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# **Studies on *Schistidium* (Grimmiaceae, Bryophyta) in Europe, with particular reference to the Alps: II. Description of two new species *S. pratense* and *S. herbertii***

MARK H. BLUM, THOMAS KIEBACHER, RAJINDA BEENHAREN-OCHTER, SYLVIA OCHTER

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# **Successful adaptive radiation of the genus *Lotus* L. (Fabaceae, Loteae, section *Pedrosia*) in the western Canary Islands, Spain, with new taxa from Tenerife and El Hierro**

ANDRÉS-ALEXANDER WELER

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# **Anatomical characterization of genus *Garchnia* (Clusiaceae) from the Western Ghats of India and their potential use in identification of species at vegetative stage**

ARUN DASOLKAR, RUTUJA RALKAR, KRISHNAN SELLAPPAN

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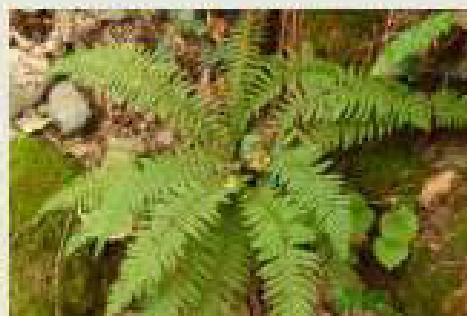
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# ***Polystichum caucasicum* sp. nov. (Dryopteridaceae), a new, surprisingly hexaploid fern species from the Caucasus**

LEON IAKI, STEFAN JESSEN, RAHEL NORDA, KATEŘINA VEJVODOVÁ, VERONIKA BALVINKOVÁ, RAHEL LUSTYK, CHRISTOPHER R. FRASER-JONES

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# **Molecular phylogeny and morphology reveal a new wood-inhabiting fungal species, *Gloeosoma cremeum* (Stereaceae, Russulales) from Yunnan Province, China**

YONGGANG ZHANG, LIU HONG, JIANG CHEN, KAIJIANG HUANG, CHANGJIN CHEN, CHEN YI, YIN LI

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## Molecular phylogeny and morphology reveal a new wood-inhabiting fungal species, *Gloeosoma cremeum* (Stereaceae, Russulales) from Yunnan Province, China

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### Abstract

In this study, *Gloeosoma cremeum* is described and illustrated as a novel species based on morphological characteristics and phylogenetic analyses of internal transcribed spacer (ITS) regions and the large subunit (nLSU) of nuclear ribosomal RNA genes. The species is characterized by smooth, membranaceous basidiomata with a cream hymenial surface, and finely echinulate, ellipsoid to semilunate basidiospores (23.5–32 × 16–20.5 µm). The phylogenetic tree inferred from ITS+nLSU sequences revealed that the new species was nested within the genus *Gloeosoma* within the family Stereaceae, forming a monophyletic lineage and grouping with *G. mirabile*.

**Key words:** Biodiversity, corticioid fungi, molecular systematics, taxonomy

### Introduction

The number of species in the kingdom Fungi is estimated to range from 2.2 to 13.2 million, with the latest estimate suggesting 2–3 million species (He *et al.* 2022, 2024; Hyde *et al.* 2024). However, only around 160,000 species have been named and classified to date, and undescribed fungi represented a vast potential resource (Hyde *et al.* 2019; He *et al.* 2024; Dong *et al.* 2025; Yang *et al.* 2025b). In the past few decades, a lot of corticioid fungi, new taxa of Russulales Kreisel ex P.M. Kirk, P.F. Cannon & J.C. David have been gathered through both morphological characteristics and DNA sequence phylogenetic analyses (Wu *et al.* 2020; Zou *et al.* 2022; Bhunjun *et al.* 2024; Deng *et al.* 2024; Dong *et al.* 2024; Zhou *et al.* 2024; He *et al.* 2025; Wang *et al.* 2025; Yang *et al.* 2025a, b).

Species in the family Stereaceae are all saprobic, causing a white rot (or white pocket rot in some species) on both conifers and hardwoods (Rajchenberg *et al.* 2021; Dong *et al.* 2025; He *et al.* 2024; Yang *et al.* 2025a). So far, the family Stereaceae contains only corticioid and stereoid wood-decaying fungi with a smooth or occasionally tuberculate or merulioid hymenophores (Bernicchia & Gorjón 2010; Xu *et al.* 2025). Species in the family mostly belong to *Aleurodiscus* s. lat., *Gloeocystidiellum* s. lat., *Stereum* Hill ex Pers. and *Xylobolus* P. Karst. (Rajchenberg *et al.* 2021; Xu *et al.* 2025). Morphologically, species of *Aleurodiscus* s. lat. divided into several smaller genera: *Acanthobasidium* Oberw., *Acanthofungus* Sheng H. Wu, *Boidin* & C.Y. Chien, *Acanthophysellum* Parmasto, *Acanthophysium* (Pilát) G. Cunn., *Aleurobotrys* Boidin, *Aleurocystidiellum* P. A. Lemke, *Aleurodiscus* s. str., *Aleuromyces* Boidin & Gilles, *Gloeosoma* Bres., and *Neoaleurodiscus* Sheng H. Wu., which were according to different combinations of

morphological characteristics, but their relationships are still unclear to a certain extent, and some species formed single-species lineages without generic names (Rajchenberg *et al.* 2021; Maekawa *et al.* 2023; Xu *et al.* 2025). Based on a complete taxonomy and phylogenetic study of the family Stereaceae focusing on the phylogenetic relationship at the generic level, included sequences of *G. vitellinum* (type species) for the first time, and showed that together with *G. decorticans* Rajchenb., Pildain & C. Riquelme, *G. mirabile* (Berk. & M.A. Curtis) Rajchenb., Pildain & C. Riquelme, and *G. zealandicum* (Cooke & W. Phillips) Rajchenb., Pildain & C. Riquelme; they formed a well-defined group of species with strong phylogenetic support. The genus *Gloeosoma* is phylogenetically related to other genera in the Stereaceae, and is distant from other clades in Stereaceae and from other genera segregated from *Aleurodiscus* s. lat. (Rajchenberg *et al.* 2021; Xu *et al.* 2025).

The genus *Gloeosoma* is characterized by the discoid, cupulate to large and auricularioid, gelatinous to fleshy basidiomata with pink to salmon-colored hymenial surface; hyphal system monomitic with clamped generative hyphae; acanthocystidia always present, gloeocystidia present in some species; basidia clavate with four sterigmata; basidiospores large, more than 20 µm long, aculeate to echinulate, thick-walled, amyloid (Bernicchia & Gorjón 2010; Rajchenberg *et al.* 2021). According to Index Fungorum ([www.indexfungorum.org](http://www.indexfungorum.org); accessed on 24 August 2025) and Mycobank (<https://www.mycobank.org/>; accessed on 24 August 2025), the genus *Gloeosoma* has only five specific names, of which four are accepted worldwide (Rajchenberg *et al.* 2021; Xu *et al.* 2025).

During surveys of wood-inhabiting fungi, we found a species of *Gloeosoma* that does not match any known species. Morphological characteristics and multi-locus molecular analyses based on ITS+nLSU sequences indicate that it is a new species and is described here.

## Materials and methods

### *Sample Collection and Herbarium Specimen Preparation*

Fresh fruit bodies of fungi growing on angiosperm branches were collected from Zhaotong, Wumengshan National Nature Reserve in Yunnan Province, China. The samples were photographed *in situ* using a Canon 80D camera (Tokyo, Japan), with fresh macroscopic details recorded (Rathnayaka *et al.* 2025), and then transported to the Southwest Forestry University mycology laboratory in plastic collection boxes. Specimens were dried in an electric food dehydrator at 45 °C, then sealed in envelopes and zip-lock plastic bags, and labeled. The dried specimens were deposited in the herbarium of the Southwest Forestry University (SWFC), Kunming, Yunnan Province, China.

### *Morphology*

The macromorphology was based on fresh and dried specimens. The color terms in the description followed Petersen (1996). The micromorphological characteristics data were systematically analyzed from the dried specimens and observed under a light microscope, aligning with established methodologies. Sections mounted in 5% KOH and 2% phloxine B dye (C<sub>20</sub>H<sub>2</sub>Br<sub>4</sub>Cl<sub>4</sub>Na<sub>2</sub>O<sub>5</sub>). Other reagents were also used, including Cotton Blue and Melzer's reagent. Micromorphology was observed following the method of Wu *et al.* (2022). The following abbreviations were used: CB = Cotton Blue, CB– = acyanophilous, KOH = 5% potassium hydroxide, IKI = Melzer's reagent, IKI– = both inamyloid and indextrinoid, W = mean spore width (arithmetic average for all spores), L = mean spore length (arithmetic 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 (Dong *et al.* 2024).

### *DNA Extraction, PCR amplification, and Sequencing*

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 the primer pair ITS5/ITS4 (White *et al.* 1990). The nuclear large subunit (nLSU) region with the primer pair LR0R/LR7 (Vilgalys & Hester 1990). The PCR procedure for ITS was as follows: 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 of 72 °C for 10 min. The PCR procedure for nLSU was as follows: 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 of

72 °C for 10 min. The PCR products were purified and sequenced at Kunming Tsingke Biological Technology Limited Company (Yunnan Province, P.R. China). All newly generated sequences were deposited in GenBank (Table 1).

Molecular Phylogeny

Additional sequences were downloaded from GenBank (Table 1). These sequences were compared with the GenBank database using the Basic Local Alignment Search Tool (BLAST), and available sequences of species in the genus containing ex-type or representative sequences were downloaded from GenBank following previous publications (Spirin *et al.* 2018; Wu *et al.* 2020; Deng *et al.* 2025; Wang *et al.* 2025; Xu *et al.* 2025; Yang *et al.* 2025a). The sequences were aligned in MAFFT version 7 using the G-INS-i strategy (Kato *et al.* 2019). The alignment was adjusted manually using AliView version 1.27 (Larsson 2014). The dataset was aligned, and the ITS and nLSU sequences were combined using Mesquite version 3.51. (1) *Vararia fissurata* Y.L. Deng & C.L. Zhao was assigned as an outgroup to root trees in the ITS+nLSU analysis (Figure 1) (Deng *et al.* 2024); (2) *Conferticium tuberculatum* Lu Wang & C.L. Zhao was assigned as an outgroup to root trees following the ITS+nLSU analysis (Figure 2) (Wang *et al.* 2025).

**TABLE 1.** Names, voucher numbers, references & corresponding GenBank accession numbers of the taxa used in the phylogenetic analyses. [\* Indicates type materials; — indicates sequence unavailability].

| Taxa                                  | Voucher no.          | Locality     | GenBank accession no. |          | References                     |
|---------------------------------------|----------------------|--------------|-----------------------|----------|--------------------------------|
|                                       |                      |              | ITS                   | LSU      |                                |
| <i>Acanthobasidium bambusicola</i>    | He2357               | China        | KU559343              | KU574833 | Tian <i>et al.</i> 2018        |
| <i>Acanthobasidium phragmitis</i>     | CBS 233.86           | France       | —                     | AY039305 | Wu <i>et al.</i> 2001          |
| <i>Aleurobotrys botryosus</i>         | He2712               | China        | KX306877              | KY450788 | Tian <i>et al.</i> 2018        |
| <i>Aleurodiscus gigasporus</i>        | He2865               | China        | MW533081              | MW528917 | Xu <i>et al.</i> 2025          |
| <i>Aleurodiscus globisporus</i>       | He5605               | China        | MW533084              | MW528920 | Xu <i>et al.</i> 2025          |
| <i>Aleurodiscus pinicola</i>          | Wu1308-54            | China        | MF043525              | MF043530 | Wu <i>et al.</i> 2019          |
| <i>Conferticium albocreum</i>         | CLZhao 35693         | China        | PQ197729              | PQ783842 | Wang <i>et al.</i> 2025        |
| <i>Conferticium tuberculatum</i>      | CLZhao 29390         | China        | PQ166603              | PQ295862 | Wang <i>et al.</i> 2025        |
| <i>Confertotrama aspella</i>          | He4626               | China        | KY860402              | KY860460 | Xu <i>et al.</i> 2025          |
| <i>Confertotrama rugulosa</i>         | He3427               | China        | MW533086              | MW528925 | Xu <i>et al.</i> 2025          |
| <i>Gelatinostereum phlebioides</i>    | He1951               | China        | MW533097              | MW528943 | Xu <i>et al.</i> 2025          |
| <i>Gelatinostereum phlebioides</i>    | He6340               | China        | MW533095              | MW528941 | Xu <i>et al.</i> 2025          |
| <i>Gloeocystidiellum cremeum</i>      | CLZhao 29477         | China        | PQ287846              | PQ295863 | Wang <i>et al.</i> 2025        |
| <i>Gloeocystidiellum cremeum</i>      | CLZhao 33623         | China        | PQ287847              | PQ295864 | Wang <i>et al.</i> 2025        |
| <i>Gloeocystidiellum fissuratum</i>   | CLZhao 32247         | China        | PQ287849              | PQ295865 | Wang <i>et al.</i> 2025        |
| <i>Gloeocystidiellum fissuratum</i>   | CLZhao 32303         | China        | PQ287850              | PQ295866 | Wang <i>et al.</i> 2025        |
| <i>Gloeomyces parvisporus</i>         | Wu1307-84            | China        | LC433897              | LC433904 | Xu <i>et al.</i> 2025          |
| <i>Gloeomyces subcerussatus</i>       | He6964               | China        | MW533099              | MW528948 | Xu <i>et al.</i> 2025          |
| <i>Gloeomyces tropicus</i>            | CBS106.54            | Netherlands  | —                     | MH868789 | Xu <i>et al.</i> 2025          |
| <i>Gloeopeniophorella bambusicola</i> | CLZhao 35561         | China        | PP819702              | —        | Yang <i>et al.</i> 2025b       |
| <i>Gloeopeniophorella convolvens</i>  | KHL10103             | —            | AF506435              | AF506435 | Yang <i>et al.</i> 2025b       |
| <b><i>Gloeosoma cremeum</i></b>       | <b>CLZhao 29621*</b> | <b>China</b> | PX046471              | PX046472 | <b>This study</b>              |
| <b><i>Gloeosoma cremeum</i></b>       | <b>CLZhao 6781</b>   | <b>China</b> | OM955790              | —        | <b>This study</b>              |
| <i>Gloeosoma decorticans</i>          | MR12666              | Chile        | MT831041              | MT831021 | Rajchenberg <i>et al.</i> 2021 |
| <i>Gloeosoma decorticans</i>          | MR12665              | Chile        | MT831042              | MT831022 | Rajchenberg <i>et al.</i> 2021 |
| <i>Gloeosoma mirabile</i>             | Dai 27192            | China        | PV191153              | —        | Unpublished                    |
| <i>Gloeosoma mirabile</i>             | Dai 12722            | China        | KU559351              | —        | Unpublished                    |
| <i>Gloeosoma mirabile</i>             | He3733               | China        | KY450787              | KY450791 | Xu <i>et al.</i> 2025          |
| <i>Gloeosoma vitellinum</i>           | 259cc                | Argentina    | MT831040              | MT831020 | Rajchenberg <i>et al.</i> 2021 |

.....continued on the next page

TABLE 1. (Continued)

| Taxa                            | Voucher no.  | Locality  | GenBank accession no. |          | References                |
|---------------------------------|--------------|-----------|-----------------------|----------|---------------------------|
|                                 |              |           | ITS                   | LSU      |                           |
| <i>Gloeosoma vitellinum</i>     | 646cc        | Argentina | MT831039              | MT831019 | Xu <i>et al.</i> 2025     |
| <i>Megalocystidium brunneum</i> | He3447       | China     | MW533078              | MW528913 | Xu <i>et al.</i> 2025     |
| <i>Megalocystidium salicis</i>  | Spirin 11933 | Russia    | MT359938              | —        | Spirin <i>et al.</i> 2021 |
| <i>Neoaleurodiscus fujii</i>    | He2921       | China     | KU559357              | KU574845 | Dai <i>et al.</i> 2017    |
| <i>Neoaleurodiscus fujii</i>    | Wu0807-41    | Japan     | —                     | FJ799924 | Dai <i>et al.</i> 2017    |
| <i>Stereodiscus antarcticus</i> | MR11265      | Argentina | MT831048              | MT831028 | Xu <i>et al.</i> 2025     |
| <i>Megalocystidium brunneum</i> | He3447       | China     | MW533078              | MW528913 | Xu <i>et al.</i> 2025     |
| <i>Megalocystidium salicis</i>  | Spirin 11933 | Russia    | MT359938              | —        | Spirin <i>et al.</i> 2021 |
| <i>Neoaleurodiscus fujii</i>    | He2921       | China     | KU559357              | KU574845 | Dai <i>et al.</i> 2017    |
| <i>Neoaleurodiscus fujii</i>    | Wu0807-41    | Japan     | —                     | FJ799924 | Dai <i>et al.</i> 2017    |
| <i>Stereodiscus antarcticus</i> | MR11265      | Argentina | MT831048              | MT831028 | Xu <i>et al.</i> 2025     |
| <i>Megalocystidium brunneum</i> | He3447       | China     | MW533078              | MW528913 | Xu <i>et al.</i> 2025     |
| <i>Megalocystidium salicis</i>  | Spirin 11933 | Russia    | MT359938              | —        | Spirin <i>et al.</i> 2021 |
| <i>Neoaleurodiscus fujii</i>    | He2921       | China     | KU559357              | KU574845 | Dai <i>et al.</i> 2017    |
| <i>Neoaleurodiscus fujii</i>    | Wu0807-41    | Japan     | —                     | FJ799924 | Dai <i>et al.</i> 2017    |
| <i>Stereodiscus antarcticus</i> | MR11265      | Argentina | MT831048              | MT831028 | Xu <i>et al.</i> 2025     |

Maximum parsimony (MP), Maximum Likelihood (ML), and Bayesian Inference (BI) analyses were applied to the combined datasets following a previous study (Zhao & Wu 2017), and the tree construction procedure was performed in PAUP\* version 4.0b10 (Swofford 2002). 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, branches of zero length were collapsed, and all parsimonious trees were saved. Clade robustness was assessed using bootstrap (BT) analysis with 1,000 replicates (Felsenstein 1985). Descriptive tree statistics, tree length (TL), consistency index (CI), retention index (RI), rescaled consistency index (RC), and homoplasy index (HI) were calculated for each maximum parsimonious tree generated. The multiple sequence alignment was also analyzed using maximum likelihood (ML) in RAxML-HPC2 (Miller *et al.* 2012). Branch support (BS) for ML analysis was determined by 1000 bootstrap replicates.

MrModeltest 2.3 (Nylander 2004) was used to determine the best-fit evolution model for each dataset for Bayesian inference (BI), which was performed with MrBayes 3.2.7a using a general time-reversible model of DNA substitution and a gamma distribution of rate variation across sites (Ronquist *et al.* 2012). Four Markov chains were run twice from a random starting tree for 0.8 million generations of the datasets (Figure 1) and for 0.8 million generations of the datasets (Figure 2); the tree was sampled every 1,000 generations. The first one-fourth of all generations were discarded as burnin. The majority rule consensus tree of all remaining trees was calculated. Branches were considered significantly supported if they received a maximum likelihood bootstrap value (BS)  $\geq 70\%$ , a maximum parsimony bootstrap value (BT)  $\geq 50\%$ , or Bayesian posterior probabilities (BPP)  $\geq 0.95$ .

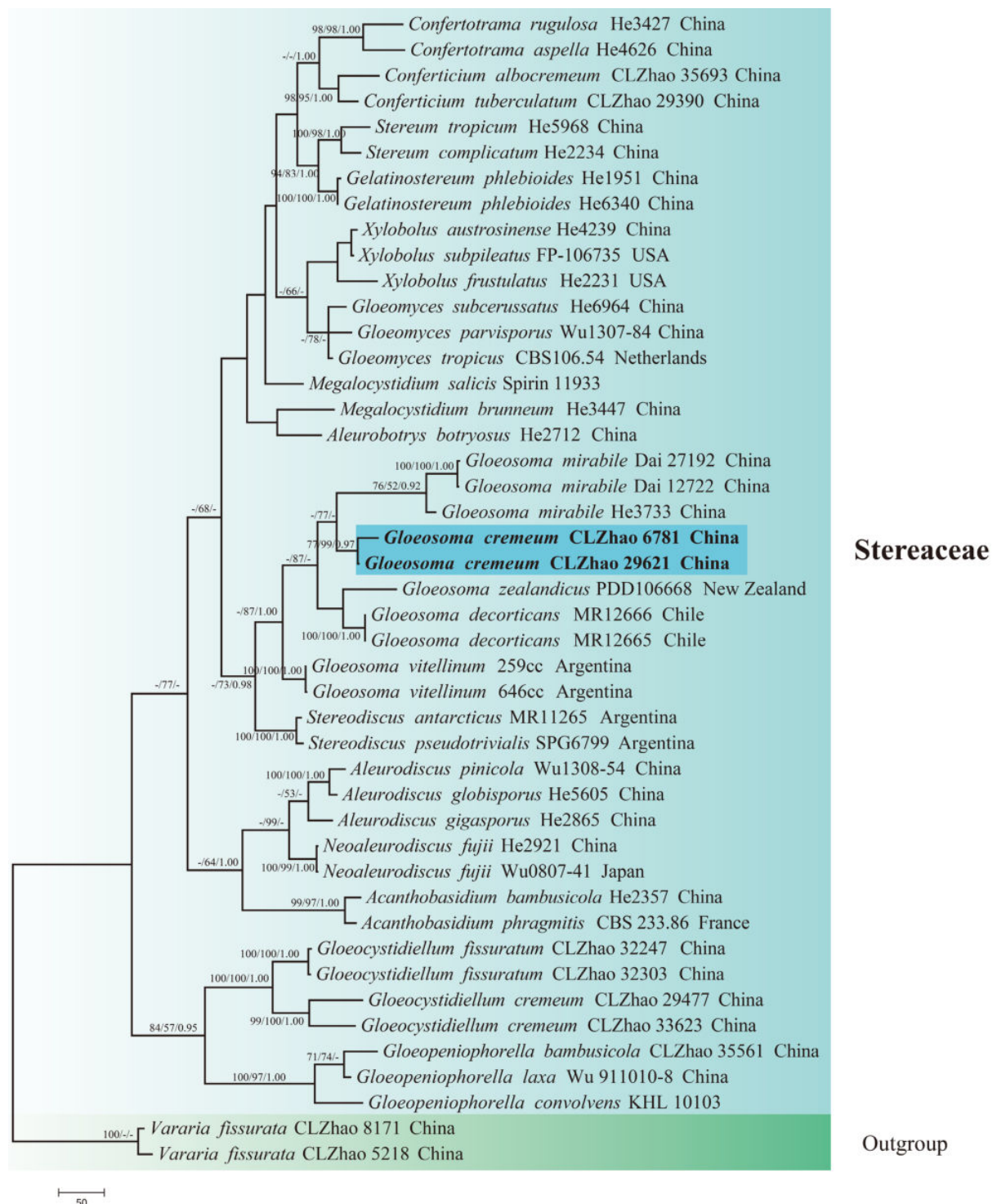
## Results

### Phylogenetic analyses

The datasets based on ITS+nLSU (Figure 1) comprise sequences from 45 fungal specimens representing 35 species. The datasets had an aligned length of 2766 characters, of which 1,231 were constant, 262 were variable and parsimony-uninformative, and 643 were parsimony-informative. Maximum parsimony analysis yielded 1 equally parsimonious tree (TL = 2766, CI = 0.5123, HI = 0.4877, RI = 0.6423, RC = 0.3290). Bayesian and ML analyses yielded a similar topology to the MP analysis, with an average standard deviation of split frequencies of 0.005504 (BI), and the effective sample size (ESS) across the two runs is double the average ESS (avg ESS) = 462.5. The phylogenetic tree (Figure 1)



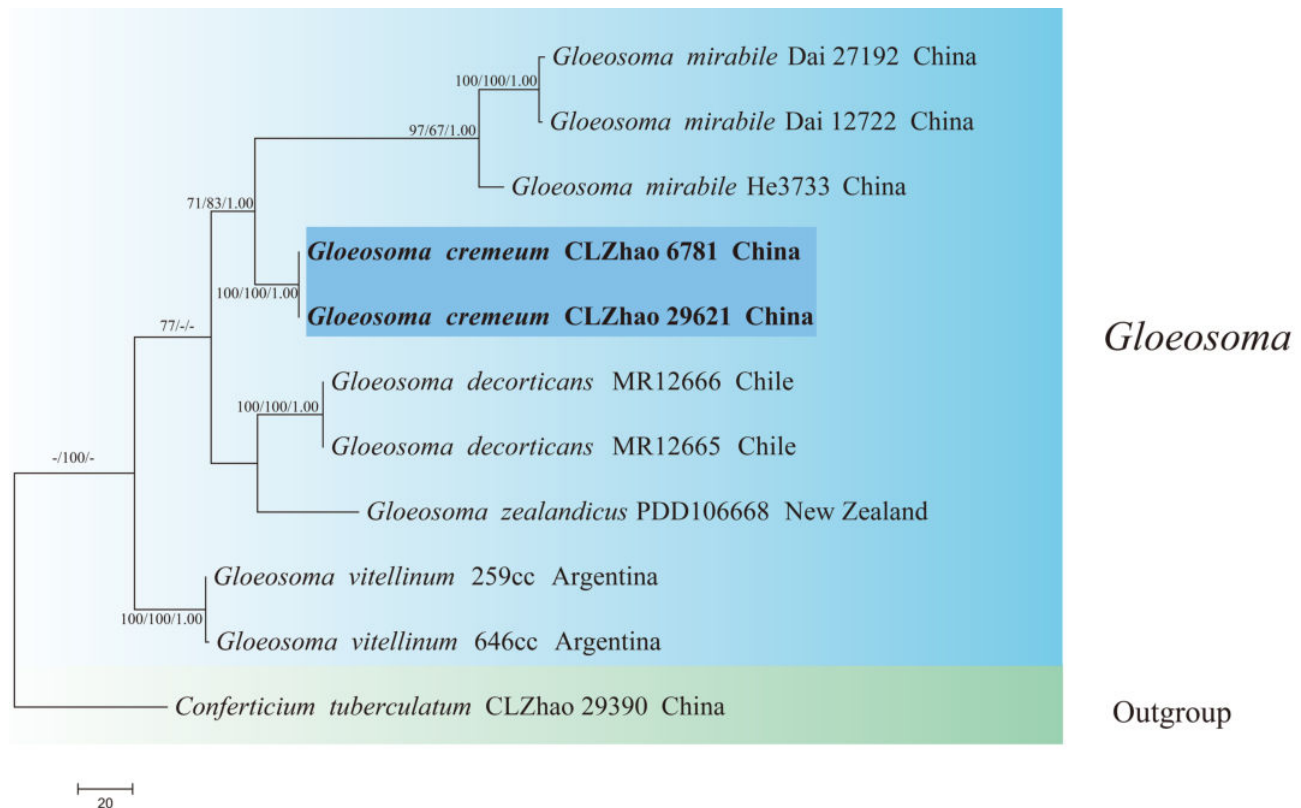
inferred from ITS and nLSU sequences showed that the new species, grouped in the genus *Gloeosoma* and clustered within the family Stereaceae (Russulales), is closely related to *G. mirabile*. The aligned sequence dataset of the phylogenetic analyses was deposited in figshare (10.6084/m9.figshare.30540785).



**FIGURE 1.** Maximum parsimony strict consensus tree illustrating the phylogeny of *Gloeosoma* and related genera in the family Stereaceae based on ITS+nLSU sequences; branches are labeled with maximum likelihood bootstrap value  $\geq 70\%$ , parsimony bootstrap value  $\geq 50\%$  and Bayesian posterior probabilities  $\geq 0.95$ .

The datasets based on ITS+nLSU (Figure 2) comprise sequences from 11 fungal specimens representing six species. The datasets had an aligned length of 1,977 characters, of which 1,692 were constant, 150 were variable and parsimony-uninformative, and 135 were parsimony-informative. Maximum parsimony analysis yielded 1 equally parsimonious tree (TL = 385, CI = 0.8701, HI = 0.1299, RI = 0.7967, RC = 0.6933). Bayesian and ML analyses resulted in a similar topology to the MP analysis, with an average standard deviation of split frequencies of 0.001540 (BI), and

the effective sample size (ESS) across the two runs is double the average ESS (avg ESS) = 1307. The phylogenetic tree (Figure 2) inferred from ITS and nLSU sequences showed that the new species grouped within the genus *Gloeosoma*, closely related to *G. mirabile*. The aligned sequence dataset of the phylogenetic analyses was deposited in figshare (10.6084/m9.figshare.30540785).



**FIGURE. 2.** Maximum parsimony strict consensus tree illustrating the phylogeny of *Gloeosoma cremeum* and related species in the genus *Gloeosoma*, based on ITS+nLSU sequences; branches are labeled with maximum likelihood bootstrap value  $\geq 70\%$ , parsimony bootstrap value  $\geq 50\%$  and Bayesian posterior probabilities  $\geq 0.95$ .

## Taxonomy

***Gloeosoma cremeum*** Y.G. Zhu & C.L. Zhao, *sp. nov.* FIGS. 3–5  
MycoBank no.: 860531

**Diagnosis:** Differs from other *Gloeosoma* species by the smooth hymenophore with cream hymenial surface, monomitic hyphal system with clamped generative hyphae, and finely echinulate, ellipsoid basidiospores ( $23.5\text{--}32 \times 16\text{--}20.5 \mu\text{m}$ ).

**Typification:** CHINA. Yunnan Province: Zhaotong, Wumengshan National Nature Reserve, GPS coordinates:  $27^{\circ}77' \text{N}$ ,  $104^{\circ}25' \text{E}$ , altitude: 1900 m asl., on the fallen angiosperm branch, leg. C.L. Zhao, 13 July 2023, CLZhao 29621 (SWFC!).

**Etymology:** *cremeum* (Lat.) refers to the species having a cream color of the hymenial surface.

**Basidiomata:** Annual, resupinate, closely adnate, ceraceous, without odor or taste when fresh, up to 6 cm long, 1 cm wide, and  $450 \mu\text{m}$  thick. Hymenophore smooth, slightly creamy when fresh, creamy upon drying. Sterile margin narrow, cream, up to 1 mm.

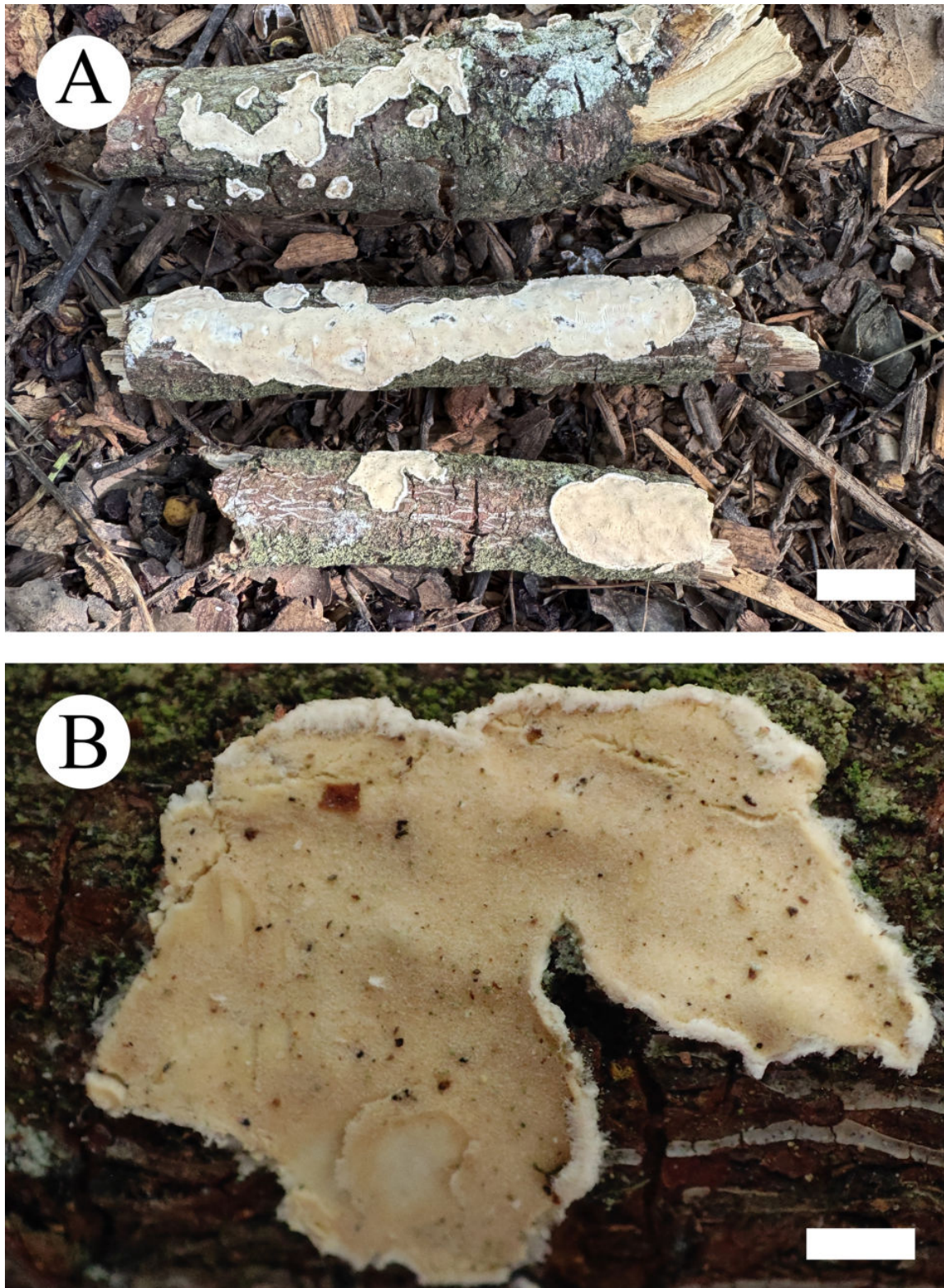
**Hyphal system:** Monomitic; generative hyphae with clamp connections, colorless, thin- to thick-walled, smooth, branched, interwoven,  $2\text{--}5 \mu\text{m}$  in diameter; IKI–, CB–; tissues unchanged in KOH.

**Hymenium:** Cystidia subclavate to obclavate, colorless, thin-walled, smooth, mostly  $48\text{--}67.5 \times 6.5\text{--}14.5 \mu\text{m}$ . Acanthophyses scattered in the hymenium, slightly thick-walled, colorless, with thorny ramifications. Basidia clavate, with a basal clamp septum and four sterigmata,  $107.5\text{--}152 \times 22\text{--}30 \mu\text{m}$ ; basidioles numerous, in shape similar to basidia but smaller.

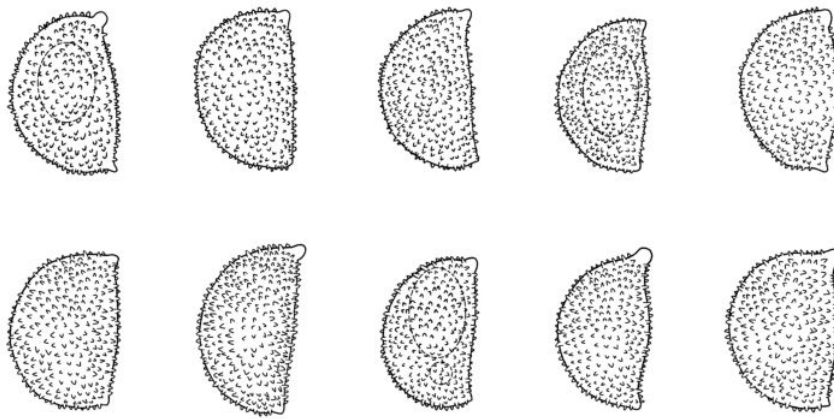


**Spores:** Basidiospores ellipsoid to semilunate, colorless, thin-walled, finely echinulate, a few with one or more oil drops, IKI+, CB–,  $(19.5\text{--}23.5\text{--}32\text{--}32.5) \times (12\text{--}16\text{--}20.5\text{--}22) \mu\text{m}$ ,  $L = 28.30 \mu\text{m}$ ,  $W = 18.00 \mu\text{m}$ ,  $Q = 1.571\text{--}1.693$  ( $n = 60/2$ ).

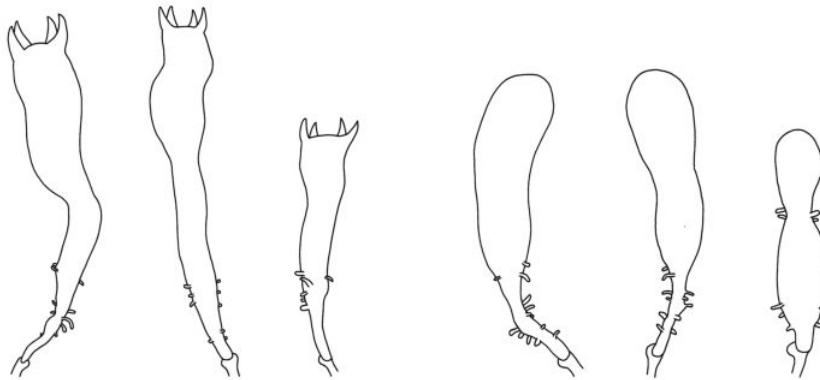
**Additional specimen examined (paratype)**—CHINA. Yunnan Province: Chuxiong, Zixishan Forestry Park, GPS coordinates:  $24^{\circ}40' \text{N}$ ,  $106^{\circ}36' \text{E}$ , altitude: 1900 m asl., on the fallen angiosperm branch, leg. C.L. Zhao, 30 June 2018, CLZhao 6781 (SWFC!).



**FIGURE 3.** Basidiomata of *Gloeosoma cremeum* (holotype CLZhao 29621). Scale bars: 1 cm (A); 1 mm (B).



**A**



**B**

**C**

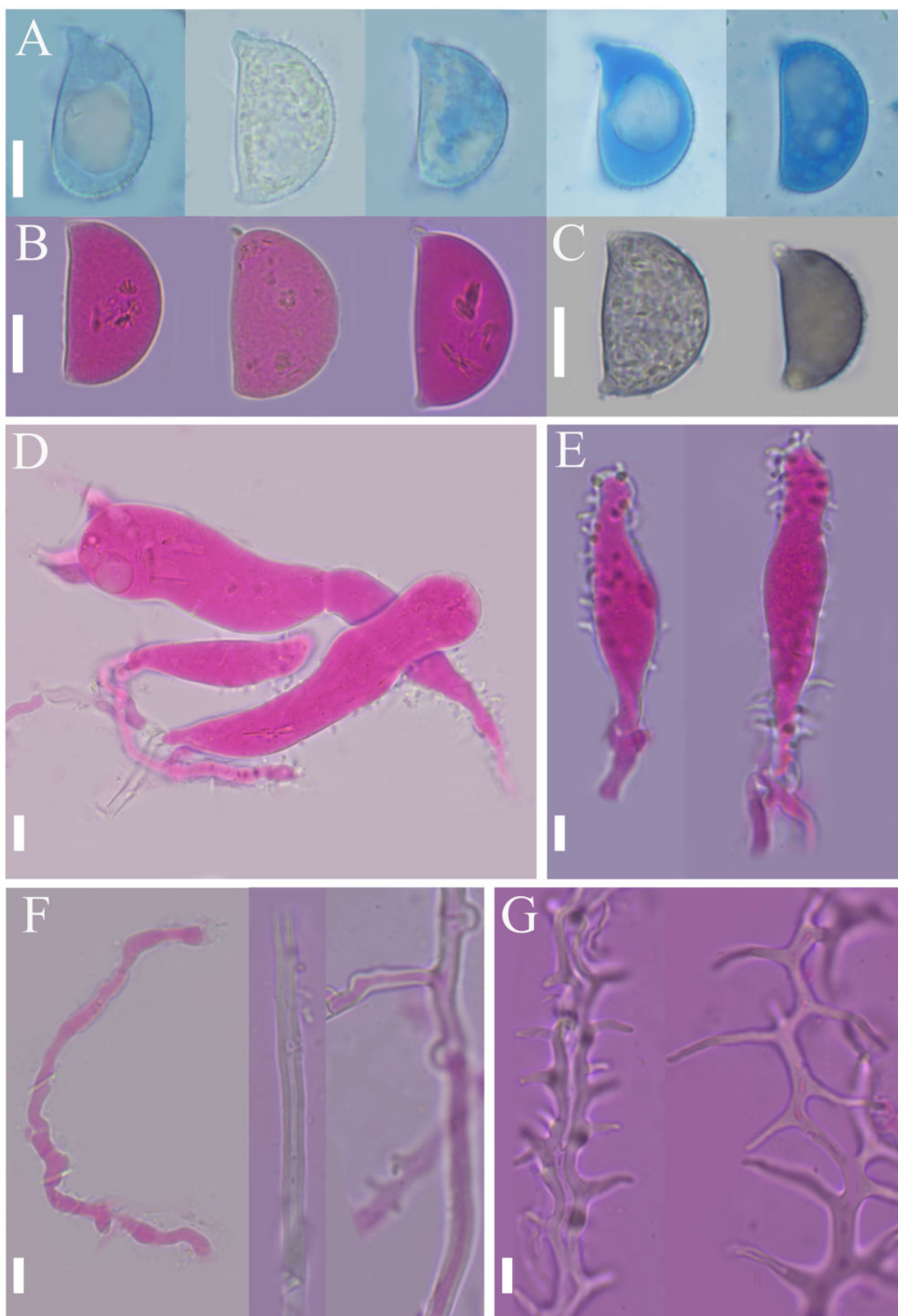


**D**

**E**

**FIGURE 4.** Microscopic structures of *Gloeosoma cremeum* (holotype CLZhao 29621): (A) basidiospores; (B) basidia; (C) basidioles; (D) cystidia; (E) a section of the hymenium. Scale bars: 10  $\mu\text{m}$  (A), 20  $\mu\text{m}$  (B–E).





**FIGURE 5.** Microscopic structures of *Gloeosoma cremeum* (holotype CLZhao 29621): (A) basidiospores in cotton blue; (B) basidiospores in 5% KOH and 2% phloxine B dye ( $C_{20}H_2Br_4Cl_4Na_2O_5$ ); (C) basidiospores in Melzer's reagent (IKI+); (D) basidia and basidioles; (E) cystidia; (F) generative hyphae with clamp connections; (G) acanthophyses. Scale bars: 10  $\mu$ m (A–G).

# Discussion

As DNA sequence data are increasingly applied in molecular phylogenetic studies of fungi, the species classification methods within the fungal kingdom are continually updated (Deng *et al.* 2024; Dong *et al.* 2024, 2025; He *et al.* 2025; Wang *et al.* 2025; Yang *et al.* 2025a, b). By collecting fungal specimens across regions, a new species, *Gloeosoma cremeum*, is described based on phylogenetic analyses and morphological characters. In the present study, the phylogenetic tree inferred from ITS+nLSU sequences revealed that the new species *Gloeosoma cremeum* was nested within the genus *Gloeosoma* within the family Stereaceae, in which it grouped with *G. mirabile*.

Morphologically, a comparison of the morphological characteristics of *G. cremeum*, *G. decorticans*, *G. mirabile*, *G. vitellinum*, and *G. zealandicum* is provided in Table 2. The species *G. cremeum* is morphologically similar to other species, with ellipsoid to semilunate basidiospores. However, *G. cremeum* has white to cream, smooth basidiomata, whereas *G. decorticans* has discoid basidiomata with furfuraceous, salmon pink hymenial surface; *G. mirabile* usually has smooth basidiomata with salmon or pink hymenial surface; *G. vitellinum* has cyphelloid basidiomata with vitellinous yellow hymenial surface; and *G. zealandicum* has cupulate basidiomata with pink or salmon hymenial surface (Núñez & Ryvarden 1997; Rajchenberg *et al.* 2021).

**TABLE 2.** Morphological characteristics used for distinguishing the clade comprising *G. cremeum*, *G. decorticans*, *G. mirabile*, *G. vitellinum*, *G. zealandicum*.

| Species name          | Basidiomata                    | Basidia                                    | Basidiospores                                                           | Habitat                              | Distribution  | References                     |
|-----------------------|--------------------------------|--------------------------------------------|-------------------------------------------------------------------------|--------------------------------------|---------------|--------------------------------|
| <i>G. cremeum</i>     | Effused, smooth                | Clavate (107.5–152 × 22–30 µm)             | Ellipsoid to semilunate, biapiculate, (23.5–32 × 16–20.5 µm)            | Hardwood                             | Asia          | This study                     |
| <i>G. decorticans</i> | Effused-reflexed, furfuraceous | Clavate (160–180 × 22–27 µm)               | Ellipsoid to broadly ellipsoid, biapiculate, (32.7–36.2 × 20.5–23.3 µm) | Hardwood                             | South America | Rajchenberg <i>et al.</i> 2021 |
| <i>G. mirabile</i>    | Effused-reflexed, smooth       | Clavate (80–160 × 16–24 µm)                | Ellipsoid to semilunate, biapiculate, (24–28 × 14–17 µm)                | Hardwood                             | America, Asia | Núñez & Ryvarden 1997          |
| <i>G. vitellinum</i>  | Cyphelloid                     | Subclavate to clavate (150–200 × 22–30 µm) | Ovoid, asperulate (20–30 × 18–24 µm)                                    | Dead stems of <i>Nothofagus</i> spp. | South America | Núñez & Ryvarden 1997          |
| <i>G. zealandicum</i> | Cupulate, ceraceous            | Subclavate (60–150 × 20–26 µm)             | Obovate, citriform or D-shaped coarsely asperulate (24–30 × 15–20 µm)   | Hardwood                             | New Zealand   | Núñez & Ryvarden 1997          |

The present study describes a new wood-rotting fungus in the small genus *Gloeosoma*, from Yunnan Province, southwest China, highlighting its role in enriching regional biodiversity and resource exploration efforts.

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