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Research Article

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Xiaojie Zhang, Siqi Shi, Jiangqing Su, Changlin Zhao

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Short Communication

**There Is More to the Taxonomy of *Schoenus apogon* (Cyperaceae) Than Meets the Eye: An Unresolved Complex With Cytological Diversity**

Yu Ito, Norio Tanaka, Jeremy J. Bruhl, Karen L. Wilson, Okihito Yano

First Published: 11 July 2026

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Short Communication

**Analysis of Culturable Endophytic Fungal Composition and Antioxidant Capacity Isolated From *Eriocaulon nudicuspe* Collected From the Tokai Hilly Land Spring-Fed Mires**

Wei Jiang, Weiwanqi Zhang, Qiong Han, Guang-Xi Wang

First Published: 10 July 2026

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## RESEARCH ARTICLE

# *Scopuloides fimbriata* (Meruliaceae, Polyporales), a New Fungal Species From Southwest China Revealed by Morphology and Phylogenetic Analyses

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## ABSTRACT

Wood-inhabiting fungi can decompose lignin, cellulose, and hemicellulose and play an integral role in the material cycle of forest ecosystems. In this study, we proposed a new species *Scopuloides fimbriata*, which was collected from Yunnan Province, southwest China. This new species is characterized by a smooth, white to buff hymenial surface and cylindrical, colorless, thin-walled basidiospores measuring  $4.5\text{--}6.3 \times 2\text{--}3 \mu\text{m}$ . The phylogenetic analysis was performed with Maximum Likelihood, Bayesian Inference, and Maximum Parsimony methods based on ITS + nLSU nuclear RNA gene regions. Phylogenetic analysis showed that *S. fimbriata* formed a monophyletic lineage within the family Meruliaceae and it is closely related to the type species of *Scopuloides*, *S. hydnoides*.

## 1 | Introduction

Fungi are well known as a diverse group of microorganisms and play important functional roles across agricultural, ecological, and economic contexts (Hibbett et al. 2025). Wood-inhabiting fungi are essential to natural ecosystems, accelerating rock weathering, responding to plant growth and nutrient cycling, and maintaining plant diversity (Larsson 2007; Justo et al. 2017; Wang et al. 2026).

Polyporales is one of the most intensively studied clades of Fungi (Justo et al. 2017; Wu et al. 2022; Zhao et al. 2025). Species in the phlebioid clade of Polyporales are wood-inhabiting fungi associated with white rot and typically produce crust-like or corticioid basidiomata with smooth or variously shaped hymenophores (Larsson 2007; Bernicchia and Gorjón 2010; Wu et al. 2022; Zhao et al. 2025). Within this clade, one well-supported subclade is recognized as the family Meruliaceae Rea (Floudas and Hibbett 2015; Gu et al. 2025; Zhao et al. 2025). The ecology, species diversity, taxonomy, and molecular systematics of taxa in these

families have been extensively studied (Floudas and Hibbett 2015; Miettinen et al. 2016; Justo et al. 2017; Dong et al. 2025). The Meruliaceae includes corticioid species, resupinate or pileate polypores, or pileate hydnaceous species, which are often ceraceous in appearance. The hyphal system is usually monomitic, rarely dimitic, and tightly arranged; generative hyphae are usually clamped, rarely simple-septate, and basidiospores are typically thin-walled, smooth, and colorless (Larsson 2007; Bernicchia and Gorjón 2010; Justo et al. 2017; Gu et al. 2025; Deng et al. 2026a).

The genus *Scopuloides*, typified by *S. hydnoides* (Cooke & Massee) Hjortstam & Ryvarden, has been recovered as monophyletic within Meruliaceae and includes species from Asia, Europe, North America, and the Neotropics (Larsson 2007; Bernicchia and Gorjón 2010; Wijesinghe et al. 2025; Deng et al. 2026a, 2026b). *Scopuloides* species are typically ceraceous, with white to buff hymenophores that are odontoid, hydnoid, or grandinoid. The genus is characterized by a compact subiculum with agglutinated, short-celled subicular hyphae, short basidia, small



basidiospores, and the presence of lamprocystidia (Wu 1990; Gilbertson and Nakasone 2003; Bernicchia and Gorjón 2010). According to MycoBank and Index Fungorum (accessed on 28 April 2026), *Scopuloides* has been recorded with 16 specific and infraspecific names, of which 11 species are widely recognized (Bernicchia and Gorjón 2010; Gu et al. 2025).

Multigene phylogenetic analyses were carried out based on two datasets as ITS + nLSU and five-gene (ITS + nLSU + *RPB1* + *RPB2* + *TEF1*) sequences to further explore species diversity in Meruliaceae, clarify the validity and circumscription of selected genera, and contribute to a well-supported and robust phylogeny of the family (Li et al. 2025). A multigene phylogeny and taxonomic study of the phlebioid clade, with implications for species diversity in Phanerochaetaceae, Irpicaceae, and Meruliaceae of Polyporales, has shown that four species of *Scopuloides* grouped together based on nucDNA ITS1-5.8S-ITS2, 28S rDNA, RNA polymerase II largest subunit (*RPB1*), RNA polymerase II second largest subunit (*RPB2*), and translation elongation factor 1- $\alpha$  (*TEF1*), with all species clustering within Meruliaceae (Chen et al. 2021).

During investigations of wood-inhabiting fungi in Yunnan Province, China, an undescribed species was discovered and is introduced herein. The aims of this study were to confirm the taxonomic affinities of the new species and to conduct a phylogenetic and taxonomic analysis of ITS and nLSU sequences to elucidate relationships among representative species of the family Meruliaceae. Accordingly, one new species *Scopuloides fimbriata* is proposed, with descriptions and illustrations based on morphological characteristics and phylogenetic analyses.

## 2 | Materials and Methods

### 2.1 | Specimen Collection and Morphological Studies

Fresh basidiomata were collected from the moist soil of broad-leaved forests in Baoshan, Yunnan Province, in July 2024. The samples were photographed in situ, and fresh macroscopic and other important collection details were recorded (Rathnayaka et al. 2025). Photographs were taken with a Nikon D7100 camera. All the photos were focus-stacked using Helicon Focus software. Macroscopic details were recorded and basidiomata were transported to a field station and dried on an electronic food drier at 45 °C (Dong et al. 2024). Once dried, the specimens were sealed in envelopes and zip-lock plastic bags and labeled (Dong et al. 2025). The dried specimens were deposited in the herbarium of the Southwest Forestry University (SWFC), Kunming, Yunnan Province, China.

The macromorphological descriptions were based on field notes and photos collected in the field and in the lab. Petersen (1996) was followed for the color terminology. Micromorphological data were obtained from dried specimens using a light microscope at 1000 $\times$  magnification. Sections of the hymenium were mounted in 5% KOH, 2% phloxine B, Cotton Blue, and Melzer's reagent. To show the variation in spore sizes, the extreme 5% of measurements at each end of the range were excluded 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, 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, and  $n = a/b$  (number of spores (a) measured from a given number (b) of specimens). The new species was registered in the MycoBank database (<http://www.mycobank.org>).

### 2.2 | 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 with the LR0R and LR7 primer pair (Vilgalys and Hester 1990; Rehner and Samuels 1994). 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 (White et al. 1990). The PCR procedure for nrLSU 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 (White et al. 1990). The PCR products were purified and sequenced at Kunming Tsingke Biological Technology Limited Company (Yunnan Province, P. R. China). Consensus sequences were generated using SnapGene (version 4.2.4; from Insightful Science; available at <https://snapgene.com>). The newly generated sequences were deposited in NCBI GenBank (Table 1).

The sequences were aligned in MAFFT version 7 (Katoh et al. 2019) using the G-INS-i strategy. Alignments were manually adjusted using AliView version 1.27 (Larsson 2014). Alignments of different loci were combined with Mesquite version 3.51 (Maddison and Maddison 2018). Two datasets were used for the phylogenetic analyses. The first dataset comprised a concatenated ITS + nLSU alignment of 20 genera in Meruliaceae, and was used to determine the genus-level placement of the studied material. The second dataset included ITS sequences of 10 *Scopuloides* species and was used to evaluate the species-level identity and phylogenetic position of the studied specimens within that genus.

Maximum parsimony (MP), Maximum Likelihood (ML), and Bayesian Inference (BI) analyses were applied to the combined three datasets following a previous study (Dong et al. 2024). 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 1000 random sequence additions. Max-trees were set to 5000, branches of zero length were collapsed, and all parsimonious trees were saved. Clade robustness was assessed using bootstrap (BT) analysis with 1000 pseudo-replicates (Felsenstein 1985). Descriptive tree statistics—tree length (TL), composite consistency index (CI), composite

**TABLE 1** | Names, sample numbers, references, and corresponding GenBank accession numbers of the taxa used in the phylogenetic analyses of this study.

| Species name                        | Sample no.       | GenBank<br>accession no. |          | Locality       | References               |
|-------------------------------------|------------------|--------------------------|----------|----------------|--------------------------|
|                                     |                  | ITS                      | nLSU     |                |                          |
| <i>Allophlebia ludoviciana</i>      | HHB-6564-Sp T    | MZ637036                 | MZ637240 | USA            | Chen et al. 2021         |
| <i>Allophlebia ludoviciana</i>      | HHB-8715-Sp T    | KY948770                 | KY948846 | USA            | Chen et al. 2021         |
| <i>Aurantipileus albidus</i>        | CIEFAP-117       | KY948739                 | KY948848 | Argentina      | Justo et al. 2017        |
| <i>Aurantipileus mayaensis</i>      | TJB10228         | HM772140                 | HM772139 | Belize         | Ginns et al. 2010        |
| <i>Aurantipileus semisupina</i>     | Cui 10 222       | KF845956                 | KF845949 | China          | Zhao and Cui 2014        |
| <i>Aurantipileus semisupina</i>     | Chen 3327        | MZ636937                 | MZ637100 | China          | Chen et al. 2021         |
| <i>Aurantiporus alboaurantius</i>   | Cui 2877         | KF845954                 | KF845947 | China          | Zhao and Cui 2014        |
| <i>Aurantiporus alboaurantius</i>   | Cui 4136         | KF845955                 | KF845948 | China          | Zhao and Cui 2014        |
| <i>Aurantiporus croceus</i>         | BRNM 737 561     | JQ821320                 | JQ821317 | Czech Republic | Dvořák et al. 2014       |
| <i>Aurantiporus orientalis</i>      | Dai 23 714       | PP702380                 | PP623071 | China          | Vlasák et al. 2012       |
| <i>Aurantiporus pseudoplacentus</i> | PRM 899 297      | JN592497                 | JN592504 | USA            | Vlasák et al. 2012       |
| <i>Aurantiporus pseudoplacentus</i> | Miettinen 18,997 | KY948744                 | KY948902 | USA            | Justo et al. 2017        |
| <i>Aurantiporus roseus</i>          | Dai 13 573       | KJ698635                 | KJ698639 | China          | Zhao et al. 2015         |
| <i>Ceriporiopsisoides guidella</i>  | HUBO 7659 T      | FJ496687                 | FJ496722 | Italy          | Tomšovský et al. 2010    |
| <i>Climacodon septentrionalis</i>   | RLG-6890-Sp      | KP135344                 | –        | USA            | Floudas and Hibbett 2015 |
| <i>Climacodon septentrionalis</i>   | AFTOL-ID 767     | AY854082                 | AY684165 | USA            | Lutzoni et al. 2004      |
| <i>Crustodontia chrysocreas</i>     | HHB-3946 T       | KP135357                 | –        | USA            | Floudas and Hibbett 2015 |
| <i>Crustodontia chrysocreas</i>     | HHB-6333-Sp T    | KP135358                 | KP135263 | USA            | Floudas and Hibbett 2015 |
| <i>Crustodontia nigrodontea</i>     | CLZhao 2729      | MT896823                 | MT896819 | China          | Huang et al. 2020        |
| <i>Crustodontia nigrodontea</i>     | CLZhao 2758      | MT896824                 | –        | China          | Huang et al. 2020        |
| <i>Geesterania carneola</i>         | MCW 388/12       | KY174999                 | KY174999 | Brazil         | Westphalen et al. 2018   |
| <i>Geesterania davidii</i>          | MCW 396/12       | KY174998                 | KY174998 | Brazil         | Westphalen et al. 2018   |
| <i>Hermanssonia centrifuga</i>      | CBS 125 890 T    | MH864088                 | MH875547 | Sweden         | Vu et al. 2019           |
| <i>Hermanssonia fimbriata</i>       | Dai 23 266 *     | ON135436                 | ON135440 | China          | Liu et al. 2022          |
| <i>Hermanssonia fimbriata</i>       | Dai 23 305       | ON135437                 | ON135441 | China          | Liu et al. 2022          |
| <i>Hydnophlebia alachuana</i>       | L-11 510-Sp      | KP135340                 | –        | USA            | Floudas and Hibbett 2015 |
| <i>Hydnophlebia alachuana</i>       | FP-103 881-Sp    | KP135341                 | KP135201 | USA            | Floudas and Hibbett 2015 |
| <i>Hydnophlebia omnivora</i>        | KKN-112-Sp       | KP135334                 | KP135216 | USA            | Floudas and Hibbett 2015 |
| <i>Hydnophlebia omnivora</i>        | ME-497           | KP135332                 | KP135218 | USA            | Floudas and Hibbett 2015 |
| <i>Hydnophlebia sinensis</i>        | He 1924          | MK860723                 | MK860733 | China          | Liu et al. 2020          |
| <i>Hydnophlebia subchrysorhiza</i>  | He 2325          | MK860718                 | MK860727 | China          | Liu et al. 2020          |
| <i>Hydnophlebia subchrysorhiza</i>  | He 3886          | MK860717                 | MK860726 | China          | Liu et al. 2020          |
| <i>Luteoporia albocitrina</i>       | Dai 19 507       | MT872218                 | MT872216 | Sri Lanka      | Liu and Yuan 2020        |
| <i>Luteoporia albocitrina</i>       | Dai 19 622       | MT872219                 | MT872217 | Sri Lanka      | Liu and Yuan 2020        |
| <i>Luteoporia straminea</i>         | CLZhao 18 947 *  | MW732407                 | MW724799 | China          | Zhao et al. 2023         |
| <i>Luteoporia straminea</i>         | CLZhao 5974      | OM897115                 | OM897114 | China          | Zhao et al. 2023         |
| <i>Meruliella lindtneri</i>         | GB-501           | KY948772                 | KY948847 | Norway         | Justo et al. 2017        |
| <i>Mycoacia aurea</i>               | RLG-5075-Sp      | KY948759                 | MZ637161 | USA            | Chen et al. 2021         |
| <i>Mycoacia aurea</i>               | Chen 3780        | MZ637000                 | MZ637160 | China          | Chen et al. 2021         |
| <i>Mycoacia kunmingensis</i>        | CLZhao 152       | KX081072                 | KX081074 | China          | Zhao and Wu 2017         |
| <i>Mycoacia kunmingensis</i>        | CLZhao 153 *     | KX081073                 | KX081075 | China          | Zhao and Wu 2017         |

(Continues)

TABLE 1 | (Continued)

| Species name                       | Sample no.        | GenBank<br>accession no. |          | Locality       | References                        |
|------------------------------------|-------------------|--------------------------|----------|----------------|-----------------------------------|
|                                    |                   | ITS                      | nLSU     |                |                                   |
| <i>Mycoacia livida</i>             | Miettinen 101     | HQ153416                 | –        | Russia         | Ghobad-Nejhad and Hallenberg 2012 |
| <i>Mycoacia livida</i>             | FBCC937           | LN611122                 | LN611122 | Finland        | Kuuskeri et al. 2015              |
| <i>Mycoaciella efibulata</i>       | WEI 16–167        | MZ637010                 | MZ637170 | China          | Chen et al. 2021                  |
| <i>Mycoaciella efibulata</i>       | CLZhao 15 876     | MW732404                 | MW724796 | China          | Zhao et al. 2023                  |
| <i>Pappia fissilis</i>             | 814 T             | HQ728291                 | HQ729001 | Czech Republic | Tomšovský 2012                    |
| <i>Pappia fissilis</i>             | BRNM 699 803 T    | HQ728292                 | HQ729002 | Czech Republic | Tomšovský 2012                    |
| <i>Phlebia acerina</i>             | FBCC345           | LN611083                 | LN611083 | Russia         | Kuuskeri et al. 2015              |
| <i>Phlebia acerina</i>             | GC 1708–40        | MZ637030                 | MZ637234 | China          | Chen et al. 2021                  |
| <i>Phlebia floridensis</i>         | FP-102 562-T      | KP135386                 | –        | USA            | Floudas and Hibbett 2015          |
| <i>Phlebia floridensis</i>         | HHB-9905-Sp       | KP135383                 | KP135264 | USA            | Floudas and Hibbett 2015          |
| <i>Phlebia niveomarginata</i>      | CLZhao 18 972     | MW732409                 | MW724801 | China          | Zhao et al. 2023                  |
| <i>Phlebia niveomarginata</i>      | CLZhao 19 089 *   | MW732410                 | MW724802 | China          | Zhao et al. 2023                  |
| <i>Phlebia poroides</i>            | CLZhao 16 121 *   | MW732405                 | MW724797 | China          | Zhao et al. 2023                  |
| <i>Phlebia poroides</i>            | CLZhao 18 421     | MW732406                 | MW724798 | China          | Zhao et al. 2023                  |
| <i>Phlebia radiata</i>             | FD-85 T           | KP135377                 | –        | USA            | Floudas and Hibbett 2015          |
| <i>Phlebia radiata</i>             | AFTOL-ID-484 5 T  | AY854087                 | –        | USA            | Floudas and Hibbett 2015          |
| <i>Phlebia rufa</i>                | FBCC297           | LN611092                 | LN611092 | Sweden         | Kuuskeri et al. 2015              |
| <i>Phlebia rufa</i>                | HHB-14 924        | KP135374                 | –        | USA            | Floudas and Hibbett 2015          |
| <i>Phlebicolorata austroasiana</i> | Dai 17 556        | ON135439                 | ON135443 | China          | Liu et al. 2022                   |
| <i>Phlebicolorata brevispora</i>   | FBCC1463 T        | LN611135                 | LN611135 | USA            | Kuuskeri et al. 2015              |
| <i>Phlebicolorata brevispora</i>   | HHB-7024-Sp T     | MZ637032                 | MZ637236 | USA            | Chen et al. 2021                  |
| <i>Phlebiodontia acanthocystis</i> | FP150571          | KY948767                 | KY948844 | USA            | Justo et al. 2017                 |
| <i>Phlebiodontia acanthocystis</i> | GC 1703–30        | LC387338                 | LC387343 | China          | Chen et al. 2018                  |
| <i>Phlebiodontia caspica</i>       | FCUG3159          | HQ153410                 | –        | Iran           | Ghobad-Nejhad and Hallenberg 2012 |
| <i>Phlebiodontia fissurata</i>     | CLZhao 2900       | MW732402                 | MW724794 | China          | Zhao et al. 2023                  |
| <i>Phlebiodontia rajchenbergii</i> | MCW626 * T        | OP265191                 | OP265189 | Brazil         | Motato-Vásquez et al. 2022        |
| <i>Phlebiodontia rajchenbergii</i> | MCW636 T          | OP265192                 | OP265190 | Brazil         | Motato-Vásquez et al. 2022        |
| <i>Phlebiporia bubalina</i>        | Dai 13 168 * T    | KC782526                 | KC782528 | China          | Chen and Cui 2014                 |
| <i>Phlebiporia bubalina</i>        | Dai 15 179 T      | KY131843                 | KY131902 | China          | Wu et al. 2017                    |
| <i>Phlebiporia crystallifera</i>   | He 20 120 720–8 * | PP549562                 | PP549595 | China          | Li et al. 2025                    |
| <i>Phlebiporia crystallifera</i>   | He 5227           | PP549563                 | PP549596 | Vietnam        | Li et al. 2025                    |
| <i>Phlebiporia ontoidea</i>        | He 4903 *         | PP549564                 | PP549597 | China          | Li et al. 2025                    |
| <i>Phlebiporia ontoidea</i>        | Wu 1210–7         | MZ637061                 | –        | China          | Chen et al. 2021                  |
| <i>Porophlebia fimbriata</i>       | Dai 11 672        | KJ698633                 | KJ698637 | China          | Zhao et al. 2015                  |
| <i>Porophlebia fimbriata</i>       | Cui 1671          | KJ698634                 | KJ698638 | China          | Zhao et al. 2015                  |
| <i>Pseudophlebia setulosa</i>      | PH5105 T          | GU461313                 | GU461313 | Spain          | Moreno et al. 2011                |
| <i>Pseudophlebia setulosa</i>      | HHB-6891-Sp T     | KP135382                 | KP135267 | USA            | Chen et al. 2021                  |
| <i>Scopuloides allantoidea</i>     | GC 1602–11        | MZ637080                 | MZ637278 | China          | Chen et al. 2021                  |
| <i>Scopuloides allantoidea</i>     | WEI 16–060        | MZ637081                 | MZ637279 | China          | Zong and Zhao 2021                |
| <i>Scopuloides amplissima</i>      | GC 1602–11        | MZ637080                 | MZ637278 | China          | Chen et al. 2021                  |
| <i>Scopuloides amplissima</i>      | WEI 16–060        | MZ637081                 | MZ637279 | China          | Chen et al. 2021                  |

(Continues)

TABLE 1 | (Continued)

| Species name                        | Sample no.             | GenBank<br>accession no. |                 | Locality     | References           |
|-------------------------------------|------------------------|--------------------------|-----------------|--------------|----------------------|
|                                     |                        | ITS                      | nLSU            |              |                      |
| <i>Scopuloides dimorpha</i>         | FP-102 935-Sp          | KP135353                 | KP135285        | USA          | Zong and Zhao 2021   |
| <i>Scopuloides dimorpha</i>         | WEI 19–073             | MZ637084                 | MZ637282        | China        | Chen et al. 2021     |
| <i>Scopuloides ellipsoidea</i>      | He 4681                | PP549568                 | PP549602        | China        | Li et al. 2025       |
| <i>Scopuloides ellipsoidea</i>      | He 4760 *              | PP549569                 | PP549603        | China        | Li et al. 2025       |
| <i>Scopuloides farinacea</i>        | CLZhao 30 005          | PV470558                 | PV474203        | China        | Gu et al. 2025       |
| <i>Scopuloides farinacea</i>        | CLZhao 30 181 *        | PV470559                 | PV474204        | China        | Gu et al. 2025       |
| <b><i>Scopuloides fimbriata</i></b> | <b>CLZhao 38 962</b>   | <b>PZ379720</b>          | <b>PZ344668</b> | <b>China</b> | <b>Present study</b> |
| <b><i>Scopuloides fimbriata</i></b> | <b>CLZhao 38 974 *</b> | <b>PZ368423</b>          | <b>PZ344669</b> | <b>China</b> | <b>Present study</b> |
| <i>Scopuloides grandinioides</i>    | RLG-5104-sp            | KP135351                 | KP135283        | USA          | Li et al. 2025       |
| <i>Scopuloides grandinioides</i>    | HHB-11 766-sp          | KP135348                 | –               | USA          | Li et al. 2025       |
| <i>Scopuloides hydnoidea</i>        | FP-150 473 T           | KP135355                 | KP135284        | USA          | Zong and Zhao 2021   |
| <i>Scopuloides hydnoidea</i>        | He 4507 T              | PP549572                 | PP549606        | China        | Li et al. 2025       |
| <i>Scopuloides rimosa</i>           | He 3320                | PP549574                 | PP549608        | China        | Li et al. 2025       |
| <i>Scopuloides rimosa</i>           | He 3620                | PP549575                 | PP549609        | China        | Li et al. 2025       |
| <i>Scopuloides yunnanensis</i>      | CLZhao 30 079          | PP511313                 | PP511316        | China        | Gu et al. 2024       |
| <i>Scopuloides yunnanensis</i>      | CLZhao 30 213 *        | PP511314                 | PP511317        | China        | Gu et al. 2024       |
| <i>Thelephora grandinioides</i>     | CLZhao 3408            | MZ400678                 | MZ400671        | China        | Liu et al. 2021      |
| <i>Thelephora grandinioides</i>     | CLZhao 3406 *          | MZ400677                 | MZ400672        | China        | Liu et al. 2021      |

Notes: New species are in bold; T is the type species of the genus; \* is the holotype, and – refers to the missing data.

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 1000 bootstrap pseudo-replicates.

MrModeltest 2.3 (Nylander 2004) was used to determine the best-fit evolution model for each dataset for the purposes of Bayesian inference (BI), which 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). 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 as significantly supported if they received a maximum likelihood bootstrap support value (BS) of  $\geq 70\%$ , a maximum parsimony bootstrap support value (BT) of  $\geq 70\%$  or a Bayesian posterior probability (BPP) of  $\geq 0.95$ .

### 3 | Results

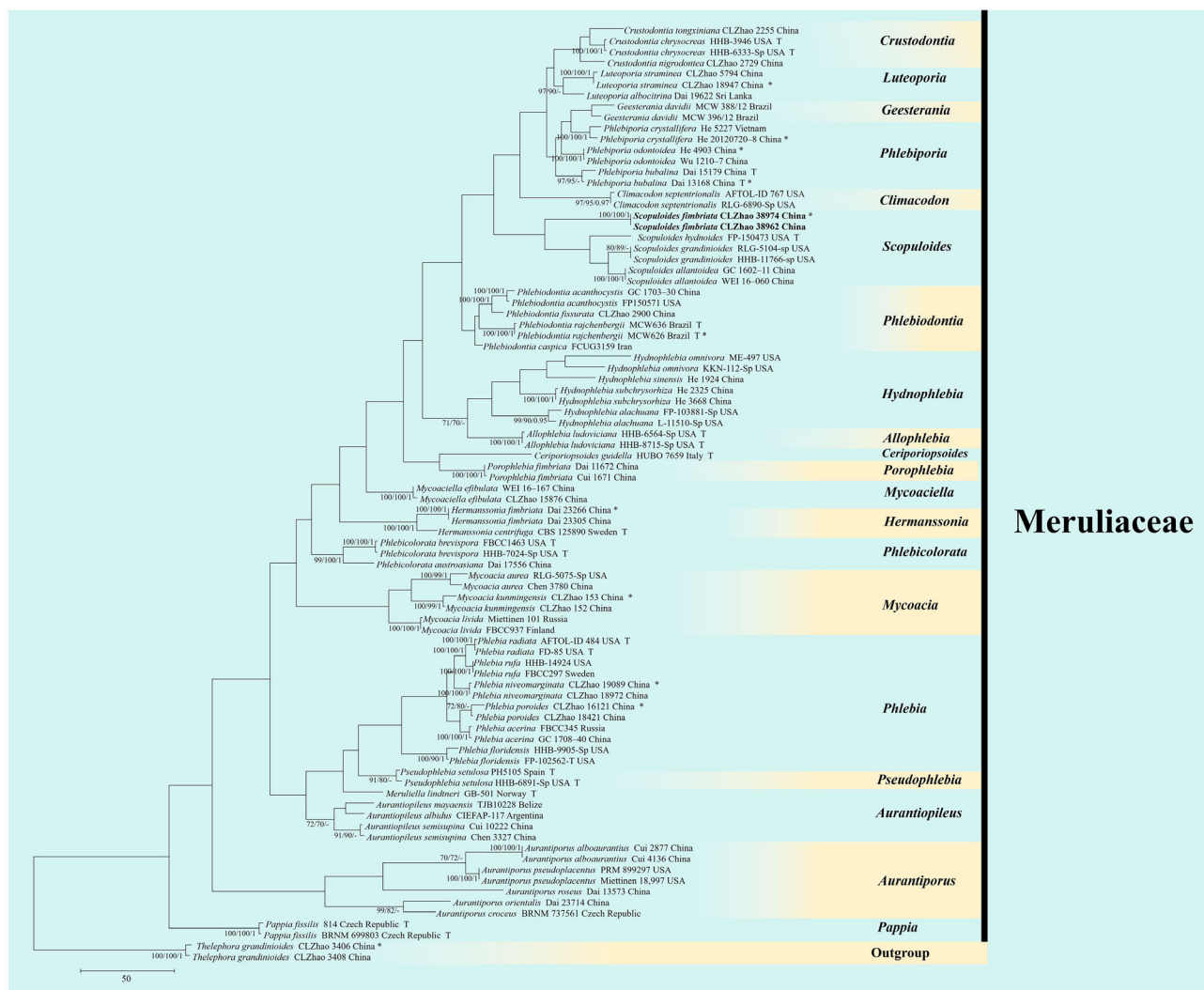
#### 3.1 | Molecular Phylogeny

The phylogeny of the new *Scopuloides* species and related Meruliaceae species based on ITS + nLSU sequences is shown in Figure 1. The aligned dataset comprised 86 specimens representing 50 taxa, including the new *Scopuloides* species. *Thelephora grandinioides* C.L. Zhao & X.F. Liu was used as

the outgroup taxon in the phylogenetic analysis (Figure 1; Liu et al. 2021). The phylogenetic tree diagram generated in this study has been deposited in the Figshare repository and is publicly available at: <https://doi.org/10.6084/m9.figshare.32674791>. The trees from the three analyses (ML, MP, and BI) showed identical topologies. Four Markov chains were run in two independent runs from random starting trees, each for 8 million generations. The dataset had an aligned length of 2,544 characters, of which 542 were constant, 560 were variable and parsimony-uninformative, and 1,442 were parsimony-informative. Maximum parsimony analysis yielded 2 equally parsimonious trees (TL = 6347, CI = 0.5028, HI = 0.4972, RI = 0.7433, RC = 0.4257). The best model for the ITS + nLSU dataset, estimated and applied in the Bayesian analysis, was GTR + I + G. Both Bayesian and ML analyses yielded a similar topology to the MP analysis, with an average standard deviation of split frequencies = 0.009452 (BI), and the effective sample size (ESS) across the two runs was twice the average ESS (avg ESS) = 431.23.

The phylogenetic tree of the new species and related *Scopuloides* species within the genus *Scopuloides* based on ITS sequences (Figure 2) showed that the aligned dataset encompassed 21 specimens representing 11 taxa, including the new species *Scopuloides fimbriata*, and *Thelephora grandinioides* was used as the outgroup taxa in the phylogenetic analysis (Liu et al. 2021). The phylogenetic tree diagram generated in this study has been deposited in the Figshare repository and is publicly available at: <https://doi.org/10.6084/m9.figshare.32674899>. Four Markov chains were run for 2 runs from random starting trees, each for 3 million generations. The dataset had an aligned length of 866 characters, of which 606 were constant, 30 were variable and





## Meruliaceae

**FIGURE 1** | Maximum Parsimony strict consensus tree illustrating the phylogeny of the new *Scopuloides* species and related species of the family Meruliaceae based on ITS + nLSU sequences. Branches are labeled with maximum likelihood bootstrap values equal to or above 70%, parsimony bootstrap values equal to or above 70% and Bayesian posterior probabilities equal to or above 0.95. The new species is in bold; T is the type species of the genus; \* is the holotype.

parsimony-uninformative, and 230 were parsimony-informative. Maximum Parsimony analysis yielded 2 equally parsimonious trees (TL = 468, CI = 0.6934, HI = 0.3066, RI = 0.7597, RC = 0.5268). The best model for the ITS dataset, estimated and applied in the Bayesian analysis, was HKY + G. Both Bayesian and ML analyses yielded a similar topology to the MP analysis, with an average standard deviation of split frequencies = 0.002691 (BI), and the effective sample size (ESS) across the two runs is double the average ESS (avg ESS) = 1552.83.

The phylogeny (Figure 2) based on ITS data showed that the new species *S. fimbriata* clustered within the genus *Scopuloides* and was closely related to *S. ellipsoidea* S.H. He, Yue Li & Nakasone and *S. leprosa* (Bourdote & Galzin) Boidin, Lanq. & Gilles.

### 3.2 | Taxonomy

***Scopuloides fimbriata*** X.J. Zhang & C.L. Zhao, sp. nov., Figures 3 and 4.

**MycoBank:** MB 863 560

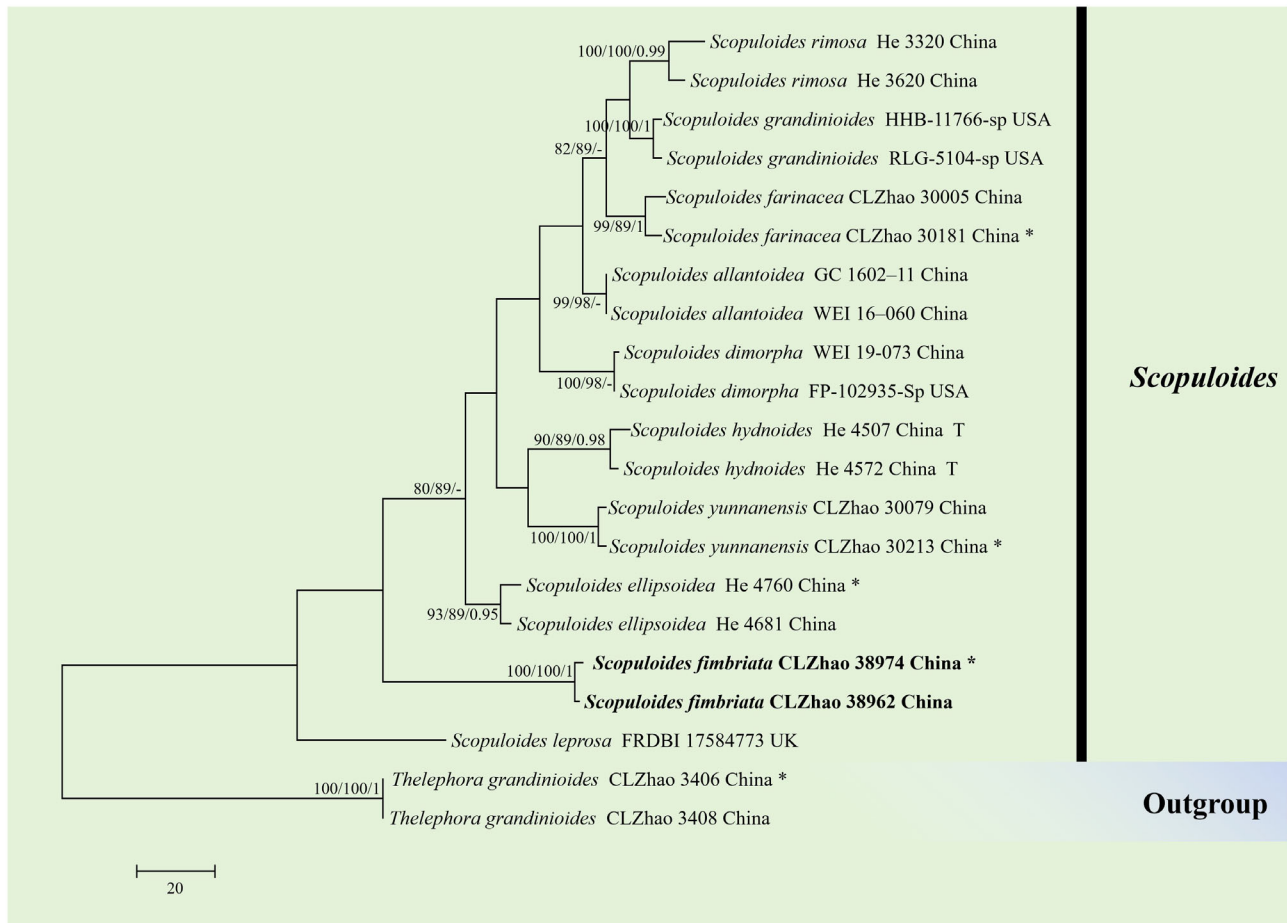
**Etymology:** *fimbriata* (Lat.): refers to the fimbriate sterile margin of the basidiomata.

**Holotype:** China, Yunnan Province, Baoshan, Tengchong, Tuantian Town, Gaoligongshan National Nature Reserve, GPS coordinates: 24°55' N, 98°40' E, elev. 2100 m asl., on the fallen angiosperm branch, leg. C.L. Zhao, 7 July 2024, CLZhao 38 974 (SWFC 00038974).

**Description:** *Basidiomata* annual, resupinate, coriaceous, without odor or taste when fresh, up to 6 cm long, 1.5 cm wide, less than 0.5 mm thick. Hymenial surface smooth, white when fresh and white to buff upon drying. Sterile margin narrow, white, up to 1 mm wide.

**Hyphal system** monomitic; generative hyphae bearing simple-septa, colorless, thin-walled to slightly thick-walled, branched, interwoven, 1.3–2.1 µm in diameter; subiculum generative





**FIGURE 2** | Maximum Parsimony strict consensus tree illustrating the phylogeny of the new species and related species of *Scopuloides* based on ITS sequences. Branches are labeled with maximum likelihood bootstrap values equal to or above 70%, parsimony bootstrap values equal to or above 70% and Bayesian posterior probabilities equal to or above 0.95, respectively. The new species is in bold; T is the type species of the genus; \* is the holotype.

hyphae, thick-walled, colorless, branched, interwoven, IKI-, CB-; tissues unchanged in KOH. *Cystidia* absent. *Basidia* clavate, thin-walled, with a simple septum at the base and four sterigmata, with oil droplet-like refractive material,  $16\text{--}23 \times 3.7\text{--}4.8 \mu\text{m}$ . Basidioles dominate the hymenium, similar to basidia but smaller. *Basidiospores* cylindrical, colorless, thin-walled, with 2–3 oil drops, IKI-, CB-,  $(4.3\text{--})4.5\text{--}6.3(-6.9) \times 2\text{--}3(-3.4) \mu\text{m}$ ,  $L = 5.44 \mu\text{m}$ ,  $W = 2.58 \mu\text{m}$ ,  $Q = 1.90\text{--}2.11$  ( $n = 60/2$ ).

**Material examined:** China, Yunnan Province, Baoshan, Tengchong, Tuantian Town, Gaoligongshan National Nature Reserve, GPS coordinates:  $24^{\circ}55' \text{ N}$ ,  $98^{\circ}40' \text{ E}$ , elev. 2100 m asl., on the fallen angiosperm branch, leg. C.L. Zhao, 7 July 2024, CLZhao 38 962 (SWFC 00038962).

#### 4 | Discussion

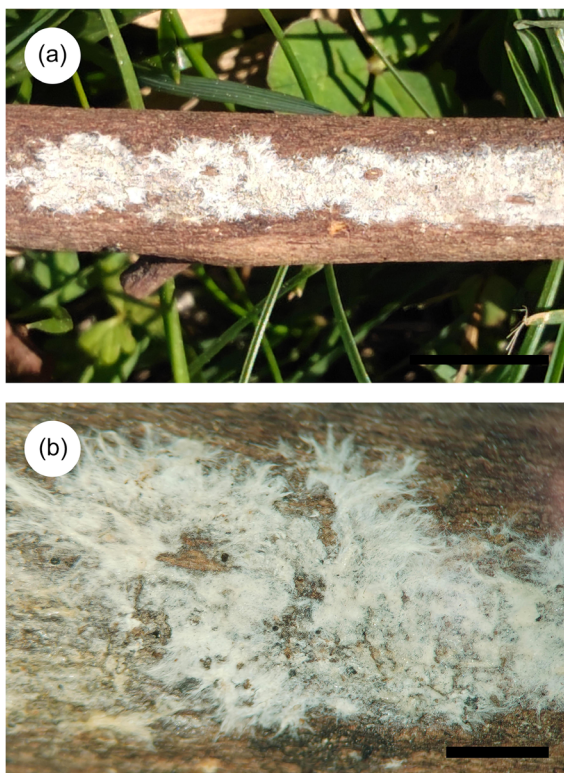
A multigene phylogeny together based on nucDNA ITS1-5.8S-ITS2, 28S rDNA, *RPB1*, *RPB2*, and *TEF1*, indicated that *Scopuloides* species grouped with related genera species within the families Meruliaceae of Polyporales (Chen et al. 2021). In the present study, one new species, *Scopuloides fimbriata*, is described based on phylogenetic analyses and morphological

characteristics. Based on the ITS + nLSU dataset, the results show that *S. fimbriata* is closely related to *S. hydroides* (Figure 1). However, morphologically, *S. hydroides* has smaller short-allantoid basidiospores ( $3.5\text{--}4 \times 1.8\text{--}2.2 \mu\text{m}$  vs.  $4.5\text{--}6.3 \times 2\text{--}3 \mu\text{m}$ ; Eriksson et al. 1984).

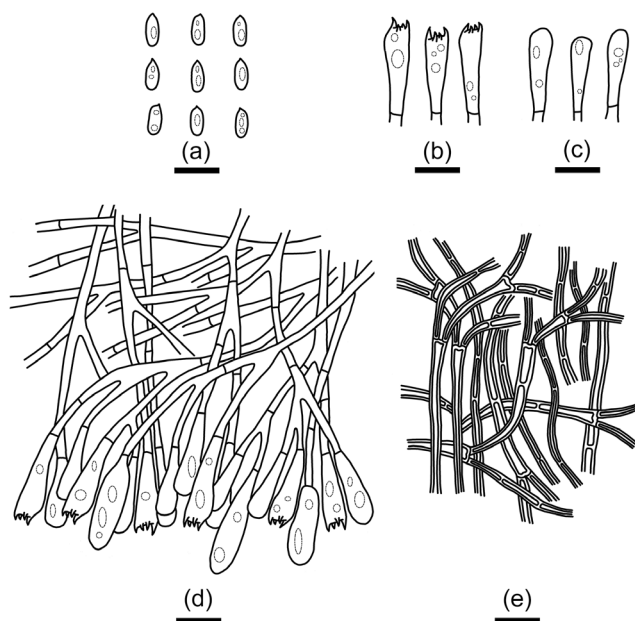
Phylogenetic analysis based on the ITS dataset showed that the new species *S. fimbriata* is closely related to *S. ellipsoidea* and *S. leprosa* (Figure 2). However, morphologically, *S. ellipsoidea* has yellowish white, gray, yellowish gray to orange gray hymenial surface and smaller basidiospores ( $2.6\text{--}3.1 \times 1.5\text{--}1.8 \mu\text{m}$  vs.  $4.5\text{--}6.3 \times 2\text{--}3 \mu\text{m}$ ; Li et al. 2025); *S. leprosa* has larger basidia ( $25\text{--}32 \times 5\text{--}6 \mu\text{m}$  vs.  $16\text{--}23 \times 3.7\text{--}4.8 \mu\text{m}$ ; Boidin et al. 1993).

Morphologically, *Scopuloides fimbriata* is similar to *S. farinacea* Z.R. Gu & C.L. Zhao and *S. yunnanensis* Z.R. Gu & C.L. Zhao. However, *S. farinacea* is distinguished from *S. fimbriata* by pale cream to buff hymenophore and its smaller basidiospores ( $2.8\text{--}3.5 \times 1.4\text{--}2 \mu\text{m}$  vs.  $4.5\text{--}6.3 \times 2\text{--}3 \mu\text{m}$ ; Gu et al. 2025). The species *S. yunnanensis* differs from *S. fimbriata* by having a white to pale cream hymenial surface and smaller basidiospores ( $2.8\text{--}3.7 \times 1.4\text{--}2 \mu\text{m}$  vs.  $4.5\text{--}6.3 \times 2\text{--}3 \mu\text{m}$ ; Gu et al. 2024).

Wood-inhabiting fungi constitute a well-studied ecological guild within Basidiomycota, encompassing poroid, smooth,



**FIGURE 3** | Basidiomata of *Scopuloides fimbriata* (holotype, CLZhao 38 974): (a) Basidiomata on the ground. (b) Macroscopic characteristics of hymenophore. Bars: a = 1 cm, b = 1 mm.



**FIGURE 4** | Microscopic structures of *Scopuloides fimbriata* (holotype, CLZhao 38 974): (a) Basidiospores. (b) Basidia. (c) Basidioles. (d) A section of the hymenium. (e) Hyphae from subiculum. Bars: a–e = 10  $\mu$ m.

grandinioid, odontoid, and hydroid basidiomata, and numerous new taxa have been described from China in recent years (Luo et al. 2022; Qu et al. 2022; Zhang et al. 2024; Liu et al. 2025; Zhao et al. 2025; Deng et al. 2026a). Based on the morphological and

phylogenetic methods, a number of wood-inhabiting fungi were recorded in China (Chen et al. 2020; Chen and Zhao 2020; Guan and Zhao 2023; Yuan et al. 2023; Yang et al. 2023, 2024; Zhou et al. 2023; 2024; Wijesinghe et al. 2025; Li et al. 2026; Zhu et al. 2026). In the present study, the new species *Scopuloides fimbriata* is reported based on a combination of morphological features and molecular evidence. This study contributes to a greater understanding of fungal diversity in these areas and continued field surveys coupled with molecular analyses will likely reveal additional undescribed taxa.

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## Conflicts of Interest

No potential conflict of interest was reported by the author(s).

## Data Availability Statement

The data that support the findings of this study are openly available in GenBank at <https://www.ncbi.nlm.nih.gov/nuccore>, reference number PZ379720, PZ368423, PZ344668, PZ344669.

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