

Additions to saprobic Dothideomycetes and Sordariomycetes from Kunming Institute of Botany, Yunnan, China

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Abstract

Our efforts to investigate microfungi in the Kunming Institute of Botany (KIB) garden have led to the discovery of several fungi on dead plant parts. Through comprehensive morphological studies, illustrations, and combined multi-locus phylogenies, we identified nine taxa from our collections, all belonging to the classes Dothideomycetes and Sordariomycetes. In particular, we introduce seven new host records and two new species, each with unique characteristics. The discovery of these new species, *Melanographium trachycarpi* and *Neohendersonia camelliae*, greatly enhances our understanding of fungal diversity and paves the way for further research. Meanwhile, *Botryosphaeria dolichospermatii* and *Pseudolachnella tengii* are reported here for the first time in their sexual form, which has the potential to further expand our knowledge. Additionally, a checklist of fungi collected from KIB between 2010 and 2025 is included for maintenance and institutional record-keeping, for those interested in fungi at KIB.

Keywords: Botanical garden, DNA, Microfungi, Phylogeny, Taxonomy

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Introduction

The capabilities of fungi are remarkable in addressing future global demands, encompassing health, sustainable agriculture, and renewable energy^[1]. Therefore, it is our responsibility to recognize the presence of concealed mycota worldwide. These newly discovered species will play a significant role in advancing agriculture, industrial biotechnology, medicine, and disease control^[1]. To achieve these advancements, we must be diligent in our scientific practices, ensuring robust taxon sampling and accurate referencing when introducing new fungal taxa. This is crucial for achieving better outcomes in fungal research and driving progress in our fields^[2]. In fungi, there are two of the two largest classes within the Ascomycota phylum: Dothideomycetes and Sordariomycetes. Members of them occur as pathogens, saprobes, endophytes, or epiphytes, and are widely utilized in economically significant industries^[3–5]. Their diverse functions as metabolites and biocontrol agents make them a fascinating area of study^[6,7]. Dothideomycetes

are primarily distinguished by the presence of bitunicate asci, which possess two wall layers and are often fissitunicate^[8–10]. In contrast, Sordariomycetes are characterized by inoperculate, unitunicate asci lacking a hinged cap and with a single wall layer^[11]. Traditional identification of fungi, especially within the diverse Ascomycota classes Dothideomycetes and Sordariomycetes, primarily relies on morphological characteristics observed under microscopy, such as the structure of fruiting bodies (ascmata), ascus type, and spore (ascospore or conidia) morphology^[9,10]. Although contemporary research incorporates DNA-based molecular techniques, traditional morphological methods continue to serve as the foundation for preliminary classification and the description of new species^[2,12,13]. Both classes exhibit a wide range of lifestyles; notably, saprobic fungi, as major decomposers of organic matter, play a crucial ecological role in terrestrial and aquatic environments^[9,11,14,15]. Their substantial influence on plant primary production, carbon mineralization, and segregation is a testament to their significant contribution to the environment^[14,16]. Moreover, fungi's adaptability

to various conditions, such as moisture levels, temperature, substrate availability, and nutrient content, significantly influences their ability to decompose organic matter^[17]. Studying fungal distribution worldwide is crucial to a better understanding of the fungal cycle and its changes^[18].

The study of fungal diversity has several crucial aspects, including biotechnology research, understanding ecosystem functioning, and protecting human health and agricultural security^[2,19,20]. Fungal biodiversity hotspots around the world significantly impact the increasing number and diversity of both micro- and macro-fungi. The magnitude of our discoveries is truly impressive. As of the present, 15,266 new fungal species have been reported in China, underscoring the country's considerable biodiversity^[21]. The majority of these species are found in Southern China and account for 8.69% of all globally described fungal species, placing China second only to the United States^[2,22,23]. These discoveries have been documented across all 34 provincial-level regions, with Yunnan Province reporting the highest number at 3,869 species, nearly one-fifth of the national total. The distinctive geographical features of Yunnan support both a highland cold-resistant biome in the west and a tropical biome in the south and southwest, making the province a key area for fungal discoveries and a leading hotspot for biotechnology research^[23–37].

This study aims to advance understanding of the diversity and distribution of saprobic fungal communities in the KIB using both morphological and molecular approaches. Dead plant material bearing fungal fruiting bodies was collected from the KIB premises in Kunming, Yunnan, China, to facilitate the identification of both novel and previously known saprobic fungal species. Through detailed morphological examination and multi-locus phylogenetic analyses, two new species and seven new records within Dothideomycetes and Sordariomycetes were identified from the KIB garden. Furthermore, this research presents the first comprehensive checklist of fungi collected at KIB, establishing a valuable resource for future studies.

Material and methods

Sample collection, morphological observations, and isolation

Dead and decaying branches, petioles, and culms with fungal fruiting bodies were collected from the garden of the Kunming Institute of Botany, Yunnan Province, China, and taken to the KIB mycology laboratory after important collection details were recorded^[38]. The specimens were examined under an Olympus SZ61 (Japan) series stereo- and light microscope, photographed with an OLYMPUS SZ2-ILST and an Industrial Digital Camera 16NP USB3.0 (Panasonic, Japan) microscope imaging system. The morphological characteristics of the fungi were recorded. We followed the method of Senanayake et al.^[38] to isolate a single spore and obtain a pure culture of the fungus on potato dextrose agar (PDA). Microstructural observation was performed using scanning electron microscopy (ZEISS GeminiSEM and ZEISS Sigma 300 apparatus). Spores or other relevant structures were carefully isolated with a needle under a stereomicroscope and transferred onto an aluminum specimen stub, pre-coated with conductive adhesive to ensure well-dispersed, non-overlapping placement. The mounted sample was rapidly frozen. In a low-temperature preparation chamber, the sample was coated with a thin layer of gold under vacuum for approximately 30 min to enhance conductivity and minimize charging during observation. After coating, the frozen

sample was maintained at a low temperature and directly transferred to the SEM chamber for imaging. Images were acquired at appropriate accelerating voltages and magnifications to examine the surface structure of the samples^[39]. The Tarosoft Image Framework program v0.9.0.7. was used to measure all microscopic structures of the fungi, and Adobe Photoshop CS3 Extended v10.0 (Adobe Systems, USA) was used to process and edit the images used in the figures. Herbarium specimens are deposited in the Kunming Institute of Botany, Academia Sinica (KUN-HKAS), while the living cultures are deposited in the Kunming Institute of Botany Culture Collection (KUNCC/KUMCC). Facesoffungi (FoF) number and Index Fungorum (IF) number were obtained as explained in Jayasiri et al.^[40] and Index Fungorum^[41], respectively. In addition, sexual/asexual morphs sporulation in the culture medium was induced following a slightly modified method of Su et al.^[42]. Sterilized toothpicks and pine needles were placed on either side of a PDA plate, and a small piece of mycelium grown on PDA was placed on the baits. The cultures were incubated at 28 °C. For *in vitro* sporulation, the plates were examined using a stereo microscope. Fungal microstructures were prepared on slides, observed, photographed, measured, and compiled into a photographic plate.

Molecular studies

Actively growing mycelium was carefully scraped from a 7–10-day-old PDA culture using a sterile scalpel and transferred into a 1.5 mL centrifuge tube for DNA extraction. The Biospin Fungus Genomic DNA Extraction Kit–BSC14S1 (BioFlux, China) was used to extract DNA, following the manufacturer's instructions, and extracted DNA was preserved at –20 °C. DNA amplifications were performed by polymerase chain reaction (PCR). A portion of the large-subunit nuclear rRNA gene (LSU) was amplified using primer pairs LR0R and LR5^[43]. The small 18S subunit nuclear rRNA gene (SSU) was amplified with primer pairs NS1 and NS4^[44]. Primer pairs ITS4 and ITS5 were used to amplify the 5.8S rDNA gene and flanking internal transcribed spacers (ITS)^[44]. The translation elongation factor 1-alpha gene (*tef1*) was amplified by using primers EF1-983F and EF1-2218R^[45], or the primers EF1-728F and EF1-986R^[46]. The RNA polymerase II second-largest subunit (*rpb2*) gene was amplified with primers fRPB2 and fRPB2-7cR^[47]. The beta-tubulin (*tub2*) gene was amplified using primers Btub2Fd and Btub4Rd^[48]. The PCR thermal cycle programs for ITS, LSU, and SSU were as follows: an initialization step of 94 °C for 3 min, followed by 35 cycles of 94 °C for 30 s, an annealing step at 55 °C for 50 s, an elongation step at 72 °C for 1 min, and a final extension step of 72 °C for 10 min. The PCR thermal cycle programs for *rpb2*, *tef1*, and *tub2* was as follows: an initialization step of 95 °C for 3 min, followed by 40 cycles of 95 °C for 50 s, an annealing step (52 °C, 30 s for *tub2*; 55 °C, 50 s for *rpb2*, and *tef1*), an elongation step at 72 °C for 90 s, and a final extension step of 72 °C for 10 min.

Phylogenetic analyses

The ITS, LSU, SSU, and protein-coding genes (*rpb2*, *tef1*, and *tub2*) were used for different fungal groups as needed. All reference sequences were retrieved from GenBank using the latest references for each fungal group. Sequences were aligned with BioEdit v5.0.6^[49] and ClustalX v1.83^[50], or with MAFFT v6.864b (<https://mafft.cbrc.jp/alignment/server/index.html>)^[51]. The alignments were visually checked and manually improved where necessary. Phylogenetic analyses were carried out with MrBayes v3.2.7a^[52] for Bayesian inference analysis (BI). A Maximum Likelihood analysis (ML) was performed via the CIPRES web portal^[53] using RAXML v7.2.8 as part of the 'RAXML-HPC2 on TG' tool^[54] or implemented

in RAXMLGUI v0.9b2^[55]. Other phylogenetic details are outlined in Jeewon et al.^[56,57]. Phylogenetic trees were drawn with FigTree v1.4^[58]. Maximum likelihood bootstrap support (MLBS) equal or greater than 50%–70% and Bayesian posterior probabilities (BYPP) values equal or greater than 0.95 are indicated on the resulting tree topology in each figure. Newly generated sequences were deposited at the NCBI GenBank. GenBank accession numbers for sequenced genes are given in the descriptions under the materials examined. The same isolate was duplicated and remade as sequences A and B.

Results

In this paper, we describe two new species and seven new records of saprobic fungal strains collected from the KIB (Yunnan, China). The novelties are morphologically illustrated, and phylogenies based on multi-locus sequence data are provided to accommodate species in their orders, families, and genera where appropriate.

Phylogenetic analyses

Analysis 1: *Botryosphaeria* phylogeny was based on combined ITS, LSU, *tef1*, and *tub2* sequence data.

Forty strains are included in the combined analyses, which comprise 2,223 characters across the ITS, LSU, *tef1*, and *tub2* alignments. *Macrophomina phaseolina* (CBS 227.33 and CBS 162.25) was used as the outgroup taxon, and related sequences were obtained as described by Tian et al.^[59]. Single-loci analyses were performed to compare the topology and clade stability with those of combined-locus analyses. The tree topology of the ML analysis is similar to that of the BI analysis. The best RAXML tree had a final likelihood value of −4756.457710. The matrix contained 267 distinct alignment patterns, with 18.94% of characters undetermined or missing. Estimated base frequencies were as follows: A = 0.226896, C = 0.273860, G = 0.274223, T = 0.225021; substitution rates AC = 0.835737, AG = 2.668379, AT = 1.055693, CG = 0.817208, CT = 6.080596, GT = 1.000000; gamma distribution shape parameter α = 0.084375. The collection (KUMCC 21-0103A, KUMCC 21-0103B) in the present study phylogenetically clustered with *B. dolichospermii* strains (CGMCC 3.19098, CGMCC 3.19097, CGMCC 3.19096).

Analysis 2: *Helminthosporium* phylogeny was based on combined LSU, SSU, ITS, and *tef1* sequence data.

Fifty-six strains were included in the analyses, comprising 3,776 characters including gaps. The tree is rooted with *Periconia pseudodigitata* (KT1395), and related sequences were obtained from Hyde et al.^[60]. The matrix contained 1,263 distinct alignment patterns, with 36.99% of characters undetermined or missing. Estimated base frequencies were as follows: A = 0.240622, C = 0.242963, G = 0.270350, T = 0.246065; substitution rates AC = 1.991544, AG = 3.170223, AT = 2.023982, CG = 0.880620, CT = 7.722965, GT = 1.000000; gamma distribution shape parameter α = 0.171719. The trees from the two analyses (ML and BI) were identical. Our collection (KKMCC 21-0076) in the present study phylogenetically clustered between *H. velutinum* strains (MFLUCC 16-1360, MFLUCC 16-1096, CPC 26297, L131, CGMCC 3.23572) with statistical support (96% MLBS/1.00BYPP).

Analysis 3: *Neohendersonia* phylogeny was based on combined SSU, LSU, and ITS sequence data.

Nineteen strains were included in the combined analyses, which comprise 2,681 characters for SSU, LSU, and ITS alignment. *Boeremia exigua* (CBS 431.74) was used as the outgroup taxon, and related sequences were obtained following Sun et al.^[61]. Single-locus

analyses were performed to compare the topology and clade stability with those of combined-locus analyses. The tree topology of the ML analysis is similar to the BI analysis. The best RAXML tree had a final likelihood value of −7346.622368. The matrix contained 461 distinct alignment patterns, with 24.34% of characters undetermined or missing. Estimated base frequencies were as follows: A = 0.250407, C = 0.221818, G = 0.276438, T = 0.251338; substitution rates AC = 1.578736, AG = 3.664305, AT = 1.349205, CG = 0.450256, CT = 6.079060, GT = 1.000000; gamma distribution shape parameter α = 0.079251. Multi-locus phylogenetic analyses showed that our strains (KUMCC 21-0056, KUMCC 21-0107) belong to *Neohendersonia* and form a well-separated lineage from *N. kickxii* and *N. tongrenensis*.

Analysis 4: *Magnibotryascoma* phylogeny was based on combined LSU, SSU, ITS, *tef1*, and *rpb2* sequence data.

Fifty-three strains were included in the analyses, comprising 4,359 characters, including gaps. The tree was rooted with *Lophiostoma arundinis* (CBS 621.86), and related sequences were obtained from Ren et al.^[62]. The matrix contained 1,143 distinct alignment patterns, with 46.56% of characters undetermined or missing. Estimated base frequencies were as follows: A = 0.242454, C = 0.254882, G = 0.276848, T = 0.225816; substitution rates AC = 1.235534, AG = 2.891989, AT = 1.669777, CG = 1.089129, CT = 8.990044, GT = 1.000000; gamma distribution shape parameter α = 0.178080. The trees from the two analyses (ML and BI) were identical. Multi-locus phylogenetic analyses show that our new isolate (KUMCC 21-0112) clusters with *M. mali* (KUMCC 21-0516) but receives low statistical support.

Analysis 5: *Apiospora* phylogeny was based on ITS sequence data.

Seventy-nine strains were included in the analyses, comprising 913 characters for the ITS alignment. *Seiridium phylicae* (CBS 133587) in Sporocadaceae (Amphisphaeriales) is used as the outgroup taxon, and related sequences are taken from Pintos & Alvarado^[63]. The tree topology of the ML analysis is similar to the Bayesian analysis. The best RaxML tree with a final likelihood value of −5256.291374 is presented. The matrix contained 439 distinct alignment patterns, with 25.11% of characters undetermined or missing. Estimated base frequencies were as follows: A = 0.239919, C = 0.248556, G = 0.233761, T = 0.277764; substitution rates AC = 0.826486, AG = 1.770838, AT = 0.788607, CG = 0.944632, CT = 2.720760, GT = 1.000000; gamma distribution shape parameter α = 0.301517. Multi-locus phylogenetic analyses show that our new isolate (KUMCC 21-0047) clusters with *A. yunnana* strains, with high statistical support (100% MLBS/1.00 BYPP).

Analysis 6: *Pseudolachnella* phylogeny was based on combined LSU, ITS, and *tef1* sequence data.

Thirty strains were included in the analyses, comprising 2,869 characters in the LSU, ITS, and *tef1* alignments. *Dinemasporium strigosum* (MAFF 244355) and *D. cruciferum* (MAFF 244327) are used as outgroup taxa, and related sequences are taken from Wu & Diao^[64]. Single-locus analyses were performed to compare the topology and clade stability with those of combined-locus analyses. The tree topology of the ML analysis is similar to the Bayesian analysis. The best RaxML tree with a final likelihood value of −3089.572070 is presented. Estimated base frequencies were as follows: A = 0.259453, C = 0.230435, G = 0.223495, T = 0.286617; substitution rates AC = 0.775950, AG = 1.961909, AT = 0.980782, CG = 0.452485, CT = 3.571483, GT = 1.000000; gamma distribution shape parameter α = 0.150142. Multi-locus phylogenetic analyses show our new isolate (KUMCC 21-0048) clustered with *P. tengii* (NN047882) with high statistical support (100% MLBS/1.00 BYPP).

Analysis 7: *Distoseptispora* phylogeny was based on combined ITS, LSU, *tef1*, and *rpb2* sequence data.

Eighty-six strains were included in the combined analyses, which comprise 3,466 characters for ITS LSU, *tef1*, and *rpb2* after alignment. *Pseudostanthughesia aquitropica* (MFLUCC 16-0569) and *P. lignicola* (MFLUCC 15-0352) were used as the outgroup taxa, and related sequences were obtained following Liao et al.^[65]. Single-locus analyses were performed to compare the topology and clade stability with those of combined-gene analyses. The tree topology of the ML analysis is similar to the Bayesian analysis. The best RaxML tree with a final likelihood value of −35748.256699 is presented. The matrix contained 1,775 distinct alignment patterns, with 28.49% of characters undetermined or missing. Estimated base frequencies were as follows: A = 0.240683, C = 0.265261, G = 0.282208, T = 0.211848; substitution rates AC = 1.367285, AG = 3.313867, AT = 1.258963, CG = 0.898119, CT = 6.927241, GT = 1.000000; gamma distribution shape parameter α = 0.254970. Multi-locus phylogenetic analyses showed that *Distoseptispora* and our strain (KUMCC 21-0039) clustered with *D. guizhouensis* (GZCC 21-0666) with high statistical support (100% MLBS/1.00 BYPP).

Analysis 8: *Peroneutypa* phylogeny was based on combined ITS and *tub2* sequence data.

Forty-three strains were included in the combined analyses, which comprised 1,182 characters in the ITS and *tub2* alignments. *Allocryptovalsa polyspora* (MFLU 17-1218) and *A. elaeidis* (MFLUCC 15-0707) were used as the outgroup taxa, and related sequences were obtained following Mao et al.^[66]. Single-locus analyses were performed to compare the topology and clade stability with those of combined-locus analyses. The tree topology of the ML analysis is similar to the Bayesian analysis. The best RaxML tree had a final likelihood value of −9820.994449. The matrix contained 748 distinct alignment patterns, with 35.42% of characters undetermined or missing. Estimated base frequencies were as follows: A = 0.214321, C = 0.280618, G = 0.243945, T = 0.261117; substitution rates AC = 0.864463, AG = 2.289966, AT = 1.381503, CG = 1.060632, CT = 3.181007, GT = 1.000000; gamma distribution shape parameter α = 0.513331. Multi-locus phylogenetic analyses show that our new isolates (KUMCC 21-0049, KUMCC 21-0100) are sister lineages to *P. scoparia* (MFLUCC 11-0478), with 70% MLBS statistical support.

Analysis 9: *Melanographium* phylogeny was based on combined LSU, ITS, SSU, *tef1*, and *rpb2* sequence data.

Fourteen strains were included in the analyses, which comprised 4,428 characters for LSU, ITS, SSU, *tef1*, and *rpb2* alignment. Related sequences are taken from Samarakoon et al.^[67]. Two strains from *Zygosporium oscheoides* (MFLUCC 14-0402 and CBS 195.79) were used as the outgroup. The tree topology of the ML analysis is similar to the Bayesian analysis. The best RaxML tree with a final likelihood value of −12077.017651 is presented. The matrix contained 622 distinct alignment patterns, with 26.22% of characters undetermined or missing. Estimated base frequencies were as follows: A = 0.243063, C = 0.249875, G = 0.264718, T = 0.242345; substitution rates AC = 1.293241, AG = 2.428649, AT = 1.255505, CG = 0.928677, CT = 6.755147, GT = 1.000000; gamma distribution shape parameter α = 0.133168. Multi-locus phylogenetic analyses show that our new isolates (KUMCC 21-0101A, KUMCC 21-0101B) are sister lineages to *M. citri* (GZCC21-0208, GZCC21-0212), with 99% MLBS/1.00 BYPP statistical support.

Taxonomy

Dothideomycetes O.E. Erikss. & Winka

Botryosphaeriales C.L. Schoch, Crous & Shoemaker

Botryosphaeriaceae Theiss. & Syd.

Botryosphaeria Ces. & De Not.

Generally, *Botryosphaeria* is regarded as a species complex, owing to the high level of intraspecific variation among its isolates,

which overlap with those of other related species, while morphological characteristics are no longer routinely employed for the identification^[59,68,69]. *Botryosphaeria* species are known as plant saprobes, pathogens, and endophytes, with a global distribution across a wide variety of mainly woody hosts^[68,70]. Diseases caused by pathogens belonging to the genus *Botryosphaeria* have resulted in significant losses in various economically important crops. To identify *Botryosphaeria* sp., it is recommended to provide ITS sequence data, combined with *tef1* and *tub2*, which can effectively distinguish closely related species^[71]. In our study, we introduced a new host record of *B. dolichospermatis* as a saprobe from *Acer* sp.

Botryosphaeria dolichospermatis Z.P. Dou, W. He & Y. Zhang, in Dou, Zhao, He & Zhang, *Mycosystema* 40(3): 479 (2021)

Index Fungorum number: IF 826937, **Figs 1, 2**

Saprobic on dead branches of *Acer* sp. **Sexual morph:** *Ascomata* 125–165 μm high $\times$ 189 190–225 μm diam. ($\bar{x}$ = 147 $\times$ 197 μm , n = 10), eustromatic, gregarious, black, semi-immersed, becoming erumpent at maturity, uniloculate, glabrous, ostiolate, with minutely papillate. *Peridium* 20–30 μm wide, thick-walled, composed of several layers of thickened, dark-brown to black pseudoparenchymatous cells of *textura angularis* or *textura globosa*, with hyaline cells towards the inner layers. *Hamathecium* 2–2.5 μm ($\bar{x}$ = 2.2 μm , n = 20) wide, thin-walled, hyaline, septate, broadly cellular pseudoparaphyses, embedded in a hyaline gelatinous matrix. *Asci* 69–86 $\times$ 10–17 μm ($\bar{x}$ = 76 $\times$ 13 μm , n = 20), 8-spored, bitunicate, fissitunicate, clavate to cylindric-clavate, short stipitate, thin at ectotunica rather thick at endotunica, 3-layered, with a prominent apical chamber, developing on a broad basal hymenial layer. *Ascospores* 17–22 $\times$ 5–7 μm ($\bar{x}$ = 20 $\times$ 6 μm , n = 20), irregularly 2-seriate in the ascus, hyaline, thin-walled, varied in shape, usually ovoid to fusoid or fusoid-ellipsoid, widest in the middle, straight or inequilateral, septate, with smooth or granular contents, sometimes guttulate, surrounded by a thin mucilaginous sheath. **Asexual morph:** See Chu et al.^[59].

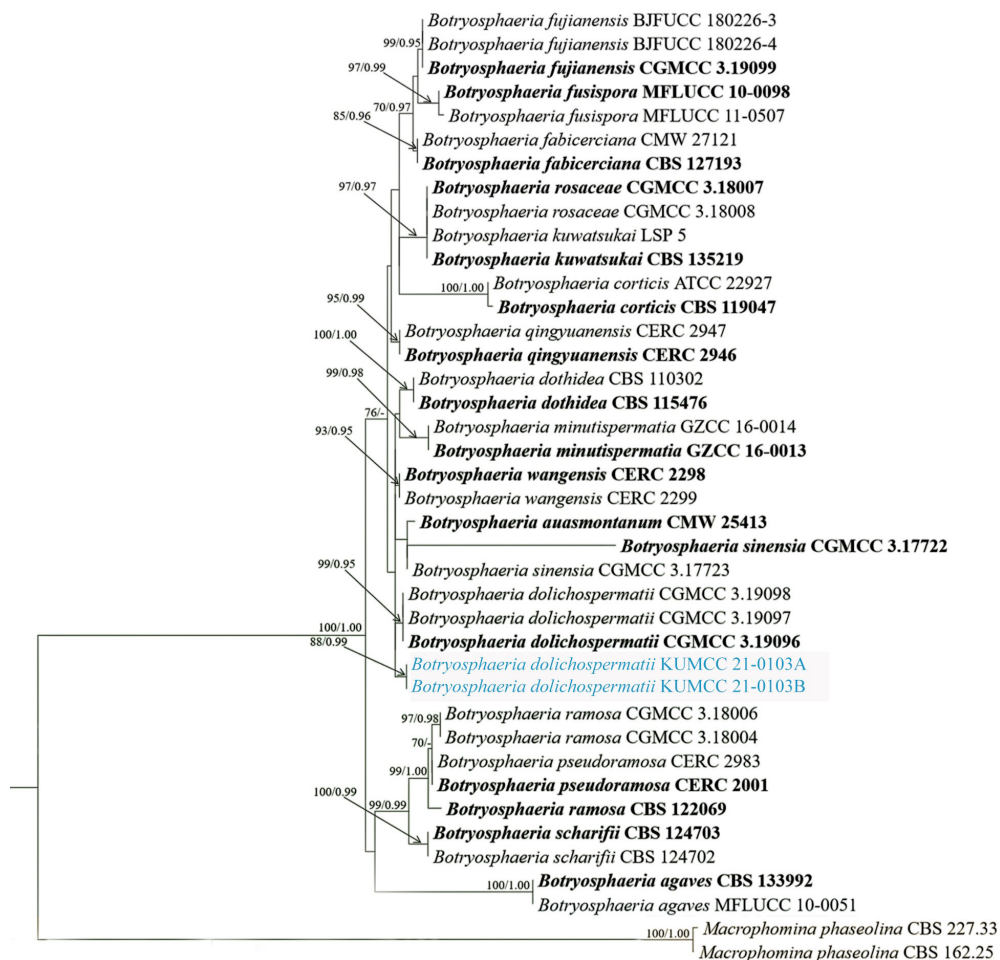
Culture characteristics: Ascospores germinate on PDA within 24 h, and germ tubes are produced from both sides. Colonies grow fast on PDA, effuse, velvety to hairy, circular, white in the first week, and brown to dark brown after 1 week from above and below.

Known host and distribution: On the cankered branch of *Vaccinium uliginosum* in Fujian, China^[59]; on dead branches of *Acer* sp. in Yunnan, China (this study).

Material examined: China, Yunnan, Kunming, Kunming Institute of Botany, Chinese Academy of Science, on dead branches of *Acer* sp. (Sapindaceae), 15 May 2020, S. Tibpromma, ST 48 (KUN-HKAS 115560, new host record), living culture KUMCC 21-0103.

GenBank accession numbers: KUMCC 21-0103: SSU: PV942129; ITS: PV873194; LSU: PV942116; *tub2*: PX055888.

Notes: Our new collection morphologically resembles the type collection of *Botryosphaeria* described in Phillips et al.^[72]. The new strain makes a weak independent clade and is closely related to *B. dolichospermatis* (CGMCC 3.19096^T) in multigene phylogenetic analysis (Fig. 1). *Botryosphaeria dolichospermatis* was initially introduced as an asexual morph^[59], while our new isolate is a sexual morph, and it fits well with the generic description of the sexual morph of *Botryosphaeria*^[73]. The sexual morph of our sample is characterized by black, uniloculate, erumpent ascomata, resembling those of other *Botryosphaeria* species such as *B. dothidea* and *B. rosaceae*^[71]. A comparison of LSU, ITS, *tef1*, and *tub2* gene sequences between the new isolate and *B. dolichospermatis* (CGMCC 3.19096^T) revealed no differences, except for two gaps in the ITS region within the areas analyzed in this study. Consequently, the new isolate is presented as the first recorded sexual morph and a new host record of *B. dolichospermatis*, supported by both morphological and phylogenetic similarities.



Outgroup

Fig. 1 Phylogram generated from Maximum Likelihood analysis based on ITS, LSU, *tef1*, and *tub2* sequence data representing *Botryosphaeria* species. Bootstrap values for ML equal to or greater than 60% and BYPP values greater than 0.95 (the rounding of values to two decimal proportions) from BI analysis are labelled on the nodes. A newly generated sequence is in blue, and type species are bold.

Pleosporales Luttr. ex M.E. Barr

Massarinaceae Munk

Helminthosporium Link

The type species of *Helminthosporium*, *H. velutinum*, is characterized by hyphomycetous with solitary, cylindrical, unbranched, brown conidiophores that produce obclavate, distoseptate conidia in integrated, terminal or intercalary, polytretic conidiogenous cells^[74–77]. Most taxa in the *Helminthosporium* complex have later been placed in other genera, initially based on morphological characters and later based on molecular data, although the status of some species remained unresolved^[78]. While a comprehensive study of the genus has been revised by Voglmayr & Jaklitsch^[79], more than 225 species were listed in *Helminthosporium*^[34,80,81]. In the present study, we collected *H. velutinum* from a branch of an unknown plant at the KIB, Yunnan, China, and this is the second strain that was reported from Yunnan Province, China.

Helminthosporium velutinum Link [as '*Helmisporium*'], Mag. Gesell. naturf. Freunde, Berlin 3(1–2): 10, tab. 1:9 (1809)

Index Fungorum number: IF 250075, Figs 3, 4

Saprobic on dead branches of an unknown plant species. **Sexual morph:** Undetermined. **Asexual morph:** Hyphomycetes. **Conidiophores** mononematous, macronematous, mostly unbranched, percurrently proliferating from cut ends, dark brown, smooth, 321–340 μm long ($\bar{x}$ = 335 μm , n = 10), 8–10 μm wide ($\bar{x}$ = 9 μm , n = 10), 10–13-septate, bulbous at base, erect or flexuous tapering

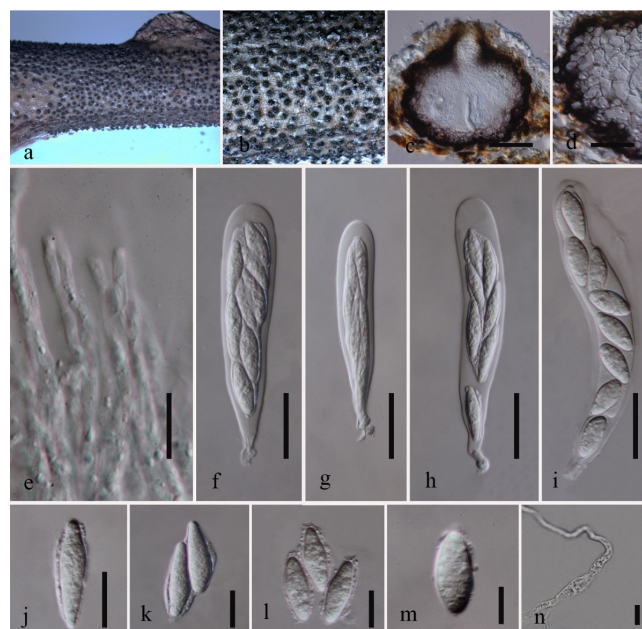


Fig. 2 *Botryosphaeria dolichospermatis* (KUN-HKAS 115560). (a), (b) Ascomata on host surface. (c) Vertical section of ascoma. (d) Peridium. (e) Pseudoparaphyses. (f)–(i) Asci. (j)–(m) Ascospores. (n) Germinated ascospore. Scale bars: (c) = 50 μm ; (d), (f)–(i) = 20 μm ; (e), (j)–(n) = 10 μm .

towards the apex, with cells towards the apex of the conidiophore guttulate, fertile. *Conidiogenous cells* polytretic, integrated, intercalary, terminal. *Conidia* 30–84 µm long ($\bar{x}$ = 64 µm, n = 20), 10–15 µm wide ($\bar{x}$ = 13 µm, n = 20), single, obclavate, pale brown to brown, 7–9-distoseptate, smooth, straight or curved, truncate at cicatrized base, dark brown, with apical cell paler than other cells, rostrate, guttulate. Conidial secession schizolytic.

Culture characteristics: Colonies on PDA, after 7 d at 25 °C in dark grey to brown with watery substrate, effuse, velvety, margin grey to white, reverse dark brown with pale-brown margin.

Known hosts and distribution: On the cankered branch of *Acer campestre* in Italy^[79], on the leaves of *Canna generalis* in Taiwan, China^[82], on the stem of *Passiflora edulis* in Australia^[83], on the twigs

of *Ulex europaeus* in Scotland (UK)^[84], on dead fruit of *Musa acuminata* in Thailand^[85], on decaying branches of an unidentified host in Sichuan, China^[78], on submerged wood in streams in Yunnan, China^[86], and on a branch of an unknown plant in Yunnan, China (this study).

Material examined: China, Yunnan, Kunming, Kunming Institute of Botany, Chinese Academy of Science, on dead branches of an unknown plant species, 17 July 2020, S. Tibpromma, ST 146 (KUN-HKAS 115606), living culture KUMCC 21-0076.

GenBank accession numbers: KUMCC 21-0076: SSU: PV942134; ITS: PV873202; LSU: PV942124; *tef1*: PX055884.

Notes: New strain (KUMCC 21-0076) clusters with the strains of *Helminthosporium velutinum* (MFLUCC 16-1096, CPC 26297, CGMCC

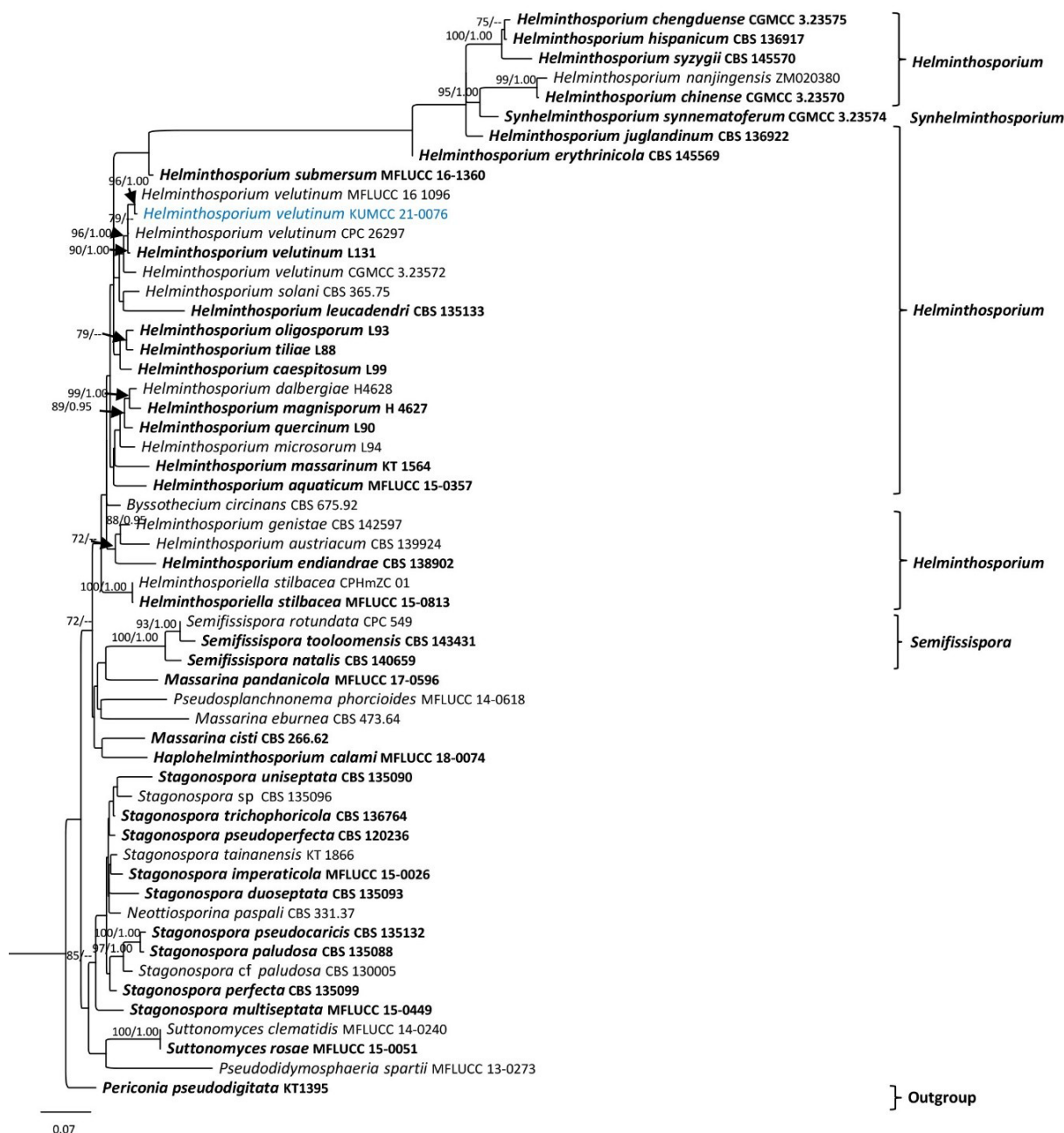


Fig. 3 Phylogram generated from Maximum Likelihood analysis based on LSU, SSU, ITS, and *tef1* sequence data. Bootstrap values for ML equal to or greater than 70% and BYPP values greater than 0.95 (rounded to two decimal places) from the BI analysis are labeled on the nodes. A newly generated sequence is in blue, and type species are bold.

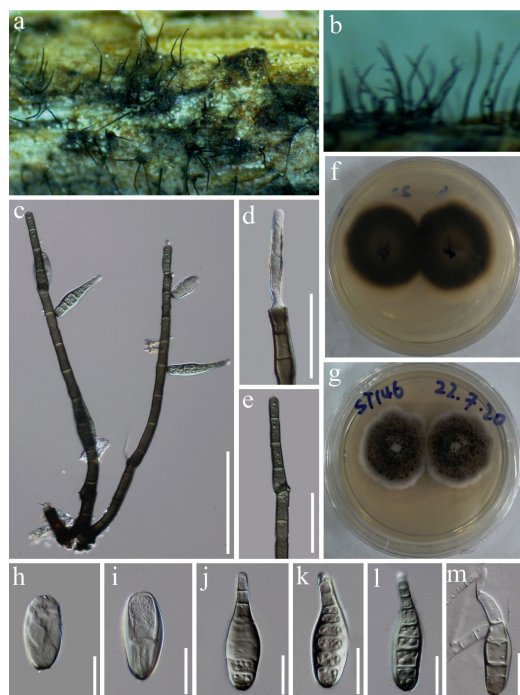


Fig. 4 *Helminthosporium velutinum* (KUN-HKAS 115606). (a), (b) Colonies on the substrate. (c) Conidiophores and conidia. (d), (e) Conidiogenesis. (f) Reverse view of culture on PDA. (g) Forward view of a few of the cultures in PDA. (h)–(l) Conidia. (m) Germinating conidium. Scale bars: (c)= 100 µm; (d), (e) = 50 µm; (h)–(m) = 20 µm.

3.23572, and L131[epitype]) and makes sister lineage to MFLUCC 16-1096 with 96% MLBS/1.00 BYPP statistic support (Fig. 3). In a BLASTn search of the NCBI GenBank, the closest match of the ITS sequence of the new isolate (KUMCC 21-0076) with 100% similarity was *H. velutinum* strains (voucher 202107001, MFLUCC 16-1096, and MFLUCC 16-1300).

Helminthosporium velutinum is found on a wide range of dead plant material, and it is cosmopolitan in distribution^[78]. Our new isolate shares a similar morphology with the type strain of *H. velutinum* (L131) in having solitary, cylindrical, unbranched, brown conidiophores that produce obclavate, distoseptate conidia^[74–77]. Based on morphology and the similarity of ITS sequences from various collections worldwide, we identified our isolates as *H. velutinum*. The species is primarily associated with dead plant material in terrestrial ecosystems worldwide^[77,82–85]. Our new isolate is also from a branch of an unidentified plant species in Yunnan, China.

Neohendersoniaceae A. Giraldo & Crous

Neohendersonia Petr.

Neohendersonia was introduced by Petrak^[87] with *N. pyriformis* as the type species. However, Giraldo et al.^[88] suggested that *N. pyriformis* should be considered synonymous with *N. kickxii*, a proposition later supported by subsequent literature; *N. kickxii* was proposed as the type species, being the older name^[88–90]. Currently, there are five species accepted in the genus; only *N. kickxii* and *N. tongrenensis* have sequence data, and all species were reported only as coelomycetes^[61,88]. In this study, we introduced a new species of this genus and its sexual morph.

Neohendersonia camelliae Jayasiri, Tibpromma & Karun., sp. nov.

Index Fungorum number: IF905408; **Facesoffungi number:** FoF 18867, Figs 5, 6

Etymology: The specific epithet reflects the host genus, *Camellia*.

Holotype: KUN-HKAS 115578

Saprobic on dead branches of *Camellia* sp. and unknown plant species. **Sexual morph:** Ascomata 233–308 high × 210–307 µm diam. ($\bar{x}$ = 305 × 264 µm, n = 10) scattered, solitary, semi-immersed to immersed, globose to subglobose, uni-loculate, with a central ostiole. Ostiole 20–40 µm long, minutely papillate, with pore-like opening. Peridium 15–35 µm thick, thick-walled, of uniform thickness, 5–7 layered, outer layers brown to dark brown, inner layers hyaline, composed of pseudoparenchymatous cells of *textura angularis*. Hamathecium composed of numerous, septate, branched, long, hyaline 1.2–2.0 µm wide pseudoparaphyses anastomosing at the apex, embedded in a gelatinous matrix. Asci 150–210 × 20–37 µm ($\bar{x}$ = 184 × 30 µm, n = 20), 6–8-spored, sometimes 4-spored, bitunicate, fissitunicate, broadly cylindrical to cylindrical-clavate, short pedicellate, sometimes with long pedicels, apically rounded, with an indistinct ocular chamber. Ascospores 35–47 × 10–16 µm ($\bar{x}$ = 42 × 14 µm, n = 30), 1–2-seriate, hyaline, becoming pale brown at maturity, broadly fusiform, smooth-walled, conical at both ends, 1-septate, with asymmetric cells, upper cell slightly larger than lower cell, with septum prominent when immature, with each cell containing a large and a small guttule, sheath when present 1.5–4 µm wide. **Asexual morph:** Undetermined.

Culture characteristics: Ascospores germinated within 12 h on PDA, colonies grown on PDA at room temperature (20–25 °C). Colonies are circular to irregular, dull, with wrinkled, yellow-green to brown aerial hyphae at the edge, dark green on the reverse, and produce a yellow-orange pigment on PDA.

Material examined: China, Yunnan, Kunming, Kunming Institute of Botany, Chinese Academy of Science, on dead branches of *Camellia* sp. (Theaceae), 08 June 2020, S. Tibpromma, ST 80 (KUN-HKAS 115578, holotype), ex-type KUMCC 21-0056; *ibid.*, on dead branches of an unidentified plant, 25 May 2020, S. Tibpromma, ST 58 (KUN-HKAS 115566, paratype), ex-paratype KUMCC 21-0107.

GenBank accession numbers: KUMCC 21-0056: SSU: PV942132; ITS: PV873199; LSU: PV942121; *tef1*: PX055881; *rpb2*: PX055870. KUMCC 21-0107: SSU: PV948970; ITS: PV873197; LSU: PV942119; *tef1*: PX055879; *rpb2*: PX055868.

Notes: *Neohendersonia camelliae* is introduced as a new species, mainly based on phylogenetic analyses of a combined SSU, ITS, LSU, *rpb2*, and *tef1* dataset and nucleotide comparison. *Neohendersonia camelliae* clusters sister lineage with the strains of *N. kickxii* with low statistical support (Fig. 5). In a BLASTn search of NCBI GenBank, the closest match of the ITS sequence of the new isolates (KUMCC 21-0056 and KUMCC 21-0107) with 92.91% similarity was the type strain of *N. kickxii* (CBS 112403). The comparison of ITS sequence between *N. camelliae* (KUMCC 21-0056) and *N. kickxii* (CBS 112403) shows a 47 bp (including gaps) difference (9.1%). Thus, we introduced our isolate as a new species in accordance with the guidelines of Jeewon & Hyde^[91]. In addition, we did not obtain the asexual morph in the culture. Therefore, a morphological comparison between our new species and *Neohendersonia kickxii* was not possible, as the latter has so far only been reported in its asexual morph^[88]. Currently, five other species are known within the genus *Neohendersonia*^[41,63,89,92]. Among other genera in the family Neohendersoniaceae, *Neohendersonia camelliae* shares a more similar morphology with the genus *Crassiparies*^[93,94] than with *Brevicollum* and *Medicopsis*. The sexual morph of *Crassiparies* (*C. quadrisporus*) is characterized by scattered, immersed, subglobose ascomata with an ostiolar neck, thin ascomata wall with polygonal to rectangular cells, septate, branched, and anastomosed pseudoparaphyses; 4-spored, cylindrical to clavate, pedicellate asci, and hyaline, broadly fusiform, 1-septate ascospores^[93,94]. However, they

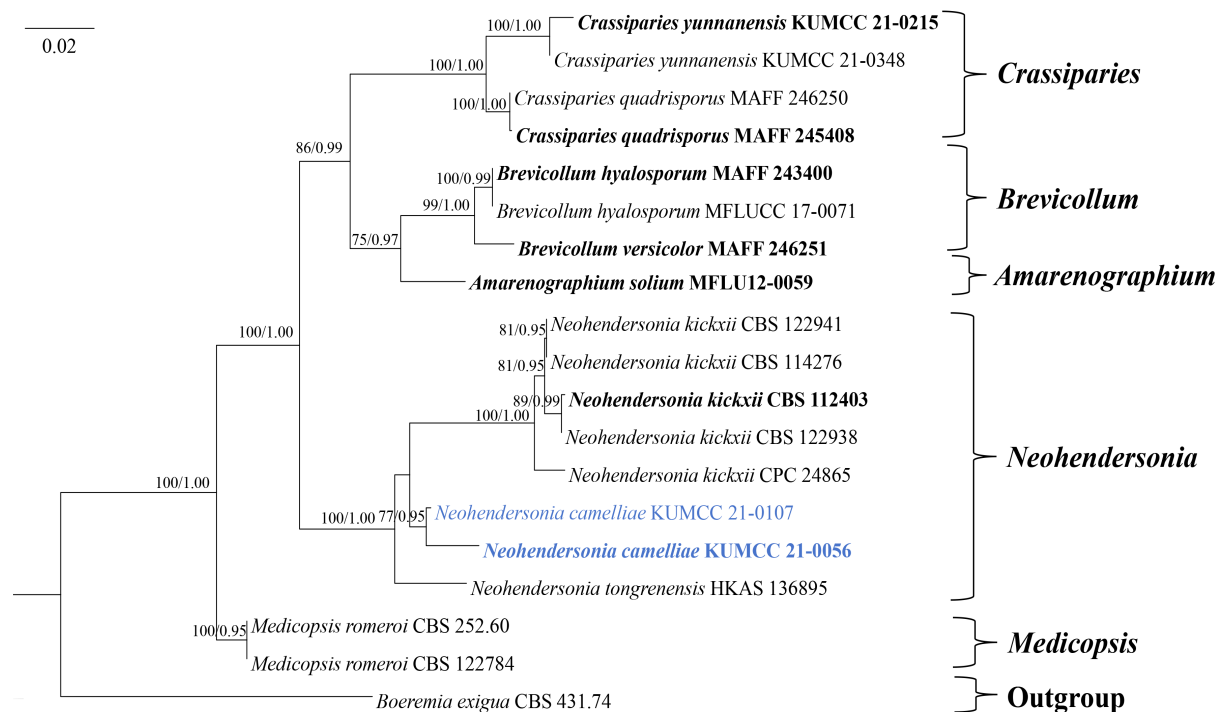


Fig. 5 Phylogram generated from Maximum Likelihood analysis based on SSU, LSU, and ITS sequence data representing *Neohendersonia* species. Bootstrap values for ML equal to or greater than 70% and BYPP greater than 0.95 (rounded to two decimal places) from the BI analysis are labeled on the nodes. Strains of the newly described species are in blue, while type strains are in bold.

are difficult to distinguish morphologically but can be well separated in phylogeny.

Notably, all strains of *Neohendersonia kickxii* identified in Austria (CBS 122938, CBS 122941), Italy (CBS 112403), and Sweden (CBS 114276) were from *Fagus* spp. whereas our two new strains were isolated from *Camellia* sp. and dead branches of an unknown species in Yunnan, China.

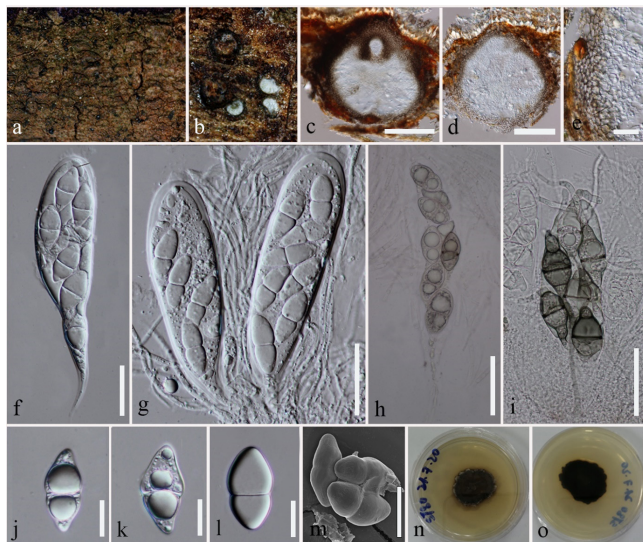


Fig. 6 *Neohendersonia camelliae* (KUN-HKAS 115578, holotype). (a), (b) Ascomata on host surface. (c), (d) Vertical section of ascomata. (e) Peridium. (f) Ascus. (g) Asci embedded in narrowly cellular pseudo-paraphyses. (h) Ascus with mature ascospores. (i) Germinated ascospores. (j)–(m) Ascospores (SEM). (n) Upper view on PDA. (o) Reverse view on PDA. Scale bars: (c), (d) = 100 µm; (e), (j)–(m) = 20 µm; (f)–(i) = 50 µm.

Teichosporaceae M.E. Barr

Magnibotryascoma Thambug. & K.D. Hyde

Thambugala et al.^[95] introduced *Magnibotryascoma* to accommodate *M. uniseriata* ($\equiv$ *Misturatosphaeria uniseriata*). *Magnibotryascoma* species have been reported as woody-based saprobes on *Acer cappadocicum*, *Clematis vitalba*, *Machilus yunnanensis*, *Malus halliana*, *Ribes sanguineum*, *Robinia pseudoacacia*, *Salix* sp., *Shorea assamica*, and *Vaccinium myrtillus* from Belgium, China, Germany, Norway, and the United Kingdom^[62,96,97]. The sexual morph of this genus is characterized by solitary or aggregated ascomata, fissitunicate, cylindrical to cylindrical-clavate asci, and partially overlapping, brown to dark brown, fusiform to elliptical, 1–3-septate ascospores^[95], while the asexual morph is characterized by pycnidial, uniloculate, semi-erumpent to superficial, subglobose to globose, dark brown to black conidiomata, multi-layered conidiomatal walls, enteroblastic, phialidic, integrated, truncate to cylindrical, hyaline conidiogenous cells, and hyaline to reddish-brown, aseptate conidia^[34,97,98]. In a previous study, Jaklitsch et al.^[96] synonymized this genus with *Teichospora*, but the morphological differences between the two genera are notable. Later, phylogenetic analyses by Hongsanan et al.^[9] positioned *Magnibotryascoma* as a distinct lineage within Teichosporaceae, separate from *Teichospora*, thereby supporting its recognition as a distinct genus. Currently, eight species are accepted in this genus^[41]. Morphological characteristics and phylogenetic analyses of combined ITS, LSU, SSU, and *tef1- α* sequence data revealed their taxonomic positions within *Magnibotryascoma*^[34,98]. In this study, we found other *M. mali* from unidentified tree species in Yunnan, China.

Magnibotryascoma mali Phukhams., Wanas. & K.D. Hyde 2017

Index Fungorum number: IF553255; **Facesoffungi number:** FoF03387, **Figs 7, 8**

Saprobic on dead branches of an unidentified tree species. **Sexual morph:** Undetermined. **Asexual morph:** Coelomycetous.

Conidiomata 147–182 µm high, 203–280 µm diam. ($\bar{x}$ = 165 × 247 µm, n = 5) pycnidial, solitary, aggregated, uniloculate, immersed, globose to subglobose, coriaceous, dark brown to brown, papillate, with a central ostiole. Pycnidial wall 10–23 µm wide, thick, 2-layered, with an outer layer composed of light brown to brown cells of *textura angularis*, lined with a hyaline innermost layer bearing conidiogenous cells. *Conidiophores* are reduced to conidiogenous cells. *Conidiogenous cells* 5.2–7.9 × 1.7–3 µm ($\bar{x}$ = 6.4 × 2 µm, n = 20), enteroblastic, annelidic, discrete, cylindrical to oblong, hyaline, arising from the inner layer of pycnidial wall. *Conidia* 3.2–4.3 × 1.9–2.6 µm ($\bar{x}$ = 4 × 2.2 µm, n = 30), subglobose, oval, guttulate, hyaline when immature, pale brown at maturity, aseptate, smooth-walled.

Culture characteristics: Colonies grow on PDA at 20 °C. Colonies after 14 d dense, circular, slightly raised, rough surface, with curled or scalloped entire margin, radiated, with four layers in surface view (Fig. 8m), pale yellowish to brown at the margin, paler towards the center, separated by pale-grey to dark-grey concentric ring near the margin, with yellow pigment diffusing in the agars, and pale to dark brown in reverse.

Known host and distribution: On decayed twigs of *Malus halliana* in Yunnan, China^[99], on a dead branch of *Metrosideros* sp. in New Zealand^[100], on dead branches of *Osmanthus fragrans* in Sichuan, China^[101], on dead branches of unknown species in Yunnan, China (this study).

Material examined: China, Yunnan, Kunming, Kunming Institute of Botany, Chinese Academy of Science, on dead branches of unknown

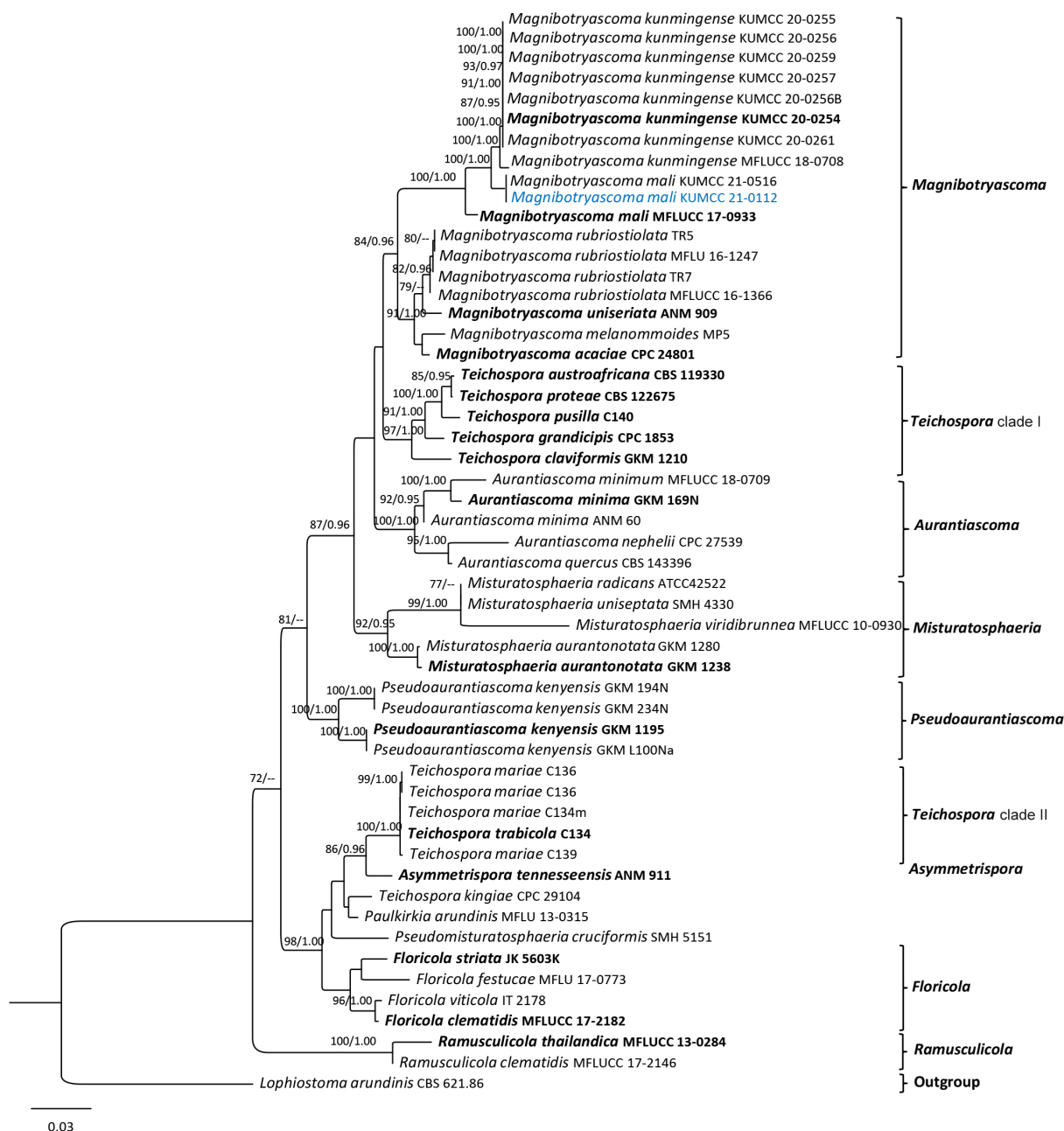


Fig. 7 Phylogram generated from maximum likelihood analysis based on LSU, SSU, ITS, *tef1*, and *rpb2* sequence data. Bootstrap values for ML equal to or greater than 70% and BYPP equal to or greater than 0.95 (rounded to two decimal places) from the BI analysis are labeled on the nodes. A newly generated sequence is in blue, and type strains are bold.

species, 09 June 2020, S. Tibpromma, ST 93 (KUN-HKAS 115583), living culture KUMCC 21-0112.

GenBank accession numbers: KUMCC 21-0112: SSU: PV942133; ITS: PV873201; LSU: PV942123; *tef1*: PX055883; *rpb2*: PX055872.

Notes: In multigene phylogenetic analyses, our new strain clustered with the strain of *Magnibotryascoma mali* (KUMCC 21-0516) with 100% MLBS/1.00 BYPP statistical support (Fig. 7). In the NCBI BLASTn search based on ITS sequence, the closest match of our new strain is *M. mali* (KUMCC 21-0516) with 100% similarity; *tef1* sequence closest match with *M. mali* (GZAAS 23-0648) with 99.70% similarity; *rpb2* sequence closest match with *M. mali* (MFLUCC 17-0933) with 98.58% similarity. Based on the phylogenetic tree, our strain clustered with *M. mali* (KUMCC 21-0516) while sister to the ex-type of *M. mali* (MFLUCC 17-0933) (Fig. 7). The morphology of our new strain matched the description by Ren et al.^[62], and also matches with the holotype of *M. mali* (MFLU 17-0559), which was introduced from decayed twigs of *Malus halliana* (Rosaceae) in Yunnan, China^[99].

According to the phylogenetic tree of Ren et al.^[62] and Chethana et al.^[101], their isolates of *M. mali* are related to *M. mali* (MFLUCC 17-0933, ex-type) but do not group together with the results of our phylogenetic analyses. Our *M. mali* does not group with the ex-type of *M. mali* (MFLUCC 17-0933) (Fig. 7). Therefore, with this conspecific status, further taxonomic work is needed to resolve identification, phylogenetic position, and relationships between *M. mali* members.

Sordariomycetes O.E. Erikss. & Winka

Sordariomycetidae O.E. Erikss. & Winka

Amphisphaeriales D. Hawksw. & O.E. Erikss.

Apiosporaceae K.D. Hyde, J. Fröhl., Joanne E. Taylor & M.E. Barr

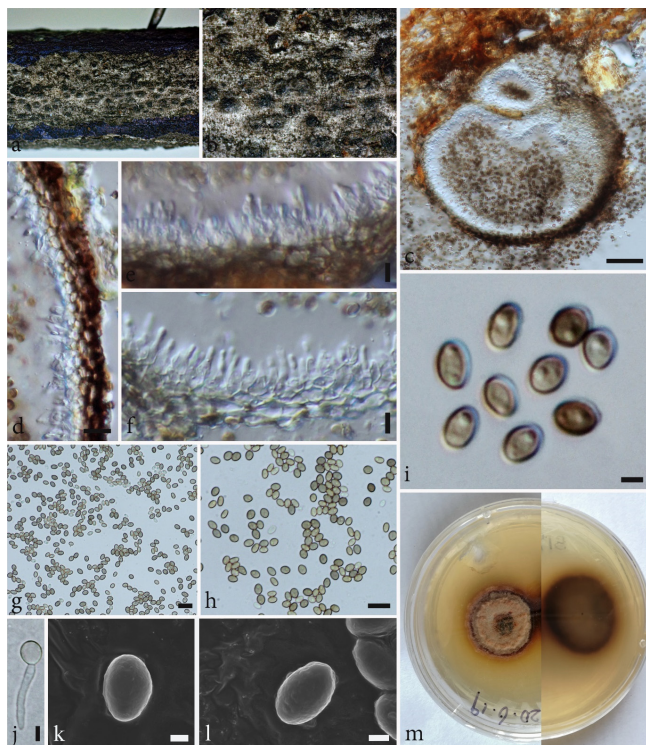


Fig. 8 *Magnibotryascoma mali* (KUN-HKAS 115583). (a), (b) Conidiomata observed on the host surface. (c) Horizontal section of a conidioma. (d) Pycnidial wall. (e), (f) Conidiogenous cells. (g)–(i), (k), (l) Conidia; (k), (l) SEM photos. (j) Germinated conidium. Scale bars: (c) = 50 μ m; (d) = 20 μ m; (e)–(h) = 10 μ m; (i), (k), (l) = 1 μ m; (j) = 2 μ m.

Apiospora Sacc.

The genus *Apiospora* was introduced by Saccardo^[102], with *A. montagnei* as the type species. Members of this genus can survive as endophytes, saprobes, or pathogens, which have a wide range of distribution in different habitats such as animal tissues, seaweeds, and even oligotrophic environments (lichens, air, and soil)^[103–105]. The genus was reported with both its sexual and asexual morphs. Sexual morphs are characterized by multi-locular stromata and 1-septate (near the lower cell) ascospores^[106]. Asexual morphs were characterized by dark-brown conidia, with a longitudinal, transparent slit or hyaline conidiophores, basauxic conidiogenous cells, and pale-brown to brown conidia^[104–107]. In this study, we collected known species *A. yunnana* as saprobic on dead bamboo culms in the KIB garden, and this is the third time that this species has been found on bamboo in China.

Apiospora yunnana (D.Q. Dai & K.D. Hyde) Pintos & P. Alvarado, Fungal Systematics and Evolution 7: 207 (2021)

Index Fungorum number: IF837739, Figs 9, 10

≡ *Arthrimum yunnanum* D.Q. Dai & K.D. Hyde, in Dai, Phookamsak, Wijayawardene, Li, Bhat, Xu, Taylor, Hyde & Chukeatirote, Fungal Diversity 82: 69 (2016)

Saprobic on dead bamboo culms. **Sexual morph:** *Ascostromata* 0.6–1.2 mm long, 0.4–0.6 mm wide, 0.2–0.3 mm high, solitary, or occasionally with two, gregarious, immersed, subepidermal, fusiform to ellipsoid, black, with a long-slit opening at the top. *Ascoma* 126–150 μ m diam. $\times$ 123–183 μ m high in section, perithecioid, subglobose, light brown to dark brown, with a distinct ostiole at the centre, crowned by a black clypeus. *Peridium* laterally 30–46 μ m thick, composed of brown and small light brown to reddish brown to hyaline elongated cells of *textura angularis*, surrounded by 100–300 μ m stromatic tissues, composed of small cells of *textura angularis*. *Hamathecium* composed of dense, 3–5 μ m broad, septate, unbranched, paraphyses. *Asci* 85–92 $\times$ 17–25 μ m ($\bar{x}$ = 88 $\times$ 21 μ m, n = 20), 8-spored, unitunicate, broadly cylindrical to subglobose, with a narrow apex. *Ascospores* 26–32 $\times$ 9–11 μ m ($\bar{x}$ = 29 $\times$ 10 μ m, n = 20), 2–3-seriate, asymmetrically 1-septate, apiospored, elliptical, with a large, curved, upper cell and small lower cell, narrowly rounded at ends, hyaline, smooth-walled, with many guttules, surrounded by a 5–10 μ m wide gelatinous sheath. **Asexual morph:** Undetermined.

Culture characteristics: Ascospores germinate on PDA within 24 h, and germ tubes develop from the upper part. Colonies fast growing on PDA at 25 $^{\circ}$ C, sparse, circular, with irregular edges, flattened, hairy to feathery, white from above, brown to dark brown in the centre from below. Mycelium is superficial to immersed in medium, with branched, septate, smooth hyphae.

Known host and distribution: On dead culms of *Phyllostachys nigra* in Yunnan, China^[106], on decaying culms of *Phyllostachys heteroclada* in Sichuan, China^[108], on dead culms of bamboo (Poaceae) in Yunnan, China (this study).

Material examined: China, Yunnan, Kunming, Kunming Institute of Botany, Chinese Academy of Science, on dead culms of bamboo (Poaceae), 15 May 2020, S. Tibpromma, ST 55 (KUN-HKAS 115564), living culture KUMCC 21-0047.

GenBank accession numbers: KUMCC 21-0047: SSU: PV942130; ITS: PV873195; LSU: PV942117; *tub2*: PX055889.

Notes: *Apiospora yunnana* was described by Dai et al.^[106] based on a specimen collected in Yunnan Province, China. This species occurred on dead culms of *Phyllostachys nigra* (black bamboo, Poaceae)^[106]. Our new strain (KUMCC 21-0047) groups within the type strain of *A. yunnana*, with statistical support 97% MLBS/1.00 BYPP (Fig. 9). The new collection has similar ascospore, ascus, and



Outgroup

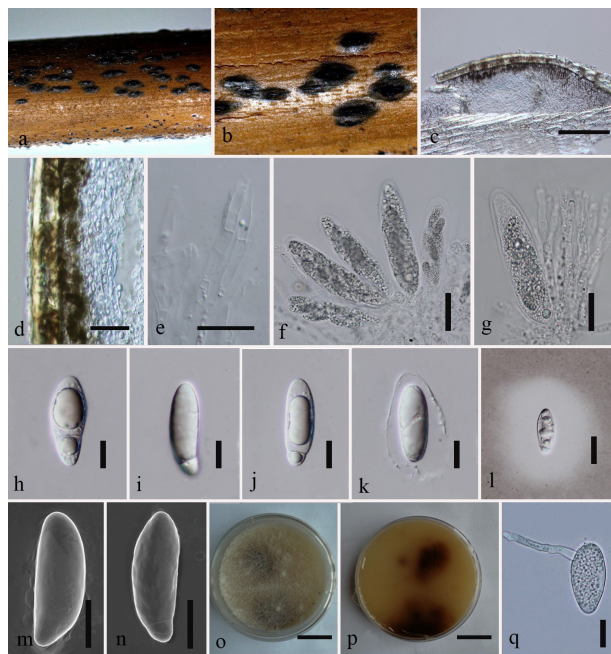


Fig. 10 *Apiospora yunnana* (HKAS 115564). (a), (b) Ascomata on host surface. (c) Vertical section of ascomata. (d) Peridium. (e) Paraphyses. (f), (g) Asci. (h)–(n) Ascospores; (l) ascospore with mucilaginous sheath in India ink; (m), (n) SEM photos. (o) Upper view on PDA. (p) Reverse view on PDA. (q) Germinated ascospore. Scale bars: (c) = 100 μ m; (d), (l) = 20 μ m; (e), (h)–(k), (m), (n), (q) = 10 μ m; (f), (g) = 30 μ m; (o), (p) = 2 cm.

ascocarp morphology to the type strain. Therefore, the strain collected from the same place and host group (bamboo) is assigned to *A. yunnana*.

Chaetosphaeriales Huhndorf, A.N. Mill. & F.A. Fernández

Chaetosphaeriaceae Réblová, M.E. Barr & Samuels

Pseudolachnella Teng

Pseudolachnella, a genus segregated from *Pseudolachnea*, was established to accommodate species with multiseptate conidia, with *P. scoleospora* as the type species^[109]. Under the genus *Pseudolachnella*, 23 species are accepted, and for many of them, ITS, LSU, and *tef1* sequences are available^[42,65]. Members of this genus have been reported only as asexual morphs and characterized by stromatic, acervular, setose conidiomata with marginal setae, phialidic conidiogenous cells, and conidia with single to multiple appendages at each end^[110,111]. Dead bamboo substrates from China, India, and Japan are common hosts for this genus^[111,112]. In this study, we introduce the sexual morph of *P. tengii*, the first for this genus.

Pseudolachnella tengii W.P. Wu & Y.Z. Diao, Fungal Diversity 116: 501 (2022)

Index Fungorum Number: IF841674, Figs 11, 12

Saprobic on a dead branch of a liana. **Sexual morph:** Ascomata 432–441 $\times$ 420–445 μ m, scattered, solitary, immersed, irregular in shape, globose to subglobose, uniloculate, with a short central ostiole. Peridium 15–35 μ m thick, thin-walled, of equal thickness, composed of 5–7 layers of flattened, dark brown, pseudoparenchymatous cells of *textura angularis*, with paler brown to hyaline towards the inner layer. Hamathecium 1.2–2.0 μ m wide, filamentous, septate, branched, long, hyaline paraphyses. Asci 150–210 $\times$ 20–37 μ m ($\bar{x}$ = 184 $\times$ 30 μ m, n = 20), 8-spored, unitunicate, cylindrical to clavate, short pedicellate, sometimes with long pedicels, apical rounded, with a J- ring. Ascospores 35–47 $\times$ 10–16 μ m ($\bar{x}$ = 42 $\times$ 14 μ m, n = 30), 1–2-seriate, hyaline when young, becoming dark

brown when mature, broadly fusiform, with rounded to acute ends, smooth-walled, muriform, with asymmetric cells, with septa becoming prominent when mature, 5–10-transverse and 2–4–8-longitudinal septum, surrounded by a thin, inconspicuous, mucilaginous sheath. **Asexual morph:** See Wu & Diao^[64].

Culture characteristics: Ascospores germinated within 12 h on PDA, colonies grown on PDA at room temperature (20–25 °C). Colonies circular to irregular, dull surface and wrinkled, yellow to dark brown, dark brown on the reverse, producing a yellow-orange pigment on PDA.

Known host and distribution: On the dead culm of *Phyllostachys* sp. in Yunnan, China^[64], on a dead branch of a liana in Yunnan, China (this study).

Material examined: China, Yunnan, Kunming, Kunming Institute of Botany, Chinese Academy of Science, on a dead branch of a liana, 26 May 2020, S. Tibpromma, ST 56 (KUN-HKAS 115565), living culture KUMCC 21-0048.

GenBank accession numbers: KUMCC 21-0048: ITS: PV873196; LSU: PV942118; *tef1*: PX055878; *rpb2*: PX055867.

Notes: In the phylogenetic analysis, the new isolate formed a sister group with *Pseudolachnella tengii* (NN047882^T), with 100% MLBS and 1.00 BYPP statistical support (Fig. 11). *Pseudolachnella tengii* was introduced as an asexual morph, and the genus *Pseudolachnella* comprised only asexual morph species^[64,110]. Therefore, morphological comparison is impossible as our new isolate is a sexual morph. As well, we are unsuccessful in getting the asexual morph from the culture. Based on nucleotide comparisons between our isolates and *P. tengii* (NN047882^T), the ITS and LSU sequences are identical, while *tef1* and *rpb2* are available for *P. tengii* (NN047882^T). In this study, we introduced the new isolate as the sexual morph of *P. tengii*, and both the holotype (HMAS 352045)^[64] and our new isolate (HKAS 115565) were collected from the KIB in Kunming, Yunnan, China.

Distoseptisporales Z.L. Luo, H.Y. Su & K.D. Hyde

Distoseptisporaceae K.D. Hyde & McKenzie

Distoseptispora K.D. Hyde, McKenzie & Maharachch

The genus *Distoseptispora* is one of the *Sporidesmium*-like genera introduced by Su et al.^[113], with the type species, *D. fluminicola*, isolated from decaying wood in Yunnan, China. *Distoseptispora*, as a single genus within Distoseptisporaceae, occurs mainly as asexual morphs, while only two species have been reported as sexual morphs, viz. *D. hyalina* and *D. licualae*^[114,115]. Species of this genus were found forming effuse, hairy colonies on decaying wood, plant stems, bamboo culms, and fallen leaves and shafts in terrestrial and freshwater habitats, mostly reported from Asia (mainly in China and Thailand)^[31,116–119]. Furthermore, members of this genus show macronematous, mononematous, septate, unbranched, cylindrical, olivaceous to brown conidiophores; mono- or polyblastic, integrated, terminal, cylindrical, determinate, or percurrently extending conidiogenous cells; and acrogenous, solitary, smooth or verruculose, euseptate or distoseptate conidia^[31]. In this study, we found known species of *Distoseptispora* (*D. guizhouensis*) from an unidentified plant in the KIB garden.

Distoseptispora guizhouensis X. Tang, Jayaward., J.C. Kang & K.D. Hyde, in Hyde et al., Mycosphere 12(1): 1126 (2021)

Index Fungorum number: IF558532, Figs 13, 14

Saprobic on decaying branch of an unidentified plant. **Sexual morph:** Undetermined. **Asexual morph:** Hyphomycetous. Colonies on wood effuse, hairy, dark brown, scattered or in small groups, glistering, usually setiform. Mycelium is partly immersed, partly superficial, composed of septate, smooth-walled, pale-brown to hyaline hyphae. Conidiophores 21–44 $\times$ 3.8–4.9 μ m ($\bar{x}$ = 32 $\times$ 4.2 μ m, n = 30),

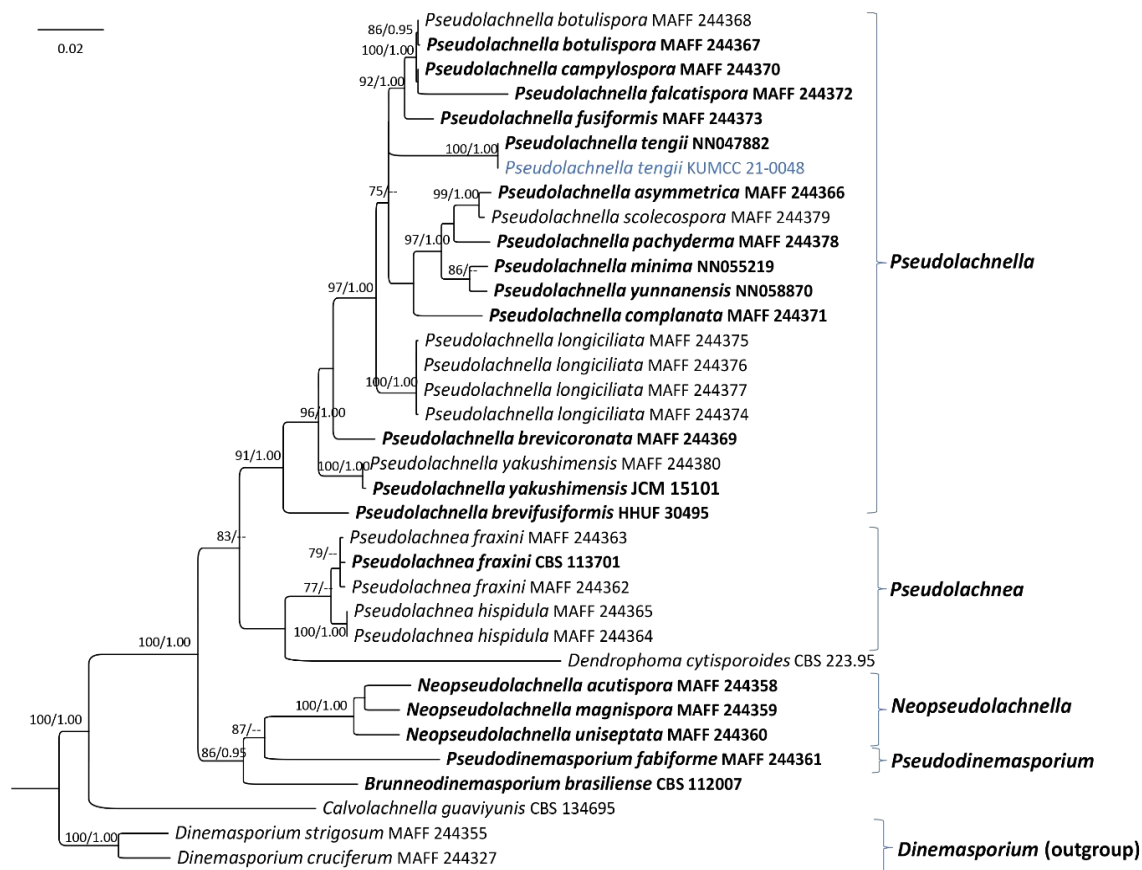


Fig. 11 Phylogram generated from Maximum Likelihood analysis based on LSU, ITS, and *tef1* sequence data representing *Pseudolachnella* and its relatives. Bootstrap values for ML equal to or greater than 70% and BYPP values equal to or greater than 0.95 (rounded to two decimal places) from the BI analysis are labelled on the nodes. A newly generated sequence is in blue, and ex-type strains are in bold.



Fig. 12 *Pseudolachnella tengii* (KUN-HKAS 115565). (a)–(c) Ascomata on host surface. (d) Paraphyses. (e) Vertical section of ascoma. (f)–(i) Asci. (j) Peridium. (k)–(p) Ascospores; (n)–(p) SEM photos. (q) Germinated ascospore. (r) Upper view on PDA. (s) Reverse view on PDA. Scale bars: (d) = 10 µm; (e) = 100 µm; (f)–(j) = 20 µm; (k)–(q) = 10 µm; (r), (s) = 2 cm.

macronematous, mononematous, erect, solitary or caespitose, straight or flexuous, cylindrical, percurrently proliferating, rounded at apex, smooth-walled, septate, unbranched, greyish brown. *Conidiogenous cells* monoblastic, integrated, terminal, determinate, cylindrical, brown, rounded, and darkened at the apex. *Conidia* 73–184 × 10–19 µm ($\bar{x}$ = 104 × 13 µm, n = 20), acrogenous, obclavate, rostrate, 12–31-distoseptate, brown to dark brown, usually paler towards the apex, rounded at apex, with a truncated base, faintly to heavily pigmented at the basal scar.

Culture characteristics: Conidia germinate on PDA within 24 h, and germ tubes are produced from both ends. Colonies growing on PDA, slow growing after 1 month at 25 °C in natural light; circular, with dense, three-layered (forward grey, white, and grey, respectively), and a dark-brown margin. In reverse, dark brown to black with a smooth margin.

Known host and distribution: Decaying wood in Guizhou^[61] and Yunnan, China (this study).

Material examined: China, Yunnan, Kunming, Kunming Institute of Botany, Chinese Academy of Science, decaying branch of unknown plant, 6 May 2020, S. Tibpromma, ST03 (KUN-HKAS 115537); living culture KUMCC 21-0039.

GenBank accession numbers: KUMCC 21-0039: SSU: PV948969; ITS: PV873190; LSU: PV951539; *tef1*: PX055874; *rpb2*: PX055863.

Notes: Our new isolate is well supported together with *Distoseptispora guizhouensis* (GZCC 21-0666^T) (100% MLBS/ 1.00 BYPP, Fig. 13). Also, it shares similar morphology with the holotype of *D. guizhouensis* (GZAAS21-0381) in having macronematous, mononematous, erect, cylindrical conidiophores, monoblastic,

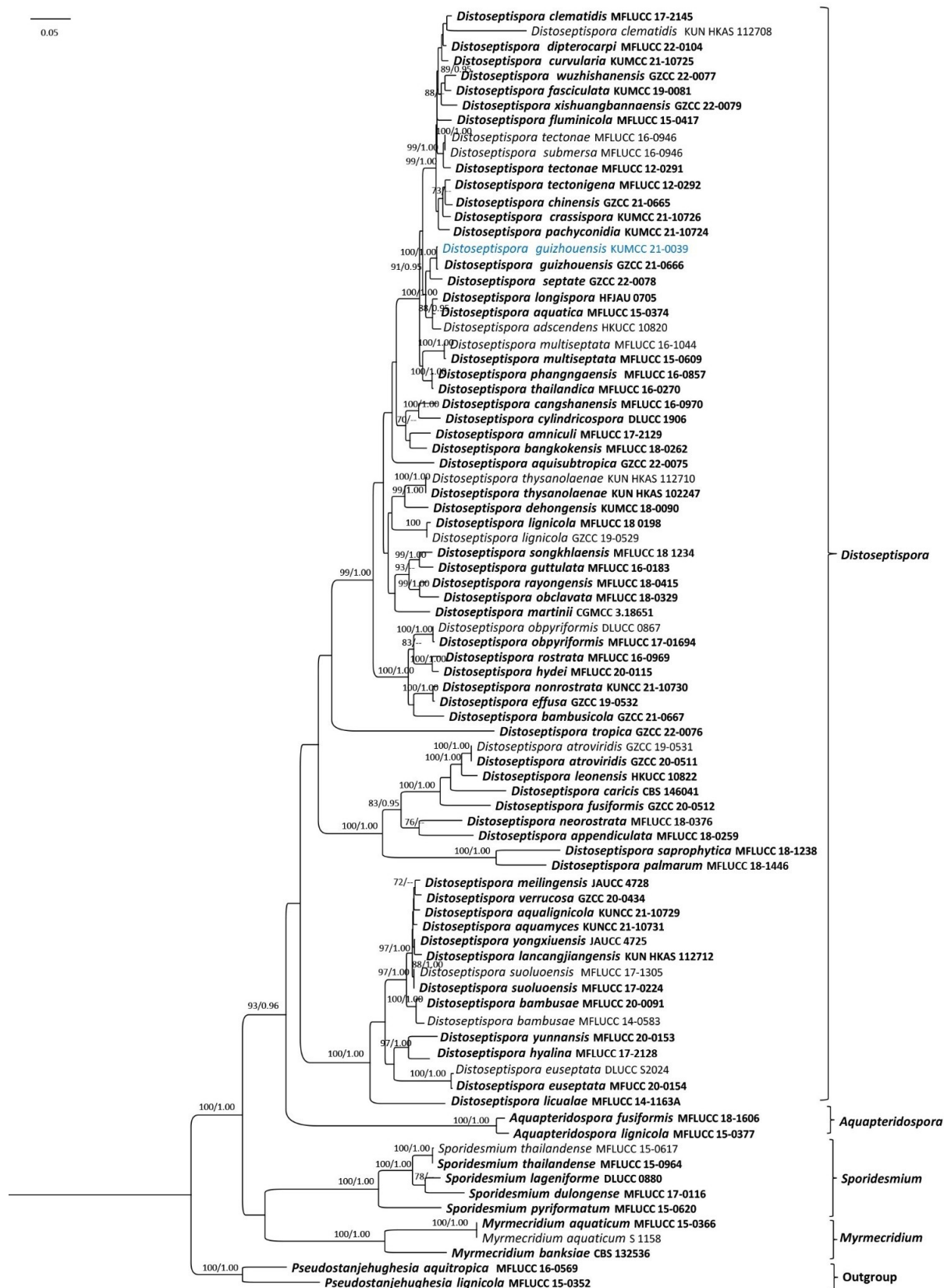


Fig. 13 Phylogram generated from Maximum Likelihood analysis based on ITS, LSU, *tef1*, and *rpb2* sequence data representing *Distoseptispora* species. Bootstrap values for ML equal to or greater than 70% and BYPP values equal to or greater than 0.95 (rounded to two decimal places) from the BI analysis are labelled on the nodes. A newly generated sequence is in blue, and type species are in bold.

integrated, terminal, determinate, cylindrical, brown conidiogenous cells, and acrogenous, obclavate, distoseptate, brown to dark-brown conidia^[61]. Conidiophore and conidia sizes of our new isolate (KUN-HKAS 115537) and holotype (GZAAS21-0381^[61]) are shown with the conidiophore overlap size ($21\text{--}44 \times 3.8\text{--}4.9 \mu\text{m}$ vs $21\text{--}50 \times 4\text{--}9 \mu\text{m}$), but the holotype conidia are bigger than our isolate ($73\text{--}184 \times 10\text{--}19 \mu\text{m}$ vs $90\text{--}273 \times 15\text{--}21$). Based on nucleotide comparisons, two base pairs differ in the ITS region between our isolates and *D. guizhouensis* (GZCC 21-0666, ex-type), whereas the LSU and *tef1* sequences are identical. Here, we report the new collection of *D. guizhouensis* in Yunnan, China, accompanied by SEM photographs of its conidia for the first time. However, the species name was corrected in the original as *D. guizhouensis*, but in Index Fungorum and MycoBank, it was recorded as *D. guizhouensis*. Therefore, it will need to be corrected in the future.

Xylariales Nannf.

Diatrypaceae Nitschke

Peroneutypa Berl.

Peroneutypa is characterized by long, prominent necks, with small, truncate apices, urn-shaped asci, and allantoid ascospores^[120–122]. Li et al.^[123] accepted *Peroneutypa* with 27 species, but approximately 76 epithets are listed in Index Fungorum^[41]. Members of *Peroneutypa* are saprobes or pathogens and are widely distributed in terrestrial and marine habitats^[124–128]. In our study, we identified the known species *Peroneutypa* (*P. scoparia*) using morphological and phylogenetic data. In addition, this is the first time *P. scoparia* has been found on *Trachycarpus* sp. in Yunnan Province, China.



Fig. 14 *Distoseptispora guizhouensis* (KUN-HKAS 115537). (a) Colonies on host surface. (b) Germinated conidium. (c)–(e) Conidiophores, conidiogenous, and developing conidia. (f)–(j) Conidia. (k) Colony on PDA. (l)–(n) SEM photographs of conidiogenous cells and conidia. Scale bars: (b)–(e), (l), (m) = 10 μm ; (f)–(j), (n) = 20 μm .

Peroneutypa scoparia (Schwein.) Carmarán & A.I. Romero

Index Fungorum number: IF500713; **Facesoffungi number:** FoF 01998, **Figs 15, 16**

Synonyms:

=*Sphaeria scoparia* Schwein.

=*Valsa scoparia* (Schwein.) M.A. Curtis.

=*Eutypella scoparia* (Schwein.) Ellis & Everh.

=*Peroneutypella scoparia* (Schwein.) Berl.

=*Eutypa scoparia* (Schwein.) L.C. Tiffany & J.C. Gilman.

=*Valsa ceratophora* sensu Cooke.

=*Valsa heteracantha* Sacc.

=*Eutypa heteracantha* (Sacc.) Sacc.

=*Engizostoma heteracanthum* (Sacc.) Kuntze.

=*Peroneutypa heteracantha* (Sacc.) Berl.

=*Peroneutypella heteracantha* (Sacc.) Rehm.

=*Peroneutypella heteracantha* f. *berberidis* Rehm.

=*Peroneutypa heteracantha* f. *arundinis-donacis* Speg.

=*Peroneutypa heteracantha* f. *ricini-communis* Speg.

=*Peroneutypa heteracantha* f. *casuarinae-strictae* Speg.

=*Peroneutypa heteracantha* f. *annonae-cherimoliae* Speg.

Saprobic on dead petioles of *Trachycarpus* sp. **Sexual morph:** **Ascomata** perithecial, 350–450 μm diam., 150–170 μm high ($\bar{x} = 421 \times 162 \mu\text{m}$, $n = 10$), solitary to 2- or 3-grouped, gregarious, immersed in the cortex, globose to subglobose, dark brown to black, coriaceous, becoming raised to erumpent by a long ostiolar canal. **Ostiolar canal** 130–180 μm long, 48–60 μm wide ($\bar{x} = 156 \times 52 \mu\text{m}$, $n = 10$), dark brown to black, glabrous, circular to irregular in shape, arranged longitudinally, periphysate. **Peridium** 15–31 μm thick, composed of two sections of layers, with the outer section comprising 3–5 layers of relatively small, brown to dark-brown thick-walled cells, arranged in *textura angularis*, and the inner part comprising 3–5 layers of hyaline cells of *textura angularis*. **Hamathecium** composed of 2.7–3.8 μm wide, dense, cylindrical, septate, hyaline paraphyses, slightly swollen at the septa. **Asci** 21–41 $\times$ 4–6 μm ($\bar{x} = 33 \times 5 \mu\text{m}$, $n = 20$), 8-spored, unitunicate, clavate to cylindro-clavate, apically rounded to truncate, J- apical ring, with a 15–20 μm long pedicel. **Ascospores** 4–5 $\times$ 1–2 μm ($\bar{x} = 4.1 \times 1.4 \mu\text{m}$, $n = 30$), 2–3-seriate to irregularly arranged, allantoid, hyaline, rounded at both ends, smooth-walled. **Asexual morph:** See Shang et al.^[129].

Culture characteristics: Ascospores germinate on PDA within 24 h, and germ tubes are produced from both ends. Colonies after 1 week white, cottony, with ropy hyphal strands near the centre with diffuse margins; reverse coloration pale yellow; after 1 month, grey to dark-brown radial strands of aerial hyphae, reverse yellow to brown.

Known host and distribution with molecular data: on leaves of *Garcinia dulcis* from Songkhla, Thailand^[105], on dead culms of bamboo and on dead wood of *Dalbergia cana*, *Microcos paniculate*, and *Azelia xylocarpa* from Chiang Rai, Thailand^[130,131], on living branches of *Broussonetia papyrifera* from Argentina^[7], on unknown bark from Chiang Mai, Thailand^[129], on diseased dieback marine wood from Phetchaburi, Thailand^[132], and on dead petioles of *Trachycarpus* sp. and unknown plants from Yunnan, China (this study).

Material examined: China, Yunnan, Kunming, Kunming Institute of Botany, Chinese Academy of Science, on dead petioles of *Trachycarpus* sp. (Arecaceae), 28 June 2020, Tibpromma, ST 63 (KUN-HKAS 115568), living culture KUMCC 21-0049; *ibid.*, on dead branches of an unidentified plant, 1 May 2020, S. Tibpromma, ST 40 (KUN-HKAS 115766), living culture KUMCC 21-0100.

GenBank accession numbers: KUMCC 21-0049: SSU: PV942131; ITS: PV873198; LSU: PV942120; *tef1*: PX055880; *tub2*: PX055890; *rpb2*:

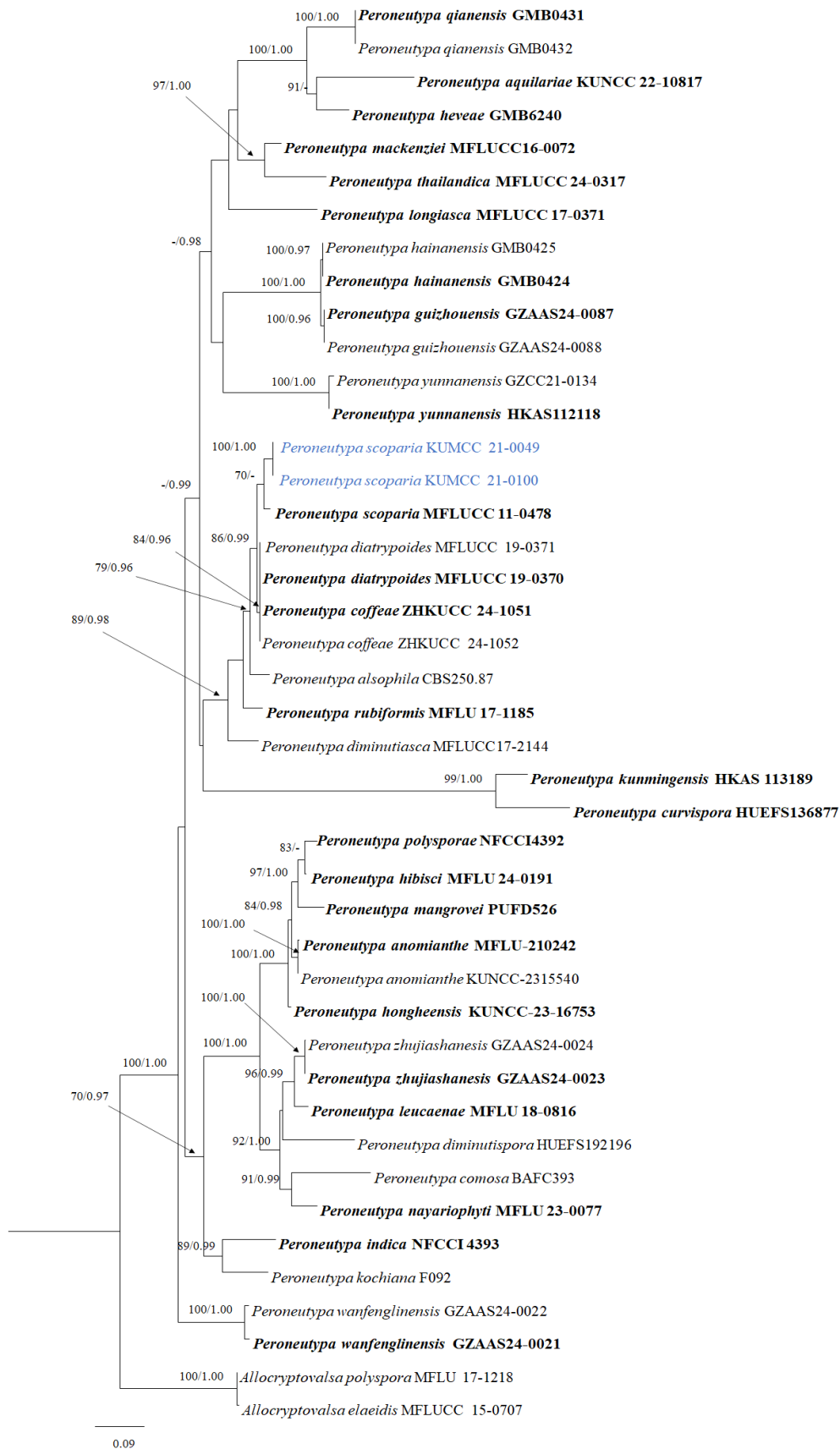


Fig. 15 Phylogram generated from Maximum Likelihood analysis based on ITS and *tub2* sequence data representing *Peroneutypa*. Bootstrap values for ML equal to or greater than 70% and BYPP values equal to or greater than 0.95 (rounded to two decimal places) from the BI analysis are labeled on the nodes. The newly generated sequences are in blue, and the type species and the reference specimens are in bold.

PX055869. KUMCC 21-0100: SSU: PV942127; ITS: PV873192; LSU: PV942114; *tef1*: PX055876; *tub2*: PX055886; *rpb2*: PX055865.

Notes: Phylogenetic analyses of a combined ITS and *tub2* sequence dataset showed that our strains (KUMCC 21-0049 and KUMCC 21-0100) cluster with *Peroneutypa scoparia* (MFLUCC 11-0478) with 70% MLBS statistical support (Fig. 15). Our sample differs slightly from *P. scoparia* (MFLU 15-1183, reference specimen) by having a relatively small ostiolar canal (130–180 × 48–60 µm vs 195–530 × 330–720 µm). Therefore, the combined ITS-*tub2* phylogeny and morphological features support our isolates as *P.*

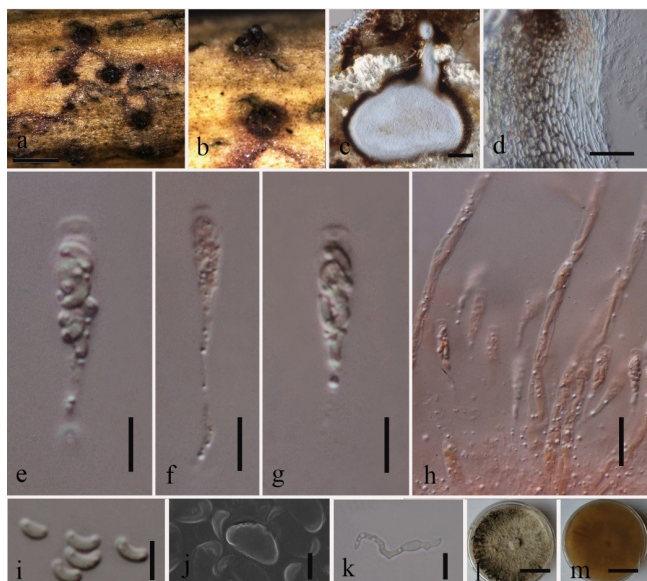


Fig. 16 *Peroneutypa scoparia* (HKAS 115568). (a), (b) Ascomata on host surface. (c) Vertical section of ascoma. (d) Peridium. (e)–(g) Asci (stained with Congo red). (h) Paraphyses (stained with Congo red). (i), (j) Ascospores; (j) SEM photo. (k) Germinated ascospore. (l) Upper view on PDA. (m) Reverse view on PDA. Scale bars: (a) = 500 µm; (c) = 50 µm; (d) = 10 cm; (e)–(i), (k) = 5 µm, (j) = 2 µm; (l), (m) = 2 cm.

scoparia. In addition, this is the first time *P. scoparia* has been found in China, and the first time SEM images of its ascospores have been provided.

Sordariomycetes genera *incertae sedis*

Melanographium Sacc.

This genus, typified by *M. selenioides*^[133], is characterized by dark and unbranched conidiophores generally arising in a group from an immersed stroma with polyblastic conidiogenous cells and sympodial proliferation^[134–136]. Conidia are pigmented, single-celled, frequently reniform in shape, and often with a hyaline germ slit^[134–136]. Species are distinguished by the length of the conidiophores, the pattern of conidiophore grouping (single, synnemata, loosely or dense fascicles), conidial shape (straight, curved, or strongly curved), and conidial size^[136]. In the Index Fungorum^[41], 19 species have been recorded, but only a few species have molecular data. In this study, we introduce a new species based on both molecular and morphological data.

Melanographium trachycarpi Jayasiri, Tibpromma & Karun., *sp. nov.*

Index Fungorum number: IF905409; **Facesoffungi number:** FoF 18869, Figs 17, 18

Etymology: The specific epithet '*trachycarpi*' refers to the host plant genus, *Trachycarpus*.

Holotype: KUN-HKAS 115558

Saprobic on dead petioles of *Trachycarpus* sp. **Sexual morph:** Undetermined. **Asexual morph:** Colonies on natural substrate superficial, effuse, velvety, tufted, dark brown. **Mycelium** immersed, composed of branched, septate, smooth, brown hyphae. **Conidiophores** 115–268 × 2.7–5.6 µm ($\bar{x}$ = 220 × 5 µm, *n* = 20), macronematous, loosely or densely fasciculate, panicle or tufted, unbranched, multiseptate, straight below, slightly flexuous above, geniculate near the apex, brown to dark brown below, brown to pale brown towards the apex, subhyaline at the tip, thick-walled, rarely with percurrent proliferations. **Conidiogenous cells** are polyblastic, integrated, terminal, sympodial, cylindrical, or slightly clavate, with minutely protruding conidiogenous scars. **Conidia** 14–19 × 7.6–10.5 µm ($\bar{x}$ = 17 × 9 µm, *n* = 50), holoblastic, acropleurogenous,

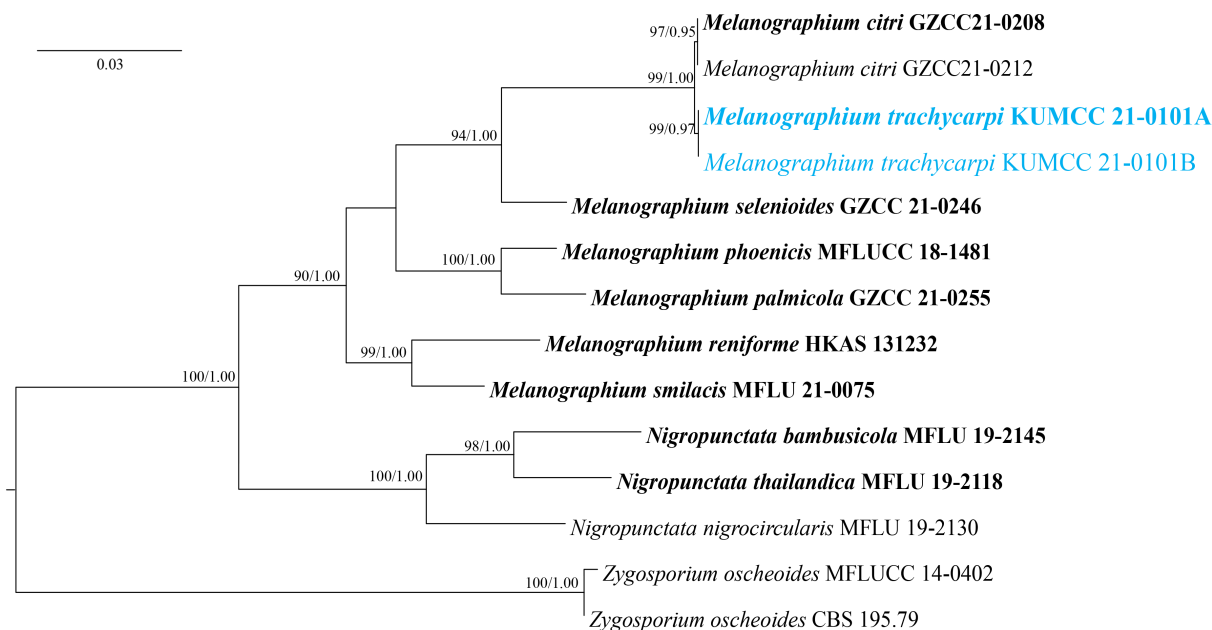


Fig. 17 Phylogram generated from Maximum Likelihood analysis based on LSU, ITS, and *rpb2* sequence data representing *Melanographium* and closely related genera. Bootstrap values for ML equal to or greater than 70% and BYPP values equal to or greater than 0.95 (rounded to two decimal places) from the BI analysis are labelled on the nodes. The newly generated sequences are in blue, and type species are in bold.

solitary, reniform or broad obovoid to semicircular, slightly curved, olivaceous brown to dark brown, aseptate, without germ-slit, verrucose or smooth-walled. Conidial secession schizolytic.

Culture characteristics: Conidiophore germinated on PDA, colony circular, flossy, velvety. Colonies after 2 weeks yellow green to green brown, flossy, velvety, entire edge, flat; reverse coloration brown to black.

Material examined: China, Yunnan, Kunming, Kunming Institute of Botany, Chinese Academy of Science, on dead petioles of *Trachycarpus* sp. (Arecaceae), 15 May 2020, S. Tibpromma, ST 45 (KUN-HKAS 115558, holotype), ex-type living culture KUMCC 21-0101.

GenBank accession numbers: KUMCC 21-0101: SSU: PV942128; ITS: PV873193; LSU: PV942115; *tef1*: PX055877; *tub2*: PX055887; *rpb2*: PX055866.

Notes: *Melanographium trachycarpi* was found on dead branches of *Trachycarpus* sp. *Melanographium trachycarpi* shares common characteristics with other *Melanographium* species, including effused and tufted colonies, loosely or densely fasciculate conidiophores, and reniform, aseptate, darkly pigmented conidia^[96–99,101,102]. Phylogenetically, *M. trachycarpi* is a sister lineage with two strains of *M. citri* (GZCC21-0208^T, GZCC21-0212) with 99% MLBS/1.00 BYPP statistical support (Fig. 17). However, *M. trachycarpi* (KUN-HKAS 115558) differs from *M. citri* (HKAS 115665, reference specimen) by having short conidiophores (115–268 µm long, 2.7–5.6 µm) with olivaceous-brown to dark-brown conidia, reniform or broad obovoid to semicircular and lacking a germ-slit, while *M. citri* has long conidiophores (130–880 µm long, 20–140 µm) with pale to dark-brown conidia, which are curved, reniform or elliptical, sometimes obovoid, with a subhyaline longitudinal germ-slit^[137]. We therefore recognize our collection as a new species, namely *M. trachycarpi*.

Discussion

At the KIB, there are over 8,000 plant species in the garden, showcasing rich biodiversity^[138]. Due to the high diversity of plant species, soil types, and often varied organic inputs, these environments support a wide range of fungi. In a previous study, several fungi were identified and introduced as new or known species, mostly found as saprobic fungi (Table 1^[139]). As KIB's garden is a

managed garden, containing diverse plant species often harbors beneficial saprobic fungi. Saprobic fungi are well known as decomposers of diverse plant litter, wood, and organic debris. Several hosts and fungi exhibit patterns that are generally non-random, influenced by evolutionary history, ecological specialization, and specific environmental factors. While some fungi are generalists, many form highly specialized relationships with specific host plants, especially within mycorrhizal networks (beneficial) and pathogenic (disease-causing) groups^[140–142]. This research study makes a significant contribution to the understanding of fungal diversity by describing two new species previously unreported and seven new host records, highlighting the rich fungal diversity at the KIB, Yunnan, China. These findings are the result of detailed morphological observations combined with multigene phylogenetic analyses (SSU, ITS, LSU, *rpb2*, *tef1*, and *tub2*), confirming the novelty and taxonomic placement of these taxa. Besides introducing them based on morphology and DNA sequences, this study presents SEM photographs of some species for the first time and provides a checklist of fungi from KIB for the years 2010–2025, which may help other researchers interested in fungi at the KIB (Table 1).

In this study, we introduced *Melanographium trachycarpi* as a new species; our new species shares common features with other *Melanographium* species, including effused and tufted colonies, loosely or densely fasciculate conidiophores, and reniform, aseptate, darkly pigmented conidia^[133–136,143,144]. Since no sequence data are available for several *Melanographium* species, we used the keys to *Melanographium* species from previous studies to identify our species, together with species with molecular data^[135–137,144,145]. We found that our collection resembles *M. palmicola* and *M. spinulosum* (loose conidiophore with length < 1,000 µm)^[133,135]. Conidia of *M. palmicola* are ellipsoidal, obovoid or subcymbiform, dark olivaceous-brown, and smaller (15–18 × 8–10 µm); while *M. spinulosum* has 17–23 × 11–15 µm, obovoid, dark reddish-brown conidia^[133,135]. Conidia in our collection measure 14–19 × 7.6–10.5 µm and are reniform or broad obovoid to semicircular, unlike those of *M. palmicola* and *M. spinulosum*. Also, phylogeny supported in our sample is well separated from other species in *Melanographium*, with a close relationship to *M. citri* (GZCC21-0208^T, GZCC21-0212), with 99% MLBS/1.00 BYPP statistical support (Fig. 17).

Phylogenetically comparable to the genus *Neohendersonia*, *N. camelliae* is introduced here as a new species with sexual morph, based on phylogenetic analyses of a combined SSU, ITS, LSU, *rpb2*, and *tef1* dataset and nucleotide comparisons. *Splanchnonema-loricatum* was considered the sexual morph of *N. kickxii*, which is characterized by large ascomata with a thick-walled peridium, but there is no unequivocal evidence for this sexual-asexual connection^[146]. The sexual morph of *N. camelliae* fits well with the generic description of the sexual morph of Neohendersoniaceae and has many more similar characteristics to members of *Crassiparies*^[93,94]. However, they are similar in morphology but can be well separated in phylogeny, and this is the first sexual morph in the genus (Fig. 5). In Fig. 7, there are two points discussed. First, two strains of *Magnibotryascoma mali* are not grouped with the type strain, as discussed in the notes of *M. mali* section. Second, *Teichospora* members are also shown not to group together, instead forming two distinct clades. These results are similar to other publications that *Teichospora* did not group together but still clustered within Teichosporaceae^[137,147,148]. With this problem, the natural generic delimitation of this genus needs to be resolved in the future through taxonomic and phylogenetic studies. Additionally, in this study, we identified another sample of *Apiospora yunnana* collected from bamboo in Yunnan, China. However, two additional collections, including the holotype, were also found on bamboo in

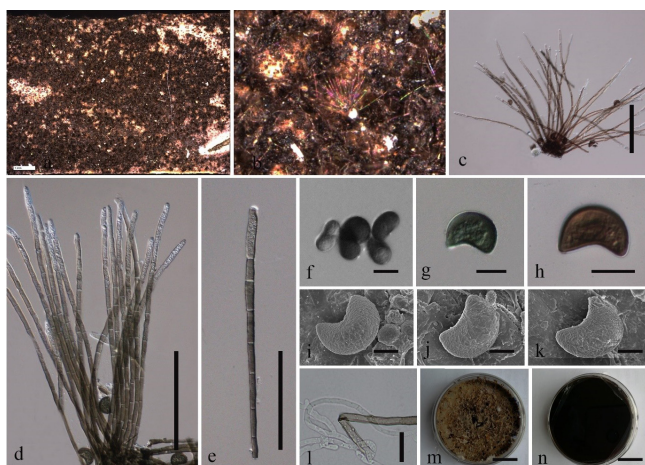


Fig. 18 *Melanographium trachycarpi* (KUN-HKAS 115558, holotype). (a), (b) Colonies on the host surface. (c)–(e) Conidiophores. (f)–(k) Conidia; (l)–(n) SEM photos. (l) Germinated conidiophore. (m) Upper view on PDA. (n) Reverse view on PDA. Scale bars: (c), (d), (e) = 100 µm; (f)–(h), (l) = 10 µm; (i)–(k) = 5 µm; (m), (n) = 2 µm.

Table 1. Checklist of fungi collected from KIB (from 2010–2025).

Species name	New taxa/ known taxa	Host/substrate	Life mode	Ref.
Ascomycota				
<i>Alternaria alternata</i>	Known	<i>Magnolia grandiflora</i>	Saprobic	Jayasiri et al. ^[149]
<i>Arthrinium yunnanum</i>	New	<i>Phyllostachys nigra</i>	Saprobic	Dai et al. ^[106]
<i>Austropleospora keteleeriae</i>	New	<i>Keteleeria fortunei</i>	Saprobic	Jayasiri et al. ^[149]
<i>Bartalinia kunmingensis</i>	New	<i>Zea mays</i>	Saprobic	Phookamsak et al. ^[150]
<i>Brunneofusispora sinensis</i>	Known	<i>Magnolia denudata</i>	Saprobic	Wanasinghe et al. ^[139]
<i>Brunneomurispora lonicerae</i>	New	<i>Lonicera maackii</i>	Saprobic	Phookamsak et al. ^[150]
<i>Camporesiomyces mali</i>	New	<i>Malus halliana</i>	Saprobic	Hyde et al. ^[144]
<i>Ceratospaeria yunnanensis</i>	New	<i>Heteropanax fregans</i>	Saprobic	Manawasinghe et al. ^[151]
<i>Cladosporium cladosporioides</i>	Known	<i>Magnolia grandiflora</i>	Saprobic	Jayasiri et al. ^[149]
<i>Diatrypella yunnanensis</i>	New	Unidentified plant	Saprobic	Hyde et al. ^[144]
<i>Diatrypella yunnanensis</i>	New	Unidentified plant	Saprobic	Hyde et al. ^[144]
<i>Didymella coffeae-arabicae</i>	Known	<i>Leucaena</i> sp.	Saprobic	Jayasiri et al. ^[149]
<i>Didymella magnoliae</i>	New	<i>Magnolia grandiflora</i>	Saprobic	Jayasiri et al. ^[149]
<i>Diplodia magnoliigena</i>	New	<i>Magnolia grandiflora</i>	Saprobic	Jayasiri et al. ^[149]
<i>Hysterobrevium constrictum</i>	Known	Unidentified plant	Saprobic	Hyde et al. ^[144]
<i>Keissleriella caraganae</i>	New	<i>Caragana arborescens</i>	Saprobic	Phookamsak et al. ^[150]
<i>Liua muriformis</i>	New	<i>Lonicera maackii</i>	Saprobic	Phookamsak et al. ^[150]
<i>Lonicericola hyaloseptispora</i>	New	<i>Lonicera maackii</i>	Saprobic	Phookamsak et al. ^[150]
<i>Montagnula aquilariae</i>	Known	Unidentified plant	Saprobic	Wanasinghe et al. ^[152]
<i>Montagnula thevetiae</i>	New	<i>Thevetia peruviana</i>	Saprobic	Wanasinghe et al. ^[152]
<i>Murilentithecia lonicerae</i>	New	<i>Lonicera maackii</i>	Saprobic	Phookamsak et al. ^[150]
<i>Neofusicoccum parvum</i>	Known	<i>Magnolia grandiflora</i>	Saprobic	Jayasiri et al. ^[149]
<i>Neoleptospora camporesiana</i>	New	<i>Heteropanax fragrans</i>	Saprobic	Manawasinghe et al. ^[151]
<i>Neosetophoma lonicerae</i>	New	<i>Lonicera maackii</i>	Saprobic	Phookamsak et al. ^[150]
<i>Nigrograna magnoliae</i>	New	<i>Magnolia denudata</i>	Saprobic	Wanasinghe et al. ^[152]
<i>Nothophoma quercina</i>	Known	<i>Keteleeria fortunei</i>	Saprobic	Jayasiri et al. ^[149]
<i>Paratrimmatostroma kunmingensis</i>	New	Fern	Saprobic	Phookamsak et al. ^[150]
<i>Paucispora kunmingense</i>	New	<i>Malus halliana</i> (Rosaceae)	Saprobic	Hyde et al. ^[153]
<i>Periconia byssoides</i>	Known	<i>Prunus armeniaca</i>	Saprobic	Yang et al. ^[154]
<i>Periconia byssoides</i>	Known	<i>Magnolia grandiflora</i>	Saprobic	Jayasiri et al. ^[149]
<i>Periconia chimonanthei</i>	New	<i>Chimonanthe praecox</i>	Saprobic	Yang et al. ^[154]
<i>Periconia cortaderiae</i>	Known	<i>Caragana arborescens</i>	Saprobic	Phookamsak et al. ^[150]
<i>Periconia kunmingensis</i>	New	Fern	Saprobic	Phookamsak et al. ^[155]
<i>Phaeopoacea muriformis</i>	New	unidentified grass species	Saprobic	Hyde et al. ^[153]
<i>Phaeosphaeria chinensis</i>	New	<i>Wisteria</i> sp.	Saprobic	Jayasiri et al. ^[149]
<i>Phaeoseptum mali</i>	New	<i>Malus halliana</i>	Saprobic	Phookamsak et al. ^[156]
<i>Phaeosphaeria cycadis</i>	New	<i>Cycas</i> sp.	Leaf spots	Phookamsak et al. ^[150]
<i>Phaeosphaeriopsis aloes</i>	Known	<i>Yucca elephantipes</i>	Saprobic	Boonmee et al. ^[157]
<i>Phragmocamarosporium hederarum</i>	Known	<i>Cycas</i>	Leaf spots	Phookamsak et al. ^[150]
<i>Plectosphaerella kunmingensis</i>	New	Water agar as a contaminated fungus	Unknown	Phookamsak et al. ^[150]
<i>Plenodomus artemisiae</i>	New	<i>Artemisia</i> sp.	Saprobic	Phookamsak et al. ^[150]
<i>Pseudolachnella tengii</i>	New	<i>Phyllostachys</i> sp.	Saprobic	Wu & Diao ^[64]
<i>Pleurotheciella dimorphospora</i>	New	<i>Malus</i> sp.	Saprobic	Boonmee et al. ^[157]
<i>Pseudochaetosphaeronema kunmingense</i>	New	<i>Cerasus pseudocerasus</i>	Saprobic	Hyde et al. ^[144]
<i>Pseudopithomyces chartarum</i>	Known	<i>Magnolia grandiflora</i>	Saprobic	Jayasiri et al. ^[149]
<i>Pseudopithomyces kunmingensis</i>	New	unidentified grass species	Saprobic	Abreu et al. ^[153]
<i>Rhytidhysterium camporesii</i>	New	Unidentified plant	Saprobic	Hyde et al. ^[144]
<i>Sclerostagonospora rosae</i>	New	<i>Rosa</i> sp.	Saprobic	Wanasinghe et al. ^[158]
<i>Septoriella neomuriformis</i>	New	unidentified grass	Saprobic	Wanasinghe & Mharachchikumbura ^[159]
<i>Shearia formosa</i>	Known	<i>Magnolia denudata</i>	Saprobic	Wanasinghe et al. ^[139]
<i>Sparticola muriformis</i>	New	unidentified grass	Saprobic	Karunaratna et al. ^[160]
<i>Sphaerellopsis paraphysata</i>	Known	<i>Liriope spicata</i>	Rust on living leaves	Phookamsak et al. ^[150]
<i>Stagonosporopsis pini</i>	New	<i>Pinus</i> sp.	Saprobic	Jayasiri et al. ^[149]
<i>Stomiopeltis chinensis</i>	New	<i>Harpephyllum</i> sp.	Saprobic	Jayasiri et al. ^[149]
<i>Tetraploa bambusae</i>	New	Bamboo	Saprobic	Phookamsak et al. ^[161]
<i>Thyronectria kunmingensis</i>	New	unidentified plant	Saprobic	Tun et al. ^[162]
<i>Torula ficus</i>	Known	<i>Magnolia grandiflora</i>	Saprobic	Jayasiri et al. ^[149]
<i>Torula gaodangensis</i>	Known	<i>Malus</i> sp.	Saprobic	Hyde et al. ^[144]
<i>Torula mackenziei</i>	Known	Unidentified plant	Saprobic	Boonmee et al. ^[157]

(to be continued)

Table 1. (continued)

Species name	New taxa/ known taxa	Host/substrate	Life mode	Ref.
<i>Vaginatisspora fuckelii</i>	Known	<i>Rosa</i> sp.	Saprobic	Hyde et al. ^[153]
<i>Wojnowiciella kunmingensis</i>	New	<i>Lonicera maackii</i>	Saprobic	Phookamsak et al. ^[150]
<i>Basidiomycota</i>				
<i>Amanita cingulata</i>	New	-		Liu et al. ^[163]
<i>Amanita exitialis</i>	New	Soil in forests dominated by Fagaceae		Cai et al. ^[164]
<i>Amanita flavipes</i>	Known	On soil in woodland		Cai et al. ^[165]
<i>Amanita fuliginea</i>	Known	On soil in forests dominated by Fagaceae		Cai et al. ^[164]
<i>Amanita fuligineoides</i>	Known	On soil in forests dominated by Fagaceae		Cai et al. ^[164]
<i>Amanita griseorosea</i>	New	Forests of Fagaceae		Cai et al. ^[164]
<i>Amanita manginiana</i>	Known	-		Cai et al. ^[165]
<i>Amanita molliuscula</i>	New	On soil under trees of <i>Pinus</i> and <i>Quercus</i>		Cai et al. ^[164]
<i>Amanita pallidorosea</i>	Known	On soil in forests of Pinaceae and Fagaceae		Cai et al. ^[164]
<i>Amanita parvixitialis</i>	New	Forests dominated by Fagaceae		Cai et al. ^[164]
<i>Amanita pseudoporphyraria</i>	Known	In woodland of <i>Coniferae</i>		Cai et al. ^[165]
<i>Amanita rimosa</i>	Known	Soil in forests dominated by Fagaceae		Cai et al. ^[164]
<i>Amanita</i> sp. (<i>Phalloideae</i>)		-		Cai et al. ^[165]
<i>Amanita subfuliginea</i>	New	On soil in forests of Fagaceae and <i>Pinus</i>		Cai et al. ^[164]
<i>Amanita subpallidorosea</i>	Known	On soil in forests dominated by <i>Quercus</i> and <i>Cyclobalanopsis</i>		Cai et al. ^[164]
<i>Amanita virosa</i>	Known	On soil in forests of Pinaceae and Fagaceae		Cai et al. ^[164]
<i>Apiculospora spartii</i>	Known delete (new host and geographical record)	Dead leaves of <i>Yucca gigantea</i>	Saprobic	Wijayawardene et al. ^[166]
<i>Cantharellus phloginus</i>	New	On soil, associated with <i>Castanopsis</i> and <i>Pinus</i>		Shao et al. ^[167]
<i>Cantharellus vaginatus</i>	New	Under mixed forest dominated by <i>Castanopsis</i> and <i>Pinus</i>		Shao et al. ^[168]
<i>Cantharellus zangii</i>	New	On ground in subalpine mixed forests dominated by <i>Larix potaninii</i> var. <i>macrocarpa</i> , and <i>Picea likiangensis</i>		Tian et al. ^[169]
<i>Chiua angusticystidiata</i>	New	On soil		Wu et al. ^[170]
<i>Chiua olivaceoreticulata</i>	New	On soil		Wu et al. ^[170]
<i>Chiua virens</i>	New	-		Wu et al. ^[170]
<i>Chiua viridula</i>	New	On soil		Wu et al. ^[170]
<i>Cibaomyces glutinis</i>	New	On buried rotten wood in broad-leaved forests dominated by Fagaceae		Hao et al. ^[171]
<i>Cyptotrama glabra</i>	New	On rotten wood of broad-leaved trees		Qin & Yang ^[172]
<i>Flammulina velutipes</i> var. <i>filiformis</i>	New	On base of dead trunk	Saprobic	Ge et al. ^[173]
<i>Flammulina velutipes</i> var. <i>himalayana</i>	New	On base of dead trunk of Betulaceae	Saprobic	Ge et al. ^[173]
<i>Flammulina yunnanensis</i>	New	On dead trunk of <i>Lithocarpus</i> or <i>Quercus</i>		Ge et al. ^[174]
<i>Hymenoboletus filiformis</i>	New	On soil, associated with <i>Lithocarpus</i> and <i>Castanopsis</i>		Li & Yang ^[175]
<i>Hymenoboletus griseoviridis</i>	New	On soil, associated with Fagaceae		Li & Yang ^[175]
<i>Hymenoboletus jiangxiensis</i>	New	On soil, associated with Fagaceae		Li & Yang ^[175]
<i>Hymenoboletus luteopurpureus</i>	New	On soil		Wu et al. ^[170]
<i>Paraxerula ellipsospora</i>	New	In forests dominated by <i>Pinus</i>		Qin et al. ^[176]
<i>Physalacria corneri</i>	New	On rotten trunk of broad-leaved trees		Qin & Yang ^[172]
<i>Physalacria lacrymispora</i>	New	On dead culm of <i>Chimonobambusa</i>	Saprobic	Qin & Yang ^[172]
<i>Physalacria sinensis</i>	New	On rotten wood of <i>Quercus variabilis</i>		Qin & Yang ^[172]
<i>Pseudolepiota zangmui</i>	New	In mixed broadleaved forest of Fagaceae		Ge & Yang ^[177]
<i>Rhodotus asperior</i>	New	On dead trunk in forest dominated by <i>Castanopsis</i> and <i>Lithocarpus</i>		Tang et al. ^[178]
<i>Suillus alpinus</i>	New	On ground under <i>Larix potaninii</i>		Shi et al. ^[179]
<i>Tuber baoshanense</i>	New	-		Wan et al. ^[180]
<i>Tuber calosporum</i>	New	In soil under mixed forest with <i>Pinus yunnanensis</i>		Wan et al. ^[181]
<i>Tuber polymorphosporum</i>	New	In soil		Wan et al. ^[180]
<i>Tuber shidianense</i>	New	In humus soil under mixed forest with <i>Pinus yunnanensis</i>		Wan et al. ^[181]
<i>Tuber sinoniveum</i>	New	In humus soil under <i>Pinus armandii</i>		Xu et al. ^[182]
<i>Tylocinum griseolum</i>	New	On soil		Wu et al. ^[170]
<i>Zangia chlorinosma</i>	New	-		Li & Yang ^[175]
<i>Zangia erythrocephala</i>	New	In mixed forests of <i>Picea</i> , <i>Pinus</i> , and <i>Quercus aquifolioides</i>		Li & Yang ^[175]
<i>Zangia olivacea</i>	New	In mixed forests of <i>Picea</i> , <i>Pinus densata</i> , and <i>Quercus semicarpifolia</i>		Li & Yang ^[175]

(to be continued)

Table 1. (continued)

Species name	New taxa/ known taxa	Host/substrate	Life mode	Ref.
<i>Zangia olivaceobrunnea</i>	New	In mixed forests of <i>Keteleeria</i> , <i>Pinus yunnanensis</i> , and <i>Quercus variabilis</i>		Li & Yang ^[175]
<i>Zangia roseola</i>	New combinations	<i>Pinus yunnanensis</i>		Li & Yang ^[175]

Remark: all taxa were kept the same name when they were introduced.

China^[106,108]. Therefore, future research should examine whether this species exhibits host specificity, referring to a fungus's ability to infect, colonize, or establish relationships with particular host organisms (Poaceae). In this study, we also identified known species (*Botryosphaeria dolichospermatis* and *Pseudolachnella tengii*) that have been reported only in asexual morphs in their life cycles. This study reported, for the first time, another advantage of their sexual morphology, with the potential to further enrich our knowledge.

Our study provides important insights into fungal diversity at the KIB, Yunnan, China, and highlights the need for further research. Expanding the sampling scope in the KIB area may reveal additional species or shed light on the distribution patterns of the taxa identified here. Additionally, future research should focus on the genetic diversity of these species across populations to explore potential intraspecific variation. Advanced molecular techniques such as whole-genome sequencing could provide deeper insights into their evolutionary history and functional capabilities.

In conclusion, this study significantly expands the known diversity of the classes Dothideomycetes and Sordariomycetes, enriching our understanding of fungal diversity in Yunnan Province, China (especially the KIB), by describing two new species and seven new records. These findings not only enhance our knowledge of the fungal taxonomy and phylogeny of these groups but also highlight the biogeographical importance of KIB as a biodiversity hotspot. Therefore, the continuous exploration of the fungal diversity of this area is crucial for uncovering undiscovered taxa, and our study underscores the need for ongoing exploration and conservation of this unique area.

Author contributions

The authors confirm their contribution to the paper as follows: study conception and design, data collection, draft manuscript preparation: Tibpromma S, Jayasiri SC, Xu RF, Liu R, Lu L, Karunarathna SC; analysis and interpretation of results: Tibpromma S, Jayasiri SC, Xu RF, Liu R, Karunarathna SC; review and editing: Jiang HB, Bhat J, Dawoud TM, Dai DQ, Tarafder E, Kumla J, Xu J; draft manuscript preparation: Wariss HM. All authors reviewed the results and approved the final version of the manuscript.

Data availability

The data generated for this study are available in NCBI, Index Fungorum, and Facesoffungi databases.

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Conflict of interest

The authors declare that they have no conflict of interest.

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