

Two New Species of Pleosporales from Pteridophytes in China

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Abstract

Pleosporales is one of the largest and most diverse orders in Dothideomycetes. This order encompasses numerous families and genera characterized by considerable morphological diversity and a wide range of ecological lifestyles. During an investigation of fungal diversity associated with pteridophytes in South China, healthy samples of *Diplopterygium chinense* and *Lepidogrammitis drymoglossoides* were collected from Yunnan and Guangdong provinces. Endophytic fungi were isolated using the tissue isolation method. Among the isolates, four strains were identified as members of Pleosporales based on multi-locus phylogenetic analyses using the internal transcribed spacer (ITS), the large subunit (LSU), the β -tubulin (*tub2*), and the RNA polymerase II subunit (*rpb2*) sequence data, together with morphological characteristics of conidiation. These strains were assigned to two species each in *Epicoccum* and *Paraconiothyrium* and are herein described as two new species, *Epicoccum diplopterygii* and *Paraconiothyrium drymoglossoidis*. Detailed morphological illustrations, taxonomic descriptions, and molecular data are provided. This study expands the current knowledge of Pleosporales diversity and host associations in pteridophytic plants, providing a foundation for future taxonomic and ecological studies of fungi associated with pteridophytes in China.

1. Introduction

Pleosporales was formally established by Luttrell (1955) and is currently recognized as the largest order in Dothideomycetes, with 91 families and 653 genera (Hyde et al. 2024, Thiyagaraja et al. 2025). Pleosporales encompasses a wide range of morphological and ecological diversity (Kirk et al. 2008, Zhang et al. 2012, Hyde et al. 2013, Wijayawardene et al. 2014, Bhunjun et al. 2021, Thiyagaraja et al. 2025). Pleosporales species are characterized by perithecial ascomata, which are flask-shaped and typically possess papillae, and ostioles. The asexual morphs are coelomycetous and hyphomycetous (Hyde et al. 2011, Pem et al. 2024, He et al. 2025). The species exhibit remarkable ecological and morphological diversity, including saprobic, plant pathogenic, endophytic, and lichenicolous fungi, as well as species from freshwater and marine habitats (Shearer et al. 2009, Hongsan et al. 2020, Phukhamsakda et al. 2020, Yang et al. 2025; Thiyagaraja et al. 2025).

Didymellaceae is a large family within the Pleosporales, which includes major genera of phoma-like fungi including *Ascochyta*, *Didymella*, and *Stagonosporopsis*, and represents an underestimated component of fungal diversity (Chen et al. 2017, 2023, Gomzhina et al. 2025). *Didymellaceae* species are predominantly plant pathogens, such as *Didymella pinodes*, which causes Ascochyta blight of field pea, and *Parastagonospora nodorum*, which causes Stagonospora nodorum blotch of wheat (Bretag et al. 1995, Solomon et al. 2006, Quaedy et al. 2013); however, several species have also been reported as opportunistic pathogens of humans and animals worldwide (Boerema et al. 2004, de Hoog et al. 2011). Moreover, numerous taxa occur as plant endophytes or saprobes, often in association with both host and non-host organisms, highlighting the ecological versatility of *Didymellaceae* (Schulz and Boyle 2005, Tahtamouni et al. 2016). Therefore, investigating *Didymellaceae* species diversity is essential for

understanding the taxonomy, evolution, and functional roles of plant-associated fungi (de Gruyter et al. 2009, Chen et al. 2015, Hou et al. 2020).

Didymosphaeriaceae represents a morphologically distinct but phylogenetically underexplored family within Pleosporales. Studies of its species diversity are important for resolving family boundaries and understanding evolutionary relationships among pleosporalean fungi (Hyde et al. 2013, Ariyawansa et al. 2014, Hyde et al. 2024). *Didymosphaeriaceae* is characterized by 1-septate ascospores and trabeculate pseudoparaphyses, which anastomose mostly above the asci (Liew et al. 2000, Hyde et al. 2013, Ariyawansa et al. 2014, Wanasinghe et al. 2016). Wanasinghe et al. (2016) introduced two new genera, *Laburnicola* and *Paramassariosphaeria*, based on combined phylogenetic analyses of LSU, SSU, and ITS sequence data. The family comprises 39 genera, with species occurring worldwide as endophytes, pathogens, and saprobes on a wide range of plant substrates (Liu et al. 2015, Wanasinghe et al. 2016, Hyde et al. 2024).

Pteridophytes are seedless vascular plants that reproduce by spores and typically inhabit moist environments (PPG 2016). In addition, they are an important part of the ground vegetation in many forest communities and, with about one-third of the species growing on the trunks and branches of trees, they are also an important component of many epiphytic plant communities (Yatskievych et al. 2003, PPG 2016). Recent studies have revealed that pteridophytes host a wide range of fungal taxa; however, knowledge of fungal diversity associated with pteridophytes remains limited (Bao et al. 2025, Zhang et al. 2025). This study is a part of an ongoing investigation of fungal diversity associated with pteridophytes in South China, in which we collected fresh healthy samples to understand the endophytic diversity in pteridophytes. The objectives of this study are to determine species composition, assess phylogenetic relationships, and enhance current knowledge of fungal diversity in pteridophyte hosts. Here we described four new taxa from *Didymellaceae* and *Didymosphaeriaceae* with updated taxonomic positions through morphology combined with phylogenetic analyses. These data will not only contribute to a better understanding of host associations and geographic distribution of Pleosporales in China but also highlight their potential as valuable fungal resources for future studies on ecosystem functions.

2. Materials and methods

2.1 Sample collection, isolation, and morphological examination

Samples of fungi were obtained from Baiyun Mountain (23°09'35"N 113°17'40"E) in Guangzhou city, Guangdong Province, and Ailao Mountain (24°31'23"N 101°03'12"E) in Yunnan Province, China. Healthy fresh leaves of *Diplazium chinense* and *Lepidogrammitis drymoglossoides* were collected, and the specimens were brought to the lab in a Ziploc bag. The fresh leaves were washed with water to remove dirt and dust. Then, leaves were cut into small pieces (5×5 mm); these small pieces were soaked for 30 s in a 75% ethanol solution, soaked for 30 s in a 2.5% sodium hypochlorite solution, and washed three times with sterilized distilled water for 30 s each. The sterilized tissue fragments were dried on sterile

filter paper and then transferred to Potato Dextrose Agar (PDA) (Senanayake et al. 2020). All PDA plates were cultured at a constant temperature of 25 °C for 2–4 days, and single hyphae were picked from the periphery of the grown colonies and inoculated on new PDA plates. After 2–3 weeks of purification, pure cultures were obtained.

For morphological characterization, potato dextrose agar medium (PDA), malt extract agar medium (MEA), synthetic nutrient-poor agar medium (SNA), water agar medium (WA), as well as on PDA, SNA, and WA supplemented with sterile pine needle segments were used. Morphological characterization was done by observing the mucus clumps produced on these media, including hyphae, ascomata, and ascospores, were observed and photographed using a Nikon Eclipse 80i microscope (Nikon, Japan). The colony morphology was recorded with a Nikon D300S digital camera (Nikon, Japan). All microscopic structures were measured using Tarosoft® Image Frame Works Version 0.9.7 and images were processed in Adobe Photoshop 2019 (Adobe Systems, San Jose, CA, USA) (Senanayake et al. 2020, Xiong et al. 2021, Manawasinghe et al. 2025). The morphological characteristics were examined using a stereomicroscope (Cnoptec sz650, China). The micro-morphological characteristics were observed and photographed using the Nikon Eclipse 80i microscope (Nikon, Japan). Colony colour (upper and reverse) was described using to the colour charts of Rayner (1970). All pure cultures were deposited in the culture collection of Zhongkai University of Agriculture and Engineering (ZHKUCC), China. Herbarium materials were deposited in the herbaria of Zhongkai University of Agriculture and Engineering (MHKU), China. Data on the new species were deposited in the Greater Mekong Subregion database (Chaiwan et al. 2021).

2.2 DNA extraction, PCR amplification, and sequencing

Genomic DNA was extracted directly from one-week-old pure cultures using a Biospin Fungal Genomic DNA Extraction Kit (BioFlux, China) following the manufacturer's instructions. The DNA was subjected to polymerase chain reaction (PCR) to amplify the internal transcribed spacer (ITS) gene using the primers ITS1 and ITS4 (White et al 1990); the large subunit (LSU) gene using the primers LROR and LR5 (Vilgalys and Hester 1990); the *β-tubulin* (*tub2*) gene using the primers TUB-2Fd and TUB-4R (Glass and Donaldson 1995); and the RNA polymerase II subunit (*rpb2*) gene using the primers fRPB2-5F and fRPB2-7cr (Liu et al. 1999). The final Polymerase chain reaction (PCR) consisted of 12.5 µL of 2×Taq Master Mix (Dye Plus) (mixture of FastTaq TM DNA Polymerase, buffer, dNTP Mixture, and stabilizer) (Beijing Qingke Biological Technology Co., Ltd., Beijing, PR China), 9 µL of ddH₂O, 1 µL of primers, and 1 µL of DNA template. PCR reactions were performed using the program for ITS, LSU, *tub2*, and *rpb2*, as described by Conforto et al. (2019) and Tennakoon et al. (2020). PCR products were analysed on 1% agarose gels and sent to Tianyi (Guangzhou, China) Co., Ltd for sequencing. All sequence data generated in this study were deposited in NCBI GenBank.

2.3 Phylogenetic analyses

The chromatograms were examined using BioEdit version 7.0.5.2 (Hall 1999), and low-quality regions were trimmed before alignment. All sequences were subjected to BLASTn searches in the National

Center for Biotechnology Information (NCBI). Based on the BLASTn search, we identified our isolates belonging to *Epicoccum* and *Paraconiothyrium*. All reference sequences used in this study were downloaded from GenBank following Cao et al. (2025), Gomzhina et al. (2025), and Manawasinghe et al. (2025) and are listed in Table 1. Alignments for each locus were generated using MAFFT 7 web servers (<http://mafft.cbrc.jp/alignment/server> (accessed 20 January 2026) and were manually improved using BioEdit 7.0.5.2 (Hall 1999). Multigene phylogenetic trees were constructed using maximum likelihood (ML) and Bayesian inference (BI) analysis.

Maximum likelihood analysis was performed using the IQ-TREE webserver (Trifinopoulos et al. 2016). The branch support of the phylogenetic tree was tested with 1000 replicates of Ultrafast bootstrap (Minh et al. 2013) and SH-aLRTtest (Guindon et al. 2010). Bayesian inference analysis was performed using MrBayes 3.2.7a on XSEDE on the CIPRES portal (Huelsenbeck et al. 2001, Miller et al. 2010, Stamatakis et al. 2014). Posterior probabilities (PP) were defined by the Markov chain Monte Carlo (MCMC) sampling method (Rannala & Yang 1996, Huelsenbeck & Ronquist 2001). Two parallel runs were conducted using the default settings. Six simultaneous Markov chains were run for 2 million generations, and trees were sampled every 1000th generation. The first 25% of trees were discarded as the burn-in phase. The remaining trees were used for calculating posterior probabilities in the majority rule consensus tree (Doll and Jacquemin 2018). Phylogenetic trees were visualized with FigTree 1.4.3 (<http://tree.bio.ed.ac.uk/software/figtree/>), and layouts were carried out with Adobe Illustrator 2018 (Adobe, USA).

3. Result

Four isolates were obtained and identified as two novel species, *Epicoccum diplopterygii* and *Paraconiothyrium drymoglossoidis*, belonging to *Didymellaceae* and *Didymosphaeriaceae*, respectively. For the updated taxonomic treatments of this study, Hyde et al. (2024) is followed. Identified taxa are listed alphabetically under the taxonomy and phylogeny section.

3.1 Taxonomy and Phylogeny

Pleosporales Luttr. ex M.E. Barr (1987)

Didymellaceae Gruyter, Aveskamp & Verkley, Mycol. Res. 113(4): 516 (2009)

Epicoccum Link, Mag. Gesell. naturf. Freunde, Berlin 7: 32 (1816) [1815]

Epicoccum was introduced by Link (1816) and presently includes 186 records in Index Fungorum (2026). Xu et al. (2023) and Gomzhina et al. (2025) are followed for the taxonomic treatment of *Epicoccum*. Two isolates obtained in this study showed morphological resemblance to species of *Epicoccum*. The multi-gene phylogenetic tree consisted of LSU, ITS, *rpb2*, and *tub2* gene regions. *Macroventuria anomochaeta* (CBS 525.71) and *Neodidymelliopsis cannabis* (CBS 121.75) were used as outgroup taxa. Ninety-eight strains were included in the combined gene analyses, comprising 3084 characters after alignment (580

for ITS, 969 for LSU, 988 for *rpb2*, and 546 for *tub2*). The best RAxML tree with a final likelihood value of -15602.333541 is presented (Fig. 1). The GTR + I+G evolutionary model was selected as the best-fit for the ITS, LSU, *rpb2*, and *tub2* gene regions in the Bayesian analysis. The phylogenetic tree resulting had a topology closely resembling the ML tree presented. In both analyses (ML and BIPP). The sequences of our collected strains nested within the clades correspond to their respective genera, confirming their affinities. Certain nodes within the clades lacked robust support (they consistently appeared stable in repeated phylogenetic analyses). In the phylogenetic analysis, the two new isolats formed a distinct, well-supported clade, supporting their recognition as a novel species: *Epicoccum diplopterygii*.

Epicoccum diplopterygii H. Li, K.D. Hyde & Manawas., **sp. nov.** Figure 2

Index Fungorum: IF 905123; Facesoffungi number: FoF 19502.

Etymology

The name refers to the host genus *Diplopterygium chinense*, from which it was isolated.

Holotype

MHKU 24–0837

Description: *Endophytic* in fresh leaves of *Diplopterygium chinense*. *Sexual morph*: Not observed. **Asexual morph**: Vegetative hyphae 3–6 µm gathering, branched, white to pale yellow. *Conidiomata* sporodochial 130–220 µm diam (n = 10) abundant, aggregated, superficial, pale brown initially, turning dark with age. *Conidiophores* 13–21 × 3–5 µm ($\bar{x}$ = 18.2 × 4.6 µm, n = 10) µm, macronematous or semi-macronematous, branched, yellow to pale brown. *Conidiophores cell* 8–15 × 6–14 µm ($\bar{x}$ = 11.6 × 10.1 µm, n = 20), verrucose, pale brown to dark brown. *Conidia* 14–20 × 11–15 µm ($\bar{x}$ = 16.1 × 13.6 µm, n = 30), solitary, acrogenous, 1–3 septate, irregular in shape, sometimes subglobose, brown to dark brown, rough-walled.

Culture characteristics

Colony on PDA reaching 40 mm diam after 4 days at 25°C in the dark. Colonies fluffy with dense mycelia, on the surface, apricot in the centre with white margin, in reverse dark coral in the centre with orange irregular margin.

Material examined

China, Yunnan Province, Puer City, Ailao Mountain, from fresh leaves of *Diplopterygium chinense*, 16 June 2023, H. Li, ZHKUCC 24-1467 (MHKU 24–0837, holotype); ex-type living culture, ZHKUCC 24-1468.

GenBank numbers: ZHKUCC 24-1467: ITS: PZ094857, LSU: PZ094861, *rpb2*: PZ094688, *tub2*: PZ094684; ZHKUCC 24-1468: ITS: PZ094858, LSU: PZ094862, *rpb2*: PZ094689, *tub2*: PZ094685.

Notes

In the phylogenetic analyses, our new isolates (ZHKUCC 24-1467 and ZHKUCC 24-1468) grouped with *Epicoccum loliicola* with 79% ML, 0.93 BIPP statistical support (Fig. 1). The asexual morph of *E. loliicola* was introduced by Xu et al. (2014) from *Lolium multiflorum* in China. Our isolates differ from *Epicoccum loliicola* (HMCE5) in having smaller conidia ($14.8 \times 11.4 \mu\text{m}$ vs. $16.1 \times 13.6 \mu\text{m}$), which are irregular in shape and 1–3-septate, whereas *E. loliicola* possesses globose to subglobose or pyriform, aseptate conidia that are brown to dark brown and verrucose (Xu et al. 2014). Pairwise sequence comparisons between the new isolate (ZHKUCC 24-1467) and *E. loliicola* (HMCE5) revealed nucleotide differences of 3/823 bp (0.4%) in LSU, 1/459 bp (0.2%) in ITS, 13/849 bp (1.5%) in *rpb2*, and 13/269 bp (5%) in *tub2*. Phylogeny also indicates that the clade containing our isolates and *E. loliicola* provides a sister lineage to *E. yunnanense*. The sexual morph of *E. yunnanense* differs from our isolate in having larger conidia ($16.1 \times 13.6 \mu\text{m}$ vs. $14 \times 7 \mu\text{m}$), and the conidia surface of *E. yunnanense* are smooth, whereas those of our new isolates are irregular (Tian et al. 2024). Hence, based on significant differences, we present our isolate as a novel species, *E. diplopterygii* from *Diplopterygium chinense*.

Didymosphaeriaceae Munk, Dansk bot. Ark. 15(no. 2): 128 (1953)

Paraconiothyrium Verkley, Stud. Mycol. 50(2): 327 (2004)

Paraconiothyrium was introduced by Verkley et al. (2004). Members of this genus play a crucial function as saprobes on dead plants, particularly dead wood, and occasionally on dead leaves (Verkley et al. 2004, Hyde et al. 2013, Ariyawansa et al. 2014, Hongsanan et al. 2020, Boonmee et al. 2021). Currently, there are 39 records of *Paraconiothyrium* in Index Fungorum (2026). In this study, the taxonomic treatment of *Paraconiothyrium* follows Tennakoon et al. (2022) and Xiong et al. (2024). Two isolates obtained in this study were morphologically similar to species of *Paraconiothyrium*. The multi-gene phylogenetic tree consists of LSU, ITS, and *tub2* gene regions. *Tremateia arundicola* (MFLU 16-1275) and *T. guiyangensis* (GZAAS01) were used as outgroup taxa (Tennakoon et al. 2022). Forty-six strains were included in the combined gene analyses, comprising 2579 characters after the alignment (729 characters for ITS, 929 characters for LSU, and 685 characters for *tub2*). The best RAxML tree with a final likelihood value of -9334.497796 is presented (Fig. 2). The GTR + I+G evolutionary model was selected as the best-fit for the LSU, ITS, and *tub2* gene regions in the Bayesian analysis. The phylogenetic tree resulting had a topology closely resembling the ML tree presented. In both analyses (ML and BIPP). The sequences of our collected strains nested within the clades correspond to their respective genera, confirming their affinities. Certain nodes within the clades lacked robust support (they consistently appeared stable in repeated phylogenetic analyses). In the phylogenetic analysis, the two new isolates formed a distinct, well-supported clade, supporting their recognition as a novel species: *Paraconiothyrium drymoglossoidis*.

Paraconiothyrium drymoglossoidis H. Li, K.D. Hyde & Manawas., sp. nov. Figure 4

Index Fungorum number: IF 905124; Facesoffungi number: FoF 19503.

Etymology

The name refers to the host genus *Lepidogrammitis drymoglossoides*, from which it was isolated.

Holotype

MHKU 24–0614

Description: *Endophytic* in fresh leaves of *Lepidogrammitis drymoglossoides*. **Sexual morph:** Not observed. **Asexual morph:** *Mycelium* 3–5 µm wide, surface and endophytic hyphae consist of septate, branched hyphae that are white, smooth-walled and thin-walled. The hyphae are occasionally swollen in the septal regions. *Chlamydospores* 10–20 × 10–20 µm ($\bar{x}$ = 16.8 × 15.6 µm, n = 30), globose, hyaline, integrated or terminal, mostly formed by the differentiation of swollen hyphae, aseptate, thick and smooth walled.

Culture characteristics

Colony on PDA reaching 20 mm diam after 6 days at 25°C in the dark. Colonies fluffy with dense mycelia, creamy white overall, slightly raised in the middle, reverse yellow spreads from dark to light from the center.

Material examined

China, Guangdong Province, Guangzhou City, Baiyun Mountain, from fresh leaves of *Lepidogrammitis drymoglossoides*, 16 August 2021, H. Li, ZHKUCC 24-1136 (MHKU 24–0614, holotype); ex-type living culture, ZHKUCC 24-1137.

GenBank numbers: ZHKUCC 24-1136: ITS: PZ094859, LSU: PZ094863, *tub2*: PZ094686; ZHKUCC 24-1137: ITS: PZ094860, LSU: PZ094864, *tub2*: PZ094687.

Notes: In the phylogenetic analyses, our new isolates (ZHKUCC 24-1136 and ZHKUCC 24-1137) grouped with *Paraconiothyrium archidendri* with 84% ML, 0.92 BIPP statistical support (Fig. 3). The asexual morph of *P. archidendri* was introduced by Verkley et al. (2014) from *Pithecellobium bigeminum* in Burma. Despite incubation for 2 months on various media (PDA, MEA, SNA, WA, and WA amended with pine needles), the isolate failed to sporulate. Only chlamydospores were produced on WA amended with pine needles, precluding morphological comparison with the asexual morph of *P. archidendri*. The compare the comparisons of our new isolate (ZHKUCC 24-1136) in LSU, ITS, and *tub2* gene regions separately, showing *P. archidendri* (CBS 168.77, LSU: 5/905, 1%; ITS:3/605, 0.5%; *tub2*: 64/416, 15.4%). Thus, we present our isolate as a new species, *P. drymoglossoidis* from *Lepidogrammitis drymoglossoides*.

4. Discussion

In this study, the asexual morphs of two novel Pleosporales species, *Epicoccum diplopterygii* and *Paraconiothyrium drymoglossoidis*, were identified using an integrative taxonomic approach combining

multigene phylogenetic analyses with morphological characterization. Both taxa were isolated as endophytes from healthy pteridophytic hosts, highlighting the ecological breadth of Pleosporales and their ability to persist in asymptomatic associations with plants (Zhang et al. 2012). Notably, increasing evidence suggests that closely related taxa within Pleosporales may occupy distinct ecological niches, with frequent transitions among endophytic, saprobic, and pathogenic lifestyles (Zanne et al. 2020, Hill et al. 2022, Bhunjun et al. 2024). The discovery of these two endophytic species from ferns further supports the view that lifestyle plasticity is a common and evolutionary significant feature within the order (Hu et al. 2024, Bhunjun et al. 2024).

Species of *Epicoccum* are important plant-associated fungi, with numerous taxa reported as pathogens causing leaf spots, blights, and roots on a wide range of hosts, while others occur as endophytes or saprobes (Chen et al. 2020, Chethana et al. 2019, Lin et al. 2018, Xu et al. 2022). The isolation of *E. diplopterygii* as an endophyte from *Diplopterygium chinense* is consistent with this ecological diversity. However, phylogenetic analyses revealed that *E. diplopterygii* is closely related to species with documented pathogenic or saprobic lifestyles (*E. loliicola* and *E. yunnanense*), indicating that endophytic isolation does not preclude pathogenic potential in phylogenetically related taxa. Such findings align with the concept of an endophyte–pathogen continuum, where asymptomatic colonization may represent a latent or conditional ecological state (Schulz and Boyle 2005, Porras-Alfaro and Bayman 2011, Hardoim et al. 2015). Consequently, the ecological role of *E. diplopterygii* warrants further investigation through pathogenicity assays and functional studies.

Paraconiothyrium is a morphologically and ecologically diverse genus within *Didymosphaeriaceae*, typically characterized by pycnidial or eustromatic conidiomata and phialidic or annellidic conidiogenesis (Verkley et al. 2004, Phukhamsakda et al. 2022, Yang et al. 2025). In the present study, *Paraconiothyrium drymoglossoides* was observed to form chlamydospores in culture, a feature that has not previously been reported for the genus. As we used molecular data, we were able to link the taxon to *Paraconiothyrium* (Shenoy et al. 2006). This first record of chlamydospore formation in *Paraconiothyrium* expands the known morphological concept of the genus and suggests that its structural diversity may have been underestimated. The presence of chlamydospores may reflect an adaptive strategy for survival under unfavorable environmental conditions (Watanabe 2002, Agrios 2005), further emphasizing the ecological flexibility of the genus.

Despite recent advances in multigene phylogenetic analyses, taxonomic instability persists within *Didymellaceae* and *Didymosphaeriaceae*, partly due to overlapping morphological characters and incomplete molecular sampling (Aveskamp et al. 2010, Ariyawansa et al. 2014, Tennakoon et al. 2022). The placement of newly described taxa, such as those reported here, underscores the necessity of integrative taxonomic approaches that combine detailed morphology with robust phylogenetic frameworks. Continued efforts to collect, culture, and sequence Pleosporales species from diverse hosts and habitats will be essential to improving phylogenetic resolution and achieving a more stable, natural classification within these families.

Declarations

Ethics approval:

Not applicable.

Consent to participate:

Not applicable.

Consent for publication:

Not applicable.

Competing interests:

The authors have no competing interests to declare that are relevant to the content of this article.

Author Contribution

All authors were involved in this research. H-L, IS-M and CH-Z sample collection, morphological observation, isolation, and preparation of related materials. The first draft of the manuscript was written by H-L. Research supervision, conceptualisation, and study design were provided by I-S-M and K-D-H. The manuscript was critically reviewed, revised, and edited by K-D-H, I-S-M, D-N-W, and C-S-B to improve clarity and meet the requirements for submission. All authors read and approved the final version of the manuscript

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Data Availability

The datasets generated for this study can be found in GenBank, NCBI and the accession numbers are given in Table 1. Newly introduced fungal names were registered at the Index Fungorum and the identification numbers are shown in their respective entries.

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Table 1

Table 1 is not available with this version.

Figures

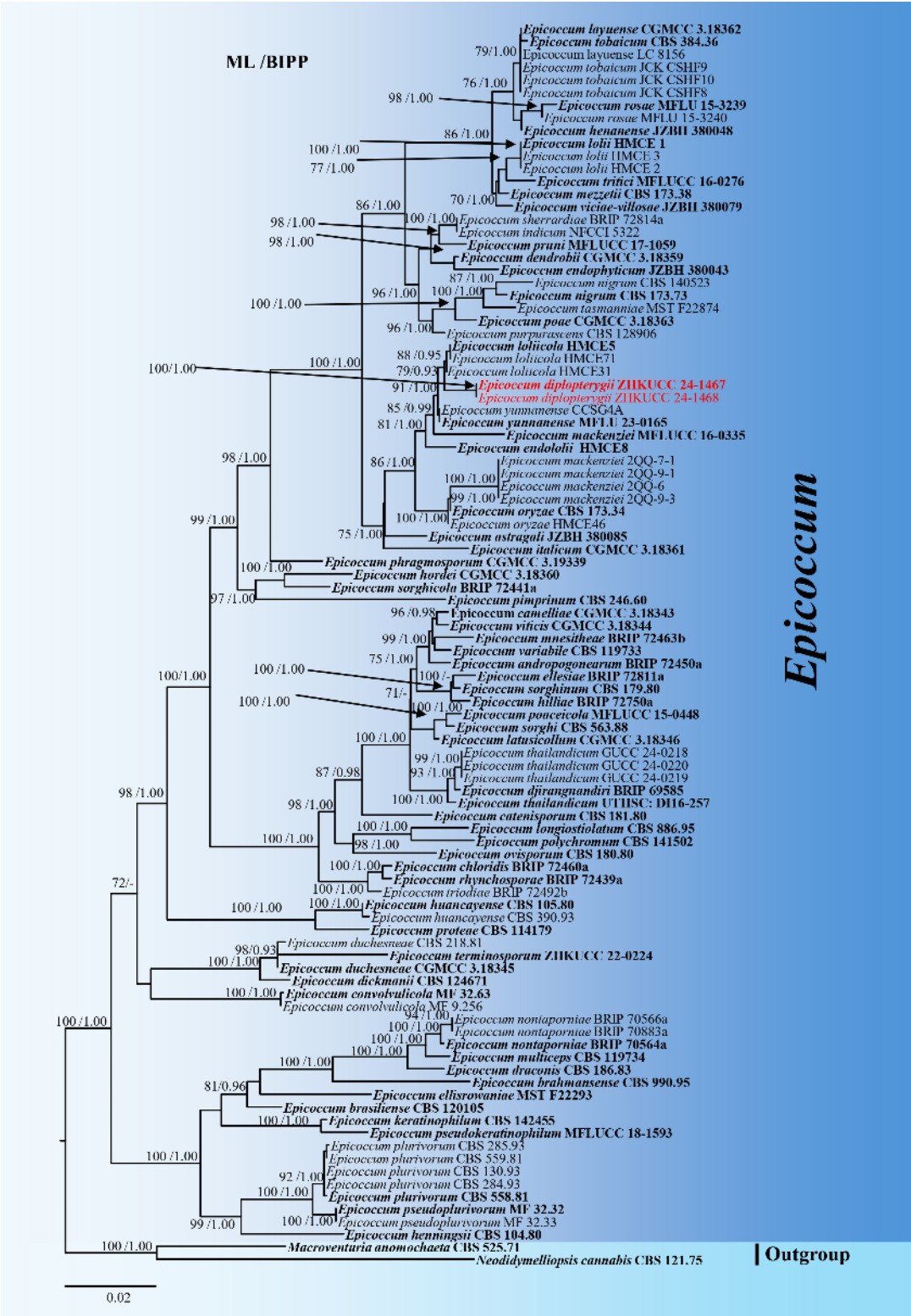


Figure 1

Phylogenetic tree generated by maximum likelihood analyses based on the combined ITS, LSU, *rpb2*, and *tub2* sequence alignments of *Epicoccum*. *Macroventuria anomochaeta* (CBS 525.71) and *Neodidymelliopsis cannabis* (CBS 121.75) are used as the outgroup taxa. Bootstrap support values for maximum likelihood (ML) equal to or greater than 70% and Bayesian posterior probabilities equal to or greater than 0.90 are indicated above branches as ML/BIPP. Ex-type strains are in bold, and the newly obtained strains are in red.

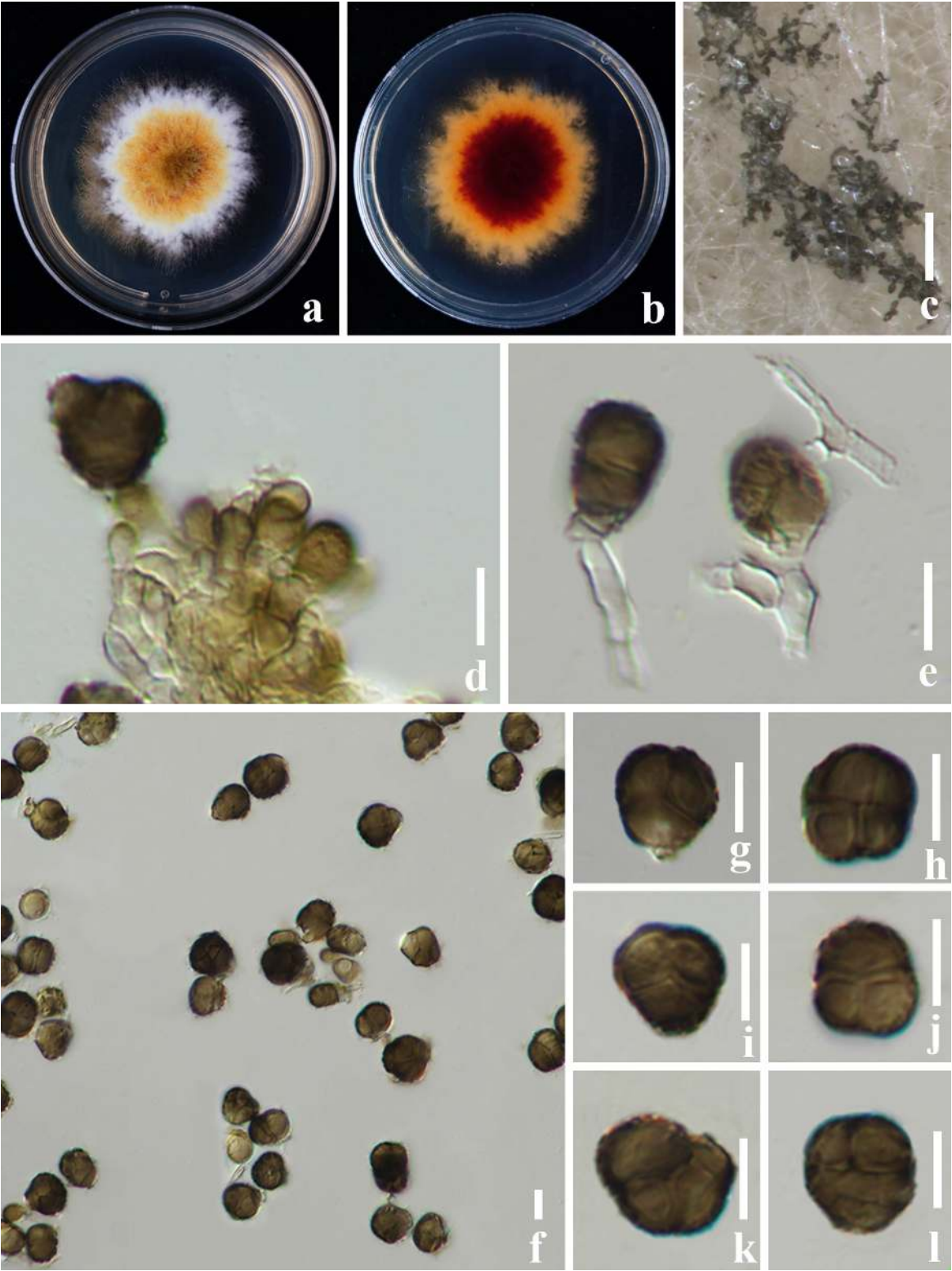


Figure 2

(GZAAS01) are used as the outgroup taxa. Bootstrap support values for maximum likelihood (ML) equal to or greater than 70% and Bayesian posterior probabilities equal to or greater than 0.90 are indicated above branches as ML/BIPP. Ex-type strains are in bold, and the newly obtained strains are in red.

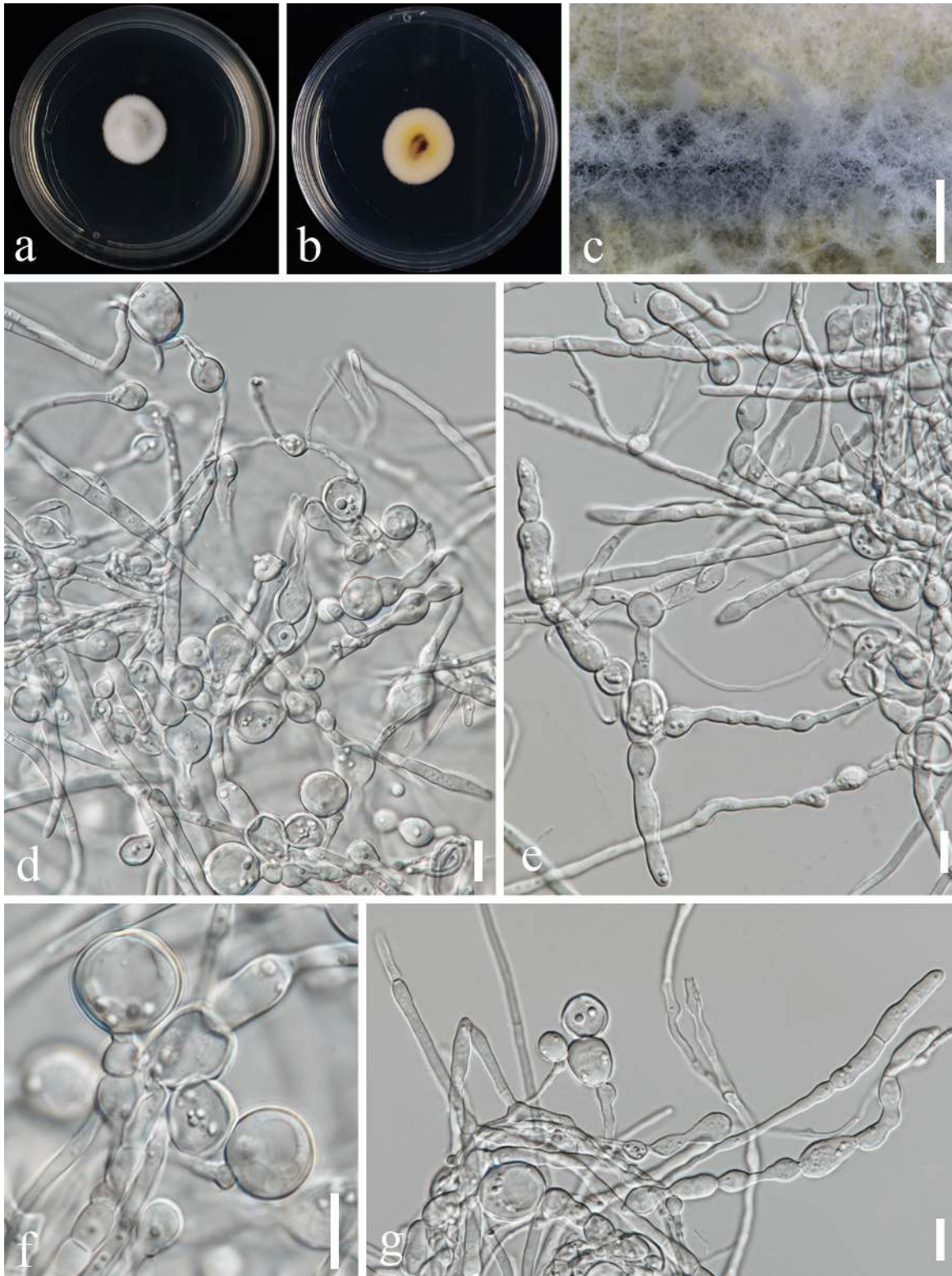


Figure 4

Paraconiothyrium drymoglossoidis (MHKU 24-0614, holotype). a, b Cultures on PDA from obverse and reverse. c Colonies on WA pine needle medium. d–g Mycelium and Chlamydospores. Scale bars: c = 1

mm, $d-f = 10\text{ }\mu\text{m}$.