chen *et al.* 2021
Efibula turgida	Wu 0910-86	MZ636972	MZ637134	China	Chen *et al.* 2021
Efibula turgida	Wu 0910-99	MZ636973	MZ637135	China	Chen *et al.* 2021
Efibula taiwanensis	He 4582	MZ422507	MZ422478	China	Li *et al.* 2022
Efibula yunnanensis	CLZhao 11641	MT611529	–	China	Ma *et al.* 2020
Efibula yunnanensis	GC 1608-1	MZ636975	MZ637137	China	Chen *et al.* 2021
Gloeoporus dichrous	CBS 446.50	MH856705	MH868222	Canada	Vu *et al.* 2019
Gloeoporus dichrous	Dai 16370A	KU360399	KU360406	China	Yuan *et al.* 2016
Gloeoporus pannocinctus	FCUG 2019	AF141612	AF141612	Sweden	Yuan *et al.* 2016
Gloeoporus pannocinctus	CBS 291.71	MH860130	MH871903	France	Vu *et al.* 2019
Gloeoporus thelephoroides	BZ-2896	MG572757	MG572741	Belize	Jung *et al.* 2018
Irpex favus	Wu 0705-1	MZ636988	MZ637149	China	Chen *et al.* 2021
Irpex favus	Wu 0705-2	MZ636989	MZ637150	China	Chen *et al.* 2021
Irpex flavus	WHC 1381	LC427029	LC427052	China	Chen *et al.* 2021
Irpex flavus	LE295997	KF856505	KF856510	Tanzania	Zmitrovich & Malysheva 2014
Irpex laceratus	WHC 1372	MZ636990	MZ637151	China	Chen *et al.* 2021
Irpex latemarginatus	Piatek 1997	KX752592	KX752592	China	Chen *et al.* 2021
Irpex lacteus	FD-9	KP135026	KP135224	USA	Chen *et al.* 2021
Irpex lenis	Wu 1608-14	MZ636991	MZ637152	China	Chen *et al.* 2021

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TABLE 1. (Continued)

Species name	Sample no.	GenBank accessions no.		Country	References
		ITS	LSU		
Irpex lenis	Wu 1608-2	MZ636992	MZ637153	China	Chen *et al.* 2021
Irpex rosea	CLZhao 18491	MW377575	MW377578	China	Wang & Zhao 2021
Irpex rosea	CLZhao 18489	MW377574	MW377577	China	Wang & Zhao 2021
Irpex rosettiformis	Meijer 3729	JN649346	JN649346	China	Chen *et al.* 2021
Leptoporus mollis	TJV-93-174-T	KY948795	EU402510	USA	Chen *et al.* 2021
Leptoporus mollis	RLG 7163	KY948794	MZ637155	USA	Chen *et al.* 2021
Meruliopsis leptocystidiata	Wu 1708-15	LC427012	LC427032	China	Chen *et al.* 2020
Meruliopsis leptocystidiata	Wu 1708-43	LC427013	LC427033	China	Chen *et al.* 2020
Meruliopsis taxicola	CBS 455.48	MH856432	MH867978	Canada	Vu *et al.* 2019
Meruliopsis taxicola	BU061013-38	MG572756	MG572740	South Korea	Jung *et al.* 2018
Phanerochaetella angustocystidiata	Wu 9606-39	MZ637020	GQ470638	China	Chen *et al.* 2021
Phanerochaetella leptoderma	Chen 1362	MZ637025	GQ470646	China	Chen *et al.* 2021
Trametopsis aborigena	Robledo 1236	KY655336	KY655338	Argentina	Gomez-Montoya *et al.* 2017
Trametopsis aborigena	Robledo 1238	KY655337	KY655339	Argentina	Gomez-Montoya *et al.* 2017
Trametopsis brasiliensis	Meijer 3637	JN710510	JN710510	Brazil	Gomez-Montoya *et al.* 2017
Trametopsis cervina	PRM900574	AY684175	AY855907	Czech Republic	Tomšovský *et al.* 2006
Phanerochaete rhodella	FD-18	KP135187	KP135258	USA	Justo *et al.* 2017

The sequences were aligned with MAFFT version 7 (Katoh *et al.* 2019) using the G-INS-i strategy. The alignment was adjusted manually using AliView version 1.27 (Larsson 2014). Each dataset was aligned separately at first, and then the ITS and nLSU regions were combined with Mesquite version 3.51. Sequences of *Phanerochaete rhodella* (Peck) Floudas & Hibbett (2015: 700) were selected as the outgroup in the ITS+nLSU analysis (Fig. 1), following a previous study (Justo *et al.* 2017). Sequences of *Byssomerulius corium* (Pers.) Parmasto (1967: 383) was selected as an outgroup in the ITS analysis (Fig. 2) as inspired by a previous study (Justo *et al.* 2017).

Maximum parsimony analysis in PAUP* version 4.0b10 (http://phylosolutions. com/paup-test/) was applied to ITS and the combined ITS+nLSU dataset following a previous study (Zhao & Wu 2017). All characters were equally weighted, and gaps were treated as missing data. Trees were inferred using the heuristic search option with TBR branch swapping and 1,000 random sequence additions. Max-trees were set to 5,000, and branches of zero length were collapsed, and all parsimonious trees were saved. Clade robustness was assessed using bootstrap (BT) analysis with 1,000 pseudo-replicates (Felsenstein 1985). Descriptive tree statistics, tree length (TL), composite consistency index (CI), composite retention index (RI), composite rescaled consistency index (RC), and composite homoplasy index (HI) were calculated for each maximum parsimonious tree generated. The combined dataset was also analyzed using Maximum Likelihood (ML) in RAxML-HPC2 through the CIPRES Science Gateway (Miller *et al.* 2012). Branch support (BS) for the ML analysis was determined by 1,000 bootstrap pseudo-replicates.

MrModeltest 2.3 was used to determine the best-fit evolutionary model for each dataset for Bayesian inference (BI) (Nylander 2004). It was performed using MrBayes 3.2.7a with a GTR+I+G model of DNA substitution and a gamma distribution rate variation across sites (Ronquist *et al.* 2012). A total of four Markov chains were run for two random starting trees, each for one million generations, for ITS+nLSU (Fig. 1) and for ITS (Fig. 2), with trees and parameters sampled every 1,000 generations. The first quarter of each generation was discarded as a burn-in. A majority rule consensus tree was computed from the remaining trees. Branches were considered significantly supported if they received a maximum likelihood bootstrap support value (BS) of ≥ 70%, a maximum parsimony bootstrap support value (BT) of ≥ 50% or a Bayesian posterior probability (BPP) of ≥ 0.95.

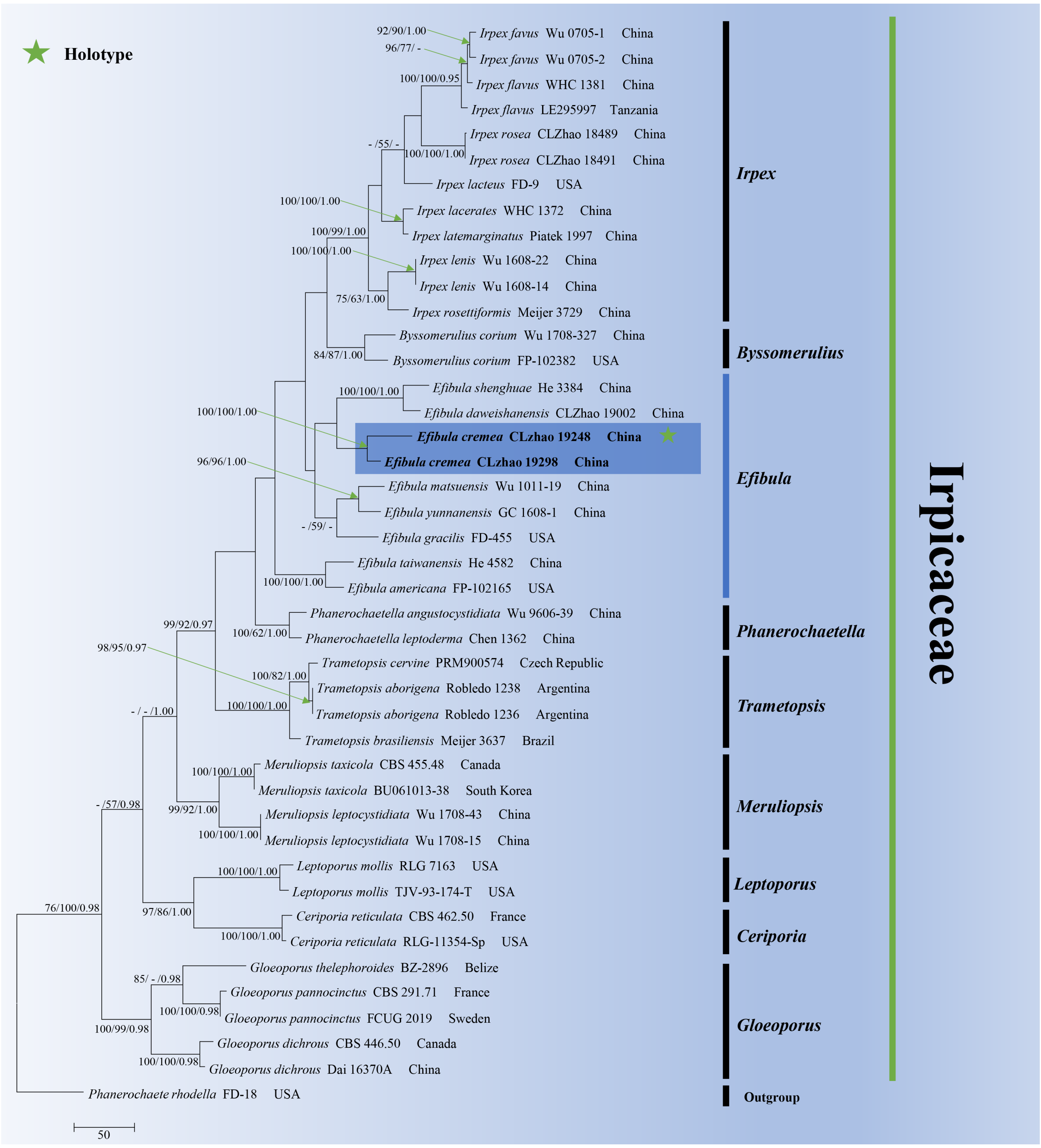

FIGURE 1. Maximum Likelihood strict consensus tree illustrating the *Efibula cremea* and related species in the family Irpicaceae based on the combined ITS+nLSU sequences. Branches are labeled with Maximum Likelihood bootstrap values equal to or above 70%, parsimony bootstrap value ≥ 50%, and Bayesian posterior probabilities ≥ 0.95. The new species is in bold.

Results

Molecular phylogeny

The ITS+nLSU dataset (Fig. 1) included sequences from 43 fungal specimens representing 31 species belonging to nine genera related to *Efibula* in the family Irpicaceae, including 4 new sequences and 80 downloaded from GenBank. The dataset had an aligned length of 2,168 characters, of which 1,544 characters were constant, 181 were variable and parsimony-uninformative, and 443 were parsimony-informative. The MP analysis yielded five equally parsimonious trees (TL = 1810, CI = 0.4884, HI = 0.5116, RI = 0.6664, RC = 0.3255). The best RAxML tree with a final likelihood value of -10038.938622 is presented. The evolutionary model GTR+GAMMA is applied to all the genes. The matrix contained 759 distinct alignment patterns, with 28.73% of characters undetermined or missing. Estimated base frequencies were as follows: A = 0.263216, C = 0.200946, G = 0.262288, T = 0.273550; substitution rates AC = 1.654906, AG = 3.906781, AT = 2.150083, CG = 1.047162, CT = 7.433342, GT = 1.000000; gamma distribution shape parameter α = 0.205643. The best-fit model for ITS+nLSU alignment estimated and applied in BI was GTR+I+G. At the end of the BI runs, the average standard deviation of split frequencies was 0.005602 (BI), and the effective sample size (ESS) across the two runs is double the average ESS (avg. ESS) = 212.5. The tree topology obtained by BI was similar to the one from MP and ML. In the phylogenetic reconstruction (Fig. 1) of the family Irpicaceae, it includes nine genera as *Byssomerulius* Parmasto (1967: 383), *Ceriporia* Donk (1933: 170), *Efibula*, *Gloeoporus* Mont (1842: 126)., *Irpex* Fr. (1825: 81), *Leptoporus* Quél. (1886: 236), *Meruliopsis* Bondartsev (1959: 274), *Phanerochaetella* C.C. Chen & Sheng H. Wu (2021: 415), and *Trametopsis* Tomšovský (2008: 7). The phylogram based on the combined ITS+nLSU sequences (Fig. 1) indicates that the species *Efibula cremea* is assigned to the genus *Efibula*.

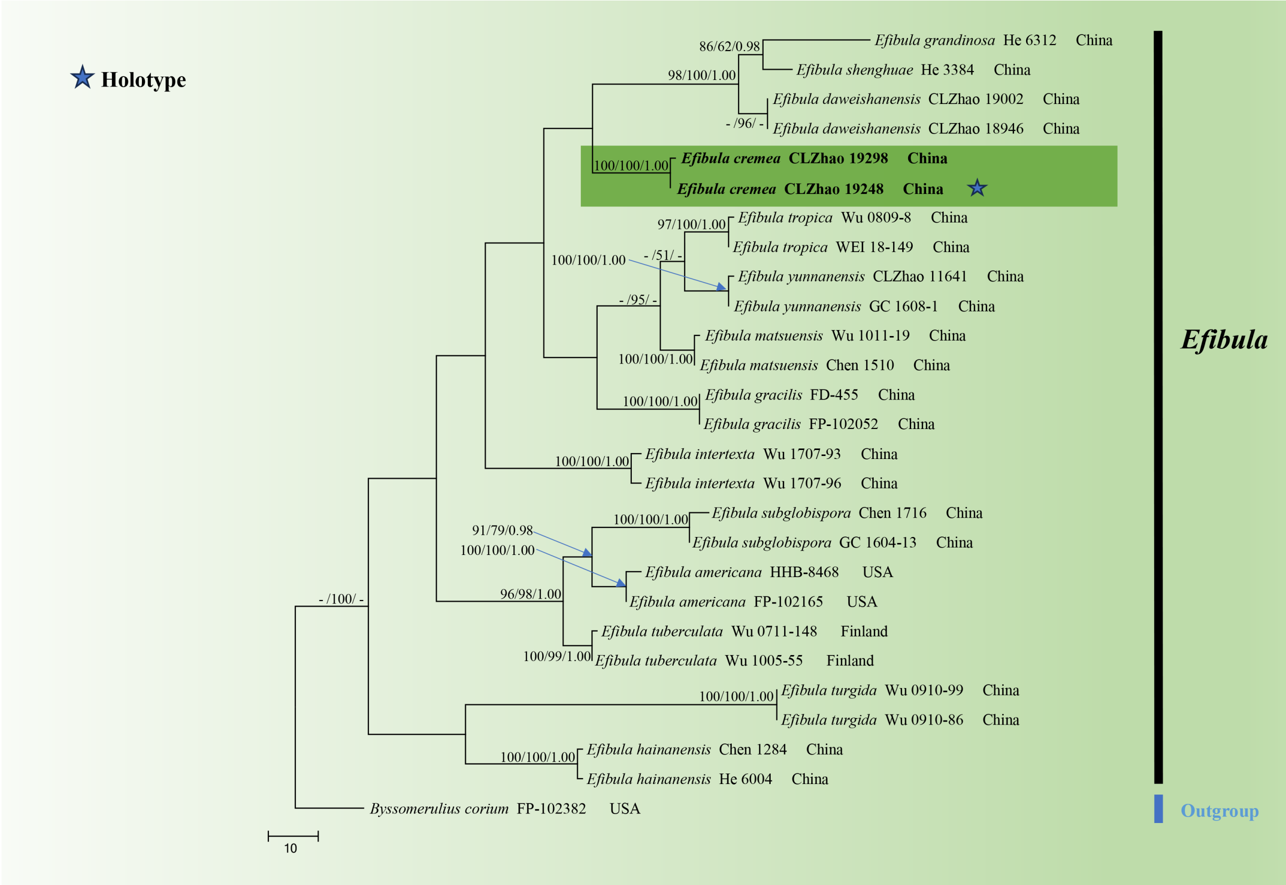

FIGURE 2. Maximum Likelihood strict consensus tree illustrating the *Efibula cremea* and related species in the genus *Efibula* based on the combined ITS sequences. Branches are labeled with Maximum Likelihood bootstrap values equal to or above 70%, parsimony bootstrap value ≥ 50%, and Bayesian posterior probabilities ≥ 0.95. The new species is in bold.

The ITS dataset (Fig. 2) included sequences from 27 fungal specimens representing 15 species. The aligned length of the data set was 634 characters, of which 414 characters were constant, 24 were variable and parsimony-uninformative, and 196 were parsimony-informative. The MP analysis yielded three equally parsimonious trees (TL = 494, CI = 0.6235, HI = 0.3765, RI = 0.7609, RC = 0.4744). The best RAxML tree, with a final likelihood of -2349.974113, is presented. The evolutionary model GTR+GAMMA is applied to all the genes. The matrix contained 253 distinct alignment patterns, with 12.22% of characters undetermined or missing. Estimated base frequencies were as follows: A = 0.254015, C = 0.202113, G = 0.217736, T = 0.326136; substitution rates AC = 1.782534, AG = 4.598351, AT = 2.021774, CG = 0.505259, CT = 6.518748, GT = 1.000000; gamma distribution shape parameter α = 0.235747. The best-fit model for the ITS alignment estimated and applied in BI was HKY+G. At the end of the BI runs, the average standard deviation of split frequencies was 0.004701 (BI), and the effective sample size (ESS) across the two runs is double the average ESS (avg. ESS) = 320. The topology based on ITS sequences (Fig. 2) shows that *E.*

cremea is grouped with the clade comprising *E. daweishanensis, E. grandinosa*, Y. Li, and S.H. He (2022: 7), and *E. shenghuae* Yue Li & S.H. He (2022: 11).

Application of the pairwise homoplasy index (PHI) test to the combined partial ITS sequence data tree locus sequences revealed no evidence of recombination among phylogenetically related species. No significant recombination events were observed in *Efibula cremea* with *E. daweishanensis, E. shenghuae,* and phylogenetically closely related species *E. americana*, *E. gracilis*, *E. matsuensis*, *E. taiwanensis,* and *E. yunnanensis* (Fig. 3). The test results of the combined partial ITS sequences dataset show that Φw = 0.9645 (Φw > 0.05), no recombination is present in the new species with *E. daweishanensis*, *E. shenghuae*, *E. americana*, *E. gracilis*, *E. matsuensis*, *E. taiwanensis,* and *E. yunnanensis* (Fig. 3).

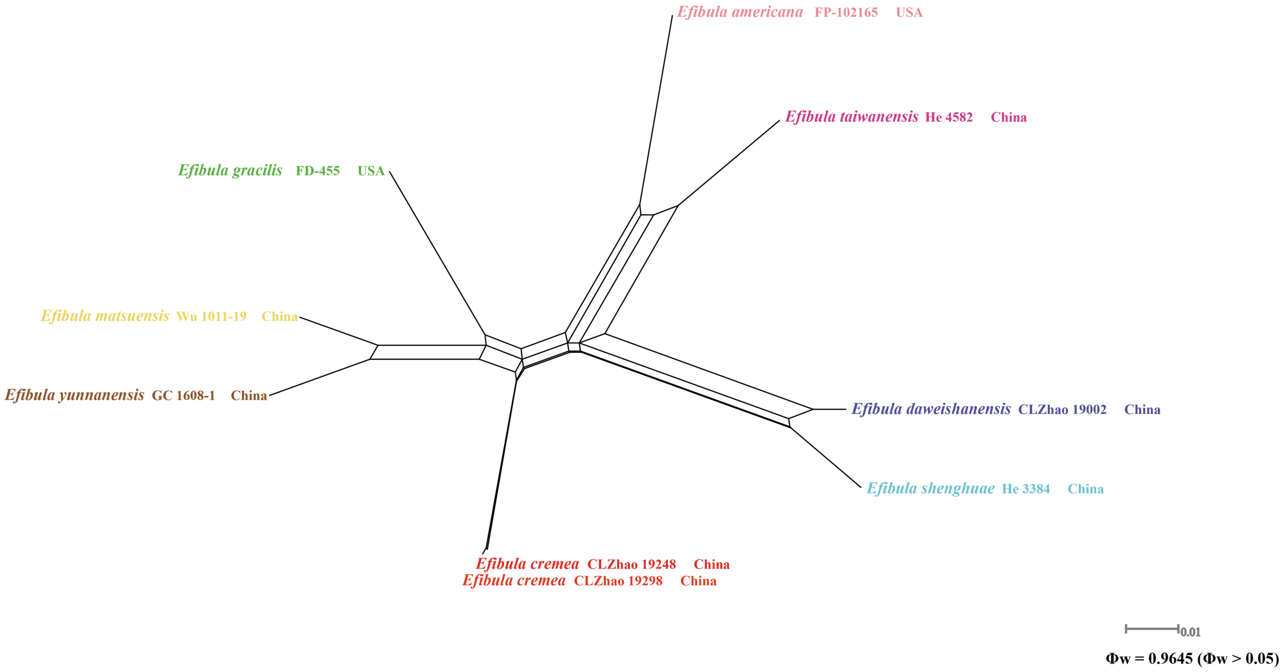

FIGURE 3. The results of the pairwise homoplasy index (PHI) test for the combined partial ITS sequence data of *Efibula cremea* and closely related taxa, using the LogDet transformation and splits decomposition. PHI test results (Φw ≤ 0.05) indicate significant recombination within the dataset. New taxa are in red.

Taxonomy

Efibula cremea Q. Li & C.L. Zhao, *sp. nov.* Figs. 4–6
MycoBank no.: 859971

***Etymology*:**—*Cremea* (Lat.) refers to the cream hymenial surface of the type specimen.

***Diagnosis*:**—Differs from other species of *Efibula* by membranous, white to cream basidiomata, grandinioid hymenial surface, a monomitic hyphal system with simple-septa on generative hyphae and ellipsoid basidiospores (4.7–5.7 × 3.3–4 µm).

***Holotype*:**—CHINA. Yunnan Province, Zhaotong, Qiaojia County, Yaoshan National Nature Reserve, Tuanbao Village, GPS coordinates 27°09′N, 103°02′E, altitude 2410 m asl., on a fallen angiosperm branch, a broad-leaf forest, dominant vegetation as Fagaceae, leg. C.L. Zhao, 17 July 2020, CLZhao 19248 (SWFC). White rot.

***Basidiomata*:**—Annual, resupinate, adnate, punctate, without odor or taste when fresh, soft coriaceous when fresh, becoming hard coriaceous upon drying, up to 5 cm long, 2 cm wide, 50–100 µm thick. Hymenial surface grandinioid, white when fresh, white to cream upon drying. Sterile margin white, narrow, up to 0.5 mm wide.

***Hyphal structure*:**—Hyphal system monomitic; generative hyphae simple-septa, colorless, thin- to thick-walled, rarely branched, interwoven, 2–5.5 µm in diameter; IKI–, CB–; tissues unchanged in KOH; numerous crystals present amongst generative hyphae.

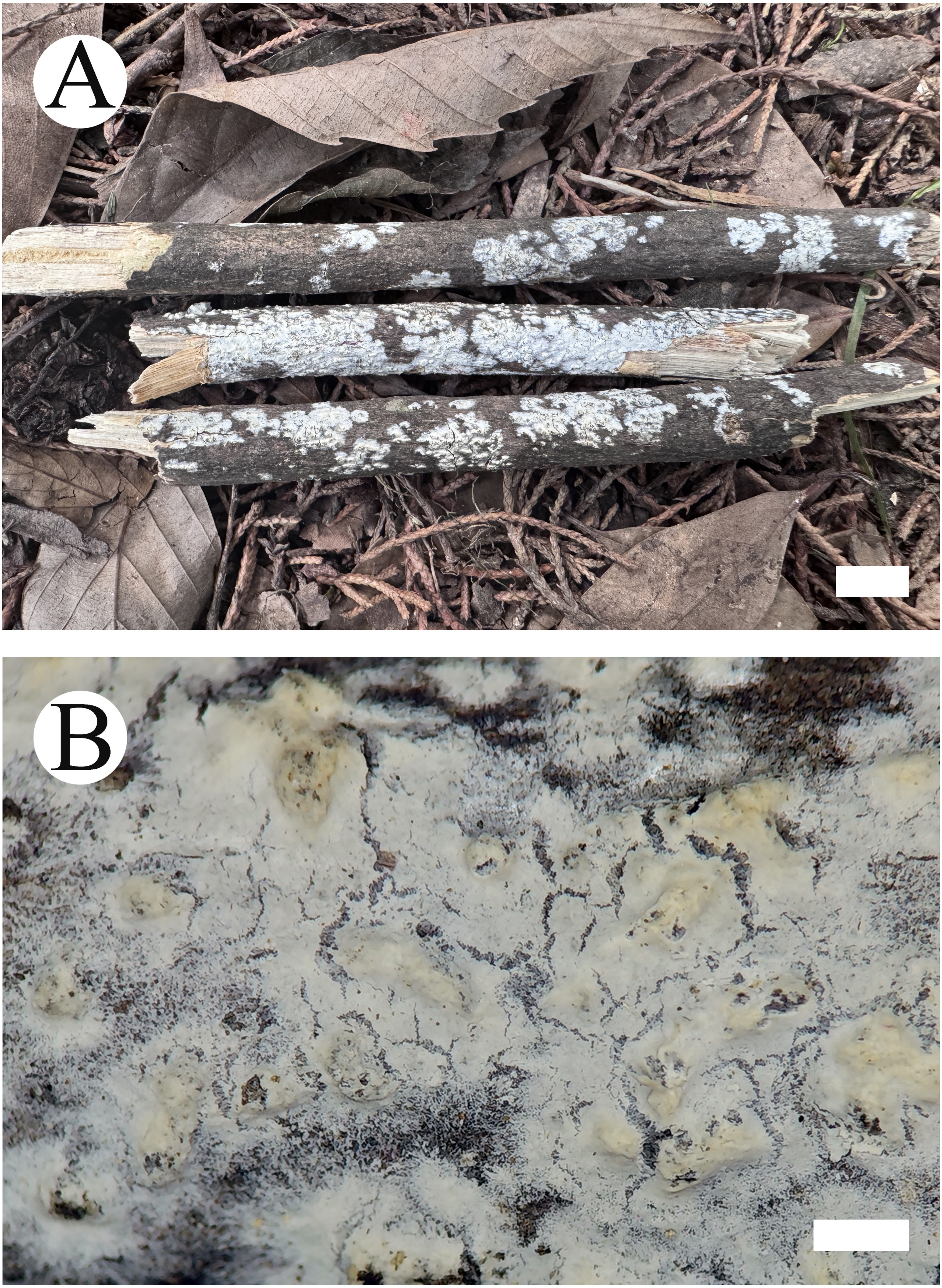

FIGURE 4. Basidiomata of *Efibula cremea* (A, B) CLZhao 19248 (holotype).

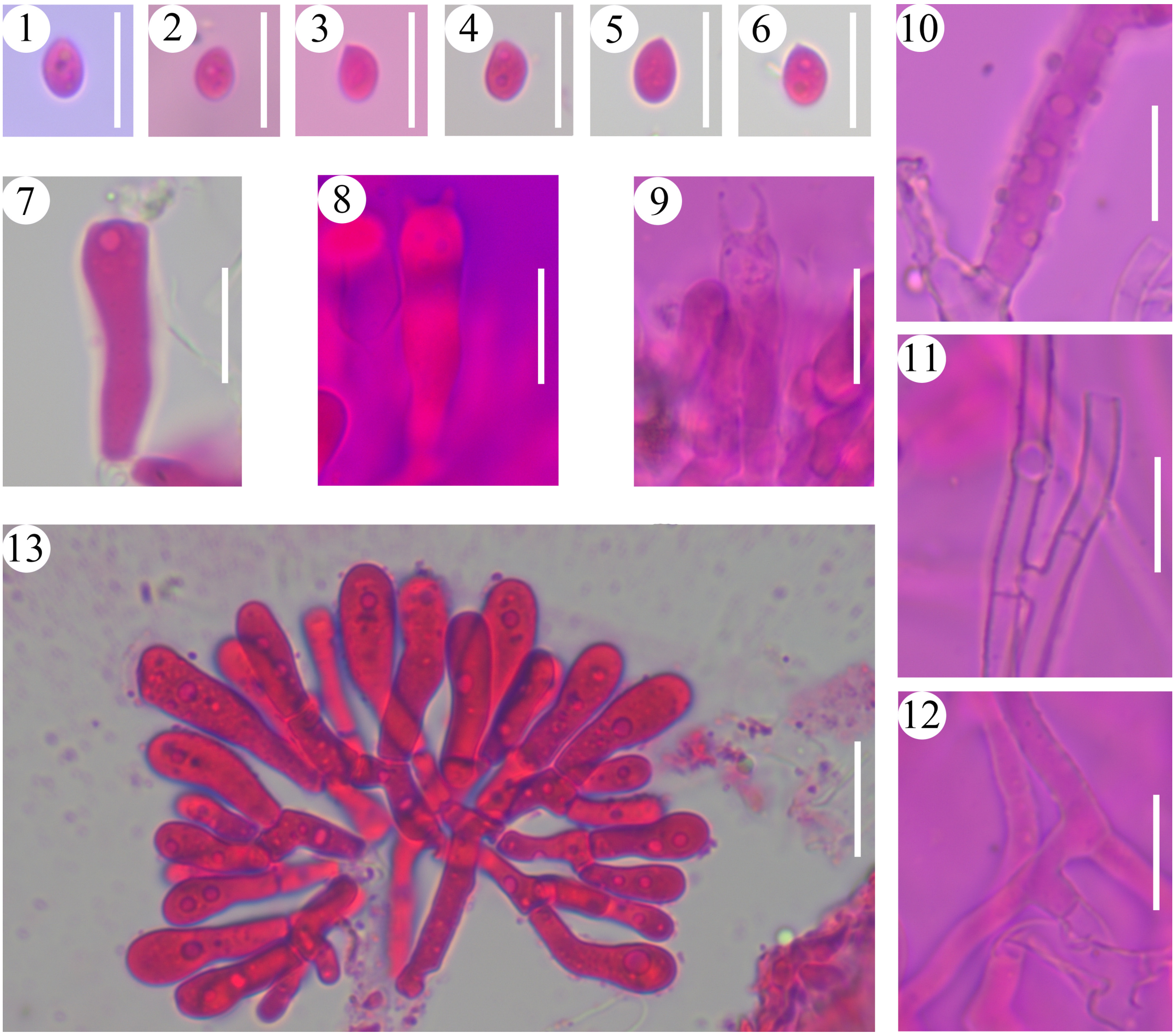

FIGURE 5. Sections of the hymenium of *Efibula cremea* (holotype, CLZhao 19248). (1–6) Basidiospores; (7–9) Basidia; (10–12) Generative hyphae; (13) Basidioles. Scale bars: 1–13 = 10 µm.

Hymenium:—Cystidia and cystidioles absent. Basidia clavate, slightly sinuous or constricted in the middle, with a few granules, 4 sterigmata and a simple septum at the base, 17.5–25 × 5–7.5 µm; basidioles dominant, similar to basidia in shape, but slightly smaller.

Basidiospores:—Ellipsoid, thin-walled, smooth, colorless, IKI–, CB–, (4.5–)4.7–5.7(–6.2) × 3.3–4(–4.2) µm, L = 5.23 µm, W = 3.68 µm, Q = 1.37–1.42 (n = 30/2).

Additional specimen examined:—CHINA. Yunnan Province, Zhaotong, Qiaojia County, Yaoshan County National Nature Reserve, Tuanbao Village, GPS coordinates 27°09′N, 103°02′E, altitude 2410 m asl., on a fallen angiosperm branch, leg. C.L. Zhao, 17 July 2020, CLZhao 19298 (SWFC). White rot.

Discussion

Phylogenetically, the molecular analyses of the family Irpicaceae were carried out based on a, in which the dataset included concatenated ITS1-5.8S-ITS2 and nrLSU sequences of 67 taxa of Irpicaceae from around the world, and the species from 14 genera were distributed in nine clades, among which five genera received high support values (Li *et al.* 2022). In the present study, the topology based on ITS and ITS+nLSU sequences (Figs. 1, 2) revealed that *Efibula cremea* grouped with the species *E. daweishanensis*, *E. grandinosa*, and *E. shenghuae*. However, *E. daweishanensis*

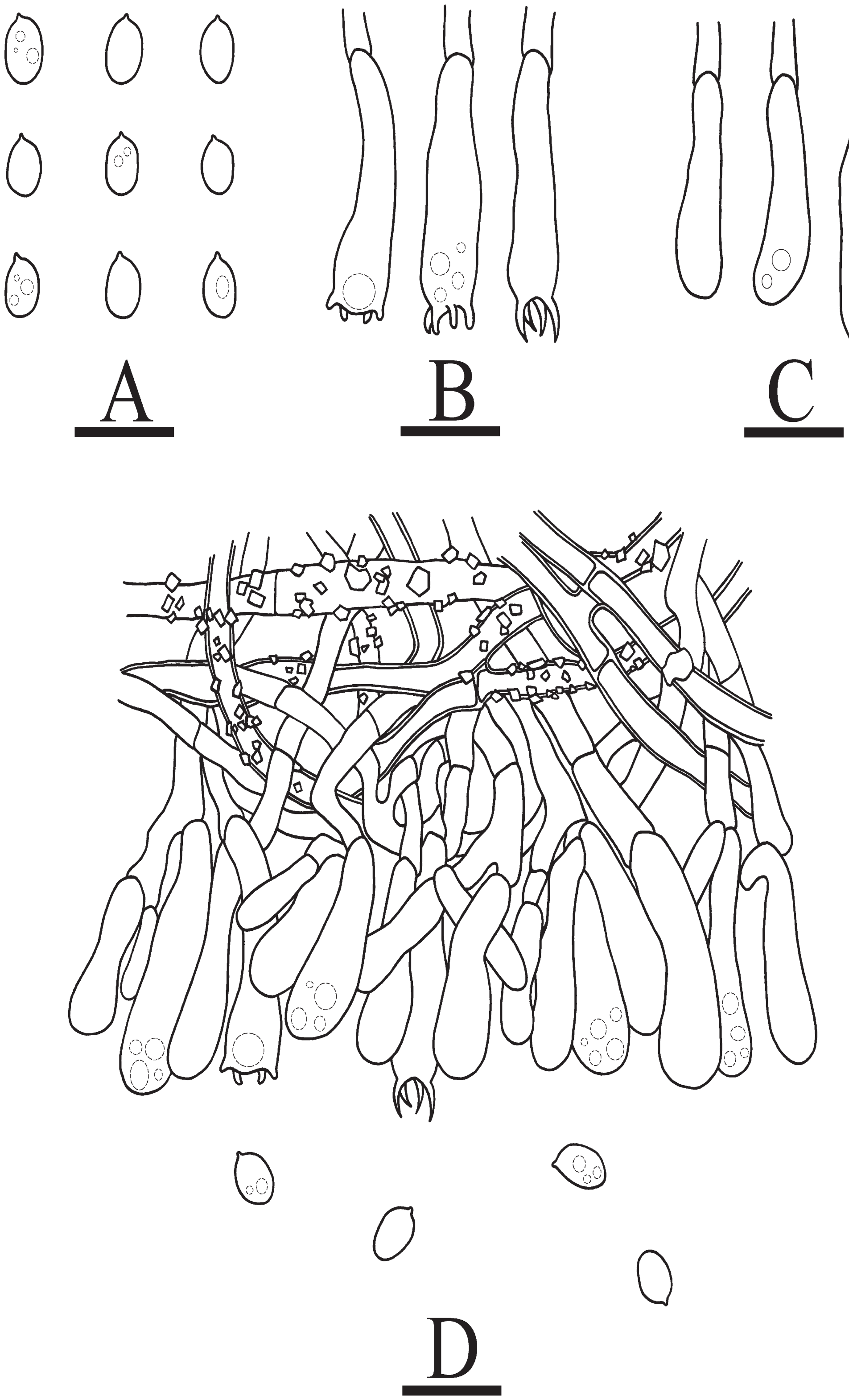

FIGURE 6. Microscopic structures of *Efibula cremea* (holotype, CLZhao 19248). (A) Basidiospores; (B) Basidia; (C) Basidioles; (D) A section of the hymenium. Scale bars: A–D = 10 µm.

differs from *E. cremea* by thin-walled generative hyphae, smaller basidia (14–19 × 5–6.5 µm *vs*. 17.5–25 × 5–7.5 µm), and larger basidiospores (6–7.5 × 3.5–4.8 µm *vs*. 4.7–5.7 × 3.3–4 µm) (Dong *et al*. 2024). *Efibula grandinosa* is different from *E. cremea* by a pale orange to grayish orange hymenial surface, and longer basidia (36–43 × 5–7 µm *vs*. 17.5–25 × 5–7.5 µm, Li *et al.* 2022). *Efibula shenghuae* is distinguished from *E. cremea* by its orange white to pale orange hymenial surface, longer basidia (23–38 × 4.5–7 µm *vs*. 17.5–25 × 5–7.5 µm) and longer basidiospores (6–6.5 × 3–3.5 µm *vs*. 4.7–5.7 × 3.3–4 µm) (Li *et al.* 2022). In the ecological distribution, the new species *E. cremea* and its lookalikes *E. daweishanensis*, *E. grandinosa*, and *E. shenghuae* are sympatric (overlapping distribution), in which *E. cremea* was found in Qiaojia County of Yunnan Province, *E. daweishanensis* was found in Pingbian County of Yunnan Province, *E. grandinosa* was found in Shizong County of Yunnan Province, and *E. shenghuae* was found in Baoshan County of Yunnan Province. All of them are distributed in the subtropics and have similar latitudes.

Morphologically, *Efibula cremea* resembles *E. grandinosa*, *E. tuberculata* (P. Karst.) Zmitr. & Spirin (2006: 33) and *E. yunnanensis* in sharing clavate basidia and ellipsoid basidiospores. However, *E. grandinosa* differs from *E. cremea* in its membranous hymenial surface, thin-walled generative hyphae, longer basidia (36–43 × 5–7 µm *vs*. 17.5–25 × 5–7.5 µm), and wider basidiospores (6–6.8 × 3.7–4 µm *vs*. 4.7–5.7 × 3.3–4 µm) (Li *et al*. 2022). *Efibula tuberculata* is distinguished from *E. cremea* by its smooth to slightly tuberculate hymenial surface and larger basidiospores (5.3–6.4 × 3.4–4.3 µm *vs*. 4.7–5.7 × 3.3–4 µm, Chen *et al.* 2021). *Efibula yunnanensis* differentiates from *E. cremea* by a smooth hymenial surface, longer basidia (25–31 × 6–7.5 µm vs. 17.5–25 × 5–7.5 µm), and larger basidiospores (5.5–7.5 ×3.6–4.5 µm vs. 4.7–5.7 × 3.3–4 µm) (Ma *et al*. 2020); in addition, *E. yunnanensis* and *E. cremea* group in different clades with a phylogenetic distance (Fig. 2).

Wood-inhabiting fungi form an ecologically important branch of the tree of life, characterized by distinct and diverse traits (Yang *et al.* 2025). Therefore, for future utilization, it is now urgent to recognize and conserve fungi (Dong *et al.* 2025).

To date, 25 species of *Efibula* have been recorded worldwide, and their diversity in China remains poorly known, especially in subtropical and tropical areas. In the present study, one new species is identified from Yunnan Province, which will further enrich our knowledge of fungal diversity in this area, and more new taxa of the genus *Efibula* will be found with further fieldwork and molecular analyses.

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