

Microfungi associated with grassland ecosystems in Yunnan, Southwest China

Gao Y^{1,5,6,9}, Wanasinghe DN^{2*}, Liu LL³, Tibpromma S⁴, Karunarathna SC⁴, Dissanayake LS^{1,9}, Eungwanichayapant PD⁵, Sun ZY^{1,7}, Cai LL⁸, Xu JC^{1,9}, Faraj T², Jayawardena RS^{5,6}, Hyde KD^{1,2,10*}, Gui H^{1,7,9,11*}.

¹Department of Economic Plants and Biotechnology, Yunnan Key Laboratory for Wild Plant Resources, Kunming Institute of Botany, Chinese Academy of Sciences, Kunming 650201, P.R. China

²Department of Soil Science, College of Food and Agriculture Sciences, King Saud University, Riyadh 11362, Saudi Arabia

³State Key Laboratory for Tea Plant Germplasm Innovation and Resource Utilization, School of Tea Science, Anhui Agricultural University, Hefei-230036, China

⁴Center for Yunnan Plateau Biological Resources Protection and Utilization & Yunnan International Joint Laboratory of Fungal Sustainable Utilization in South and Southeast Asia, College of Biology and Food Engineering, Qujing Normal University, Qujing 655099, China

⁵School of Science, Mae Fah Luang University, Chiang Rai 57100, Thailand

⁶Center of Excellence in Fungal Research, Mae Fah Luang University, Chiang Rai 57100, Thailand

⁷University of Chinese Academy of Sciences, Beijing 100049, China

⁸School of Forestry, Southwest Forestry University, Kunming 650224, China

⁹Centre for Mountain Futures (CMF), Kunming Institute of Botany, Chinese Academy of Sciences, Kunming, 650201, P.R. China

¹⁰Department of Botany and Microbiology, College of Science, King Saud University, P.O. Box 22452, Riyadh 11495, Saudi Arabia

¹¹State Key Laboratory of Plant Diversity and Specialty Crops, Xiangshan, Haidian, Beijing 100093, China

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Abstract

During a survey of microfungi associated with grassland vegetation in Yunnan Province, China, various fungal taxa belonging to Dothideomycetes and Sordariomycetes were isolated. This study presents detailed morphological descriptions, illustrations, and multigene phylogenetic analyses of those fungal species to understand their taxonomic placements. Based on 138 fungal collections, the present work introduces a new genus (*Keisslerielloides*), 31 new species, four new combinations, the first sexual morph record for two species, the first asexual morph record for four species, both morphs for three species, and new host or geographic records for 47 species. Among them, *Apiospora poacearum*, *Camarosporioides kunmingensis*, *Dinemasporium poacearum*, *Epicoccum kunmingense*, *Heterosporicola qujingensis*, *Keissleriella graminicola*, *K. lolii*, *K. zhaotongensis*, *Leptosphaeria chinensis*, *Massarina yunnanensis*, *Neoascochyta zhaotongensis*, *Ne. dactylidis*, *Nigrospora dactylidis*, *Occultithea yunnanensis*, *Ophiobolopsis dipsaci*, *O. poacearum*, *Paraophiobolus bidentis*, *Periconia poacearum*, *P. todei*, *Phaeosphaeria kunmingensis*, *Ph. lolii*, *Pseudocyclothyriella lolii*, *Ps. yunnanensis*, *Pseudolophiostoma kunmingense*, *Schizothecium dactylidis*, *Septoriella graminearum*, *S. longispora*, *S. yunnanensis*, *S. zhaotongensis*, *Setophoma dactylidis*, and *Stagonospora dactylidis* are introduced as new Ascomycota species. The new combinations are *Keisslerielloides bambusicola* (= *Keissleriella bambusicola*), *K. caraganae* (= *Keissleriella caraganae*), *K. yonaguniensis* (= *Keissleriella*

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***Corresponding Author:** Wanasinghe DN – dnadeeshan@gmail.com, Kevin D. Hyde – e-mail – kdhyde3@gmail.com, Heng Gui – e-mail – guiheng@mail.kib.ac.cn

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yonaguniensis), *K. yunnanensis* (= *Keissleriella yunnanensis*). We also introduce new host or geographical records for *Apiospora arundinis*, *A. locuta-pollinis*, *A. rasikravindrae*, *Aplosporella javeedii*, *Astrocystis sublimbata*, *Catenuliconidia uniseptata*, *Comoclathris sedi*, *Cucurbitaria lijiangensis*, *Dinemasporium americanum*, *Discosia macrozambiae*, *Epicoccum dendrobii*, *E. mackenziei*, *E. viciae-villosae*, *Floricola sulcata*, *Keissleriella gloeospora*, *K. poagena*, *Keisslerielloides yunnanensis*, *Letendreaa helminthicola*, *Lophiopoacea paramacrostoma*, *Montagnula shangrilana*, *Neoascochyta humicola*, *Neoleptospora camporesiana*, *N. fusiformispora*, *Occultibambusa jonesii*, *Ophiosphaerella aquatica*, *Paraphaeosphaeria michotii*, *Periconia cortaderiae*, *P. wurfbainiae*, *Phaeosphaeria septata*, *Ph. tabebuiae*, *Phaeosphaeriopsis aloes*, *Pha. grevilleae*, *Plenodomus artemisiae*, *Pl. sinensis*, *Praeclarispora herbicola*, *Pseudopithomyces chartarum*, *Ps. rosae*, *Sclerostagonospora rosae*, *Septoriella paradactylidis*, *S. tridentina*, *S. vagans*, *Stagonospora poaceicola*, *Torula chromolaenae*, *T. fici*, *Tremateia arundicola*, *Truncatella angustata*, and *Xylaria xylarioides*. The new sexual/asexual links are reported in *Keissleriella gloeospora*, *Neoascochyta humicola*, *Paraphaeosphaeria michotii*, *Phaeosphaeriopsis grevilleae*, *Praeclarispora herbicola*, *Pseudocyclothyriella lolii*, and *Stagonospora poaceicola*. This study enhances the understanding of microfungal diversity in grassland ecosystems and highlights the rich, yet understudied, fungal biodiversity of Yunnan Province.

Keywords – 4 new combinations – 32 new taxa – 47 new records – Dothideomycetes – Sordariomycetes – Taxonomy

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INTRODUCTION

As decomposers, pathogens, and mutualists, fungi play an essential role in ecosystem functions (Carris et al. 2012, Sun et al. 2019, Hyde et al. 2020a, Niego et al. 2023a, b, Nimalrathna et al. 2025). According to the latest research, fungi comprise 19 phyla, 83 classes, 1,220 families, 10,685 genera, and 140,000 known species (Hyde et al. 2024a). However, the estimated fungal species could be 1.5 to 3.8 million, with a “best estimate” at 2.5 million fungal species (Niskanen et al. 2023, Hyde et al. 2024b). The emergence of modern molecular methods has significantly accelerated fungal research in recent years, leading to many new taxonomic discoveries being reported from diverse substrates such as grassland ecosystems, soil, and freshwater (Boonmee et al. 2021, Maharachchikumbura et al. 2021b, Hyde et al. 2023a, Leifheit et al. 2024). In Asia, there has been a notable growth in mycology studies and associated publications (Hyde et al. 2020a).

Especially in Yunnan Province, China, Feng & Yang (2018) indicated that Yunnan possesses an extremely rich diversity of higher fungi, with approximately 104,000 species potentially existing, however, only around 6,000 species have been described, including about 3,000 species of higher fungi (Ascomycota and Basidiomycota). This suggests that only a small portion of the known species in the province have been described. Wang et al. (2021) documented many new fungal species from Yunnan Province, bringing the total to more than 1,300, accounting for nearly 25% of the total number of fungal species in China. This supports Hyde et al. (2018, 2020a), who stated that continued exploration of new environments, aided by modern methods, would result in the description of many more taxa, providing a promising future for mycology.

Grasslands, the largest terrestrial ecosystems, cover approximately 40% of the land area in China and around 25% of the terrestrial surface of the Earth (Chen et al. 2023). They play a crucial role in reducing soil erosion, preserving biodiversity, regulating the climate, and storing carbon (Bengtsson et al. 2019). Additionally, grasslands serve as vital carbon and biomass reservoirs, containing over 10% of the terrestrial biomass on Earth and 20% of the global soil carbon (Korth et al. 2015, Chen et al. 2019), thus having a significant influence on the carbon and water cycles of terrestrial ecosystems. Grasslands are a biome characterized by periodic drought, with grasses and herbaceous plants predominant (Rogers 1979). Key benefits of grasslands are: (1) Grasslands host a vast array of plant and animal species, contributing to global biodiversity, this diversity ensures ecosystem resilience and provides resources for food, medicine, and cultural practices (Söderström et al. 2001, Parr et al. 2014, Bengtsson et al. 2019, Petermann & Buzhdygan 2021, Kose et al.

2022); (2) Grasslands are vital grazing grounds for livestock, forming the backbone of agriculture and pastoralism in many regions. They provide nutritious forage that is essential for the health and productivity of animals, thereby supporting the livelihoods of the farmers and pastoralists, and food security (O'Mara 2012, Bengtsson et al. 2019, Su et al. 2023, Wu et al. 2023); (3) Grasslands play a crucial role in mitigating climate change by sequestering carbon in their soils. The carbon stored in grassland ecosystems helps regulate the global carbon cycle, which is important for reducing the impacts of greenhouse gases and maintaining a stable climate (Kerlin 2018, Bai & Cotrufo 2022, Liu et al. 2023a); (4) Grasslands contribute significantly to the regulation of water cycles by influencing water infiltration and storage, to reduce the risks of both floods and droughts by moderating runoff and improving groundwater recharge (Bilotta et al. 2008, Bilotta et al. 2010, Joyce et al. 2016).

Most research has primarily concentrated on the grasslands of northern China due to their significant regional and global importance, while studies on grasslands in southwest China remain relatively scarce (Yan et al. 2019, Chen et al. 2023, Xu et al. 2023, Fang et al. 2025, Wanasinghe et al. 2025). Yunnan province, located at the crossroads of the Himalayan mountains and the Southeast Asian peninsula, boasts a wide variety of grassland and plant community types (Cheng et al. 2022). As the second-largest grassland area in southern China, Yunnan plays a crucial role in the regional carbon cycle (Cheng et al. 2022). Most researchers focus on the interaction between climate and grasslands, whereas studies on microfungi associated with grasslands are relatively scarce (Cheng et al. 2022, Cao et al. 2022, Zhang et al. 2023, Qin et al. 2024, Fang et al. 2025). In the grasslands of Yunnan Province, China, diverse vegetation provides the primary carbohydrate source and fodder for livestock. Within the grassland biome, various organisms, including herbivorous mammals, insects, fungi (saprobic, pathogenic, and symbiotic), play crucial roles in sustaining biomass and biodiversity (Karunarathna et al. 2021). Specifically, fungi play a vital role in maintaining and shaping the ecosystem, with each fungal community associated with grassland vegetation contributing to specific ecological functions (Karunarathna et al. 2022). Fungi are highly responsive to environmental shifts and global warming, potentially leading to the extinction of numerous species unable to adapt quickly to the pace of ecological transformation (Wanasinghe et al. 2022). To address species loss and understand their ecological importance, comprehensive fungal sampling across diverse grasslands in various geographic areas is critically needed. Consequently, we are conducting ongoing surveys of grassland-associated microfungi in Yunnan, China.

Saprobic fungi are important decomposers in ecosystems, playing a crucial role in nutrient cycling, soil improvement, and the maintenance of plant biodiversity (Niego et al. 2023a, b). They secrete enzymes to break down organic materials, releasing mineral nutrients into the surrounding soil, thereby improving soil fertility (Kubicek & Druzhinina 2007). Saprobic fungi play an important role in degrading lignocellulose, the most abundant terrestrial organic material, and are critical for facilitating carbon cycling in nature (Vos et al. 2021).

In this study, we conducted molecular sequence data analysis and detailed morphological descriptions of grassland-associated microfungi in Yunnan Province, China. This integrated approach, designed to significantly enhance existing knowledge and facilitate future research, has yielded remarkable findings. We have collected numerous fungal specimens representing diverse families within the Ascomycota. Saprobes are collected from four different locations, and our findings include the documentation of 31 novel species, a new genus, three new combinations, and new host associations and geographic distribution records for 47 previously described species. This research represents the most comprehensive effort to fill the knowledge gap regarding the diversity, taxonomy, and phylogeny of microfungi in the grasslands of Yunnan.

MATERIALS AND METHODS

Sample collection, isolation, and morphological examination

Samples were collected from different sites of grasslands in Yunnan Province, China, during 2020–2022 (Fig. 1). The host plants were identified by a thorough process that involved observing their morphological features, such as leaves, flowers, seeds, and root systems, in combination with the book Flora of China series by Wu & Chen (2004). In addition, using plant databases and identification tools, such as the Flora of China database and plant image recognition systems, for online query and comparison, comparing with herbarium specimens, and consulting with botanists or plant experts added layers of assurance to the identification process. Visible fungal fruiting bodies growing on plants were collected from the grasslands. Specimens were stored in plastic zip-lock or paper bags and returned to the mycology laboratory at the Kunming Institute of Botany. Samples were examined using an Olympus SZ-61 (Tokyo, Japan) dissecting microscope. Fungal fruiting structures were manually sectioned and mounted in water on a slide for microscopic observation. Micro-morphological characteristics were examined using a Nikon ECLIPSE Ni-U 80i (Tokyo, Japan) compound microscope with differential interference contrast (DIC) and phase contrast (PC) illumination. Photos of microscopic structures were captured using a Nikon DS-Ri2 camera. Fungal colonies were photographed by a digital phone camera (iPhone 8, Apple Inc., US). Photoplates and measurements were processed using Adobe Photoshop CS6 Extended version 13.0.1 (Adobe Systems, CA, USA). $L/W = (L_{\min} + L_{\max}) / (W_{\min} + W_{\max})$, where, for a given taxon and a given micromorphological structure, $L_{\min}$ and $L_{\max}$ stand for the length minimum and maximum dimensions, respectively, and $W_{\min}$ and $W_{\max}$ stand for the width minimum and maximum dimensions, respectively (Pereira & Phillips 2024). Single spore isolation of conidia or ascospores was conducted, and germinated spores were processed by following the methods described in Senanayake et al. (2020a). Pure cultures were grown in potato dextrose agar (PDA) medium at 27°C. The living cultures were deposited in duplicates, which were maintained at the China General Microbiological Culture Collection Center (CGMCC) and the Culture Collection of Kunming Institute of Botany (KUNCC). Herbarium specimens were deposited in the herbarium of the Kunming Institute of Botany, Academia Sinica (HKAS). The new taxa have been registered and can be referenced using their Index Fungorum and Faces of Fungi (FoF) numbers (Jayasiri et al. 2015, Index Fungorum 2025). Taxonomic novelties were introduced using a polyphasic approach that integrates morphological, molecular, and ecological data, in line with contemporary taxonomic standards (Jayawardena et al. 2021, Maharachchikumbura et al. 2021a).

DNA extraction, PCR amplification, and sequencing

Fungal mycelia were scraped from two or three-weeks colonies grown on PDA at 25–27°C, and the DNA was extracted using the Biospin Fungus Genomic DNA Extraction Kit (BioFlux® Hangzhou, China) according to the manufacturer's protocol. Due to some fungal spores did not germinate, the E.Z.N.A. Forensic DNA Kit-D3591 (Omega Biotek, Inc., Norcross, Georgia) was used to extract DNA directly from fruiting bodies. Polymerase chain reactions (PCRs) were conducted to amplify regions of the small nuclear ribosomal subunit rDNA (SSU), large nuclear ribosomal subunit rDNA (LSU), internal transcribed spacer region (ITS), translation elongation factor 1- α gene (*tef1- α*), β -tubulin (*tub2*), RNA polymerase II second largest subunit (*rpb2*) and actin genes (*act*), using the following primer pairs: NS1/NS4 for SSU (White et al. 1990), LR0R/LR5 for LSU (Vilgalys & Hester 1990), ITS5/ITS4 for ITS (White et al. 1990), EF1-983F/EF1-2218R for *tef1- α* (Rehner & Buckley 2005), T1/T22 for *tub2* (O'Donnell & Cigelnik 1997), fRPB2-5F/fRPB2-7cR for *rpb2* (Liu et al. 1999) and ACT512F/ACT783 for *act* (Hsieh et al. 2005). PCR was performed in a 25 μ L reaction volume containing 12.5 μ L 2X PCR MasterMix (TIANGEN Co., Beijing, China), 8.5 μ L double-distilled water, 2 μ L genomic DNA, and 1 μ L of each forward and reverse primer (stock of 10 pM). PCR thermal cycles for SSU, LSU, ITS, *tef1- α* , *tub2*, and *rpb2*, the protocols of Gao et al. (2023, 2024). PCR products were sequenced at the Qingke Company, Yunnan Province, China, and Shanghai Sangon Biological Engineering Technology and Service Company, China. Sequences were deposited in GenBank.

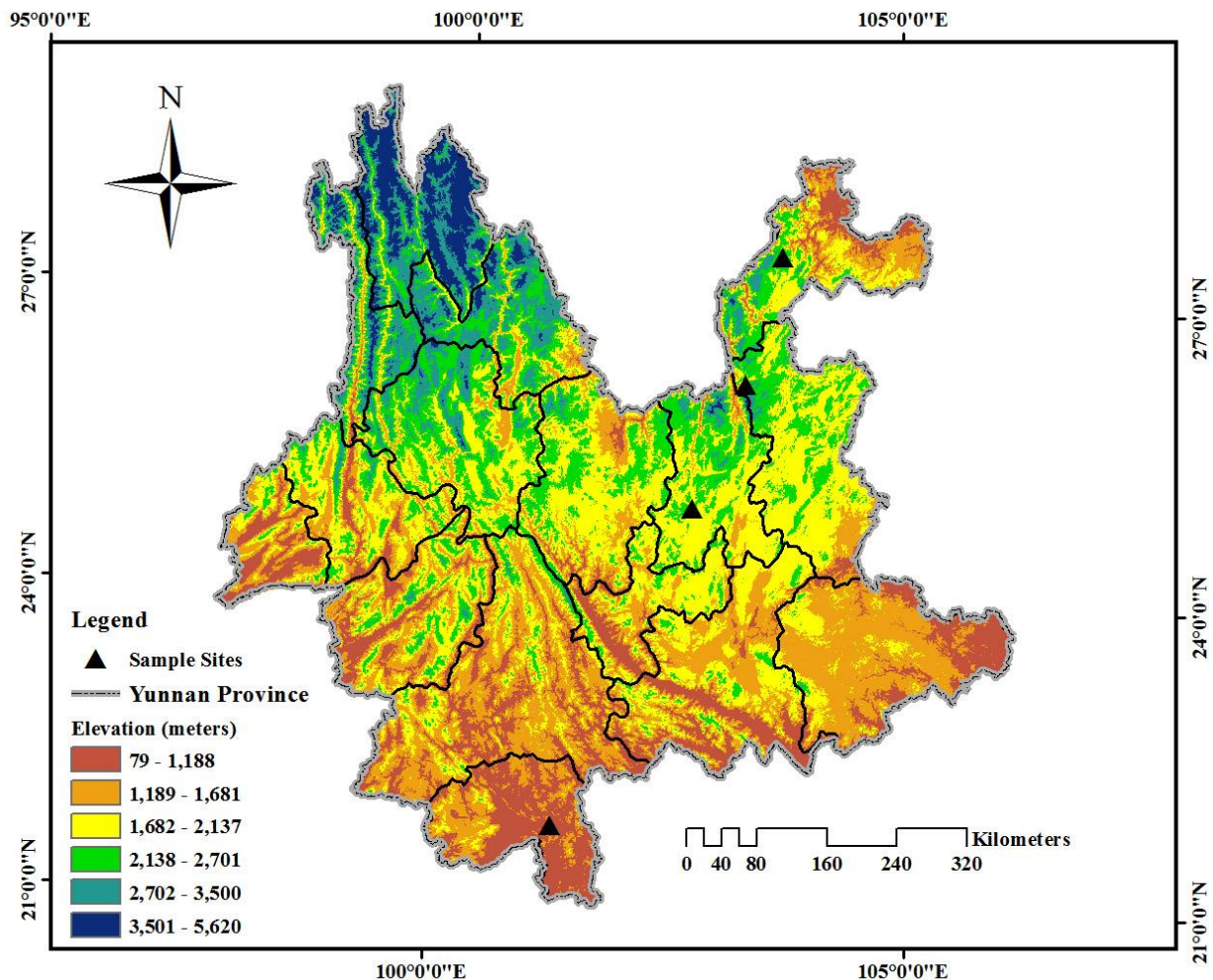


Figure 1 – Sampling locations in Yunnan, China. For each site, the elevation was extracted from the top to the bottom of the sampling sites: Zhaotong, Qujing, Kunming, and Xishuangbanna. The map was created with ArcGIS 10.8 (ESRI, Redlands, CA, USA).

Phylogenetic analyses

The quality of the original sequences was checked using BioEdit v. 7.0.5.3 (Hall 1999), and both reverse and forward sequences generated in this study were assembled with the Geneious Program (9.1.2). In our study, the newly generated assembled sequences were used for NCBI BLAST searches in GenBank (<https://blast.ncbi.nlm.nih.gov/Blast.cgi>). The BLAST search results and sequences from the latest publications were used to obtain sequence data for the phylogenetic analyses. Individual gene regions were aligned using MAFFT v.7 (<http://mafft.cbrc.jp/alignment/server/>) (Katoh et al. 2019). Sequence data trimmed with trimAL v1.2 (Capella-Gutiérrez et al. 2009). Then, multigene sequence alignments are combined by the Sequence Matrix program (1.7.8) (Vaidya et al. 2011). The FASTA files have been transferred to the format in the AliView program (Larsson 2014), PHYLIP for maximum likelihood analysis (ML), and NEXUS for Bayesian analysis (PP).

Maximum-likelihood (ML) analysis was performed via the online portal CIPRES Science Gateway v. 3.3 (Miller et al. 2010), using the RAxML-HPC v. 8 tool on XSEDE (8.2.12), with the GTRGAMMA nucleotide substitution model and 1,000 rapid bootstrap replicates. Bayesian inference analysis (PP) was performed using MrBayes v. 3.2 on the XSEDE tool on the CIPRES portal (Miller et al. 2010). The evolutionary model of nucleotide substitution for Bayesian inference analysis was selected independently for each locus using MrModeltest 2.3 (Nylander et al. 2008) via PAUP v. 4.0 b10 (Ronquist & Huelsenbeck 2003). Six simultaneous Markov chains were run

for $1 \times 10^5 - 1 \times 10^9$ generations, with trees sampled every 200 generations, until it was stopped when the standard deviation of split frequencies between the two simultaneous runs dropped below 0.01. Phylogenetic trees were visualized with FigTree v.1.4.0 (Rambaut 2012) and edited using Microsoft PowerPoint (Microsoft, 2010) and Adobe Illustrator® CS6 v.26.0 (Adobe Systems, San Jose, CA, USA).

RESULTS

Taxonomy

Ascomycota Caval.-Sm., Biol. Rev. Cambridge Philos. Soc. 73: 247 (1998)

Dothideomycetes O.E. Erikss. & Winka, Myconet 1: 5 (1997)

Botryosphaeriales C.L. Schoch, Crous & Shoemaker, Mycologia 98 (6): 1050 (2007)

Aplosporellaceae Slippers, Boissin & Crous, Stud. Mycol. 76(1): 41 (2013)

Notes – Aplosporellaceae, introduced by Slippers et al. (2013), was established to include the genera *Aplosporella* and *Bagnisiella*. *Aplosporella*, initially described by Spegazzini (1880a), was previously classified under Botryosphaeriaceae. Slippers et al. (2013) redefined this genus and assigned it to the newly proposed family Aplosporellaceae. *Bagnisiella* is recognized as a sexual genus within Aplosporellaceae, and many studies suggest that *Aplosporella* may represent its asexual morph (Hyde et al. 2012, Slippers et al. 2013, Wijayawardene et al. 2014, Verma et al. 2021). However, this link has yet to be confirmed through culture-based studies (Damm et al. 2007, Slippers et al. 2013). The sexual morphs of Aplosporellaceae are characterized by pseudothecial ascomata, predominantly multilocular, bitunicate, clavate asci that can be either stalked or sessile, with a well-developed apical chamber; and ascospores that range from hyaline to pigmented, septate or aseptate, ellipsoid to ovoid in shape (Slippers et al. 2013, Verma et al. 2021). The asexual morphs are coelomycetous, featuring uni- to multilocular pycnidial conidiomata embedded in stromatic tissue; hyaline, phialidic conidiogenous cells that proliferate percurrently or display periclinal thickening at the apex; and ellipsoid to subcylindrical conidia that are aseptate, initially hyaline, later become pigmented (Slippers et al. 2013, Verma et al. 2021).

Aplosporella Speg., Anales Soc. Ci. Argent. 10 (4): 157 (1880)

Notes – *Aplosporella* was initially described by Spegazzini (1880a), with *A. chlorostroma* as the type species. The genus comprises saprobes, plant pathogens, and endophytes (Jami et al. 2014, Fan et al. 2015, Ekanayaka et al. 2016, Dou et al. 2017, Du et al. 2017, Zhu et al. 2018). Index Fungorum (2025) records approximately 340 epithets under *Aplosporella*. This genus is characterized by multiloculate pycnidia, aseptate, brown, spinulose conidia, hyaline, fusiform, aseptate spermatia paraphyses (Du et al. 2017). *Aplosporella* was well-defined, with species described from living cultures and identified a close genetic relationship between *Aplosporella* and *Bagnisiella*, suggesting that *Bagnisiella* represents the sexual morph and should be synonymized with *Aplosporella* (Schoch et al. 2009, Slippers et al. 2013). Ekanayaka et al. (2016) described a new species, *Aplosporella thailandica*, from Thailand, which morphologically aligns with *Bagnisiella*. Phillips et al. (2019) formally recognized *Bagnisiella* as a synonym of *Aplosporella*. The most recent phylogenetic tree of *Aplosporella* species was provided by Lin et al. (2023). In this study, a new record, *Aplosporella javeedii* is introduced based on morphology and molecular data, together with description and illustrations (Fig. 3). An updated phylogenetic tree based on combined ITS, LSU, and *tef1-α* sequence data is presented in Fig. 2.

Aplosporella javeedii Jami, Slippers, M.J. Wingf. & Gryzenh., Fungal Biology 118 (2): 174 (2013)
Fig. 3

Index Fungorum number: IF803637; Facesoffungi number: FoF07383

Saprobic on a dead stem of *Sisyrinchium rosulatum* and grasses. Sexual morph: Undetermined. Asexual morph: *Conidiomata* 230–360 µm diam. × 150–210 µm high ($\bar{x}$ = 318 × 177 µm, n = 10), immersed to erumpent through host tissue, solitary or scattered, with 2–3 locules,

subglobose to globose, thick-walled, black, ostiolar neck central, with minute papilla. *Conidiomata* wall 35–70 μm wide ($\bar{x}$ = 52 μm , n = 35), comprising several layers of dark brown to black cells of *textura angularis*. *Paraphyses* 1.7–2.5 μm wide ($\bar{x}$ = 2 μm , n = 30), filiform, septate, branching, hyaline. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 8.5–15.5 $\times$ 3–5 μm ($\bar{x}$ = 11 $\times$ 3.8 μm , n = 15), cylindrical or elliptical, hyaline. *Conidia* 20–25 $\times$ 8–10 μm ($\bar{x}$ = 22 $\times$ 9 μm , n = 25), ellipsoid or oval to reniform, aseptate, hyaline when immature, becoming brown to dark brown with finely verruculose walls observed clearly when mature. Asexual morph on PDA (Fig. 3, p–s): *Conidiomata* pycnidial, gregarious, semi-immersed or bulging on mycelial surface, globose to subglobose, dark brown to black. *Conidiophores* septate, subcylindrical, simple or rarely branched at base, hyaline to subhyaline. *Conidiogenous cells* are holoblastic, discrete, cylindrical, smooth-walled, hyaline. *Conidia* 18–23 $\times$ 8–10 μm ($\bar{x}$ = 20 $\times$ 9.5 μm , n = 25), ellipsoid or reniform, aseptate, hyaline to pale yellow when immature, becoming brown to dark brown when mature.

Culture characteristics – Colonies on PDA reaching 60 mm diam. after five weeks at 27°C, colonies from above, dense, fluffy, umbonate, circular, grey with white aerial mycelium, grey with black hyphal lumps, papillate; from below, brown with black spots. Mycelium 2–5 μm wide ($\bar{x}$ = 3 μm , n = 25), septate, hyaline, branched.



Figure 2 – RAXML phylogram generated from a combined dataset of partial ITS, LSU, and *tef1- α* DNA sequence analyses for *Aplosporella*. Related sequences are obtained following Lin et al. (2023). Thirty-eight strains were included in the combined analyses, which comprised 1,714 characters in the combined ITS, LSU, and *tef1- α* alignment. *Alanomyces indica* (MCC 1039) was used as the outgroup taxon. The best-scoring RAXML tree with a final likelihood value of -4066.202609 is presented. The matrix contained 265 distinct alignment patterns, with 27.42% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.231173, C = 0.244331, G = 0.281624, T = 0.242871; substitution rates AC = 4.682590, AG = 5.637899, AT = 2.565118, CG = 3.171346, CT = 10.545497, GT = 1.000000. The tree topology of the ML analysis is similar to the Bayesian analysis. Bootstrap values for ML equal to or greater than 70% and PP values greater than 0.95 (rounding of values to 2 decimal places) are labelled on the nodes. Strains

of the newly described species are in orange, while type strains are in bold. (LSU: 839 bp, ITS: 570 bp, *tef1-α*: 305 bp).

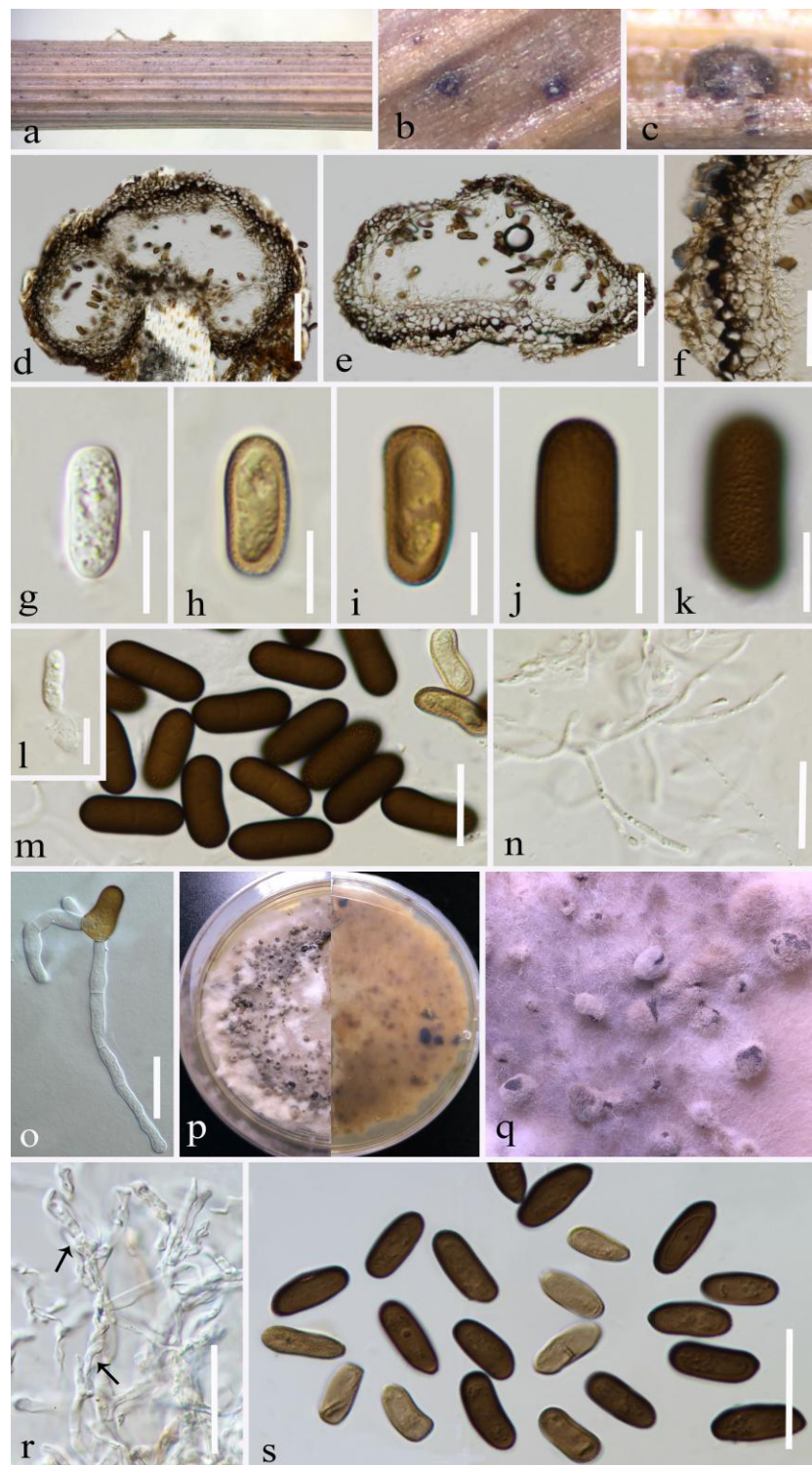


Figure 3 – *Aplosporella javeedii* (HKAS 132961, a new host record). a–c Appearance of conidiomata on the host substrate. d, e Vertical sections of conidiomata. f Conidioma wall. l Conidiogenous cells and developing conidia. g–k, m Conidia. n Hamathecium with paraphyses. o A germinated conidium. p Colony on PDA (left: above, right: below). q Conidiomata on PDA. r Mycelium (arrowheads indicate conidiogenous cells). s Conidia. Scale bars: d, e = 100 μ m, f = 50 μ m, r, s = 30 μ m, m–o = 20 μ m, g–l = 10 μ m.

Material examined – China, Yunnan Province, Kunming, on a decaying stem of *Sisyrinchium rosulatum* (Iridaceae), 13 June 2022, Y. Gao, DG8 (HKAS 132961), living culture KUNCC 25-19196; on a decaying stem of *Dietes iridioides* (Iridaceae), 16 June 2022, Y. Gao, KG14 (HKAS 146001), living culture KUNCC 25-19197.

Known hosts and distribution – endophyte from healthy wood sections of *Celtis africana* (Cannabaceae) and *Searsia lancea* (Anacardiaceae) in South Africa (Jami et al. 2015), on infected stems of *Broussonetia papyrifera* (Moraceae) and on infected branches of *Albizia julibrissin* (Fabaceae), *Gleditsia sinensis* (Fabaceae), *Juniperus chinensis* (Cupressaceae), *Styphnolobium japonicum* (Fabaceae) and in China (Fan et al. 2015), on dead stem of *Sisyrinchium rosulatum* (Iridaceae) and *Dietes iridioides* (Iridaceae) in Yunnan Province, China (This study).

GenBank numbers – KUNCC 25-19196: ITS = PV608643, LSU = PV607389; KUNCC 25-19197: ITS = PV608644, LSU = PV607390.

Notes – *Aplosporella javeedii* was previously reported as an endophyte from healthy trees of two dicotyledonous host species in South Africa (Jami et al. 2014). Fan et al. (2015) identified six botryosphaeriaceous strains as *Aplosporella javeedii* on infected branches of hosts (*Albizia julibrissin*, *Broussonetia papyrifera*, *Gleditsia sinensis*, *Juniperus chinensis*, *Styphnolobium japonicum*). Botryosphaeriaceous fungi might shift from endophytic to pathogenic habits when hosts are subjected to stress (Slippers & Wingfield 2007, Manawasinghe et al. 2022). Therefore, Fan et al. (2015) raised the question of whether *Aplosporella javeedii* has pathogenic potential. Our two new collections are identified as saprobic and based on morphological observations and multigene phylogenetic analyses, our collections grouped with *Aplosporella javeedii* (CFCC 50052, CFCC 50053, CFCC 50054, CFCC 89657, CFCC 89658 and CFCC 89659) with 88% ML and 0.99 PP support (Fig. 2). Our new collections share similar morphological characters with *Aplosporella javeedii* (CFCC 89657, ex-type), such as immersed to erumpent, multi-locular conidiomata, ellipsoid or oval to reniform with verruculose wall observed clearly when mature, aseptate conidia (Fan et al. 2015). A comparison of nucleotide sequences between our two new collections and *Aplosporella javeedii* (CFCC 50052, CFCC 50053, CFCC 50054, CFCC 89657T, CFCC 89658, and CFCC 89659) revealed no base pair differences in the ITS locus. Therefore, our new collections represent new records of *Aplosporella javeedii* from Poaceae hosts in China.

Pleosporales Luttr. ex M.E. Barr, Prodrum to class Loculoascomycetes: 67 (1987)

Cucurbitariaceae G. Winter, Rabenhorst's Kryptogamen-Flora, Pilze – Ascomyceten 1(2): 308 (1885)

Notes – Cucurbitariaceae was established by Winter (1885) with *Cucurbitaria* as its type genus. There are 15 genera recognized within this family (Hyde et al. 2024a). It is primarily distinguished by its sexual morph, characterized by globose to subglobose, uni-loculate ascomata; a black ostiole with inconspicuous or papillate to cylindrical; light brown to reddish-brown, multi-layered peridium; septate, cellular pseudoparaphyses; fissitunicate, bitunicate, cylindrical to clavate asci with furcate pedicel and minute ocular chamber; 1-seriate, or partially overlapping, ellipsoidal, golden brown to dark brown, multi-septate, muriform ascospores (Hongsanan et al. 2020a). The asexual morphs are coelomycetous, resembling *Phoma* or *Pyrenochaeta* (Doilom et al. 2013, Jaklitsch et al. 2018). This study reports a new record species of *Cucurbitaria* discovered on *Artemisia carvifolia* in China. An updated phylogenetic tree based on combined ITS, LSU, *tef1-α*, and *rpb2* sequence data is presented in Fig. 4.

Cucurbitaria Gray, A natural arrangement of British plants 1: 519 (1821)

Notes – *Cucurbitaria* was introduced by Gray & Shury (1821), with the type species *Cucurbitaria berberidis*. The characteristics of *Cucurbitaria* by erumpent, gregarious, perithecioid ascomata, a thickened, elongated peridium on the surface of the hypostroma, cylindrical or fissitunicate asci, brown, muriform, uniseriate ascospores (Welch 1926, Appadoo et al. 2021, Ren et al. 2024a). The asexual morphs are pyrenochaeta- or phoma-like (Wanasinghe et al. 2017, Jaklitsch et al. 2018, Hongsanan et al. 2020a). *Cucurbitaria* comprises necrotrophic and Saprobiic

fungi, mostly on the stems, leaves, and bark of various shrubs and trees (Doilom et al. 2013, Valenzuela-Lopez et al. 2018). The genus is reported to occur preferentially in temperate and Mediterranean climates; however, more collections are required to confirm its distribution (Jaklitsch et al. 2018, Farr & Rossman 2025). Index Fungorum (2025) lists 473 species epithets, of which only 94 are validated. The morphological characteristics presented by Welch (1926) were insufficiently detailed, resulting in the misclassification of unrelated species under *Cucurbitaria*. Contemporary phylogenetic analyses have revealed that several species historically classified as *Cucurbitaria* actually belong to different families, including Nectriaceae and Melanommataceae (Checa et al. 2013, Jaklitsch & Voglmayr 2017). To address this, Wanasinghe et al. (2017) established *Neocucurbitaria* to accommodate cucurbitaria-like species distinguished by solitary fruiting bodies with periphyses and muriform ascospores. Similarly, Valenzuela-Lopez et al. (2018) proposed *Allocucurbitaria* for a cucurbitaria-like species phylogenetically linked to *Cucurbitaria* and introduced *Paracucurbitaria* for phylogenetically distinct species exhibiting traits similar to the asexual form of *Cucurbitaria*. In this study, a new record of *C. lijiangensis* is introduced based on morphology and molecular data, together with a description and illustrations (Fig. 5).

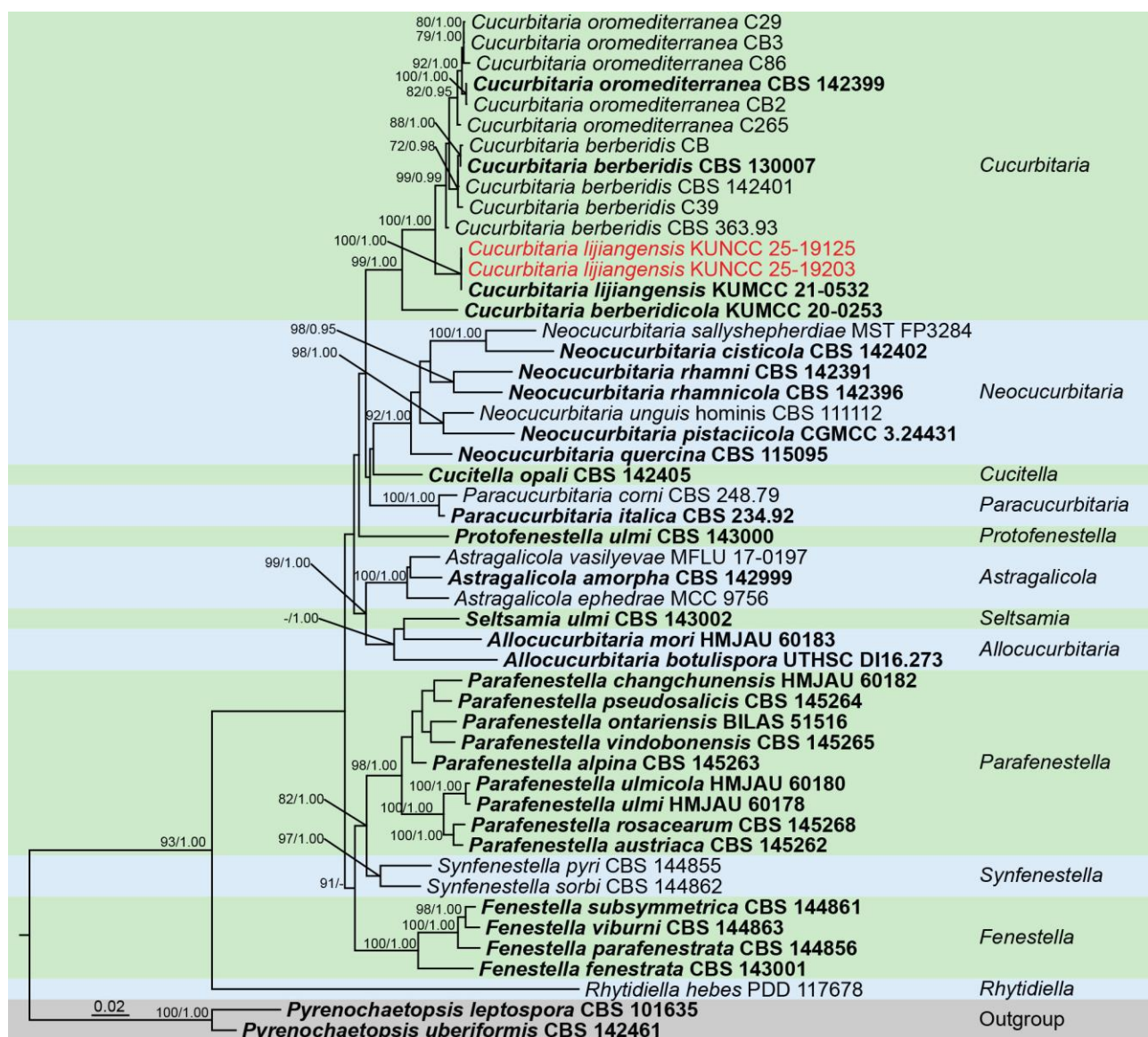


Figure 4 – RAxML phylogram generated from a combined dataset of partial ITS, LSU, *tef1-α*, and *rpb2* DNA sequence analyses for Cucurbitariaceae. Related sequences are obtained following Appadoo et al. (2021) and Ren et al. (2024a). Fifty strains were included in the combined analyses, which comprised 3,668 characters in the combined ITS, LSU, *tef1-α*, and *rpb2* alignment.

Pyrenochaetopsis leptospora (CBS 101635) and *Pyrenochaetopsis uberiformis* (CBS 142461) were used as the outgroup taxa. The best-scoring RAXML tree with a final likelihood value of -22662.279899 is presented. The matrix contained 1,143 distinct alignment patterns, with 14.65% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.240438, C = 0.261041, G = 0.266337, T = 0.232184; substitution rates AC = 1.285831, AG = 4.659840, AT = 1.516935, CG = 1.218431, CT = 8.611901, GT = 1.000000. The tree topology of the ML analysis is similar to the Bayesian analysis. Bootstrap values for ML equal to or greater than 70% and PP values greater than 0.95 (the rounding of values to 2 decimal places) are labelled on the nodes. Strains of the newly described species are in orange, while type strains are in bold. (LSU: 851 bp, ITS: 545 bp, *tef1-α*: 1205 bp, *rpb2*: 1067 bp).

Cucurbitaria lijiangensis G.C. Ren & K.D. Hyde, Mycosphere 15 (1): 1000 (2024)

Fig. 5

Index Fungorum number: IF901350; Facesoffungi number: FoF13879

Saprobic on the dead stem of *Artemisia carvifolia*. Sexual morph: *Ascomata* 410–500 µm diam. × 310–450 µm high ($\bar{x}$ = 460 × 390 µm, n = 10), subglobose to globose, superficial, clustered, coriaceous, uni-loculate, black. *Peridium* 55–110 µm wide ($\bar{x}$ = 85 µm, n = 30), composed of the dark outermost layers, inner layers comprising hyaline to reddish-brown, flattened, thick-walled cells of *textura angularis*. *Hamathecium* comprises 1–2 µm wide ($\bar{x}$ = 1.4 µm, n = 30), composing numerous, dense, filamentous, branched, septate, hyaline pseudoparaphyses, embedded in a gelatinous matrix. *Asci* 130–230 × 18–32 µm ($\bar{x}$ = 195 × 23 µm, n = 30), 6–8-spored, cylindrical to cylindric-clavate, apically rounded, bitunicate, fissitunicate, short pedicellate, thick-walled, with a minute ocular chamber. *Ascospores* 27–41 × 13–20 µm ($\bar{x}$ = 35 × 17 µm, n = 30), uniseriate, muriform, ellipsoidal to broadly fusiform, ends remaining cone-shaped, with acute ends, with 6–13 transverse septa and 2–6 longitudinal septa, slightly constricted at the central septum, smooth, with guttulate, hyaline to pale brown when young, becoming brown at maturity. Asexual morph: Undetermined.

Culture characteristics – Ascospores germinated within 48 h on PDA. 6 cm diam. after three weeks at 27°C. Cultures from above, grey to greenish brown with pale yellow mycelium, floccose, umbonate, flat; from below, gray to black.

Material examined – China, Yunnan Province, Zhaotong grassland, on dead stems of *Artemisia carvifolia* (Asteraceae), 28 August 2021, Y. Gao, ZG15A (HKAS 126578), living culture KUNCC 25-19125; *ibid.*, ZG15B (HKAS 135334), living culture KUNCC 25-19203.

Known hosts and distribution – on dead woody twigs of *Rhododendron rubiginosum* (Ericaceae) in China (Ren et al. 2024a), on dead stems of *Artemisia carvifolia* (Asteraceae) in Yunnan Province, China (This study).

GenBank numbers – KUNCC 25-19125: ITS = PV608517, LSU = PV607363, *tef1-α* = PV626414, *rpb2* = PV640438; KUNCC 25-19203: ITS = PV608518, LSU = PV607364, *tef1-α* = PV626415, *rpb2* = PV640439.

Notes – In the multigene phylogenetic analyses, our collections (KUNCC 25-19125 and KUNCC 25-19203) grouped with *Cucurbitaria lijiangensis* (KUMCC 21-0532, ex-type) with 100% ML and 1.00 PP support values (Fig. 4). Morphologically, our collections resemble *C. lijiangensis* (KUMCC 21-0532) by its subglobose to globose, coriaceous, uni-loculate ascomata; cylindrical to cylindric-clavate, short pedicellate, with a minute ocular chamber; muriform, ellipsoidal to broadly fusiform asci, clearly showing changing the transverse septa with maturity ascospores. In addition, the nucleotides in ITS, LSU, *tef1-α*, and *rpb2* of our collection (KUNCC 25-19125 and KUNCC 25-19203) are not different from *Cucurbitaria lijiangensis* (KUMCC 21-0532). Thus, we identified our collections as *Cucurbitaria lijiangensis* based on phylogenetic analyses and morphological characters. it is a new host record on *Artemisia carvifolia*.

Dictyosporiaceae Boonmee & K.D. Hyde, Fungal Diversity 80: 462 (2016)

Notes – Dictyosporiaceae was established by Boonmee et al. (2016) to accommodate a holomorphic group characterized by cheiросporous, digitate, and/or dictyosporous, pale brown to

brown conidia, as well as globose to subglobose, dark brown to black ascomata, bitunicate asci, septate, hyaline ascospores, which may be sheathed or unsheathed. Dictyosporiaceae (Pleosporales, Dothideomycetes) comprises 20 genera with a global distribution. Members of Dictyosporiaceae primarily act as saprobes on plant debris, as well as on dead or decaying wood in both aquatic and terrestrial environments (Boonmee et al. 2016, Li et al. 2017b, Yang et al. 2018, Wijayawardene et al. 2020, Atienza et al. 2021, Shen et al. 2022, Tian et al. 2022b, Liu et al. 2023b). An updated phylogenetic tree based on combined ITS, LSU, SSU, and *tefl*- α sequence data is presented in Fig. 6.

Pseudocyclothyriella Phukhams. & Phookamsak, *Frontiers in Microbiology* 12 (no. 656235): 8 (2021) **amended**.

Index Fungorum number: IF557441; Facesoffungi Number: FoF09539

Type species – *Pseudocyclothyriella clematidis* (Phukhams. & K.D. Hyde) Phukhams. & Phookamsak

Sexual morph: Semi-immersed to erumpent through the host surface, solitary, subglobose to globose, uni-loculate, ascomata. Composed of light brown to brown cells of *textura angularis* peridium. Numerous, dense, septate, filamentous, branched, embedded in a gelatinous matrix hamathecium. Eight-spored, clavate to broad cylindrical-clavate, fissitunicate, bitunicate, short pedicellate, ocular chamber visible when immature asci. Obovoid to sub-fusiform, biseriate, rounded at apex, acute at the ends, hyaline to yellowish, 1-5-septate, guttulate, deeply constricted at the middle septum ascospores (This study). Asexual morph: See Phukhamsakda et al. (2020) and Jiang et al. (2021a).

Notes – Jiang et al. (2021a) introduced a monotypic genus, *Pseudocyclothyriella*, to accommodate a single coelomycetous species, *P. clematidis*, which was previously described as *Pseudocoleophoma clematidis* by Phukhamsakda et al. (2020) collected from *Clematis vitalba* (Ranunculaceae) in Italy. The asexual form of *Pseudocyclothyriella* is characterized by subglobose to subconical, solitary to gregarious, black, immersed to erumpent, shiny with oval, papilla, conidiomata, thick-walled, multi-layered scleroplectenchymatous cells, dark brown to black cells of *textura angularis* to *textura globulosa* of outer layer, hyaline to pale brown cells of inner layer pycnidial wall, cylindrical to subcylindrical, or ampulliform, holoblastic, determinate, phialidic, hyaline, discrete, smooth-walled, aseptate conidiogenous cells, oval to oblong, slightly curved toward the ends, hyaline to yellowish brown, smooth-walled, aseptate conidia (Jiang et al. 2021a). We introduce two new *Pseudocyclothyriella* species, *P. lolii* and *P. yunnanensis*, together with descriptions and illustrations (Figs. 7, 8), expanding *Pseudocyclothyriella* from a monotypic to a polytypic genus. In addition, the sexual morphology of *Pseudocyclothyriella* is introduced in this study.

Pseudocyclothyriella lolii Y. Gao, H. Gui & K.D. Hyde, sp. nov.

Fig. 7

Index Fungorum number: IF903812; Facesoffungi number: FoF17689

Holotype – HKAS 132981

Etymology – The specific epithet is derived from *Lolium perenne* (Poaceae), from which the holotype was collected.

Saprobic on a dead leaf blade of *Lolium perenne* (Perennial ryegrass). Sexual morph: *Ascomata* 145–175 μm diam. $\times$ 110–150 μm high ($\bar{x}$ = 155 $\times$ 120 μm , n = 10), subglobose to globose to subglobose, semi-immersed to erumpent through host surface, scattered, solitary, uni-loculate, black. *Peridium* 8–15 μm wide ($\bar{x}$ = 11 μm , n = 30), composed of 3–4 layers of light brown to brown cells of *textura angularis*, heavily pigmented at the outer layers, lined with a hyaline layer. *Hamathecium* comprises 2–4 μm wide ($\bar{x}$ = 2.5 μm , n = 30), composed of numerous, dense, filamentous, branched, septate, pseudoparaphyses, embedded in a gelatinous matrix. *Asci* 53–87 $\times$ 10–18 μm ($\bar{x}$ = 71 $\times$ 15 μm , n = 30), 8-spored, clavate to broad cylindrical-clavate, apically rounded, uniseriate when immature, biseriate when mature, fissitunicate, short pedicellate,

thick-walled, ocular chamber visible when immature. *Ascospores* $20\text{--}27 \times 6\text{--}9\ \mu\text{m}$ ($\bar{x} = 25 \times 8\ \mu\text{m}$, $n = 35$), biseriate, partially overlapping, obovoid to sub-fusiform, rounded at apex, acute at the ends, hyaline to yellowish, 1-5-septate, deeply constricted at the middle septum, smooth, with guttulate. Asexual morph: Undetermined.

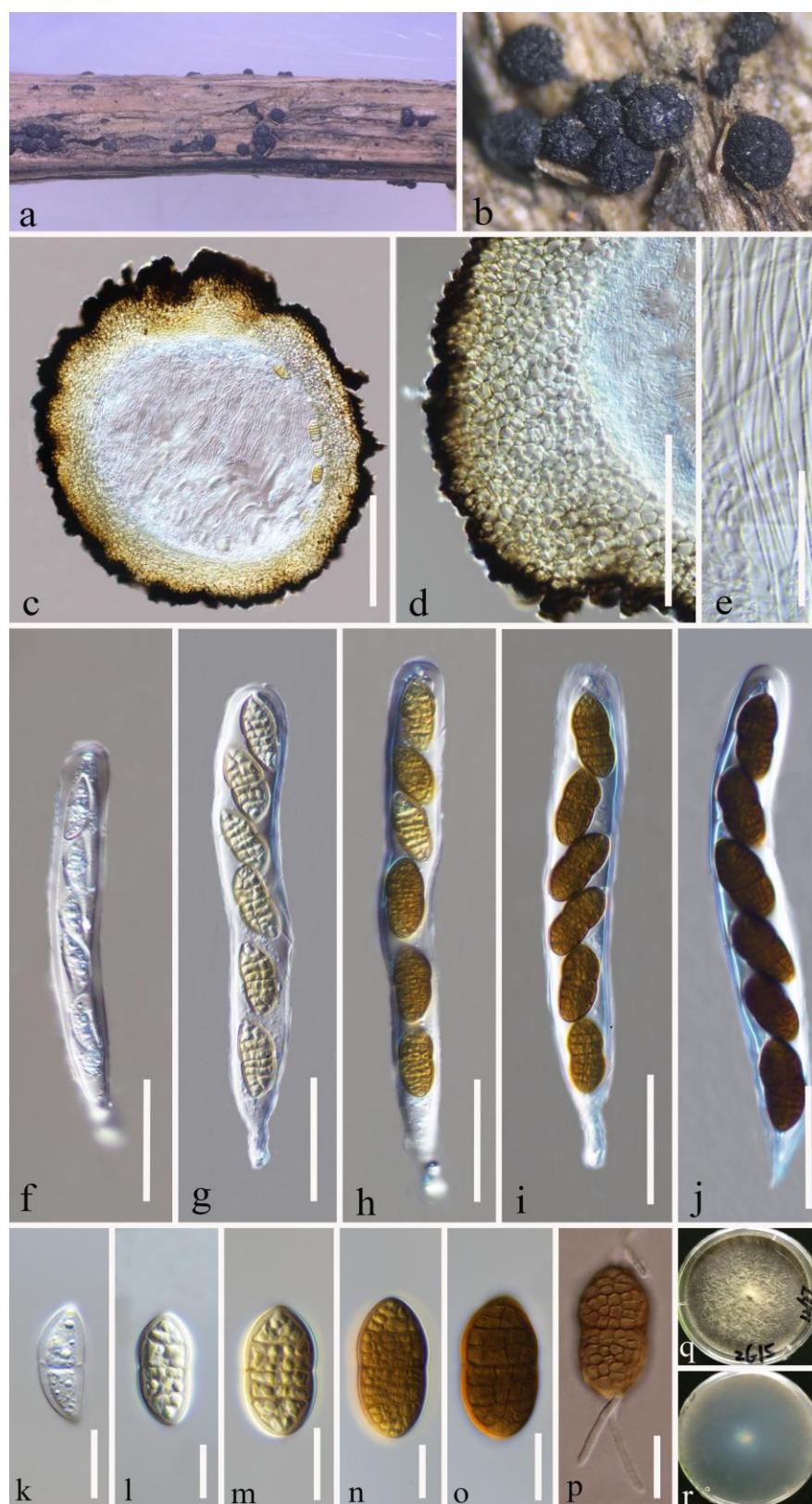


Figure 5 – *Cucurbitaria lijiangensis* (HKAS 126578, a new host record). a, b Appearance of ascomata on the host substrate. c A section of an ascoma. d Peridium. e Pseudoparaphyses. f–j

Asci. k–o Ascospores. p A germinated ascospore. q, r Culture characters on PDA (q: above, r: below). Scale bars: c = 150 μ m, d = 100 μ m, f–j = 50 μ m, e = 30 μ m, p = 20 μ m, k–o = 15 μ m.

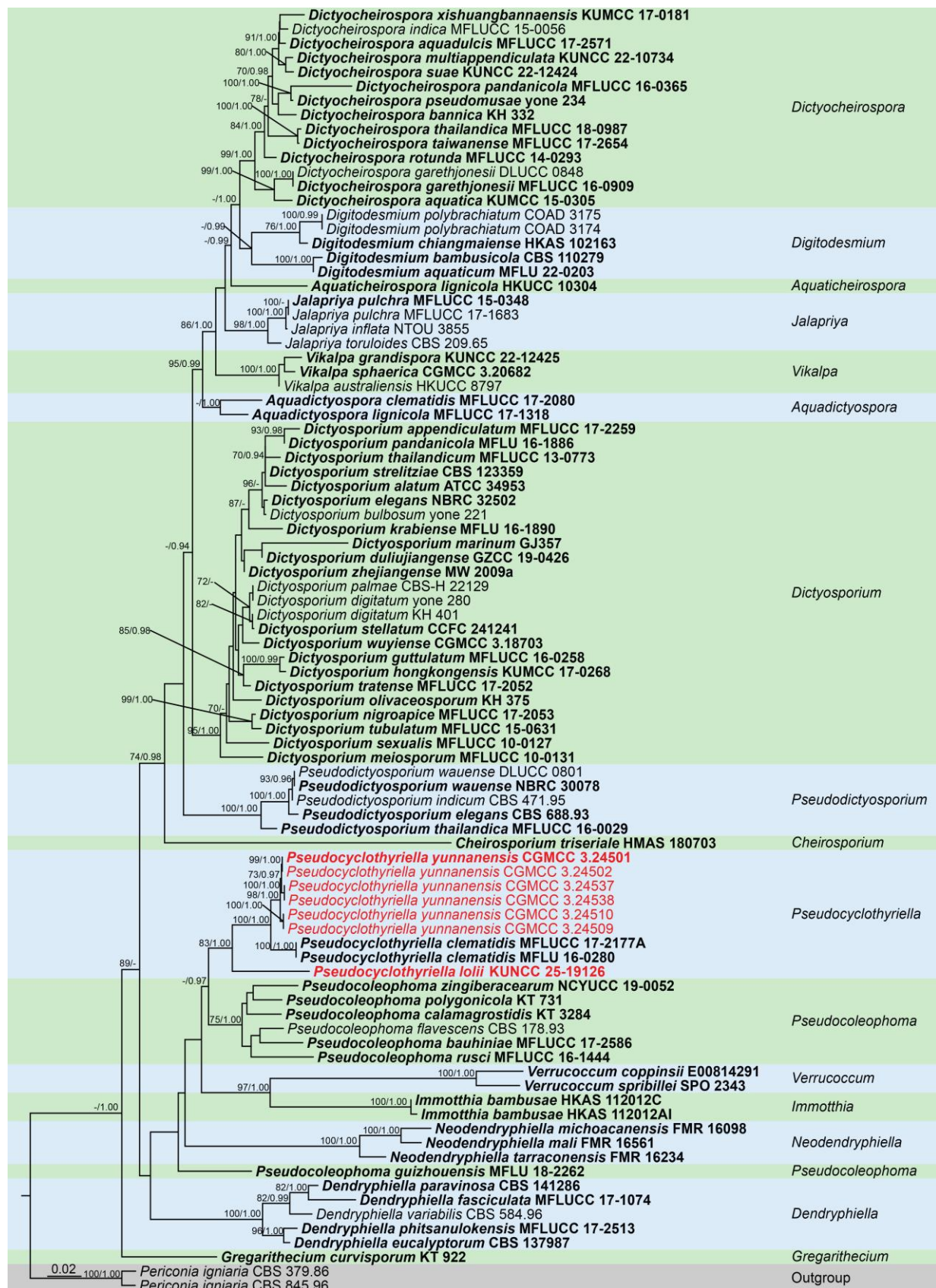


Figure 6 – RAxML phylogram generated from a combined dataset of partial ITS, LSU, SSU, and *tef1*- α DNA sequence analyses for Dictyosporiaceae. Related sequences are obtained following

Jiang et al. (2021a) and Liu et al. (2023b). Ninety strains were included in the combined analyses, which comprised 3,717 characters in the combined ITS, LSU, SSU, and *tef1-α* alignment. *Periconia igniaria* (CBS 379.86 and CBS 845.96) were used as the outgroup taxa. The best-scoring RAxML tree with a final likelihood value of -23324.802965 is presented. The matrix contained 1268 distinct alignment patterns, with 35.48% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.242659, C = 0.243125, G = 0.268984, T = 0.245232; substitution rates AC = 1.505187, AG = 3.350360, AT = 2.204293, CG = 0.807367, CT = 8.344023, GT = 1.000000. The tree topology of the ML analysis is similar to the Bayesian analysis. Bootstrap values for ML equal to or greater than 70% and PP values greater than 0.90 (rounding of values to 2 decimal places) are labelled on the nodes. Strains of the newly described species are in orange, while type strains are in bold. (ITS: 514 bp, LSU: 1255 bp, SSU: 1047 bp, *tef1-α*: 901 bp)

Culture characteristics – Asci and ascospores germinated within 48 h on PDA. 1.5 cm diam. after two weeks at 27°C. cultures from above, white, dense, circular, umbonate, fluffy, slightly radiating in the lower part; from below, cream-white, radiating outwardly.

Material examined – China, Yunnan Province, Qujing grassland, on a dead leaf blade of *Lolium perenne* (Poaceae), 27 August 2022, Y. Gao, QG28B (HKAS 132981, holotype), ex-type living culture KUNCC 25-19126.

GenBank numbers – KUNCC 25-19126: ITS = PV608525, LSU = PV607371, SSU = PV607278, *tef1-α* = PV626422.

Notes – Based on our phylogenetic analysis of the combined SSU, LSU, ITS, and *tef1-α* sequence data, the collection of our novel species *Pseudocyclothyriella lolii* (KUNCC 25-19126, ex-type) is closely related to *P. clematidis* (MFLUCC 17-2177A, ex-type) with 83% ML and 1.00 PP statistical support (Fig. 6). *Pseudocyclothyriella lolii* (KUNCC 25-19126) and *P. clematidis* (MFLUCC 17-2177A) showed a 11.75% (63/536 bp, with 5 gaps) base pair difference in the ITS region, 2.25% (17/756 bp, without gaps) base pair difference in the LSU gene region, 6.5% (46/707 bp, without gaps) base pair difference in *tef1-α* region. Previously, the sexual morphology of *Pseudocyclothyriella* had never been reported (Phukhamsakda et al. 2020, Jiang et al. 2021a). *Pseudocyclothyriella* was established to accommodate *P. clematidis*, and it was known only from its asexual morph. Our new collection, *Pseudocyclothyriella lolii* is from a dead leaf blade of *Lolium perenne* (Poaceae), which reports the sexual morph. Hence, we amend the description of the *Pseudocyclothyriella* genus to accommodate its sexual morph. Therefore, based on the polyphasic approach recommended for species boundaries delimitation (Jayawardena et al. 2021, Maharachchikumbura et al. 2021a), we introduce *Pseudocyclothyriella lolii* as a novel species.

Pseudocyclothyriella yunnanensis Y. Gao, H. Gui & K.D. Hyde, sp. nov.

Fig. 8

Index Fungorum number: IF903813; Facesoffungi number: FoF17690

Holotype – HKAS 128785

Etymology – The specific epithet “yunnanensis” refers to Yunnan Province, where the holotype was collected.

Saprobic on a dead stem of grass. Sexual morph: Undetermined. Asexual morph: *Conidiomata* 300–320 µm diam. × 130–290 µm high ($\bar{x}$ = 314 × 230 µm, n = 15), superficial, solitary or scattered, uniloculate, conical or subglobose to globose, thick-walled, black, ostiolar neck central, with minute papilla. *Conidioma wall* 40–110 µm wide ($\bar{x}$ = 74 µm, n = 30), multilayered, outer layer composed of light brown to brown cells of *textura angularis*, lined with a thick hyaline layer bearing conidiogenous cells, loosely arranged and wider at the sides and the bottom. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 2.5–4.5 × 3–5 µm ($\bar{x}$ = 3.5 × 4 µm, n = 20), subglobose or phialidic, determinate, discrete, arising from inner layers of conidioma. *Conidia* 3.5–4.5 × 2–3 µm ($\bar{x}$ = 4 × 2.5 µm, n = 30), oval, aseptate, with 1(–2) guttules in each cell, smooth-walled, hyaline when immature, yellowish brown at maturity.

Culture characteristics – Colonies on PDA reaching 15 mm diam. after three weeks at 25°C, colonies from above, circular, dense, white, umbonate, papillate with fluffy; from below, cream, radiating outwardly.

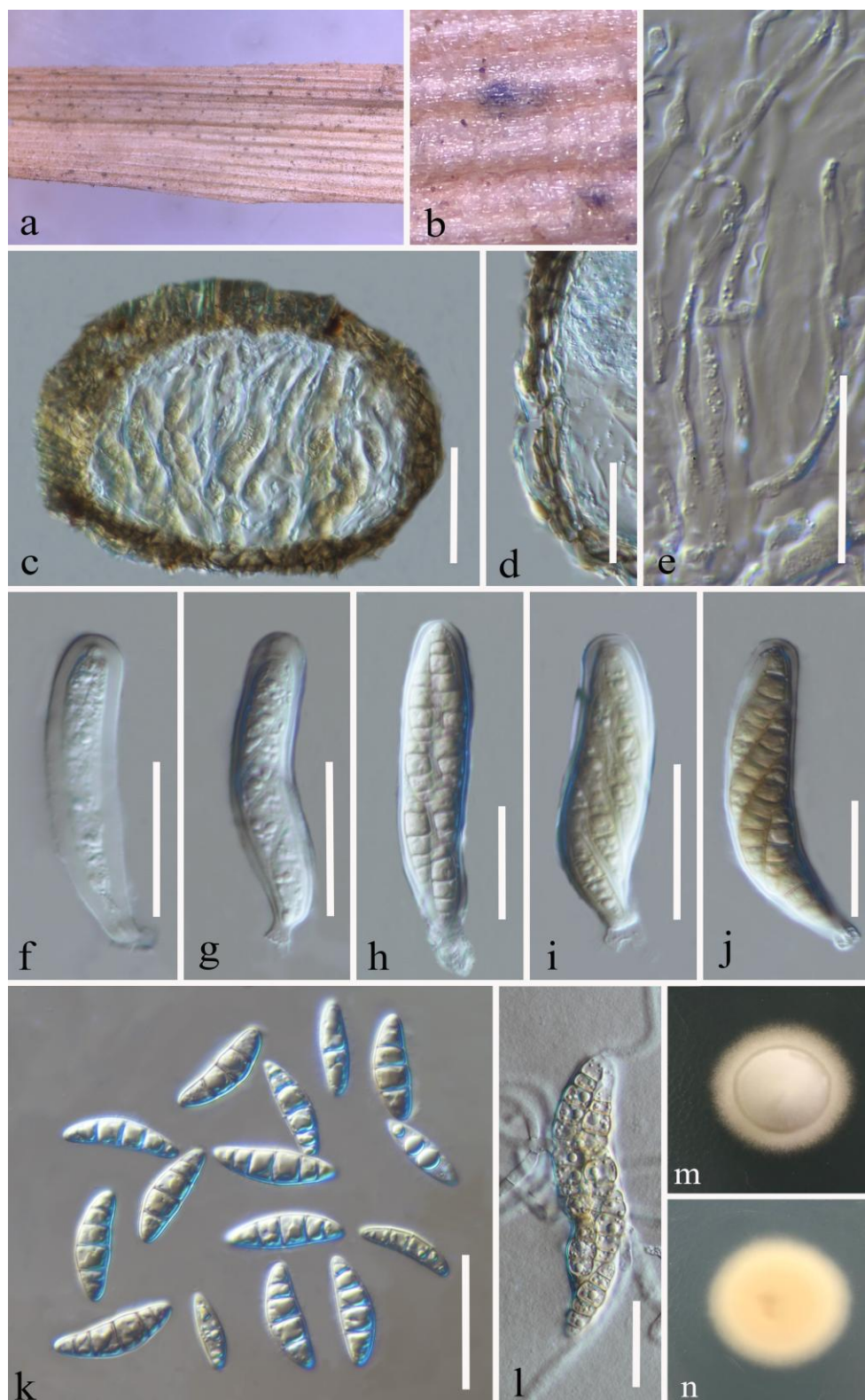


Figure 7 – *Pseudocyclothyriella lolii* (HKAS 132981, holotype). a, b Appearance of ascomata on the host substrate. c A section of an ascoma. d Peridium. e Pseudoparaphyses. f–j Asci. k Ascospores. l Germinated ascospores. m, n Culture characters on PDA (m: above, n: below). Scale bars: c = 50 μ m, d–l = 30 μ m.

Material examined – China, Yunnan Province, Zhaotong grassland, on a decaying stem of unidentified grass, 25 August 2022, Y. Gao, QG5A (HKAS 128785, holotype), ex-type living culture CGMCC 3.24501; *ibid.*, QG5B (HKAS 128786, isotype), ex-isotype, CGMCC 3.24502;

China, Yunnan Province, Qujing, on a decaying stem of unidentified grass, 27 August 2022, Y. Gao, QG18A (HKAS 128797, paratype), ex-paratype, CGMCC 3.24509; *ibid.*, QG18B (HKAS 128798, CGMCC 3.24510); *ibid.*, QG107A (HKAS 128783, CGMCC 3.24537); *ibid.*, QG107B (HKAS 128784, CGMCC 3.24538).

GenBank numbers – CGMCC 3.24501: ITS = PV608519, LSU = PV607365, SSU = PV607272, *tef1*- α = PV626416; CGMCC 3.24502: ITS = PV608520, LSU = PV607366, SSU = PV607273, *tef1*- α = PV626417; CGMCC 3.24509: ITS = PV608521, LSU = PV607367, SSU = PV607274, *tef1*- α = PV626418; CGMCC 3.24510: ITS = PV608522, LSU = PV607368, SSU = PV607275, *tef1*- α = PV626419; CGMCC 3.24537: ITS = PV608523, LSU = PV607369, SSU = PV607276, *tef1*- α = PV626420; CGMCC 3.24538: ITS = PV608524, LSU = PV607370, SSU = PV607277, *tef1*- α = PV626421.

Notes – *Pseudocyclothyriella yunnanensis* is introduced as a new species based on its distinct morphology and the phylogeny of the combined SSU, LSU, ITS, and *tef1*- α sequence data. Our collections formed a sister lineage to *Pseudocyclothyriella clematidis* (MFLUCC 17-2177A, MFLU 16-0280) with 100% ML and 1.00 PP support values (Fig. 6). Sequence comparison between *Pseudocyclothyriella yunnanensis* (CGMCC 3.24501) and *P. clematidis* (MFLUCC 17-2177A, ex-type) showed a 3.74% (20/535 bp, with 2 gaps) base pair difference in the ITS region, 0.63% (5/793 bp, without gaps) base pair difference in the LSU region, 2.84% (20/705 bp, without gaps) base pair difference in *tef1*- α region. Morphologically, *Pseudocyclothyriella yunnanensis* differs from *P. clematidis* (MFLUCC 17-2177A) in its conidiomata size (300–320 $\times$ 130–290 μ m, L/W = 1.5 vs. 130–150 $\times$ 100–130 μ m, L/W = 1.2), thickness of conidiomatal wall (40–110 vs. 20–30 μ m wide), the size of conidia (3.5–4.5 $\times$ 2–3 μ m, L/W = 1.6 vs. 5–8 $\times$ 2–4 μ m, L/W = 2.2) (Phukhamsakda et al. 2020). Therefore, based on the approaches recommended by Jayawardena et al. (2021) and Maharachchikumbura et al. (2021a) for species delimitation, we introduce *Pseudocyclothyriella yunnanensis* as a new species.

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

Notes – Didymellaceae was introduced by de Gruyter et al. (2009) with the type genus *Didymella*. It is the largest family in Pleosporales, comprising 50 genera as noted by Hyde et al. (2024a). The sexual morph of this family is characterized mainly by immersed, globose to flattened, pseudothecia with ostioles and pseudoparenchymatal cells, 8-spored, bitunicate asci, clavate or saccate to cylindrical, 1-septate ascospores (didymospores) or multi-septate dictyospores. The asexual morphs are coelomycetous conidiomata with pycnidial, erumpent, unilocular with cells of *textura angularis*, conidiophores are absent, filiform, branched, septate, enteroblastic conidiogenous cells, doliiform to lageniform, phialidic, smooth-walled, and conidia of various shapes: globose, ellipsoid, fusiform, cylindrical, pyriform, guttulate, hyaline or pigmented, aseptate or septate (Hongsan et al. 2020a). Species in Didymellaceae are cosmopolitan and are commonly plant pathogens, causing leaf and stem lesions on a wide range of hosts (de Gruyter et al. 2009, Chen et al. 2017). They also exhibit diverse lifestyles, functioning as endophytes, saprobes, fungicolous fungi, or lichenicolous fungi (Aveskamp et al. 2010). An updated phylogenetic tree based on combined ITS, LSU, *tub2*, and *rpb2* sequence data is presented in Fig. 9.

Epicoccum Link, Mag. Neuesten Entdeck. Gesamten Naturk. Ges. Naturf. Freunde Berlin 7: 32 (1815)

Notes – *Epicoccum* was established by Link (1815), with *Epicoccum nigrum* designated as its type species, later revised by Chen et al. (2015). Members of this genus exhibit diverse ecological roles, functioning as saprobes (Jayasiri et al. 2017), pathogens (Raza et al. 2019) and endophytes (Fávaro et al. 2012, Dzoyem et al. 2017), inhabiting various plant tissues in both aquatic and terrestrial environments (Voronin et al. 2021, Barreto et al. 2022). *Epicoccum* displays both hyphomycetous and coelomycetous synanamorphs (Chen et al. 2015, Thambugala et al. 2017). The hyphomycetous asexual morph is distinguished by dark sporodochia with branched conidiophores and mono- to polyblastic, hyaline conidiogenous cells that generate pigmented, occasionally

verruculose, dictyoconidia (Link 1815, Chen et al. 2015, de Silva et al. 2021). The coelomycetous asexual morph produces conidia within pycnidial conidiomata (Chen et al. 2015). Index Fungorum (2025) lists 179 records for *Epicoccum*. However, sequence data are lacking for the majority of species described before the year 2000, with only 48 species supported by molecular data (de Silva et al. 2021, Keirnan et al. 2021, Tian et al. 2024). In this study, we report three new records (*E. dendrobii*, *E. mackenziei*, and *E. viciae-villosae*) and describe one new species (*E. kunmingense*) with descriptions, illustrations and the phylogenetic analyses (Figs. 9–13).

Epicoccum dendrobii Q. Chen, Crous & L. Cai, Studies in Mycology 87: 140 (2017)
Index Fungorum number: IF818964; Facesoffungi number: FoF18348

Fig. 10

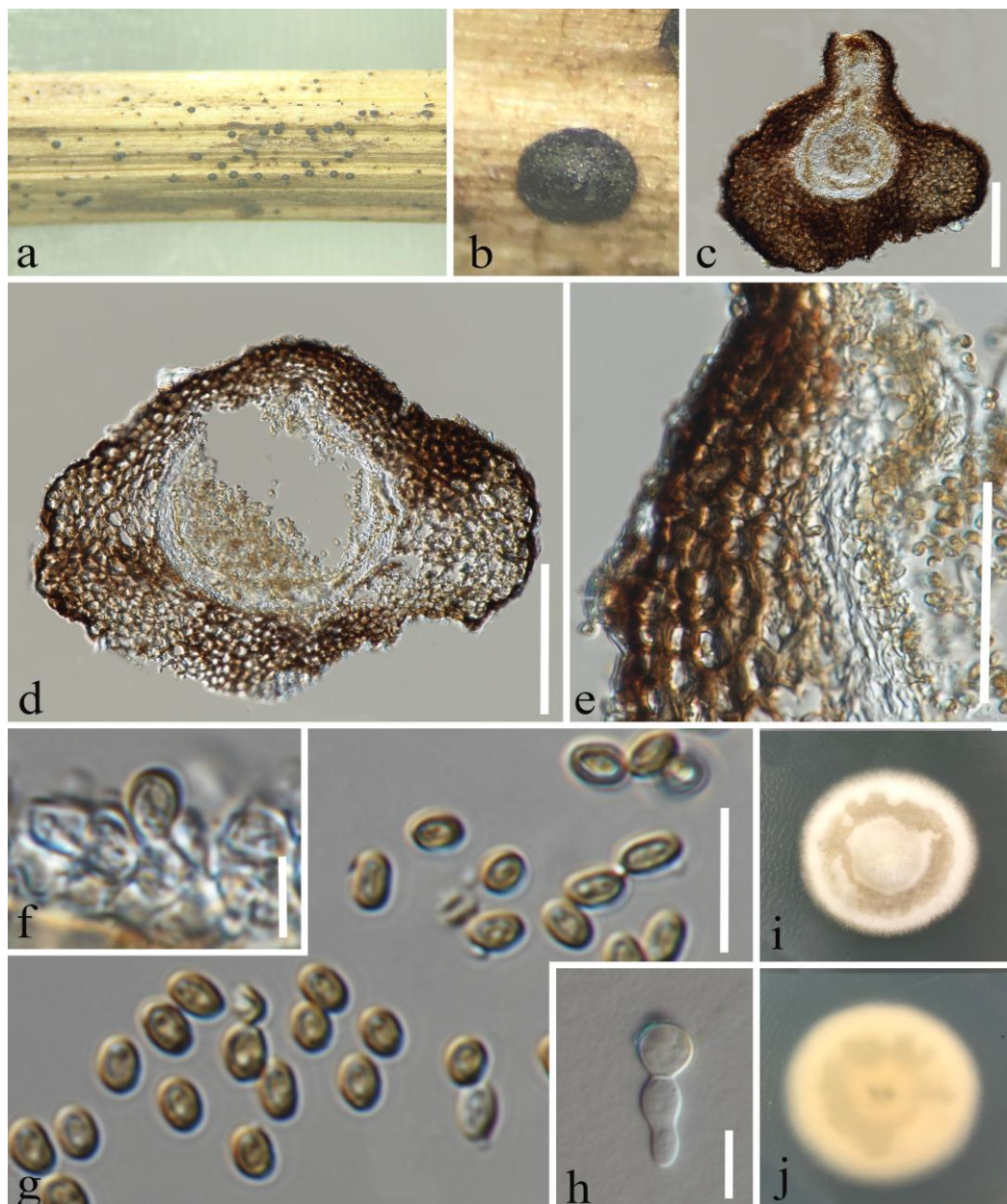


Figure 8 – *Pseudocyclothyriella yunnanensis* (HKAS 128785, holotype). a, b Appearance of conidiomata on the host substrate. c, d Vertical sections through conidiomata. e Section of conidioma wall. f Conidiogenous cells and conidia. g Conidia. h A germinated conidium. i, j Colony on PDA (i: above, j: below). Scale bars: c, d = 100 μ m, e = 50 μ m, g = 10 μ m, f, h = 5 μ m.

Saprobic on a dead leaf blade of grass. Sexual morph: Undetermined. Asexual morph: Colonies effuse on the natural substrate, scattered, dark brown to dark. *Conidiomata*, immersed or semi-immersed, conical, globose to lenticular. *Conidiophores* micronematous, reduced to holoblastic conidiogenous cells. *Conidia* $18\text{--}22 \times 11\text{--}17\ \mu\text{m}$ ($\bar{x} = 19.5 \times 14\ \mu\text{m}$, $n = 20$), irregular ellipsoid or rarely globose to subglobose, brown to dark brown, rough, verruculose, truncate at base, sometimes with a basal cell.

Culture characteristics – *Conidia* germinated within 48 h on PDA. 6 cm diam. after three weeks at 27°C, cultures from above, dense, circular, umbonate, yellow; from below, pale yellow.

Material examined – China, Yunnan Province, Kunming, on dead stems of unidentified grass (Poaceae), 13 June 2022, Y. Gao, DG7A (HKAS 135359), living culture KUNCC 25-19130.

Known hosts and distribution – on leaf spots of *Dendrobium fimbriatum* (Orchidaceae) in China (Chen et al. 2017), on dead stems of grass (Poaceae) in Yunnan Province, China (This study).

GenBank numbers – KUNCC 25-19130: ITS = PV608531, LSU = PV607377, *rpb2* = PV665020.

Notes – In the multigene phylogenetic analyses, our collection (KUNCC 25-19130) grouped with *E. dendrobii* (CGMCC 3.18359, LC 8146, SMEL1) (Fig. 9). Morphologically, our collection (KUNCC 25-19130) is similar to *E. dendrobii* (CGMCC 3.18359, ex-type) in having globose or subglobose-pyriform conidia, which are smooth when young, later become multicellular-phragmosporous, verrucose, and brown. Our new collection is a saprophyte and it is reported as a new host record on grass in China based on phylogeny and morphology

Epicoccum kunmingense Y. Gao, H. Gui & K.D. Hyde, sp. nov.

Fig. 11

Index Fungorum number: IF903815; Facesoffungi number: FoF17692

Holotype – HKAS 133002

Etymology – The specific epithet “kunmingense” refers to the type locality of this fungus, Kunming City, China.

Saprobic on dead stems of grass. Sexual morph: Undetermined. Asexual morph: Colonies effuse on the natural substrate, aggregated, dark brown to dark. *Conidiomata* sporodochial, irregular, gregarious, superficial. *Conidiophores* $7\text{--}17 \times 5\text{--}7.5\ \mu\text{m}$ ($\bar{x} = 14.5 \times 6.5\ \mu\text{m}$, $n = 15$), micronematous, reduced to holoblastic conidiogenous cells. *Conidiogenous cells* $5\text{--}8 \times 3\text{--}5.5\ \mu\text{m}$ ($\bar{x} = 7 \times 4.2\ \mu\text{m}$, $n = 25$), short cylindrical, yellow to brown. *Conidia* $15\text{--}20 \times 7\text{--}13\ \mu\text{m}$ ($\bar{x} = 16.5 \times 10.5\ \mu\text{m}$, $n = 25$), mostly ellipsoid, rarely globose to subglobose, brown to dark brown, verruculose, truncate at base, sometimes with a basal cell.

Culture characteristics – *Conidia* germinated within 48 h on PDA. 6 cm diam. after three weeks at 27°C. cultures from above, dense, circular, umbonate, fluffy, pale yellow-brown with white or pink spots; from below, pale yellow.

Material examined – China, Yunnan Province, Kunming, on dead stems of unidentified grass (Poaceae), 23 June 2021, Y. Gao, CCSG4A (HKAS 133002, holotype), *ibid.*, CCSG4B (HKAS 145992).

GenBank numbers – HKAS 133002: ITS = PV608529, LSU = PV607375, *tub2* = PV613301, *rpb2* = PV654117, HKAS 145992: ITS = PV608530, LSU = PV607376, *tub2* = PV613302, *rpb2* = PV654118.

Notes – In the multigene phylogenetic analyses, our new collections (HKAS 133002, HKAS 145992) grouped with *E. mackenziei* (MFLUCC 16-0335, ex-type) with 73% ML and 0.87 PP support values (Fig. 9). *Epicoccum mackenziei* was reported with its sexual morph by Jayasiri et al. (2017), however, the asexual morph was not observed. The pairwise nucleotide comparison showed that our collection (HKAS 133002) differs from *Epicoccum mackenziei* (MFLUCC 16-0335) in 27/554 bp of *rpb2* (4.87%, without gaps). Morphologically, our collection differs from *Epicoccum mackenziei* (KUNCC 25-19128, KUNCC 25-19129) in its conidiomata (irregular, gregarious vs.

globose, scattered), conidiogenous cells ($5\text{--}8 \times 3\text{--}5.5\text{ }\mu\text{m}$, $L/W = 1.5$, cylindrical vs. $4\text{--}6 \times 2.5\text{--}4\text{ }\mu\text{m}$, $L/W = 1.5$, cylindrical or globose), conidia ($15\text{--}20 \times 7\text{--}13\text{ }\mu\text{m}$, $L/W = 1.8$ vs. $9\text{--}13 \times 5\text{--}9\text{ }\mu\text{m}$, $L/W = 1.6$), colony characters (from above pale yellow-brown with white or pink spots from below pale yellow vs. from above white, from below white to cream). Based on the polyphasic taxonomic approach recommended for species boundaries delimitation (Jayawardena et al. 2021, Maharachchikumbura et al. 2021a), *Epicoccum kunmingense* is introduced as a novel taxon by an asexual morph from China in this study.

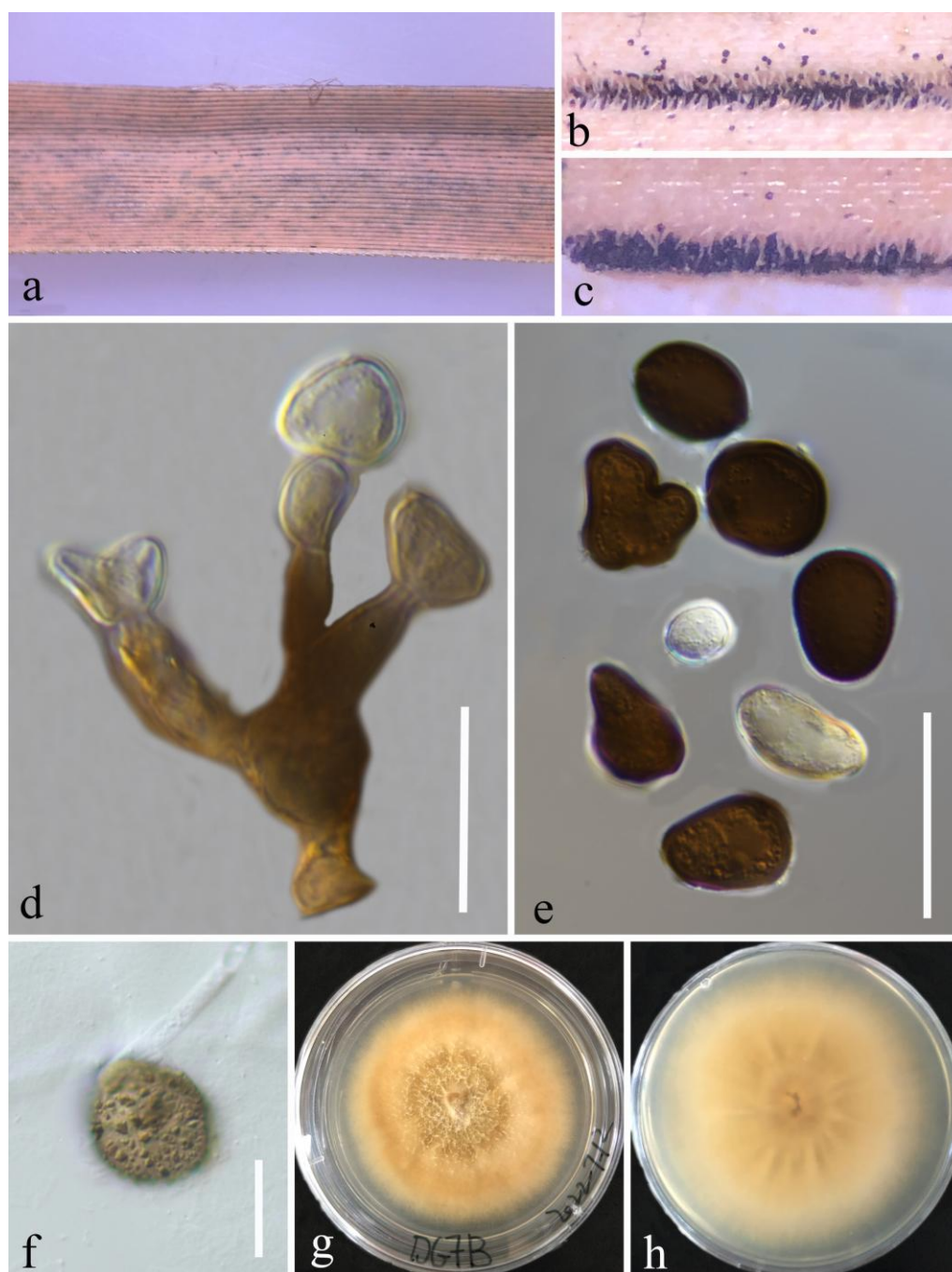


Figure 10 – *Epicoccum dendrobii* (HKAS 135359, a new host record). a–c Colonies on the host substrate. d Conidiogenous cells with attached conidium. e Conidia. f A germinated conidium. g, h Culture characters on PDA (g: above, h: below). Scale bars: e = $30\text{ }\mu\text{m}$, d, f = $15\text{ }\mu\text{m}$.

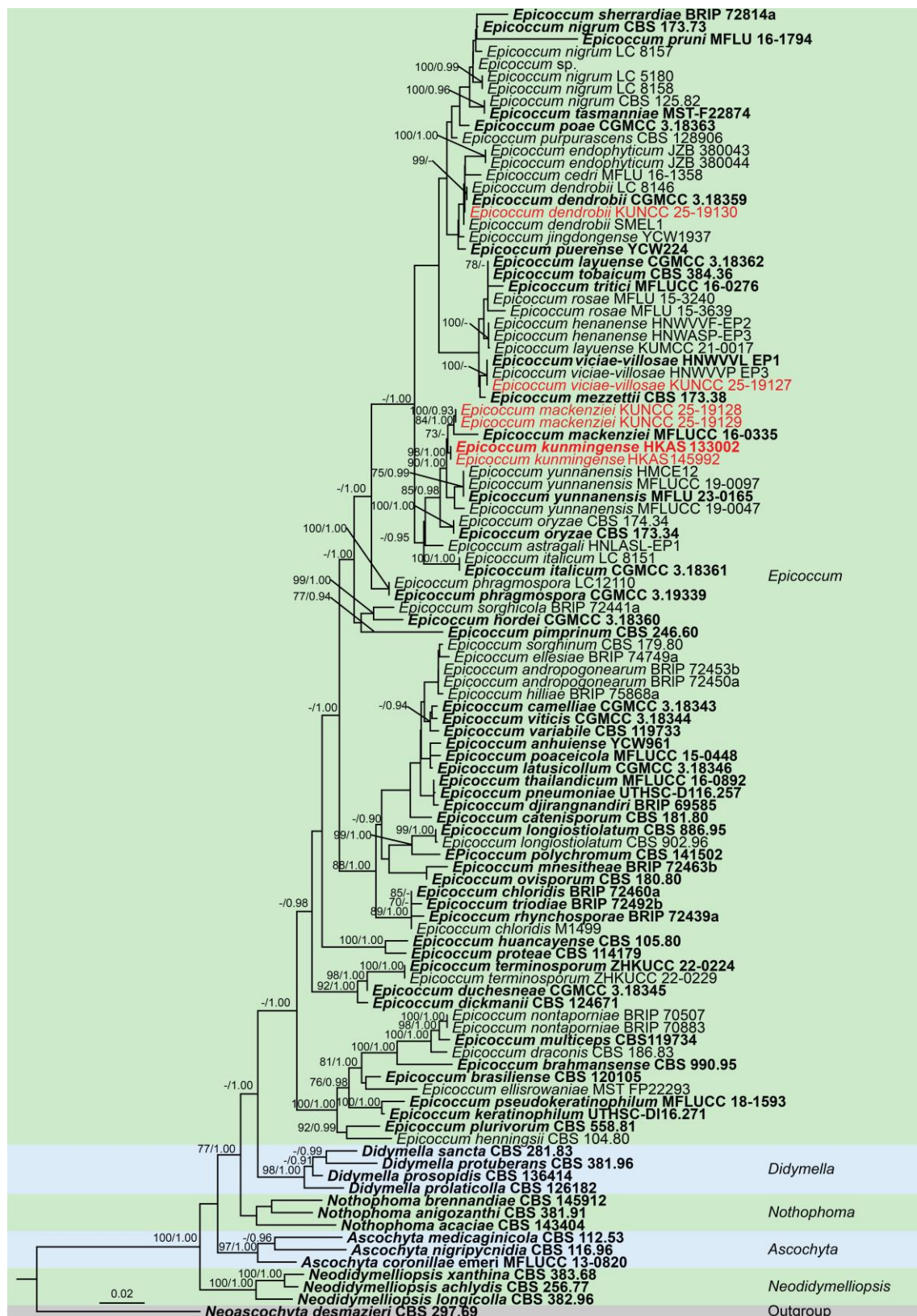


Figure 9 – RAxML phylogram generated from a combined dataset of partial ITS, LSU, *tub2*, and *rpb2* DNA sequence analyses for *Epicoccum*. Related sequences are obtained following Tian et al. (2024). One hundred and six strains were included in the combined analyses, which comprised 2,295 characters in the combined ITS, LSU, *tub2*, and *rpb2* alignment. *Neosascochyta desmazieri* (CBS 297.69) was used as the outgroup taxon. The best-scoring RAxML tree with a final likelihood value of -15447.513440 is presented. The matrix contained 685 distinct alignment patterns, with 15.90% of undetermined characters or gaps. Estimated base frequencies were as

follows; A = 0.239405, C = 0.245214, G = 0.274757, T = 0.240624; substitution rates AC = 1.530143, AG = 5.765732, AT = 1.863354, CG = 0.931494, CT = 11.601279, GT = 1.000000. The tree topology of the ML analysis is similar to the Bayesian analysis. Bootstrap values for ML equal to or greater than 70% and PP values greater than 0.90 (rounding of values to 2 decimal places) are labelled on the nodes. Strains of the newly described species are in orange, while type strains are in bold. (ITS: 486 bp, LSU: 880 bp, *tub2*: 333 bp, *rpb2*: 596 bp)

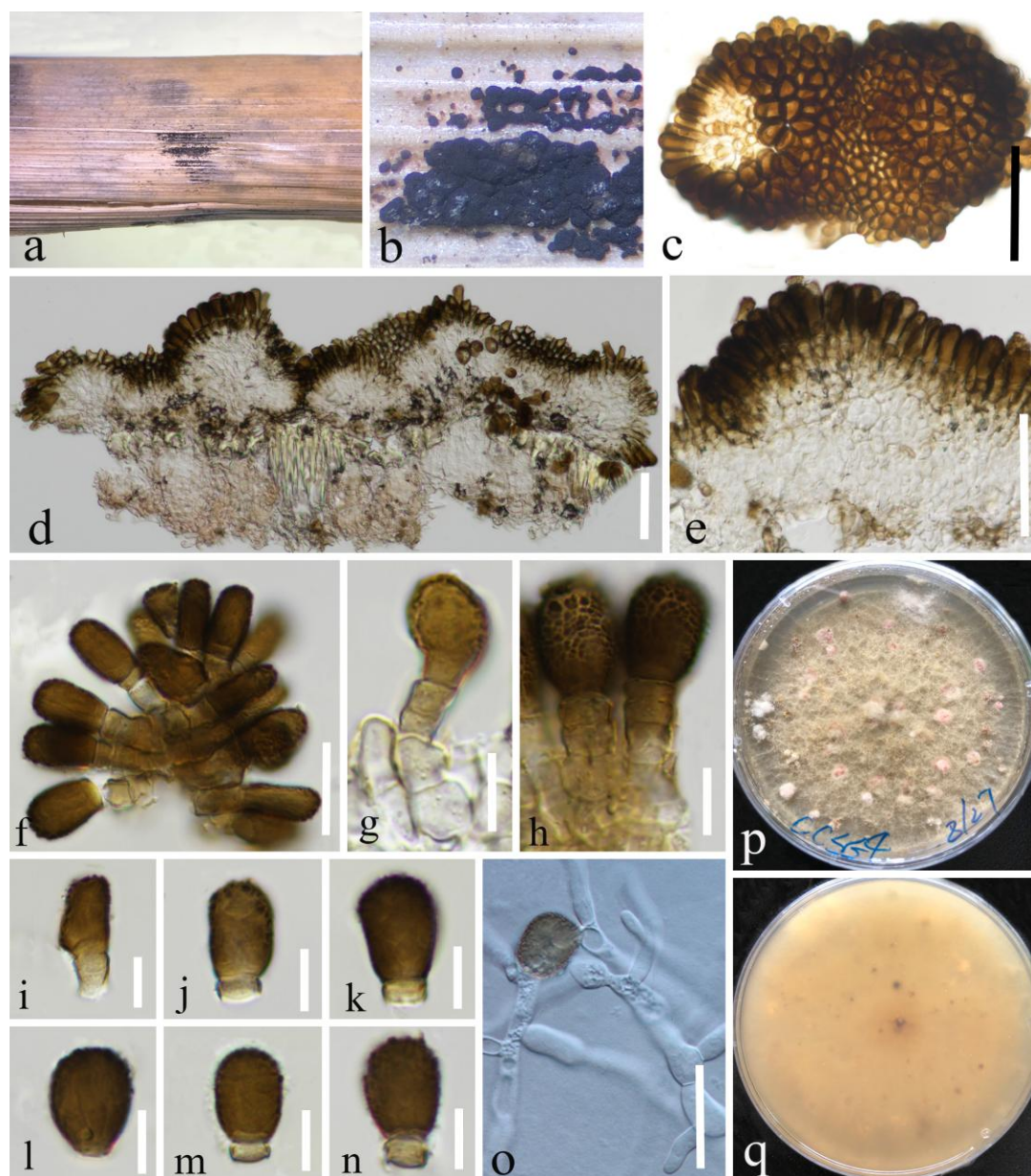


Figure 11 — *Epicoccum kunmingense* (HKAS 133002, holotype). a, b Colonies on the host substrate. c Sporodochium. d, e Vertical sections of sporodochia. f–h Conidiogenous cells with attached conidium. i–n Conidia. o A germinated conidium. p Colony on PDA (p: above, q: below). Scale bars: c–e = 50 μ m, o = 30 μ m, f = 20 μ m, g–n = 10 μ m.

Epicoccum mackenziei Jayasiri, Camporesi & K.D. Hyde, Mycosphere 8 (8): 1093 (2017)
Fig. 12

Index Fungorum number: IF552362; Facesoffungi number: FoF02503

Saprobic on the dead stem of *Lolium perenne*. Sexual morph: Undetermined. Asexual morph: Colonies effuse on the natural substrate, scattered, dark brown to dark. *Conidiomata* 80–110 $\times$ 65–85 μ m ($\bar{x}$ = 96 $\times$ 76 μ m, n = 10), sporodochial, globose, scattered, superficial. *Conidiophores*

micronematous, reduced to holoblastic conidiogenous cells. *Conidiogenous cells* $4\text{--}6 \times 2.5\text{--}4\ \mu\text{m}$ ($\bar{x} = 5 \times 3\ \mu\text{m}$, $n = 20$), short cylindrical or globose, yellow to brown. *Conidia* $9\text{--}13 \times 5\text{--}9\ \mu\text{m}$ ($\bar{x} = 12 \times 7\ \mu\text{m}$, $n = 25$), mostly ellipsoid, rarely globose to subglobose, brown to dark brown, verruculose, truncate at base, sometimes with a basal cell.

Culture characteristics – Conidia germinated within 48 h on PDA. 2 cm diam. after two weeks at 27°C. cultures from above, dense, circular, umbonate, fluffy, white; from below, white to cream.

Material examined – China, Yunnan Province, Zhaotong grassland, on dead stems of *Lolium perenne* (Poaceae), 25 August 2022, Y. Gao, QG60A (HKAS 135355), living culture KUNCC 25-19128, *ibid.*, QG60B (HKAS 145983) living culture KUNCC 25-19129.

Known hosts and distribution – on dead aerial stems of *Ononis spinosa* (Fabaceae) in Italy (Jayasiri et al. 2017), on dead stems of *Lolium perenne* (Poaceae) in Yunnan Province, China (This study).

GenBank numbers – KUNCC 25-19128: ITS = PV608527, LSU = PV607373, *rpb2* = PV665021. KUNCC 25-19129: ITS = PV608528, LSU = PV607374, *rpb2* = PV665022.

Notes – In the multigene phylogenetic analyses, our collections (KUNCC 25-19128, KUNCC 25-19129) grouped with *Epicoccum mackenziei* (MFLUCC 16-0335, ex-type) with 84% ML and 1.00 PP support values (Fig. 9). However, the asexual morph of *E. mackenziei* (MFLUCC 16-0335) was not observed, and the morphs of our collection and *E. mackenziei* (MFLUCC 16-0335) could not be compared (Jayasiri et al. 2017). The pairwise nucleotide comparison showed that our collection (KUNCC 25-19128) differs from *E. mackenziei* (MFLUCC 16-0335) in 23/555 bp of *rpb2* (4.14%, with 1 gap), in 0/490 bp of ITS (0.00%), 0/845 bp of LSU (0.00%). Therefore, based on the polyphasic approach recommended for species boundaries delimitation (Jayawardena et al. 2021, Maharachchikumbura et al. 2021a), we introduce our collections as a new host and a geographical record of *E. mackenziei*, and provide its asexual morph.

Epicoccum viciae-villosae W.S. Zhao, Q. Ning & J.Y. Yan, Mycosphere 14 (1): 19 (2023) Fig. 13

Index Fungorum number: IF558424; Facesoffungi number: FoF10794

Saprobic on dead stems of *Lolium perenne*. Sexual morph: Undetermined. Asexual morph: Colonies effuse on the natural substrate, scattered, dark brown to dark. *Conidiomata* sporodochial, irregular, scattered, superficial. *Conidiophores* micronematous, reduced to holoblastic conidiogenous cells. *Conidia* $16\text{--}26 \times 15\text{--}29\ \mu\text{m}$ ($\bar{x} = 20 \times 21\ \mu\text{m}$, $n = 25$), multicellular-phragmosporous, mostly globose to subglobose, brown to dark brown, rough, verruculose, truncate at base, sometimes with a basal cell.

Culture characteristics – Conidia germinated within 48 h on PDA. 2 cm diam. after two weeks at 27°C. cultures from above, dense, circular, umbonate, fluffy, white; from below, white to cream.

Material examined – China, Yunnan Province, Kunming, on dead stems of unidentified grass (Poaceae), 25 March 2021, Y. Gao, GY46 (HKAS 135340), living culture KUNCC 25-19127.

Known hosts and distribution – from *Vicia villosa* (Fabaceae) in China (Abeywickrama et al. 2023), on dead stems of grass (Poaceae) in Yunnan Province, China (This study).

GenBank numbers – KUNCC 25-19127: ITS = PV608526, LSU = PV607372.

Notes – In the phylogenetic analyses of ITS, LSU, *tub2*, and *rpb2*, our collection (KUNCC 25-19127) grouped with *Epicoccum viciae-villosae* (HNWVVL EP1, HNWVVP EP3) (Fig. 9). Our collection (HKAS 135340) is morphologically similar to *Epicoccum viciae-villosae* (HNWVVL EP1, ex-type) in having scattered conidiomata and multicellular, globose to subglobose conidia. The comparison of nucleotides shows our collection has 100% (489/489) and 100% (776/776) similarities with *Epicoccum viciae-villosae* in ITS and LSU sequence data, respectively. Therefore, based on the polyphasic approach recommended for species boundaries delimitation (Jayawardena et al. 2021, Maharachchikumbura et al. 2021a), we identified our collection as *Epicoccum viciae-*

villosae based on morphological characters and phylogenetic analyses. Our new collection is a new host record of grass (Poaceae) in China.

Neoascochyta Qian Chen & L. Cai, Stud. Mycol. 82: 198 (2015)

Notes – Chen et al. (2015) established *Neoascochyta* to accommodate taxa that exhibit morphological similarities to *Ascochyta* but are phylogenetically distinct. This genus is classified within the family Didymellaceae, whose members are predominantly parasitic on woody substrates and on dead herbaceous stems and leaves (Hyde et al. 2013). There were 21 species accepted in the genus *Neoascochyta* (Index Fungorum 2025). This genus is morphologically characterized by pseudothecial ascomata, cylindrical or subclavate asci, hyaline, cylindrical to ovoid, 1-septate ascospores. The asexual morph is coelomycetous, with pycnidial conidiomata, a pseudoparenchymatous wall, ampulliform to doliiform or obpyriform conidiogenous cells, and fusoid to cylindrical, hyaline, obclavate-ovoid to ellipsoidal conidia (Chen et al. 2015). In this study, we introduce a new host record for *Neoascochyta humicola* and a new species, *N. zhaotongensis*, together with descriptions and illustrations (Figs. 15, 16). An updated phylogenetic tree based on combined ITS, LSU, *tub2*, and *rpb2* sequence data is presented in Fig. 14.

Neoascochyta humicola L.W. Hou, L. Cai & Crous, Stud. Mycol. 96: 389 (2020)

Fig. 15

Index Fungorum number: IF834683; Facesoffungi number: FoF18349

Saprobic on dead stems of grass. Sexual morph: Undetermined. Asexual morph: *Conidiomata* 115–150 µm diam. × 90–120 µm high ($\bar{x}$ = 140 × 100 µm, n = 10), immersed or erumpent, with dark brown to black spots on the host surface, subglobose to globose, scattered or gregarious, black, ostiolate. *Ostiole* circular, papillate. *Conidioma* wall 13–25 µm wide ($\bar{x}$ = 18 µm, n = 30), composed of thick-walled, brown to hyaline cells of *textura angularis*. *Conidiogenous cells* 5–15 × 2–9 µm ($\bar{x}$ = 5 × 10 µm, n = 15), enteroblastic, phialidic, cylindrical, discrete or integrated, indeterminate, smooth, arising from inner layers of conidioma. *Conidia* 15.5–19 × 4–6 µm ($\bar{x}$ = 17 × 5 µm, n = 30), fusiform, 1-septate, slightly constricted at the septa, straight, obtuse at both ends, smooth-walled, guttulate, hyaline.

Culture characteristics – Colonies on PDA reaching 50 mm diam. after four weeks at 27°C, colonies from above, circular, dense, papillate with fluffy, gray with white spots; from below, gray with black spots, paler toward margins.

Material examined – China, Yunnan Province, Kunming, on a decaying stem of unidentified grass (Poaceae), 1 October 2022, Y. Gao, MG12 (HKAS 132974), living culture KUNCC 25-19131.

Known hosts and distribution – from soil in the United States (Hou et al. 2020), on dead stems of grass (Poaceae) in Yunnan Province, China (This study).

GenBank numbers – KUNCC 25-19131: ITS = PV608532, LSU = PV607378, *rpb2* = PV655529.

Notes – *Neoascochyta humicola* was introduced by Hou et al. (2020), who concluded from a phylogenetic perspective that *N. humicola* (CBS 127323, ex-type) formed a distinct sister lineage with *N. fusiformis* (CBS 876.72, ex-type). However, the morphological information of *Neoascochyta humicola* (CBS 127323) was not provided. In this study, our collection (KUNCC 25-19131) grouped with the ex-type strain of *Neoascochyta humicola* (CBS 127323) with 72% ML and 1.00 PP statistical support (Fig. 14). Morphologically, *Neoascochyta humicola* differs from *N. fusiformis* by conidiomata (115–150 × 90–120, L/W = 1.3 vs. 230–600 × 220–440 µm, L/W = 1.3), conidiogenous cells (5–15 × 2–9, L/W = 1.8 vs. 7.5–11 × 6–10 µm, L/W = 1.2), conidia length (15.5–19 vs. 16–25.5 µm) (Hou et al. 2020). Therefore, we introduce our collection as a new host and a geographical record of *Neoascochyta humicola* from grass (Poaceae) in China and provide a detailed morphological description.

Neoascochyta zhaotongensis Y. Gao, H. Gui & K.D. Hyde, sp. nov.

Fig. 16

Index Fungorum number: IF903816; Facesoffungi number: FoF17693

Holotype – HKAS 132989

Etymology – The specific epithet “zhaotongensis” refers to Zhaotong City, where the holotype was collected.

Saprobic on a dead leaf blade of *Dactylis glomerata* (Cock's-foot or orchard grass). Sexual morph: *Ascomata* 50–75 μm diam. ($\bar{x}$ = 66 μm , n = 15), subglobose to globose, semi-immersed to erumpent through the host surface, scattered, solitary, uni-loculate, dark brown. *Peridium* 6–10 μm wide ($\bar{x}$ = 8 μm , n = 20), composed of 1–3 layers of light brown to brown cells of *textura angularis* or *textura globulosa*. *Asci* 38–72 $\times$ 17–26.5 μm ($\bar{x}$ = 56 $\times$ 20 μm , n = 30), 8-spored, broad cylindrical-clavate, bitunicate, fissitunicate, apically rounded, short pedicellate, thick-walled, with an ocular chamber. *Ascospores* 20–25 $\times$ 6–8 μm ($\bar{x}$ = 23 $\times$ 7 μm , n = 30), biserial, broad fusiform with acute ends, tapering towards the ends, 1-septate, constricted at the septum, smooth, with guttulate, hyaline. Asexual morph: Undetermined.

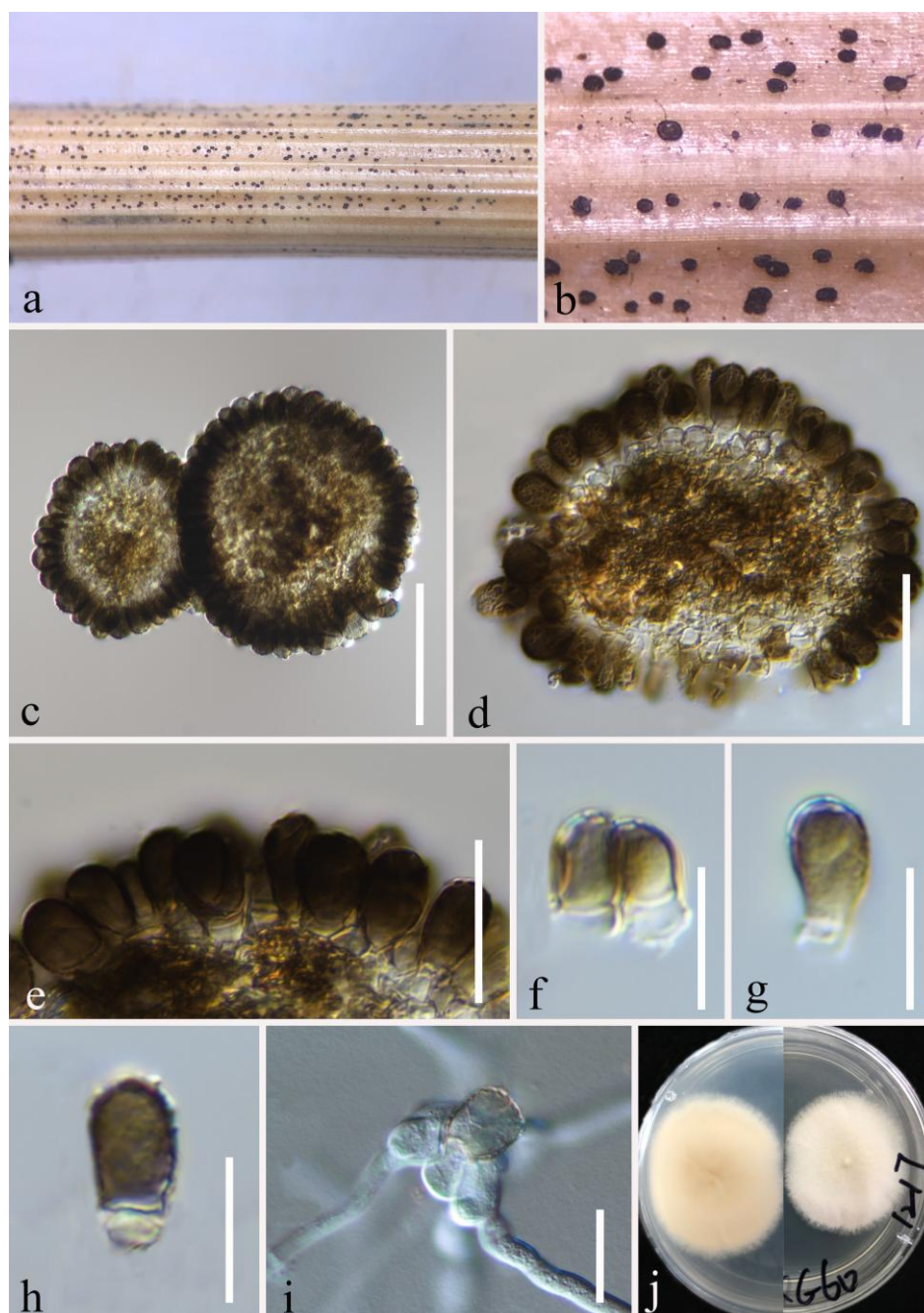


Figure 12 – *Epicoccum mackenziei* (HKAS 135355, a new host and a geographical record). a, b Colonies on the host substrate. c, d Conidiomata. e Conidiogenous cells with attached conidia. f–h

Conidia. i A germinated conidium. j Culture characters on PDA (left: below, right: above). Scale bars: c = 50 μ m, d = 30 μ m, e, i = 20 μ m, f–h = 10 μ m.

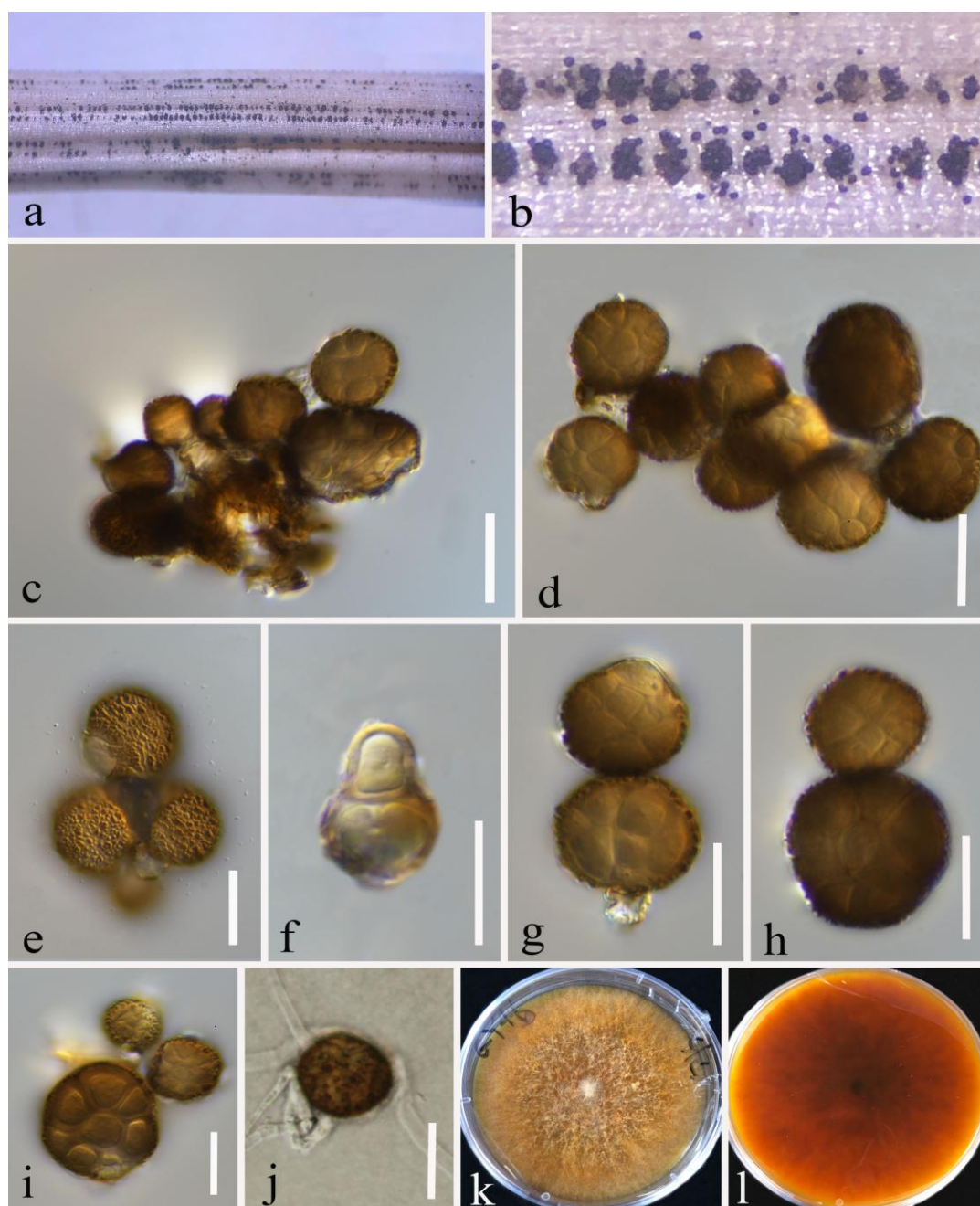


Figure 13 – *Epicoccum viciae-villosae* (HKAS 135340, a new host record). a, b Colonies on the host substrate. c Sporodochia. d–i Conidia. j A germinated conidium. k, l Culture characters on PDA (k: above, l: below). Scale bars: c, d, j = 20 μ m, e–i = 15 μ m.

Culture characteristics – Asci germinated within 48 h on PDA. 1.5 cm diam. after two weeks at 27°C. cultures from above, dense, circular, umbonate, fluffy, gray; from below, pale gray at the margin and gray at the center.

Material examined – China, Yunnan Province, Zhaotong grassland, on dead stems of *Dactylis glomerata* (Poaceae), 27 August 2022, Y. Gao, QG90 (HKAS 132989, holotype), ex-type living culture KUNCC 25-19132.

GenBank numbers – KUNCC 25-19132: ITS = PV608533, LSU = PV607379, *rpb2* = PV655530.

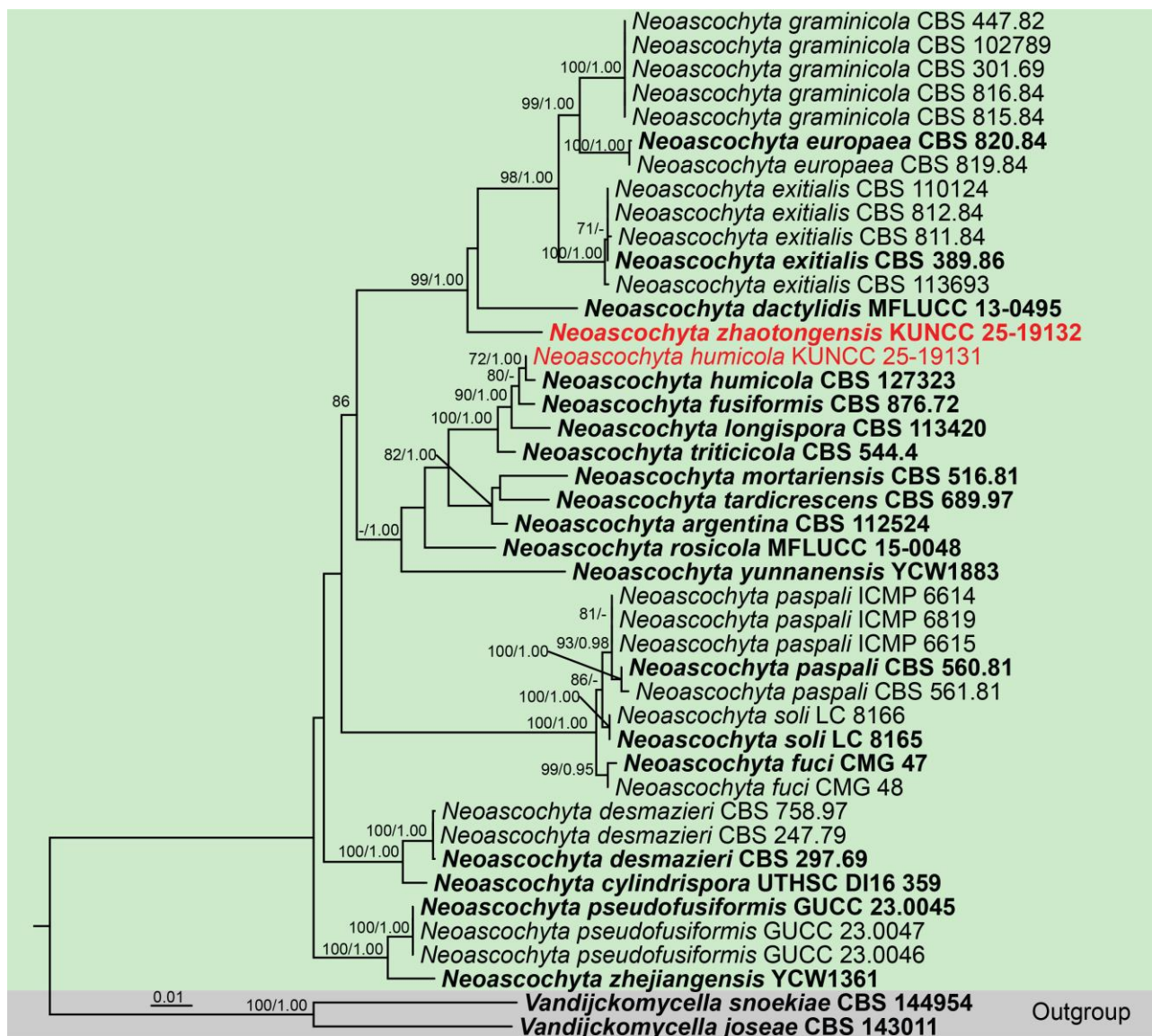


Figure 14 – RAxML phylogram generated from a combined dataset of partial ITS, LSU, *tub2*, and *rpb2* DNA sequence analyses for *Neoascochyta*. Related sequences are obtained following Fu et al. (2024). Forty-three strains were included in the combined analyses, which comprised 2,376 characters in the combined ITS, LSU, *tub2*, and *rpb2* alignment. *Vandijckomyces joseae* (CBS 143011) and *Vandijckomyces snoekiae* (CBS 144954) were used as the outgroup taxa. The best-scoring RAxML tree with a final likelihood value of -8682.499472 is presented. The matrix contained 462 distinct alignment patterns, with 15.33% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.238376, C = 0.242965, G = 0.278387, T = 0.240272; substitution rates AC = 2.504713, AG = 8.499645, AT = 2.121347, CG = 1.106325, CT = 15.690257, GT = 1.000000. The tree topology of the ML analysis is similar to the Bayesian analysis. Bootstrap values for ML equal to or greater than 70% and PP values greater than 0.95 (rounding of values to 2 decimal places) are labelled on the nodes. Strains of the newly described species are in orange, while type strains are in bold. (ITS: 487 bp, LSU: 960 bp, *tub2*: 333 bp, *rpb2*: 596 bp)

Notes – Morphological characteristics and multigene analyses have demonstrated that *Neoascochyta zhaotongensis* (KUNCC 25-19132) is a phylogenetically distinct species, showing the close relationship to *N. dactylidis* (MFLUCC 13-0495, ex-type) with 99% ML and 1.00 PP support values (Fig. 14). *Neoascochyta dactylidis*, previously collected on dead aerial stems of *Dactylis glomerata* (Poaceae) in Italy (Li et al. 2020a), but the authors have not provided the sexual

morph for this fungus. Therefore, the morphological comparison between our new species and *Neoscochyta dactylidis* is not possible. The pairwise nucleotide comparison showed that our collection *Neoscochyta zhaotongensis* (KUNCC 25-19132) differs from *N. dactylidis* (MFLUCC 13-0495) in 16/476 bp of ITS (3.4%, with 4 gaps), 3/877 bp of LSU (0.3%, without gaps). Based on both phylogeny and morphology, *Neoscochyta zhaotongensis* is described as a new species from China.

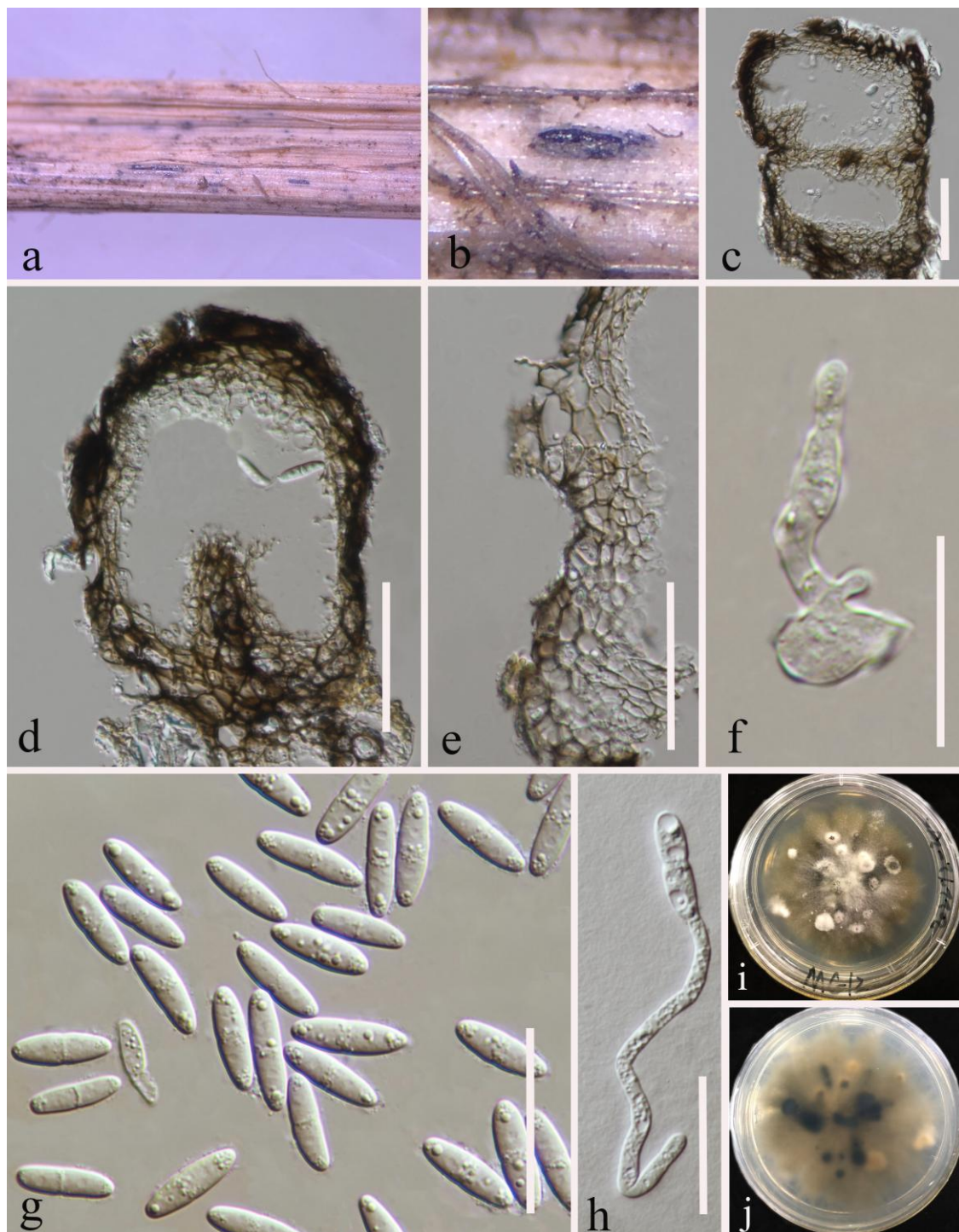


Figure 15 – *Neoscochyta humicola* (HKAS 132974, a new host and a geographical record). a, b Appearance of conidiomata on the host substrate. c, d Vertical sections of conidiomata. e Conidioma wall. f Conidiogenous cells. g Conidia. h A germinated conidium. i, j Colony on PDA (i: above, j: below). Scale bars: c–e = 50 μ m, g, h = 30 μ m, f = 20 μ m.

Didymosphaeriaceae Munk, Dansk botanisk Arkiv 15 (2): 128 (1953)

Notes – Didymosphaeriaceae was established by Munk (1953), with *Didymosphaeria* as the type genus. Didymosphaeriaceae comprises 38 genera and 255 species (Hyde et al. 2024a). The sexual morphs of this family are characterized by globose to subglobose, centrally ostiolate ascomata, trabeculate pseudoparaphyses that predominantly anastomose above the asci (Liew et al. 2000), cylindric or oblong pedicellate asci, and brown, thick-walled, septate ascospores (Aptroot 1995, Ariyawansa et al. 2014a). The asexual morphs are described as fusicladium-like and phoma-like (Hyde et al. 2013). Members of Didymosphaeriaceae primarily inhabit terrestrial and aquatic environments, functioning as endophytes, saprobes, pathogens, and hemibiotrophs on herbaceous stems, woody branches, and leaves. They can also parasitize other fungi (Ariyawansa et al. 2014a, Thambugala et al. 2017, Phookamsak et al. 2019). An updated phylogenetic tree based on combined ITS, LSU, SSU, and *tef1*- α sequence data is presented in Fig. 17.

Letendraea Sacc., Michelia 2 (6): 73 (1880)

Notes – *Letendraea* was reported by Saccardo (1880), with *L. eurotioides* designated as its type species. Members of this genus exhibit saprobic lifestyles in terrestrial ecosystems, while some act as pathogens causing leaf spot disease in *Cordyline* species (Ariyawansa et al. 2014a). Additionally, certain species have been documented in marine environments (Huang et al. 2019). There are 15 species accepted under *Letendraea* (Index Fungorum 2025). In this study, we introduce a new host record for *Letendraea helminthicola*, based on morphology and molecular data, together with descriptions and illustrations (Fig. 18).

Letendraea helminthicola (Berk. & Broome) Weese ex Petch, Transactions of the British Mycological Society 21 (3–4): 277 (1938) Fig. 18

Index Fungorum number: IF252540; Facesoffungi number: FoF09440

Saprobic on a dead leaf blade of an unidentified plant. Sexual morph: *Ascomata* 130–155 μm diam. $\times$ 120–150 μm high ($\bar{x}$ = 145 $\times$ 130 μm , n = 10), globose or subglobose, immersed black dots on the host substrate, solitary, scattered, uni-loculate, brown to dark brown. *Peridium* 12–23 μm wide ($\bar{x}$ = 16 μm , n = 30), composed of 2–4 layers of pale brown to brown cells of *textura angularis*, inner layers comprising thin, hyaline cells. *Hamathecium* comprises 2–3.5 μm wide ($\bar{x}$ = 2.5 μm , n = 30), numerous filamentous, branched, hyaline, septate, guttulate, pseudoparaphyses. *Asci* 45–80 $\times$ 8–12 μm ($\bar{x}$ = 65 $\times$ 9.5 μm , n = 20), 8-spored, bitunicate, cylindrical-clavate, apically rounded, short pedicellate. *Ascospores* 14–19 $\times$ 4–8 μm ($\bar{x}$ = 17 $\times$ 5.5 μm , n = 25), biseriate, ellipsoidal to fusiform, 1-septate, straight or slightly curved, acute at both ends, thick-walled, olivaceous brown. Asexual morph: Undetermined.

Culture characteristics – Ascospores germinated within 48 h on PDA. Colonies on PDA were irregular and approx., 5.5 cm diam. after four weeks at 27 °C. Culture from above, cream, brown in the middle, edge white, dense, flattened, umbonate; from below, cream, thin, with flat parchment-like sheets.

Material examined – China, Yunnan Province, Kunming, on a dead leaf blade of an unidentified plant from grassland, 06 June 2021, Y. Gao, GY111 (HKAS 126573), living culture KUNCC 25-19133.

Known hosts and distribution – on *Helminthosporium appendiculatum* in the United Kingdom (Petch 1938), healthy leaves of *Magnolia candolli* (Magnoliaceae) in China (De Silva et al. 2021), on a dead leaf blade of an unidentified plant from grassland in Yunnan Province, China (This study).

GenBank numbers – KUNCC 25-19133: ITS = PV642533, LSU = PV607380, SSU = PV607279, *tef1*- α = PV626423.

Notes – The sexual morph of *Letendraea helminthicola* was introduced as a hyper-pathogenic fungus by Petch (1938). Our new collection, KUNCC 25-19133, is phylogenetically related to *Letendraea helminthicola* (MFLUCC 19-0055, CBS 884.85) with 86% ML and 0.56 PP support (Fig. 17). Our new collection and *Letendraea helminthicola* (MFLUCC 19-0055) have similar

morphological characters (Petch 1938). Therefore, based on morphology and phylogenetic affinity, we identify our collection as *Letendraea helminthicola* and report it here as a new host record.

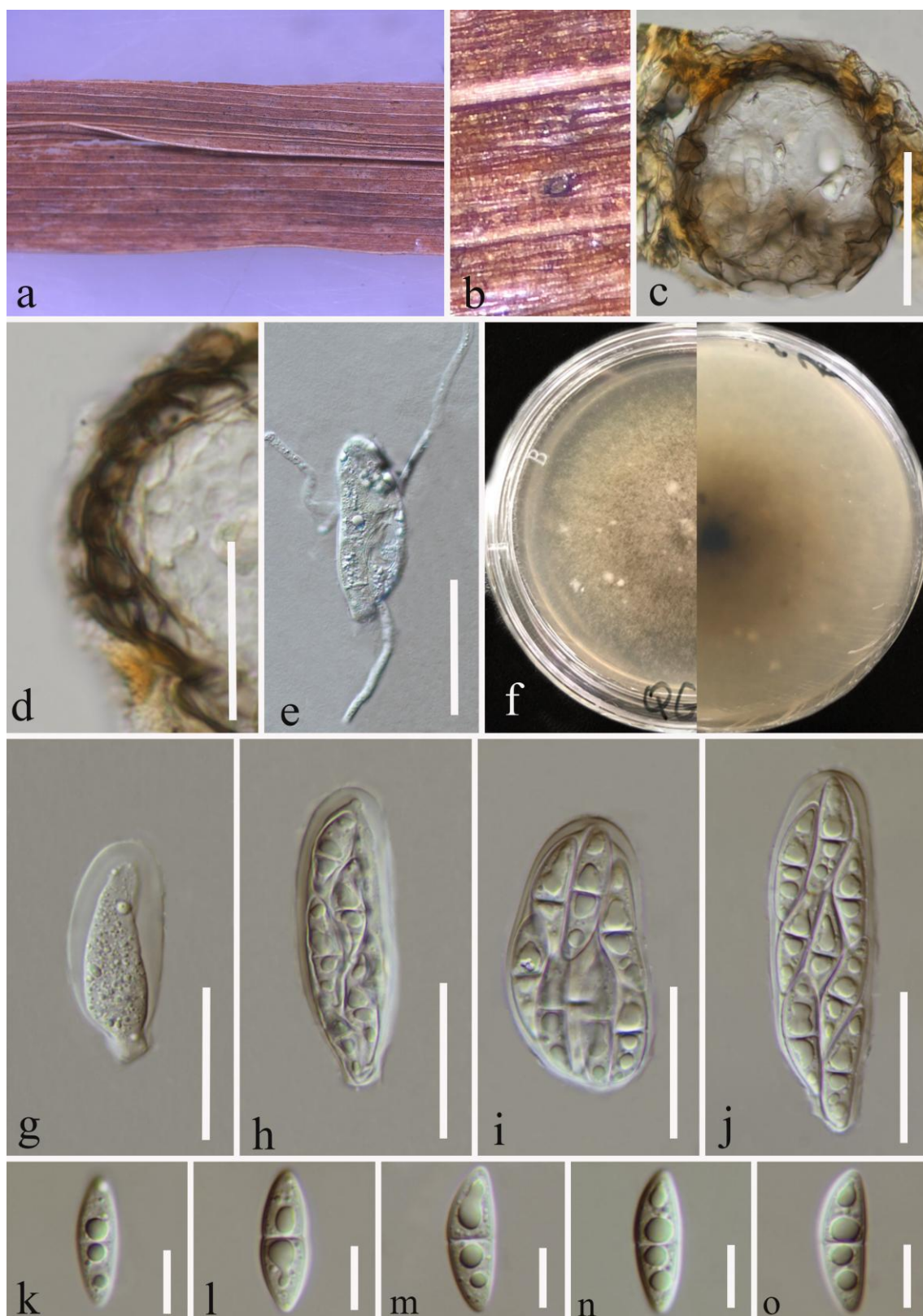


Figure 16 – *Neoascochyta zhaotongensis* (HKAS 132989, holotype). a, b Appearance of ascomata on the host substrate. c Section of an ascoma. d Peridium. e A germinated ascus. f Culture characters on PDA (left: above, right: below). g–j Asci. k–o Ascospores. Scale bars: c–e = 50 µm, g–j = 30 µm, k–o = 10 µm.

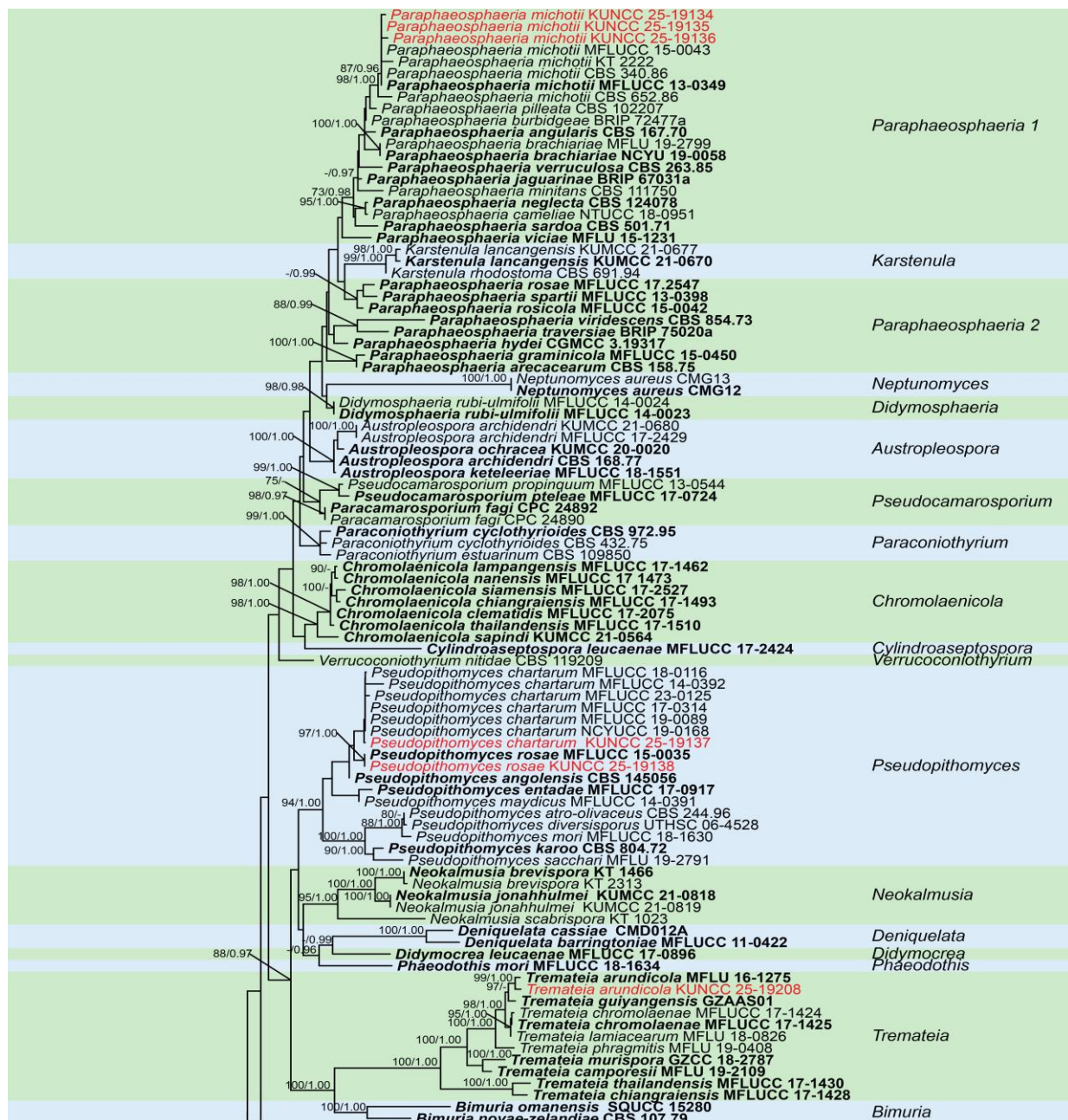


Figure 17 – RaxML phylogram generated from a combined dataset of partial ITS, LSU, SSU, and *tef1-α* DNA sequence analyses for Didymosphaeriaceae. Related sequences are obtained following De Silva et al. (2021), Tennakoon et al. (2021a, 2022), Ren et al. (2022), Devadatha et al. (2023) and Wanasinghe et al. (2024). One hundred and seventy strains were included in the combined analyses, which comprised 3,237 characters in the combined ITS, LSU, SSU, and *tef1-α* alignment. *Bambusistroma didymosporum* (MFLU 15-0057 and MFLU 15-0058) were used as the outgroup taxa. The best-scoring RaxML tree with a final likelihood value of -27064.588944 is presented. The matrix contained 1,333 distinct alignment patterns, with 26.29% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.238953, C = 0.251099, G = 0.271454, T = 0.238494; substitution rates AC = 1.531349, AG = 2.848178, AT = 1.654540, CG = 1.056237, CT = 7.510174, GT = 1.000000. The tree topology of the ML analysis is similar to the Bayesian analysis. Bootstrap values for ML equal to or greater than 70% and PP values greater than 0.95 (rounding of values to 2 decimal places) are labelled on the nodes. Strains of the newly described species are in orange, while type strains are in bold. (ITS: 445 bp, LSU: 923 bp, SSU: 950 bp, *tef1-α*: 919 bp)



Figure 17 – Continued.

Montagnula Berl., Icones Fungorum. Pyrenomycetes 2: 68 (1896)

Notes – *Montagnula* was initially established by Berlese (1896) to accommodate the species *M. infernalis*. Later, Ariyawansa et al. (2014a) assigned this genus to the Didymosphaeriaceae based on Phylogenetic analysis. Members of *Montagnula* are primarily saprobic organisms that thrive on decaying plant material (Ariyawansa et al. 2014a, Mapook et al. 2020). The sexual morph is characterized by immersed, globose ascomata with a clypeus, claviform asci, ellipsoid or fusoid ascospores with transverse septa and longitudinal septa (Ariyawansa et al. 2014a, Mapook et al. 2020). There are 57 species accepted in the genus *Montagnula* (Index Fungorum 2025). In this study, we introduce a new host record for *Montagnula shangrilana*, based on morphology and molecular data, together with descriptions and illustrations (Fig. 19).

Montagnula shangrilana Wanas., MycoKeys 101: 213 (2024)

Fig. 19

Index Fungorum number: IF850095; Facesoffungi number: FoF18350

Saprobic on dead woody litter of herbaceous plants. Sexual morph: *Ascomata* 370–430 µm diam. × 200–250 µm high ($\bar{x}$ = 400 × 230 µm, n = 10), globose or subglobose, immersed, solitary, scattered, uni-loculate, flattened base, brown to black with a central ostiole. *Ostiole* central, papillate. *Peridium* 7–24 µm wide ($\bar{x}$ = 13 µm, n = 35), fused with host tissues, comprising two layers of hyaline to brown cells of *textura angularis*. *Hamathecium* comprises 2–5 µm wide ($\bar{x}$ = 3 µm, n = 35), numerous filamentous, branched, hyaline, septate, guttulate, pseudoparaphyses. *Asci* 120–165 × 18–26 µm ($\bar{x}$ = 150 × 21 µm, n = 20), 8-spored, bitunicate, cylindrical-clavate, apically

rounded, slightly curved, short-stalked. *Ascospores* $25\text{--}35.5 \times 8\text{--}13.5 \mu\text{m}$ ($\bar{x} = 32.5 \times 10.5 \mu\text{m}$, $n = 30$), biseriate, fusiform, 1-septate, pale yellow to yellow-brown when immature, 3-septate, dark brown when mature, conical at both ends, guttulate, without appendages, and mucilaginous sheath. Asexual morph: Undetermined.

Culture characteristics – Ascospores germinated within 48 h on PDA. Colonies on PDA were irregular and approx. 6 cm diam. after three weeks at 27°C. Culture from above, grey, filiform, umbonate; from below, light yellow-brown, radiating outwardly.

Material examined – China, Yunnan Province, Qujing grassland, on dead stems of unidentified herbaceous plants, 27 August 2022, Y. Gao, QG14A (HKAS 128793), living culture CGMCC 3.25082; *ibid.*, QG14B (HKAS 128794), living culture CGMCC 3.25083.

Known hosts and distribution – on dead woody litter of *Rhododendron* sp. (Ericaceae) in China (Wanasinghe et al. 2024), on dead stems of an unidentified herbaceous plant from grassland in Yunnan Province, China (This study).

GenBank numbers – CGMCC 3.25082: ITS = PV608534, LSU = PV607381, SSU = PV607280, *tef1- α* = PV626424; CGMCC 3.25083: ITS = PV608535, LSU = PV607382, SSU = PV607281, *tef1- α* = PV626425.

Notes – Our phylogenetic analysis showed that our new collections (CGMCC 3.25082 and CGMCC 3.25083) grouped with *Montagnula shangrilana* (KUNCC 23-14433, KUNCC 23-14434) with 100% ML and 1.00 PP support values (Fig. 17). Our collections (CGMCC 3.25082 and CGMCC 3.25083) differ from *M. shangrilana* (KUNCC 23-14434, ex-type) in its ascomata ($370\text{--}430 \times 200\text{--}250 \mu\text{m}$, L/W = 1.8 vs. $150\text{--}210 \times 120\text{--}180 \mu\text{m}$, L/W = 1.2), asci ($120\text{--}165 \times 18\text{--}26 \mu\text{m}$, L/W = 6.5 vs. $90\text{--}140 \times 20\text{--}30 \mu\text{m}$, L/W = 4.6), ascospores ($25\text{--}35.5 \times 8\text{--}13.5 \mu\text{m}$, L/W = 2.8 vs. $48\text{--}60 \times 17\text{--}22 \mu\text{m}$, L/W = 2.8). However, Comparisons of the SSU, LSU, ITS, and *tef1- α* sequences of our collections (CGMCC 3.25082 and CGMCC 3.25083) and *M. shangrilana* (KUNCC 23-14434) showed 99.9% (1014/1015 bp), 100% (840/840 bp), 99.57% (460/462 bp) and 99.43% (876/881 bp) similarity, respectively. Based on morphological characteristics and phylogenetic analyses, we report our collections as a new host record of *Montagnula shangrilana* from decaying herbaceous plants in China.

Paraphaeosphaeria O.E. Erikss., Ark. Bot. Ser. 2. 6 (4–5): 405 (1967)

Notes – *Paraphaeosphaeria* was introduced by Eriksson (1967) to accommodate four species, which have oblong-cylindric ascospores with *P. michotii* as the type species. The sexual morphs of *Paraphaeosphaeria* are characterized by semi-immersed or immersed ascomata, short pedicellate asci, and yellowish-brown, broadly elliptical, multi-septate ascospores (Ariyawansa et al. 2014a, Hongsanan et al. 2020a). Asexual morphs have pycnidial conidiomata and 1-septate or aseptate conidia (Wanasinghe et al. 2018, Hongsanan et al. 2020a). Ariyawansa et al. (2014a) verified the phylogenetic placement of this genus in Didymosphaeriaceae. There are 41 species accepted in the genus *Paraphaeosphaeria* (Index Fungorum 2025). In this study, we introduce a new host and geographical record for *Paraphaeosphaeria michotii*, based on both morphological and molecular data, along with descriptions and illustrations (Figs. 20, 21).

Paraphaeosphaeria michotii (Westend.) O.E. Erikss., Cryptogams of the Himalayas 6: 405 (1967)
Figs. 20, 21

Index Fungorum number: IF335615; Facesoffungi number: FoF00058

Saprobic on a dead stem of *Stipa capillata*. Sexual morph: *Ascomata* $95\text{--}105 \mu\text{m}$ diam. $\times$ $70\text{--}90 \mu\text{m}$ high ($\bar{x} = 102 \times 80 \mu\text{m}$, $n = 10$), globose or subglobose, superficial, solitary, scattered, uniloculate, flattened base, brown to black. *Peridium* $10\text{--}20 \mu\text{m}$ wide, ($\bar{x} = 15 \mu\text{m}$, $n = 25$), wide at the sides, outermost layer comprising reddish-brown to dark brown, thick-walled, loosely packed cells of *textura angularis*, an inner layer composed of hyaline, flattened, thin-walled cells of *textura angularis*. *Hamathecium* comprises $1.5\text{--}3.5 \mu\text{m}$ wide ($\bar{x} = 2.5 \mu\text{m}$, $n = 25$), numerous filamentous, branched, hyaline, septate, pseudoparaphyses. *Asci* $50\text{--}75 \times 10\text{--}13 \mu\text{m}$ ($\bar{x} = 61 \times 11.5 \mu\text{m}$, $n = 25$), 8-spored, cylindric-clavate, bitunicate, fissitunicate, rounded at the apex, slightly curved,

pedicellate. *Ascospores* $14\text{--}18 \times 4\text{--}5.5 \text{ }\mu\text{m}$ ($\bar{x} = 16 \times 5 \text{ }\mu\text{m}$, $n = 25$), overlapping, biserial, narrowly fusiform, 2-septate, hyaline and guttulate at the beginning, becoming brown at maturity, rounded at the ends, rough-walled. Asexual morph: *Conidiomata* $90\text{--}110 \text{ }\mu\text{m}$ diam. $\times 100\text{--}115 \text{ }\mu\text{m}$ high, ($\bar{x} = 101 \times 106 \text{ }\mu\text{m}$, $n = 10$), pycnidial, globose or subglobose, superficial on the host substrate, solitary, scattered, uni-loculate, dark brown to black. *Conidiomata* wall thin, comprising the cells of *textura angularis*, outer wall brown, hyaline towards the inner layer. *Conidiophores* are reduced to conidiogenous cells. *Conidiogenous cells* $4.5\text{--}6.5 \times 3.5\text{--}6 \text{ }\mu\text{m}$ ($\bar{x} = 5.8 \times 4.5 \text{ }\mu\text{m}$, $n = 20$), ampulliform, phialidic, hyaline, smooth. *Conidia* $5.5\text{--}8.5 \times 3\text{--}4.5 \text{ }\mu\text{m}$ ($\bar{x} = 6 \times 4 \text{ }\mu\text{m}$, $n = 30$), oblong or ellipsoid with obtuse ends, thick-walled, aseptate, golden brown.

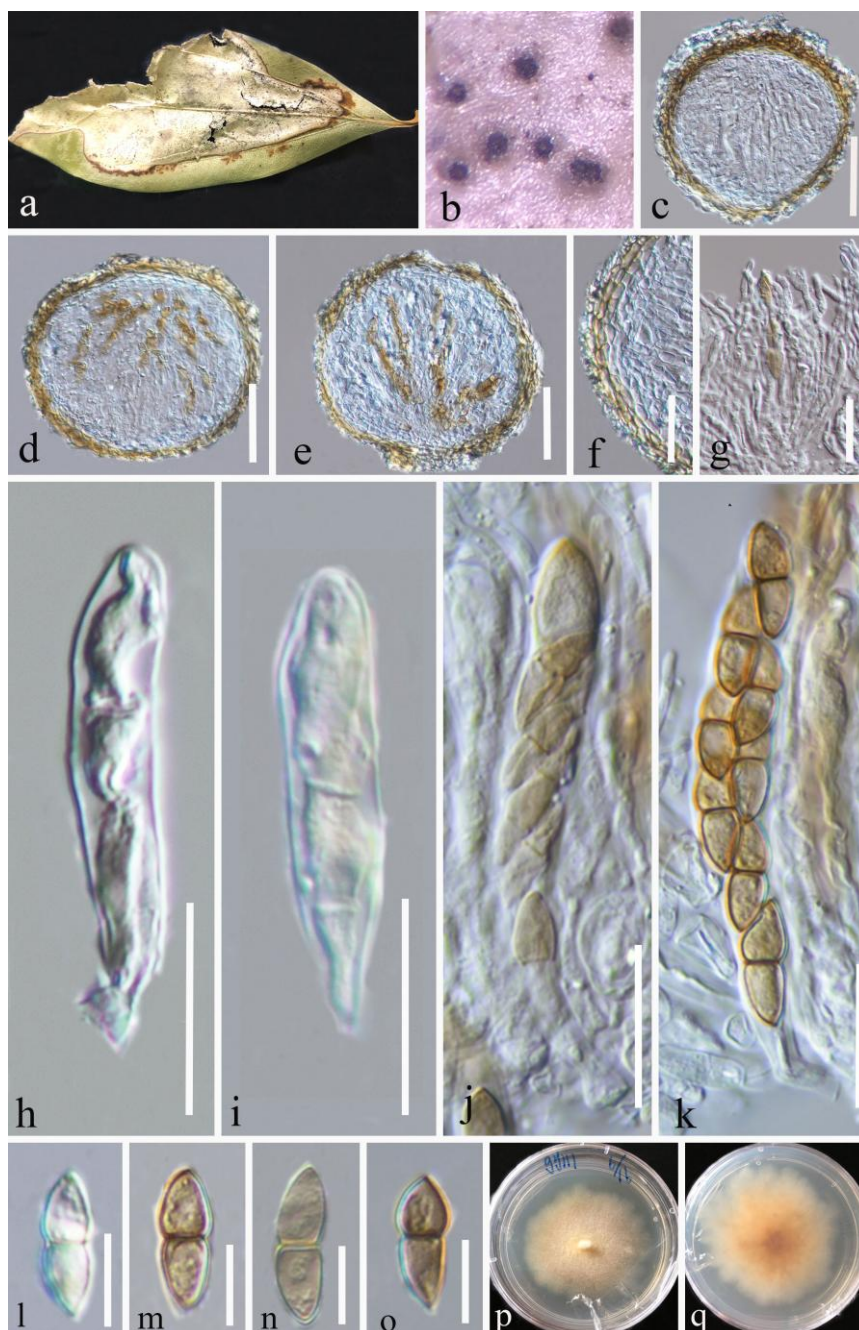


Figure 18 – *Letendraea helminthicola* (HKAS 126573, a new host record). a, b Appearance of ascomata on the host substrate. c–e Sections of ascomata. f Peridium. g Pseudoparaphyses. h–k Asci. l–o Ascospores. p, q Culture characters on PDA (p: above, q: below). Scale bars: c–e = $50 \text{ }\mu\text{m}$, f, g = $30 \text{ }\mu\text{m}$, h–k = $20 \text{ }\mu\text{m}$, l–o = $10 \text{ }\mu\text{m}$.

Culture characteristics – Ascospores germinated on PDA within 24 hours, colonies growing on PDA reaching 50 mm within four weeks at 27°C, mycelia from above, circular, dense, flat, umbonate, rough with undulate edge, white, velvety; from below, pale yellow at the center, white at the margin (Fig. 20). Conidia germinated on PDA within 20 hours, a germ tube was initially produced from the end of the conidia. Colonies on PDA reached 25 mm in three weeks at room temperature (27°C). Colony dense, circular, low convex, from above, smooth, with edge entire, floccose, white; from below, yellow at the edge, brown at the center, producing pigmentation in agar. *Mycelium* 1–2.5 µm broad ($\bar{x}$ = 2.1 µm, n = 25), septate, hyaline, branched, sporulated after six months. Asexual morph on PDA: *Conidiomata*, irregular shapes, pycnidial, gregarious, immersed, dark brown to black. *Peridium* thin, composed of brown cells of *textura angularis* to *globulosa*. *Microconidiogenous cells* 3–5 × 1.8–4 µm ($\bar{x}$ = 3.5 × 3 µm, n = 25), globose or subglobose, hyaline. *Microconidia* 5–7 × 3–5 µm ($\bar{x}$ = 6 × 4 µm, n = 25), hyaline to golden brown, aseptate, round to oblong or ellipsoidal, with small guttules (Fig. 21).

Material examined – China, Yunnan Province, Kunming, on dead stems of *Stipa capillata* (Poaceae), 27 July 2021, Y. Gao, GY170 (HKAS 135348), living culture KUNCC 25-19134; China, Yunnan Province, Zhaotong grassland, on dead stems of *Lolium persicum* (Poaceae), 25 September 2022, Y. Gao, LG1 (HKAS 132962), living culture KUNCC 25-19135; 27 August 2022, Y. Gao, QG73 (HKAS 132988), living culture KUNCC 25-19136.

Known hosts and distribution – On dead leaves of Poaceae sp. in Italy (Ariyawansa et al. 2014a), On dead leaves of *Phragmites australis* (Poaceae) in France, on *Typha latifolia* (Typhaceae) in Germany (Verkley et al. 2014), on dead leaves of *Typha latifolia* (Typhaceae) in Japan (Tanaka et al. 2015), on dried aerial spines of *Rosa canina* (Rosaceae) in Italy (Wanasinghe et al. 2018), on dead stems of *Stipa capillata* (Poaceae) and on dead stems of *Lolium persicum* (Poaceae) in Yunnan Province, China (This study).

GenBank numbers – KUNCC 25-19134: ITS = PV608536, LSU = PV607383, *tefl-α* = PV626426; KUNCC 25-19135: ITS = PV608537, LSU = PV607384, *tefl-α* = PV626427; KUNCC 25-19136: ITS = PV608538, LSU = PV607385, SSU = PV607282, *tefl-α* = PV626428.

Notes – Multigene phylogenetic analyses reveal that the three collections of KUNCC 25-19134, KUNCC 25-19135, and KUNCC 25-19136 are grouped with *Paraphaeosphaeria michotii* (MFLUCC 13-0349, MFLUCC 15-0043, KT 2222, CBS 340.86, CBS 652.86), forming a monophyletic clade (Fig. 17). The sexual and asexual morphologies of our new collections did not differ from the original descriptions of *P. michotii* (MFLUCC 13-0349, ex-type). Additionally, we report here, for the first time, the asexual morph of *P. michotii* observed in culture (Fig. 21). Its morphological characteristics closely align closely with those previously described for the species. Based on the above evidence, we confirm our collections are *Paraphaeosphaeria michotii* and it is a new host and a geographical record.

***Pseudopithomyces* Ariyaw. & K.D. Hyde, Fungal Diversity 75: 64 (2015)**

Notes – *Pseudopithomyces* was introduced by Ariyawansa et al. (2015b) with the type species *P. chartarum*. *Pseudopithomyces* species have been reported as parasitic or saprobic on dead plant stems and leaves, and on humans. *Pseudopithomyces* is characterized by flexuous, aseptate conidiophores, blastic or monoblastic, terminal determinate conidiogenous cells, fusiform, dark, verruculose conidia, and producing brown to black colonies on the host (Ariyawansa et al. 2015b, Hyde et al. 2017, Jayasiri et al. 2019, Tennakoon et al. 2021a, Tian et al. 2024). There were 16 species accepted in the genus *Pseudopithomyces* (Index Fungorum 2025). In this study, we introduce new host and geographical records for two species, *Pseudopithomyces chartarum* and *P. rosae*, based on morphology and molecular data, along with descriptions and illustrations (Figs. 22, 23).

***Pseudopithomyces chartarum* (Berk. & M.A. Curtis) J.F. Li, Ariyaw. & K.D. Hyde, in Ariyawansa et al., Fungal Divers. 75: 66 (2015)** Fig. 22

Index Fungorum number: IF551393; Facesoffungi number: FoF00938

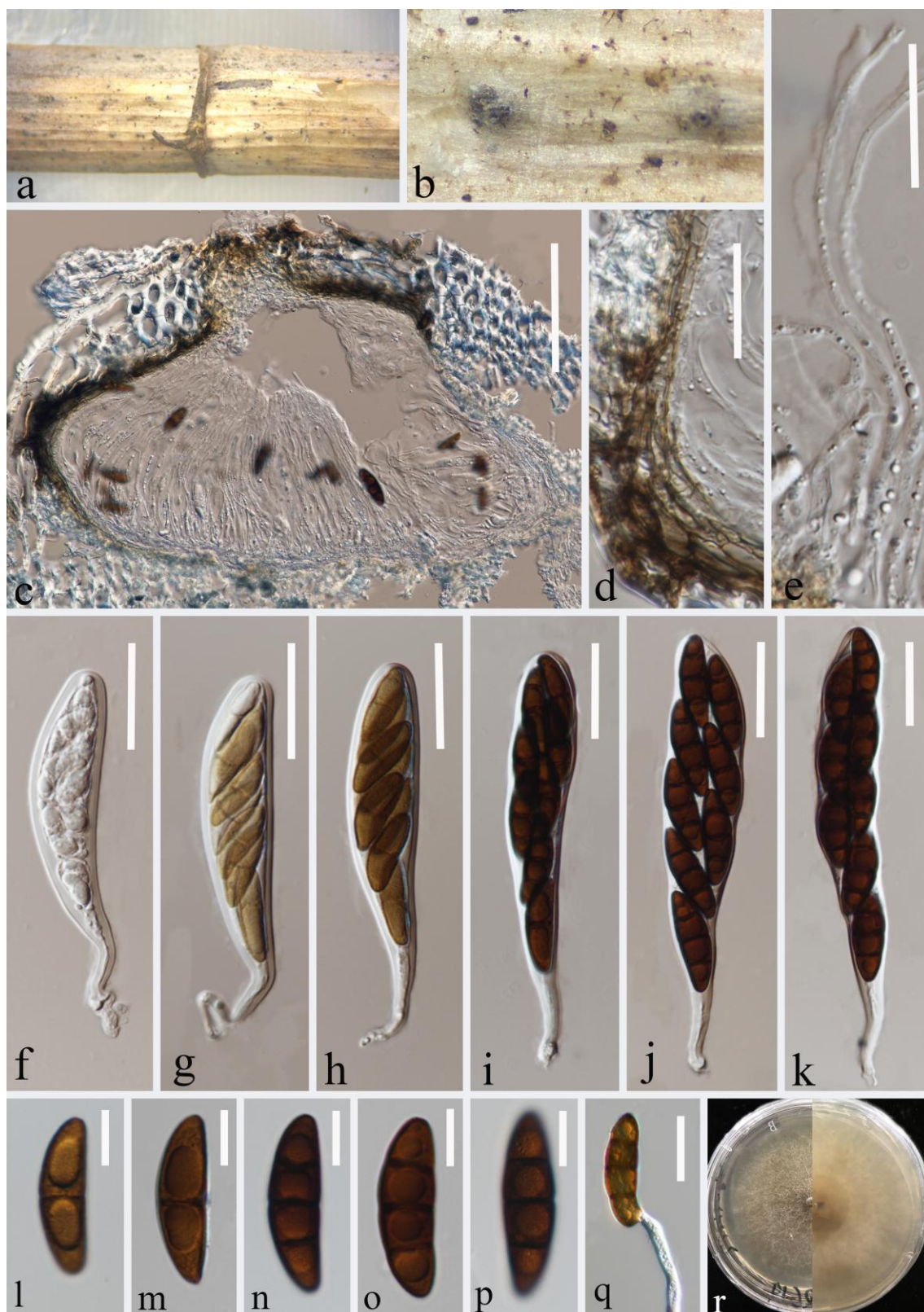


Figure 19 – *Montagnula shangrilana* (HKAS 128793, a new host record). a, b Appearance of ascomata on the host substrate. c A section of an ascoma. d Peridium. e Pseudoparaphyses. f–k Asci. l–p Ascospores. q A germinated ascospore. r Culture characters on PDA (left: above, right: below). Scale bars: c = 100 μ m, d–k = 30 μ m, q = 20 μ m, l–p = 10 μ m.

Saprobic on dead stems of *Dactylis glomerata*. Sexual morph: Undetermined. Asexual morph on the host substrare: Hyphomycetous. *Colonies* black, separate, and later become confluent.

Conidiophores formed laterally and irregularly on the hyphae, micronematous, mononematous, hyaline to yellowish, smooth or occasionally verruculose, septate, and branched. *Conidiogenous cells* 5.5–11 × 3–3.5 µm ($\bar{x}$ = 7.5 × 3.2 µm, n = 15), integrated, holoblastic, monoblastic, hyaline. *Conidia* 16–32 × 9–22 µm ($\bar{x}$ = 23 × 15.5 µm, n = 25), acropleurogenous or pleurogenous, muriform, broadly ellipsoid, 2–3 transverse septate, 1–2 longitudinal septate, sometimes constricted at the septa, light brown to dark brown, verruculose to echinulate, often carrying part of conidiogenous cell at base. Asexual morph on PDA: *Conidia* 19–27 × 13–17 µm ($\bar{x}$ = 23 × 15.5 µm, n = 25), aggregated, globose, muriform, broadly ellipsoid, 2–3 transverse septate, 1–2 longitudinal septate, sometimes constricted at the septa, light brown to dark brown, verruculose to echinulate, often carrying part of conidiogenous cell at base.

Culture characteristics – *Conidia* germinated on PDA within 20 hours. Colonies on PDA reached 35 mm in three weeks at room temperature (27°C). Colony dense, circular, from above, low convex, surface smooth, with edge entire, floccose, white; from below, pale brown at the edge, black at the center, not producing pigmentation in agar. *Mycelium* 1.8–4 µm broad ($\bar{x}$ = 2.8 µm, n = 30), septate, hyaline, branched, sporulated after six months.

Material examined – China, Yunnan Province, Zhaotong grassland, on dead stems of *Dactylis glomerata* (Poaceae), 25 September 2022, Y. Gao, LG4 (HKAS 132964), living culture KUNCC 25-19137.

Known hosts and distribution – On dead leaves and stems of *Acoelorrhaphe wrightii*, *Arachis hypogaea*, *Bridelia ferruginea*, *Cajanus indica*, *Calopogonium mhcamoides*, *Centrosema pubescens*, *Foeniculum vulgare*, *Holcus lanatus*, *Ipomoea* sp., *Jatropha podagrica*, *Jatropha* sp., *Musa sapientum*, *Neboulidia laevis*, *Nicotiana tabacum*, *Oryza sativa*, *Pandanus amaryllifolius*, *Pueraria phaseoloides*, *Sorghum* sp., *Trifolium repens*, *Triticum vulgare* and *Zea mays* from China, Ghana, Jamaica, Malaya, Mauritius, New Zealand, Northern Rhodesia, Nyasaland, Philippines, Sierra Leone, Southern Rhodesia, the Sudan Republic, Thailand, the United States (Berkeley 1874, Ellis 1960, Ariyawansa et al. 2015b, Hyde et al. 2017, Tibpromma et al. 2018a, Tian et al. 2024); on dead stems of *Dactylis glomerata* (Poaceae) in Yunnan Province, China (This study).

GenBank numbers – KUNCC 25-19137: ITS = PV608539, LSU = PV607386, SSU = PV607283, *tef1-α* = PV626429.

Notes – Tian et al. (2024) synonymized *Pseudopithomyces pandanicola* (MFLUCC 18-0116) and *P. palmicola* (MFLUCC 14-0392) under *P. chartarum* based on phylogenetic and morphological analyses. In our phylogenetic analyses, our collection (KUNCC 25-19137) grouped with *P. chartarum* (MFLUCC 18-0116, MFLUCC 14-0392, MFLUCC 23-0125, MFLUCC 17-0314, MFLUCC 19-0089, NCYUCC 19-0168) and shares similar morphological characteristics with *P. chartarum* (MFLUCC 19-0089) in having broadly ellipsoid, brown, septate conidia (Ram 1989, Ariyawansa et al. 2015b, Tian et al. 2024). Hence, we introduce *P. chartarum* (KUNCC 25-19137) as a new host and geographical record from *Dactylis glomerata* in China based on morphology and phylogeny. In addition, our phylogenetic analyses showed that *Pseudopithomyces kunmingnensis* (MFLUCC 17-0314) grouped within the *P. chartarum* clade (Fig. 17). Morphologically, *Pseudopithomyces kunmingnensis* is not different from *P. chartarum* by its conidiogenous cells and conidia (Hyde et al. 2017). The base-pair similarity between *Pseudopithomyces kunmingnensis* and *P. chartarum* is 99% in ITS (499/500 bp), 100% in LSU (809/809 bp), and 100% in SSU (923/923 bp). Thus, we synonymized *Pseudopithomyces kunmingnensis* under *P. chartarum*. In this study, we identified that our collection belongs to *Pseudopithomyces chartarum*, and it is a new host record.

Pseudopithomyces rosae Phukhams., Camporesi & K.D. Hyde, Fungal Diversity 89: 43 (2018)
Fig. 23

Index Fungorum number: IF554136; Facesoffungi number: FoF03974

Saprobic on dead stems of grass (Poaceae). Sexual morph: Undetermined. Asexual morph: Hyphomycetous. Colonies brown to black, effuse. *Conidiophores* formed laterally and irregularly on the hyphae, micronematous, mononematous, hyaline to yellowish, smooth or occasionally

verruculose, septate, and branched. *Conidiogenous cells* $3.5\text{--}10 \times 2.5\text{--}6 \mu\text{m}$ ($\bar{x} = 8 \times 4 \mu\text{m}$, $n = 15$), globose or subglobose or oblong, integrated, holoblastic, hyaline. *Conidia* $20\text{--}31 \times 14.5\text{--}22 \mu\text{m}$ ($\bar{x} = 25 \times 19 \mu\text{m}$, $n = 30$), muriform or broadly ellipsoid, 3-transverse septate, 1-longitudinal septate, verruculose to echinulate, ovoid, thin-walled, pale brown to dark brown. Asexual morph on PDA: *Conidiogenous cells* $10\text{--}14 \times 2\text{--}3.5 \mu\text{m}$ ($\bar{x} = 11 \times 2.5 \mu\text{m}$, $n = 10$), polyphialidic, integrated or terminal, cylindrical, straight to slightly, hyaline. *Conidia* $18.5\text{--}29 \times 12\text{--}20 \mu\text{m}$ ($\bar{x} = 23 \times 15 \mu\text{m}$, $n = 30$), aggregated, globose or muriform, broadly ellipsoid, 3-transverse septate, 1-longitudinal septate, sometimes slightly constricted at the septa, verruculose to echinulate, light brown to dark brown, often carrying part of conidiogenous cell at base.

Culture characteristics – *Conidia* germinated on PDA within 24 hours. Colonies on PDA reached 50 mm in three weeks at room temperature (27°C). Colony from above, circular, low convex, filamentous, with entire edge, floccose, white mycelium cover; from below, circular zonate, pale yellow at the edge, with brown margin, dark brown at the center, not producing pigmentation in agar. *Mycelium* $1.3\text{--}3 \mu\text{m}$ wide ($\bar{x} = 2 \mu\text{m}$, $n = 30$), septate, hyaline, branched, sporulated after six months.

Material examined – China, Yunnan Province, Kunming, on dead stems of unidentified grass (Poaceae), 01 October 2022, Y. Gao, MG5 (HKAS 135333), living culture KUNCC 25-19138.

Known hosts and distribution – On dead aerial spines of *Rosa canina* (Rosaceae) in Italy (Wanasinghe et al. 2018), on dead stems of grass (Poaceae) in Yunnan Province, China (This study).

GenBank numbers – KUNCC 25-19138: ITS = PV608540, LSU = PV607387, SSU = PV607284, *tef1-α* = PV626430.

Notes – Phylogenetic analyses showed that our strain (KUNCC 25-19138) is grouped within *Pseudopithomyces rosae* (MFLUCC 15-0035, ex-type) with 97% ML and 1.00 PP support values (Fig. 17). *Pseudopithomyces rosae* was reported by Wanasinghe et al. (2018) on dead aerial spines of *Rosa canina* in Italy, which was introduced with the asexual morph. Our collection (KUNCC 25-19138) resembles *P. rosae* (MFLUCC 15-0035) in having mononemous, micronematous conidiophores and muriform conidia; conidia are similar in size ($20\text{--}31 \times 14.5\text{--}22 \mu\text{m}$ vs. $13\text{--}30 \times 9\text{--}20 \mu\text{m}$) (Wanasinghe et al. 2018). The asexual morphs of our collection (KUNCC 25-19138) were observed on both the host and culture in China. Thus, we identified that our collection belongs to *Pseudopithomyces rosae*, and it represents a new host and geographical record based on phylogenetic analyses and morphological characteristics.

Tremateia Kohlm., Volkm.-Kohlm. & O.E. Erikss., Bot. Mar. 38: 165 (1995)

Notes – *Tremateia* was introduced by Kohlmeyer et al. (1995) to accommodate *T. halophile* as a facultative marine genus, which is characterized by immersed, depressed globose ascomata, numerous cellular pseudoparaphyses, fissitunicate, clavate asci, ellipsoid muriform ascospores. *Tremateia* produced both sexual and Phoma-like asexual morphs. Through a comprehensive phylogenetic and morphological study, Ariyawansa et al. (2014a) established the taxonomic position of *Tremateia* within Didymosphaeriaceae. Subsequent studies conducted by Hyde et al. (2016) and Feng et al. (2019) provided further evidence supporting the terrestrial habitat preference of *Tremateia* species. There were 11 species accepted in the genus *Tremateia* (Index Fungorum 2025). In this study, we introduce a new geographical record for *Tremateia arundicola*, based on morphology and molecular data, together with descriptions and illustrations (Fig. 24).

Tremateia arundicola Wanas., E.B.G. Jones & K.D. Hyde (2016)

Fig. 24

Index Fungorum number: IF552134; Facesoffungi number: FoF02210

Saprobic on dead stems of herbaceous plants. Sexual morph: *Ascomata* $185\text{--}285 \mu\text{m}$ diam. $\times$ $190\text{--}275 \mu\text{m}$ high ($\bar{x} = 245 \times 246 \mu\text{m}$, $n = 10$), globose or subglobose, immersed in host tissue, with papilla, solitary, scattered, uni-loculate, flattened base, brown to dark brown, ostiolate. *Peridium* $10\text{--}25 \mu\text{m}$ wide ($\bar{x} = 17.5 \mu\text{m}$, $n = 25$), thick, with 3–5 layers, comprising dark brown cells of *textura angularis*. *Hamathecium* comprises $1.5\text{--}3 \mu\text{m}$ wide ($\bar{x} = 2 \mu\text{m}$, $n = 30$), numerous,

filamentous, branched, septate, pseudoparaphyses. *Asci* 70–115 × 13–17 µm ($\bar{x}$ = 95 × 15 µm, n = 25), 8-spored, cylindrical to cylindric-clavate bitunicate, fissitunicate, apically rounded, thick-walled at the apex, short pedicellate, with furcated pedicel when immature, with minute ocular chamber. *Ascospores* 18.5–23 × 7–10 µm ($\bar{x}$ = 20.5 × 8 µm, n = 25), overlapping, 2-seriate, muriform, ellipsoid to broad fusiform, with 3–7-transverse septa, 1–2-longitudinal septum in each row, obviously constricted in the central septum and slightly constricted at other septa, initially hyaline, becoming golden-brownish to brown when mature, with a distinct gelatinous sheath. Asexual morph: Undetermined.

Culture characteristics – Ascospores germinated within 48 h on PDA. Colonies on PDA, 5 cm diam. after four weeks at 27°C. The colonies from above, rough, mycelia superficial, circular, dense, flat, entire edge, white; from below, white to cream margin, dark brown at the center.

Material examined – China, Yunnan Province, Kunming, on dead stems of unidentified herbaceous plants, 23 June 2021, Y. Gao, CCSG31 (HKAS 133005), living culture KUNCC 25-19208.

Known hosts and distribution – on herbaceous stems in the United Kingdom (Hyde et al. 2016), on dead stems of herbaceous plants in Yunnan Province, China (This study).

GenBank numbers – KUNCC 25-19208: ITS = PV642534, LSU = PV607388, SSU = PV607285, *tef1-α* = PV626431.

Notes – Based on multigene phylogenetic analyses, our collection (KUNCC 25-19208) is grouped close to *Tremateia arundicola* (MFLU 16-1275, holotype) with 99% ML and 1.00 PP statistical support (Fig. 17). *Tremateia arundicola* was introduced by Hyde et al. (2016) on herbaceous plants in the United Kingdom. The pairwise nucleotide comparison showed that our collection (KUNCC 25-19208) differs from *T. arundicola* (MFLU 16-1275) in 0/938 bp of SSU (0.00%), 0/851 bp of LSU (0.00%), 12/654 bp of ITS (1.83%, with 5 gaps), 1/756 bp of *tef1-α* (0.13%, without gaps). Our collection (KUNCC 25-19208) is similar to *T. arundicola* (MFLU 16-1275) in the character of ascomata (185–285 × 190–275 µm, L/W = 1 vs. 250–350 × 200–300 µm, L/W = 1.2), asci (70–115 × 13–17 µm, L/W = 6.2 vs. 170–200 × 15–20 µm, L/W = 10.6) and ascospores (2-seriate, 3–7-transverse septa, 1–2-longitudinal septum vs. uni-seriate, 3–6 transversely septate, with 1 vertical septum). We identified our collection is *T. arundicola* based on phylogenetic analyses and morphological characteristics and it is a new geographical record.

Lentitheciaceae Y. Zhang et al., C.L. Schoch, J. Fourn., Crous & K.D. Hyde, *Studies in Mycology* 64: 93 (2009)

Notes – Lentitheciaceae was introduced to accommodate massarina-like species, including *Katumotoa*, *Keissleriella*, with the type genus, *Lentithecium* (Zhang et al. 2009, 2012). Twenty genera have been accepted into the family (Hyde et al. 2024a, Tian et al. 2024). Species in Lentitheciaceae have been documented as saprobes on twigs and stems of both herbaceous and woody plants across marine, terrestrial and freshwater environments. Additionally, endophytic species of *Darksidea* have been isolated from semiarid regions (Wanasinghe et al. 2014, Tanaka et al. 2015, Hongsanan et al. 2020a, Liu et al. 2021). The sexual morphs are characterized by having globose to lenticular, immersed to superficial ascomata; composed of hyaline to brown, thin-walled cells, polygonal to angular peridium; cellular, branched, septate pseudoparaphyses; cylindrical to broadly clavate, fissitunicate, bitunicate asci; narrowly fusiform to broadly cylindrical, septate, hyaline, with an entire mucilaginous sheath or elongated appendage-like sheath ascospores (Zhang et al. 2009, Hongsanan et al. 2020a). The asexual morphs are characterized by globose, pycnidial, ostiolate conidiomata; phialidic or blastic conidiogenous cells; cylindrical to oblong, one-celled to muriform, hyaline to pigmented conidia (Hongsanan et al. 2020a). An updated phylogenetic tree based on combined ITS, LSU, SSU, and *tef1-α* sequence data is presented in Fig. 25.

Keissleriella Höhn., *Sitzungsber. Kaiserl. Akad. Wiss., Wien. Math.-Naturwiss. Cl., Abt. 1* 128: 582 (1919)

Notes – *Keissleriella* was introduced by Höhnelt (1919) with *K. aesculin* as the type species. Zhang et al. (2009) included *Keissleriella* in Lentitheciaceae. This genus is characterized by black setae on the ascomata, uni- or multi-septate, hyaline to pale brown, with mucilaginous sheath ascospores (Barr 1990, Liu et al. 2015, Tibpromma et al. 2017, Wanasinghe et al. 2018, Phookamsak et al. 2019). The asexual morph comprises unbranched or branched, flexuous, smooth, hyaline conidiophores, phialidic conidiogenous cells, aseptate or septate, hyaline to brown conidia (Hyde et al. 2020a). There were 45 species accepted in the genus *Keissleriella* (Index Fungorum 2025). In this study, we introduce a new geographical record for two species (*Keissleriella gloeospora* and *K. poagensis*). Three new *Keissleriella* species (*K. graminicola*, *K. lolii*, *K. zhaotongensis*) are introduced, based on morphology and molecular data, together with descriptions and illustrations (Figs. 26–30).

Keissleriella gloeospora (Berk. & Curr.) S.K. Bose, *Phytopathologische Zeitschrift* 41: 190 (1961)

Fig. 26

Index Fungorum number: IF316017; Facesoffungi number: FoF18351

Saprobic on dead stems of grass. Sexual morph: Undetermined. Asexual morph: *Conidiomata* 60–90 µm diam. × 55–75 µm high ($\bar{x}$ = 81 × 65 µm, n = 10), globose or subglobose, semi-immersed in the host, solitary, scattered, uni-loculate, dark brown to black. *Conidiomata wall* 9–16 µm wide ($\bar{x}$ = 14 µm, n = 20), comprising 3–7 layers of polygonal cells, brown. *Conidiogenous cells* 3.5–7 × 2.3–6.5 µm ($\bar{x}$ = 5 × 4 µm, n = 20), enteroblastic, phialidic, oblong to ampulliform, hyaline, thin-walled, smooth. *Conidia* 4.5–11 × 1.5–3 µm ($\bar{x}$ = 7.5 × 2.5 µm, n = 25), oblong to obovoid, aseptate, smooth-walled, hyaline.

Culture characteristics – Colonies on PDA reaching 15 mm diam. after two weeks. Colony from above, dense, circular, low convex, surface smooth, with edge entire, floccose, white; from below, yellow at the edge, with white to cream margin, dark yellow at the center.

Material examined – China, Yunnan Province, Kunming, on dead stems of unidentified grass (Poaceae), 13 June 2021, Y. Gao, XJK20 (HKAS 135351), living culture KUNCC 25-19141.

Known hosts and distribution – on dead culms of *Setaria faberii* (Poaceae) in Japan (Tanaka et al. 2015), on dead stems of grass (Poaceae) in Yunnan Province, China (This study).

GenBank numbers – KUNCC 25-19141: ITS = PV642537, LSU = PV607393, SSU = PV607290.

Notes – Multigene phylogenetic analyses (Fig. 25) show that our collection (KUNCC 25-19141) grouped with *Keissleriella gloeospora* (KT 829), with 100% ML and 1.00 PP support values (Fig. 25). Comparisons of SSU, LSU, and ITS sequence data reveal there are no bp differences between our new collection (KUNCC 25-19141) and *K. gloeospora* (KT 829). *K. gloeospora* had previously been described only in sexual form (Bose 1961, Shearer et al. 1993, Tanaka et al. 2015). In our study, we identified our collection as *K. gloeospora*, representing the first record of the asexual morph and a new geographical record for this fungus.

Keissleriella graminicola Y. Gao, H. Gui & K.D. Hyde, sp. nov.

Fig. 27

Index Fungorum number: IF903817; Facesoffungi number: FoF17694

Holotype – HKAS 128781

Etymology – The specific epithet is derived from the host family Gramineae, in which the holotype was found.

Saprobic on dead stems of *Dactylis glomerata*. Sexual morph: *Ascomata* 125–210 µm diam. × 80–175 µm high ($\bar{x}$ = 170 × 130 µm, n = 10), conical to mammiform, with flattened base, semi-immersed to erumpent through the host surface, scattered, solitary, uni-loculate, black, ostiolate, papillate. *Peridium* 11–28 µm wide ($\bar{x}$ = 18.5 µm, n = 30), composed of two type cell layers, inner layer comprising 2–3 strata of flattened, pale brown, thin-walled, pseudoparenchymatous cells, arranged in *textura angularis* to *textura prismatica*, outer layer comprising several strata, of brown, thick-walled, scleroplectenchymatous cells, *textura angularis*. *Hamathecium* comprises 1–3 µm wide ($\bar{x}$ = 2 µm, n = 30), filiform branches, anastomosing above asci, reaching the ostiole part,

transverse septate, trabeculate pseudoparaphyses. *Asci* 80–115 × 6–10 µm ($\bar{x}$ = 94.5 × 8 µm, n = 30), 8-spored, narrowly clavate, apically rounded, with furcated pedicel, bitunicate, fissitunicate, thick-walled, ocular chamber visible when immature. *Ascospores* 19–27 × 2.5–5 µm ($\bar{x}$ = 22 × 3.5 µm, n = 35), uniseriate, fusiform, conical at the ends, 1-3-septate, deeply constricted at the middle septum, hyaline, smooth, with guttulate, lacking a mucilaginous sheath. Asexual morph: Undetermined.

Culture characteristics – Ascospores germinated within 48 h on PDA. 5 cm diam. after three weeks at 27°C. colonies circular, from above, raised, cottony, grey at the center, pale grey at the margin; from below, pale grey at the center, white at the margin, not producing pigment in agar.

Material examined – China, Yunnan Province, Zhaotong grassland, on dead stems of *Dactylis glomerata* (Poaceae), 25 August 2022, Y. Gao, QG106A (HKAS 128781, holotype), ex-type living culture CGMCC 3.25086; *ibid.*, QG106B (HKAS 128782, isotype), ex-isotype living culture CGMCC 3.25087.

GenBank numbers – CGMCC 3.25086: ITS = PV608545, LSU = PV607396, SSU = PV607293, *tef1*-α = PV626438; CGMCC 3.25087: ITS = PV608546, LSU = PV607397, SSU = PV607294, *tef1*-α = PV626439.

Notes – In our phylogenetic analysis, our collections (CGMCC 3.25086 and CGMCC 3.25087) formed a distinct branch with *Keissleriella lolii* (CGMCC 3.24521, CGMCC 3.24522) (Fig. 25). The comparison of ITS, LSU, and *tef1*-α sequence data between our collections and *K. lolii* revealed nucleotide differences of 54/585 (9.23%, with 9 gaps), 14/833 (1.68%), 42/943 (4.45%), respectively. *Keissleriella graminicola* (CGMCC 3.25086, ex-type) is distinguished from *K. lolii* (CGMCC 3.24521, ex-type) by its ascomata, asci, and ascospores (see the notes under *K. lolii* in this study). Based on these phylogenetic and morphological distinctions, we introduced *K. graminicola* as a novel species collected from *Dactylis glomerata* in China.

Keissleriella lolii Y. Gao, H. Gui & K.D. Hyde, sp. nov.

Fig. 28

Index Fungorum number: IF903818; Facesoffungi number: FoF17695

Holotype – HKAS 128809

Etymology – The specific epithet is derived from the genus of *Lolium perenne* (Poaceae), in which the holotype was found.

Saprobic on dead stems of *Lolium perenne*. Sexual morph: *Ascomata* 185–255 µm diam. × 155–220 µm high ($\bar{x}$ = 240 × 200 µm, n = 10), globose or subglobose, immersed in host tissue, with minute papilla, solitary, scattered, uni-loculate, flattened base, brown to dark brown, opened pore, easily open, ostiolate with black setae on the papilla. *Peridium* 9.5–21 µm wide ($\bar{x}$ = 12.5 µm, n = 30), comprising dark brown to brown cells of *textura angularis*, inner layers comprising thin, hyaline cells. *Hamathecium* comprises 1.5–2.3 µm wide ($\bar{x}$ = 1.7 µm, n = 30), filiform branches, anastomosing above asci, reaching the ostiole part, transverse septate, trabeculate pseudoparaphyses. *Asci* 70–110 × 8.5–11.5 µm ($\bar{x}$ = 95 × 10 µm, n = 25), 8-spored, cylindric-clavate to narrowly clavate, apically rounded, with furcated pedicel, bitunicate, fissitunicate, thick-walled, ocular chamber visible when immature. *Ascospores* 23–30.5 × 3–5.5 µm ($\bar{x}$ = 25 × 4.5 µm, n = 25), uniseriate, narrowly fusiform, 1-septate, constricted at the septa, hyaline, smooth, with an entire gelatinous sheath. Asexual morph: Undetermined.

Culture characteristics – Ascospores germinated within 48 h on PDA. 2 cm diam. after three weeks at 27°C. colonies circular, from above, raised, cottony, fluffy, pale brown to black at the center, white at the narrow margin; from below, dark grey at the center, white at the margin, not producing pigment in agar.

Material examined – China, Yunnan Province, Zhaotong grassland, on dead stems of *Lolium perenne* (Poaceae), 25 August 2022, Y. Gao, QG48A (HKAS 128809, holotype), ex-type living culture CGMCC 3.24521; *ibid.*, QG48B (HKAS 128810, isotype), ex-isotype living culture CGMCC 3.24522.

GenBank numbers – CGMCC 3.24521: ITS = PV608543, LSU = PV607394, SSU = PV607291, *tefl*- α = PV626436; CGMCC 3.24522: ITS = PV608544, LSU = PV607395, SSU = PV607292, *tefl*- α = PV626437.

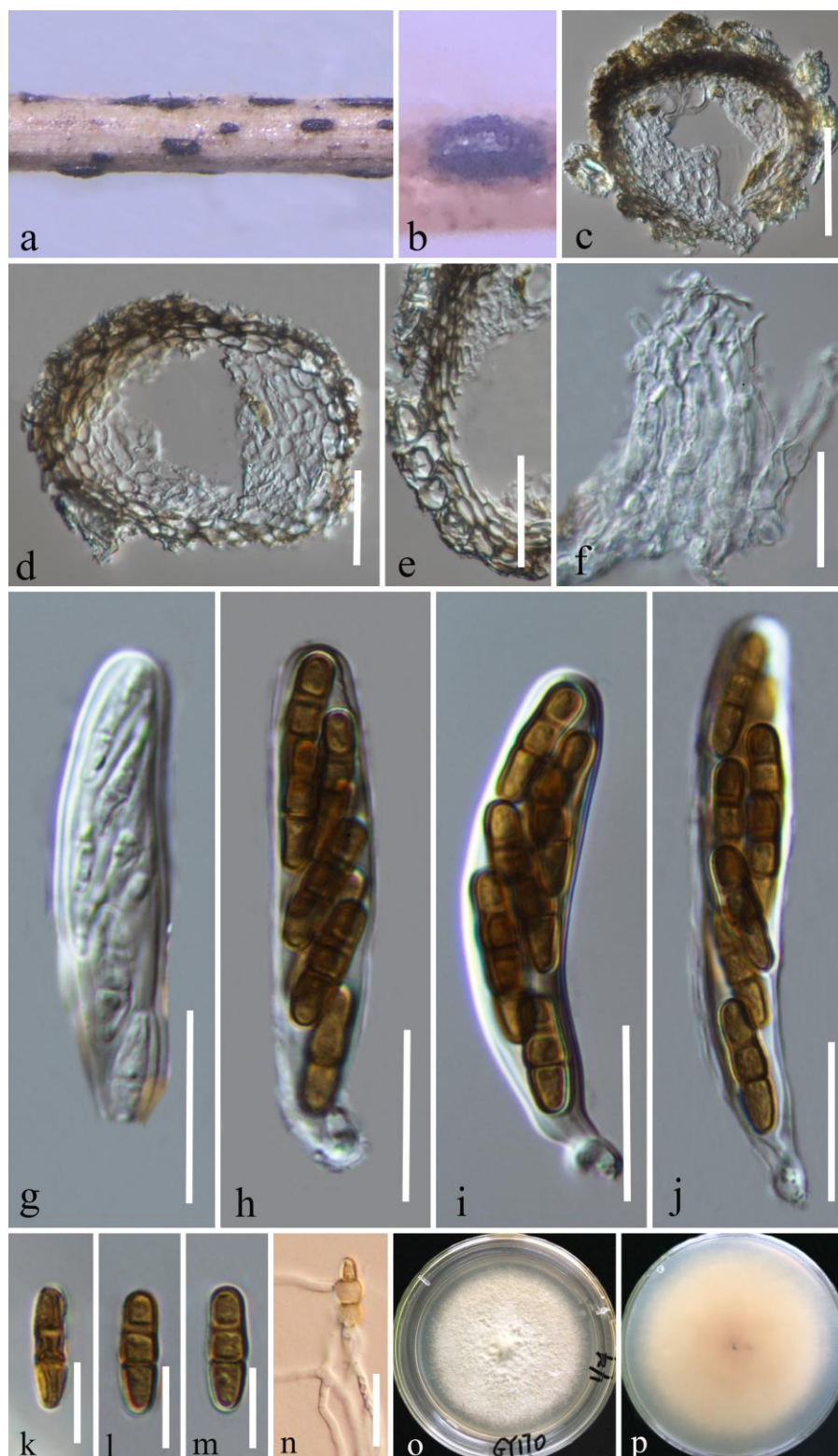


Figure 20 – *Paraphaeosphaeria michotii* (HKAS 135348, sexual morph, a new host and a geographical record). a, b Ascomata on a dead stem of *Stipa capillata*. c, d Vertical sections through ascomata. e Peridium. f Pseudoparaphyses. g–j Asci. k–m Ascospores. n A germinated ascospore. o, p Culture characters on PDA (o: above, p: below). Scale bars: c = 50 μ m, d, e = 30 μ m, f–j, n = 20 μ m, k–m = 10 μ m.

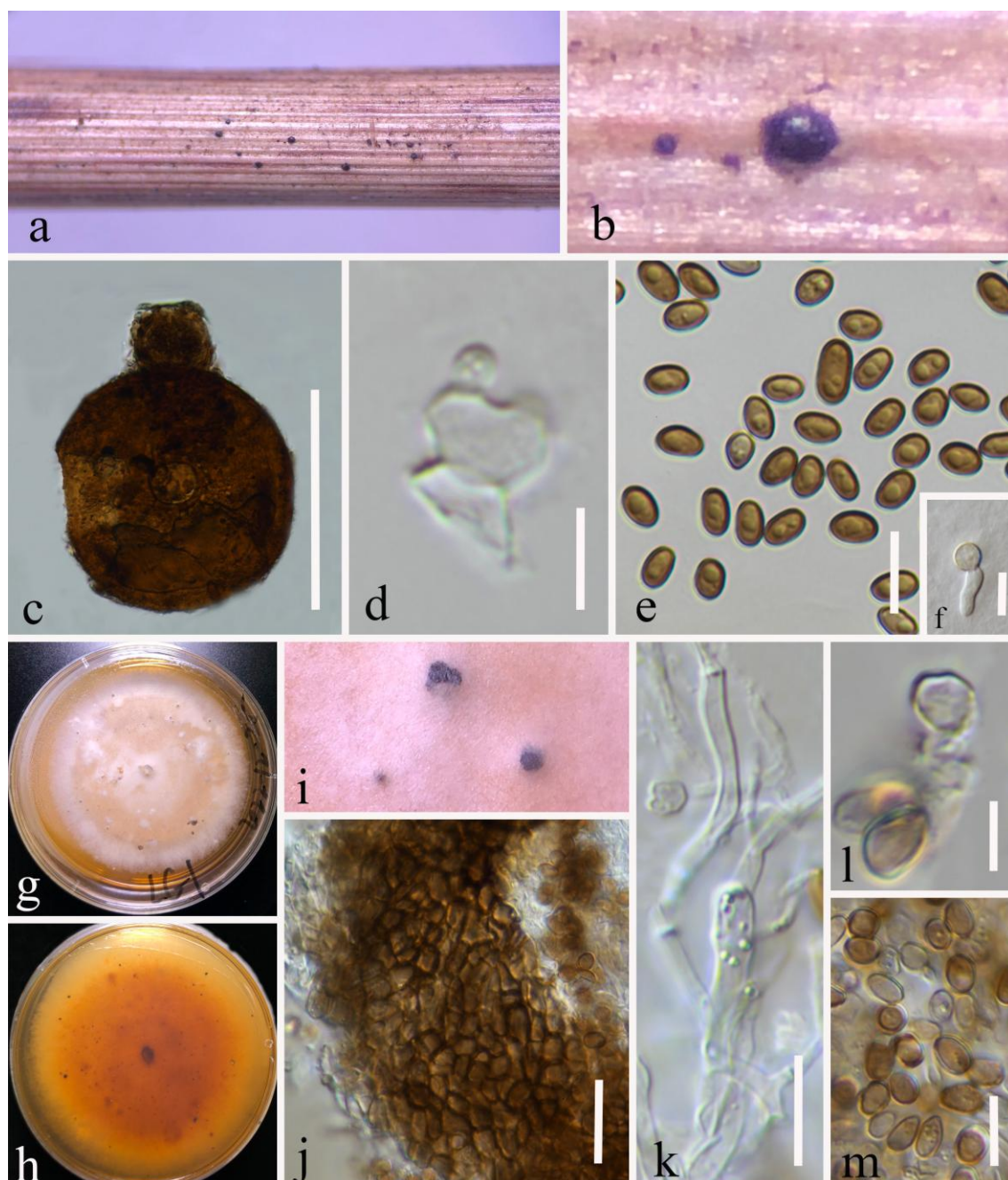


Figure 21 – *Paraphaeosphaeria michotii* (HKAS 132962, asexual morph, a new host and a geographical record). a, b Conidiomata on the dead stem of *Lolium persicum*. c Conidiomata. d Developing state of conidiogenous cells. e Conidia. f A germinated conidium. g, h Colony of the sexual morphic stage after six months on PDA (g: above, h: below). i Conidiomata produced in culture. j Conidioma wall. k Mycelium. l Conidiogenous cells and developing conidia. m Conidia. Scale bars: c = 100 μ m, e, f, j, k, m = 10 μ m, d, l = 5 μ m.

Notes – *Keissleriella lolii* (CGMCC 3.24521 and CGMCC 3.24522) are isolated from the dead stems of *Lolium perenne*. The newly obtained sequences of this fungus formed a monophyletic clade closely related to *Keissleriella graminicola* (CGMCC 3.25086 and CGMCC 3.25087) (Fig. 25). Morphologically, *K. lolii* (CGMCC 3.24521, ex-type) differs from *K. graminicola* (CGMCC 3.25086, ex-type) in its ascomata (globose or subglobose vs. conical to mammiform), asci (72–110 $\times$ 8.5–11.5 μ m, L/W = 9.1 vs. 81–115 $\times$ 6–10 μ m, L/W = 12.3), ascospores (23–30.5 $\times$ 3–5.5 μ m, L/W = 6.3, 1-septate, vs. 19–27 $\times$ 2.5–5 μ m, L/W = 6.1, 1-3-septate) (Figure 27, 28). Also, *K. lolii* (CGMCC 3.24521 and CGMCC 3.24522) differs from *K. graminicola* (CGMCC 3.25086 and CGMCC 3.25087) by 54/585 (9.23%, with 9 gaps) differences

in the ITS region, 14/833 (1.68%) differences in the LSU region, 0/1020 differences in the SSU region, and 42/943 (4.45%) differences in the *tef1*- α region. Therefore, based on the polyphasic approach recommended for delimiting species boundaries (Jayawardena et al. 2021, Maharachchikumbura et al. 2021a), we introduce *Keissleriella lolii* as a new species.

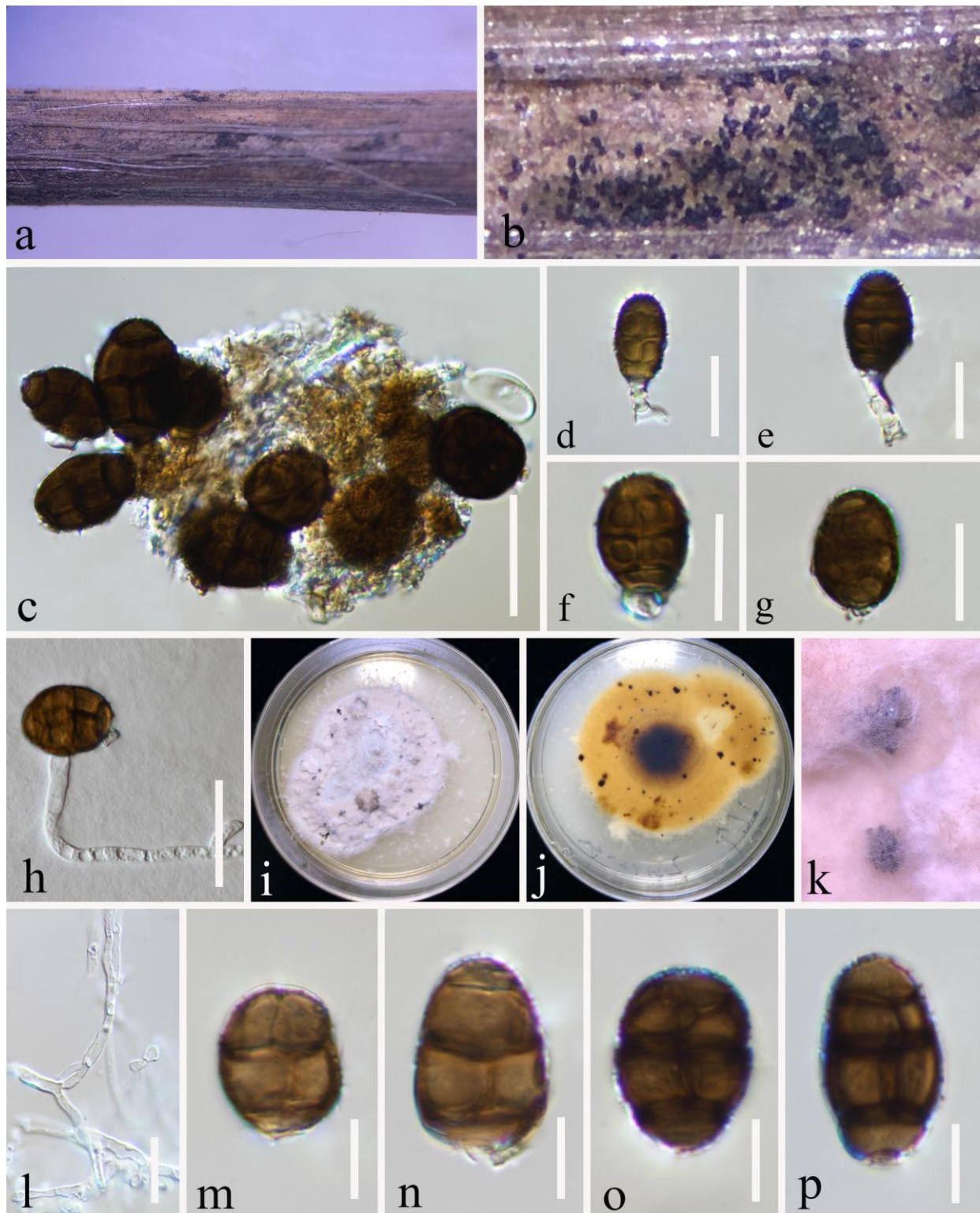


Figure 22 – *Pseudopithomyces chartarum* (HKAS 132964, a new host record). a, b Colonies on the dead stem of *Dactylis glomerata*. c Conidiophore with conidia. d, e Conidia with conidiogenous cells. f, g Conidia. h A germinated conidium. i, j Colonies on PDA (i: above, j: below). k Asexual morph produced in culture. l Mycelium. m–p Conidia. Scale bars: c = 30 µm, h, l = 20 µm, d–g = 15 µm, m–p = 10 µm.

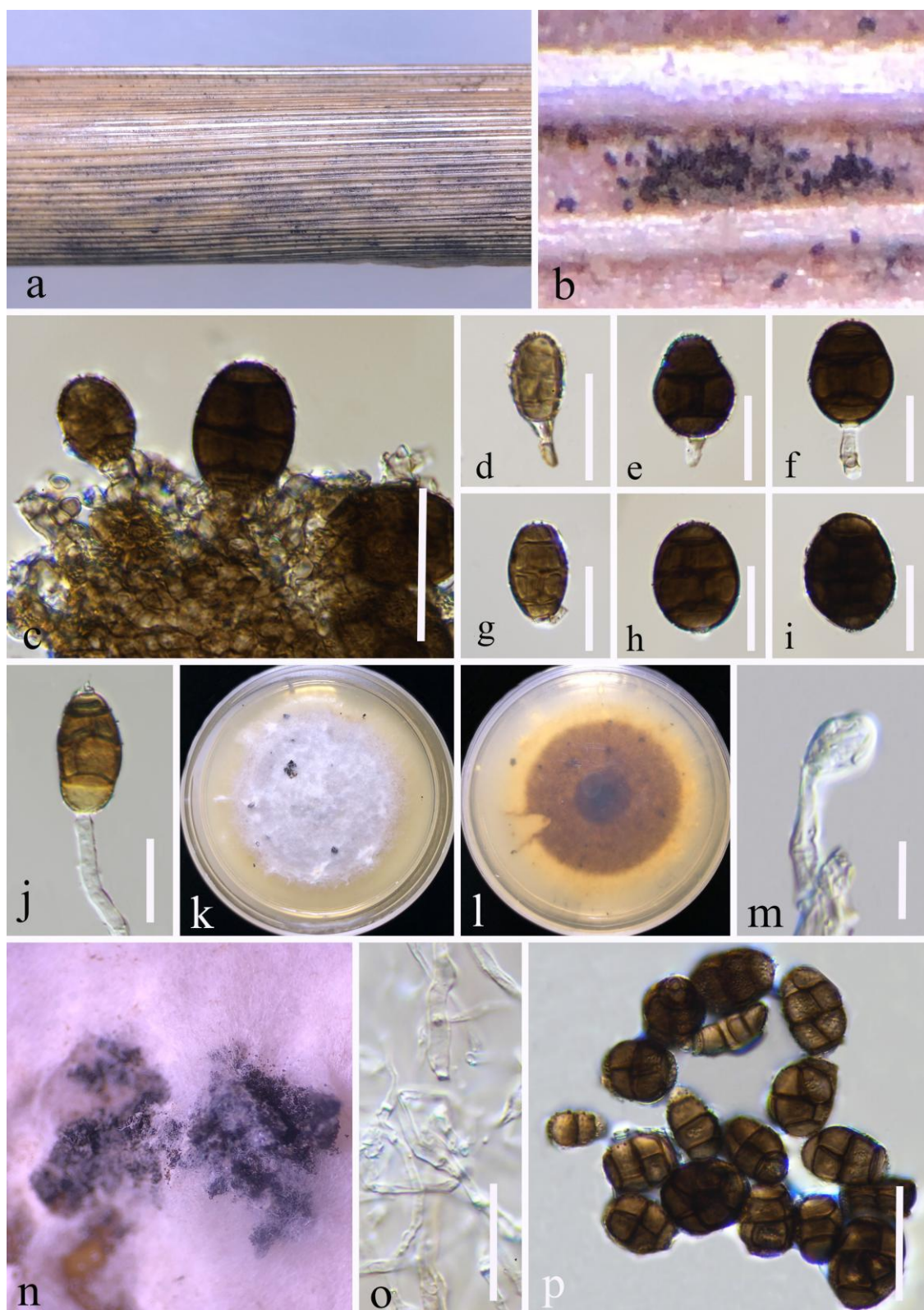


Figure 23 – *Pseudopithomyces rosae* (HKAS 135333, a new host and a geographical record). a, b Colonies on the dead stem of grass. c Conidiophore with conidia. d–f Conidia with conidiogenous cells. g–i Conidia. j A germinated conidium. k, l Colonies on PDA (k: above, l: below). m Conidia with conidiogenous cells. n Asexual morph produced in culture. o Mycelium. p Conidia. Scale bars: c, p = 30 μm , d–j, o = 20 μm , m = 10 μm .



Figure 24 – *Tremateia arundicola* (HKAS 133005, a new geographical record). a, b Appearance of ascomata on host substrate. c, d Sections of ascomata. e Peridium. f Pseudoparaphyses. g–k Asci. l–q Ascospores. r Ascospore stained in Indian ink to show the mucilaginous sheath. s A germinated ascospore. t Culture characters on PDA (left: above, right: below). Scale bars: c, d = 100 μ m, g–k = 30 μ m, e, f, r, s = 20 μ m, l–q = 10 μ m.

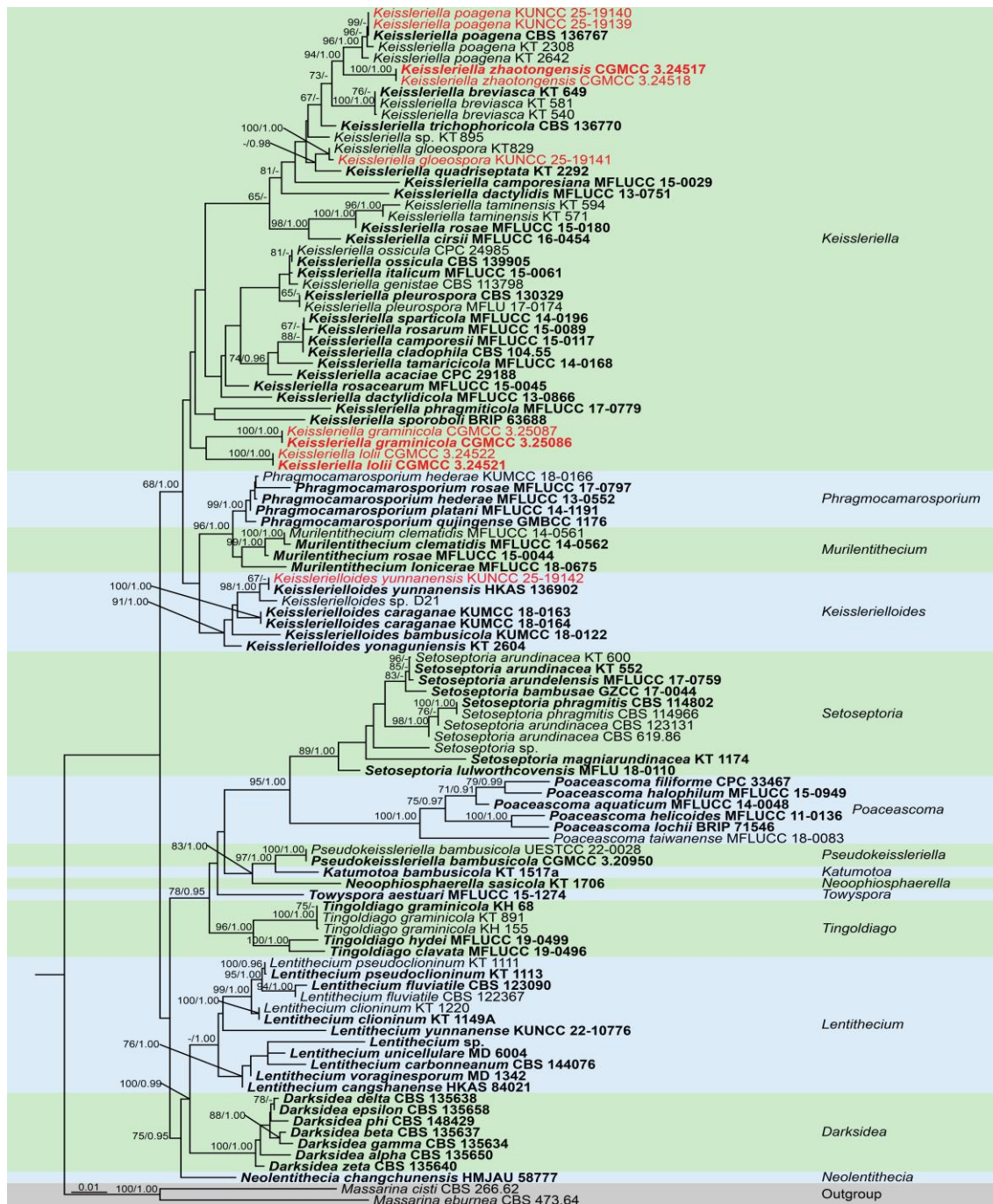


Figure 25 – RAXML phylogram generated from a combined dataset of partial ITS, LSU, SSU, and *tefl-α* DNA sequence analyses for Lentithecaceae. Related sequences are obtained following Jiang et al. (2019), Brahmanage et al. (2020), Hyde et al. (2020a), Crous et al. (2022a), Sun et al. (2025a). One hundred and six strains were included in the combined analyses, which comprised 3,313 characters in the combined ITS, LSU, SSU, and *tefl-α* alignment. *Massarina cisti* (CBS 266.62) and *Massarina eburnea* (CBS 473.64) were used as the outgroup taxa. The best-scoring RAXML tree with a final likelihood value of -19003.178742 is presented. The matrix contained 1,027 distinct alignment patterns, with 22.37% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.239230, C = 0.249439, G = 0.272330, T = 0.239001; substitution rates AC = 1.426864, AG = 2.532389, AT = 1.431346, CG = 1.219603, CT = 8.141791, GT = 1.000000. The tree topology of the ML analysis is similar to the Bayesian analysis. Bootstrap values for ML equal to or greater than 65% and PP values greater than 0.95 (rounding of values to 2 decimal places) are labelled on the nodes. Strains of the newly described species are in orange, while type strains are in bold. (ITS: 525 bp, LSU: 854 bp, SSU: 1016 bp, *tefl-α*: 918bp)

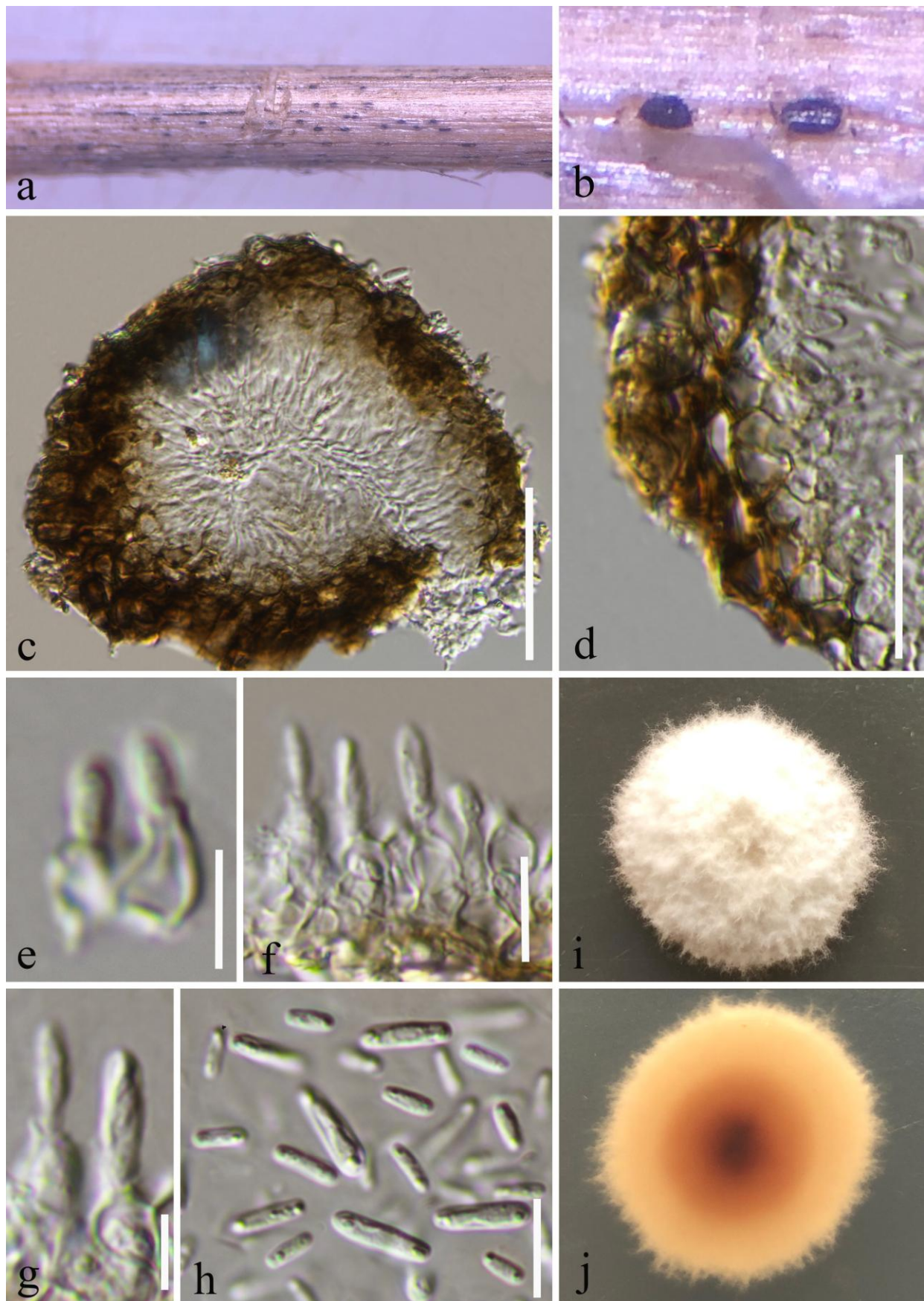


Figure 26 – *Keissleriella gloeospora* (HKAS 135351, a new morph record and a new geographical record). a, b Appearance of conidiomata on the host substrate. c A section of a conidioma. d Conidiomata wall. e–g Conidiogenous cells. h Conidia. i, j Culture characters on PDA (i: above, j: below). Scale bars: c = 30 μ m, d = 20 μ m, f, h = 10 μ m, e, g = 5 μ m.

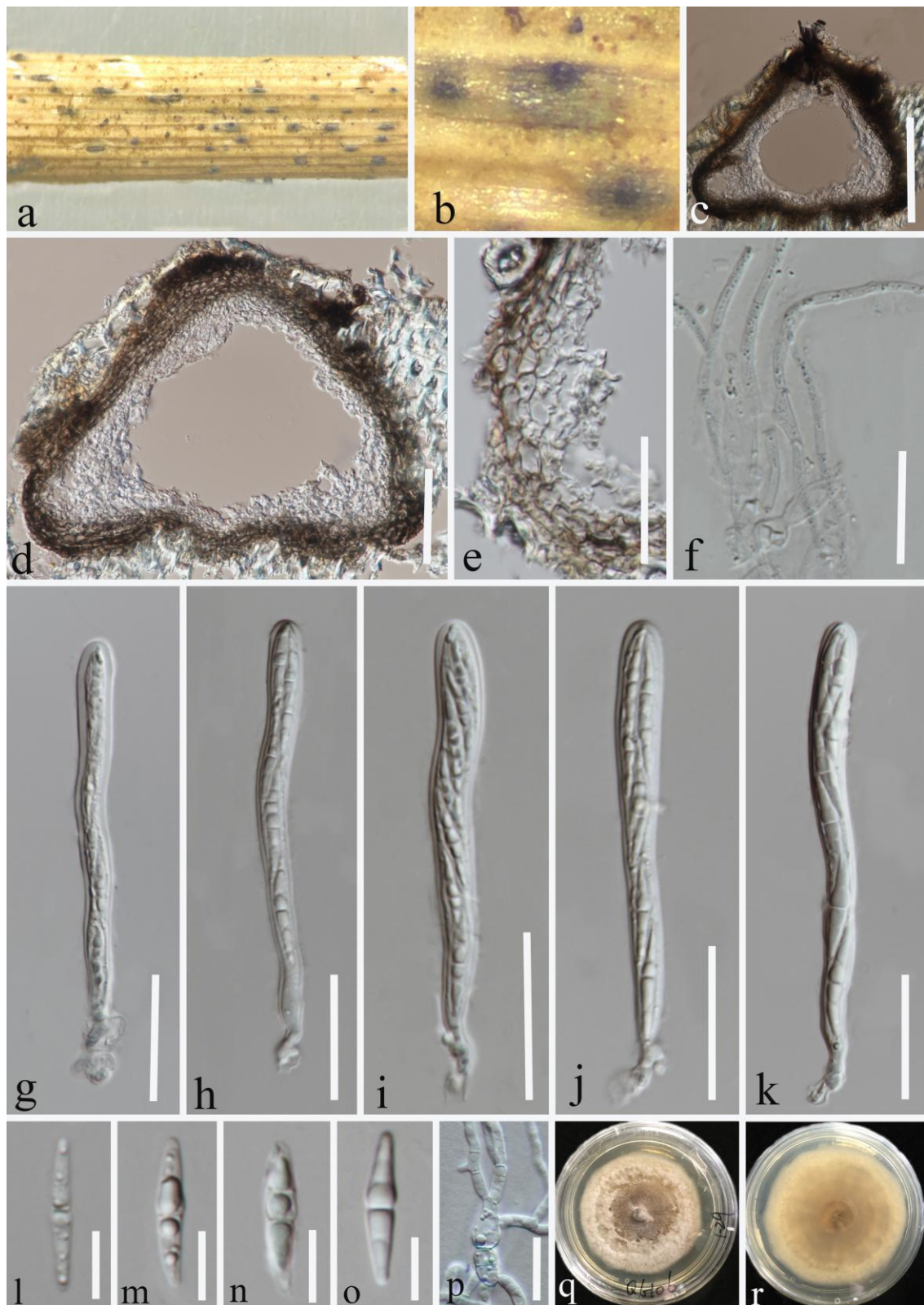


Figure 27 – *Keissleriella graminicola* (HKAS 128781, holotype). a, b Appearance of ascomata on the host substrate. c, d Sections of ascomata. e Peridium. f Pseudoparaphyses. g–k Asci. l–o Ascospores. p A germinated ascospore. q, r Culture characters on PDA (q: above, r: below). Scale bars: c = 100 μ m, d = 50 μ m, e, g–k = 30 μ m, f, p = 20 μ m, l–o = 10 μ m.

Keissleriella poagens Crous & Quaedvl, Persoonia 32: 191 (2014)

Fig. 29

Basionym: *Keissleriella culmifida* (P. Karst.) S.K. Bose ex J.K. Mitch. & Bensch, Schlechtendalia 40: 340 (2023)

Index Fungorum number: IF808887; Facesoffungi number: FoF18352

Saprobic on dead stems of *Dactylis glomerata*. Sexual morph: *Ascomata* 160–260 µm high × 130–240 µm diam. ($\bar{x}$ = 205 × 190 µm, n = 15), globose or subglobose, semi-immersed in host tissue, with minute papilla, solitary, scattered, uni-loculate, flattened base, brown to dark brown. *Peridium* 15–25 µm wide ($\bar{x}$ = 19 µm, n = 30), multi-layer, comprising dark brown to brown cells of *textura angularis*, inner layers comprising thin, hyaline cells. *Hamathecium* comprises 1.5–2.7 µm wide ($\bar{x}$ = 2 µm, n = 30), numerous, filamentous branches, septate, pseudoparaphyses. *Asci* 70–100 × 11–14 µm ($\bar{x}$ = 84.5 × 13 µm, n = 30), 8-spored, bitunicate, fissitunicate, thick-walled, cylindric-clavate to clavate, apically rounded, with furcated pedicel, ocular chamber visible when immature. *Ascospores* 20–23.5 × 4.5–6 µm ($\bar{x}$ = 22 × 5 µm, n = 30), biseriate, narrowly fusiform, conical and narrowly rounded at the ends, 3-septate, smooth, surrounded by an entire gelatinous sheath, hyaline. Asexual morph: Undetermined.

Culture characteristics – Colonies on PDA reaching 20 mm diam. after two weeks. Colony from above, dense, circular, low convex, surface smooth, with edge entire, floccose, white; from below, yellow at the edge, with white to cream margin, brown at the center, slightly radiating outwards colony; not produced pigmentation on agar medium.

Material examined – China, Yunnan Province, Zhaotong grassland, on dead stems of *Dactylis glomerata* (Poaceae), 21 August 2021, Y. Gao, ZG19 (HKAS 132992), living culture KUNCC 25-19139; *ibid.*, ZG26 (HKAS 132994), living culture KUNCC 25-19140.

Known hosts and distribution – on *Poa* sp. (Poaceae) in the Netherlands (Crous et al. 2014), on dead stems of *Agrostis flaccida* (Poaceae) in Japan (Tanaka et al. 2015), on dead stems of *Dactylis glomerata* (Poaceae) in Yunnan Province, China (This study).

GenBank numbers – KUNCC 25-19139: ITS = PV608541, LSU = PV607391, SSU = PV607288, *tefl-α* = PV626434; KUNCC 25-19140: ITS = PV608542, LSU = PV607392, SSU = PV607289, *tefl-α* = PV626435.

Notes – Our collections (KUNCC 25-19139 and KUNCC 25-19140) grouped with *Keissleriella poagensis*, and by forming a distinct clade in Lentitheciaceae (Fig. 25). ITS and LSU sequences of our collections completely matched with those from *K. poagensis* (CBS 136767, ex-type) (GenBank KJ869112, KJ869170) showed 516/516 bp (100%) and 686/686 (100%), separately. Nucleotide comparison of the *tefl-α* region between our collections and *K. culmifida* (KT 2308, KT 2642) showed 0.56% and 0.91% base pair difference (5/886 bp and 8/884 bp, without gaps) in *tefl-α* regions, the base pair differences in ITS gene (0/505 bp, 0.00%; 0/505 bp, 0.00%), the base pair differences in LSU gene (0/839 bp, 0.00%; 0/839 bp, 0.00%). Our collections (KUNCC 25-19139 and KUNCC 25-19140), *K. poagensis* (CBS 136767), and *K. culmifida* (KT 2308, KT 2642) are morphologically similar (Crous et al. 2014, Tanaka et al. 2015). Based on the combined molecular and morphological evidence, we propose that *Keissleriella poagensis* is a synonym of *K. culmifida*. In this study, we identified that our collection is *Keissleriella poagensis*, and it is a new host and a geographical record.

Keissleriella zhaotongensis Y. Gao, H. Gui & K.D. Hyde, sp. nov.

Fig. 30

Index Fungorum number: IF903819; Facesoffungi number: FoF17696

Holotype – HKAS 128805

Etymology – The specific epithet “zhaotongensis” refers to Zhaotong City, where the holotype was found.

Saprobic on dead stems of *Dactylis glomerata*. Sexual morph: *Ascomata* 130–155 µm diam. × 100–130 µm high ($\bar{x}$ = 140 × 110 µm, n = 10), globose or subglobose, immersed in host tissue, with minute papilla, solitary, scattered, uni-loculate, flattened base, brown to dark brown. *Peridium* 7.5–21 µm wide ($\bar{x}$ = 12 µm, n = 30), multi-layered, thin at the base, thick at the top, comprising brown to dark brown cells of *textura angularis* or *textura globulosa*, inner layers comprising thin, hyaline cells. *Hamathecium* comprises 2–3 µm wide ($\bar{x}$ = 2.5 µm, n = 30), filiform, anastomosing above asci, reaching the ostiole part, transverse septate, trabeculate pseudoparaphyses. *Asci* 55–90 × 10–16 µm ($\bar{x}$ = 77 × 13 µm, n = 30), 8-spored, bitunicate, fissitunicate, thick-walled, cylindric-

clavate to clavate, apically rounded, with furcated pedicel, ocular chamber visible when immature. *Ascospores* $20\text{--}22 \times 4.5\text{--}6.5 \mu\text{m}$ ($\bar{x} = 21 \times 5.5 \mu\text{m}$, $n = 30$), biseriate, fusiform, 3-septate, smooth, surrounded by an entire gelatinous sheath, hyaline. Asexual morph: Undetermined.

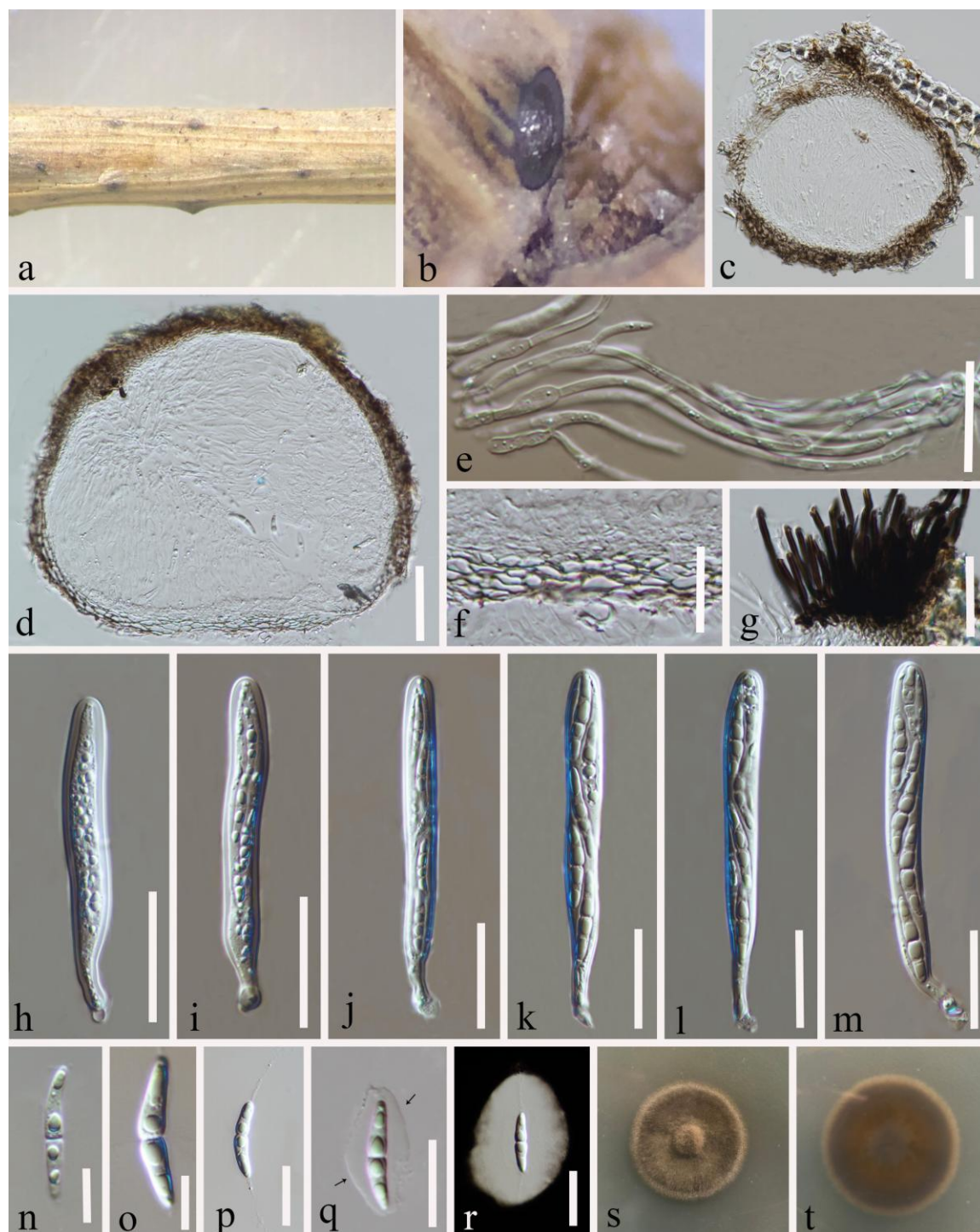


Figure 28 – *Keissleriella lolii* (HKAS 128809, holotype). a Appearance of ascomata on the host substrate. b–d Sections of ascomata. e Pseudoparaphyses. f. Peridium. g Apical setae of ascoma. h–m Asci. n–q Ascospores (q arrowheads indicate gelatinous sheath). r Ascospore stained with India ink showed mucilaginous sheath. s, t Culture characters on PDA (s: above, t: below). Scale bars: c, d = 50 μm , g–m = 30 μm , e, f, p–r = 20 μm , n, o = 10 μm .

Culture characteristics – Ascospores germinated within 48 h on PDA. Colonies on PDA were irregular and approx. 2 cm diam. after four weeks at 27°C. The colonies from above, have rough,

knobly protuberances, curled margin, white to cream at the edge, gray-green at the center; from below, white to cream margin, dark yellowish at the center.

Material examined – China, Yunnan Province, Zhaotong grassland, on dead stems of *Dactylis glomerata* (Poaceae), 27 August 2022, Y. Gao, QG40A (HKAS 128805, holotype), ex-type living culture CGMCC 3.24517; *ibid.*, QG40B (HKAS 128806, isotype), ex-isotype living culture CGMCC 3.24518.

GenBank numbers – CGMCC 3.24517: ITS = PV642535, SSU = PV607286, *tef1-α* = PV626432; CGMCC 3.24518: ITS = PV642536, SSU = PV607287, *tef1-α* = PV626433.

Notes – Based on multigene phylogenetic analyses, our collections (CGMCC 3.24517 and CGMCC 3.24518) are grouped with *Keissleriella poagens* (CBS 136767, KT 2308, KT 2642, KUNCC 25-19139, KUNCC 25-19140) with 94% ML, 1.00 PP statistical support (Fig. 25). *Keissleriella poagens* (KT 2308, KT 2642) were reported on dead stems of *Agrostis flaccida* (Poaceae) in Japan (Tanaka et al. 2015). Our collections morphologically resemble *K. poagens* (KT 2642) in its ascomata (100–130 µm high vs. 120–145 µm high) and asci (55–90 × 10–16 µm, L/W = 5.6 vs. 70.5–84 × 10.5–13 µm, L/W = 6.6) (Tanaka et al. 2015). However, the pairwise nucleotide comparison showed that our collections (CGMCC 3.24517 and CGMCC 3.24518) differ from *K. poagens* (KT 2642) in 12/474 bp of ITS (2.53%, with 2 gaps), 8/1018 bp of SSU (0.79%, with 1 gap), 25/856 bp of *tef1-α* (2.92%, without gaps). Here, *Keissleriella zhaotongensis* is introduced as a new species based on its distinct morphology and phylogeny.

Keisslerielloides Wanas., Y. Gao, H. Gui & K.D. Hyde, gen. nov.

Index Fungorum number: IF903820; Facesoffungi number: FoF17696

Etymology – Referring to its similarity with *Keissleriella*.

Saprobic on dead branches and leaves blade. Asexual morph: Undetermined. Sexual morph: *Ascomata* semi-immersed to erumpent, solitary to gregarious, scattered or clustered, dark brown to blackened, subglobose to ampulliform, often with a slightly flattened base, featuring individual ostioles surrounded by short, dark setae. *Peridium* is composed of several layers of flattened, brown to dark brown pseudoparenchymatous cells, arranged in a *textura angularis* to *textura prismatica*, with outer layers being darker and inner layers more hyaline. *Hamathecium* consists of dense, septate, anastomosed pseudoparaphyses, embedded in a hyaline gelatinous matrix. *Asci* 8-spored, bitunicate, fissitunicate, cylindrical to clavate, with short pedicels and well-developed ocular chambers. *Ascospores* ellipsoidal to fusiform, with rounded ends, range from 1 to 6 septate, initially hyaline to pale yellowish, becoming yellowish brown at maturity, with or without surrounded by a mucilaginous sheath (Tanaka et al. 2015, Jiang et al. 2019, Phookamsak et al. 2019, this study).

Type species – *Keisslerielloides yunnanensis* (Y.R. Sun, Yong Wang bis & K.D. Hyde) Wanas., Y. Gao, H. Gui & K.D. Hyde, comb. nov.

Notes – Multigene phylogenetic analyses based on combined ITS, LSU, SSU, and *tef1-α* sequence data show that *Keisslerielloides* species form a monophyletic clade in Lentitheciaceae (Fig. 25). Our results are similar to previous studies (Brahmanage et al. 2020, Hyde et al. 2020a, Yang et al. 2022c, Sun et al. 2025a). *Keisslerielloides* and *Keissleriella* are morphologically similar in terms of dark, immersed to erumpent ascomata with papillate ostioles bearing short, dark setae, bitunicate (fissitunicate) asci, and hyaline to pale brown, septate ascospores that may be surrounded by a mucilaginous sheath. However, *Keisslerielloides* differs from *Keissleriella* in that its ascomata are subglobose to ampulliform and often slightly flattened at the base (vs. globose to subglobose in *Keissleriella*); and its ascospores are ellipsoidal to fusiform with rounded ends, (1–)3–6-septate, and become yellowish-brown at maturity (vs. hyaline to pale brown, ellipsoidal to fusiform with sharper ends, and generally with fewer septa in *Keissleriella*) (Sun et al. 2025a). Our phylogenetic analyses (Fig. 25) recover all *Keisslerielloides* species as a well-supported, monophyletic lineage that is clearly distinct from *Keissleriella*, *Murilentithecium*, and *Phragmocamarosporium*. Phylogenetically, the *Keisslerielloides* is closely related to *Murilentithecium*. However, *Murilentithecium* and *Keisslerielloides* have differences in morphology. *Murilentithecium* is characterized by its broadly oblong ascomata, thick peridium with multiple layers, muriform

ascospores with complex septation, and a thick mucilaginous sheath (Wanasinghe et al. 2014). *Keisslerielloides* typically have smaller, subglobose to ampulliform ascomata with dark setae, a thinner peridium, and ascospores with only transverse septa. These differences highlight the distinct morphological and taxonomic features of the two genera. Therefore, we introduce *Keisslerielloides* as a new genus to accommodate four new taxonomic combinations (*K. bambusicola*, *K. caraganae*, *K. yonaguniensis*, *K. yunnanensis*) based on morphology and phylogeny.

Keisslerielloides bambusicola (H.B. Jiang, Phookamsak & K.D. Hyde) Wanas., Y. Gao, H. Gui & K.D. Hyde, comb. nov.

Basionym: *Keissleriella bambusicola* H.B. Jiang, Phookamsak & K.D. Hyde, Phytotaxa 423 (3): 136 (2019)

Index Fungorum number: IF903846; Facesoffungi number: FoF06256

Holotype – China, Yunnan Province, Kunming City, Golden Temple, on dead bamboo branches, 5 December 2017, H.B. Jiang & R. Phookamsak, GT005 (HKAS 101767, holotype), ex-type living culture KUMCC 18-0122.

Morphological description – Jiang et al. (2019)

Notes – In our multigene phylogenetic study, *Keisslerielloides bambusicola* (KUMCC 18-0122, ex-type) was grouped within *Keisslerielloides*. The species also shares similar morphological characters with other *Keisslerielloides* spp., such as subglobose to ampulliform, slightly flattened base, ascomata with dark setae, anastomosed pseudoparaphyses, cylindrical to cylindric-clavate, short pedicellate, apically rounded, with well-developed ocular chamber asci, ellipsoidal to fusiform, (4–)5(–6)-septate, constricted at the septa ascospores (Jiang et al. 2019).

Keisslerielloides caraganae (Chaiwan, Phookamsak, Wanas. & K.D. Hyde) Wanas., Y. Gao, H. Gui & K.D. Hyde, comb. nov.

Basionym: *Keissleriella caraganae* Chaiwan, Phookamsak, Wanas. & K.D. Hyde, Fungal Diversity 95: 16 (2019)

Index Fungorum number: IF903847; Facesoffungi number: FoF04965

Holotype – China, Yunnan Province, Kunming Institute of Botany, on a dead hanging branch of *Caragana arborescens* Lam. (Fabaceae), 2 November 2017, R. Phookamsak, KIB018 (KUN-HKAS 102236, holotype), ex-type KIB018A (KUMCC 18-0163 = MFLUCC 18-0682), KIB018B (KUMCC 18-0164).

Morphological description – Phookamsak et al. (2019)

Notes – *Keissleriella caraganae* was introduced by Phookamsak et al. (2019) in *Keissleriella* based on the sexual morph similarity to other *Keissleriella* species in ostiolar neck ascomata with short, aseptate, brown periphyses, broadly cylindrical to cylindric-clavate, bitunicate asci and septate ascospores with mucilaginous sheath (Tanaka et al. 2015, Wanasinghe et al. 2018). However, in our multigene phylogenetic study, *Keissleriella caraganae* (KUMCC 18-0163 and KUMCC 18-0164) was grouped within *Keisslerielloides*. The sexual morph of *Keissleriella caraganae* is similar to other *Keisslerielloides* spp., with ascomata subglobose to ampulliform, often with a slightly flattened base and ascospores ellipsoidal to fusiform with rounded ends, becoming yellow at maturity.

Keisslerielloides yonaguniensis (Kaz. Tanaka & K. Hiray.) Wanas., Y. Gao, H. Gui & K.D. Hyde, comb. nov.

Basionym: *keissleriella yonaguniensis* Kaz. Tanaka & K. Hiray., Studies in Mycology 82: 98 (2015)

Index Fungorum number: IF903888; Facesoffungi number: FoF04965

Holotype – Japan, Okinawa, Isl. Yonaguni, Kubura pond, on dead leaves of *Typha latifolia*, 23 Nov. 2008, K. Tanaka & K. Hirayama KT2604 (HHUF 30138, holotype), ex-type CBS 139693 (JCM 19419 = MAFF 243851)

Morphological description – Tanaka et al. (2015)

Notes – In our multigene phylogenetic study, *Keissleriella yonaguniensis* (KT2604, holotype) was grouped within *Keisslerielloides*. The sexual morph of this species is similar to other *Keisslerielloides* species.

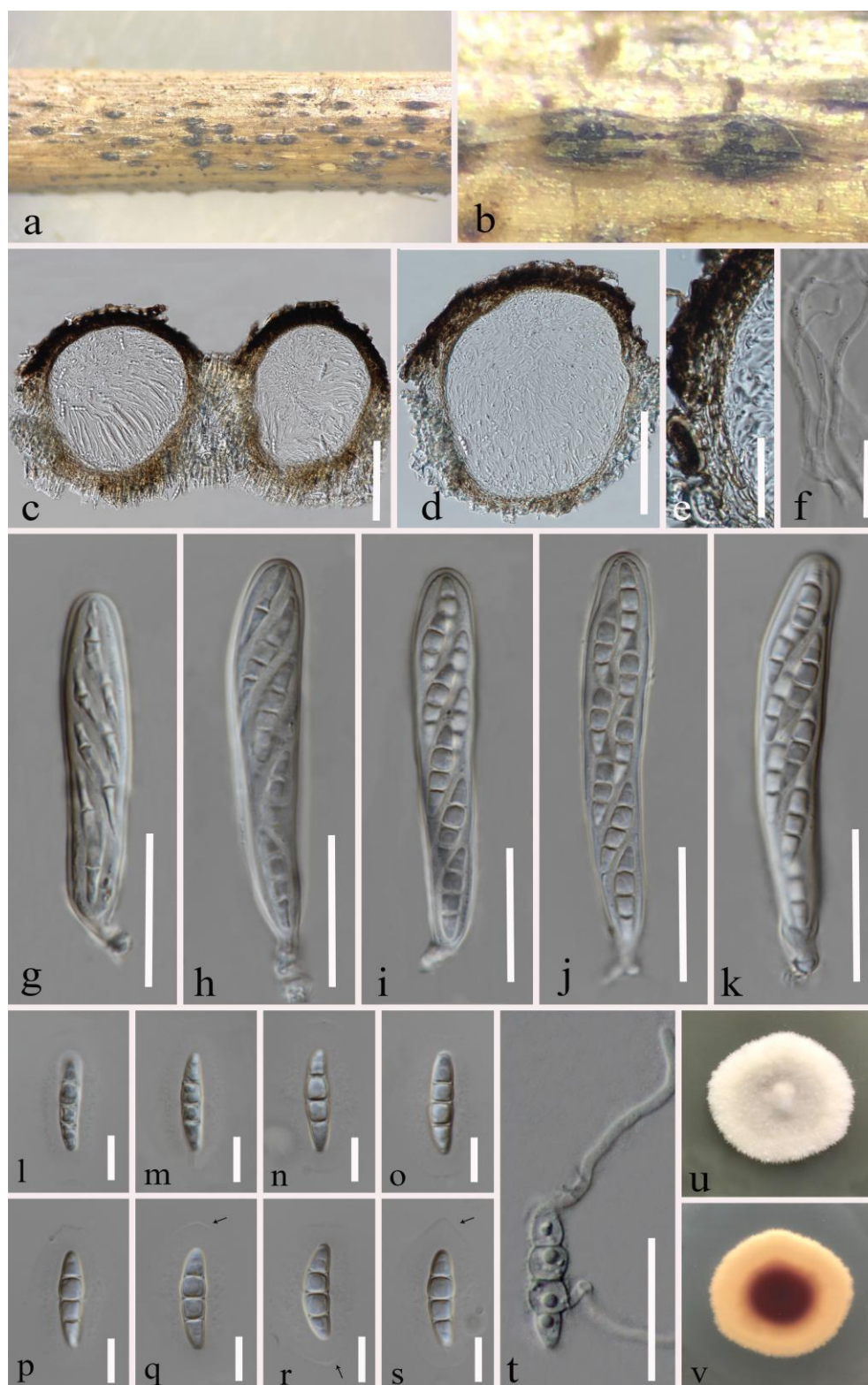


Figure 29 – *Keissleriella poagens* (HKAS 132992, a new host and a geographical record). a, b Appearance of ascomata on the host substrate. c, d Sections of ascomata. e Peridium. f Pseudoparaphyses. g–k Asci. l–s Ascospores. t A germinated ascospore. u, v Culture characters on PDA (u: above, v: below). Scale bars: c, d = 100 μ m, e, g–k = 30 μ m, f, t = 20 μ m, l–s = 10 μ m.

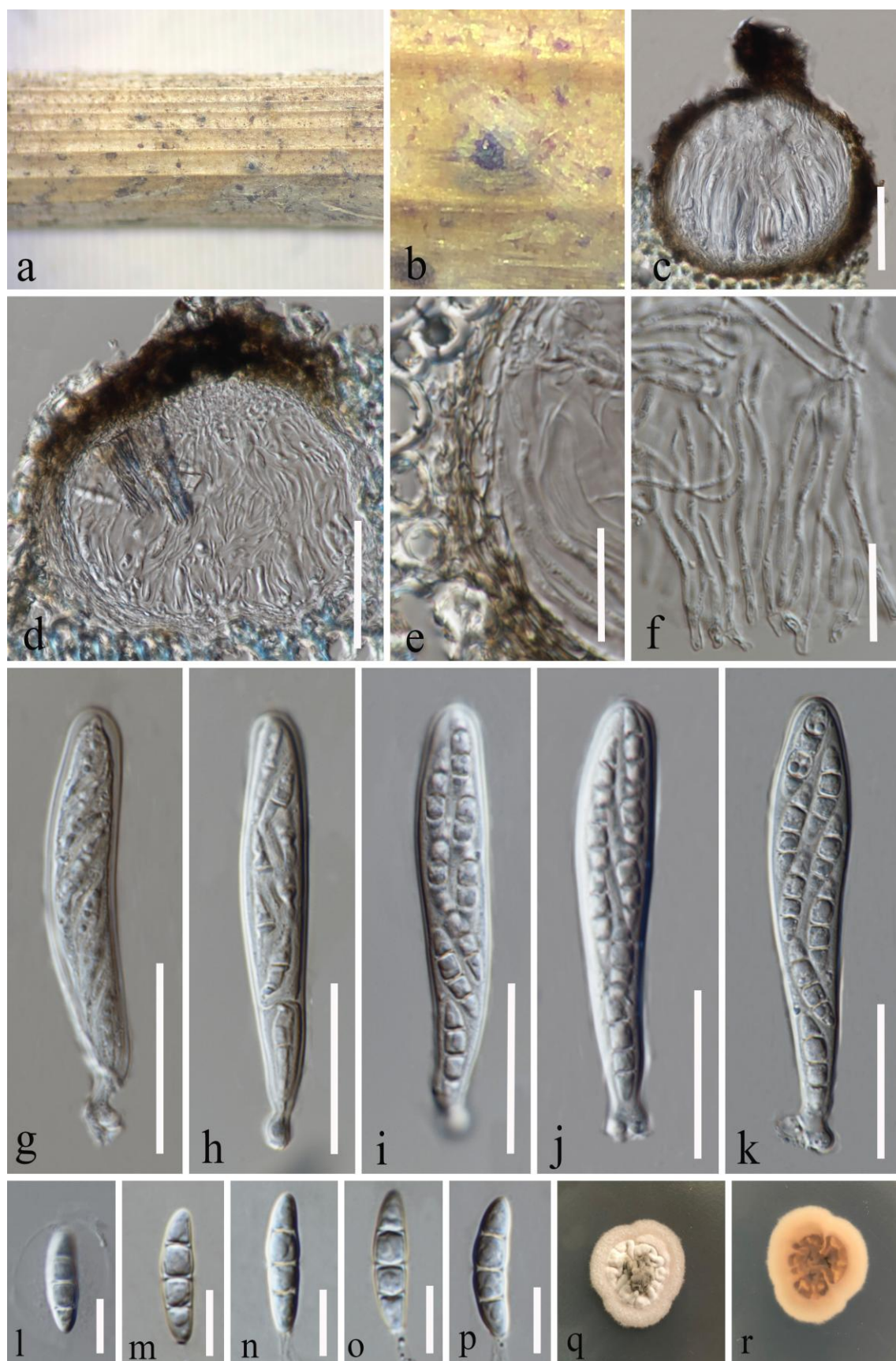


Figure 30 – *Keissleriella zhaotongensis* (HKAS 128805, holotype). a Material examined. b Appearance of ascomata on the host substrate. c, d Sections of ascomata. e Peridium. f Pseudoparaphyses. g–k Asci. l Ascospore with mucilaginous sheath. m–p Ascospores. q, r Culture characters on PDA (q: above, r: below). Scale bars: c, d = 50 μ m, g–k = 30 μ m, e, f = 20 μ m, l–p = 10 μ m.

Keisslerielloides yunnanensis (Y.R. Sun, Yong Wang bis & K.D. Hyde) Wanas., Y. Gao, H. Gui & K.D. Hyde, comb. nov. Fig. 31

Basionym: *Keissleriella yunnanensis* Y.R. Sun, Yong Wang bis & K.D. Hyde, Fungal Diversity 10.1007/s13225-024-00549-4: [54] (2025)

Index Fungorum number: IF903821; Facesoffungi number: FoF16424

Holotype – HKAS 136902

Saprobic on dead stems of grass. Sexual morph: *Ascomata* 150–180 μm high $\times$ 120–170 μm diam. ($\bar{x}$ = 170 $\times$ 140 μm , n = 10), pyriform or globose to subglobose, semi-immersed, visible as raised, black dots on the host surface, solitary, scattered, uni-loculate, brown to dark brown, individually ostiole of each locule, with minute papilla, ostiole surrounded by short, dark setae. *Peridium* 12.5–20 μm wide ($\bar{x}$ = 16 μm , n = 20), composed of several layers of small, flattened, brown to dark brown pseudoparenchymatous cells, arranged in a *textura angularis*, intermixed with the host cells. *Hamathecium* comprised of 1.5–2.5 μm wide ($\bar{x}$ = 2.2 μm , n = 30), filiform branches, dense, broad filamentous, distinctly septate, anastomosed pseudoparaphyses, embedded in a hyaline gelatinous matrix. *Asci* 60–90 $\times$ 8.5–12 μm ($\bar{x}$ = 77 $\times$ 10 μm , n = 20), 8-spored, cylindric-clavate to clavate, apically rounded, short pedicellate, bitunicate, fissitunicate, thick-walled, with well-developed ocular chamber. *Ascospores* 20.5–25 $\times$ 4–5.5 μm ($\bar{x}$ = 23 $\times$ 5 μm , n = 20), biseriate, fusiform, conical at the ends, 1-3-5-septate, hyaline when immature, becoming pale yellow when mature, smooth, with guttulate, lacking a mucilaginous sheath. Asexual morph: Undetermined.

Culture characteristics – Ascospores germinated within 48 h on PDA. 2.5 cm diam. after three weeks at 27°C. Colony dense, circular, from above, low convex, surface smooth, with edge entire, floccose, grey; from below, white at the narrow edge, black at the center.

Material examined – China, Yunnan Province, Kunming, on dead stems of unidentified grass (Poaceae), 25 August 2022, Y. Gao, XG6 (HKAS 132968), living culture KUNCC 25-19142.

Known hosts and distribution – on leaves of *Spineless yucca* (Asparagaceae) in China (Sun et al. 2025a); on dead stems of unidentified grass (Poaceae) in China (This study)

GenBank numbers – KUNCC 25-19142: ITS = PV608547, LSU = PV607398, SSU = PV607295, *tefl*- α = PV626440.

Notes – Based on our phylogenetic analysis of the combined ITS, LSU, SSU, and *tefl*- α sequence data, our collection (KUNCC 25-19142) is closely related to *Keisslerielloides yunnanensis* (HKAS 136902, holotype) with 67% ML and 1.00 PP statistical support (Fig. 25). Our specimen (HKAS 132968) is morphologically similar to *K. yunnanensis* (HKAS 136902) (Sun et al. 2025a). A pairwise nucleotide comparison showed that KUNCC 25-19142 and HKAS 136902 are identical. Therefore, based on morphological characterization and phylogenetic analyses, we introduce our collection (KUNCC 25-19142) as a new host record on dead stems of unidentified grass (Poaceae) in China.

Leptosphaeriaceae M.E. Barr, Mycotaxon 29: 503 (1987)

Notes – Leptosphaeriaceae was introduced by Barr (1987) and has been reviewed by Ariyawansa et al. (2015a). There are 18 genera accepted in Leptosphaeriaceae (Hyde et al. 2024a). Species of Leptosphaeriaceae are widely distributed and exhibit diverse lifestyles, including saprobic, epiphytic, fungicolous, parasitic, and hemibiotrophic on herbaceous and woody plants (Ariyawansa et al. 2015a, Phookamsak et al. 2019, Sun et al. 2019, Lestari et al. 2021, Gao et al. 2023). The sexual morphs of Leptosphaeriaceae are characterized by having subglobose to globose, obpyriform ascomata; peridium composed of large, thin-walled, pigmented, plectenchymatous or scleroplectenchymatous cells; cellular pseudoparaphyses; bitunicate, fissitunicate, cylindrical to oblong, with a pedicel and ocular chamber asci; oblong or filiform, fusoid, obovoid, septate, reddish brown or yellowish brown ascospores (Hongsanant et al. 2020a, Ren et al. 2024a). The asexual morphs of this family are either hyphomycetous or coelomycetous (Ariyawansa et al. 2015a). Coelomycetous members are characterized by globose, immersed to nearly superficial conidiomata; scleroplectenchymatous conidiomata wall; ellipsoidal to subcylindrical or oblong

conidia (Ariyawansa et al. 2015a). Hyphomycetous members are characterized by solitary or small groups, pale to chestnut brown, 3–6-septate conidiophores; cylindrical, terminal to intercalary, integrated, sympodial, yellowish to pale brown conidiogenous cells; cylindrical to subcylindrical, solitary, subhyaline to pale brown, aseptate or presenting of transversely septate conidia (Zhang et al. 2012, Ren et al. 2024a). An updated phylogenetic tree based on combined ITS, LSU, SSU, *tub2*, and *rpb2* sequence data is presented in Fig. 32.

Heterosporicola Crous, Fungal Diversity 86: 208 (2017)

Notes – *Heterosporicola* was introduced to accommodate *Heterospora* by Wijayawardene et al. (2018) as the remaining species of *Phoma* and *Heterosporicola chenopodii* as the type species of the *Heterosporicola*. De Gruyter et al. (2013) raised *Heterospora* to the status of an independent genus, incorporating two previously classified *Phoma* sect. *Heterospora* species (*H. chenopodii* and *H. dimorphospora*) demonstrated phylogenetic affinity with the Leptosphaeriaceae. Three species were accepted in *Heterosporicola* (*H. beijingensis*, *H. chenopodii*, *H. dimorphospora*) (Index Fungorum 2025). However, no sexual morph characters are available for this genus (Wijayawardene et al. 2018, Brahmanage et al. 2020). In this study, we introduce a new species, *Heterosporicola qujingensis*, based on morphology and molecular data, together with descriptions and illustrations (Fig. 33).

Heterosporicola qujingensis Y. Gao, H. Gui & K.D. Hyde, sp. nov.

Fig. 33

Index Fungorum number: IF903822; Facesoffungi number: FoF17697

Holotype – HKAS 128795

Etymology – The specific epithet “qujingensis” refers to Qujing City, where the holotype was found.

Saprobic on dead stems of host plants. Sexual morph: *Ascomata* 150–270 µm high × 170–220 µm diam. ($\bar{x}$ = 204 × 200 µm, n = 15), immersed, globose or subglobose, with a flattened base, scattered or in small groups, uni-loculate, glabrous, dark brown to black, ostiolate. *Ostiole* apex conical and with papilla. *Peridium* 9–18 µm wide ($\bar{x}$ = 13 µm, n = 30), composed of 2–3 layers of flattened, dark brown cells of *textura angularis*. *Hamathecium* comprises 1.5–4 µm wide ($\bar{x}$ = 2.5 µm, n = 30), septate, hyaline, branched, cellular pseudoparaphyses. *Asci* 70–90 × 12–15 µm ($\bar{x}$ = 84 × 13 µm, n = 25), 8-spored, cylindric-clavate to clavate, apically rounded, short pedicellate, fissitunicate, bitunicate, slightly curved, with ocular chamber. *Ascospores* 23–30 × 4.5–7.5 µm ($\bar{x}$ = 26.5 × 6 µm, n = 25), biserial, fusiform, 3–4-septate, often slightly constricted at the septum, broader cells above central septum, hyaline when immature, becoming pale yellow when mature, with guttulate. Asexual morph: Undetermined.

Culture characteristics – Ascospores germinated within 48 h on PDA. 1.5 cm diam. after three weeks at 27 °C. Colony dense, circular, from above, convex, surface smooth, with edge entire, floccose, white; from below, pale yellow at the edge, golden at the center, not producing pigmentation in agar.

Material examined – China, Yunnan Province, Qujing grassland, on dead stems of *Bidens Pilosa* (Asteraceae), 27 August 2022, Y. Gao, QG17A (HKAS 128795, holotype), ex-type living culture CGMCC 3.24507; *ibid.*, QG17B (HKAS 128796, isotype), ex-isotype living culture CGMCC 3.24508.

GenBank numbers – CGMCC 3.24507: ITS = PV608558, LSU = PV607409, *tub2* = PV613312, *rpb2* = PV655485; CGMCC 3.24508: ITS = PV608559, LSU = PV607410, *tub2* = PV613313, *rpb2* = PV655486.

Notes – *Heterosporicola qujingensis* (CGMCC 3.24507, CGMCC 3.24508) forms a separate clade sister to *H. chenopodii* (CBS 115.96, CBS 448.68) with 93% ML and 0.84 PP support values

(Fig. 32). *Heterosporicola chenopodii* (= *Phoma variospora*) was a widespread pathogen affecting *Chenopodium* species in Europe (Wijayawardene et al. 2017). Due to the presence of septate macroconidia in vivo, it is occasionally mistaken for *Ascochyta caulina*. The sexual morph of *Heterosporicola* remains unknown (De Gruyter et al. 2013). Sequence comparison for the ITS region between *Heterosporicola qujingensis* and *H. chenopodii* (CBS 448.68, ex-type) showed a 5.42% (27/498 bp, with 2 gaps) base pair difference in ITS region, 1.43% (12/842 bp, without gaps) base pair difference in the LSU region, 4.83% (51/1055 bp, with 1 gap) base pair difference in the *rpb2* region, respectively. In this study, we report *Heterosporicola qujingensis* as a new species from the dead stems of *Bidens Pilosa* in China. This is also the first sexual species reported in *Heterosporicola*.

Leptosphaeria Ces. & De Not., Comment. Soc. Crittog. Ital. 1 (4): 234 (1863)

Notes – *Leptosphaeria* was reported by Cesati & De Notaris (1863) and is typified by *Leptosphaeria doliolum* and lectotype designated by Shearer et al. (1990). The sexual morph of *Leptosphaeria* is characterized by coriaceous, semi-immersed to erumpent ascomata, thick-walled, composed of scleroplectenchymatous cells peridium, cylindrical or cylindric-clavate asci, ellipsoidal to fusiform, reddish to yellowish brown, septate ascospores and phoma-like and coelomycetous coniothyrium-like asexual morphs (Ariyawansa et al. 2015b, Dayarathne et al. 2015). Ariyawansa et al. (2015b) extensively examined the taxonomic reclassification of this genus. While the Index Fungorum (2025) records more than 1600 taxonomic names associated with *Leptosphaeria*, only a limited number of *Leptosphaeria* species have been validated through molecular phylogenetic studies (Ariyawansa et al. 2015a, Pem et al. 2020, Lestari et al. 2021, Gao et al. 2023). The majority of *Leptosphaeria* taxa remain without sufficient genetic data to establish their precise phylogenetic relationships (Ariyawansa et al. 2015a). In this study, we introduce a new species, *Leptosphaeria chinensis*, based on morphology and molecular data, together with descriptions and illustrations (Fig. 34).

Leptosphaeria chinensis Y. Gao, H. Gui & K.D. Hyde, sp. nov.

Fig. 34

Index Fungorum number: IF903823; Facesoffungi number: FoF17698

Holotype – HKAS 128791

Etymology – The specific epithet “chinensis” refers to China, where the holotype was found.

Saprobic on dead stems of host plants. Sexual morph: *Ascomata* 190–260 µm diam. × 145–165 µm high ($\bar{x}$ = 240 × 150 µm, n = 10), immersed in the epidermis of the host, globose or subglobose, with a flattened base, scattered or in small groups, coriaceous, uni-loculate, glabrous, dark brown to black, ostiolate. *Ostiole* apex conical and with papilla. *Peridium* 22–40 µm wide ($\bar{x}$ = 30 µm, n = 30), thick-walled, composed of 3–6 layers of flattened, hyaline to dark brown, scleroplectenchymatous cells of *textura angularis*. *Hamathecium* comprises 1–3.5 µm wide ($\bar{x}$ = 1.8 µm, n = 30), septate, hyaline, branched, cellular pseudoparaphyses, partially embedded in gelatinous matrix. *Asci* 70–100 × 11–16.5 µm ($\bar{x}$ = 84 × 14 µm, n = 25), 8-spored, cylindric-clavate to clavate, apically rounded, short pedicellate, bitunicate, fissitunicate, slightly curved, with ocular chamber. *Ascospores* 17–23 × 5–8 µm ($\bar{x}$ = 19 × 6.5 µm, n = 30), biseriate, fusiform, 3-septate, broader cells above the central septum, often slightly constricted at the septum, pale yellow when immature, becoming brown when mature, with guttulate, lacking a mucilaginous sheath. Asexual morph: Undetermined.

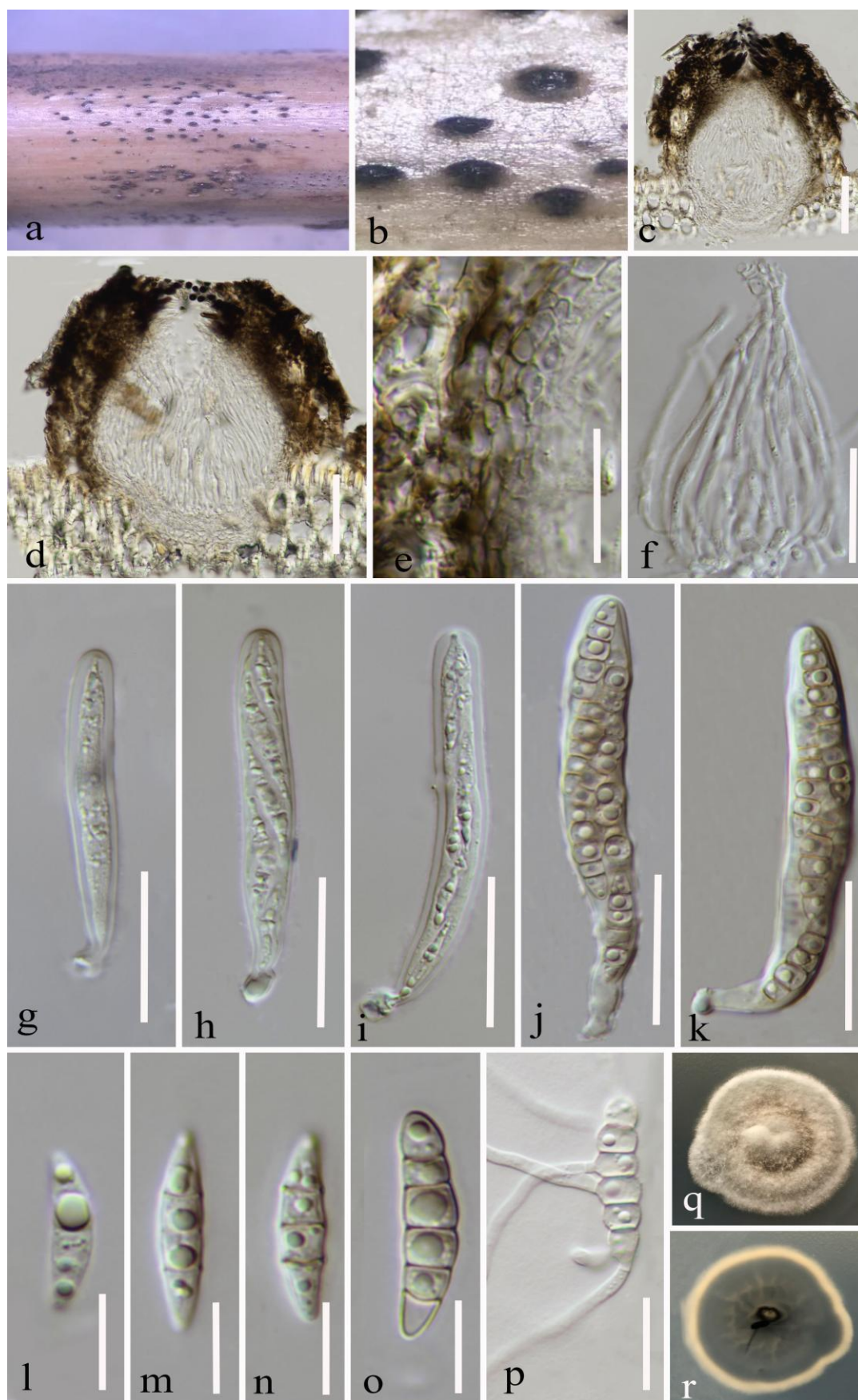


Figure 31 – *Keisslerielloides yunnanensis* (HKAS 132968, a new host record). a, b Appearance of ascomata on the host substrate. c, d Sections of ascomata. e Peridium. f Pseudoparaphyses. g–k Asci. l–o Ascospores. p A germinated ascospore. q, r Culture characters on PDA (q: above, r: below). Scale bars: c, d = 50 μ m, f–k = 30 μ m, e = 20 μ m, p = 15 μ m, l–o = 10 μ m.

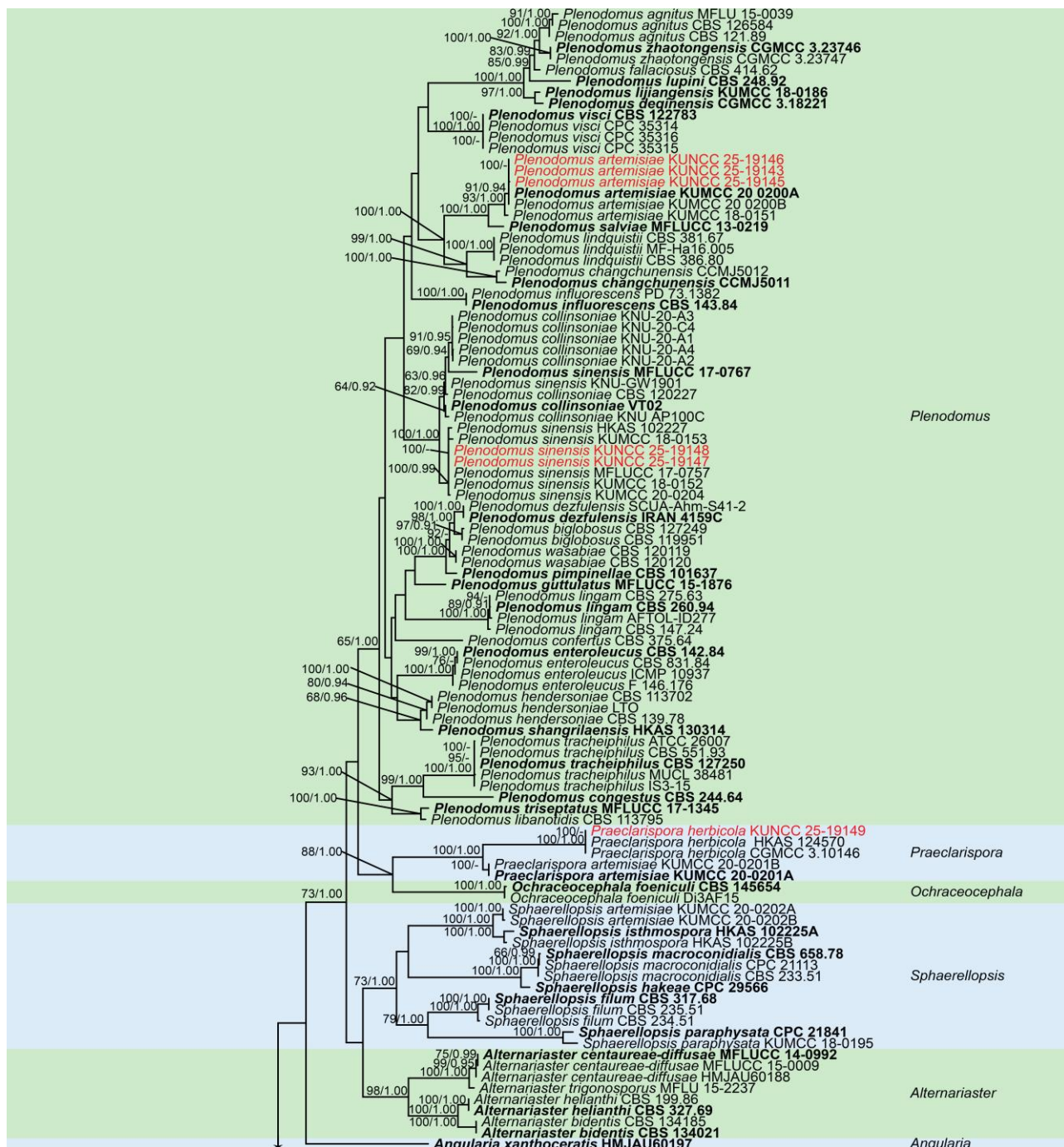


Figure 32 – RAXML phylogram generated from a combined dataset of partial ITS, LSU, SSU, *tub2*, and *rpb2* DNA sequence analyses for Leptosphaeriaceae. Related sequences are obtained following Gao et al. (2023). One hundred and ninety-five strains were included in the combined analyses, which comprise 3600 characters in the combined ITS, LSU, SSU, *tub2*, and *rpb2* alignment. *Didymella exigua* (CBS 183.55) and *Didymella maydis* (CBS 588.69) were used as the outgroup taxa. The best-scoring RAXML tree with a final likelihood value of -31512.435042 is presented. The matrix contained 1,276 distinct alignment patterns, with 41.72% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.243579, C = 0.231538, G = 0.269605, T = 0.255278; substitution rates AC = 1.643526, AG = 4.740372, AT = 1.990611, CG = 0.932698, CT = 8.529234, GT = 1.000000. The tree topology of the ML analysis is similar with the Bayesian analysis. Bootstrap values for ML equal to or greater than 60% and PP values greater than 0.95 (rounding values to 2 decimal places) are labelled on the nodes. Strains of the newly described species are in orange, while type strains are in bold. (ITS: 526 bp, LSU: 862 bp, SSU: 1018 bp, *tub2*: 333 bp, *rpb2*: 861 bp)



Figure 32 – Continued.

Culture characteristics – Ascospores germinated within 48 h on PDA. 3 cm diam. after three weeks at 27°C. Colony dense, irregular, from above, convex, surface smooth, with edge entire, floccose, white; from below, yellow at the narrow edge, reddish-brown at the center, producing pigmentation in agar.

Material examined – China, Yunnan Province, Zhaotong grassland, on dead stems of unidentified herbaceous plants, 25 August 2022, Y. Gao, QG11A (HKAS 128791, holotype), ex-type living culture CGMCC 3.24505; *ibid.*, QG11B (HKAS 128792, isotype), ex-isotype, CGMCC 3.24506; on dead stems of *Dactylis glomerata* (Poaceae), QG100A (HKAS 128775, paratype), ex-paratype, CGMCC 3.24531; *ibid.*, QG100B (HKAS 128776, CGMCC 3.24532).

GenBank numbers – CGMCC 3.24505: ITS = PV608548, LSU = PV607399, SSU = PV607296, *tub2* = PV613303, *rpb2* = PV655476; CGMCC 3.24506: ITS = PV608549, LSU = PV607400, SSU = PV607297, *tub2* = PV613304, *rpb2* = PV655477; CGMCC 3.24531: ITS = PV608550, LSU = PV607401, SSU = PV607298, *tub2* = PV613305, *rpb2* = PV655478; CGMCC

3.24532: ITS = PV608551, LSU = PV607402, SSU = PV607299, *tub2* = PV613306, *rpb2* = PV655479.

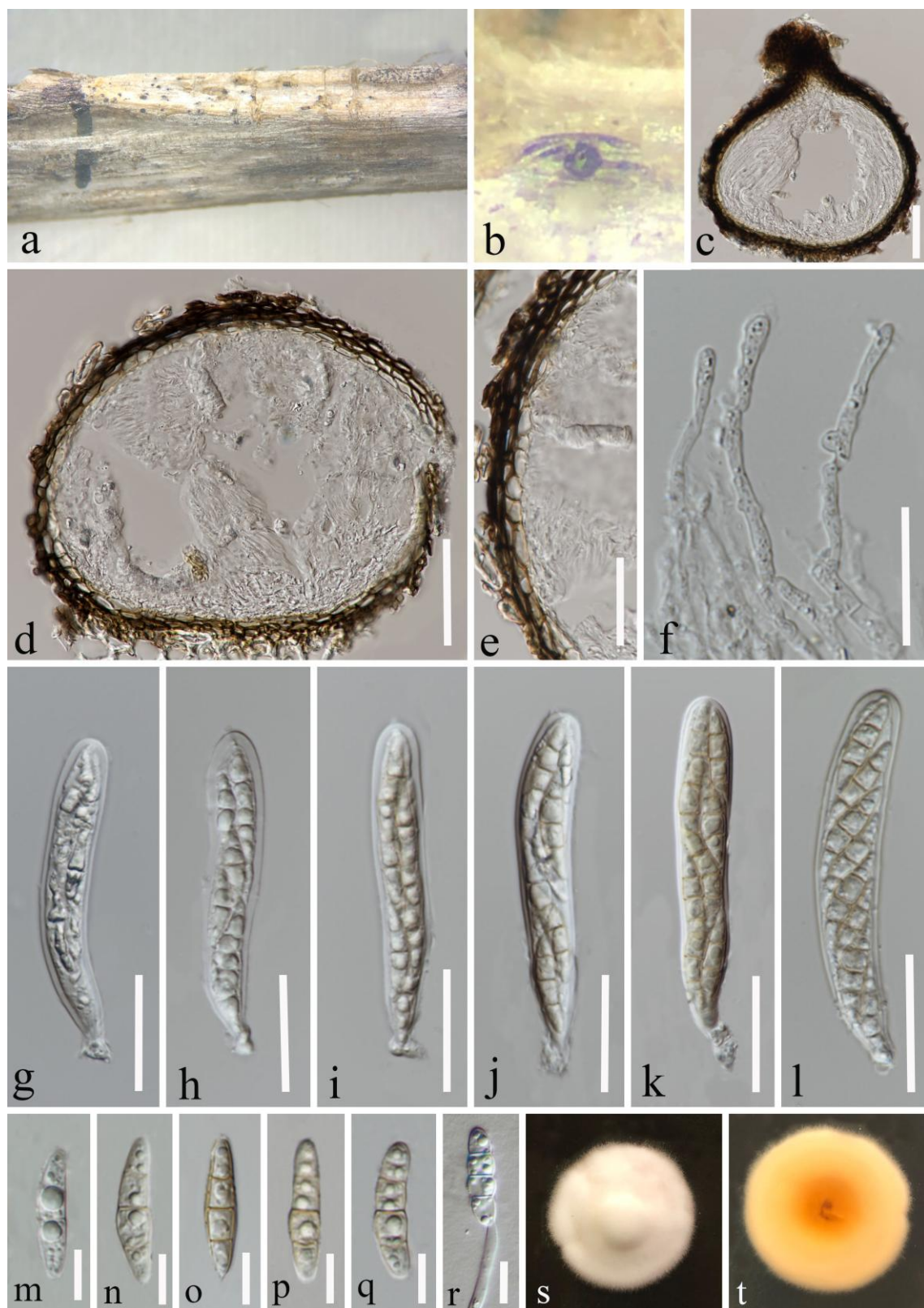


Figure 33 – *Heterosporicola qujingensis* (HKAS 128795, holotype). a, b Ascomata on the host substrate. c, d Sections of ascomata. e Peridium. f Pseudoparaphyses. g–l Asci. m–q Ascospores. r A germinated ascospore. s, t Culture characters on PDA (s: above, t: below). Scale bars: c, d = 50 μ m, e, g–l = 30 μ m, f = 20 μ m, m–r = 10 μ m.

Culture characteristics – Ascospores germinated within 48 h on PDA. 3 cm diam. after three weeks at 27°C. Colony dense, irregular, from above, convex, surface smooth, with edge entire, floccose, white; from below, yellow at the narrow edge, reddish-brown at the center, producing pigmentation in agar.

Material examined – China, Yunnan Province, Zhaotong grassland, on dead stems of unidentified herbaceous plants, 25 August 2022, Y. Gao, QG11A (HKAS 128791, holotype), ex-type living culture CGMCC 3.24505; *ibid.*, QG11B (HKAS 128792, isotype), ex-isotype, CGMCC 3.24506; on dead stems of *Dactylis glomerata* (Poaceae), QG100A (HKAS 128775, paratype), ex-paratype, CGMCC 3.24531; *ibid.*, QG100B (HKAS 128776, CGMCC 3.24532).

GenBank numbers – CGMCC 3.24505: ITS = PV608548, LSU = PV607399, SSU = PV607296, *tub2* = PV613303, *rpb2* = PV655476; CGMCC 3.24506: ITS = PV608549, LSU = PV607400, SSU = PV607297, *tub2* = PV613304, *rpb2* = PV655477; CGMCC 3.24531: ITS = PV608550, LSU = PV607401, SSU = PV607298, *tub2* = PV613305, *rpb2* = PV655478; CGMCC 3.24532: ITS = PV608551, LSU = PV607402, SSU = PV607299, *tub2* = PV613306, *rpb2* = PV655479.

Notes – *Leptosphaeria chinensis* is introduced as a new species based on its distinct morphology and the phylogeny of the combined ITS, LSU, SSU, *tub2*, and *rpb2* sequence data. Our collections (CGMCC 3.24505, CGMCC 3.24506, CGMCC 3.24531, CGMCC 3.24532) formed a sister clade to *Leptosphaeria pedicularis* (CBS 126582, CBS 390.80) with 64% ML and 0.98 PP support values (Fig. 32). De Gruyter et al. (2013) reclassified *Phoma pedicularis* to *Leptosphaeria pedicularis* based on phylogenetic studies. Sequence comparison for the ITS region between *Leptosphaeria chinensis* (CGMCC 3.24505, ex-type) and *L. pedicularis* (CBS 126582) showed an 11.8% (61/517 bp, with 12 gaps) base pair difference in ITS region, 0.72% (6/835 bp, without gaps) base pair difference in LSU region, 7.83% (26/332 bp, with 1 gap) base pair difference in *tub2* region. The SSU and *rpb2* sequences of *Leptosphaeria pedicularis* are not provided (De Gruyter et al. 2013). Herein, *Leptosphaeria chinensis* is introduced as a new species on dead stems of *Dactylis glomerata* and herbaceous plants in China.

***Plenodomus* Preuss, Linnaea 24: 145 (1851)**

Notes – *Plenodomus* was originally established by Preuss (1851), designating *P. rabenhorstii* as its type species. However, Boerema & Kesteren (1964) proposed *P. lingam* as the type combination over *P. rabenhorstii*, as the original type material of *P. rabenhorstii* was destroyed during World War II, as documented by multiple studies (de Gruyter et al. 2013, Ariyawansa et al. 2015a, Phookamsak et al. 2019). Species of *Plenodomus* are parasitic or saprobic on plants in terrestrial habitats (Ariyawansa et al. 2015a). Through molecular phylogenetic analyses, de Gruyter et al. (2013) conducted a taxonomic revision of *Phoma* section *Plenodomus*, transferring its synonymized species to *Plenodomus* within Leptosphaeriaceae. The Index Fungorum (2025) listed 103 *Plenodomus* epithets; however, few species have been confirmed by phylogenetic analyses. Most *Plenodomus* species lack molecular data to clarify their phylogenetic placements. This study introduces two new host records of *Plenodomus* species (*Plenodomus artemisiae* and *P. sinensis*), together with descriptions and illustrations (Figs. 35–37).

***Plenodomus artemisiae* Karun., Phookamsak & K.D. Hyde, Fungal Diversity 95: 23 (2019) Fig. 35**

Index Fungorum number: IF556118; Facesoffungi number: FoF05696

Saprobic on dead stems of host plants. Sexual morph: *Ascomata* 117–140 µm diam. × 95–140 µm high ($\bar{x}$ = 125 × 117 µm, *n* = 10), semi-immersed or superficial, globose or subglobose, dark brown, solitary, with truncate base, scattered, ostiolate, papillate. *Ostioles* central, beak-like papilla, ostiolar canal filled with paraphyses. *Peridium* 13.5–23 µm wide ($\bar{x}$ = 17.5 µm, *n* = 25), thick-walled, composed of 2–4 thick-walled layers of unequal, composed of several cell layers of dark brown scleroplectenchymatous cells, arranged in a *textura angularis* to *textura globulosa*. *Hamathecium* comprises 2–3.5 µm wide ($\bar{x}$ = 2.8 µm, *n* = 30), composed of hyaline, filamentous, pseudoparaphyses, anastomosing, septate, constricted at the septum, embedded in a hyaline

gelatinous matrix. *Asci* 55–84 × 9–12.5 µm ($\bar{x}$ = 70 × 11 µm, n = 25), 8-spored, cylindric-clavate to clavate, bitunicate, fissitunicate, pedicellate, apically rounded with a distinct ocular chamber. *Ascospores* 22–36 × 3–6 µm ($\bar{x}$ = 31 × 5 µm, n = 30), overlapping 2–3-seriate, fusiform, 5-septate, often slightly constricted at the septum, hyaline when immature, becoming pale brown when mature, with guttulate, lacking a mucilaginous sheath and appendages. Asexual morph: Undetermined.

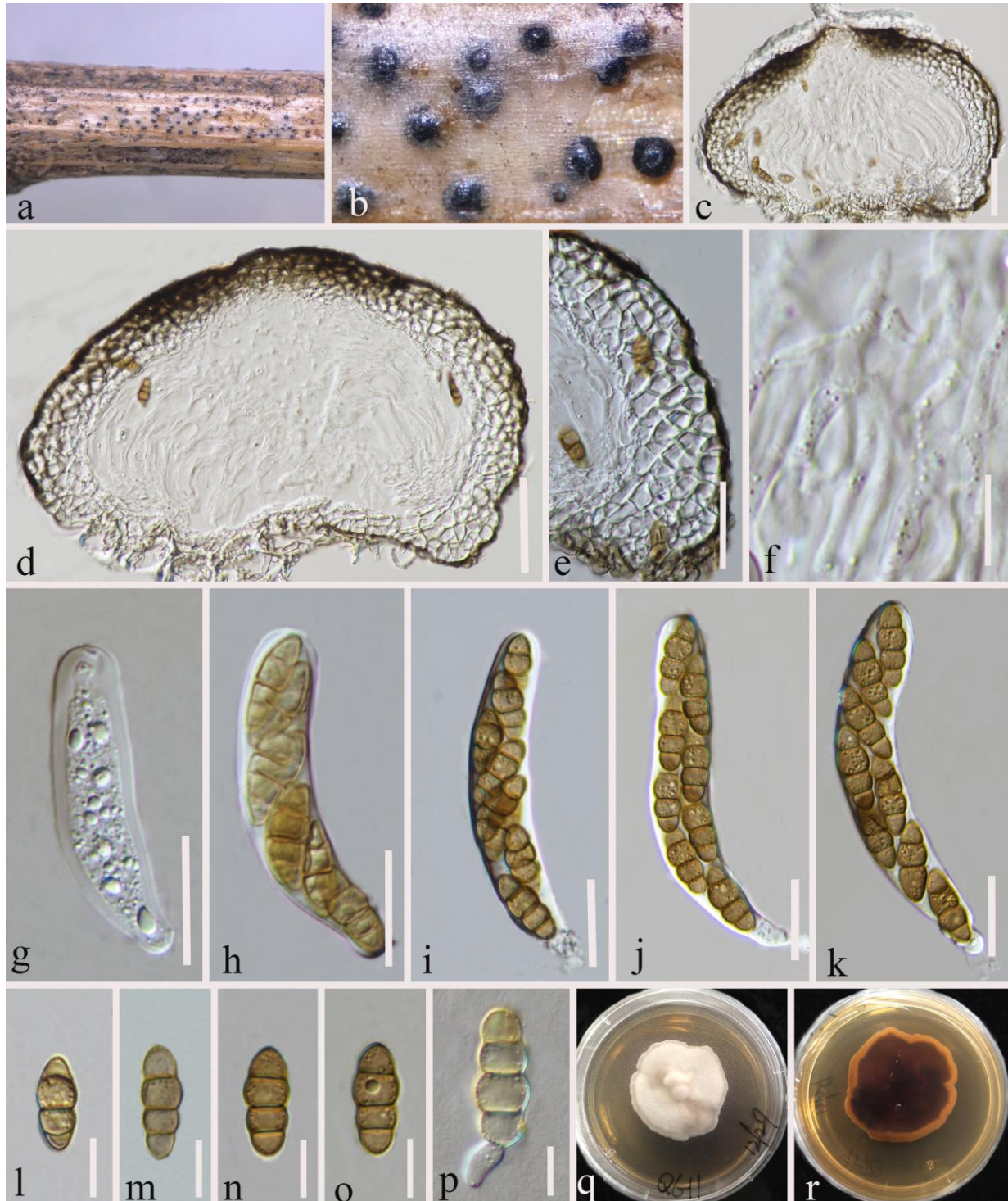


Figure 34 – *Leptosphaeria chinensis* (HKAS 128791, holotype). a, b Appearance of ascomata on the host substrate. c, d Sections of ascomata. e Peridium. f Hamathecium. g–k Asci. l–o Ascospores. p A germinated ascospore. q, r Culture characters on PDA (q: above, r: below). Scale bars: c, d = 50 µm, e = 30 µm, g–k = 20 µm, f, l–o = 10 µm.

Culture characteristics – Colonies on PDA reaching 15 mm diam. after two weeks. Colony from above, fimbriate, marginal hyphae emission, dense, flat, gray with white spots; from below, white to cream margin, gray at the center.

Material examined – China, Yunnan Province, Zhaotong, on dead stems of unidentified grass (Poaceae), 25 August 2022, Y. Gao, QG37 (HKAS 132982), living culture KUNCC 25-19143; *ibid.*, QG15 (HKAS 146004), living culture KUNCC 25-19145; *ibid.*, QG55 (HKAS 146005), living culture KUNCC 25-19146;

Known hosts and distribution – on dead branches and stems of *Artemisia* sp. in China (Phookamsak et al. 2019), on dead stems of *Artemisia argyi* (Asteraceae) in China (Doilom et al. 2021), on dead stems of grass (Poaceae) in Yunnan Province, China (This study).

GenBank numbers – KUNCC 25-19143: ITS = PV608552, LSU = PV607403, SSU = PV607300, *tub2* = PV613307, *rpb2* = PV655480; KUNCC 25-19145: ITS = PV608553, LSU = PV607404, SSU = PV607301, *tub2* = PV613308, *rpb2* = PV655481; KUNCC 25-19146: ITS = PV608554, LSU = PV607405, SSU = PV607302, *tub2* = PV613309, *rpb2* = PV655482.

Notes – In the present study, the multigene phylogeny indicates that our collections (KUNCC 25-19143, KUNCC 25-19145, KUNCC 25-19146) grouped within *Plenodomus artemisiae* (KUMCC 20-0200A, KUMCC 20-0200B, KUMCC 18-0151) with 91% ML and 0.94 PP support values (Fig. 32). Our collection (KUNCC 25-19143) shares similar characters with the type species *Plenodomus artemisiae* (KUMCC 20-0200A, ex-type) by having semi-immersed or superficial, globose to subglobose ascomata with papillate; cylindric-clavate to clavate, pedicellate, apically rounded with distinct ocular chamber asci; and fusiform, 5-septate ascospores lacking a mucilaginous sheath and appendages (Phookamsak et al. 2019). However, our collection differs from *Plenodomus artemisiae* (KUMCC 20-0200A) in having small ascomata (117–140 × 95–140 µm, L/W = 1.1 vs. 300–450 × 140–280 µm, L/W = 1.8) (Phookamsak et al. 2019). Based on both morphological similarities in asci and ascospores and phylogenetic support, we report our saprobic collections (KUNCC 25-19143, KUNCC 25-19145, KUNCC 25-19146) as a new host record of *Plenodomus artemisiae* on Poaceae hosts in China.

Plenodomus sinensis Tennakoon, Phookamsak & K.D. Hyde, Phytotaxa 324 (1): 76 (2017)
Figs. 36, 37

Index Fungorum number: IF553195; Facesoffungi number: FoF03235

Saprobic on dead stems of host plants. Sexual morph: *Ascomata* 290–360 µm diam. × 185–250 µm high ($\bar{x}$ = 330 × 210 µm, *n* = 15), superficial, globose or subglobose, smooth, scattered, uniloculate, coriaceous, with minutely ostiolate papilla, easily removed from the host substrate, with a flattened base, black. *Peridium* 50–100 µm wide ($\bar{x}$ = 65 µm, *n* = 30), thick-walled, slightly thin at the base, inner layer comprising 2–3 cell layers of flattened, light brown cells, arranged in a *textura angularis*, middle layer comprising several layers of sub-hyaline cells arranged in a *textura globulosa*, outer layer composed of heavily pigmented, thick-walled, dark brown cells, *textura angularis*. *Hamathecium* comprises 2–3 µm wide ($\bar{x}$ = 2.5 µm, *n* = 30), branched, cellular pseudoparaphyses, septate, slightly constricted at the septa. *Asci* 75–95 × 9–11 µm ($\bar{x}$ = 88 × 10 µm, *n* = 25), 8-spored, bitunicate, fissitunicate, cylindrical, short pedicel, apically rounded, with a distinct ocular chamber. *Ascospores* 27–39 × 4–5.5 µm ($\bar{x}$ = 33 × 5 µm, *n* = 25), overlapping 1–2-seriate, fusiform, with obtuse ends, 6–7-septate, often slightly constricted at the middle septum, hyaline when immature, becoming yellowish when mature, with guttulate, smooth-walled, with mucilaginous globoid-shaped appendages at both ends. Asexual morph: *Conidiomata* 65–110 µm diam. × 45–60 µm high ($\bar{x}$ = 81 × 65 µm, *n* = 10), globose or subglobose, superficial on the host, solitary, scattered, uni-loculate, dark brown to black. *Conidiomata wall* 5.5–10 µm wide ($\bar{x}$ = 8 µm, *n* = 25), comprising 2–3 layers of *textura angularis*, inner layer hyaline, outer layer brown. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 3.5–6 × 3–5.5 µm ($\bar{x}$ = 4.5 × 4 µm, *n* = 20), subglobose to ampulliform, phialidic, hyaline, smooth. *Conidia* 4.5–7 × 2–3 µm ($\bar{x}$ = 5.5 × 2.5 µm, *n* = 30), oblong to obovoid, aseptate, smooth-walled, hyaline.

Culture characteristics – Colonies on PDA reaching 15 mm diam. after two weeks. Colony from above, fimbriate, marginal hyphae emission, dense, flat, gray with white spots; from below, white to cream margin, gray at the center.

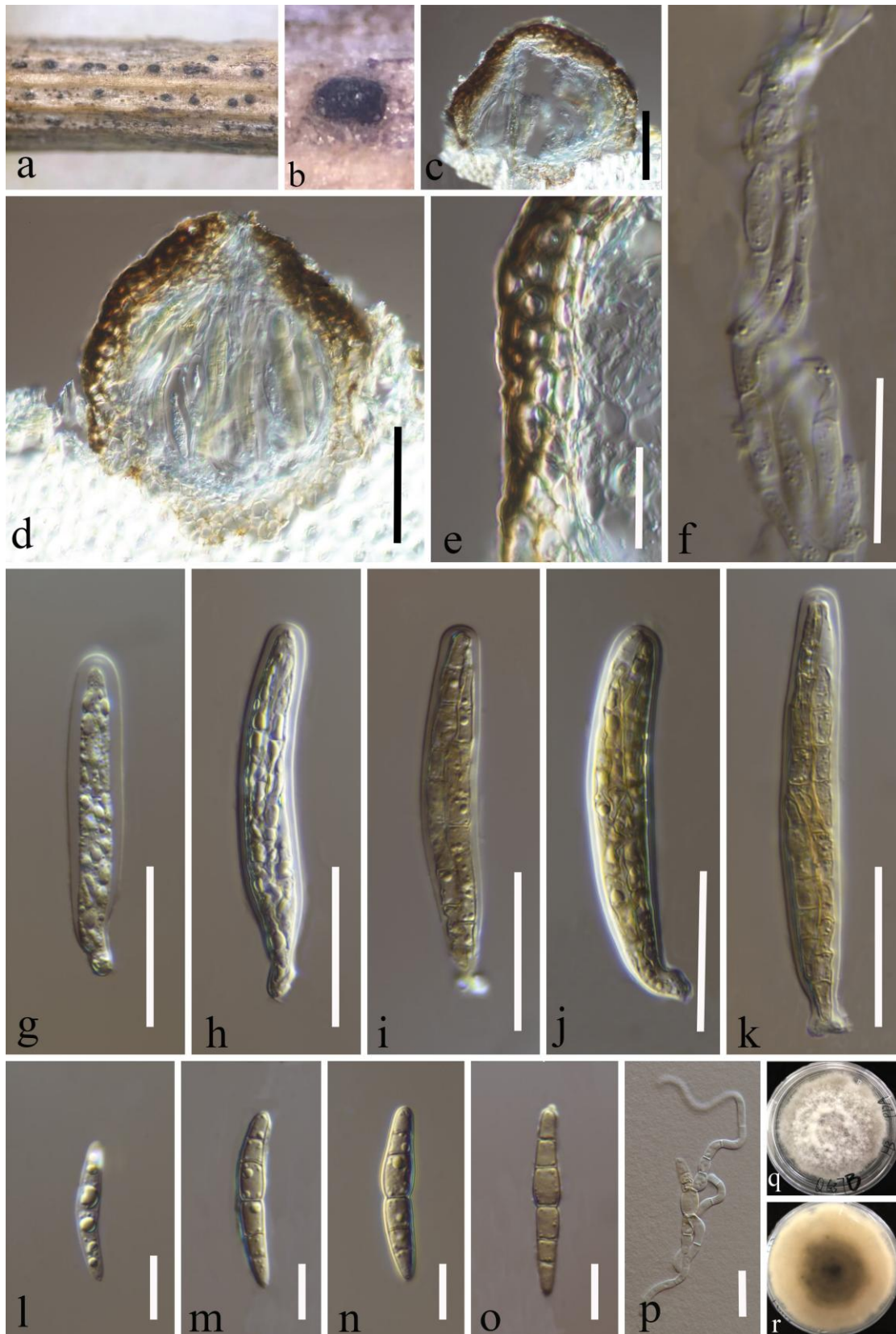


Figure 35 – *Plenodomus artemisiae* (HKAS 132982, a new host record). a, b Ascomata on the host substrate. c, d Sections of ascomata. e Peridium. f Pseudoparaphyses. g–k Asci. l–o Ascospores.

p A germinated ascospore. q, r Culture characters on PDA (q: above, r: below). Scale bars: c, d = 50 µm, g–k = 30 µm, e, f, p = 20 µm, f, l–o = 10 µm.

Material examined – China, Yunnan Province, Zhaotong grassland, 25 August 2022, on dead stems of *Dipsacus* sp. (Caprifoliaceae), Y. Gao, QG41B (HKAS 135356, sexual morph), living culture KUNCC 25-19147; on dead stems of *Pedicularis oxycarpa* (Orobanchaceae), QG65 (HKAS 132998, asexual morph), living culture KUNCC 25-19148.

Known hosts and distribution – on dead branch of *Tamarindus indica* (Fabaceae) and on the dead branch of *Plukenetia volubilis* (Euphorbiaceae) in China (Tennakoon et al. 2017), on dead fronds of fern and on dead stems of *Cirsium* sp. (Asteraceae) in China (Phookamsak et al. 2019), from soil samples in Korea (Moe et al. 2020), on dead stems of *Artemisia argyi* (Asteraceae) in China (Doilom et al. 2021), on dead stems of *Dipsacus* sp. (Caprifoliaceae, sexual morph) and *Pedicularis oxycarpa* (Orobanchaceae, asexual morph) in Yunnan Province, China (This study).

GenBank numbers – KUNCC 25-19147: ITS = PV608555, LSU = PV607406, SSU = PV607303, *tub2* = PV613310, *rpb2* = PV655483; KUNCC 25-19148: ITS = PV608556, LSU = PV607407, SSU = PV607304, *tub2* = PV613311, *rpb2* = PV655484.

Notes – Our collections (KUNCC 25-19147 and KUNCC 25-19148) are similar to the morphological characteristics of the holotype of *Plenodomus sinensis* (MFLU 17-0767) based on its globose or subglobose, superficial, uniloculate, coriaceous ascomata; 6–7-septate, fusiform, with mucilaginous globoid-shaped appendages at both ends of ascospores (Tennakoon et al. 2017). The asexual morph of *P. sinensis* (KUMCC 18-0152), which was reported by Phookamsak et al. (2019), is similar to our collections (KUNCC 25-19147 and KUNCC 25-19148). Multigene phylogeny shows that our collections clustered with *P. sinensis* (HKAS 102227, KUMCC 18-0153, MFLUCC 17-0757, KUMCC 18-0152, KUMCC 20-0204); however, they separate from the *P. sinensis* (MFLUCC 17-0767, ex-type). Nevertheless, (MFLUCC 17-0767) clusters with *P. collinsoniae* (CBS 120227) (Fig. 32) differ in having larger asci, longer ascospores with olivaceous to yellowish pigmentation as discussed in Tennakoon et al. (2017) and Doilom et al. (2021). Morphologically, our collections are more similar to *P. sinensis* (MFLUCC 17-0757, paratype). *Plenodomus sinensis* appears to have a wide host range (Tennakoon et al. 2017, Phookamsak et al. 2019, Moe et al. 2020, Doilom et al. 2021). Our collections are identified as new host records of *Plenodomus sinensis* on *Dipsacus* sp. (sexual morph) and *Pedicularis oxycarpa* (asexual morph) in China.

Praeclarispora Doilom, W. Dong, K.D. Hyde & C.F. Liao, *Frontiers Microbiol.* 12 (no. 660261): 3 (2021)

Notes – *Praeclarispora* was established by Doilom et al. (2021), with *Praeclarispora artemisiae* as its type species. *Praeclarispora* was distinguished from other genera in Leptosphaeriaceae by having versicolored ascospores (Doilom et al. 2021). The sexual morph of the genus is characterized by subglobose, coriaceous, erumpent to superficial ascomata; bitunicate, fissitunicate, short pedicel with indistinct ocular chamber asci, fusiform, curved, pale brown to brown in median celled ascospores (Doilom et al. 2021, Xu et al. 2024a). Two species are accepted in *Praeclarispora*, however, the asexual morph for this genus has not been reported (Doilom et al. 2021, Xu et al. 2024a). In this study, we introduce a new host record of *Praeclarispora herbicola*, together with descriptions and illustrations (Figs. 38, 39).

Praeclarispora herbicola (W.Y. Zhuang & W.Y. Li) S. Xu, H.B. Jiang & Phookamsak, *Phytotaxa* 634 (3): 281 (2024) Figs. 38, 39

Index Fungorum number: IF900846, Facesoffungi number: FoF14799

Saprobic on dead stems of *Artemisia carvifolia*. Sexual morph: *Ascomata* 370–470 µm high × 340–465 µm diam. ($\bar{x}$ = 440 × 410 µm, n = 10), raised, semi-immersed to erumpent or superficial, globose or subglobose, solitary, scattered, uni-loculate, glabrous, dark brown to black, ostiolate. *Peridium* 51–87 µm wide ($\bar{x}$ = 73 µm, n = 25), unequally thick, thinner at the base, thick at the sides towards the apex, composed of several layers, of two types of cells, scleroplectenchymatous

(at the apex) and pseudoparenchymatous (at base and sides), with inner layers composed of hyaline to pale brown to brown, flattened cells, of *textura angularis* to *textura prismatica*, outer layers composed of dark brown to black, thick-walled cells of *textura angularis* to *textura globulosa*. *Hamathecium* comprises 2–3.5 μm wide ($\bar{x}$ = 2.5 μm , n = 30), septate, hyaline, branched, cellular pseudoparaphyse. *Asci* 100–140 $\times$ 20–26 μm ($\bar{x}$ = 127 $\times$ 23.5 μm , n = 25), 8-spored, broadly cylindrical to cylindric-clavate, apically rounded, short pedicellate, fissitunicate, bitunicate, with ocular chamber. *Ascospores* 23–30 $\times$ 4.5–7.5 μm ($\bar{x}$ = 26.5 $\times$ 6 μm , n = 25), biserial, fusiform, with acute ends, slightly curved, 6–10-septate, often slightly constricted at the median septum, hyaline when immature, becoming versicolor when mature, the middle cells turn brown to golden brown at the 4th to 6th cells, slightly rough with small guttules, somewhat sectorial, arranged in a row, with distoseptate-like, subhyaline to pale yellowish brown towards the end cells. Asexual morph: sporulated on PDA after two months on PDA (Fig. 39): Hyphae 2–3 μm diam. ($\bar{x}$ = 2.5 μm , n = 30), branched, hyaline, septate, smooth, thin-walled, forming hyphal coils. *Conidiophores* micronematous, mononematous, solitary, erect, subcylindrical, hyaline, unbranched, straight or flexuous, smooth-walled, sometimes reduced to conidiogenous cells. *Conidiogenous cells* are smooth, straight or slightly curved, cylindrical or ampulliform, sometimes ovate or obpyriform, arising from hyphae, terminal or lateral, either solitary or aggregated in clusters. *Conidia* 4–7.5 $\times$ 3.5–7 μm ($\bar{x}$ = 5.2 $\times$ 5 μm , n = 25), globose or ellipsoidal, hyaline, aseptate, with small guttules.

Culture characteristics – Ascospores germinated within 48 h on PDA. 4.5 cm diam. after two weeks at 27°C. Colony dense, circular, from above, convex, surface smooth, with edge entire, floccose, white; from below, white to cream, not producing pigmentation in agar.

Material examined – China, Yunnan Province, Kunming, on dead stems of *Artemisia carvifolia* (Asteraceae), 20 June 2021, Y. Gao, CCSG29 (HKAS 135332), living culture (KUNCC 25-19149)

Known hosts and distribution – on dead stems of an unidentified herbaceous plant in China (Zhuang & Li 2009), on a dead stem of *Bidens pilosa* (Asteraceae) in China (Xu et al. 2024a), on dead stems of *Artemisia carvifolia* (Asteraceae) in Yunnan Province, China (This study).

GenBank numbers – KUNCC 25-19149: ITS = PV608557, LSU = PV607408.

Notes – *Praeclarispora herbicola* (*Phragmogibbera herbicola*) was introduced by Zhuang & Li (2009) based on morphological characteristics. Zhuang & Li (2009) acquired the molecular data for the species (including LSU and SSU sequences), however, they did not construct a phylogenetic tree to determine its evolutionary relationships. Later, the ex-type strain of *Phragmogibbera herbicola* (CGMCC 3.10146) was assigned to *Praeclarispora* based on phylogenetic analysis and new morphological analyses (Xu et al. 2024a). Our new collections (KUNCC 25-19149, KUNCC 25-19204) share similar characteristics with *P. herbicola* (CGMCC 3.10146, ex-type) by having unilocular, globose to subglobose ascomata with an ostiole; broadly cylindrical to cylindric-clavate, with an ocular chamber, short pedicel asci; fusiform, with acute ends, 6–10-septate ascospores with guttules (Zhuang & Li 2009, Xu et al. 2024a). The multigene phylogenetic analyses showed that our collections (KUNCC 25-19149, KUNCC 25-19204) grouped with *P. herbicola* (CGMCC 3.10146 and HKAS 124570) with 100% ML and 1.00 PP support values (Fig. 32). Based on characteristics and phylogenetic analyses, we report our collections as the first asexual morph and a new host record of *Praeclarispora herbicola* from decaying wood of *Artemisia carvifolia* in China.

Lophiostomataceae Sacc., Syll. Fung. 2: 672 (1883)

Notes – Lophiostomataceae was first recognized by Nitschke (1869). Later, Saccardo (1883) formally established the family with *Lophiostoma* as the type genus. Thambugala et al. (2015) reported 16 genera in this family, including 11 new genera. Afterward, 13 genera, viz., *Crassichypeus*, *Desertiserpentina*, *Flabellascoma*, *Kiskunsagia*, *Lentistoma*, *Leptoparies*, *Lophiomurispora*, *Magnopulchromyces*, *Neopaucispora*, *Neovaginatisspora*, *Parapaucispora*, *Pseudopaucispora*, *Pseudocapulatispora* were accepted in Lophiostomataceae (Hashimoto et al. 2018, Wanasinghe et al. 2018, Crous et al. 2019a, Mapook et al. 2020, Yuan et al. 2020, Maharachchikumbura et al. 2021b). Andreasen et al. (2021) synonymized 14 genera,

Alpestrisphaeria, *Biappendiculispora*, *Capulatispora*, *Coelodictyosporium*, *Guttulispora*, *Lophiohelichrysum*, *Lophiopoacea*, *Neopaucispora*, *Neotrematosphaeria*, *Platystomum*, *Pseudocapulatispora*, *Pseudolophiostoma*, *Pseudoplatystomum*, *Sigarispora*, under *Lophiostoma* based on multigene analysis. Li et al. (2023) introduced *Oleaginea* as a new genus in Lophiostomataceae. The sexual morph of Lophiostomataceae is characterized by semi-immersed to densely erumpent or superficial, carbonaceous, dark-brown to black, slit-like ostioles with crest-like apex ascomata; cylindrical to clavate, furcate pedicel, with minute ocular chamber asci; hyaline to pale brown, fusiform phragmospores or muriform ascospores (Hongsan et al. 2020a, Maharachchikumbura et al. 2021b, Ren et al. 2024b). The asexual morph is characterized by globose to subglobose, immersed to superficial, dark brown to black, unilocular, circular ostiole conidiomata; phialidic, cylindrical conidiogenous cells; cylindrical or subglobose, aseptate, hyaline conidia (Hongsan et al. 2020a). Species of Lophiostomataceae are predominantly found as saprobes in terrestrial, freshwater, and marine environments, inhabiting a diverse range of hosts (Hashimoto et al. 2018, Bao et al. 2019, Manawasinghe et al. 2022, Ren et al. 2024b). An updated phylogenetic tree based on combined ITS, LSU, SSU, *tef1-α*, and *rpb2* sequence data is presented in Fig. 40.

Lophiopoacea Ariyaw., Thambug. & K.D. Hyde, Fungal Diversity 74: 220 (2015)

Notes – *Lophiopoacea* was established by Thambugala et al. (2015). *Lophiopoacea* includes only two species, *L. paramacrostroma* as the type species and *L. winteri* (Index Fungorum 2025). *Lophiopoacea paramacrostroma* was reported on dead *Arundo pliniana* (Poaceae) in Italy (Thambugala et al. 2015). *Lophiopoacea winteri* was reported on stems of *Polygonum* sp. in Japan (Thambugala et al. 2015). Thambugala et al. (2015) conducted a morphological comparison between *L. paramacrostroma* and *L. macrostromum* (the type species of *Lophiostoma*). Thambugala et al. (2015) noted that *Lophiopoacea paramacrostroma* differs by having a reduced crest, a peridium composed of two strata with hyaline to brown, large cells of *textura angularis*, wider pseudoparaphyses, and larger, fusiform ascospores. Furthermore, our phylogenetic analyses revealed that the ex-type strain of *L. paramacrostroma* formed a distinct cluster alongside two putatively identified strains of *Lophiostoma winteri* (JCM 17648, MAFF 239454). This research result is similar to previous studies (Thambugala et al. 2015, Ren et al. 2024b). As a result, *Lophiopoacea winteri* is proposed as the new designation for *Lophiostoma winteri* and is recognized as the second species within *Lophiopoacea*. However, Andreasen et al. (2021) later suggested synonymizing *Lophiopoacea* under *Lophiostoma*. In this study, we followed Thambugala et al. (2015) for our taxonomic conclusions of *Lophiopoacea* (Fig. 40). We also introduce a new host and a geographical record for *Lophiopoacea paramacrostroma*, together with descriptions and illustrations (Fig. 41).

Lophiopoacea paramacrostroma Ariyaw., Thambug., Camporesi & K.D. Hyde, Fungal Diversity 74: 221 (2015) Fig. 41

Index Fungorum number: IF551241; Facesoffungi number: FoF00807

Saprobic on dead stems of *Dactylis glomerata*. Sexual morph: *Ascomata* 145–330 µm diam. × 205–290 µm high, ($\bar{x}$ = 260 × 250 µm, n = 15), immersed, globose or subglobose, with a flattened base, scattered, uni-loculate, glabrous, dark brown to black, ostiolate. *ascoma* apex crest-like, central, carbonaceous, with a pore-like ostiole. *Peridium* 15–35 µm wide ($\bar{x}$ = 20 µm, n = 30), composed of several layers of pale brown to black, thick-walled *pseudoparenchymatous* cells, pale inside, fusing with host tissue at the outside. *Hamathecium* comprises 1.5–2.5 µm wide ($\bar{x}$ = 2 µm, n = 30), filiform, branched or simple, septate, cellular, pseudoparaphyses. *Asci* 85–130 × 11–17 µm ($\bar{x}$ = 110 × 14 µm, n = 20), 8-spored, cylindric-clavate, slightly curved, bitunicate, fissitunicate, with a long pedicel, rounded at the apex, with ocular chamber. *Ascospores* 32–36 × 4.5–7 µm ($\bar{x}$ = 34 × 5.5 µm, n = 25), fusiform with narrow, acute ends, uniseriate to bi-seriate, overlapping, 1-3-septate, constricted at the middle septum, region above central septum widest, guttulate, smooth-walled, hyaline, lacking a mucilaginous sheath. Asexual morph: Undetermined.

Culture characteristics – Ascospores germinated within 48 h on PDA. 1.5 cm diam. after three weeks at 27°C. Colony dense, circular, from above, convex, surface smooth, with edge entire, floccose, gray-green at the edge, white at the center; from below, brown, not producing pigmentation in agar.

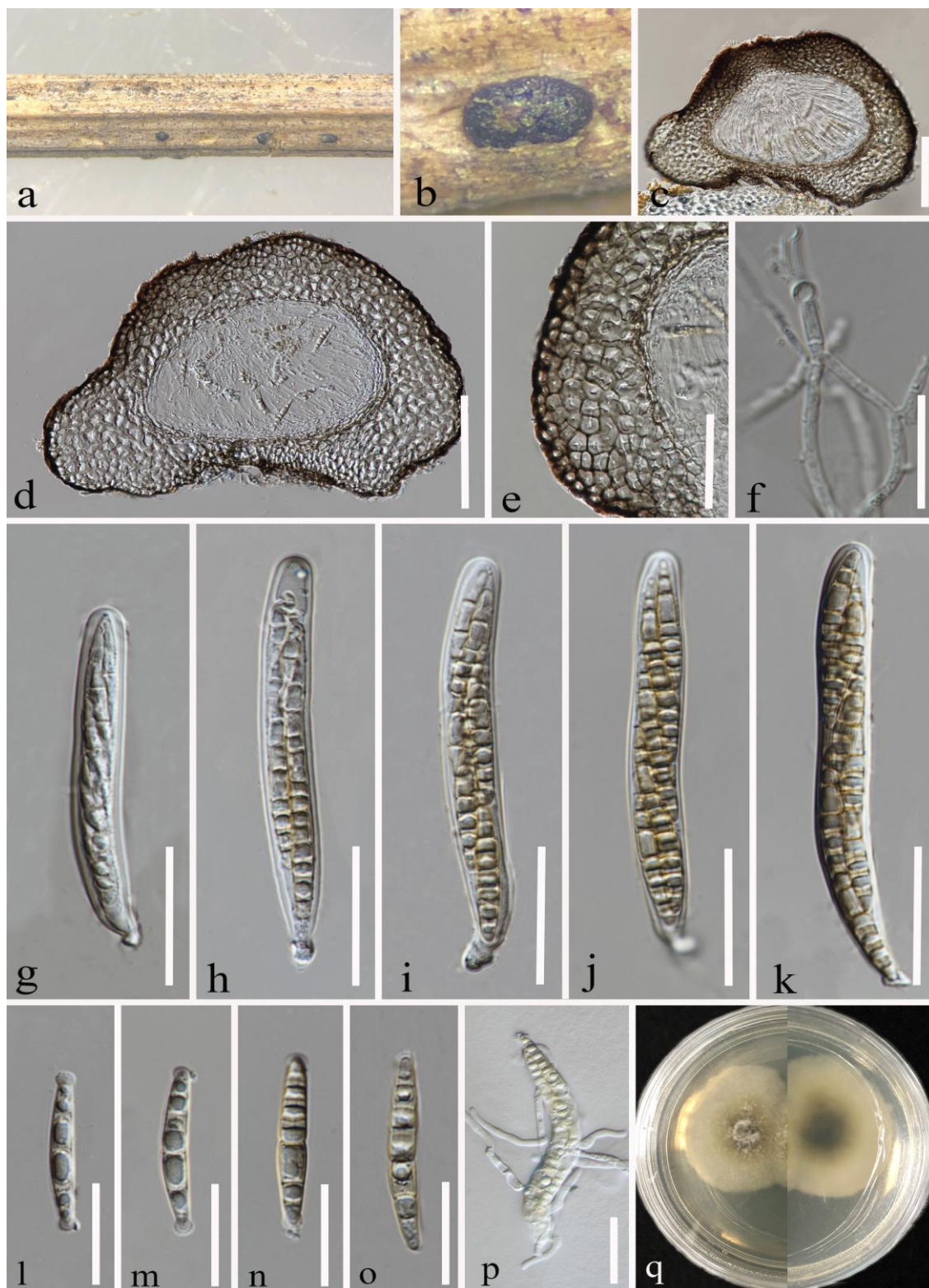


Figure 36 – *Plenodomus sinensis* (HKAS 135356, sexual morph, a new host record). a, b Ascomata on the host substrate. c, d Sections of ascomata. e Peridium. f Pseudoparaphyses. g–k Asci. l–o Ascospores. p Germinated ascospores. q Culture characters on PDA (left: above, right: below). Scale bars: c, d = 100 μ m, e = 50 μ m, g–k, p = 30 μ m, f, l–o = 20 μ m.

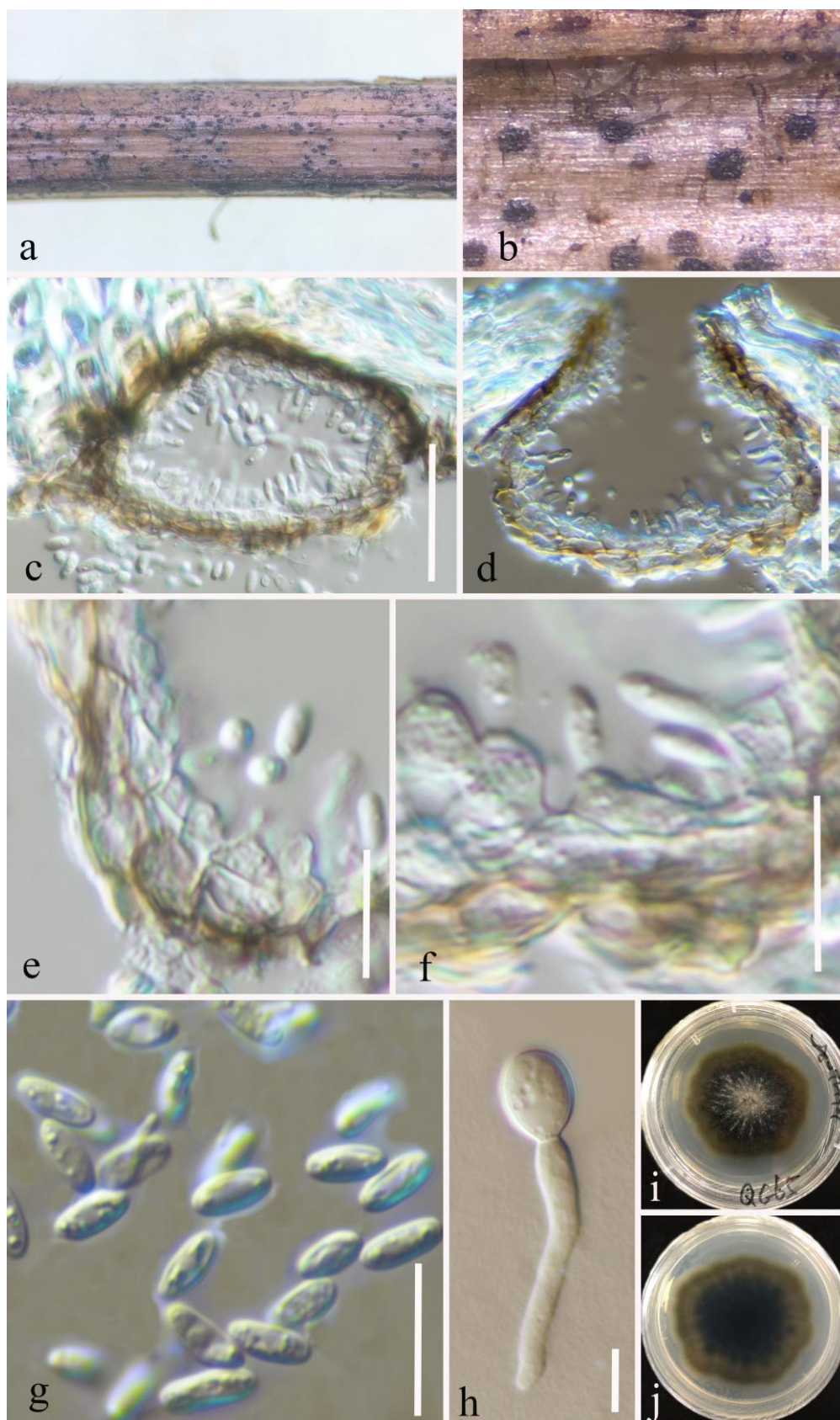


Figure 37 – *Plenodomus sinensis* (HKAS 132998, asexual morph, a new host record). a, b Appearance of conidiomata on the host substrate. c, d Sections of conidiomata. e Conidiomata wall. f Conidiogenous cells. g Conidia. h A germinated conidium. i, j Culture characters on PDA (i: above, j: below). Scale bars: c, d = 30 μm , e–g = 10 μm , h = 5 μm .

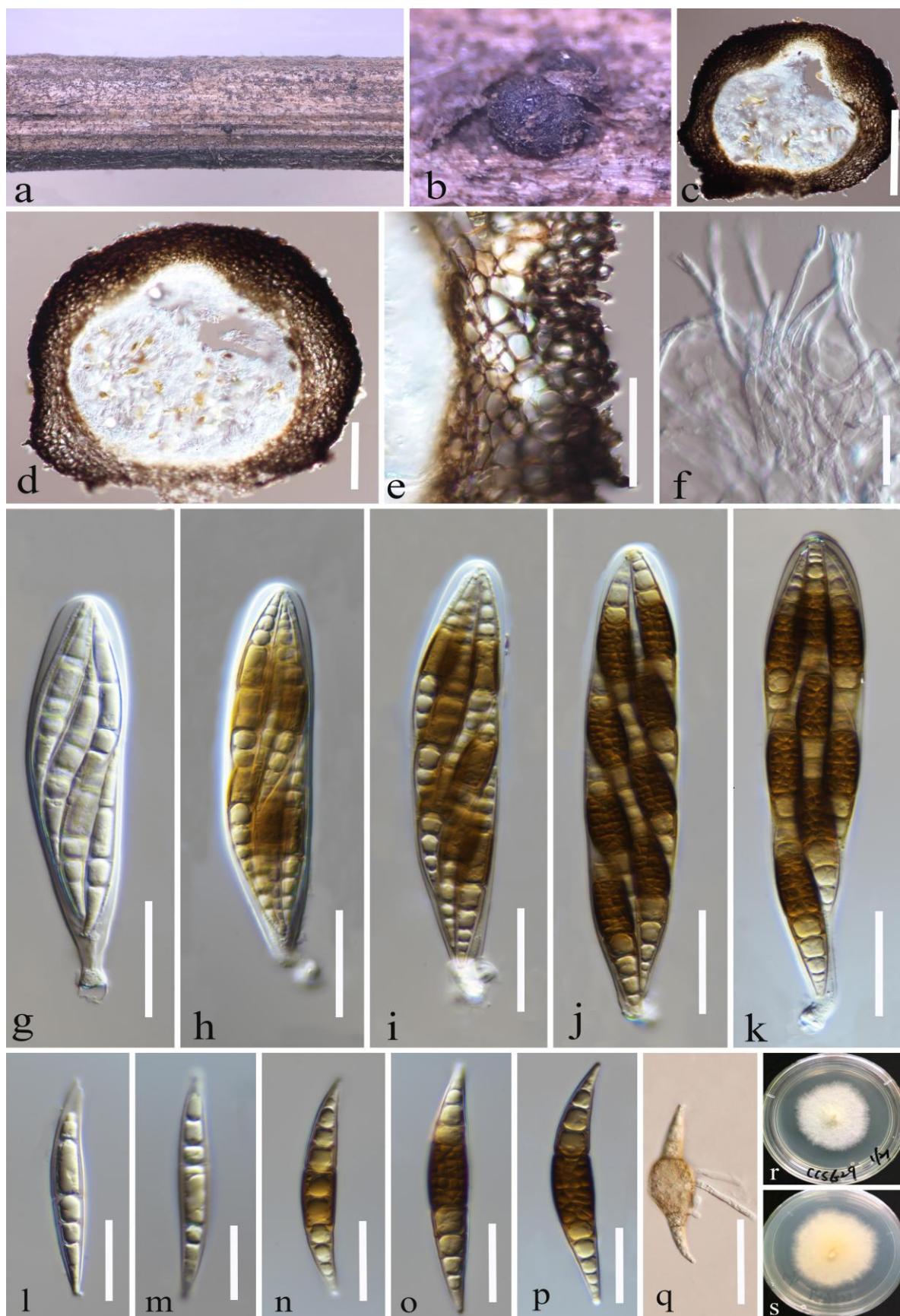


Figure 38 – *Praeclarispora herbicola* (HKAS 135332, sexual morph, a new host record). a, b Ascomata on a dead stem of *Artemisia carvifolia* (Asteraceae). c, d Sections of ascomata. e Peridium. f Pseudoparaphyses. g–k Asci. l–p Ascospores. q A germinated ascospore. r, s Culture

characters on PDA (r: above, s: below). Scale bars: c = 200 μ m, d = 100 μ m, e = 50 μ m, g–k, q = 30 μ m, f, l–p = 20 μ m.

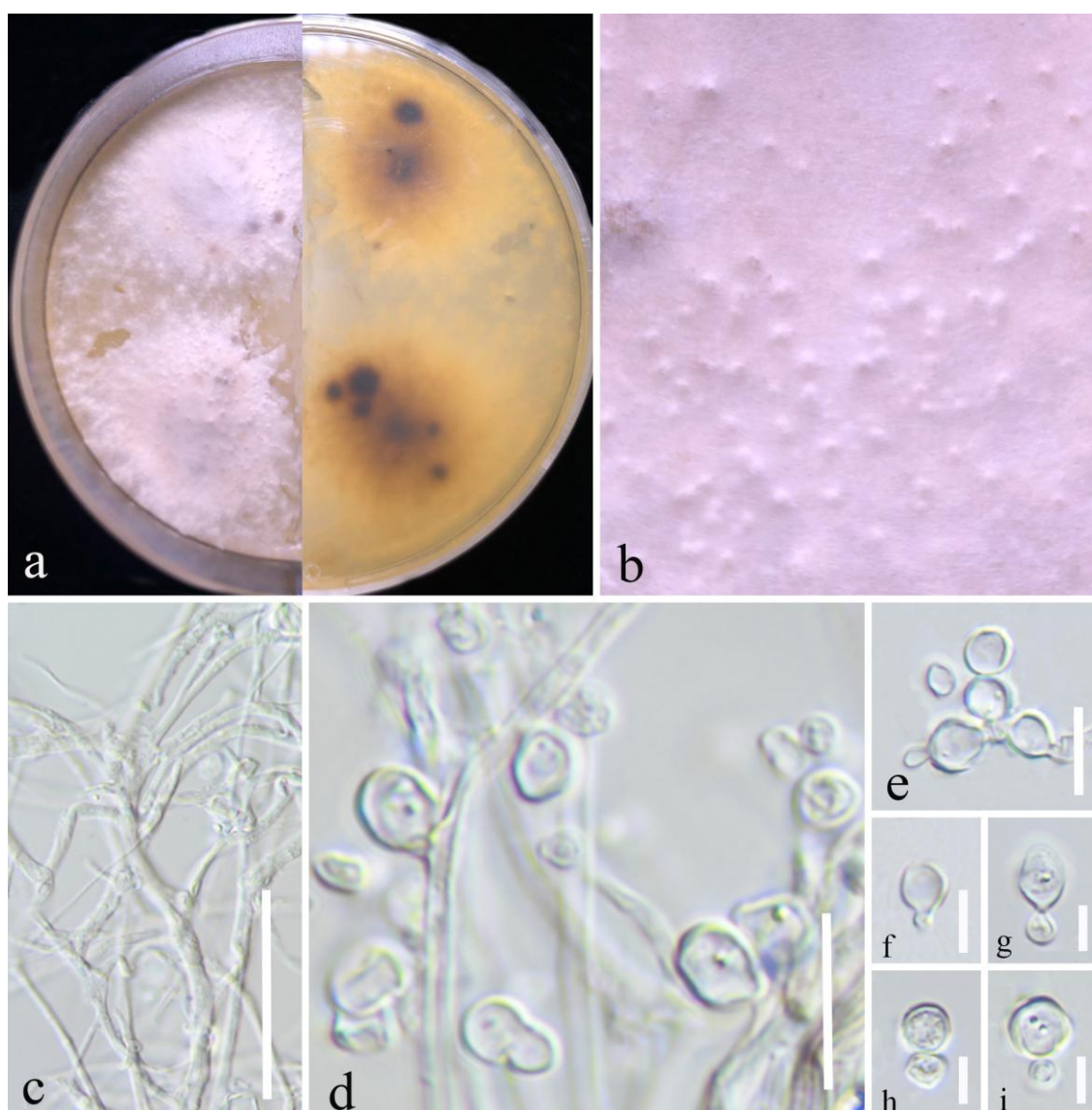


Figure 39 – *Praeclarispora herbicola* (KUNCC 25-19149, asexual morph, a new host record). a Culture characteristic on PDA (left: above, right: below). b Conidia on aerial mycelia on PDA. c Mycelium. d, e Conidiophores with conidiogenous cells. f–i Conidia. Scale bars: c = 30 μ m, d, e = 10 μ m, f–i = 5 μ m.

Material examined – China, Yunnan Province, Zhaotong grassland, on dead stems of *Dactylis glomerata* (Poaceae), 25 August 2022, Y. Gao, QG8A (HKAS 128789, holotype), ex-type living culture CGMCC 3.24503; *ibid.*, QG8B (HKAS 128790, isotype), ex-isotype living culture CGMCC 3.24504; *ibid.*, QG7A (HKAS 128787), living culture, CGMCC 3.25080; *ibid.*, QG7B (HKAS 128788, CGMCC 3.25081).

Known hosts and distribution – on dead *Arundo pliniana* (Poaceae) in Italy (Thambugala et al. 2015), on dead stems of *Dactylis glomerata* (Poaceae) in Yunnan Province, China (This study).

GenBank numbers – CGMCC 3.24503: ITS = PV608562, LSU = PV607413, SSU = PV607307, *tef1*- α = PV626443, *rpb2* = PV655489; CGMCC 3.24504: ITS = PV608563, LSU = PV607414, SSU = PV607308, *tef1*- α = PV626444, *rpb2* = PV655490; CGMCC 3.25080: ITS = PV608564, LSU = PV607415, SSU = PV607309, *tef1*- α = PV626445, *rpb2* = PV655491; CGMCC

3.25081: ITS = PV608565, LSU = PV607416, SSU = PV607310, *tef1-α* = PV626446, *rpb2* = PV655492.

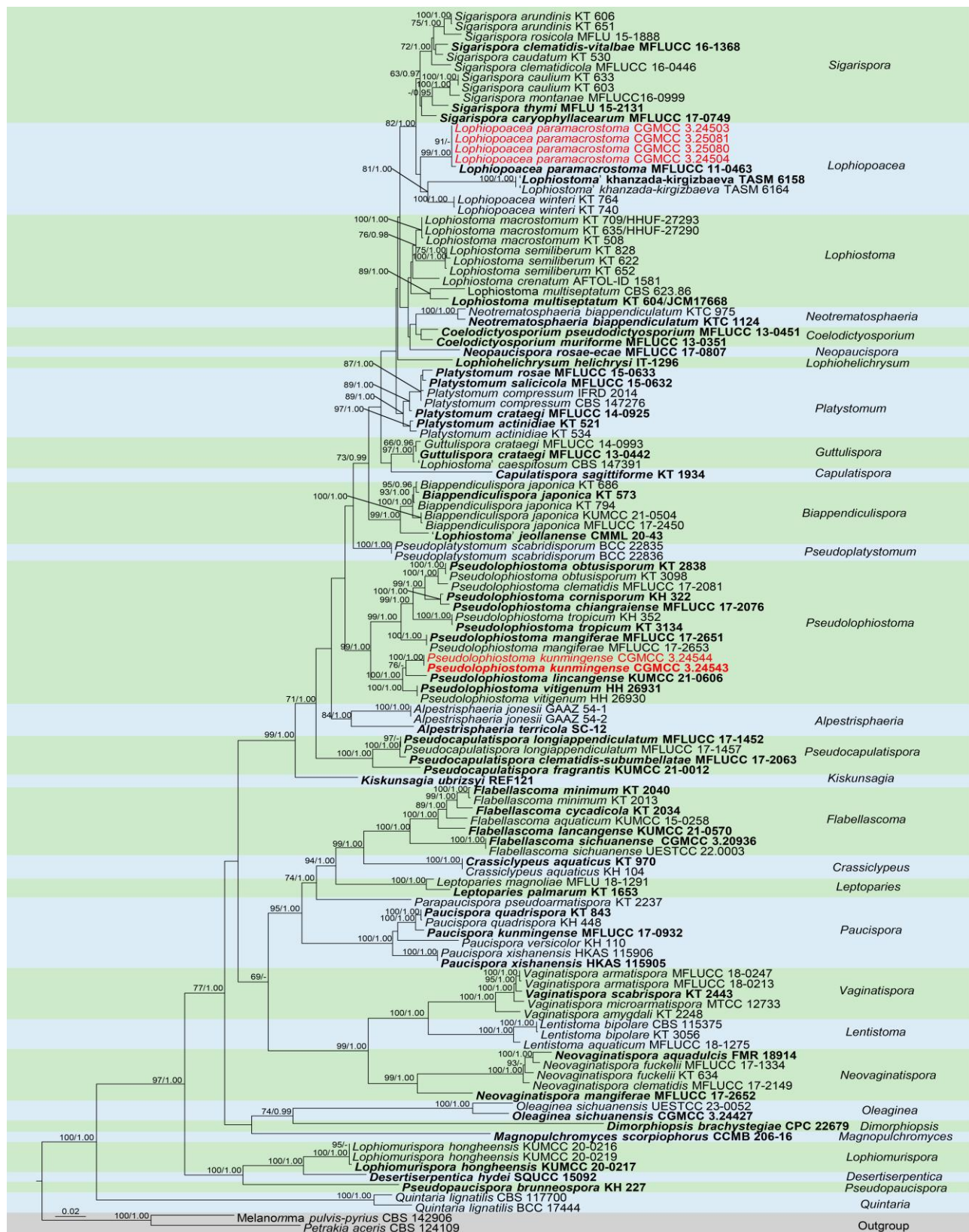


Figure 40 – RAxML phylogram generated from a combined dataset of partial ITS, LSU, SSU, *tef1-α*, and *rpb2* DNA sequence analyses for Lophiostomataceae. Related sequences are obtained following Ren et al. (2024c). One hundred and twenty strains were included in the combined analyses, which comprised 4,445 characters in the combined ITS, LSU, SSU, *tef1-α*, and *rpb2*

alignment. *Melanomma pulvis-pyrius* (CBS 142906) and *Petrakia aceris* (CBS 124109) were used as the outgroup taxa. The best-scoring RAxML tree with a final likelihood value of -38500.111793 is presented. The matrix contained 1,930 distinct alignment patterns, with 22.40% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.250105, C = 0.247019, G = 0.265802, T = 0.237073; substitution rates AC = 1.345758, AG = 3.787209, AT = 1.245576, CG = 1.159744, CT = 7.563499, GT = 1.000000. The tree topology of the ML analysis is similar to the Bayesian analysis. Bootstrap values for ML equal to or greater than 70% and PP values greater than 0.95 (rounding values to 2 decimal places) are labelled on the nodes. Strains of the newly described species are in orange, while type strains are in bold. (ITS: 640 bp, LSU: 848 bp, SSU: 997 bp, *tef1*- α : 926 bp, *rpb2*: 1034 bp)

Notes – Based on multigene phylogenetic analyses, our collections (CGMCC 3.24503, CGMCC 3.24504, CGMCC 3.25080, CGMCC 3.25081) grouped with *Lophiopoacea paramacrostoma* (MFLUCC 11-0463, ex-type) with robust statistical support (99% ML and 1.00 PP, Fig. 40). The nucleotide comparison showed that our collections (CGMCC 3.24503, CGMCC 3.24504, CGMCC 3.25080, CGMCC 3.25081) are similar to *L. paramacrostoma* (MFLUCC 11-0463) in 716/717 bp of LSU (99.86%, without gaps), 1008/1008 bp of SSU (100%). *Lophiopoacea paramacrostoma* (MFLUCC 11-0463) lacks available ITS, *tef1*- α , and *rpb2* sequences and was therefore excluded from the comparison. We identify our collections as *Lophiopoacea paramacrostoma* based on the phylogenetic analysis and morphological characteristics. We isolated *L. paramacrostoma* from *Dactylis glomerata* collected in Italy, and we introduce these collections as a new host and geographical record.

Pseudolophiostoma Thambug., Kaz. Tanaka & K.D. Hyde, Fungal Diversity 74: 235 (2015)

Notes – *Pseudolophiostoma* was established by Thambugala et al. (2015), with *P. vitigenum* as the type species. This genus comprises eight accepted species in Index Fungorum (2025). *Pseudolophiostoma* species are typically saprobes found on various woody, herbaceous, and vine plants distributed across China (Taiwan), Japan, and Thailand (Thambugala et al. 2015, Hashimoto et al. 2018, Phukhamsakda et al. 2020, Ren et al. 2024c). In this study, we introduce a new species, *Pseudolophiostoma kunmingense*, together with descriptions and illustrations (Fig. 42).

Pseudolophiostoma kunmingense Y. Gao, H. Gui & K.D. Hyde, sp. nov.

Fig. 42

Index Fungorum number: IF903824; Facesoffungi number: FoF17699

Holotype – HKAS 126568

Etymology – The specific epithet “kunmingense” refers to the type location, Kunming City.

Saprobic on dead stems of host plants. Sexual morph: *Ascomata* 225–290 μ m high $\times$ 135–160 μ m diam. ($\bar{x}$ = 260 $\times$ 150 μ m, n = 10), immersed, elliptical or subglobose, with a flattened base, uni-loculate, scattered, glabrous, dark brown to black, ascoma apex crest-like, central, carbonaceous, with a pore-like ostiole. *Peridium* 18–35 μ m wide ($\bar{x}$ = 26 μ m, n = 30), composed of two strata, inner stratum comprising several layers with lightly pigmented cells of *textura angularis*, outer stratum comprising several layers of dark brown to black, somewhat flattened cells of *textura angularis*, fusing and indistinguishable from the host tissues. *Hamathecium* comprises 1.3–2 μ m wide ($\bar{x}$ = 1.7 μ m, n = 30), filiform, branched or simple, septate, cellular, pseudoparaphyses. *Asci* 75–140 $\times$ 12–20 μ m ($\bar{x}$ = 95 $\times$ 15 μ m, n = 25), 8-spored, cylindric-clavate to clavate, apically rounded, fissitunicate, bitunicate, short pedicellate, with ocular chamber. *Ascospores* 30–50 $\times$ 6.5–10.5 μ m ($\bar{x}$ = 38 $\times$ 8.5 μ m, n = 30), biseriate, fusiform, 1-3-septate, often slightly constricted at the middle septum, hyaline, with guttulate, smooth-walled, with thin mucilaginous appendages. Asexual morph: Undetermined.

Culture characteristics – Ascospores germinated within 48 h on PDA. 1 cm diam. after two weeks at 27°C. Colony dense, circular, from above, convex, surface smooth, with edge entire, floccose, white; from below, white at the edge, pale brown at the center, not producing pigmentation in agar.

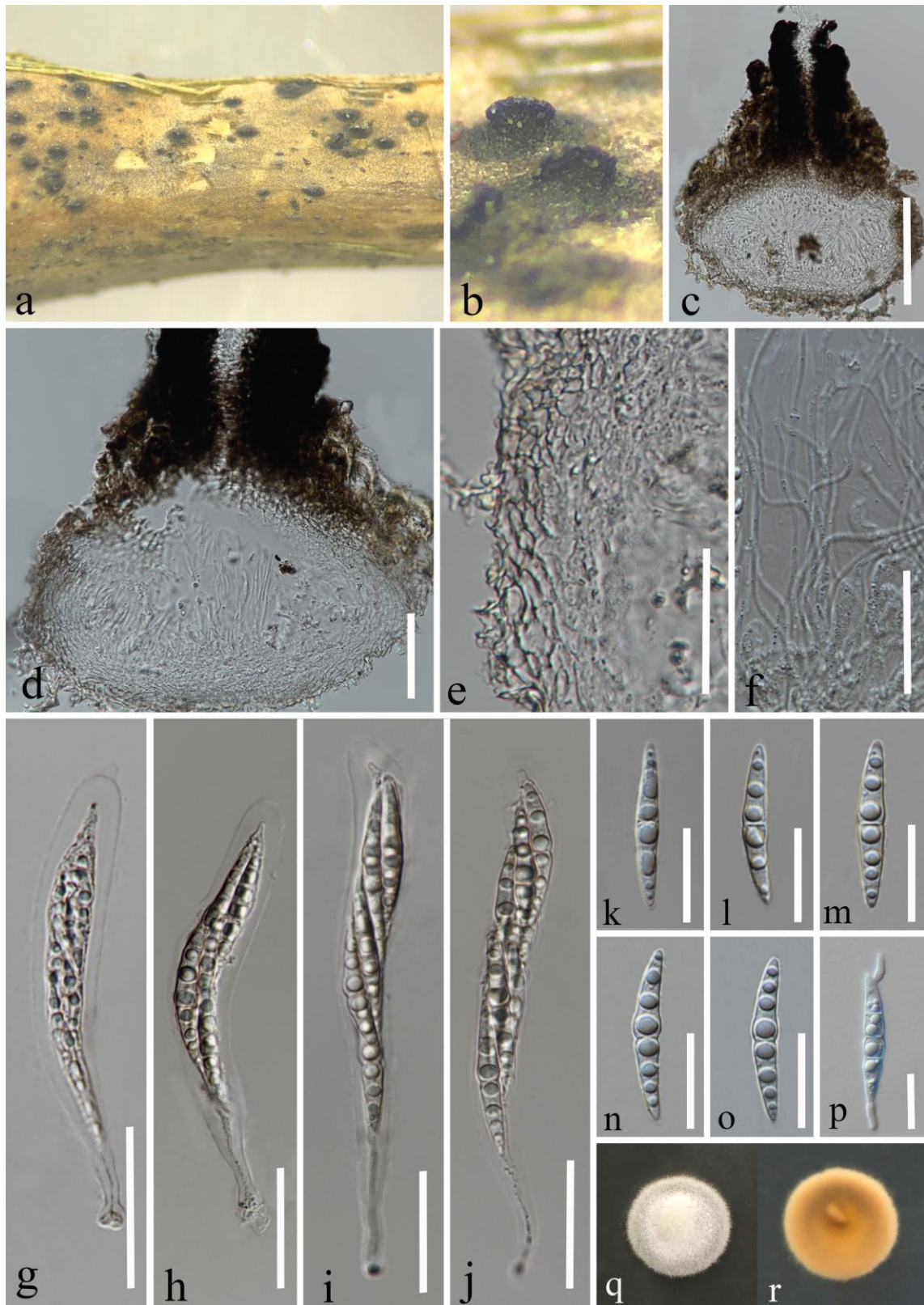


Figure 41 – *Lophiopoacea paramacrostoma* (HKAS 128789, a new host and a geographical record). a, b Ascomata on the host. c, d Sections of ascomata. e Peridium. f Pseudoparaphyses. g–j Asci. k–o Ascospores. p A germinated ascospore. q, r Culture characters on PDA (q: above, r: below). Scale bars: c = 100 μ m, d = 50 μ m, e–j = 30 μ m, k–p = 20 μ m.

Material examined – China, Yunnan Province, Kunming, on the dead unidentified wood from grassland, 13 May 2021, Y. Gao, GY63A (HKAS 126568, holotype), ex-type living culture

CGMCC 3.24543; *ibid.*, GY63B (HKAS 128757, isotype), ex-isotype living culture CGMCC 3.24544.

GenBank numbers – CGMCC 3.24543: ITS = PV608560, LSU = PV607411, SSU = PV607305, *tef1*- α = PV626441, *rpb2* = PV655487; CGMCC 3.24544: ITS = PV608561, LSU = PV607412, SSU = PV607306, *tef1*- α = PV626442, *rpb2* = PV655488.

Notes – *Pseudolophiostoma kunmingense* is introduced as a new species based on its distinct morphology and the phylogeny of the combined SSU, LSU, ITS, *tef1*- α , and *rpb2* sequence data. In our phylogenetic study, our collections (CGMCC 3.24543 and CGMCC 3.24544) formed a sister clade to *Pseudolophiostoma lincangense* (KUMCC 21-0606, ex-type), with 76% ML and 0.84 PP statistical support values (Fig. 40). A pairwise nucleotide comparison showed that *P. kunmingense* (CGMCC 3.24543) differs from *P. lincangense* (KUMCC 21-0606) in 21/549 bp of ITS (3.83%, with 3 gaps), 5/840 bp of LSU (0.60% without gaps), 0/976 bp of SSU (0.00%), 11/863 bp of *tef1*- α (1.27% without gaps), 36/1044 bp of *rpb2* (3.59% without gaps). *P. kunmingense* (CGMCC 3.24543) differs from the type species of *P. lincangense* (KUMCC 21-0606) in ascomata (225–290 $\times$ 135–160 μ m, L/W = 1.7 vs. 280–330 $\times$ 230–290 μ m, L/W = 1.2), ascospores (6.5–10.5 μ m wide, cylindric-clavate to clavate vs. 5–5.8 μ m wide, fusiform) (Ren et al. 2024c). In this study, based on morphological characterization and phylogenetic analyses, *Pseudolophiostoma kunmingense* is introduced as a new saprobic fungus from dead wood in China.

Massarinaceae Munk, Friesia 5 (3-5): 305 (1956)

Notes – Massarinaceae was introduced by Munk (1956) to accommodate *Massarina*, with *Massarina* designated as the type genus and described based on the sexual morph (Saccardo 1883). Currently, eleven genera were accepted in Massarinaceae, namely, *Byssothecium*, *Haplohelminthosporium*, *Helminthosporiella*, *Helminthosporium*, *Massarina*, *Mirohelminthosporium*, *Pseudodidymosphaeria*, *Pseudosplanchnonema*, *Semifissispora*, *Stagonospora*, *Suttonomyces*, and *Synhelminthosporium* (Hongsan et al. 2020b, Wijayawardene et al. 2020, Konta et al. 2021, Chen et al. 2022, Hyde et al. 2024a). In this study, we introduce two new species of *Massarina* and *Stagonospora* and a new record species of *Stagonospora*. An updated phylogenetic tree based on combined ITS, LSU, SSU, *tef1*- α , and *rpb2* sequence data is presented in Fig. 43.

Massarina Sacc., Syll. Fung. 2: 153 (1883)

Notes – *Massarina* was introduced by Saccardo (1883) with *M. eburnea* as the type species. There were 125 species accepted in the genus *Massarina* (Index Fungorum 2025), however, only four species have been confirmed by molecular information (Tibpromma et al. 2018b). The sexual morph of *Massarina* is characterized by its depressed, globose, immersed, hemispherical ascomata, hyaline, broadly fusiform, with rounded ends, multi-septate ascospores (Tanaka et al. 2015). The asexual morph of *Massarina* was reported as pycnidial conidiomata, ceratophoma-like, hyaline, aseptate conidia, enteroblastic conidiogenous cells, hyaline, oblong to globose-ovoid, one-celled conidia (Tibpromma et al. 2018b). In this study, we introduce a new species, *Massarina yunnanensis*, together with descriptions and illustrations (Fig. 44).

Massarina yunnanensis Y. Gao, H. Gui & K.D. Hyde, sp. nov.

Fig. 44

Index Fungorum number: IF903825; Facesoffungi number: FoF17700

Holotype – HKAS 126575

Etymology – The specific epithet “yunnanensis” refers to the type location, Yunnan Provinc.

Saprobic on dead branches. Sexual morph: *Ascomata* 140–190 μ m diam. $\times$ 90–140 μ m high ($\bar{x}$ = 170 $\times$ 120 μ m, n = 10), globose to subglobose, immersed, solitary or aggregated, brown or black. *Peridium* 16–26.5 μ m wide ($\bar{x}$ = 21 μ m, n = 30), composed of thick-walled, brown to dark brown cells of *textura angularis* or *textura globulosa*. *Hamathecium* comprises 1.8–3 μ m wide ($\bar{x}$ = 2.4 μ m, n = 30), filiform branches, composed of dense, broad filamentous, distinctly septate, narrowly at the septum, anastomosed pseudoparaphyses. *Asci* 62–100 $\times$ 9.5–16.5 μ m ($\bar{x}$ = 83.5 $\times$ 13

µm, n = 25), 8-spored, cylindric-clavate to clavate, apically rounded, bitunicate, fissitunicate, short pedicellate, thick-walled, with ocular chamber. *Ascospores* 17.5–22 × 5–6.5 µm ($\bar{x}$ = 20 × 5.8 µm, n = 35), biseriate, fusiform with acute angular ends, most of the 2-septate, slightly constricted at the septum, hyaline, smooth, with guttulate, surrounded by a thin mucilaginous sheath. Asexual morph: Undetermined.

Culture characteristics – Ascospores germinated within 48 h on PDA. 6 cm diam. after two weeks at 27°C. Colony from above, dense, circular, low convex, surface smooth, with edge entire, floccose, white at the margin, pale yellow at the center; from below, white at the edge, black at the center.

Material examined – China, Yunnan Province, Zhaotong grassland, on the dead unidentified branches found on the grassland, 21 August 2021, Y. Gao, ZG6A (HKAS 126575, holotype), ex-type living culture CGMCC 3.24567 and CGMCC 3.24568; *ibid.*, ZG12 (HKAS 126577, isotype), ex-isotype living culture CGMCC 3.24569 and CGMCC 3.24570.

GenBank numbers – CGMCC 3.24567: ITS = PV642538, LSU = PV607420, SSU = PV607314, *tef1-α* = PV626449; CGMCC 3.24568: ITS = PV642539, LSU = PV607421, SSU = PV607315, *tef1-α* = PV626450; CGMCC 3.24569: ITS = PV608569, LSU = PV607422, SSU = PV607316, *tef1-α* = PV626451; CGMCC 3.24570: ITS = PV608570, LSU = PV607423, SSU = PV607317, *tef1-α* = PV626452.

Notes –In phylogenetic analysis, our collections (CGMCC 3.24567, CGMCC 3.24568, CGMCC 3.24569, CGMCC 3.24570) grouped with *Massarina tangneyae* (BRIP 72527f, holotype) and *M. pandanicola* (MFLUCC 17-0596, ex-type) (Fig. 43). Sequence comparison between *Massarina yunnanensis* (CGMCC 3.24567) and *M. tangneyae* (BRIP 72527f) showed a 10.52% (49/466 bp, with 17 gaps) base pair difference in the ITS region, 3.37% (29/861 bp, without gaps) base pair difference in the LSU region. Our collections also have 12.86% (49/381 bp, with 9 gaps), 3.90% (33/841 bp, with 1 gap), 2.00% (19/949 bp, with 3 gaps), 8.96% (75/837 bp, with 2 gaps) difference from the ex-type strain of *M. pandanicola* (MFLUCC 17-0596) in ITS, LSU, SSU, and *tef1-α* sequence data, respectively. *Massarina pandanicola* was reported only from its asexual morph on healthy leaves of *Pandanus* sp. (Pandanaceae) in Thailand (Tibpromma et al. 2018b). *Massarina tangneyae* was introduced by Tan & Shivas (2022) from necrotic leaf spot on *Pandanus tectorius* (Pandanaceae) in Australia based on phylogenetic analyses. However, no morphological analysis of *Massarina tangneyae* (BRIP 72527f) was provided. Therefore, we were unable to compare our new species with *M. tangneyae* and *M. pandanicola*. Based on the phylogenetic evidence, we introduce *Massarina yunnanensis* as a new species.

***Stagonospora* (Sacc.) Sacc., Syll. Fung. 3: 445 (1884)**

Notes – *Stagonospora* was established by Saccardo (1884) and typified with *Stagonospora paludosa* based on the basionym *Hendersonia paludosa* (Wijayawardene et al. 2022). The asexual morph of *Stagonospora* is characterized by globose, immersed, black pycnidia, phialidic, hyaline conidiogenous cells, subcylindrical, septate, guttulate conidia (Quaedvlieg et al. 2013, Jayasiri et al. 2015, Brahmanage et al. 2020). The sexual morph is distinguishable by erumpent on host tissue, globose, brown ascomata, septate pseudoparaphyses, clavate, bitunicate asci, ellipsoidal, with guttules in each cell, 1-septate ascospores (Quaedvlieg et al. 2013). *Stagonospora* species are globally distributed and a species-rich genus in the family Massarinaceae and are commonly associated with grasses (Quaedvlieg et al. 2013, Hyde et al. 2016, Thambugala et al. 2017). Presently, more than 490 species are accepted in the genus *Stagonospora* (Index Fungorum 2025). These fungal organisms demonstrate a particular ecological preference for monocotyledonous hosts, with frequent occurrences observed in various grass species, according to studies by Quaedvlieg et al. (2013) and Thambugala et al. (2017). Ecologically, these *Stagonospora* species function as decomposers of plant litter, colonizing dead grass tissues and foliar debris, while also exhibiting pathogenic potential by causing foliar lesions on economically important crops such as wheat (Poaceae) and various sedge species (Cyperaceae) (Kobayashi et al. 2005). In this study, we introduce a new species, *Stagonospora dactylidis*, and a new asexual morph record for

Stagonospora poaceicola, based on morphology and molecular data, together with descriptions and illustrations (Figs. 45, 46).

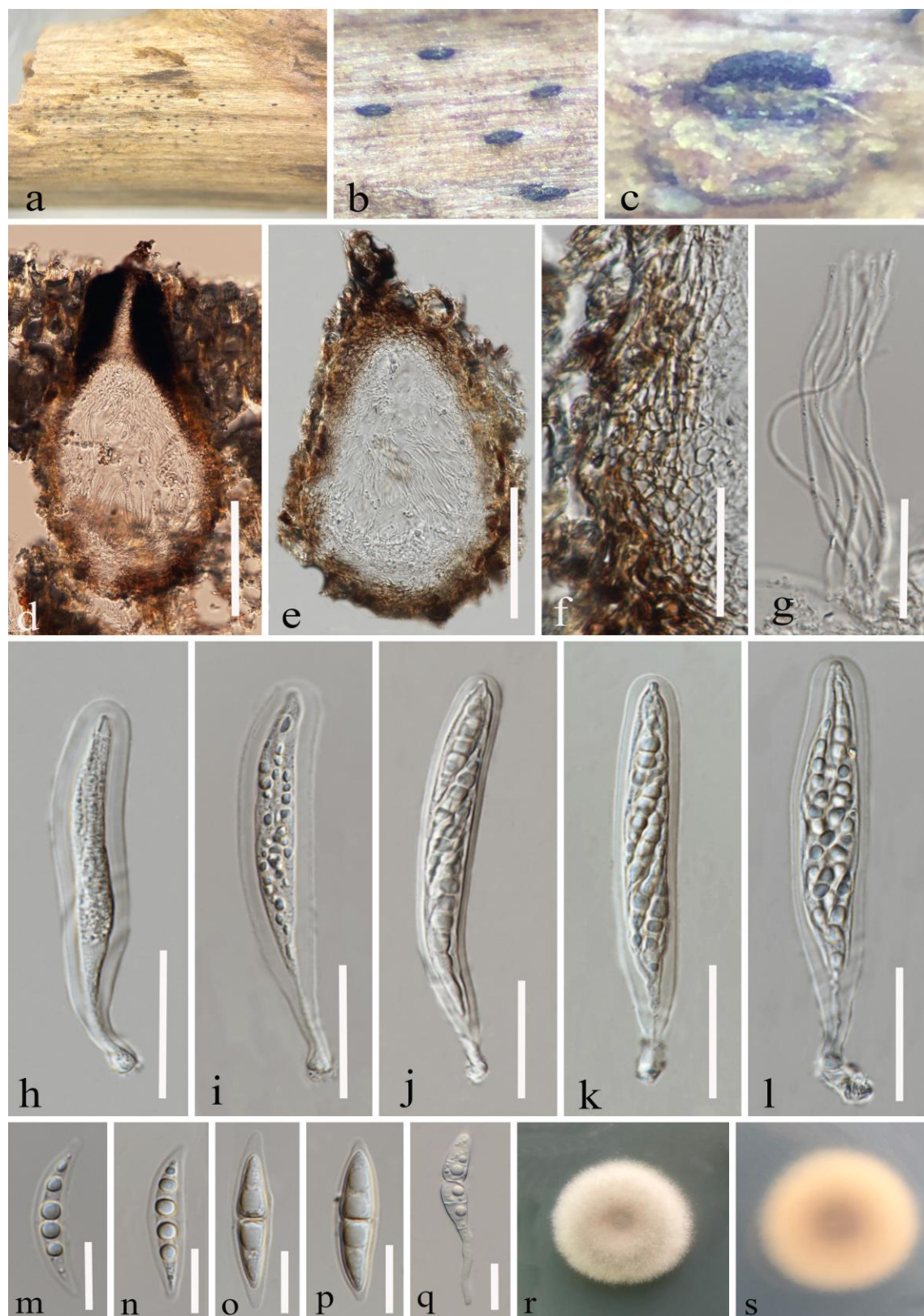


Figure 42 – *Pseudolophiostoma kunmingense* (HKAS 126568, holotype). a–c Ascomata on the host substrate. d, e Sections of ascomata. f Peridium. g Pseudoparaphyses. h–l Asci. m–p Ascospores. q A germinated ascospore. r, s Culture characters on PDA (r: above, s: below). Scale bars: d, e = 100 μ m, f–l = 30 μ m, q = 20 μ m, m–p = 15 μ m.

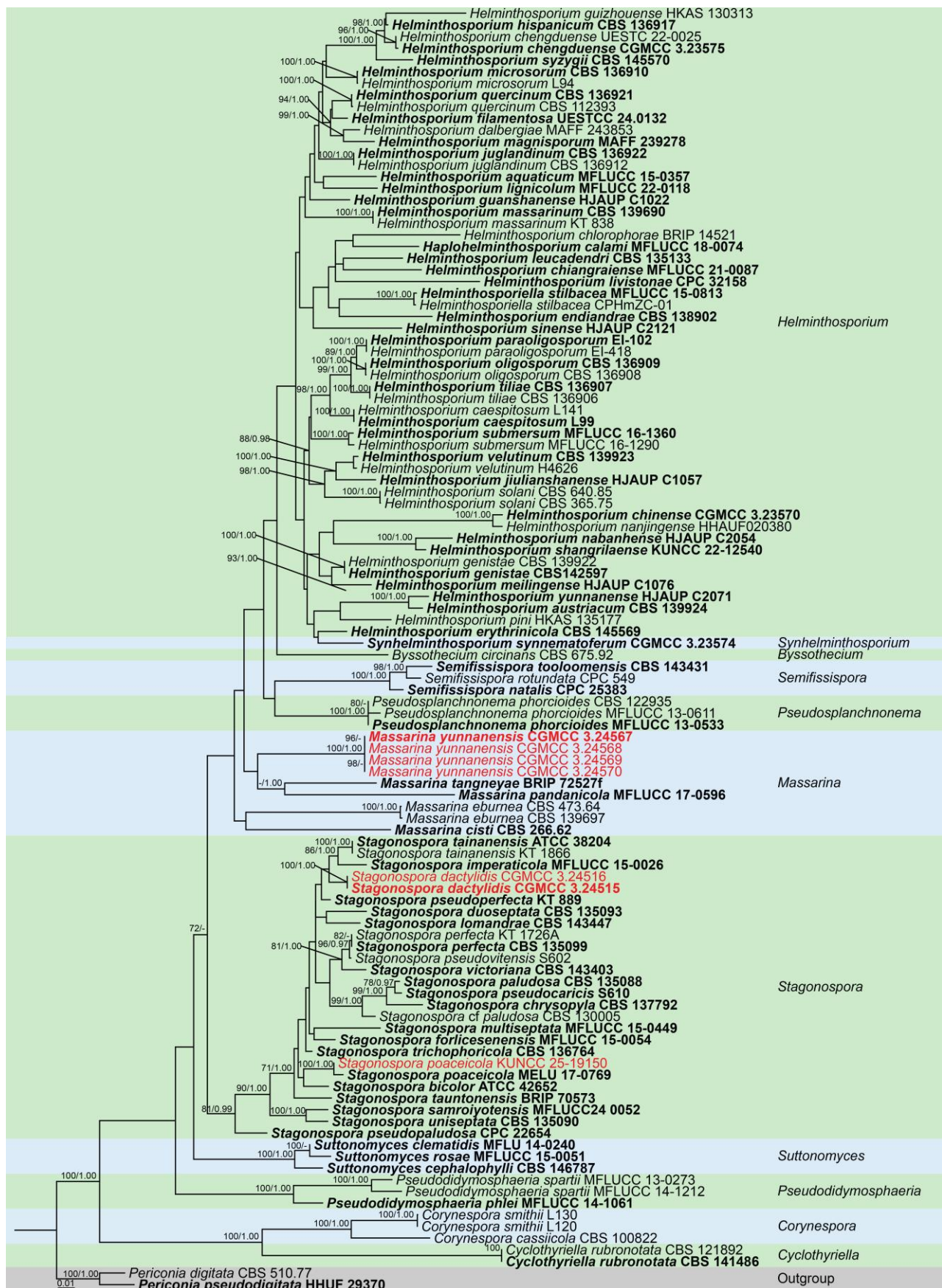


Figure 43 – RAxML phylogram generated from a combined dataset of partial ITS, LSU, SSU, *tef1*- α , and *rpb2* DNA sequence analyses for Massarinaceae. Related sequences are obtained following Chen et al. (2022), Hu et al. (2023), Hyde et al. (2023b), Bhagya et al. (2024). One hundred and ten strains were included in the combined analyses, which comprised 4,547 characters in the combined

ITS, LSU, SSU, *tef1- α* , and *rpb2* alignment. *Periconia digitata* (CBS 510.77) and *Periconia pseudodigitata* (HHUF 29370) were used as the outgroup taxa. The best-scoring RAXML tree with a final likelihood value of -35536.920938 is presented. The matrix contained 1,940 distinct alignment patterns, with 39.18% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.238395, C = 0.250495, G = 0.270143, T = 0.240967; substitution rates AC = 1.706369, AG = 4.511386, AT = 1.846981, CG = 0.973329, CT = 8.639418, GT = 1.000000. The tree topology of the ML analysis is similar to the Bayesian analysis. Bootstrap values for ML equal to or greater than 60% and PP values greater than 0.90 (rounding of values to 2 decimal places) are labelled on the nodes. Strains of the newly described species are in orange, while type strains are in bold. (ITS: 580 bp, LSU: 866 bp, SSU: 1043 bp, *tef1- α* : 930 bp, *rpb2*: 1128)

Stagonospora dactylidis Y. Gao, H. Gui & K.D. Hyde, sp. nov.

Fig. 45

Index Fungorum number: IF903826; Facesoffungi number: FOF01303

Holotype – HKAS 128803

Etymology – The specific epithet is derived from the genus *Dactylis* (Poaceae), in which the holotype was found.

Saprobic on dead stems of *Dactylis glomerata*. Sexual morph: *Ascomata* 170–320 μ m high $\times$ 160–290 μ m diam. ($\bar{x}$ = 240 $\times$ 215 μ m, n = 15), globose to subglobose, semi-immersed or superficial, solitary or aggregated, coriaceous, black, with papilla. *Peridium* 20–50 μ m wide ($\bar{x}$ = 30 μ m, n = 30), composed of thick-walled, pale brown to dark brown cells of *textura angularis* or *textura globulosa*. *Hamathecium* comprises 1.5–4 μ m wide ($\bar{x}$ = 3 μ m, n = 30), filiform branches, composed of dense, broad filamentous, distinctly septate, anastomosed pseudoparaphyses. *Asci* 70–125 $\times$ 13–20 μ m ($\bar{x}$ = 93 $\times$ 15 μ m, n = 20), 8-spored, cylindric-clavate to clavate, apically rounded, short pedicellate, bitunicate, fissitunicate, thick-walled, with a shallow ocular chamber. *Ascospores* 26–35 $\times$ 4–8.5 μ m ($\bar{x}$ = 33 $\times$ 5.5 μ m, n = 30), overlapping, narrowly fusiform with acute angular ends, 1-3-septate, slightly constricted at the middle septum, smooth, hyaline, with guttulate, surrounded by a thin mucilaginous sheath. Asexual morph: Undetermined.

Culture characteristics – Ascospores germinated within 48 h on PDA. 5.5 cm diam. after two weeks at 27 °C. Colony from above, dense, circular, low convex, surface smooth, with edge entire, floccose, white; from below, white at the margin, grey at the center.

Material examined – China, Yunnan Province, Zhaotong grassland, on dead stems of *Dactylis glomerata* (Poaceae), 26 August 2022, Y. Gao, QG32A (HKAS 128803, holotype), ex-type living culture CGMCC 3.24515; *ibid.*, QG32B (HKAS 128804, isotype), ex-isotype living culture CGMCC 3.24516.

GenBank numbers – CGMCC 3.24515: ITS = PV608567, LSU = PV607418, SSU = PV607312, *tef1- α* = PV626447, *rpb2* = PV655493; CGMCC 3.24516: ITS = PV608568, LSU = PV607419, SSU = PV607313, *tef1- α* = PV626448, *rpb2* = PV655494.

Notes – Based on multigene phylogenetic analyses, our collections (CGMCC 3.24515 and CGMCC 3.24516) constituted an independent lineage within *Stagonospora* (Fig. 43). It grouped between *Stagonospora imperaticola* (MFLUCC 15-0026, ex-type) and *S. pseudoperfecta* (KT 889, holotype). The pair-wise nucleotide comparison showed that our collections (CGMCC 3.24515 and CGMCC 3.24516) differ from *S. imperaticola* (MFLUCC 15-0026) by 19/526 bp of ITS (3.61%, with 1 gap), 4/834 bp of LSU (0.48%, without gaps), 30/824 bp of *tef1- α* (3.64%, without gaps), 37/803 bp of *rpb2* (4.61%, without gaps). Our collections differ from *S. pseudoperfecta* (KT 889) by 10/498 bp of ITS (2.01%, with 1 gap), 2/832 bp of LSU (0.24%, without gaps), 1/998 bp of SSU (0.1%, without gaps and 20/924 bp of *tef1- α* (2.16%, without gaps). *S. imperaticola* was introduced only from its asexual morph (Thambugala et al. 2017), therefore, it cannot be compared morphologically with *Stagonospora dactylidis*. Our collection differs from *S. pseudoperfecta* (KT 8890) in ascomata (170–320 $\times$ 160–290 μ m, L/W = 1.1 vs. 210–260 $\times$ 200–250 μ m, L/W = 1.0), asci (70–125 μ m vs. 66–100 μ m), ascospores (26–35 $\times$ 4–8.5 μ m, L/W = 4.9 vs. 21–30.5 $\times$ 5–7 μ m, L/W = 4.3) (Tanaka et al. 2015). Both phylogenetic analyses and morphological characteristics supported our collections as a new species, *Stagonospora dactylidis*.

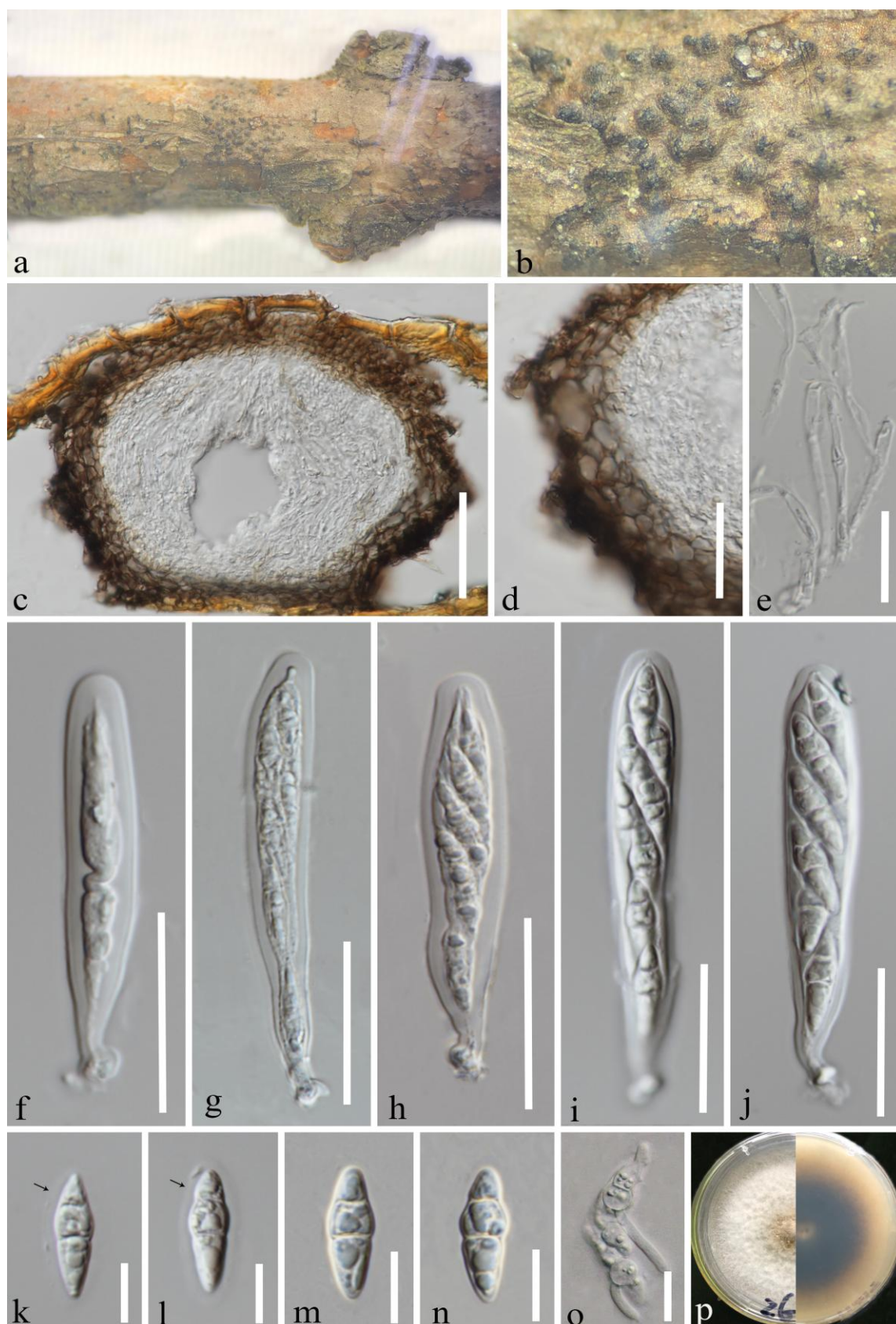


Figure 44 – *Massarina yunnanensis* (HKAS 126575, Holotype). a, b Appearance of ascomata on the host substrate. c A section of an ascoma. d A section of peridium. e Pseudoparaphyses. f–j Asci. k–n Ascospores (k, l arrowheads indicate gelatinous sheath). o Germinated ascospores. p Culture characters on PDA (left: above, right: below). Scale bars: c = 50 μm , d, f–j = 30 μm , e, o = 20 μm , k–n = 10 μm .

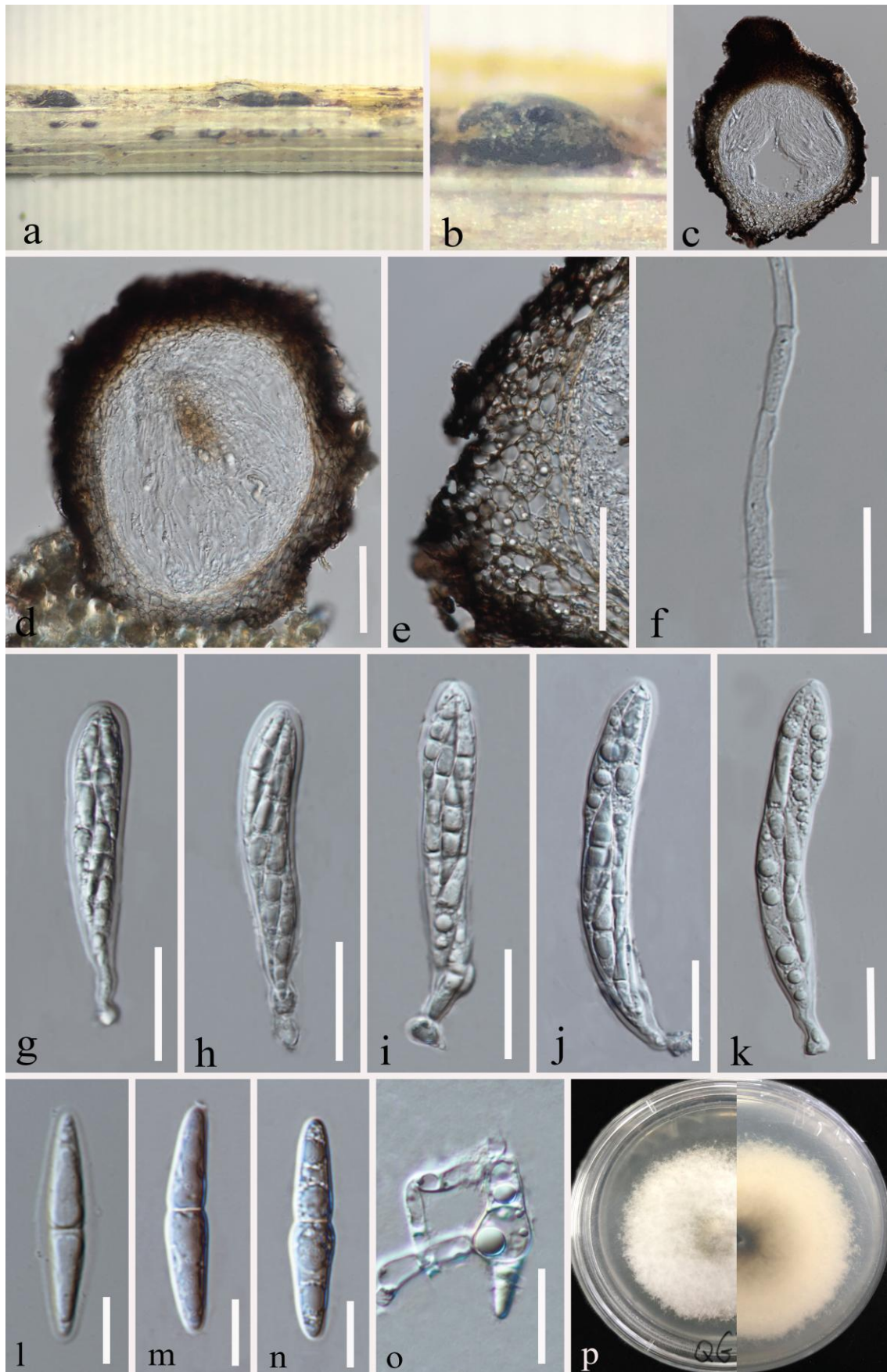


Figure 45 – *Stagonospora dactylidis* (HKAS 128803, holotype). a, b Appearance of ascomata on the host substrate. c, d Sections of ascomata. e A Section of peridium. f Pseudoparaphyses. g–k Asci. l–n Ascospores. o A germinated ascospore. p Culture characters on PDA (left: above, right: below). Scale bars: c = 100 μ m, d, e = 50 μ m, g–k = 30 μ m, f, o = 20 μ m, l–n = 10 μ m.

Stagonospora poaceicola Tennakoon, Phookamsak & K.D Hyde, Mycosphere 11 (1): 2505 (2020) amended Fig. 46

Index Fungorum number: IF557371; Facesoffungi number: FoF07748

Saprobic on dead stems of grass. Sexual morph: Described by Brahmanage et al. (2020). Asexual morph: *Conidiomata* 130–175 µm diam. × 85–130 µm high ($\bar{x}$ = 150 × 115 µm, n = 10), globose or subglobose, semi-immersed with the dark brown spot visible in the surface view, scattered, solitary, uni-loculate, dark brown to black, ostiolate. *Ostiole* circular, centrally located. *Conidiomata wall* 12–40 µm wide ($\bar{x}$ = 23 µm, n = 30), composed of thick-walled, dark brown cells of *textura angularis* in the outer layer, becoming hyaline cells in the inner layer. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 3.5–9 × 5–11 µm ($\bar{x}$ = 6.7 × 7.5 µm, n = 15), phialidic, enteroblastic, ampulliform, hyaline, thin-walled, smooth. *Conidia* 24–31 × 7–10 µm ($\bar{x}$ = 28 × 8.5 µm, n = 25), cylindrical, rounded at apex, subtruncate at base, straight, 3-septate, smooth-walled.

Culture characteristics – Colonies on PDA reaching 60 mm diam. after two weeks. Colony from above, dense, circular, low convex, surface smooth, with edge entire, floccose, with white to cream margin, brown at the center; from below, pale brown at the edge, brown margin, black at the center.

Material examined – China, Yunnan Province, Kunming, on dead stems of unidentified grass (Poaceae), 13 June 2021, Y. Gao, XJK31 (HKAS 135352), living culture KUNCC 25-19150.

Known hosts and distribution – on dead stems of grass (Poaceae) in China (Brahmanage et al. 2020), on dead stems of grass (Poaceae) in Yunnan Province, China (This study).

GenBank numbers – KUNCC 25-19150: ITS = PV608566, LSU = PV607417, SSU = PV607311.

Notes – *Stagonospora poaceicola* (MELU 17-0769, holotype) was introduced from dead stems of an unknown grass sp. (Poaceae) from Thailand. It was known only for its sexual morphology (Brahmanage et al. 2020). In the multigene phylogenetic analyses, our collection of the asexual species (KUNCC 25-19150) formed a sister clade with the type strain of *Stagonospora poaceicola* (MELU 17-0769) with 100% ML and 1.00 PP support values (Fig. 43). A comparison of SSU, ITS, and LSU sequence data reveals no significant difference between our new collection and *S. poaceicola* (MELU 17-0769). Therefore, we report our collection (KUNCC 25-19150) as a new record of the asexual species *Stagonospora poaceicola* on dead stems of grass (Poaceae) in China.

Occultibambusaceae D.Q. Dai & K.D. Hyde, Fungal Diversity 82: 25 (2016)

Notes – *Occultibambusaceae* was established by Dai et al. (2017) with *Occultibambusa* as its type genus. The family recognized five genera, viz. *Brunneofusispora*, *Neooccultibambusa*, *Occultibambusa*, *Seriascoma* and *Versicolorisporium* (Dai et al. 2017, Phookamsak et al. 2019, Hyde et al. 2024a). The sexual morph of *Occultibambusaceae* is characterized by subglobose to conical, immersed, solitary to gregarious uni- or multi-loculate, with black ostioles ascomata; cylindrical to clavate, bitunicate, (6)–8-spored, with short, furcate or bulb-like pedicels asci; fusiform, hyaline to dark brown, 1–3 septa, ascospores (Dai et al. 2017, Doilom et al. 2017, Phookamsak et al. 2019, Jiang et al. 2021b). *Occultibambusaceae* is phylogenetically related to *Biatrisporaceae*; however, members of *Occultibambusaceae* later develop manglicolous, the dark brown ascospores usually having hyaline, rounded, swollen ends, which will release mucilage (Hyde et al. 2013, Dai et al. 2017). Members of *Occultibambusaceae* are usually reported on monocotyledons; however, they can also be found on hardwood trees (Dai et al. 2017, Doilom et al. 2017).

Occultibambusa D.Q. Dai & K.D. Hyde, Fungal Diversity 82: 10.1007/s13225-016-0367-8, [26] (2016)

Notes – *Occultibambusa* was introduced by Dai et al. (2017), with *O. bambusae* being the type species of *Occultibambusa* characterized by dark, immersed, with periphysate ostioles

ascomata, broad cylindrical to clavate asci, 1-septate, dark, brown, fusiform ascospores (Dai et al. 2017). Twelve species are accepted in *Occultibambusa*, all species were isolated from Poaceae (Hyde et al. 2016, Zhang et al. 2017, Jiang et al. 2021b, Yu et al. 2021, Wang et al. 2024a, Wei et al. 2024). In this study, we introduce a new host record for *Occultibambusa jonesii*, based on morphology and molecular data, together with descriptions and illustrations (Fig. 48).

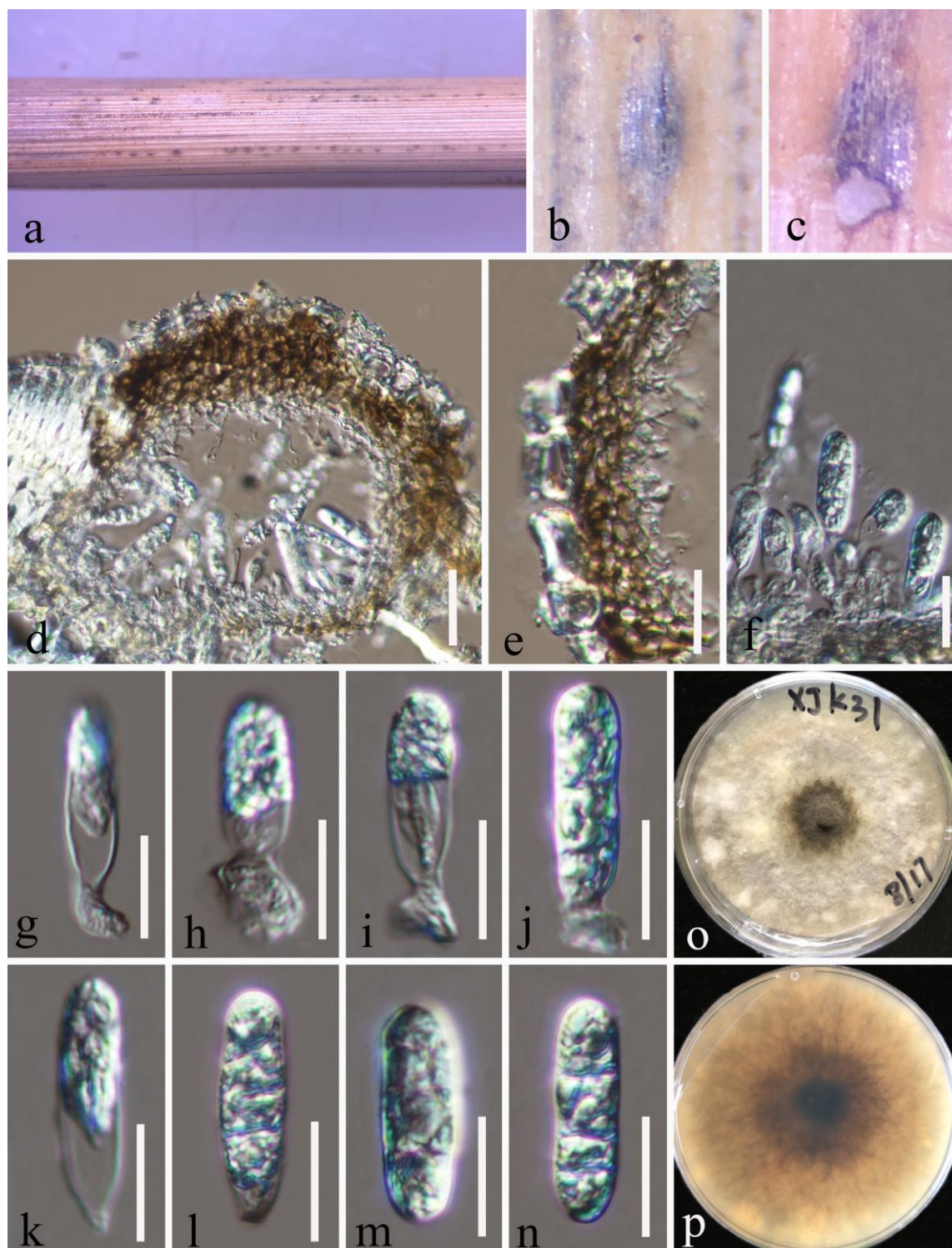


Figure 46 – *Stagonospora poaceicola* (HKAS 135352, a new asexual morph record). a, b Appearance of conidiomata on the host substrate. c, d Sections of conidiomata. e Conidiomata wall. f–j Conidiogenous cells and developing conidia. k–n Conidia. o, p Culture characters on PDA (o: above, p: below). Scale bars: d = 30 μ m, e, f = 20 μ m, g–n = 15 μ m.

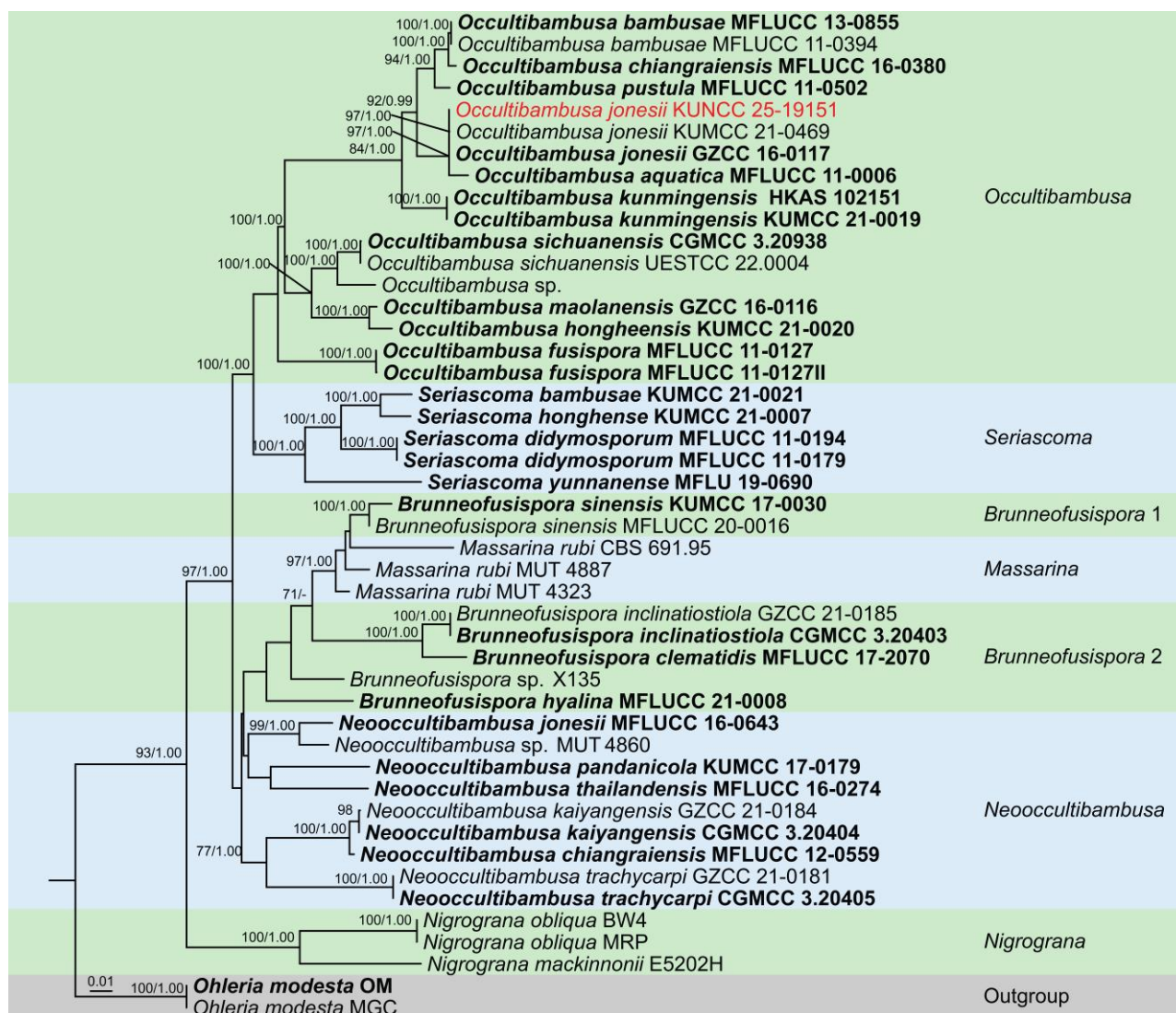


Figure 47 – RAxML phylogram generated from a combined dataset of partial ITS, LSU, SSU, *tef1*- α , and *rpb2* DNA sequence analyses for Occultibambusaceae. Related sequences are obtained following Xu et al. (2022). Forty-six strains were included in the combined analyses, which comprised 4,278 characters in the combined ITS, LSU, SSU, *tef1*- α , and *rpb2* alignment. *Ohleria modesta* (OM and MGC) were used as the outgroup taxa. The best-scoring RAxML tree with a final likelihood value of -22875.010352 is presented. The matrix contained 1,384 distinct alignment patterns, with 22.04% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.246063, C = 0.252070, G = 0.269823, T = 0.232045; substitution rates AC = 2.150914, AG = 4.916442, AT = 1.699996, CG = 1.609965, CT = 10.733651, GT = 1.000000. The tree topology of the ML analysis is similar to the Bayesian analysis. Bootstrap values for ML equal to or greater than 70% and PP values greater than 0.95 (rounding values to 2 decimal places) are labelled on the nodes. Strains of the newly described species are in orange, while type strains are in bold. (ITS: 486 bp, LSU: 844 bp, SSU: 1006 bp, *tef1*- α : 945 bp, *rpb2*: 997).

Occultibambusa jonesii Jin F. Zhang, Jian K. Liu, K.D. Hyde & Zi Y. Liu, in Zhang, Liu, Hyde, Yang & Liu, *Mycosphere* 8(4): 553 (2017) Fig. 48

Index Fungorum number: IF552743; Facesoffungi number: FoF02873

Saprobic on dead stems of unidentified grass. Sexual morph: *Ascomata* 170–230 μm diam. $\times$ 130–205 high μm ($\bar{x}$ = 200 $\times$ 175 μm , n = 10), ampulliform or subconical to hemispherical, semi-immersed, scattered, uni-loculate, glabrous, flattened at the base, brown or black, central ostiole, with minute papilla, ostiole filled with periphyses. *Peridium* 20–35 μm wide ($\bar{x}$ = 28 μm , n = 25), thin at the base, thick at the sides towards and apex, composed of several layers, of brown to dark

brown, pseudoparenchymatous cells, arranged in a *textura angularis*, with palisade-like cells at the rim, outer layers intermixed with host tissue. *Hamathecium* comprises 2–3 µm wide ($\bar{x}$ = 2.5 µm, n = 30), filamentous, branched, dense, distinct septate, cellular pseudoparaphyses, anastomosed above the asci, embedded in hyaline gelatinous matrix. *Asci* 55–80 × 10–14 µm ($\bar{x}$ = 70 × 12 µm, n = 25), 8-spored, cylindrical to cylindric-clavate, apically rounded, bitunicate, fissitunicate, short pedicellate, thick-walled, with ocular chamber. *Ascospores* 25–30 × 5–7 µm ($\bar{x}$ = 27 × 5.5 µm, n = 20), biseriate, fusiform with acute angular or conical at the end, 1-septate, slightly constricted at the septum, hyaline when young and pale brown to brown when mature, smooth, with guttulate. Asexual morph: Undetermined.

Culture characteristics – Asci and ascospores germinated within 48 h on PDA. 6 cm diam. after three weeks at 27°C. Colony from above, dense, circular, low convex, surface smooth, with edge entire, white at the edge, dark brown at the center with white spots; from below, black.

Material examined – China, Yunnan Province, Xishuangbanna, on dead stems of an unidentified grass (Poaceae) found on the grassland, 23 May 2022, Y. Gao, BG2 (HKAS 132954), living culture KUNCC 25-19151.

Known hosts and distribution – on dead bamboo culms (Poaceae) in China (Zhang et al. 2017), on culms of *Brachiaria mutica* (Poaceae) submerged in a freshwater stream in China (Xu et al. 2022), on dead stems of grass (Poaceae) in Yunnan Province, China (This study).

GenBank numbers – KUNCC 25-19151: ITS = PV642540, LSU = PV607424, SSU = PV607318, *tefl-α* = PV626453, *rpb2* = PV655495.

Notes – Multigene phylogenetic analyses indicated that our collection (KUNCC 25-19151) grouped with *Occultibambusa jonesii* (GZCC 16-0117 and KUMCC 21-0469) and *O. aquatica* (MFLUCC 11-0006, ex-type), distancing from *O. kunmingensis* (KUN-HKAS 102151 and KUMCC 21-0019) (Fig. 47). Pairwise nucleotide comparison of ITS, LSU, SSU, *tefl-α*, and *rpb2* sequence data showed that our collection (KUNCC 25-19151) is consistent with *O. jonesii* (GZCC 16-0117, ex-type), with 100% similarity for each gene region. Our collection is morphologically similar to *O. jonesii* (GZCC 16-0117 and KUMCC 21-0469) (Zhang et al. 2017, Xu et al. 2022). Therefore, our new collection is identified as a new host record of *Occultibambusa jonesii*.

Periconiaceae (Sacc.) Nann., Repertorio sistematico dei miceti dell'uomo e degli animali 4: 482 (1934)

Notes – Periconiaceae was revised by Tanaka et al. (2015) and placed in Pleosporales based on morphological and phylogenetic evidence, with *Periconia* as its type genus. Periconiaceae comprises the genera *Flavomyces* and *Periconia* (= *Bambusistroma*; = *Noosia*) (Tanaka et al. 2015, Knapp et al. 2015, Yang et al. 2022a, Hyde et al. 2024a). The sexual morph is mainly characterized by globose, immersed to erumpent, scattered to grouped ascomata with ostiolar neck central, papillate; hyaline paraphyses; ascomatal wall composed of several layers of thin-walled, pale brown to brown cells; branched, cellular, anastomosed pseudoparaphyses; oblong to cylindrical, fissitunicate, 8-spored asci; fusiform, 1-septate, smooth, hyaline, with an entire sheath ascospores (Tanaka et al. 2015). The asexual morph is mainly characterized by noosia- or periconia-like conidiomata; mononematous, macronematous conidiophores; pale brown to brown, smooth to slightly echinulate branches; conidial heads spherical; discrete on stipe, monoblastic to polyblastic, branches conidiogenous cells; globose to ellipsoidal, catenate, aseptate, verruculose to echinulate, brown conidia (Tanaka et al. 2015). *Periconia* species have been reported as endophytes, saprobes, pathogens, and are widely distributed in terrestrial habitats and rarely in aquatic and marine environments (Goga 2000, Teles et al. 2006, Phookamsak et al. 2019, Gunasekaran et al. 2021, Liao et al. 2024). An updated phylogenetic tree based on combined ITS, LSU, SSU, *tefl-α*, and *rpb2* sequence data is presented in Fig. 49.

Periconia Tode, Fungi Mecklenburgenses Selecti 2: 2 (1791)

Notes – *Periconia* was introduced by Tode (1791), with *P. lichenoides* as the type species. The majority of *Periconia* species are classified as hyphomycetous, although a few species have

been documented to exhibit sexual morphs (Tanaka et al. 2015, Phookamsak et al. 2019). The asexual morph of the genus is characterized by mononematous, macronematous, branched or unbranched conidiophores, with spherical apices, monoblastic, holoblastic, polyblastic conidiogenous cells, which form at the intercalary parts or terminal ends of the conidiophores, spherical to sub-spherical, brown, smooth or verruculose, aseptate, catenate or solitary conidia (Liu et al. 2017, Phookamsak et al. 2019, Hongsanan et al. 2020a, Tian et al. 2024). The sexual morph is characterized by necks ascomata, fusiform, hyaline, with a median septum, and gelatinous sheath ascospores (Tanaka et al. 2015). Species of *Periconia* are mostly endophytes, saprobes, and plant pathogens of herbaceous plants (Leukel 1948, Rao & Rao 1964, Ellis 1971, Markovskaja & Kačergius 2014, Voronin et al. 2021, Tian et al. 2024). *Periconia* has 238 records in Index Fungorum (2025). However, about 30 species of *Periconia* have been transferred to other genera (Schubert et al. 2007, Chlebicki 2008, Videira et al. 2017, Yin et al. 2020). There were 210 species accepted in the genus *Periconia* (Index Fungorum 2025), and 63 species have molecular data (Bao et al. 2025, He et al. 2025, Hongsanan et al. 2025, Sun et al. 2025b). In this study, we introduce two new host records for *Periconia* species (*P. cortaderiae* and *P. wurfbainiae*), two new species (*P. poacearum* and *P. todei*) based on morphology and molecular data, together with descriptions and illustrations (Figs. 50–53).

Periconia cortaderiae Thambug. & K.D. Hyde, Mycosphere 8 (4): 734 (2017)

Fig. 50

Index Fungorum number: IF553165, Facesoffungi number: FoF03226

Saprobic on dead grasses. Sexual morph: Undetermined. Asexual morph: Colony powdery, gregarious, effuse, black. *Mycelium* is composed of cottony, branched hyphae, forming dark clusters with conidia scattered on the host surface. *Conidiophores* 280–520 µm long × 6–10 µm wide ($\bar{x}$ = 450 × 8 µm, n = 15), macronematous, mononematous, single or rarely 2–3 together on stromata, erect, or bent, thick-walled, brown to dark brown, septate, smooth. *Conidiogenous cells* 7–14 × 4–6 µm ($\bar{x}$ = 11 × 5 µm, n = 15), terminal, integrated, cylindrical or subglobose, polyblastic with smooth, pale brown to brown. *Conidia* 5.8–9.5 × 5–8 µm ($\bar{x}$ = 7.5 × 6.5 µm, n = 35), solitary or catenate, oval to globose, echinulate, or verruculose, aseptate, brown to dark brown.

Culture characteristics – Conidia germinated within 48 h on PDA. 2 cm diam. after three weeks at 27 °C. Colony from above, dense, circular, surface smooth, brown at the edge, pale brown at the center; from below, yellow at the edge, dark brown at the center.

Material examined – China, Yunnan Province, Kunming, on the dead unidentified grass (Poaceae) found on the grassland, 13 May 2021, Y. Gao, GY60 (HKAS 132996), living culture KUNCC 25-19152.

Known hosts and distribution – on dead stems and leaves of *Cortaderia* sp. (Poaceae) in Thailand (Thambugala et al. 2017), on dead hanging branches of *Caragana arborescens* (Fabaceae) in China (Phookamsak et al. 2019), on dead leaves of *Musa* sp. (Musaceae) in Thailand (Samarakoon et al. 2021), on dying leafstalk of *Musa basjoo* (Musaceae) in Russia (Jayawardena et al. 2022), on the dead grass (Poaceae) in Yunnan Province, China (This study).

GenBank numbers – KUNCC 25-19152: ITS = PV608575, LSU = PV607429.

Notes – Phylogenetic analyses showed that our collection (KUNCC 25-19152) grouped within *Periconia cortaderiae* (MFLUCC 15-0451, MFLUCC 15-0453, MFLUCC 15-0457) with 100% ML and 1.00 PP support values (Fig. 49). A comparison of the ITS and LSU nucleotide base pairs indicates that our collection is identical to the type strain of *P. cortaderiae*, which is not significantly different. Our collection differs from *Periconia cortaderiae* (MFLUCC 15-0457, ex-type) has shorter conidiophores (280–520 × 6–10 µm, L/W = 50 vs. 400–800 × 4–9.4 µm, L/W = 89.5), *Conidiogenous cells* (7–14 × 4–6 µm, L/W = 2.1 vs. 5.7–9.5 × 4–6 µm, L/W = 1.5), conidia (5.8–9.5 × 5–8 µm, L/W = 1.2 vs. 4–7 × 4–6.6 µm, L/W = 1.0) (Thambugala et al. 2017). *Periconia* species exhibit morphological variability across different hosts and geographic regions, yet molecular data from informative genes can resolve their conspecificity (Phookamsak et al. 2019). Therefore, identify our collection as *P. cortaderiae*, and it is a new host record.

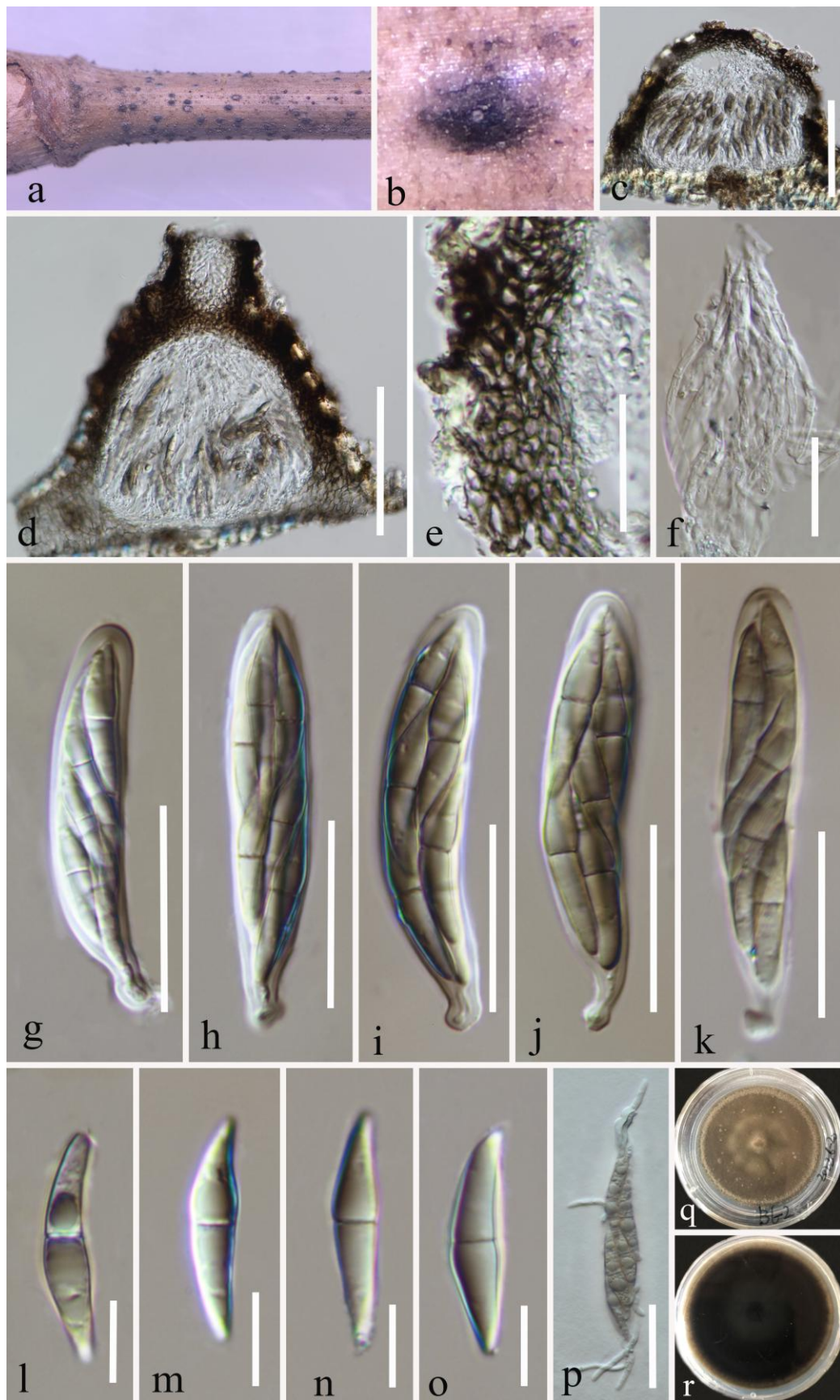


Figure 48 – *Occultibambusa jonesii* (HKAS 132954, a new host record). a, b Appearance of ascomata on the host substrate. c, d Sections of ascomata. e A section of peridium. f Pseudoparaphyses. g–k Asci. l–o Ascospores. p A germinated ascus. q, r Culture characters on PDA (q: above, r: below). Scale bars: c, d = 100 μ m, e–k, p = 30 μ m, l–o = 10 μ m.



Figure 49 – RAxML phylogram generated from a combined dataset of partial ITS, LSU, SSU, *tef1*- α , and *rpb2* DNA sequence analyses for *Periconia*. Related sequences are obtained following Yang et al. (2022a), Su et al. (2023), Liao et al. (2024), Shen et al. (2024). Ninety-two strains were

included in the combined analyses, which comprised 4,256 characters in the combined ITS, LSU, SSU, *tef1- α* , and *rpb2* alignment. *Massarina cisti* (CBS 266.62) and *Massarina eburnea* (CBS 473.64) were used as the outgroup taxa. The best-scoring RAXML tree with a final likelihood value of -22888.353300 is presented. The matrix contained 1,443 distinct alignment patterns, with 35.65% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.237376, C = 0.258378, G = 0.270535, T = 0.233711; substitution rates AC = 1.756347, AG = 4.178223, AT = 1.782255, CG = 1.248072, CT = 10.190747, GT = 1.000000. The tree topology of the ML analysis is similar to the Bayesian analysis. Bootstrap values for ML equal to or greater than 60% and PP values greater than 0.90 (rounding values to 2 decimal places) are labelled on the nodes. Strains of the newly described species are in orange, while type strains are in bold. (ITS: 532 bp, LSU: 841 bp, SSU: 1005 bp, *tef1- α* : 887 bp, *rpb2*: 991).

Periconia poacearum Y. Gao, H. Gui & K.D. Hyde, sp. nov.

Fig. 51

Index Fungorum number: IF903827; Facesoffungi number: FoF17701

Holotype – HKAS 126569

Etymology – The specific epithet is derived from the host family Poaceae, in which the holotype was found.

Saprobic on dead grasses. Sexual morph: Undetermined. Asexual morph: numerous, effuse, brown to dark brown, hairy colonies on the natural substrate. *Conidiophores* 80–110 μm long $\times$ 4.5–6 μm wide ($\bar{x}$ = 93.5 $\times$ 5.3 μm , n = 10), mononematous, macronematous, straight or slightly flexuous, unbranched, solitary, brown to dark brown, 2–3-septate, smooth to minutely verruculose, thick-walled. *Conidiogenous cells* terminal, integrated, subglobose, polyblastic, pale brown to brown, smooth to verruculose. *Conidia* 5.5–7 μm diam. ($\bar{x}$ = 6.3 μm , n = 35), solitary or catenate, oval to globose, brown to dark brown, aseptate, echinulate, or verruculose.

Culture characteristics – *Conidia* germinated within 48 h on PDA. 3 cm diam. after two weeks at 27°C. Colony from above, dense, circular, low convex, surface smooth, with edge entire, floccose, black at the edge, pale brown at the center; from below, black at the margin, gray at the center.

Material examined – China, Yunnan Province, Kunming, on the dead unidentified grass (Poaceae), 13 May 2021, Y. Gao, GY64A (HKAS 126569, holotype), ex-type living culture CGMCC 3.24545; *ibid.*, GY64B (HKAS 128758, isotype), ex-isotype living culture CGMCC 3.24546.

GenBank numbers – CGMCC 3.24545: ITS = PV608571, LSU = PV607425, SSU = PV607319, *tef1- α* = PV626454, *rpb2* = PV655496; CGMCC 3.24546: ITS = PV608572, LSU = PV607426, SSU = PV607320, *tef1- α* = PV626455, *rpb2* = PV655497.

Notes – In our phylogenetic analysis, *Periconia poacearum* (CGMCC 3.24545 and CGMCC 3.24546) grouped as a sister clade to *P. banksiae* (CBS 129526, ex-type) and *P. philadelphia* (CBS H-25197, holotype) (Fig. 49). Sequence comparison between *P. poacearum* (CGMCC 3.24545) and *P. banksiae* (CBS 129526) showed 8.72% (51/585 bp, with 20 gaps) base pair difference in the ITS region, 1.05% (9/862 bp, without gaps) base pair difference in the LSU region. Sequence comparison between *Periconia poacearum* (CGMCC 3.24545) and *P. philadelphia* (CBS H-25197) showed 5.93% (32/540 bp, with 13 gaps) base pair difference in the ITS region, 0.82% (7/856 bp, without gaps) base pair difference in the LSU region. Morphologically, our new species differs from *P. philadelphia* (CBS H-25197) in conidiophores (80–110 long μm vs. up to 500 long μm , up to 20-septate); conidia (5.5–7 μm vs. 6–11 μm , diam.) (Crous et al. 2023). Therefore, *Periconia poacearum* is introduced as a new species based on its distinct morphology and phylogenetic analyses of a combined ITS, LSU, SSU, *tef1- α* , and *rpb2* sequence data.

Periconia todei Y. Gao, H. Gui & K.D. Hyde, sp. nov.

Fig. 52

Index Fungorum number: IF903828; Facesoffungi number: FoF17702

Holotype – HKAS 128738

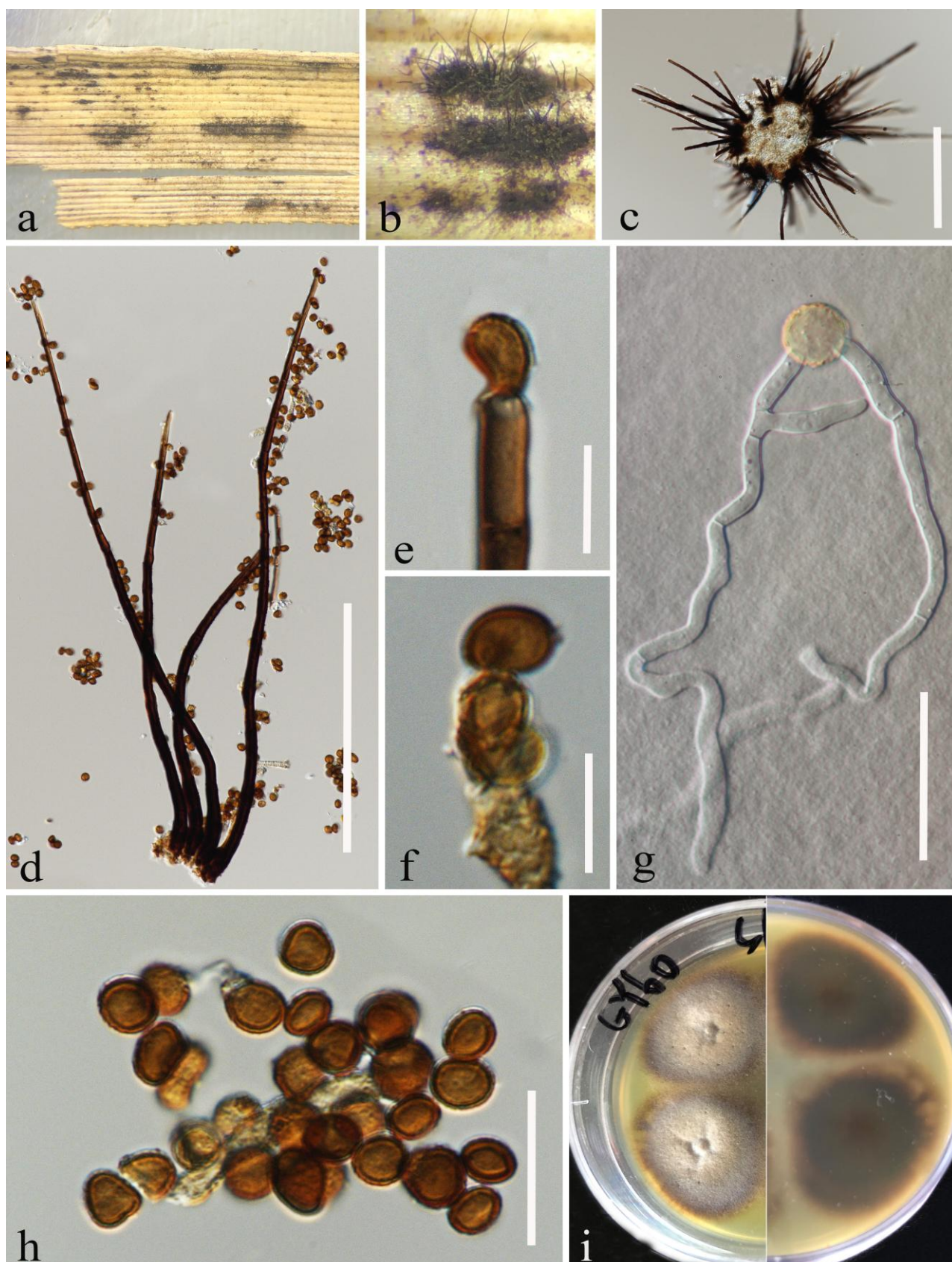


Figure 50 – *Periconia cortaderiae* (HKAS 132996, a new host record). a–c Colonies on the host substrate. c, d Conidiophores with spherical conidial heads. e, f Conidiogenous cells bearing conidia in short chains. g A germinated conidium. h Conidia. i Culture characters on PDA (left: above, right: below). Scale bars: c, d = 200 μ m, g = 30 μ m, h = 20 μ m, e, f = 10 μ m.

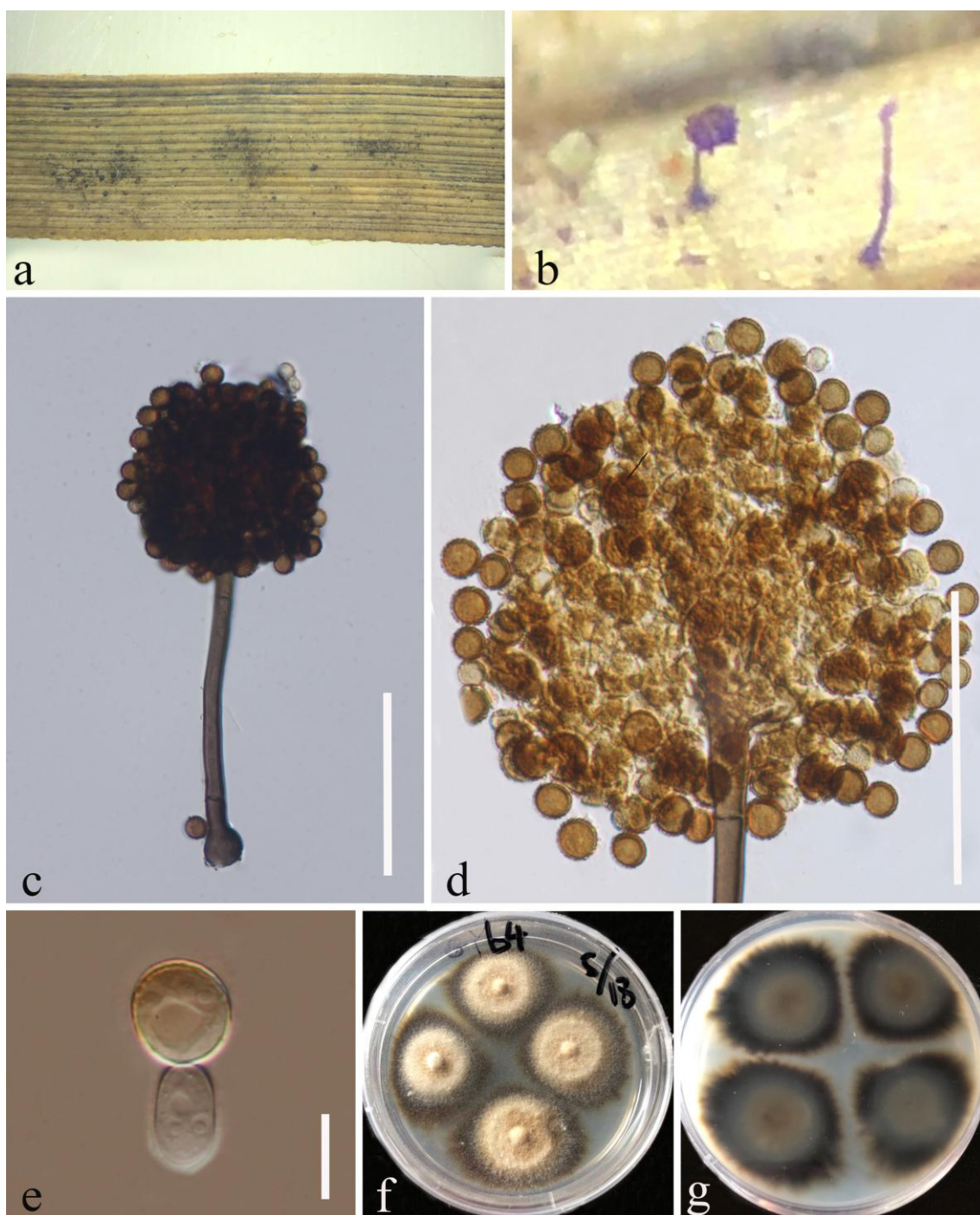


Figure 51 – *Periconia poacearum* (HKAS 126569, holotype). a, b Colonies on the host substrate. c Conidiophores with spherical conidial heads. d Apically branched conidiophores with conidia. e A germinated conidium. f, g Culture characters on PDA (f: above, g: below). Scale bars: c, d = 50 μ m, e = 10 μ m.

Etymology – The species epithet is in honor of Heinrich Julius Tode (1733–1797), a German mycologist who introduced the genus *Periconia*

Saprobic on dead grasses. Sexual morph: Undetermined. Asexual morph: numerous, effuse, brown to dark brown, hairy colonies on the natural substrate. *Conidiophores* 335–365 μ m long $\times$ 7.5–14 μ m wide ($\bar{x}$ = 380 $\times$ 10 μ m, n = 15), mononematous, macronematous, brown to dark brown, straight or slightly flexuous, unbranched, solitary, 2–4-septate, smooth to minutely verruculose, thick-walled. *Conidiogenous cells* terminal, integrated, subglobose, polyblastic with smooth to

verruculose, pale brown to brown. *Conidia* 6.2–9.5 μm diam. ($\bar{x}$ = 8 μm , n = 35), solitary or catenate, oval to globose, aseptate, echinulate, or verruculose, brown to dark brown.

Culture characteristics – *Conidia* germinated within 48 h on PDA. 6 cm diam. after two weeks at 27°C. Colony from above, dense, circular, surface smooth, with edge entire, black at the margin, white at the center; from below, black.

Material examined – China, Yunnan Province, Kunming, on the dead unidentified grass (Poaceae) found on the grassland, 1 October 2022, Y. Gao, MG11A (HKAS 128738, holotype), ex-type living culture CGMCC 3.24565; *ibid.*, MG11B (HKAS 128739, isotype), ex-isotype living culture CGMCC 3.24566.

GenBank numbers – CGMCC 3.24565: ITS = PV608573, LSU = PV607427, SSU = PV607321, *tef1*- α = PV626456; CGMCC 3.24566: ITS = PV608574, LSU = PV607428, SSU = PV607322, *tef1*- α = PV626457.

Notes – *Periconia todei* (CGMCC 3.24565, CGMCC 3.24566) is introduced as a new species based on its distinct morphology and phylogenetic analysis of combined ITS, LSU, SSU, *tef1*- α , and *rpb2* sequence data. Our collections grouped with *Periconia pseudodigitata* (CBS 139699, JCM 13164, JCM 13165) with support in ML and Bayesian analysis (95% ML, 100 PP, Fig. 49). A pairwise nucleotide comparison showed that *Periconia todei* (CGMCC 3.24565) differs from *P. pseudodigitata* (CBS 139699, ex-type) in 8/839 bp of LSU (0.95%, without gaps), 4/1022 bp of SSU (0.39%, without gaps), 22/521 bp of ITS (4.22%, with 3 gaps), 24/915 bp of *tef1*- α (2.62%, without gaps). Morphologically, the asexual morph of *Periconia todei* (CGMCC 3.24565) differs from that of *P. pseudodigitata* (CBS 139699) by its conidiophores (335–365 $\times$ 7.5–14 μm , L/W = 32.6, 2–4-septate vs. 250–450 $\times$ 8.5–15 μm , L/W = 29.8, 4–7-septate) (Tanaka et al. 2015). Therefore, *Periconia todei* is introduced as a new species on dead grasses from China.

Periconia wurfbainiae C.F. Liao, Doilom & K.D. Hyde, Diversity 16 (3, no. 141): 8 (2024)
Fig. 53

Index Fungorum number: IF851409; Facesoffungi number: FoF15277

Saprobic on dead branches. Sexual morph: *Ascomata* 150–220 high μm $\times$ 140–200 μm diam. ($\bar{x}$ = 200 $\times$ 175 μm , n = 10), pyriform or globose to subglobose, immersed to semi-immersed, scattered, brown or black, papillate stain the substrate purple, visible as black dots on the host surface. *Peridium* 10–23 μm wide ($\bar{x}$ = 14 μm , n = 30), composed of brown to dark brown cells of *textura angularis*. *Hamathecium* comprises 1.4–3 μm wide ($\bar{x}$ = 2.5 μm , n = 25), filiform, comprises dense, trabeculate, septate, branching pseudoparaphyses. *Asci* 50–80 $\times$ 8–11 μm ($\bar{x}$ = 72 $\times$ 10 μm , n = 25), 8-spored, bitunicate, fissitunicate, cylindric-clavate to clavate, apically rounded, short pedicellate, thick-walled, with an obscured ocular chamber. *Ascospores* 17–21 $\times$ 4–6 μm ($\bar{x}$ = 19.3 $\times$ 5 μm , n = 25), overlapping, fusiform with acute angular ends, 1-septate, constricted at the septum, hyaline, smooth, with guttulate, surrounded by a thin mucilaginous sheath. Asexual morph: Undetermined.

Culture characteristics – Ascospores germinated within 48 h on PDA. 6 cm diam. after two weeks at 27°C. Colony from above, dense, circular, low convex, surface smooth, with edge entire, floccose, white at the margin, pale yellow at the center; from below, white at the edge, black at the center.

Material examined – China, Yunnan Province, Xishuangbanna, on the dead branches of unidentified grass (Poaceae), 21 August 2021, Y. Gao, BG8A (HKAS 128732); *ibid.*, BG8B (HKAS 128733).

Known hosts and distribution – on dead stems of *Wurfbainia villosa* (Zingiberaceae) in China (Liao et al. 2024), on the dead branches of grass (Poaceae) found on the grassland in Yunnan Province, China (This study)

GenBank numbers – HKAS 128732: ITS = PV608576, LSU = PV607430; HKAS 128733: ITS = PV608577, LSU = PV607431.

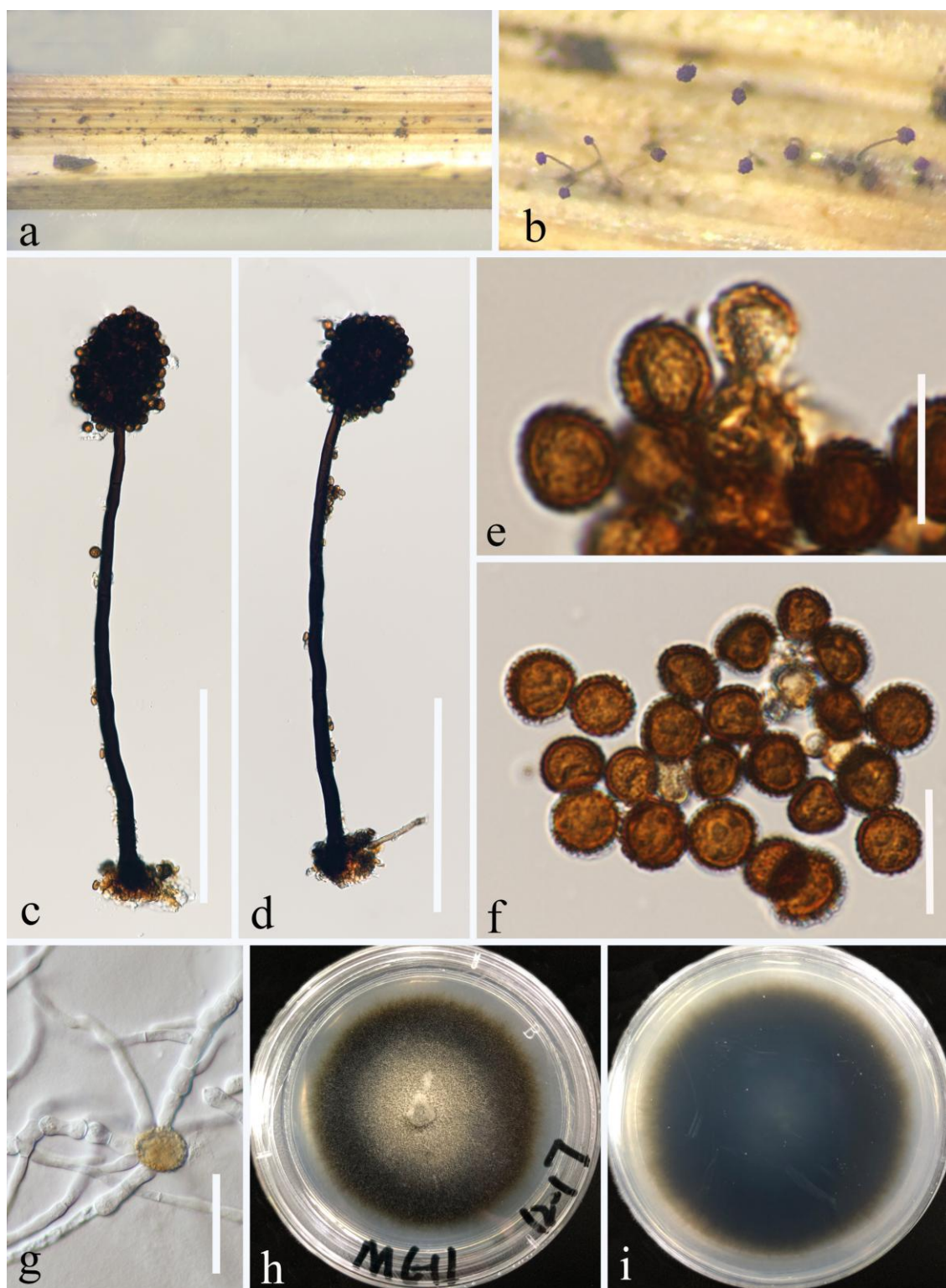


Figure 52 – *Periconia todei* (HKAS 128738, holotype). a, b Colonies on the host substrate. c, d Conidiophores with spherical conidial heads. e, f Conidia. g A germinated conidium. h, i Culture characters on PDA (h: above, i: below). Scale bars: c, d = 150 μ m, g = 20 μ m, f = 15 μ m, e = 10 μ m.

Notes – Phylogenetic analyses showed that our collections (HKAS 128732, HKAS 128733) grouped within *Periconia wurfbainiae* (ZHKUCC 23-0999, ZHKUCC 23-1000) with 100% ML and 1.00 PP support values (Fig. 49). A comparison of the ITS and LSU nucleotide base pair indicates that our collection is identical to *Periconia wurfbainiae* (ZHKUCC 23-0999, ex-type).

Based on morphological and phylogenetic evidence, we introduce our collection as a new host record of *Periconia wurfbainiae* on grass in China.



Figure 53 – *Periconia wurfbainiae* (HKAS 128732, a new host record). a, b Appearance of ascomata on the host substrate. c, d Sections of ascomata. e peridium. f Paraphyses. g–k Asci. l–q Ascospores. Scale bars: c, d = 100 μ m, e–k = 30 μ m, l–q = 10 μ m.

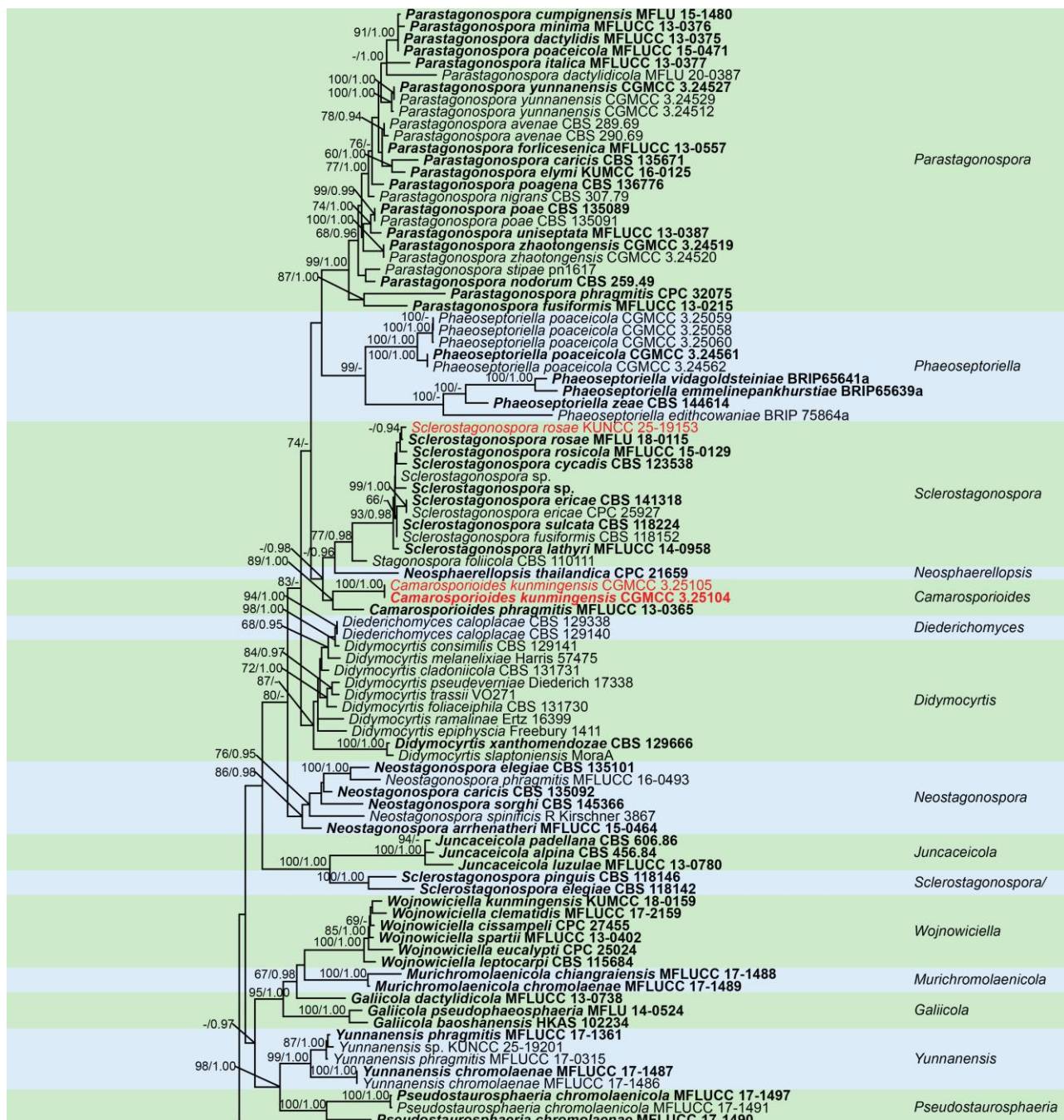


Figure 54 – RAXML phylogram generated from a combined dataset of partial ITS, LSU, SSU, *tef1*- α , and *rpb2* DNA sequence analyses for Phaeosphaeriaceae. Related sequences are obtained following Wanasinghe & Maharachchikumbura (2023). Four hundred and twelve strains were included in the combined analyses, which comprised 4,247 characters in the combined ITS, LSU, SSU, *tef1*- α , and *rpb2* alignment. *Quixadomyces hongheensis* (HKAS112346 and KUMCC 20-0215) were used as the outgroup taxa. The best-scoring RAXML tree with a final likelihood value of -76664.023527 is presented. The matrix contained 2,321 distinct alignment patterns, with 38.72% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.244462, C = 0.238009, G = 0.266349, T = 0.251180; substitution rates AC = 1.298553, AG = 4.274299, AT = 1.878641, CG = 0.774392, CT = 7.772803, GT = 1.000000. The tree topology of the ML analysis is similar to the Bayesian analysis. Bootstrap values for ML equal to or greater than 60% and PP values greater than 0.90 (rounding values to 2 decimal places) are labelled on the nodes. Strains of the newly described species are in orange, while type strains are in bold. (ITS: 561 bp, LSU: 835 bp, SSU: 1000 bp, *tef1*- α : 869 bp, *rpb2*: 981 bp).

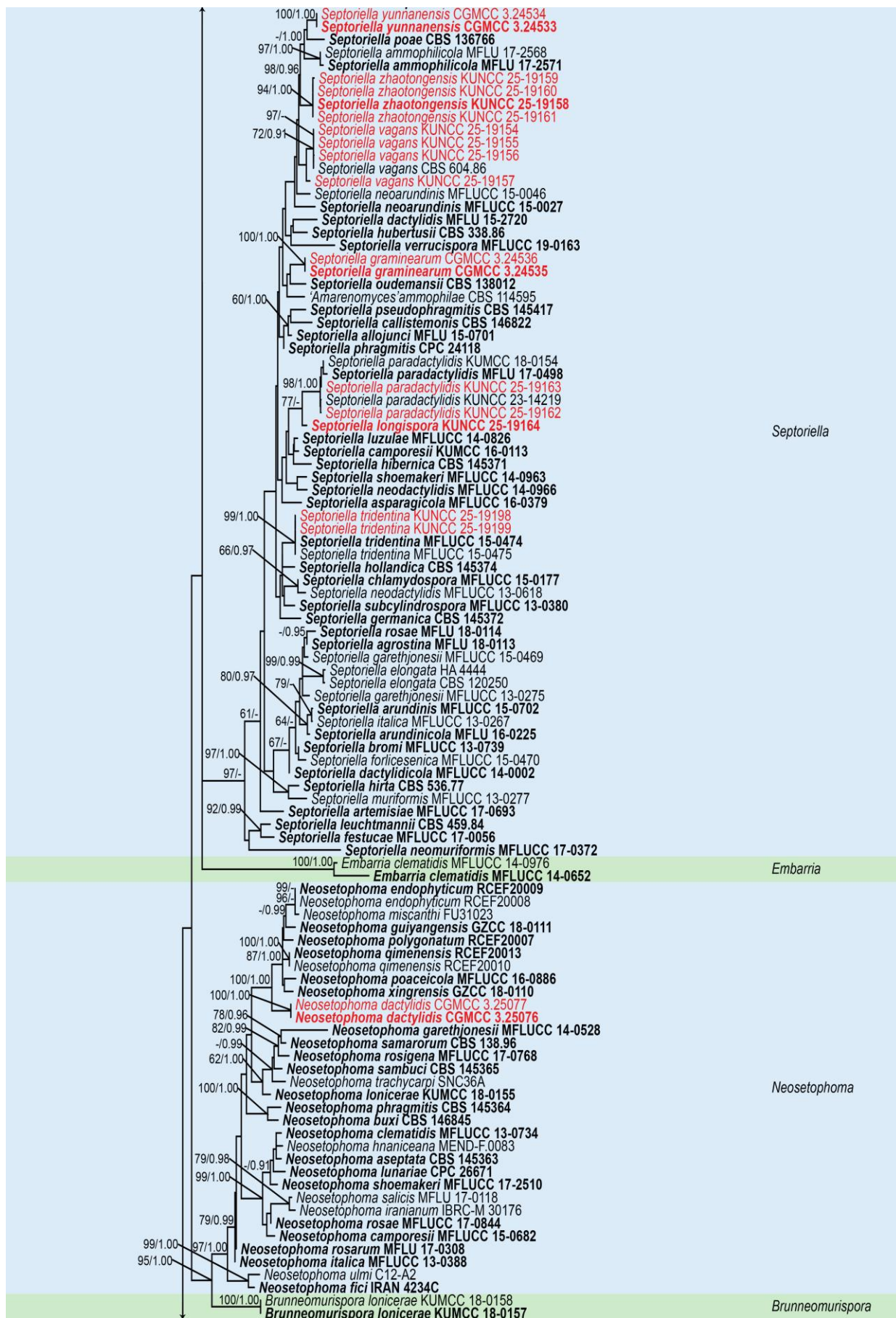


Figure 54 – Continued.

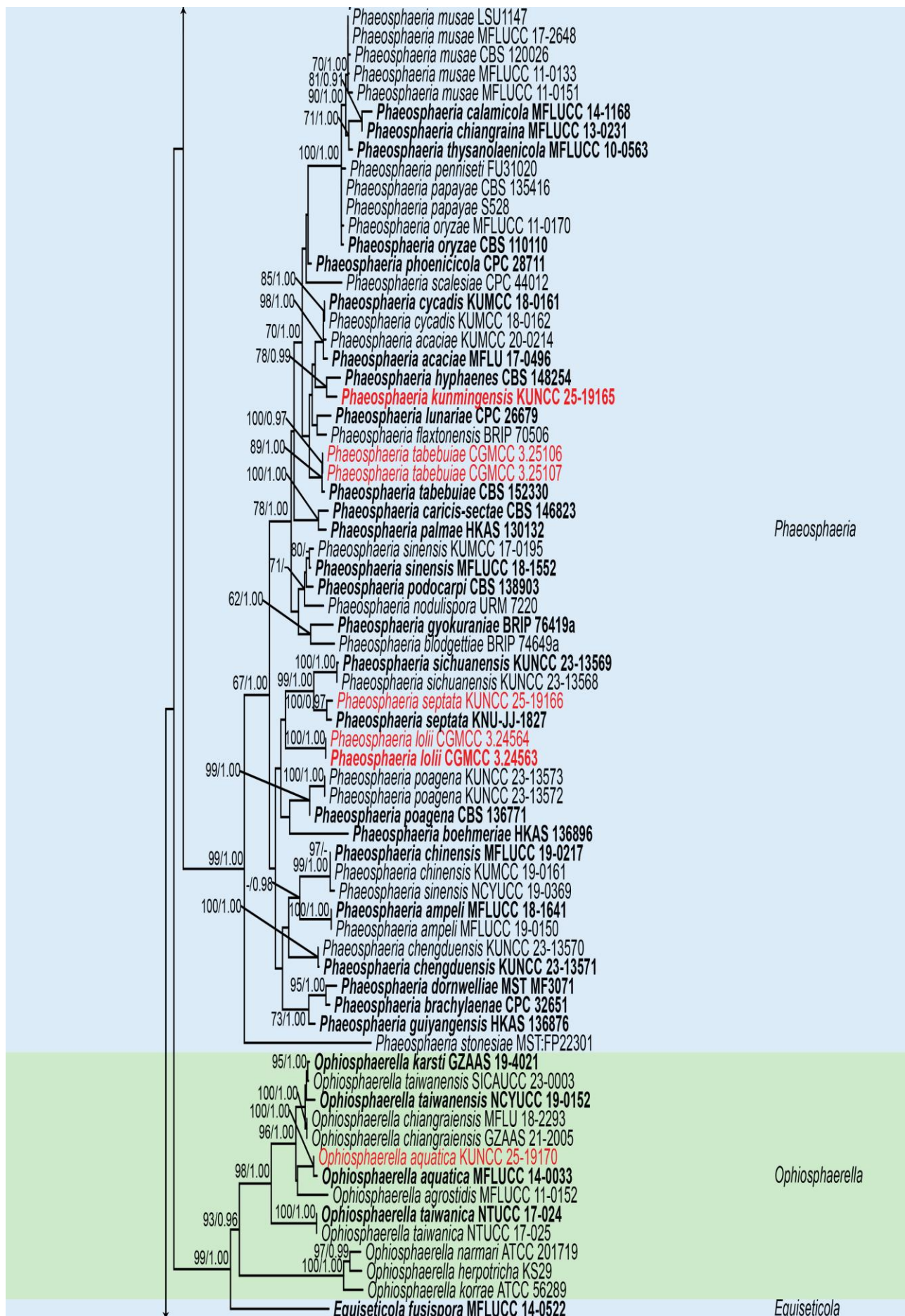


Figure 54 – Continued.

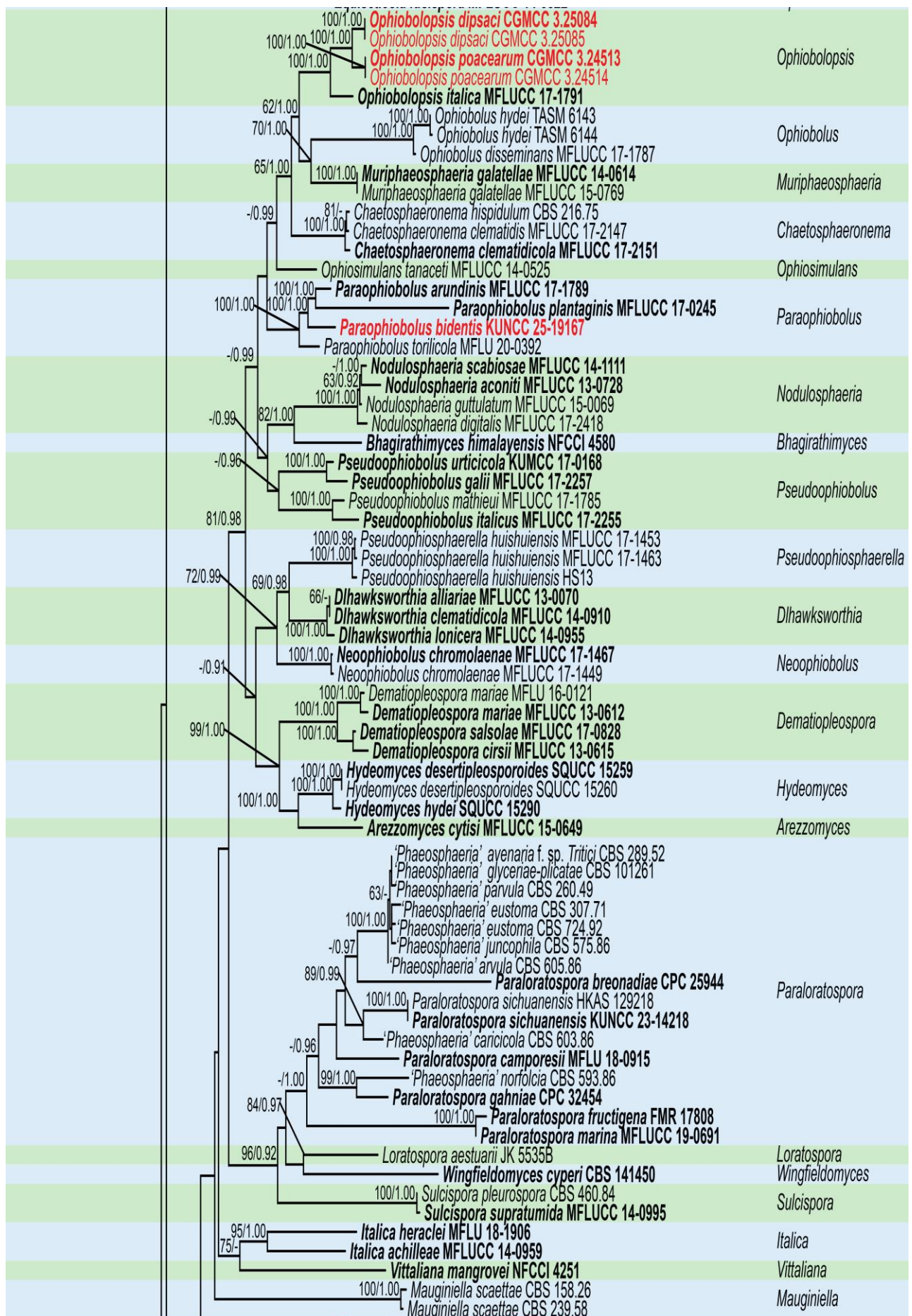


Figure 54 – Continued.

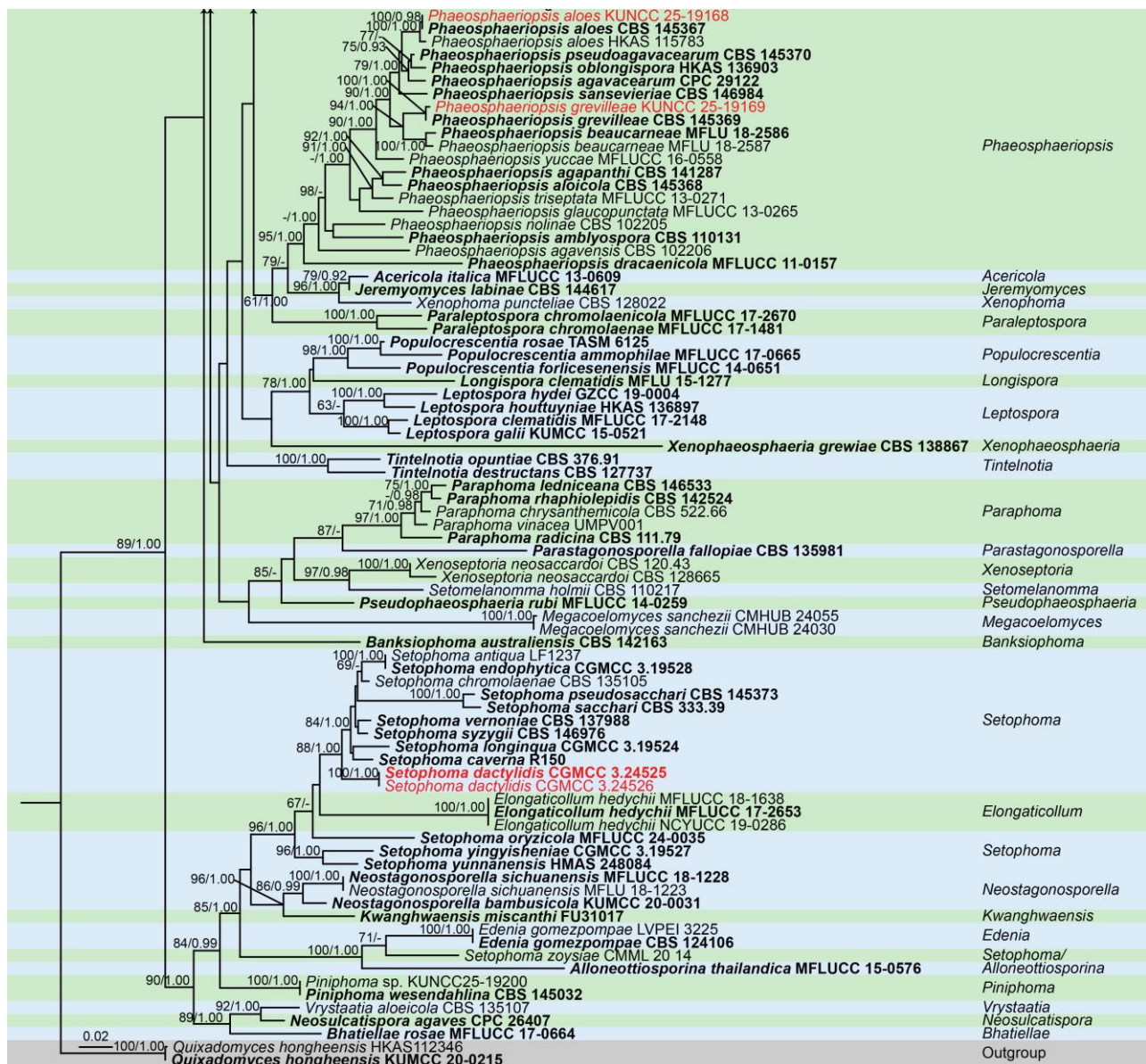


Figure 54 – Continued.

Phaeosphaeriaceae M.E. Barr, Mycologia 71: 948 (1979)

Notes – Phaeosphaeriaceae was first established by Barr (1979). It is large and significant within Pleosporales, with *Phaeosphaeria* as the type genus (Miyake 1909). The recent treatment of the Phaeosphaeriaceae was provided by Hyde et al. (2024a), which included 87 valid genera. Species in this family are highly diverse and have been reported as saprobes, plant pathogens, and endophytes on various plant hosts (Hyde et al. 2013, Hongsanan et al. 2020b). An updated phylogenetic tree based on combined ITS, LSU, SSU, *tef1-α*, and *rpb2* sequence data is presented in Fig. 54.

Camarosporioides W.J. Li & K.D. Hyde, Fungal Diversity 80: 83 (2016)

Notes – *Camarosporioides* was established by Hyde et al. (2016), designating *C. phragmitis* as its type species collected on dead stems of *Phragmites australis* (Poaceae) in Germany. The asexual morphs of *Camarosporioides* are characterized by immersed, separate or aggregated, yellowish to brown, obpyriform, pycnidial, unilocular conidiomata, single, circular, with hyaline periphyses, papillate ostiole, subcylindrical, hyaline, with obtuse apex, unbranched, septate periphyses. thick-walled, brown cells of *textura angularis* conidiomata wall. hyaline to pale brown, holoblastic, discrete, long lageniform, swollen at the base, determinate conidiogenous cells.

ellipsoidal to oval, obtuse at the apex, pale brown to brown, thick-walled, slightly truncate at base, with primary transverse septa, with a longitudinal septum, constricted at septa, verruculose conidia. In this study, we introduce a new species, *Camarosporioides kunmingensis*, together with descriptions and illustrations (Fig. 55).

Camarosporioides kunmingensis Y. Gao, H. Gui & K.D. Hyde, sp. nov.

Fig. 55

Index Fungorum number: IF903829, Faces of Fungi number: FoF17703

Holotype – HKAS 128749

Etymology – The specific epithet “kunmingensis” refers to the type location, Kunming City.

Saprobic on dead stems of grass. Sexual morph: *Conidiomata* 110–170 µm high × 100–150 µm diam. ($\bar{x}$ = 138 × 127 µm, n = 10), immersed, solitary, globose to subglobose or pyriform, yellowish to brown, uniloculate, papillate, with a central ostiole. *Conidiomata* wall 14–32 µm wide ($\bar{x}$ = 20 µm, n = 30), composed of 3–5 layers of pale brown cells of *textura angularis*. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 4–8 × 3.5–6.5 µm ($\bar{x}$ = 5.8 × 4.7 µm, n = 20), long lageniform, swollen at the base, discrete, determinate, formed from the cells lining the inner wall of the pycnidium, hyaline. *Conidia* 27–40 × 2.7–4.2 µm ($\bar{x}$ = 33 × 3.5 µm, n = 30), elongate fusiform with pointed ends, 3-septate, slightly curved, guttulate, hyaline to yellow, thick-walled. Asexual morph: Undetermined.

Culture characteristics – Colonies on PDA reaching 15 mm diam. after three weeks at 25°C, colonies from above, slightly raised, white, dense, circular with filamentous edges; from below, pale yellow at the center, white at the edges.

Material examined – China, Yunnan Province, Kunming, Shilin County, on decaying stems of unidentified grass (Poaceae), 11 July 2022, Y. Gao, XG8A (HKAS 128749, holotype), ex-type living culture CGMCC 3.25104; *ibid.*, XG8B (HKAS 128750, paratype), ex-paratype living culture CGMCC 3.25105.

GenBank numbers – CGMCC 3.25104: ITS = PV608578, LSU = PV607432, SSU = PV607323, *tef1-α* = PV626458, *rpb2* = PV655498; CGMCC 3.25105: ITS = PV608579, LSU = PV607433, SSU = PV607324, *tef1-α* = PV626459, *rpb2* = PV655499.

Notes – *Camarosporioides kunmingensis* is introduced as a new species based on its distinct morphology and phylogenetic analysis of combined ITS, LSU, SSU, *tef1-α*, and *rpb2* sequence data. *C. kunmingensis* (CGMCC 3.25104, CGMCC 3.25105) is sister to *C. phragmitis* (MFLUCC 13-0365, ex-type) with 89% ML and 1.00 PP statistical support (Fig. 54). A pairwise nucleotide comparison showed that *C. kunmingensis* differs from *C. phragmitis* (MFLUCC 13-0365) 35/558 in bp of ITS (6.27%, with 7 gaps), 13/833 bp of LSU (1.56%, with 2 gaps), 14/880 bp of *tef1-α* (1.6%, without gaps). *Camarosporioides phragmitis* was reported as saprobic on dead stems of *Phragmites australis* (Poaceae) in Germany (Hyde et al. 2016). *C. kunmingensis* differs from *C. phragmitis* (MFLUCC 13-0365) in conidiomata (110–170 × 100–150 µm, L/W = 1.1 vs. 160–177 × 143–170 µm, L/W = 1.0) and conidia (27–40 × 2.7–4.2 µm, L/W = 9.7, elongate fusiform with pointed at the end, 3-septate vs. 11–18 × 5–8 µm, L/W = 2.2, ellipsoidal to oval, with 1–3 primary transverse septa, occasionally 1–2 longitudinal septum) (Hyde et al. 2016). Therefore, based on the guidelines for new species boundaries delimitation (Jayawardena et al. 2021, Maharachchikumbura et al. 2021a), we introduce *Camarosporioides kunmingensis* as a novel species.

Neosetophoma Gruyter, Aveskamp & Verkley, Mycologia 102 (5): 1075 (2010)

Notes – *Neosetophoma* was established by de Gruyter et al. (2010) to accommodate *N. samarorum*. Species within *Neosetophoma* predominantly exhibit asexual reproductive forms, characterized by yellowish conidia that taper at one extremity. These fungi are recognized as pathogenic agents that cause leaf spot diseases across a range of host plants (Phookamsak et al. 2014). Twenty-nine species are known in *Neosetophoma* (Index Fungorum 2025). In this study, we introduce a new species (*Neosetophoma dactylidis*), together with descriptions and illustrations (Fig. 56).

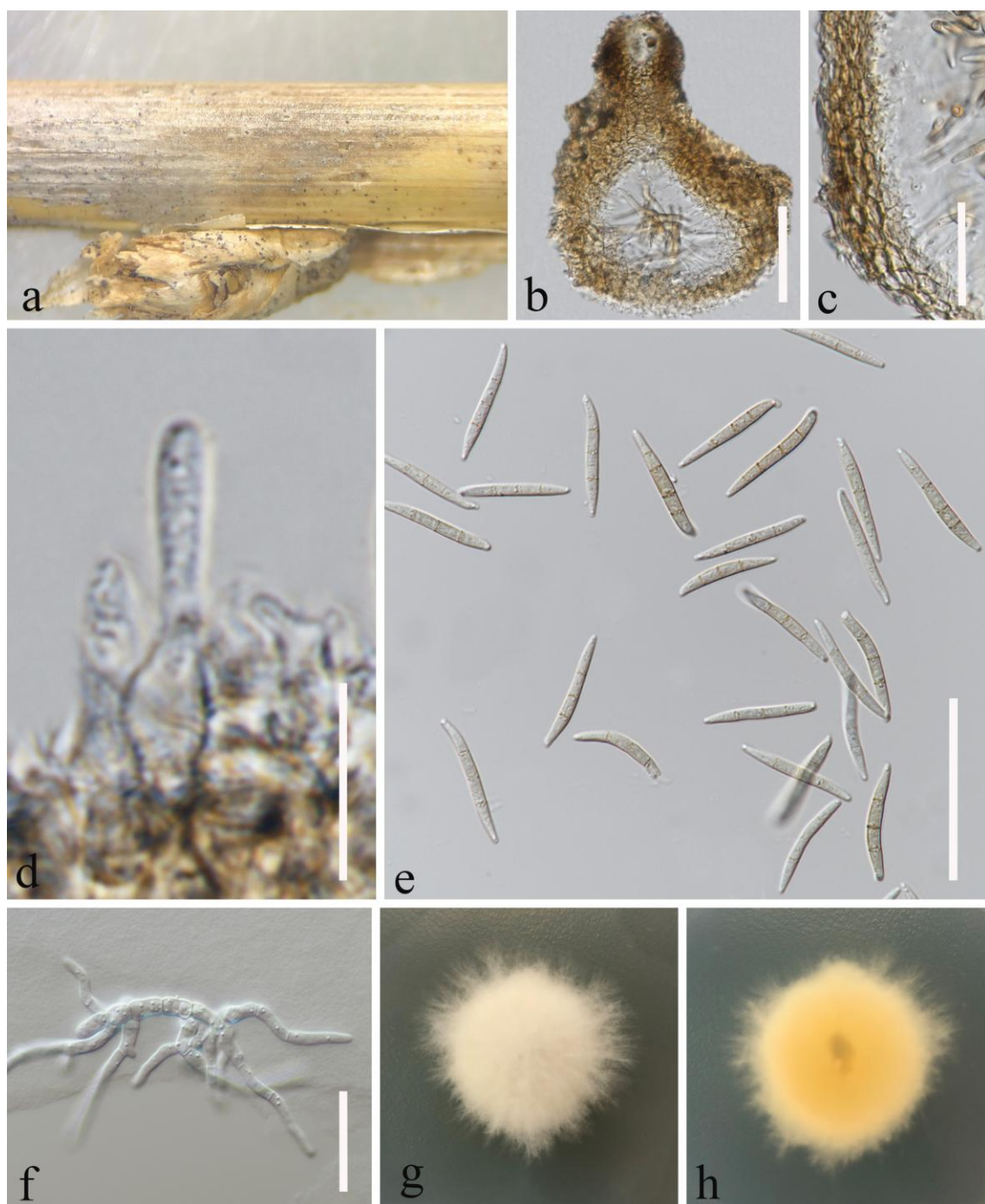


Figure 55 – *Camarosporioides kunmingensis* (HKAS 128749, holotype). a Appearance of black conidiomata on the host substrate. b Vertical section of conidioma. c Conidiomata wall. d Conidiogenous cells with developing conidia. e Conidia. f A germinated conidium. g, h Colony on PDA (g: above, h: below). Scale bars: b, e = 50 μ m, c, f = 30 μ m, d = 10 μ m.

Neosetophoma dactylidis Y. Gao, H. Gui & K.D. Hyde, sp. nov.

Fig. 56

Index Fungorum number: IF903830; Facesoffungi number: FoF17704

Holotype – HKAS 145994

Etymology – The specific epithet is derived from the genus *Dactylis* (Poaceae), which the holotype was found.

Saprobic on a dead leaf blade of *Dactylis glomerata*. Sexual morph: *Ascomata* 155–180 μ m diam. $\times$ 125–170 μ m high ($\bar{x}$ = 170 $\times$ 150 μ m, n = 10), immersed to erumpent, subglobose to globose, solitary, scattered, black, uni-loculate, papillate, with ostiolate. *Peridium* 8.5–16 μ m wide ($\bar{x}$ = 12 μ m, n = 30), composed of dark brown cells of *textura angularis*. *Hamathecium* comprises

1.5–3.5 μm wide ($\bar{x}$ = 2.5 μm , n = 30), consisting of numerous, dense, filamentous, broad, branched, septate, pseudoparaphyses. *Asci* 70–84 $\times$ 8.5–11.5 μm ($\bar{x}$ = 77 $\times$ 10 μm , n = 25), 8-spored, clavate to cylindrical-clavate, apically rounded, bitunicate, fissitunicate, short pedicellate, with an obscured ocular chamber. *Ascospores* 24.5–28 $\times$ 3.5–5 μm ($\bar{x}$ = 26.5 $\times$ 4.5 μm , n = 30), overlapping 1–2-seriate, fusiform, with acute ends, slightly curved, hyaline to yellow, mostly 5-septate, slightly constricted at the septum, smooth, with guttulate. Asexual morph: Undetermined.

Culture characteristics – *Asci* and *ascospores* germinated within 48 h on PDA. 6 cm diam. after three weeks at 27 °C. cultures from above, dense, circular, flat, surface smooth, white, with aerial mycelium, radially furrowed, fluffy, entire margins; from below, orange and radially furrowed at the center, black towards the edge, with white margin.

Material examined – China, Yunnan Province, Zhaotong grassland, on a dead leaf blade of *Dactylis glomerata* (Poaceae), 25 September 2022, Y. Gao, LG6A (HKAS 145994, holotype), ex-type living culture CGMCC 3.25076; *ibid.*, LG6B (HKAS 145998), living culture CGMCC 3.25077.

GenBank numbers – CGMCC 3.25076: ITS = PV608596, LSU = PV607450, *tef1- α* = PV626475; CGMCC 3.25077: ITS = PV608597, LSU = PV607451, *tef1- α* = PV626476.

Notes – Phylogenetically, our collections (CGMCC 3.25076, CGMCC 3.25077) reside in a clade of *Neosetophoma* and is closely related to *N. poaceicola* (MFLUCC 16-0886, ex-type) (100% ML and 1.00 PP) (Fig. 54). Both *Neosetophoma dactylidis* and *N. poaceicola* (MFLUCC 16-0886) share some different characteristics, such as *ascmata* (155–180 $\times$ 125–170 μm , L/W = 1.1 vs. 135–160 $\times$ 130–145 μm , L/W = 1.1), *Hamathecium* (1.5–3.5 μm wide vs. 0.9–1.8 μm wide), *ascospores* (24.5–28 $\times$ 3.5–5 μm , L/W = 6.2, 5-septate vs. 18.5–22.5 $\times$ 3.5–5 μm , L/W = 4.8, long, 1-septate) (Thambugala et al. 2017). A pairwise nucleotide comparison showed that *Neosetophoma dactylidis* differs from *N. poaceicola* (MFLUCC 16-0886) in 21/539 bp of ITS (3.9%, without gaps), 1/819 bp of LSU (0.12%, without gaps). Protein sequence data of *Neosetophoma poaceicola* were not provided. Therefore, based on the guidelines for new species boundaries delimitation (Jayawardena et al. 2021, Maharachchikumbura et al. 2021a), we introduce *Neosetophoma dactylidis* as a novel species.

Ophiobolopsis Phookamsak, Wanas. & K.D. Hyde, Fungal Diversity 87: 316 (2017)

Notes – *Ophiobolopsis* was established by Phookamsak et al. (2017) with *O. italica* as the type species, collected from dead and aerial stems of *Ononis spinosa* (Fabaceae) in Italy. In this study, we introduce two new species (*O. dipsaci* and *O. poacearum*), together with descriptions and illustrations (Figs. 57, 58).

Ophiobolopsis dipsaci Y. Gao, H. Gui & K.D. Hyde, sp. nov.

Fig. 57

Index Fungorum number: IF903831; Facesoffungi number: FoF17705

Holotype – HKAS 128807

Etymology – The specific epithet is derived from the genus of *Dipsacus* sp. (Caprifoliaceae), which the holotype was found.

Saprobic on dead stems of herbaceous plants. Sexual morph: *Ascomata* 415–480 μm diam. $\times$ 280–410 μm high ($\bar{x}$ = 450 $\times$ 360 μm , n = 15), globose or subglobose to ampulliform, semi-immersed to erumpent through the host epidermis, solitary, scattered, papillate, black, uni-loculate, glabrous, with ostiole. *Peridium* 56–117 μm wide ($\bar{x}$ = 87 μm , n = 30), composed of several cell layers of small to large, brown to dark brown pseudoparenchymatous cells, arranged in *textura angularis* to *textura prismatica*. *Hamathecium* comprises 2.5–5.2 μm wide ($\bar{x}$ = 3.5 μm , n = 30), consisting of numerous, septate, branched, dense, filamentous, pseudoparaphyses, narrower towards the apex, anastomosing, embedded in a hyaline gelatinous matrix. *Asci* 130–160 $\times$ 13–15 μm ($\bar{x}$ = 150 $\times$ 14 μm , n = 25), 8-spored, long cylindrical to cylindric-clavate, apically rounded, short pedicellate, curved or straight, bitunicate, fissitunicate, with an obscured ocular chamber. *Ascospores* 110–146 $\times$ 4–5.6 μm ($\bar{x}$ = 130 $\times$ 4.8 μm , n = 30), overlapping, fasciculate, scolecosporous, elongate cylindrical, tapering towards both ends, pale brown to yellowish brown, 10–13-septate, smooth, with guttulate. Asexual morph: Undetermined.

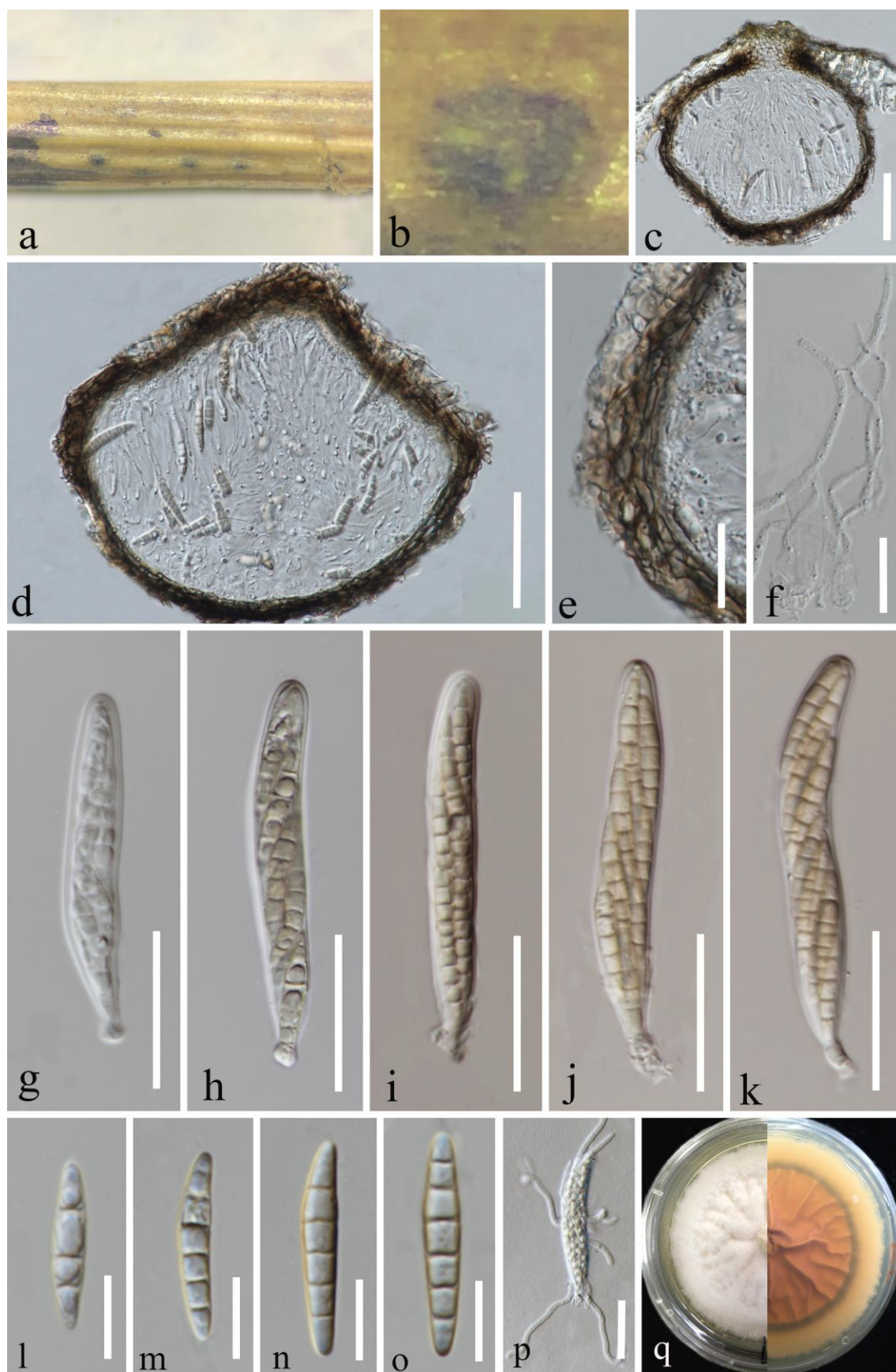


Figure 56 – *Neosetophoma dactylidis* (HKAS 145994, holotype). a, b Appearance of ascomata on the host substrate. c, d Sections of ascomata. e Peridium. f Pseudoparaphyses. g–k Asci. l–o Ascospores. p A germinated ascus. q Colony on PDA (left: above, right: below). Scale bars: c, d = 50 μ m, g–k, p = 30 μ m, e, f = 20 μ m, l–o = 10 μ m.

Culture characteristics – Asci and ascospores germinated within 48 h on PDA. 2.5 cm diam. after three weeks at 27°C. cultures from above, circular, dense, lobate edge, raised at the center, surface smooth, white at the margin, light brown at the center; from below, white at the edge, black at the center.

Material examined – China, Yunnan Province, Zhaotong grassland, on dead stems of *Dipsacus* sp. (Caprifoliaceae) on the grassland, 25 August 2022, Y. Gao, QG41CA (HKAS 128807, holotype), ex-type living culture CGMCC 3.25084; *ibid.*, QG41CB (HKAS 128808), living culture CGMCC 3.25085.

GenBank numbers – CGMCC 3.25084: ITS = PV608604, LSU = PV607458, SSU = PV607345, *tef1*- α = PV626483; CGMCC 3.25085: ITS = PV608605, LSU = PV607459, SSU = PV607346, *tef1*- α = PV626484.

Notes – In our phylogenetic analysis, *Ophiobolopsis dipsaci* (CGMCC 3.25084, CGMCC 3.25085) grouped with *O. poacearum* (CGMCC 3.24513, CGMCC 3.24514) with 100% ML and 1.00 PP support values (Fig. 54). A pairwise nucleotide comparison showed that *Ophiobolopsis dipsaci* differs from *O. poacearum* (CGMCC 3.24513, ex-type) in 7/577 bp of ITS (1.2%, without gaps), 0/830 bp of LSU (0.00%), 1/994 bp of SSU (0.1%, without gaps), 21/906 bp of *tef1*- α (2.32%, without gaps). The BLASTn search of the ITS sequence showed that the ITS sequence was close with 94.46% similarity to the type species *Ophiobolopsis italica* (MFLUCC 17-1791, ex-type). *Ophiobolopsis dipsaci* (CGMCC 3.25084) differs from *O. poacearum* (CGMCC 3.24513) and *O. italica* (MFLUCC 17-1791) in having large ascomata, wider peridium, and longer ascospores (Table 1). Therefore, *Ophiobolopsis dipsaci* is introduced as a new species based on its distinct morphology and phylogenetic position.

Ophiobolopsis poacearum Y. Gao, H. Gui & K.D. Hyde, sp. nov.

Fig. 58

Index Fungorum number: IF903832; Facesoffungi number: FoF17706

Holotype – HKAS 128801

Etymology – The specific epithet is derived from the host family Poaceae, in which the holotype was found.

Saprobic on dead stems of herbaceous plants. Sexual morph: *Ascomata* 240–290 μ m diam. $\times$ 155–200 μ m high ($\bar{x}$ = 267 $\times$ 178 μ m, *n* = 15), globose or subglobose, solitary, scattered, semi-immersed to erumpent through the host epidermis, black, uni-loculate, glabrous, papillate, with ostiolate. *Peridium* 9.5–28 μ m wide ($\bar{x}$ = 20 μ m, *n* = 30), composed of several cell layers of small to large, brown to dark brown pseudoparenchymatous cells, arranged in *textura angularis* to *textura prismatica*. *Hamathecium* comprises 2–4.2 μ m wide ($\bar{x}$ = 3 μ m, *n* = 30), consisting of numerous, septate, branched, dense, filamentous, pseudoparaphyses, anastomosing, embedded in a hyaline gelatinous matrix. *Asci* 100–120 $\times$ 12–15 μ m ($\bar{x}$ = 105 $\times$ 14 μ m, *n* = 25), 8-spored, bitunicate, fissitunicate, cylindrical to cylindric-clavate, apically rounded, short pedicellate, curved or straight, with an obscured ocular chamber. *Ascospores* 85–103 $\times$ 3–5.5 μ m ($\bar{x}$ = 91.5 $\times$ 4 μ m, *n* = 25), overlapping, fasciculate, scolecosporous, elongate cylindrical, with rounded ends, slightly tapered towards the lower cell, curved, pale brown to yellowish brown, 15–21-septate, swollen near the septa between the 4th and 5th, or 6th cells, smooth, with guttulate. Asexual morph: Undetermined.

Culture characteristics – Ascospores germinated within 48 h on PDA. 5 cm diam. after three weeks at 27°C. cultures from above, circular, dense, lobate edge, raised at the center, surface smooth, white; from below, white at the edge, black at the center, orange between the edge and center.

Material examined – China, Yunnan Province, Qujing grassland, on dead stems of unidentified herbaceous plants on the grassland, 27 August 2022, Y. Gao, QG24A (HKAS 128801, holotype), ex-type living culture CGMCC 3.24513; *ibid.*, QG24B (HKAS 128802), living culture CGMCC 3.24514.

GenBank numbers – CGMCC 3.24513: ITS = PV608606, LSU = PV607460, SSU = PV607347, *tef1*- α = PV626485; CGMCC 3.24514: ITS = PV608607, LSU = PV607461, SSU = PV607348, *tef1*- α = PV626486.



Figure 57 – *Ophiobolopsis dipsaci* (HKAS 128807, holotype). a Appearance of ascomata on the host substrate. b, c Sections of ascomata. d Peridium. e Pseudoparaphyses. f–j Asci. k–o Ascospores. p A germinated ascus. q Colony on PDA (left: above, right: below). Scale bars: b–d = 100 μm , f–o = 50 μm , p = 40 μm , e = 30 μm .

Notes – In the phylogenetic analyses of the present study, our collections (CGMCC 3.24513, CGMCC 3.24514) formed a sister clade to *Ophiobolopsis italica* (MFLUCC 17-1791, ex-type) with 100% ML and 1.00 PP support values (Fig. 54). A pairwise nucleotide comparison showed that *Ophiobolopsis poacearum* differs from *O. italica* (MFLUCC 17-1791) in 30/542 bp of ITS (5.54%, with 3 gaps), 4/830 bp of LSU (0.48%), 1/1014 bp of SSU (0.1%, without gaps), 27/906 bp of *tef1-α* (2.98%, without gaps). In addition, there are also significant differences in morphology (Table 1). Thus, we introduced *Ophiobolopsis poacearum* as a new species, based on phylogenetic and morphological evidence.

Ophiosphaerella Speg., Anales Mus. Nac. Hist. Nat. Buenos Aires Ser. 3, 12: 401 (1909)

Notes – *Ophiosphaerella* was established by Spegazzini (1909) with *O. graminicola* as the type species. The sexual morph of *Ophiosphaerella* is characterized by papillate ascomata, cylindrical, fissitunicate, narrower near the base, short furcate pedicel asci, filamentous, multi-septate, pale brown, without swollen cells or separating into part spores (Spegazzini 1909, Thambugala et al. 2017, Tennakoon et al. 2020). Most species of *Ophiosphaerella* are found as saprobes or pathogens worldwide on Cyperaceae or Poaceae (Phookamsak et al. 2014). Seventeen *Ophiosphaerella* species are listed in Index Fungorum (2025). In this study, we introduce a new host and geographical record for *Ophiosphaerella aquatica*, together with descriptions and illustrations (Fig. 59).

Ophiosphaerella aquatica Z.L. Luo, Hong Y. Su & K.D. Hyde, Fungal Diversity 75: 111 (2015)

Fig. 59

Index Fungorum number: IF634687; Facesoffungi number: FoF00951

Saprobic on a dead leaf blade of grasses. Sexual morph: *Ascomata* 280–360 µm diam. × 195–320 µm high ($\bar{x}$ = 315 × 280 µm, n = 10), immersed, subglobose to globose, with brown spots on the host surface, solitary, black, scattered, uni-loculate, with ostiolate. *Peridium* 12–28 µm wide ($\bar{x}$ = 19 µm, n = 30), composed of several layers of pseudoparenchymatous cells, the outer part comprising dark brown, occluded, thickened cells, fusing with the host, inner part comprising several layers of thin-walled, flattened, brown-walled cells of *textura angularis*. *Hamathecium* comprises 2–4 µm wide ($\bar{x}$ = 3 µm, n = 30), consisting of numerous, septate, constricted at the septum, branched, filamentous, narrower towards the apex, pseudoparaphyses, embedded in a mucilaginous matrix. *Asci* 110–170 × 8.5–10 µm ($\bar{x}$ = 140 × 9.5 µm, n = 25), 8-spored, fissitunicate, bitunicate, cylindrical to cylindric-clavate, apically rounded, with a short furcate pedicel, slightly curved, with an ocular chamber. *Ascospores* 95–155 × 2.3–3.5 µm ($\bar{x}$ = 135 × 3 µm, n = 25), overlapping, fasciculate, scolecosporous, filiform, pale yellow to brown, slightly narrowing towards the end cells, not obviously septate, straight or curved, lacking a mucilaginous sheath. Asexual morph: Undetermined.

Culture characteristics – Ascospores germinated within 48 h on PDA. 3 cm diam. after three weeks at 27°C. cultures from above, circular, dense, flat, raised, white; from below, white at the edge, pale brown at the center.

Material examined – China, Yunnan Province, Xishuangbanna, on a dead leaf blade of unidentified grass (Poaceae) on grassland, 23 May 2022, Y. Gao, BG7 (HKAS 132956), living culture KUNCC 25-19170.

Known hosts and distribution – on decaying wood submerged in a stream in Thailand (Ariyawansa et al. 2015b), on a dead leaf blade of grass (Poaceae) in Yunnan Province, China (This study).

GenBank numbers – KUNCC 25-19170: ITS = PV608611, LSU = PV607465, SSU = PV607352, *tef1-α* = PV626490, *rpb2* = PV655523.

Notes – The sexual form of *Ophiosphaerella aquatica* was isolated from decaying wood submerged in a stream and was introduced by Ariyawansa et al. (2015b). In this study, our collection (KUNCC 25-19170) from a sexually reproductive fungus formed a monophyletic clade

with *O. aquatica* (MFLUCC 14-0033, ex-type) with 100% ML and 1.00 PP statistical support (Fig. 54). A comparison of the ITS nucleotides between our collection (KUNCC 25-19170) and *O. aquatica* (MFLUCC 14-0033) revealed only one base pair difference. Sequence comparison of *tef1- α* revealed three base pair differences. Furthermore, the sexual morph is similar to that of *O. aquatica* (MFLUCC 14-0033) in terms of ascomata, asci, and ascospore characteristics (Ariyawansa et al. 2015b). Therefore, we introduce our taxon as a new host and new geographical record of *Phaeosphaeropsis aloes*.

Paraophiobolus Phookamsak, Wanas. & K.D. Hyde, Fungal Diversity 87: 318 (2017)

Notes – *Paraophiobolus* was established by Phookamsak et al. (2017) with *P. arundinis* as the type species. Three species were accepted in *Paraophiobolus* (Phookamsak et al. 2017, Brahmanage et al. 2020). In this study, we introduce a new species, *Paraophiobolus bidentis*, with descriptions and illustrations (Fig. 60).

Paraophiobolus bidentis Y. Gao, H. Gui & K.D. Hyde, sp. nov.

Fig. 60

Index Fungorum number: IF903833; Facesoffungi number: FoF17707

Holotype – HKAS 132978

Etymology – The specific epithet is derived from the genus of *Bidens pilosa* (Asteraceae), in which the holotype was found.

Saprobic on dead stems of *Bidens pilosa*. Sexual morph: *Ascomata* 210–235 μ m diam. $\times$ 120–180 μ m high ($\bar{x}$ = 222 $\times$ 155 μ m, n = 10), globose or subglobose, superficial, solitary, scattered, black, uni-loculate, glabrous, papillate, with ostiolate. *Peridium* 17.5–38 μ m wide ($\bar{x}$ = 25 μ m, n = 30), composed of brown to dark brown, thick-walled cells, arranged in a *textura angularis*, thicker towards the apex. *Hamathecium* consisting of 2–4 μ m wide ($\bar{x}$ = 2.5 μ m, n = 30), numerous, septate, branched, dense, filamentous, cellular pseudoparaphyses, anastomising, embedded in a hyaline gelatinous matrix. *Asci* 85–120 $\times$ 6.5–10.5 μ m ($\bar{x}$ = 104 $\times$ 8.5 μ m, n = 25), 8-spored, bitunicate, fissitunicate, cylindrical to cylindric-clavate, apically rounded, with short furcate pedicel, curved or straight, with an obscured ocular chamber. *Ascospores* 65–100 $\times$ 2.5–4 μ m ($\bar{x}$ = 83.5 $\times$ 2.5 μ m, n = 30), overlapping, fasciculate, scolecosporous, filiform, with rounded ends, tapered towards the lower cell, curved, pale yellow to yellowish brown, 5–7-septate, slightly constricted and swollen near the base of the 2nd or 3rd cell, smooth, with guttulate. Asexual morph: Undetermined.

Culture characteristics – Ascus and ascospores germinated within 48 h on PDA. 5 cm diam. after three weeks at 27°C. cultures from above, circular, dense, lobate edge, curled, raised at the center, floccose, hyaline mycelium with white spots; from below, yellow, producing pigmentation on PDA media.

Material examined – China, Yunnan Province, Qujing grassland, on dead stems of *Bidens pilosa* (Asteraceae) on the grassland, 27 August 2022, Y. Gao, QG16 (HKAS 132978, holotype), ex-type living culture KUNCC 25-19167.

GenBank numbers – KUNCC 25-19167: ITS = PV608608, LSU = PV607462, SSU = PV607349, *tef1- α* = PV626487, *rpb2* = PV655520.

Notes – Multigene phylogenetic analyses of combined ITS, LSU, SSU, *tef1- α* , and *rpb2* sequence data indicate that *Paraophiobolus bidentis* groups with the members of *Paraophiobolus* with robust statistical support (100% ML, 1.00 PP), *P. bidentis* (KUNCC 25-19167) is phylogenetically closely related to *P. arundinis* (MFLUCC 17-1789, ex-type) and *P. plantaginis* (MFLUCC 17-0245, ex-type) (Fig. 54). However, *P. bidentis* is different from *P. arundinis* (MFLUCC 17-1789) in having relatively small ascomata (210–235 $\times$ 120–180 μ m, L/W = 1.5 vs. 170–410 $\times$ 110–400 μ m, L/W = 1.1) and the number of ascospore septa (5–7 vs 12–16). *P. bidentis* is distinguished from *P. plantaginis* (MFLUCC 17-0245) in ascospore (65–100 $\times$ 2.5–4 μ m, L/W = 25.4 vs. 50–72 $\times$ 4–6 μ m, L/W = 12.2). A synopsis of the host and the morphological characteristics of *Paraophiobolus* species is given in Table 2. Thus, based on phylogeny and morphology, we introduce *Paraophiobolus bidentis* as a new species.



Figure 58 – *Ophiobolopsis poacearum* (HKAS 128801, holotype). a, b Appearance of ascomata on the host substrate. c Sections of ascomata. d Peridium. e Pseudoparaphyses. f–j Asci. k–n Ascospores. o A germinated ascospore. p Colony on PDA (p: above, q: below). Scale bars: c = 50 μm , d–o = 30 μm .

Table 1 Synopsis of *Ophiobolopsis dipsaci*, *O. poacearum*, and *O. italica* species with Sexual morphological features discussed in this study.

Species		<i>Ophiobolopsis dipsaci</i>	<i>O. italica</i>	<i>O. poacearum</i>
Ascomata	Size (µm)	415–480 × 280–410, L/W = 1.3	370–470 × 270–370, L/W = 1.3	240–290 × 155–200, L/W = 1.5
	Shape	Globose or subglobose to ampulliform, black	Subglobose to ampulliform, or irregular in shape, dark brown to black	Globose or subglobose, black
Peridium	Size (µm)	56–117	25–55	9.5–28
Asci	Size (µm)	130–160 × 13–15, L/W = 10.4	145–170 × 12–15, L/W = 11.7	100–120 × 12–15, L/W = 8.1
	Shape	8-spored, long cylindrical to cylindric-clavate	4-spored, cylindrical to cylindric-clavate	8-spored, cylindrical to cylindric-clavate
Ascospores	Size (µm)	110–146 × 4–5.6, L/W = 26.6	100–120 × 4–5, L/W = 24.4	85–103 × 3–5.5, L/W = 22.1
	Shape	Overlapping, elongate cylindrical, tapers towards both ends, 10–13-septate	Elongate cylindrical, with rounded ends, slightly tapered towards the lower cell, curved, 9(–12)-septate	Overlapping, elongate cylindrical, with rounded ends, slightly tapered towards the lower cell, curved, 15–21-septate
Reference		This study	Phookamsak et al. (2017)	This study

Phaeosphaeria I. Miyake, Bot. Mag. (Tokyo) 23: 93 (1909)

Notes – *Phaeosphaeria* was established by Miyake (1909) with *P. oryzae* as the type species. *Phaeosphaeria* is widely recognized for its remarkable diversity, comprising a substantial number of documented species alongside many that remain undiscovered. Species within this genus have been identified across diverse ecosystems, ranging from terrestrial to freshwater habitats (Hongsanan et al. 2020a, Magaña-Dueñas et al. 2021). These fungi demonstrate a high degree of adaptability, thriving across various climatic conditions and substrates, enabling their widespread distribution in both temperate and tropical zones. Among the species in this genus, some function as saprophytes, contributing to essential ecological processes such as decomposition and nutrient recycling. They are frequently found in association with decomposing plant matter, dead wood, or monocotyledonous organic residues. Conversely, certain species of *Phaeosphaeria* are known to act as plant pathogens, infecting a variety of hosts, including agricultural crops and forest trees (Phookamsak et al. 2014, Hongsanan et al. 2020a, Wanasinghe & Maharachchikumbura 2023). There were 234 epithets listed in *Phaeosphaeria* and 199 species accepted in the genus (Index Fungorum 2025), and 42 species have molecular data (Sun et al. 2025a, Yang et al. 2025). In this study, we introduce four new species, *Phaeosphaeria kunmingensis*, *P. lolii*, *P. poacearum*, and *P. yunnanensis*, based on morphology and molecular data, and provide descriptions and illustrations (Figs. 61–64).

Phaeosphaeria kunmingensis Y. Gao, H. Gui & K.D. Hyde, sp. nov.

Fig. 61

Index Fungorum number: IF903834, Faces of Fungi number: FoF17708

Holotype – HKAS 135326

Etymology – The specific epithet “kunmingensis” refers to the type locality, Kunming City.



Figure 59 – *Ophiosphaerella aquatica* (HKAS 132956, a new host and a new geographical record). a–c Appearance of ascomata on the host substrate. d A section of an ascoma. e Peridium. f Pseudoparaphyses. g–k Asci. l–o Ascospores. p Germinated ascospores. q Ccolony on PDA (left: above, right: below). Scale bars: d = 100 μm, e–p = 30 μm.



Figure 60 – *Paraophiobolus bidentis* (HKAS 132978, holotype). a, b Appearance of ascomata on the host substrate. c, d Sections of ascomata. e Peridium. f Pseudoparaphyses. g–k Asci. l–p Ascospores. q A germinated ascus. r Colony on PDA (r: above, s: below). Scale bars: c = 100 μ m, d = 50 μ m, e, g–q = 30 μ m, f = 20 μ m.

Table 2 Synopsis of *Paraophiobolus* species discussed in this study.

Species	Hosts	Ascomata (µm)	Asci (µm)	Ascospores (µm)	Reference
<i>P. arundinis</i>	<i>Arundo pliniana</i>	170–410 × 110–400, L/W = 1.1	75–110 × 7–12, L/W = 9.7	70–85 × 2.5–3, L/W = 28.2, 12(–16)-septate	Phookamsak et al. (2017)
<i>P. bidentis</i>	<i>Bidens pilosa</i>	210–235 × 120–180, L/W = 1.5	84.5–117 × 6.5–10.5, L/W = 11.9	65–100 × 2.5–4, L/W = 25.4, 5–7-septate	In this study
<i>P. plantaginis</i>	<i>Plantago</i> sp.	145–205 × 135–220, L/W = 1	69–124 × 7.4–9.5, L/W = 11.4	50–72 × 4–6, L/W = 12.2, 5–8-septate	Hyde et al. (2017)
<i>P. torilicola</i>	<i>Torilis arvensis</i>	100–110 × 102–106, L/W = 1	45–100 × 4.5–5, L/W = 15.3	40–60 × 1–2, L/W = 33.3, 11–13-septate	Brahmanage et al. (2020)

Saprobic on a dead blade of grass. Sexual morph: *Conidiomata* 90–100 µm high × 80–85 µm diam. ($\bar{x}$ = 95 × 83 µm, n = 10), globose to subglobose, solitary, brown to black, immersed to erumpent, with black dots on the host surface, unilocular, papillate, with a central ostiole. *Conidiomata* wall 8–17 µm wide ($\bar{x}$ = 12.5 µm, n = 25), consist of thin-walled cells arranged in a *textura angularis* pattern, composed of brown to dark brown cells. Conidiophores reduced to conidiogenous cells. *Conidiogenous cells* 3.5–6.5 µm diam. ($\bar{x}$ = 4.5 µm, n = 30), globose to subglobose, hyaline, arising from the inner layer of the pycnidium wall. *Conidia* 15–20 × 3.5–5 µm ($\bar{x}$ = 17 × 4.2 µm, n = 25), fusiform to cylindrical, obtuse at apex and base, mostly 3-septate, hyaline to pale brown, guttulate. Asexual morph: Undetermined.

Culture characteristics – Colonies on PDA reaching 15 mm diam. after three weeks at 25°C, colonies from above, irregular, dense, floccose and velvety, slightly raised with fimbriate margin, white-grey; from below, dark grey.

Material examined – China, Yunnan Province, Kunming, on a dead leaf blade of unidentified grass (Poaceae), 13 May 2021, Y. Gao, GY61 (HKAS 135326, holotype), living culture KUNCC 25-19165.

GenBank numbers – KUNCC 25-19165: ITS = PV608598, LSU = PV607452, SSU = PV607339, *tef1-α* = PV626477, *rpb2* = PV655514.

Notes – Our phylogenetic analysis shows *Phaeosphaeria kunmingensis* (KUNCC 25-19165) is closely related to *P. hyphaenes* (CBS 148254, ex-type) with 78% ML and 0.99 PP statistical support (Fig. 54). A pairwise nucleotide comparison showed that *P. kunmingensis* differs from *P. hyphaenes* (CBS 148254) in 12/509 bp of ITS (2.36%, without gaps), 28/837 bp of *rpb2* (3.35%, without gaps). *P. hyphaenes* was introduced by Crous et al. (2022b) on leaves of *Hyphaene* sp. (Arecaceae) in South Africa. *P. kunmingensis* differs from *P. hyphaenes* (CBS 148254) in its conidiomata (90–100 × 80–85 µm, L/W = 1.2 vs. 150–300 × 150–300 µm, L/W = 1), conidia (15–20 × 3.5–5 µm, L/W = 4.1, 3-septate vs. 7–13 × 2.5–3 µm, L/W = 3.6, 1–3-septate). Therefore, based on the guidelines for new species boundary delimitation (Jayawardena et al. 2021, Maharachchikumbura et al. 2021a), we introduce *Phaeosphaeria kunmingensis* as a novel taxon.

Phaeosphaeria lolii Y. Gao, H. Gui & K.D. Hyde, sp. nov.

Fig. 62

Index Fungorum number: IF903835; Facesoffungi number: FoF17709

Holotype – HKAS 128743

Etymology – The specific epithet is derived from the genus of *Lolium perenne* (Poaceae), in which the holotype was collected.

Saprobic on a dead stem of grass. Sexual morph: *Ascomata* 95–115 µm diam. × 85–100 µm high ($\bar{x}$ = 105 × 90 µm, n = 10), immersed, subglobose to globose, solitary, scattered, black, uniloculate, with ostiole. *Peridium* 8.5–21.5 µm wide ($\bar{x}$ = 15 µm, n = 20), composed of 2–4 layers of brown cells of *textura angularis*. *Hamathecium* consisting of 1.5–3.5 µm wide ($\bar{x}$ = 2.5 µm, n = 30), numerous, septate, branched, dense, filamentous, pseudoparaphyses, embedded in a gelatinous matrix. *Asci* 70–90 × 14.5–19 µm ($\bar{x}$ = 82 × 16.5 µm, n = 20), 8-spored, clavate to cylindrical-clavate, apically rounded, short pedicellate, slightly curved, bitunicate, fissitunicate, with an

obscured ocular chamber. *Ascospores* 23–30 × 6–9 µm ($\bar{x}$ = 26 × 7.3 µm, n = 25), overlapping 1–2-seriate, fusiform, with acute ends, mostly 3–5-septate, yellow to brown, slightly constricted at the septum, smooth, with guttulate. Asexual morph: Undetermined.

Culture characteristics – Ascospores germinated within 48 h on PDA. 2 cm diam. after three weeks at 27°C. cultures from above, circular, dense, flat, lobate edge, raised at the center, grayish white; from below, white at the edge, black at the center, pale yellow between the edge and center.

Material examined – China, Yunnan Province, Zhaotong grassland, on a dead stem of *Lolium perenne* (Poaceae) on the grassland, 25 September 2022, Y. Gao, LG12A (HKAS 128743, holotype), ex-type living culture CGMCC 3.24563; *ibid.*, LG12B (HKAS 128744), living culture CGMCC 3.24564.

GenBank numbers – CGMCC 3.24563: ITS = PV608602, LSU = PV607456, SSU = PV607343, *tefl*-α = PV626481, *rpb2* = PV655518; CGMCC 3.24564: ITS = PV608603, LSU = PV607457, SSU = PV607344, *tefl*-α = PV626482, *rpb2* = PV655519.

Notes – Based on the phylogenetic analysis of multiple genes, *Phaeosphaeria lolii* (CGMCC 3.24563 and CGMCC 3.24564) shares a relationship with *P. septata* (KNU-JJ-1827, type). The sexual morphology of *P. septata* was not provided by Das et al. (2021). It cannot be compared with *P. lolii*. But a pairwise nucleotide comparison showed that *Phaeosphaeria lolii* differs from *P. septata* in 15/520 bp of ITS (2.88%, without gaps), 4/825 bp of LSU (0.48%, without gaps), 1/1008 bp of SSU (0.1%, without gaps), 16/892 bp of *tefl*-α (1.79%, without gaps), 120/1029 bp of *rpb2* (11.66%, without gaps). Thus, we introduced our collection as a new species based on phylogenetic and morphological evidence.

Phaeosphaeria septata (K. Das, S.Y. Lee & H.Y. Jung) Y.R. Sun, Yong Wang bis & K.D. Hyde, Fungal Diversity 131: 188 (2025) Fig. 63

Index Fungorum number: IF903095; Facesoffungi number: FoF16442

Saprobic on a dead blade of grass. Sexual morph: *Conidiomata* 120–165 µm diam. × 80–150 µm high. ($\bar{x}$ = 145 × 125 µm, n = 10), globose to subglobose, solitary, brown to black, semi-immersed, black dots on the host surface, unilocular, papillate, with a central ostiole. *Conidiomata wall* 9–20 µm wide ($\bar{x}$ = 12 µm, n = 35), composed of 1–3 layers of yellow to dark brown cells of *textura angularis*. Conidiophores reduced to conidiogenous cells. *Conidiogenous cells* 3.5–5.5 × 3–5 µm ($\bar{x}$ = 4.5 × 4 µm, n = 20), globose to subglobose, hyaline, arising from the inner layer of pycnidium wall. *Conidia* 8.5–12.5 × 2–4.5 µm ($\bar{x}$ = 10 × 3 µm, n = 25), ovoid to ellipsoid in shape, with a conically rounded apex and base, 0–1-septate, initially, the conidia are hyaline but they become pale brown to brown, the conidia are not constricted at the septa and have a smooth surface. Asexual morph: Undetermined.

Culture characteristics – Colonies on PDA reaching 15 mm diam. after three weeks at 25°C, colonies from above, irregular, dense, floccose and velvety, slightly raised, yellow-grey; from below, yellow at the margin, dark brown at the center.

Material examined – China, Yunnan Province, Kunming, on a dead leaf blade of unidentified grass (Poaceae), 13 May 2021, Y. Gao, GY62 (HKAS 145996), living culture KUNCC 25-19166.

Known hosts and distribution – Isolated from soil in Korea (Das et al. 2021), on a dead leaf blade of grass (Poaceae) in China (in this study).

GenBank numbers – KUNCC 25-19166: ITS = PV608601, LSU = PV607455, SSU = PV607342, *tefl*-α = PV626480, *rpb2* = PV655517.

Notes – *Didymocyrtis septata* was introduced by Das et al. (2021). Later, Sun et al. (2025a) transferred *Didymocyrtis septata* to the genus *Phaeosphaeria* and named *Phaeosphaeria septata*. According to our morphological analysis and multigene phylogenetic analyses of a combined ITS, LSU, SSU, *tefl*-α, and *rpb2* sequence data. Our collection (KUNCC 25-19166) was grouped within *P. septata* (KNU-JJ-1827, type) with 100% ML and 0.97 PP support values (Fig. 54). A pairwise nucleotide comparison showed that our strain differs from *P. septata* (KNU-JJ-1827) in 492/496 bp of ITS (0.81%, with 1 gap), 731/731 bp of LSU (0.00%). Our collection differs from *P. septata* (KNU-JJ-1827) in (morphology found in plant specimens vs. morphology found in the culture

medium), conidia ($8.5\text{--}12.5 \times 2\text{--}4.5 \mu\text{m}$, $L/W = 3.2$ vs. $7\text{--}9.5 \times 2\text{--}3 \mu\text{m}$, $L/W = 3.3$) (Das et al. 2021). Therefore, we introduce our collection as a new host and a geographical record on a dead leaf blade of grass in China, and provide SSU, *tef1- α* , and *rpb2* for *Phaeosphaeria septata*.

Phaeosphaeria tabebuiae Crous, Alfenas & R.F. Alfenas, Fungal Syst. Evol. 14: 442 (2024) Fig. 64

Index Fungorum number: IF856113; Facesoffungi number: FoF17746

Saprobic on a dead stem of grass. Sexual morph: *Ascomata* 91–116 μm high $\times$ 100–110 μm diam. ($\bar{x} = 107 \times 105 \mu\text{m}$, $n = 10$), immersed to erumpent, subglobose to globose, solitary, scattered, black, uni-loculate, with ostiolate. *Peridium* 9.5–21 μm wide ($\bar{x} = 15 \mu\text{m}$, $n = 30$), composed of dark brown cells of *textura angularis*. *Hamathecium* comprises 1.5–3 μm wide ($\bar{x} = 2.5 \mu\text{m}$, $n = 30$), consisting of numerous, branched, dense, filamentous, broad, septate, pseudoparaphyses. *Asci* 43.5–61 $\times$ 8–11 μm ($\bar{x} = 51 \times 9 \mu\text{m}$, $n = 30$), 8-spored, clavate to cylindrical-clavate, apically rounded, slightly curved, bitunicate, fissitunicate, short pedicellate, with an obscured ocular chamber. *Ascospores* 16.5–23 $\times$ 4–6.5 μm ($\bar{x} = 20 \times 5 \mu\text{m}$, $n = 30$), overlapping 1–2-seriate, fusiform, with acute ends, mostly 3-septate, yellow to brown, slightly constricted at the septum, smooth, with guttulate. Asexual morph: Undetermined.

Culture characteristics – Ascus and ascospores germinated within 48 h on PDA. 2 cm diam. after three weeks at 27°C. cultures from above, dense, circular, slightly raised, surface smooth, with even edge, white at the margin, green-grayish at the center; from below, white at the margin, brownish-yellow at the center.

Material examined – China, Yunnan Province, Kunming, on a dead stem of unidentified grass (Poaceae) on the grassland, 11 July 2022, Y. Gao, XG12A (HKAS 128751), living culture CGMCC 3.25106; *ibid.*, XG12B (HKAS 128752), living culture CGMCC 3.25107.

Known hosts and distribution – on a leaf of *Tabebuia* sp. (Bignoniaceae) in Brazil (Crous et al. 2024), on a dead stem of grass (Poaceae) in China (in study).

GenBank numbers – CGMCC 3.25106: ITS = PV608599, LSU = PV607453, SSU = PV607340, *tef1- α* = PV626478, *rpb2* = PV655515; CGMCC 3.25107: ITS = PV608600, LSU = PV607454, SSU = PV607341, *tef1- α* = PV626479, *rpb2* = PV655516.

Notes – In our phylogenetic analysis, our collections (CGMCC 3.25106 and CGMCC 3.25107) grouped with *Phaeosphaeria tabebuiae* (CBS 152330, ex-type) with 89% ML and 1.00 PP support values (Fig. 54). A pairwise nucleotide comparison showed that our collections not differ from *P. tabebuiae* (CBS 152330) in 510/512 bp of ITS (0.39%, without gap), 800/800 bp of LSU (0.00%), 860/862 bp of *tef1- α* (0.23%), 864/867 bp of *rpb2* (0.35%). Morphologically, the sexual morph is similar to *P. tabebuiae* (CBS 152330) in terms of its subglobose to globose, solitary ascomata, clavate to cylindrical-clavate, bitunicate, short pedicellate asci, and bi- to triseriate, fusiform, 3-septate, yellow to brown ascospores with similar size ($16.5\text{--}23 \times 4\text{--}6.5 \mu\text{m}$ vs. $19\text{--}25 \times 4\text{--}5 \mu\text{m}$) (Crous et al. 2024). Therefore, we introduce our collections as a new host and geographical record on a dead stem of grass in China.

Phaeosphaeriopsis M.P.S. Câmara, M.E. Palm & A.W. Ramaley, Mycol. Res. 107 (5): 519 (2003)

Notes – *Phaeosphaeriopsis* was established by Câmara et al. (2003) with *P. glaucopunctata* as the type species. The sexual morph of the genus is characterized by having immersed, globose to subglobose to pyriform, sub-epidermal ascomata, cylindric asci, punctate or verrucose, septate ascospores (Câmara et al. 2003, Phookamsak et al. 2014, Thambugala et al. 2014, Tibpromma et al. 2017, Al-Jaradi et al. 2020, Tennakoon et al. 2020, Crous et al. 2021). There are 18 *Phaeosphaeriopsis* species accepted in Index Fungorum (2025). In this study, we introduce two new records for *Phaeosphaeriopsis aloes* and *P. grevilleae*, with descriptions and illustrations (Figs. 65, 66).

Phaeosphaeriopsis aloes Crous & Y. Marín, Studies in Mycology 94: 61 (2019)

Fig. 65

Index Fungorum number: IF829642; Facesoffungi number: FoF09952

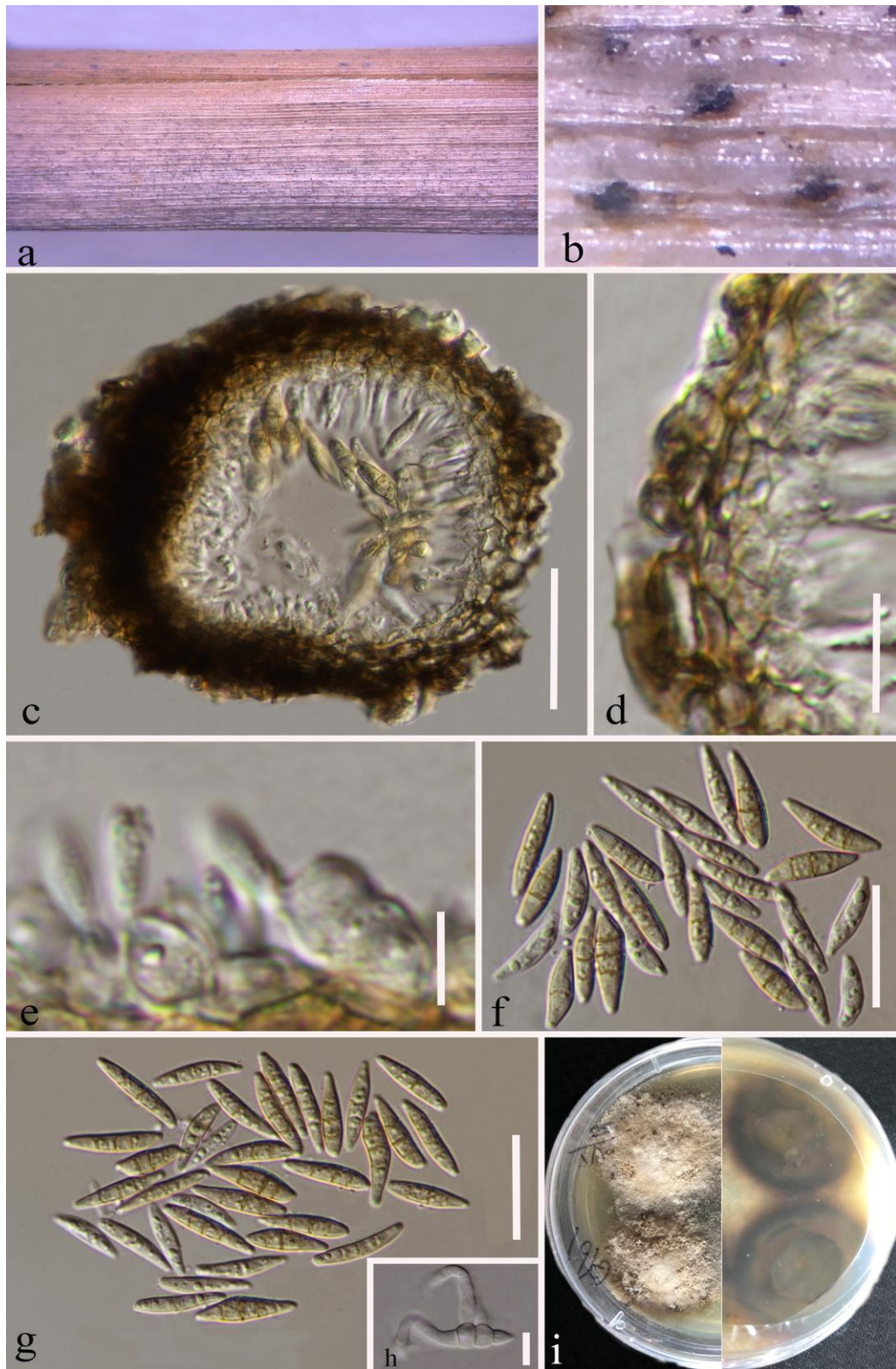


Figure 61 – *Phaeosphaeria kunmingensis* (HKAS 135326, holotype). a, b Conidiomata observed on the host substrate. c Vertical section of conidioma. d Conidiomata wall. e Conidiogenous cells with developed conidia. f, g Conidia. h A germinated conidium. i Colony on PDA (left: above, right: below). Scale bars: c = 30 μm , f, g = 20 μm , d, h = 15 μm , e = 5 μm .



Figure 62 – *Phaeosphaeria lolii* (HKAS 128743, holotype). a Appearance of ascomata on the host substrate. b A section of an ascoma. c Peridium. d Pseudoparaphyses. e–i Asci. j Ascospores. k A germinated ascospore. l, m Colony on PDA (l: above, m: below). Scale bars: b, d–i, k = 30 μ m, c, j = 20 μ m.

Saprobic on a dead stem of herbaceous plants. Sexual morph: *Ascomata* 125–265 μ m diam. $\times$ 120–160 μ m high ($\bar{x}$ = 205 $\times$ 140 μ m, n = 10), immersed, subglobose to globose, solitary, scattered, with black spots on the host surface, uni-loculate, with ostiolate. *Peridium* 11.5–24.5 μ m wide ($\bar{x}$ = 19 μ m, n = 30), thick-walled, of equal thickness, composed of dark brown to brown, thick-walled, pseudoparenchymatous cells of *textura angularis*. *Hamathecium* comprises 1.5–4.5 μ m wide ($\bar{x}$ = 3 μ m, n = 30), consisting of numerous, septate, constricted at the septum, branched, filamentous, pseudoparaphyses, embedded in a mucilaginous matrix. *Asci* 56–88 $\times$ 9–11 μ m ($\bar{x}$ = 75 $\times$ 9.5 μ m, n = 25), 8-spored, fissitunicate, bitunicate, cylindrical to cylindric-clavate, apically rounded, short pedicellate, slightly curved, with a well-developed ocular chamber. *Ascospores* 16–21 $\times$ 4–5.3 μ m ($\bar{x}$ = 18.5 $\times$ 4.5 μ m, n = 30), overlapping 1–2-seriate, oblong to cylindrical, slightly narrowing towards the end cells, mostly 5-septate, yellowish to light brown, constricted at the septa, straight or slightly curved, lacking a mucilaginous sheath. Asexual morph: Undetermined.

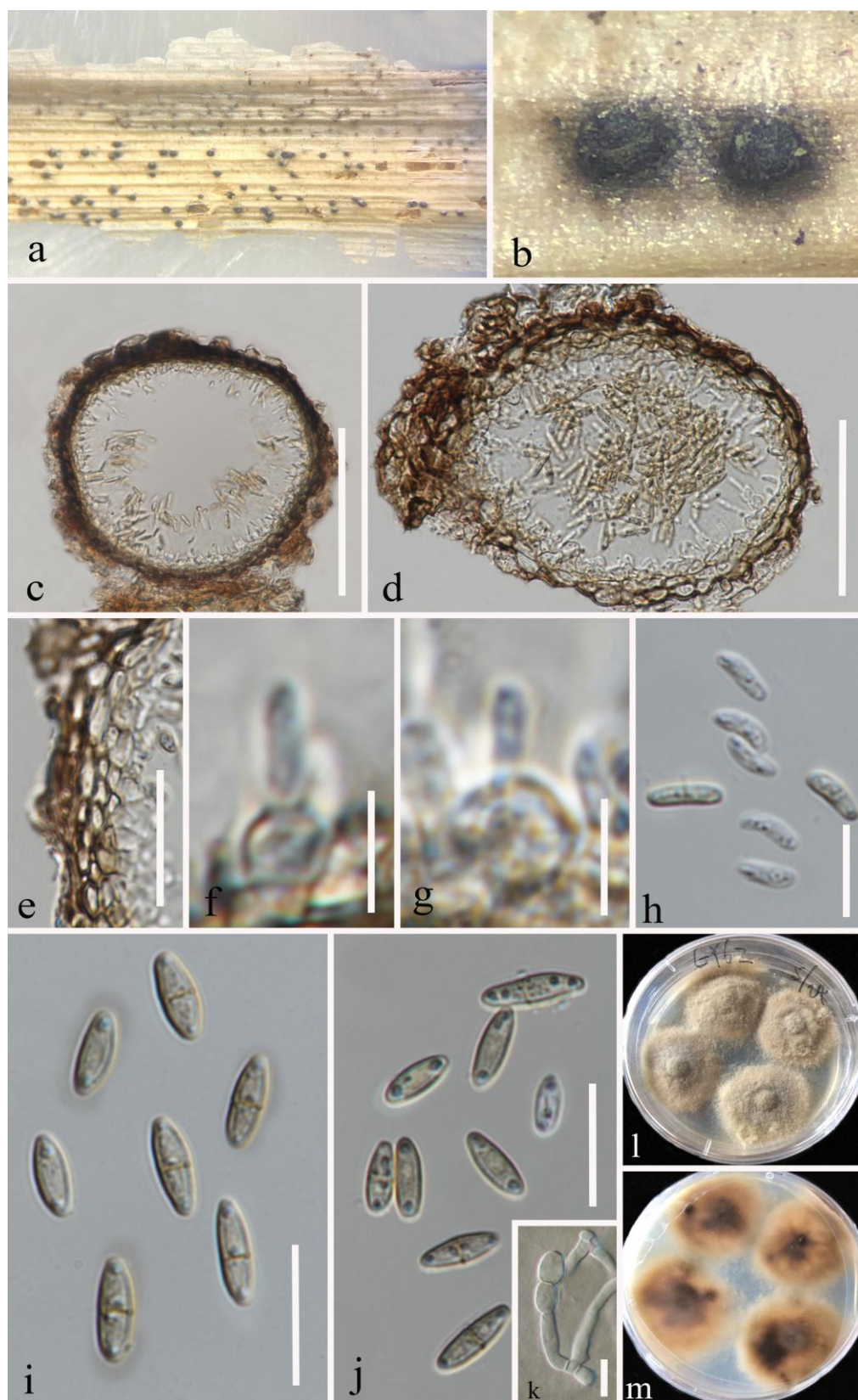


Figure 63 – *Phaeosphaeria septata* (HKAS 145996, a new host and a geographical record). a, b Conidiomata observed on the host. c, d Vertical sections of conidiomata. e Conidiomata wall. f, g Conidiogenous cells developing conidia. h–j Conidia. k A germinated conidium. l, m Colony on PDA (l: above, m: below). Scale bars: c = 100 μ m, d = 50 μ m, e = 20 μ m, i, j = 15 μ m, h, k = 10 μ m, f, g = 5 μ m.



Figure 64 – *Phaeosphaeria tabebuiae* (HKAS 128751, a new host and a geographical record). a, b Appearance of ascomata on the host substrate. c, d Sections of ascomata. e Peridium. f Pseudoparaphyses. g–k Asci. l–o Ascospores. p Germinated ascospores. q, r Colony on PDA (q: above, r: below). Scale bars: c, d = 50 μ m, e, g–k, p = 30 μ m, f = 20 μ m, l–o = 10 μ m.

Culture characteristics – Ascospores germinated within 48 h on PDA. 2 cm diam. after three weeks at 27°C. cultures from above, circular, dense, flat, raised at the center, white; from below, white at the edge, yellowish at the center.

Material examined – China, Yunnan Province, Kunming, on a dead stem of unidentified herbaceous plants on the grassland, 13 May 2021, Y. Gao, GY77 (HKAS 145997), living culture KUNCC 25-19168.

Known hosts and distribution – on leaves of *Aloe* sp. (Aloaceae) in the United States (Marin-Felix et al. 2019), on dead leaves of *Yucca elephantipes* (Asparagaceae) in China (Boonmee et al. 2021), on a dead stem of herbaceous plants in Yunnan Province, China (This study).

GenBank numbers – KUNCC 25-19168: ITS = PV608609, LSU = PV607463, SSU = PV607350, *tef1-α* = PV626488, *rpb2* = PV655521.

Notes – *Phaeosphaeriopsis aloes* was introduced as an asexual morph on leaves of *Aloe* sp. from the United States (Marin-Felix et al. 2019). Boonmee et al. (2021) provided the sexual form of *P. aloes* on dead leaves of *Yucca elephantipes* (Asparagaceae) in China. In this study, we have acquired DNA from a sexual morph, and in multigene phylogeny, our collection (KUNCC 25-19168) with *P. aloes* (HKAS 115783, CBS 145367) group in a well-supported (100% ML and 0.98 PP) monophyletic clade (Fig. 54). Morphologically, the sexual morph is similar to *P. aloes* (HKAS 115783) in terms of its ascomata, asci, and ascospore characteristics (Boonmee et al. 2021). We therefore name our collection (KUNCC 25-19168) as *Phaeosphaeriopsis aloes*, a new host record on herbaceous plants in China.

Phaeosphaeriopsis grevilleae Crous & Y. Marín, Studies in Mycology 94: 62 (2019) Fig. 66

Index Fungorum number: IF829644; Facesoffungi number: FoF18353

Saprobic on a dead stem of herbaceous plants. Sexual morph: *Ascomata* 210–270 µm diam. × 190–240 µm high ($\bar{x}$ = 250 × 215 µm, n = 10), immersed, subglobose to globose, solitary, scattered, with brown spots on the host surface, uni-loculate, with ostiolate. *Peridium* 22–35.5 µm wide ($\bar{x}$ = 30 µm, n = 30), equal thickness, composed of pale yellow to brown, thick-walled, pseudoparenchymatous cells of *textura angularis*. *Hamathecium* comprises 1.7–4 µm wide ($\bar{x}$ = 3 µm, n = 30), consisting of numerous, septate, constricted at the septum, branched, filamentous, pseudoparaphyses, embedded in a mucilaginous matrix. *Asci* 70–90 × 8–10 µm ($\bar{x}$ = 80 × 9 µm, n = 25), 8-spored, fissitunicate, bitunicate, cylindrical to cylindric-clavate, apically rounded, short pedicellate, slightly curved, with a well-developed ocular chamber. *Ascospores* 16–21 × 4–6.3 µm ($\bar{x}$ = 18 × 5 µm, n = 25), overlapping 1–2-seriate, oblong to cylindrical, slightly narrowing towards the end cells, 3–5-septate, constricted at the septa, yellowish to brown, verruculose, straight or slightly curved, lacking a mucilaginous sheath. Asexual morph: Undetermined.

Culture characteristics – Ascospores germinated within 48 h on PDA. 2 cm diam. after three weeks at 27°C. cultures from above, circular, dense, flat, raised, white; from below, white to cream.

Material examined – China, Yunnan Province, Kunming, on a dead stem of unidentified herbaceous plants on grassland, 19 May 2021, Y. Gao, GY81 (HKAS 135341), living culture KUNCC 25-19169.

Known hosts and distribution – on leaves of *Grevillea* sp. (Proteaceae) in Australia (Marin-Felix et al. 2019), on a dead stem of herbaceous plants in Yunnan Province, China (This study).

GenBank numbers – KUNCC 25-19169: ITS = PV608610, LSU = PV607464, SSU = PV607351, *tef1-α* = PV626489, *rpb2* = PV655522.

Notes – *Phaeosphaeriopsis grevilleae* was introduced by Marin-Felix et al. (2019) as an asexual morph on leaves of *Grevillea* sp. (Proteaceae) in Australia. In our study, we have acquired DNA from a sexual morph, and the multigene phylogeny of combined ITS, LSU, SSU, *tef1-α*, and *rpb2* sequence data shows our collection (KUNCC 25-19169) and *P. grevilleae* (CBS 145369, ex-type) group in a well-supported monophyletic clade (Fig. 54). The sexual morphology of *P. grevilleae* (CBS 145369) has not been reported (Marin-Felix et al. 2019). The sexual morph is similar to *Phaeosphaeriopsis beaucarnea* (MFLU 18-2586, holotype) in terms of its ascospore characteristics (Tennakoon et al. 2020). However, *Phaeosphaeriopsis grevilleae* and *P.*

beaucarneae are not closely related phylogenetically (Fig. 54). Therefore, we introduce our collection as the sexual morph of *Phaeosphaeriopsis grevilleae*, and it is a new host and a geographical record

***Sclerostagonospora* Höhn., Hedwigia 59: 252 (1917)**

Notes – *Sclerostagonospora* was introduced by Von Höhnelt (1917) with *S. heraclei* as the type species. Morphologically, *Sclerostagonospora* species are characterized by pycnidia with holoblastic conidiomata, determinate, ampulliform to irregular, discrete conidiogenous cells, subcylindrical, 3-septate, verruculose, pale brown conidia (Sutton 1980, Quaedylic et al. 2013, Phookamsak et al. 2014, Wanasinghe et al. 2018). There are 17 *Sclerostagonospora* species listed in Index Fungorum (2025), however, only nine species have sequence data in GenBank. In this study, we introduce a new record species for *Sclerostagonospora rosae*, with descriptions and illustrations (Fig. 67).

***Sclerostagonospora rosae* Wanas., E.B.G. Jones & K.D. Hyde, Fungal Diversity 89: 141 (2018)
Fig. 67**

Index Fungorum number: IF554195, Facesoffungi number: FoF04037

Saprobic on a dead leaf blade unidentified plant. Sexual morph: *Conidiomata* 70–120 μm high $\times$ 75–100 μm diam. ($\bar{x}$ = 94 $\times$ 85 μm , n = 10), globose to subglobose, sub-epidermal, erumpent at maturity, solitary, scattered, unilocular, brown, slightly concave at the top. *Conidiomata wall* 8–15 μm wide ($\bar{x}$ = 11.5 μm , n = 30), composed of 2–3 layers of dark yellow cells of *textura angularis*. Conidiophores reduced to conidiogenous cells. *Conidiogenous cells* 5–10 $\times$ 2–4 μm ($\bar{x}$ = 7.5 $\times$ 3 μm , n = 25), enteroblastic, phialidic, ampulliform, discrete, determinate, smooth, hyaline. *Conidia* 7.5–11 $\times$ 4–5 μm ($\bar{x}$ = 9 $\times$ 4.5 μm , n = 30), ellipsoidal, straight or slightly curved, both ends rounded or rarely truncate at base, mostly 1-transverse septate, slightly constricted at septa, thick and smooth-walled. Asexual morph: Undetermined.

Culture characteristics – Colonies on PDA reaching 10 mm diam. after three weeks at 25°C, colonies from the above, slightly raised, floccose, dense, yellow spot in the center surrounded by white and hyaline edges; from below, white to hyaline at the margins, dark brown to yellow at the center.

Material examined – China, Yunnan Province, Kunming, on rotten unidentified leaves blade, 13 May 2021, Y. Gao, GY90 (HKAS 132997), living culture KUNCC 25-19153.

Known hosts and distribution – *Sclerostagonospora rosae* (MFLU 18-0115) on *Rosa* sp. (Rosaceae) in China (Wanasinghe et al. 2018), *Sclerostagonospora rosae* (KUNCC 25-19153) on a dead leaf blade of a herbaceous plant in Yunnan Province, China (This study).

GenBank numbers – KUNCC 25-19153: ITS = PV608580, LSU = PV607434, SSU = PV607325, *rpb2* = PV655500.

Notes – The phylogenetic analyses show our collection (KUNCC 25-19153) grouped together with *Sclerostagonospora rosae* (MFLU 18-0115, holotype) (Fig. 54). Morphologically, our collection (KUNCC 25-19153) is similar to *S. rosae* (MFLU 18-0115) in having globose to subglobose, sub-epidermal, erumpent at maturity, solitary, scattered conidiomata; ellipsoidal, straight or slightly curved, both ends rounded or rarely truncate at base, 1-transverse septate conidia. Thus, we identified our collection (KUNCC 25-19153) as *Sclerostagonospora rosae* based on phylogenetic analyses and morphological characters. Our collection is reported as a new host in China.

***Septoriella* Oudem., Ned. Kruidk. Arch. ser. 2, 5 (3): 504 (1889)**

Notes – *Septoriella* was first described by Oudemans (1889), however, it garnered little attention, with only a handful of species being identified. Crous et al. (2015a) recently redefined the genus, designating an epitype (CBS H-22281) and an ex-epitype strain (CBS 140065) for its type species, *S. phragmitis*. This genus is widely distributed and comprises a diverse range of species. *Septoriella* species are frequently associated with various host plants, including cereals, grasses,

and other herbaceous vegetation (Marin-Felix et al. 2019). Over time, its taxonomy and classification have undergone substantial revisions, driven by the discovery of new species and the reassessment of existing ones through molecular and morphological analyses (Li et al. 2015, Thambugala et al. 2017, Marin-Felix et al. 2019, Hyde et al. 2020a, Wanasinghe & Maharachchikumbura 2023). Marin-Felix et al. (2019) further revealed that the ex-type strains of the sexual genera *Allophaeosphaeria*, *Poaceicola*, and *Vagicola* grouped within the clade representing *Septoriella*, leading to their synonymization with this genus in their study. Wanasinghe & Maharachchikumbura (2023) reported eight species to *Septoriella*: a new species, *Septoriella shoemaker*, five new combinations, *S. ammophilicola*, *S. asparagicola*, *S. festucae*, *S. luzulae*, *S. verrucispora*, two new names, *Septoriella paradactylidis*, *S. neomuriformis*. There are 57 *Septoriella* species listed in Index Fungorum (2025). In this study, we introduce four new species, *Septoriella longispora*, *S. graminearum*, *S. yunnanensis*, *S. zhaotongensis*, three new records for *Septoriella paradactylidis*, *S. tridentina*, *S. vagans* based on morphology and molecular data, with descriptions and illustrations (Figs. 68–74).

Septoriella longispora Y. Gao, H. Gui & K.D. Hyde, sp. nov.

Fig. 68

Index Fungorum number: IF903836, Facesoffungi number: FoF17710

Holotype – HKAS 132975

Etymology – The specific epithet “longispora” refers to the holotype with long spores

Saprobic on dead stems of *Dactylis glomerata*. Sexual morph: *Conidiomata* 90–135 µm high × 85–130 µm diam. ($\bar{x}$ = 112 × 110 µm, n = 15), solitary, immersed to erumpent, black dots on the host surface, unilocular, globose to subglobose, carbonaceous, brown to black, papillate, with a central ostiole. *Conidiomata wall* 10–21.5 µm wide ($\bar{x}$ = 14 µm, n = 30), composed of 2–5 layers of pale yellow to brown cells of *textura angularis*. Conidiophores reduced to conidiogenous cells. *Conidiogenous cells* 3.5–7 µm diam. ($\bar{x}$ = 4.5 µm, n = 30), globose to subglobose, hyaline, arising from the inner layer of pycnidium wall. *Conidia* 43–58 × 4–5 µm ($\bar{x}$ = 53 × 4.3 µm, n = 30), long fusiform to cylindrical, obtuse at apex and base, sometimes slightly truncate at base, 7–9-septate, slightly constricted at the septum, guttulate, hyaline to pale brown, with polar appendages at both ends. Asexual morph: Undetermined.

Culture characteristics – Colonies on PDA reaching 15 mm diam. after three weeks at 25°C, colonies from above, circular, flat, slightly raised, white; from below, zonate, white at the margin, pale brown at the center, gray at the zonate.

Material examined – China, Yunnan Province, Zhaotong grassland, on dead stems of *Dactylis glomerata* (Poaceae), 25 August 2022, Y. Gao, QG1 (HKAS 132975, holotype), living culture KUNCC 25-19164.

GenBank numbers – KUNCC 25-19164: ITS = PV608595, LSU = PV607449, SSU = PV607338, *tef1-α* = PV626474, *rpb2* = PV655513.

Notes – In the phylogenetic analyses of combined ITS, LSU, SSU, *tef1-α*, and *rpb2* sequence data, our collection (KUNCC 25-19164) formed a separate branch and clusters with *Septoriella paradactylidis* (MFLU 17-0498, MFLUCC 14-0207, KUMCC 18-0154, KUNCC 25-19162, KUNCC 25-19163, KUNCC 23-14219) with 77% ML and 0.86 PP support values (Fig. 54). Our collection (KUNCC 25-19164) differs from *S. paradactylidis* (MFLU 17-0498, holotype) in 3.13% (17/543, with 4 gaps, NR_164251), 0.36% (3/830, with 2 gaps, NG_070411), 0.00% (0/997, OR206404), 1.27% (11/869, without gaps, OR195711), 3.02% (31/1026, without gaps, OR195720), in the ITS, LSU, SSU, *tef1-α*, and *rpb2* regions, respectively. *S. paradactylidis* was introduced from its sexual morph (Hyde et al. 2017, Wanasinghe & Maharachchikumbura 2023), while we introduced *Septoriella longispora* from its asexual morph. Therefore, we were unable to compare our new species and *S. paradactylidis*. However, based on the phylogenetic distinctiveness, *Septoriella longispora* is introduced as a new species on dead stems of *Dactylis glomerata* in China.

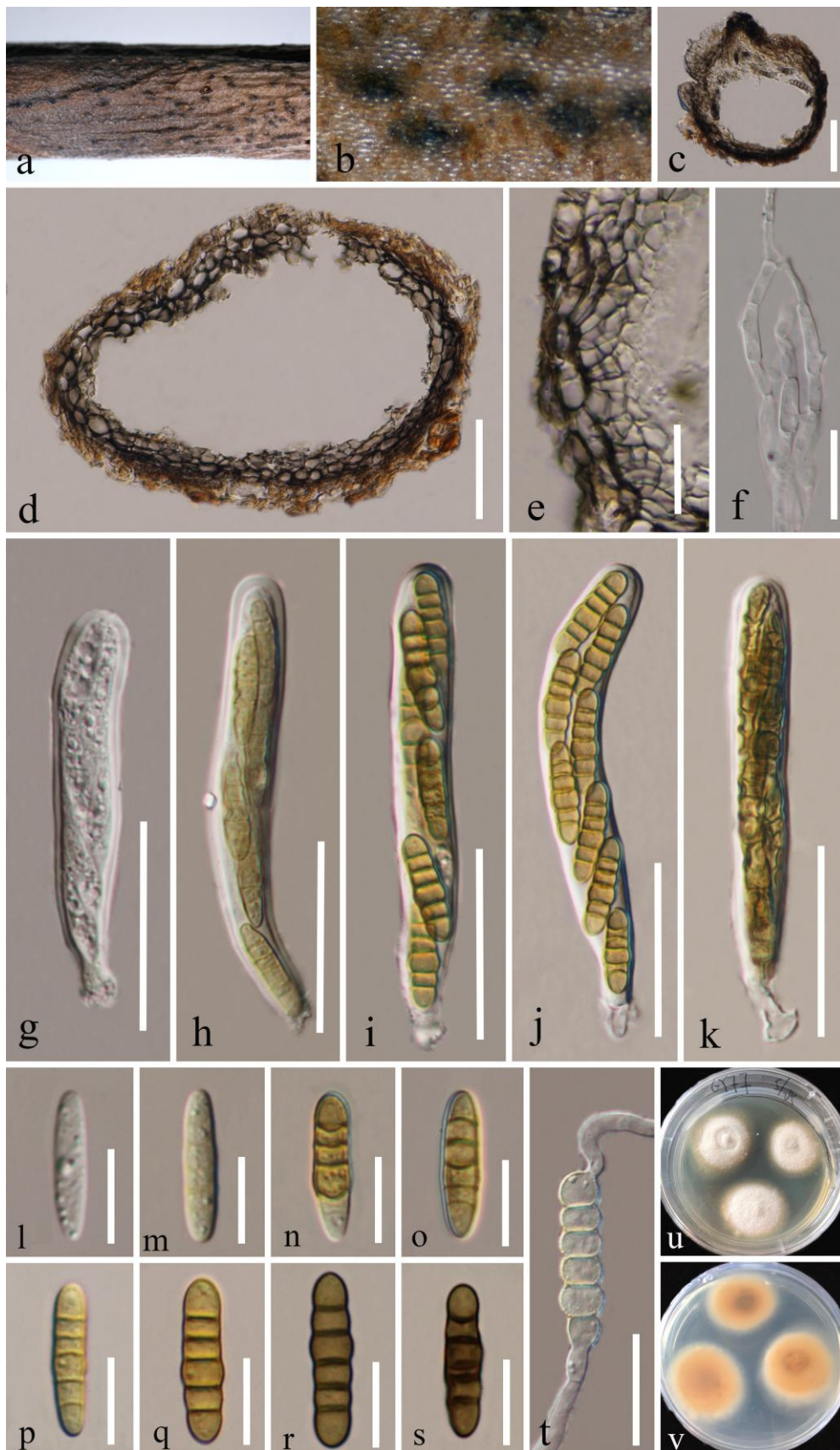


Figure 65 – *Phaeosphaeriopsis aloes* (HKAS 145997, a new host record). a, b Appearance of ascomata on the host substrate. c, d Sections of ascomata. e Peridium. f Pseudoparaphyses. g–k Asci. l–s Ascospores. t A germinated ascospore. u, v Colony on PDA (u: above, v: below). Scale bars: c, d = 50 μ m, g–k = 30 μ m, e, f, t = 20 μ m, l–s = 10 μ m.

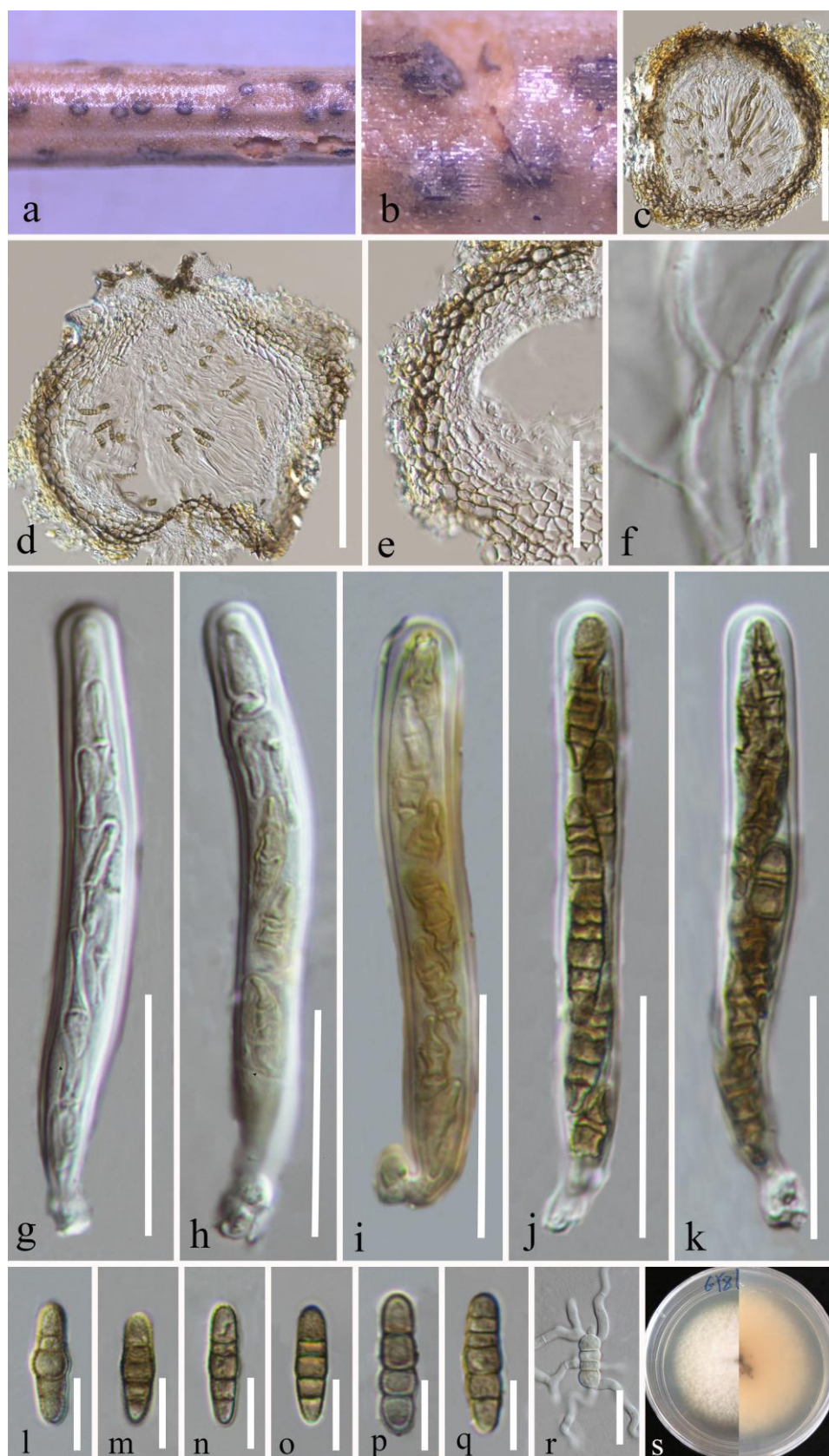


Figure 66 – *Phaeosphaeriopsis grevilleae* (HKAS 135341, a new host and a geographical record). a, b Appearance of ascomata on the host substrate. c, d Sections of ascomata. e Peridium. f Pseudoparaphyses. g–k Asci. l–q Ascospores. r A germinated ascospore. s Colony on PDA (left: above, right: below). Scale bars: c, d = 100 μ m, e = 50 μ m, g–k = 30 μ m, r = 20 μ m, f, l–q = 10 μ m.

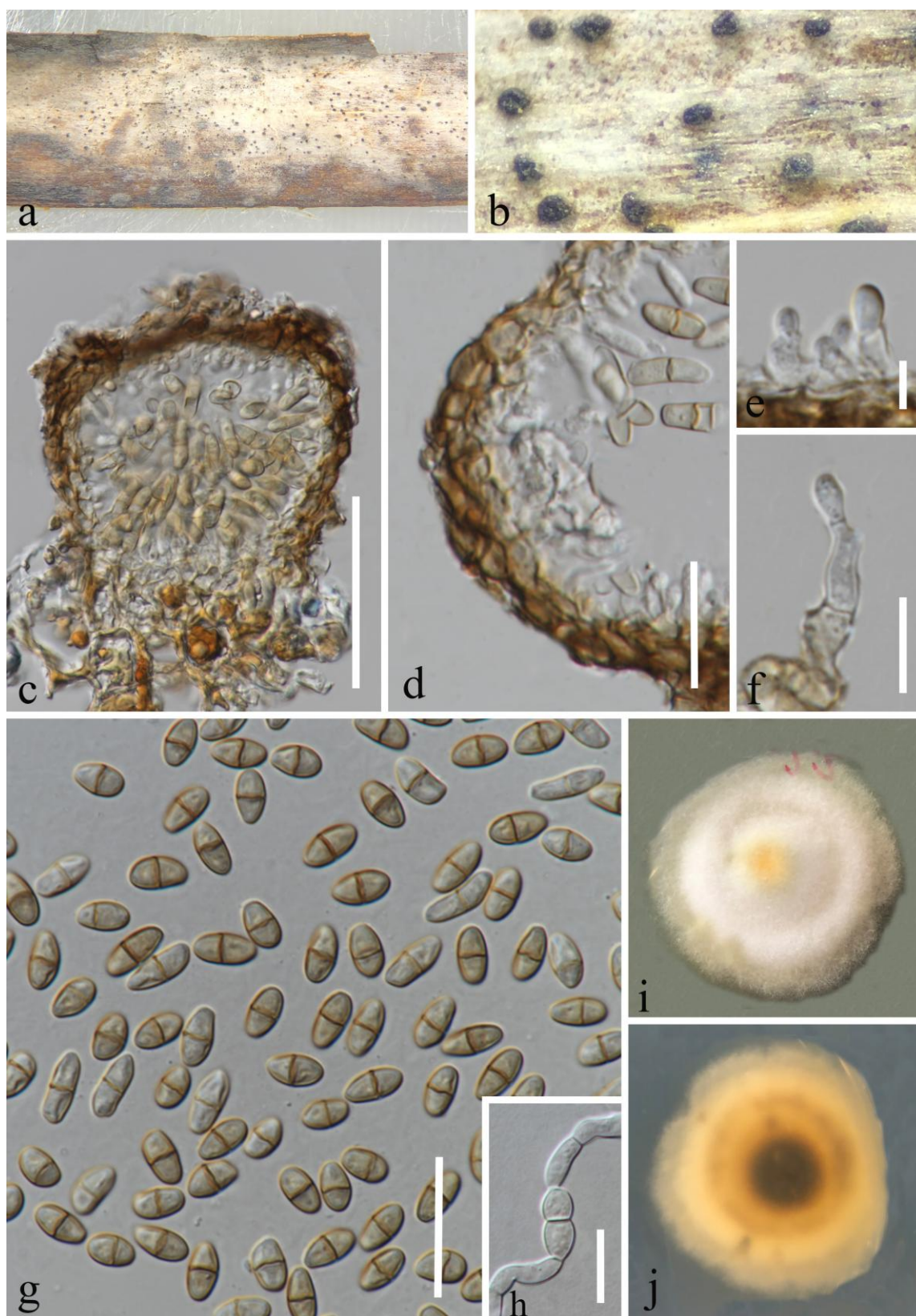


Figure 67 – *Sclerostagonospora rosae* (HKAS 132997, a new host record). a, b Conidiomata observed on host substrate. c Vertical section of a conidioma. d Conidiomata wall. e, f Conidiogenous cells developing conidia. g Conidia. h A germinated conidium. i, j Colony on PDA (i: above, j: below). Scale bars: c = 50 μ m, d, g = 20 μ m, h = 15 μ m, f = 10 μ m, e = 5 μ m.

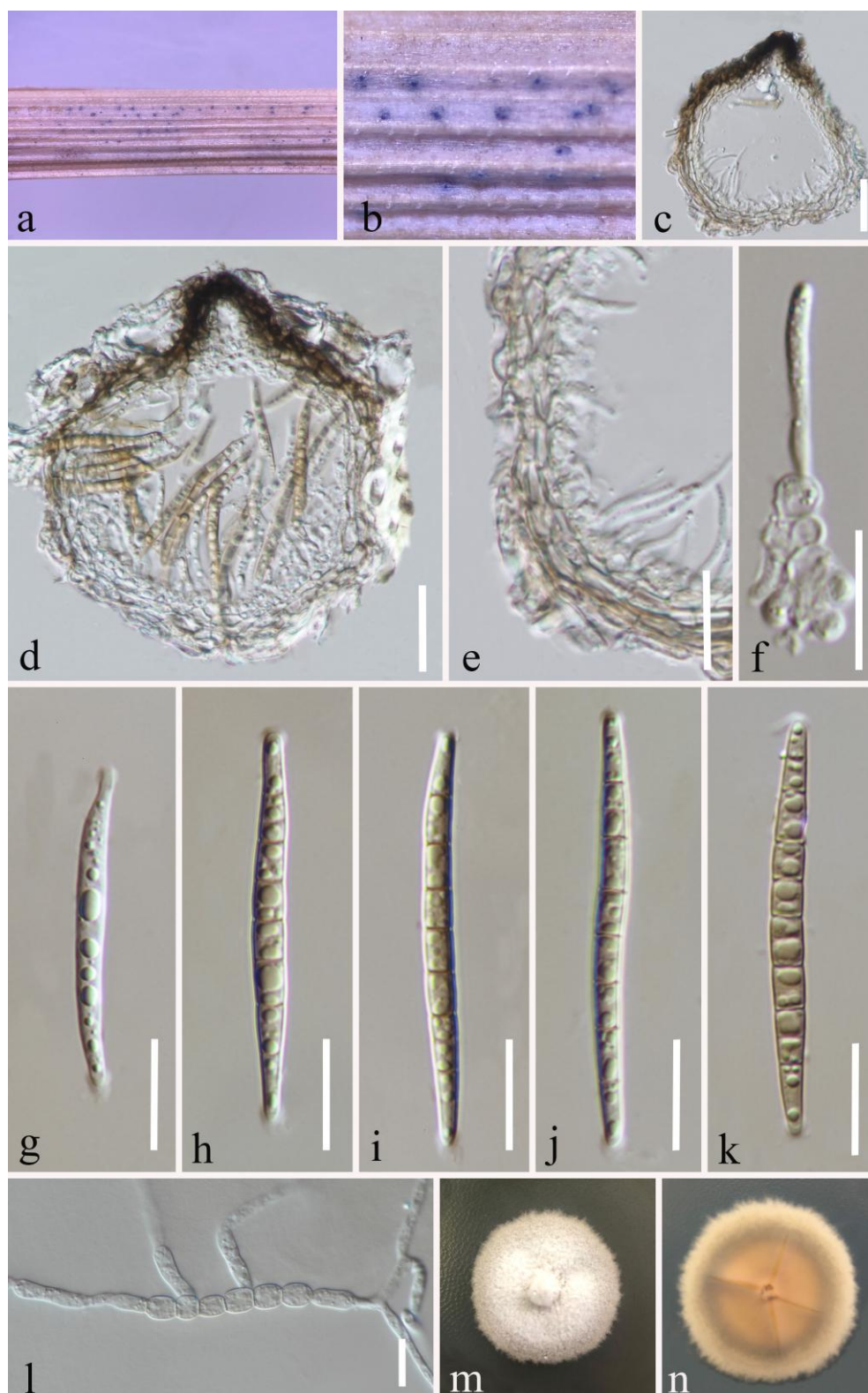


Figure 68 – *Septoriella longispora* (HKAS 132975, holotype). a, b Conidiomata observed on the host substrate. c, d Vertical sections of conidiomata. e Conidiomata wall. f Conidiogenous cells with developing conidia. g–k Conidia. l A germinated conidium. m, n Colony on PDA (m: above, n: below). Scale bars: c, d = 30 μ m, e = 20 μ m, f–l = 15 μ m.

Septoriella graminearum Y. Gao, H. Gui & K.D. Hyde, sp. nov.

Index Fungorum number: IF903837; Facesoffungi number: FoF17711

Holotype – HKAS 128779

Fig. 69

Etymology – The specific epithet is derived from the host family Gramineae, which the holotype was found.

Saprobic on a dead stem of *Dactylis glomerata*. Sexual morph: *Ascomata* 280–340 µm diam. × 220–285 µm high ($\bar{x}$ = 320 × 250 µm, n = 15), immersed to erumpent, subglobose to globose, scattered, solitary, uni-loculate, black, papillate, with ostiole. *Peridium* 16–36 µm wide ($\bar{x}$ = 24 µm, n = 30), composed of dark brown cells of *textura angularis*. *Hamathecium* comprises 2–4.5 µm wide ($\bar{x}$ = 3 µm, n = 30), consisting of numerous, dense, broad, filamentous, branched, septate, pseudoparaphyses. *Asci* 90–99.5 × 11–13.5 µm ($\bar{x}$ = 100 × 12.5 µm, n = 25), 8-spored, clavate to cylindrical-clavate, bitunicate, fissitunicate, apically rounded, thick-walled, short pedicellate, with an obscured ocular chamber. *Ascospores* 28.5–37 × 4.5–6 µm ($\bar{x}$ = 34 × 5.5 µm, n = 30), overlapping 1–2-seriate, long fusiform, apex sub-obtusely to obtusely rounded, hyaline to yellow, 7–9-septate, 4th cell is enlarged, slightly constricted at the septum, smooth, with guttulate. Asexual morph: Undetermined.

Culture characteristics – Ascospores germinated within 48 h on PDA. 5.5 cm diam. after three weeks at 27°C. cultures from above, dense, circular, flat, umbonate, fimbriate, white; from below, white to cream.

Material examined – China, Yunnan Province, Zhaotong grassland, on a dead stem of *Dactylis glomerata* (Poaceae), 25 August 2022, Y. Gao, QG103A (HKAS 128779, holotype), ex-type living culture CGMCC 3.24535; *ibid.*, QG103B (HKAS 128780), living culture CGMCC3.24536.

GenBank numbers – CGMCC 3.24535: ITS = PV608591, LSU = PV607445, *tef1-α* = PV626470, *rpb2* = PV655509; CGMCC 3.24536: ITS = PV608592, LSU = PV607446, *tef1-α* = PV626471, *rpb2* = PV655510.

Notes – *Septoriella graminearum* is introduced as a new species based on its distinct morphology and phylogenetic analysis. *Septoriella graminearum* (CGMCC 3.24535, CGMCC 3.24536) is closely related to *S. oudemansii* (CBS 138012, ex-type) (Fig. 54). A pairwise nucleotide comparison showed that *S. oudemansii* (CGMCC 3.24535) differs from *S. oudemansii* (CBS 138012) in 18/585 bp of ITS (3.08%, with 2 gaps), 8/834 bp of LSU (0.6%, without gaps). *S. oudemansii* (CBS 138012) did not provide *tef1-α* and *rpb2* sequences, so comparison could not be performed. *Septoriella oudemansii* was introduced by Crous et al. (2014) from *Phragmites australis* and *Dendryphon europaeum* from *Hedera helix* (Germany) and *H. sphondylium* (the Netherlands). *Septoriella oudemansii* has not been reported from its sexual morph. In this study, we describe a new species, *Septoriella graminearum*, as a saprobe on dead blades of *Dactylis glomerata*.

Septoriella paradactylidis Wanas. & Maharachch., J. Fungi 9 (8, no. 853): 23 (2023) Fig. 70

Index Fungorum number: IF849366; Facesoffungi number: FoF18354

Saprobic on a dead stem of *Dactylis glomerata*. Sexual morph: *Ascomata* 140–160 diam. µm × 110–140 µm high ($\bar{x}$ = 150 × 120 µm, n = 10), globose to subglobose, immersed, visible as raised, black dots on the host surface, solitary, uni-loculate, scattered, brown or black, papillate, with ostiole. *Peridium* 8–18 µm wide ($\bar{x}$ = 13 µm, n = 30), comprising pale brown to brown cells of *textura angularis*. *Hamathecium* comprises 1.5–3 µm wide ($\bar{x}$ = 2.3 µm, n = 30), filiform, comprises dense, trabeculate, septate, narrow contraction at the septum, branching pseudoparaphyses, embedded in a gelatinous matrix. *Asci* 52–78 × 9.5–13 µm ($\bar{x}$ = 72.5 × 11 µm, n = 25), 8-spored, cylindric-clavate to clavate, bitunicate, fissitunicate, apically rounded, short pedicellate, with an obscured ocular chamber. *Ascospores* 18–30 × 4–6 µm ($\bar{x}$ = 24 × 5 µm, n = 25), biserial, partially overlapping, fusiform with acute ends, 5–7-septate, slightly constricted at the septum, cell above median septum enlarged, with guttules in each cell, slightly curved, hyaline to yellow, smooth, lacking a sheath or appendages. Asexual morph: Undetermined.

Culture characteristics – Asci and ascospores germinated within 48 h on PDA. 5.5 cm diam. after three weeks at 27°C. Colony from above, dense, circular, low convex, floccose, brown at the

edge, pale yellow with white spots at the center; from below, dark brown at the center, yellow at the edge, producing pigmentation on agar medium.



Figure 69 – *Septoriella graminearum* (HKAS 128779, holotype). a, b Appearance of ascomata on the host substrate. c, d Sections of ascomata. e Peridium. f Pseudoparaphyses. g–k Asci. l–o

Ascospores. p Colony on PDA (left: above, right: below). Scale bars: c, d = 100 μ m, e, g–k = 30 μ m, f = 20 μ m, l–o = 10 μ m.

Material examined – China, Yunnan Province, Zhaotong grassland, on dead stems of *Dactylis glomerata* (Poaceae) found on the grassland, 25 August 2022, Y. Gao, QG2 (HKAS 132976), living culture KUNCC 25-19162; *ibid.*, QG45 (HKAS 146003), living culture KUNCC 25-19163.

Known hosts and distribution – on dead aerial stems of *Dactylis glomerata* (Poaceae) in Italy (Hyde et al. 2017), on dead culms of *Lolium perenne* (Poaceae) in China (Wanasinghe & Maharachchikumbura 2023), on dead stems of *Dactylis glomerata* (Poaceae) in Yunnan Province, China (This study).

GenBank numbers – KUNCC 25-19162: ITS = PV608593, LSU = PV607447, SSU = PV607336, *tef1*- α = PV626472, *rpb2* = PV655511; KUNCC 25-19163: ITS = PV608594, LSU = PV607448, SSU = PV607337, *tef1*- α = PV626473, *rpb2* = PV655512.

Notes – Our phylogenetic analyses have revealed that our collections (KUNCC 25-19162 and KUNCC 25-19163) grouped with *Septoriella paradactylidis* (MFLU 17-0498, MFLUCC 14-0207, KUMCC 18-0154, KUNCC 23-14219) with 98% ML and 1.00 PP support values (Fig. 54). Our collections (KUNCC 25-19162 and KUNCC 25-19163) are similar to *S. paradactylidis* (MFLU 17-0498, holotype) in having a similar size range of the ascomata, asci, ascospores, as well as the ascospore septation (Hyde et al. 2017, Wanasinghe & Maharachchikumbura 2023). Therefore, we report our collections as *Septoriella paradactylidis* on *Dactylis glomerata* (Poaceae) from the grassland, representing a new record of *S. paradactylidis* on that host in China.

Septoriella tridentina Thambug., Camporesi & K.D. Hyde, Mycosphere 8 (4): 759 (2017)

Fig. 71

Index Fungorum number: IF552992; Facesoffungi number: FoF03211

Saprobic on a dead stem. Sexual morph: *Ascomata* 110–150 μ m diam. ($\bar{x}$ = 130 μ m, n = 10), immersed to semi-immersed, globose to subglobose, black dots on the host surface, scattered, brown or black. *Peridium* 6–12 μ m wide ($\bar{x}$ = 9 μ m, n = 25), comprising 1–3 layers of pale brown to brown cells of *textura angularis*. *Hamathecium* comprises 1–2 μ m wide ($\bar{x}$ = 2.5 μ m, n = 30), filiform, comprises septate, rarely branched pseudoparaphyses. *Asci* 65–100 $\times$ 13–16 μ m ($\bar{x}$ = 80 $\times$ 15 μ m, n = 25), 8-spored, fissitunicate, bitunicate, cylindrical to cylindric-subclavate, straight or slightly curved, apically rounded, short pedicellate, with an ocular chamber. *Ascospores* 20–25 $\times$ 6–8 μ m ($\bar{x}$ = 24 $\times$ 7 μ m, n = 30), overlapping 1–2-seriate, cylindric-fusiform, 4–5-septate, slightly curved, hyaline to yellowish-brown, guttulate, smooth, with a mucilaginous sheath. Asexual morph: Undetermined.

Culture characteristics – Asci and ascospores germinated within 24 h on PDA. 3 cm diam. after two weeks at 27°C. Colony from above, circular, low convex, surface flocculent, white, surface smooth, with edge entire; from below, white at the margin, grey in the center.

Material examined – China, Yunnan Province, Zhaotong grassland, on dead stems of *Dactylis glomerata* (Poaceae) found on the grassland, 25 August 2022, Y. Gao, QG75 (HKAS 145987), living culture KUNCC 25-19198; *ibid.*, QG88 (HKAS 145988), living culture KUNCC 25-19199.

Known hosts and distribution – on dead aerial stems of *Dactylis glomerata* (Poaceae) in Italy (Thambugala et al. 2017), on dead stems of *Dactylis glomerata* (Poaceae) in Yunnan Province, China (This study).

GenBank numbers – KUNCC 25-19198: ITS = PV608615, LSU = PV607469, SSU = PV607356, *rpb2* = PV655524; KUNCC 25-19199: ITS = PV608616, LSU = PV607470, SSU = PV607357, *rpb2* = PV655525.

Notes – The phylogenetic analyses show our collections (KUNCC 25-19198 and KUNCC 25-19199) grouped with *Septoriella tridentina* (MFLUCC 15-0474 and MFLUCC 15-0475) (Fig. 54). Morphologically, our descriptions of our collections (KUNCC 25-19198 and KUNCC 25-19199) did not differ from the morphological descriptions of *S. tridentina* (MFLUCC 15-0474, ex-type) (Thambugala et al. 2017). Thus, we identified our collections as *Septoriella tridentina* based

on phylogenetic analyses and morphological characteristics, and we reported them as a new geographical record in China.

Septoriella vagans (Niessl) Y. Marín & Crous, *Studies in Mycology* 94: 111 (2019) Fig. 72

Index Fungorum number: IF829710; Facesoffungi number: FoF00909

Saprobic on dead stems. Sexual morph: *Ascomata* 165–200 diam. $\mu\text{m} \times 125\text{--}155 \mu\text{m}$ high ($\bar{x} = 175 \times 140 \mu\text{m}$, $n = 10$), globose to subglobose, immersed to semi-immersed, visible as raised, black dots on the host surface, scattered, brown or black. *Peridium* 9–18 μm wide ($\bar{x} = 12 \mu\text{m}$, $n = 25$), comprising 2–4 layers of pale brown to brown cells of *textura angularis*. *Hamathecium* comprises 2–3 μm wide ($\bar{x} = 2.5 \mu\text{m}$, $n = 30$), filiform, comprises dense, trabeculate, septate, branching pseudoparaphyses, embedded in a gelatinous matrix. *Asci* 70–100 $\times 13.5\text{--}19 \mu\text{m}$ ($\bar{x} = 90 \times 16 \mu\text{m}$, $n = 30$), 8-spored, bitunicate, fissitunicate, broadly cylindric-clavate to clavate, apically rounded, short pedicellate, with an obscured ocular chamber. *Ascospores* 20.5–31 $\times 6\text{--}8.5 \mu\text{m}$ ($\bar{x} = 27.5 \times 7.5 \mu\text{m}$, $n = 30$), overlapping 1–2-seriate, fusiform with rounded at end, 5-septate, constricted at the septum, slightly curved, hyaline to yellowish-brown, smooth, with guttulate, lacking a sheath or appendages. Asexual morph: Undetermined.

Culture characteristics – Asci and ascospores germinated within 48 h on PDA. 2 cm diam. after two weeks at 27°C. Colony from above, dense, circular, low convex, surface smooth, with edge entire, floccose, white; from below, white at the edge, brown at the center.

Material examined – China, Yunnan Province, Zhaotong grassland, on dead stems of *Dactylis glomerata* (Poaceae) found on the grassland, 25 August 2022, Y. Gao, QG80 (HKAS 135336), living culture KUNCC 25-19154; *ibid.*, QG93 (HKAS 146006), living culture KUNCC 25-19155; *ibid.*, QG21 (HKAS 132979), living culture KUNCC 25-19156; 25 September 2022, Y. Gao, LG8 (HKAS 146002), living culture KUNCC 25-19157.

Known hosts and distribution – On Poaceae in Germany (Niessl 1876), on *Calamagrostis arundinacea* (Poaceae) in Sweden (Quaedvlieg et al. 2013), on dead stems of *Dactylis glomerata* (Poaceae) in Yunnan Province, China (This study).

GenBank numbers – KUNCC 25-19154: ITS = PV608581, LSU = PV607435, SSU = PV607326, *tef1- α* = PV626460, *rpb2* = PV655501; KUNCC 25-19155: ITS = PV608582, LSU = PV607436, SSU = PV607327, *tef1- α* = PV626461, *rpb2* = PV655502; KUNCC 25-19156: ITS = PV608583, LSU = PV607437, SSU = PV607328, *tef1- α* = PV626462, *rpb2* = PV655503; KUNCC 25-19157: ITS = PV608584, LSU = PV607438, SSU = PV607329, *tef1- α* = PV626463, *rpb2* = PV655504.

Notes – The phylogenetic analyses show our collections (KUNCC 25-19154, KUNCC 25-19155, KUNCC 25-19156, KUNCC 25-19157) grouped with *Septoriella vagans* (CBS 604.86) (Fig. 54). Morphologically, our descriptions of our new collections (KUNCC 25-19154, KUNCC 25-19155, KUNCC 25-19156, KUNCC 25-19157) did not differ from the morphological descriptions of *S. vagans* (CBS 604.86) (Quaedvlieg et al. 2013). Thus, we identified our collections as *S. vagans* based on phylogenetic analyses and morphological characters. Our new species is reported as a new host on dead stems of *Dactylis glomerata* in China.

Septoriella yunnanensis Y. Gao, H. Gui & K.D. Hyde, sp. nov. Fig. 73

Index Fungorum number: IF903838; Facesoffungi number: FoF17712

Holotype – HKAS 128777

Etymology – The specific epithet “yunnanensis” refers to the type locality, Yunnan Province.

Saprobic on a dead stem of *Dactylis glomerata*. Sexual morph: *Ascomata* 95–140 μm diam. $\times 81\text{--}145 \mu\text{m}$ high ($\bar{x} = 120 \times 105 \mu\text{m}$, $n = 10$), subglobose to globose, semi-immersed, scattered, solitary, uni-loculate, black. *Peridium* 9–17 μm wide ($\bar{x} = 14 \mu\text{m}$, $n = 20$), composed of 3–6 layers of light brown to brown cells of *textura angularis* or *textura globulosa*. *Hamathecium* comprises 2.5–3.5 μm wide ($\bar{x} = 3 \mu\text{m}$, $n = 30$), composed of numerous, dense, filamentous, branched, multi-septate, pseudoparaphyses, embedded in a gelatinous matrix. *Asci* 100–140 $\times 14.5\text{--}23 \mu\text{m}$ ($\bar{x} = 123 \times 19 \mu\text{m}$, $n = 25$), 8-spored, bitunicate, fissitunicate, clavate to broad cylindrical-clavate, apically

rounded, short pedicellate, with an obscured ocular chamber. *Ascospores* $32\text{--}43 \times 7\text{--}10\ \mu\text{m}$ ($\bar{x} = 39 \times 8.5\ \mu\text{m}$, $n = 30$), overlapping 1–2-seriate, fusiform, acute at the ends, hyaline to yellowish, mostly 5-septate, constricted at the septum, smooth, with guttulate. Asexual morph: Undetermined.

Culture characteristics – Asci and ascospores germinated within 48 h on PDA. 6 cm diam. after three weeks at 27°C. cultures from above, dense, circular, flat, umbonate, surface rough, dull, fimbriate, slightly covered with white aerial mycelium, pale gray margin, dark gray at the center; from below, black at the center, dark yellow at the edge.

Material examined – China, Yunnan Province, Zhaotong grassland, on a dead stem of *Dactylis glomerata* (Poaceae), 25 August 2022, Y. Gao, QG102A (HKAS 128777, holotype), ex-type living culture CGMCC 3.24533; *ibid.*, QG102B (HKAS 128778), living culture CGMCC 3.24534.

GenBank numbers – CGMCC 3.24533: ITS = PV608585, LSU = PV607439, SSU = PV607330, *tef1- α* = PV626464; CGMCC 3.24534: ITS = PV608586, LSU = PV607440, SSU = PV607331, *tef1- α* = PV626465.

Notes – Based on our phylogenetic analysis show our collections (CGMCC 3.24533 and CGMCC 3.24534) are closely related to *Septoriella poae* (CBS 136766, ex-type) (Fig. 54). A pairwise nucleotide comparison showed that *Septoriella yunnanensis* differs from *S. poae* (CBS 136766) in 15/537 bp of ITS (2.79%, with 2 gaps) and 3/829 bp of LSU (0.36%, without gaps). *S. poae* was introduced by Crous et al. (2014) on *Poa* sp. (Poaceae) in the Netherlands. *S. poae* was only provided with an asexual morphology analysis. Therefore, based on the polyphasic approach recommended for species boundaries delimitation (Jayawardena et al. 2021, Maharachchikumbura et al. 2021a), we introduce *Septoriella yunnanensis* as a novel species.

Septoriella zhaotongensis Y. Gao, H. Gui & K.D. Hyde, sp. nov.

Fig. 74

Index Fungorum number: IF903839; Facesoffungi number: FoF17713

Holotype – HKAS 132966

Etymology – The specific epithet “zhaotongensis” refers to the type locality, Zhaotong City.

Saprobic on a dead stem of *Dactylis glomerata*. Sexual morph: *Ascomata* 115–160 μm diam. $\times$ 105–120 μm high ($\bar{x} = 147 \times 112\ \mu\text{m}$, $n = 10$), immersed to erumpent, subglobose to globose, scattered, solitary, uniloculate, black. *Peridium* 7.5–16 μm wide ($\bar{x} = 11\ \mu\text{m}$, $n = 30$), composed of 2–3 layers of brown cells of *textura angularis* or *textura globulosa*. *Hamathecium* comprises 1.7–3.5 μm wide ($\bar{x} = 2.5\ \mu\text{m}$, $n = 30$), composed of numerous, dense, filamentous, branched, multi-septate, pseudoparaphyses, embedded in a gelatinous matrix. *Asci* 60–100 $\times$ 11–20 μm ($\bar{x} = 83 \times 14.5\ \mu\text{m}$, $n = 25$), 8-spored, clavate to cylindrical-clavate, bitunicate, fissitunicate, apically rounded, short pedicellate, with an obscured ocular chamber. *Ascospores* $23\text{--}30 \times 6\text{--}8\ \mu\text{m}$ ($\bar{x} = 25 \times 7\ \mu\text{m}$, $n = 25$), overlapping 1–2-seriate, broadly fusiform, pale yellow to yellowish, 5-septate, constricted at the septum, smooth, with guttulate. Asexual morph: Undetermined.

Culture characteristics – Asci and ascospores germinated within 48 h on PDA. 6 cm diam. after three weeks at 27°C. cultures from above, dense, circular, flat, umbonate, surface rough, dull, fimbriate, dark brown at the margin, grayish white at the center; from below, black at the center, gray at the edge.

Material examined – China, Yunnan Province, Zhaotong grassland, on a dead stem of *Dactylis glomerata* (Poaceae), 25 September 2022, Y. Gao, LG15 (HKAS 132966, holotype), ex-type living culture KUNCC 25-19158; 25 August 2022, Y. Gao, QG92 (HKAS 146000), living culture KUNCC 25-19159; *ibid.*, QG83 (HKAS 146008), living culture KUNCC 25-19160; on a dead leaf blade of *Holcus lanatus* (Poaceae), 25 August 2022, Y. Gao, QG25 (HKAS 132980), living culture KUNCC 25-19161.

GenBank numbers – KUNCC 25-19158: ITS = PV608587, LSU = PV607441, SSU = PV607332, *tef1- α* = PV626466, *rpb2* = PV655505; KUNCC 25-19159: ITS = PV608588, LSU = PV607442, SSU = PV607333, *tef1- α* = PV626467, *rpb2* = PV655506; KUNCC 25-19160: ITS = PV608589, LSU = PV607443, SSU = PV607334, *tef1- α* = PV626468, *rpb2* = PV655507; KUNCC

25-19161: ITS = PV608590, LSU = PV607444, SSU = PV607335, *tef1-α* = PV626469, *rpb2* = PV655508.

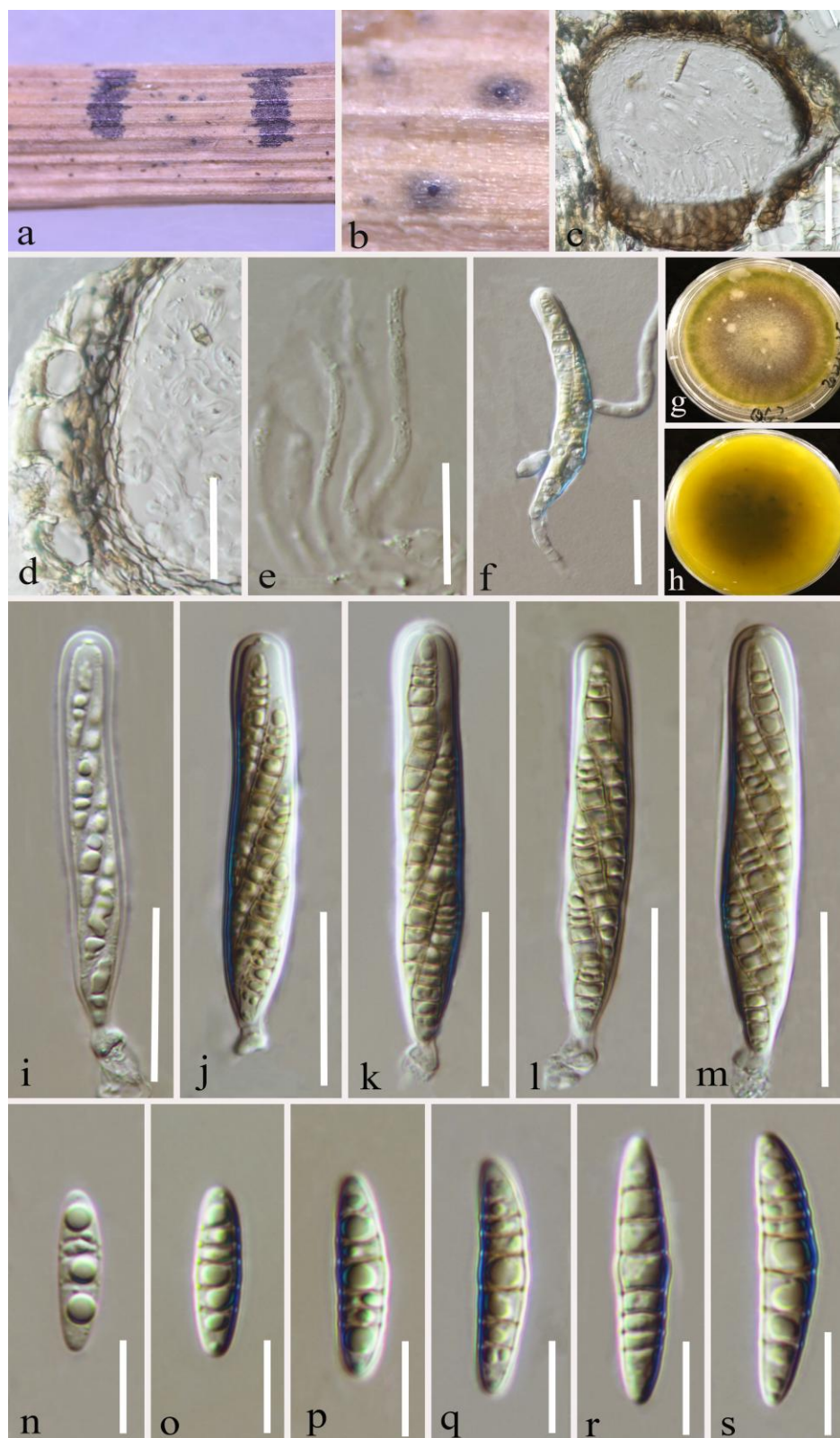


Figure 70 – *Septoriella paradactylidis* (HKAS 132976, a new host record). a, b Appearance of ascomata on the host substrate. c Section of an ascoma. d Peridium. e Pseudoparaphyses. f A germinated ascus. g, h Colony on PDA (g: above, h: below). i–m Asci. n–s Ascospores. Scale bars: c = 50 μ m, d, f, i–m = 30 μ m, e = 20 μ m, n–s = 10 μ m.

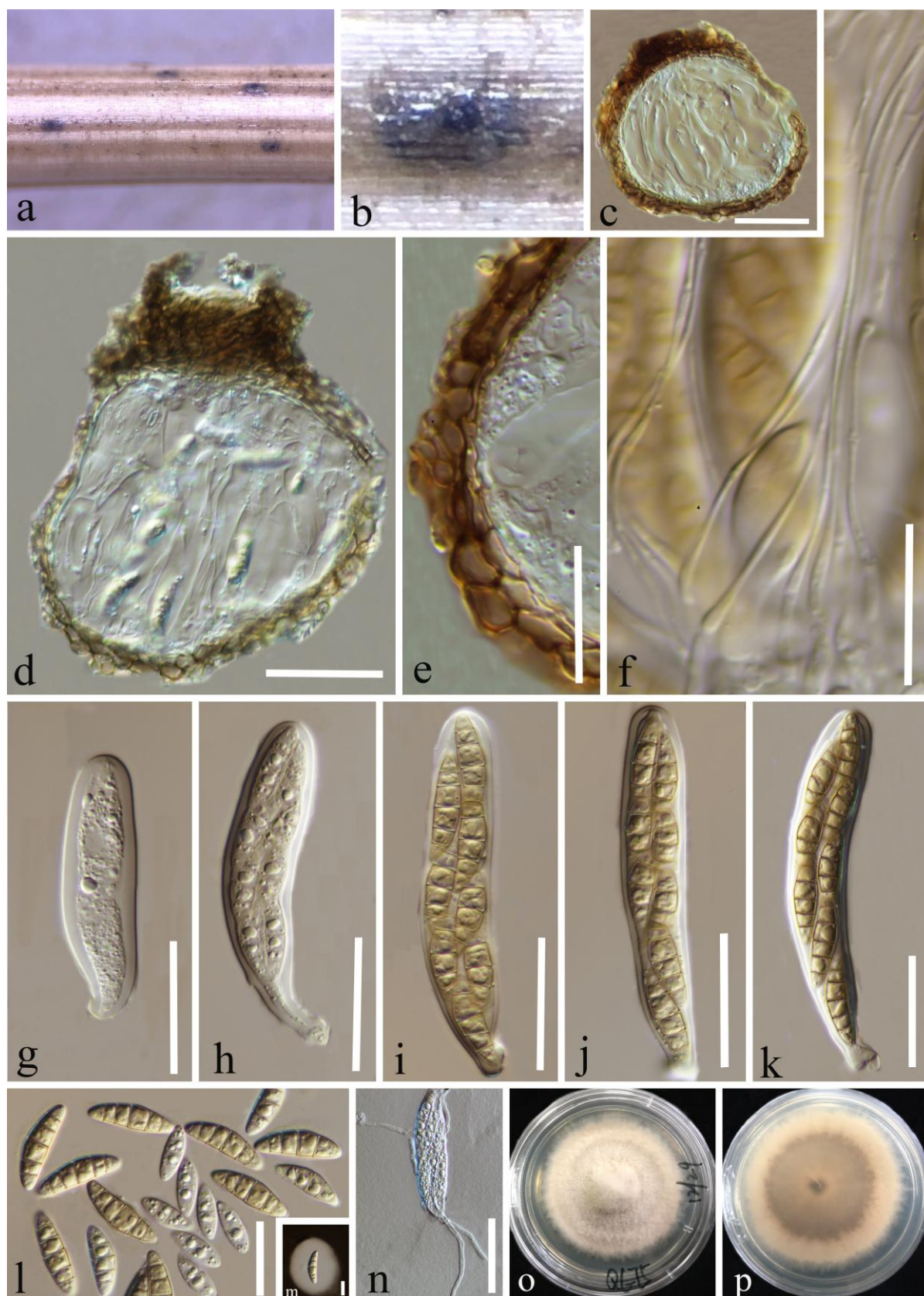


Figure 71 – *Septoriella tridentina* (HKAS 145987, a new geographical record). a, b Appearance of ascomata on the host substrate. c, d Sections of ascomata. e Peridium. f Pseudoparaphyses. g–k Asci. l Ascospores. m Ascospore stained with India ink showed a mucilaginous sheath. n A germinated ascus. o, p Colony on PDA (o: above, p: below). Scale bars: c, d, n = 50 μ m, g–k = 30 μ m, e, f, l = 20 μ m, m = 10 μ m.

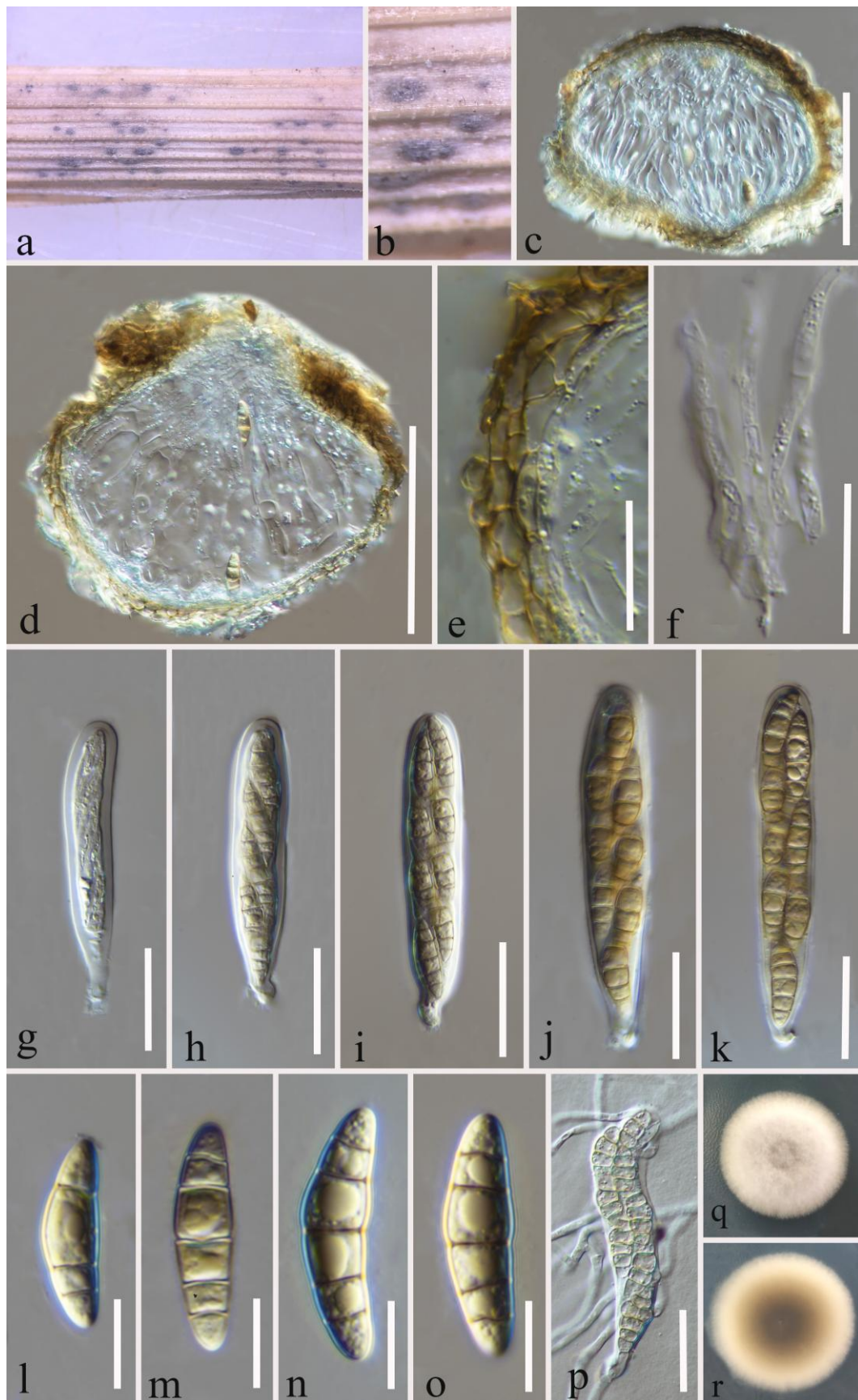


Figure 72 – *Septoriella vagans* (HKAS 135336, a new host and a geographical record). a, b Appearance of ascomata on the host substrate. c, d Sections of ascomata. e Peridium. f Pseudoparaphyses. g–k Asci. l–o Ascospores. p A germinated ascus. q, r Colony on PDA (q: above, r: below). Scale bars: c, d = 100 μ m, g–k, p = 30 μ m, e, f = 20 μ m, l–o = 10 μ m.

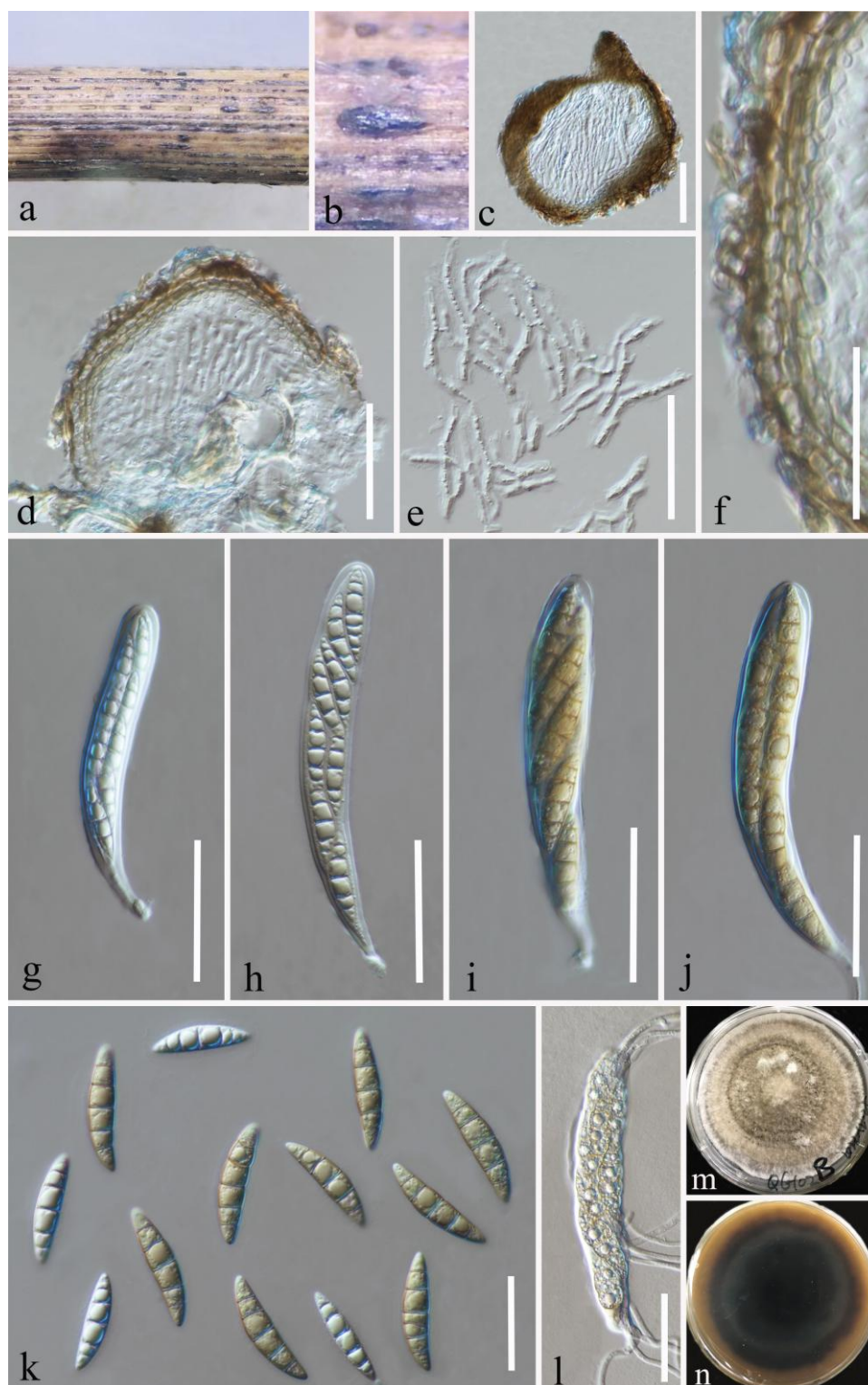


Figure 73 – *Septoriella yunnanensis* (HKAS 128777, holotype). a, b Appearance of ascomata on the host substrate. c, d Sections of ascomata. e Pseudoparaphyses. f Peridium. g–j Asci. k Ascospores. l A germinated ascus. m, n Colony on PDA (m: above, n: below). Scale bars: c–e, g–j, l = 50 μ m, f, k = 30 μ m.

Notes – Based on our phylogenetic analysis of the combined ITS, LSU, SSU, *tef1*- α , and *rpb2* sequence data, our novel species *Septoriella zhaotongensis* (KUNCC 25-19158, KUNCC 25-19159, KUNCC 25-19160, KUNCC 25-19161) is closely related to *S. ammophilicola* (MFLU 17-2571 and MFLU 17-2568) with 98% ML and 0.96 PP statistical support (Fig. 54). *Septoriella ammophilicola* was collected from the leaf of Marram grass (*Ammophila arenaria*) in the United

Kingdom (Dayarathne et al. 2020). *Septoriella zhaotongensis* differs from *S. ammophilicola* (MFLU 17-2571, holotype) in ascomata (115–160 × 105–120 µm, L/W = 1.2 vs. 300–320 × 150–170 µm, L/W = 1.9), Peridium (7.5–16 µm wide vs. 25–30 µm wide), asci (65–99.5 × 11–20 µm, L/W = 5.3 vs. 130–138 × 30–35 µm, L/W = 4.1), ascospores (23–30 × 6–8 µm, L/W = 3.8, 5-septate vs. 40–45 × 15–18 µm, L/W = 2.6, 6-septate) (Dayarathne et al. 2020). In addition, the ITS pairwise nucleotide comparison of these species showed 8/532 bp differences (1.5%, without gaps). Our collection differs from *Septoriella ammophilicola* (MFLU 17-2571) in 2.42% (21/869 bp, without gaps) in the *tef1-α* regions. Therefore, based on the polyphasic approach recommended for species boundaries delimitation (Jayawardena et al. 2021, Maharachchikumbura et al. 2021a), we introduce *Septoriella zhaotongensis* as a novel species.

Setophoma Gruyter, Aveskamp & Verkley, Mycologia 102 (5): 1077 (2009)

Notes – *Setophoma* was reported to accommodate *Phoma terrestris* and *Pyrenochaeta sacchari* (de Gruyter et al. 2010) with *Setophoma terrestris* as the type species. *Setophoma* are characterized as having setose pycnidia, phialidic conidiogenous cells, ellipsoidal to subcylindrical, hyaline, aseptate conidia (de Gruyter et al. 2010, Quaadvlieg et al. 2013). There are 17 *Setophoma* species listed in Index Fungorum (2025). In this study, we introduce a new species, *Setophoma dactylidis*, with descriptions and illustrations (Fig. 75).

Setophoma dactylidis Y. Gao, H. Gui & K.D. Hyde, sp. nov.

Fig. 75

Index Fungorum number: IF903840; Facesoffungi number: FoF17714

Holotype – HKAS 128769

Etymology – The specific epithet is derived from the genus *Dactylis* (Poaceae), which the holotype was found.

Saprobic on dead stems of *Dactylis glomerata*. Sexual morph: *Ascomata* 145–190 µm diam. × 120–155 µm high ($\bar{x}$ = 167 × 143 µm, n = 10), immersed, subglobose to globose, with brown spots on the host surface, brown to black, solitary, scattered, uni-loculate, with ostiolate. *Peridium* 10–21 µm wide ($\bar{x}$ = 15 µm, n = 30), composed of several layers of outer thick-walled cells of *textura prismatica* and inner, hyaline cells of *textura prismatica* to *textura angularis*. *Hamathecium* comprises 1.5–3 µm wide ($\bar{x}$ = 2.5 µm, n = 30), consisting of numerous, septate, branched, filamentous, pseudoparaphyses, embedded in a mucilaginous matrix. *Asci* 68.5–101 × 9–14 µm ($\bar{x}$ = 80 × 10 µm, n = 30), 8-spored, fissitunicate, bitunicate, cylindrical to cylindric-clavate, with a short pedicel, apically rounded, slightly curved, ocular chamber present. *Ascospores* 21–33.5 × 4.5–6 µm ($\bar{x}$ = 26.5 × 5.5 µm, n = 25), overlapping 1–2-seriate, fusiform, with acute ends, mostly 7-septate, constricted at the septa, yellowish to brown, straight or slightly curved, guttulate, lacking a mucilaginous sheath. Asexual morph: Undetermined.

Culture characteristics – Ascospores germinated within 48 h on PDA. 5.5 cm diam. after three weeks at 27°C. cultures from above, circular, dense, flat, raised, pink white; from below, white at the edge, yellow at the center.

Material examined – China, Yunnan Province, Zhaotong grassland, on dead stems of *Dactylis glomerata* (Poaceae), 25 August 2022, Y. Gao, QG62A (HKAS 128769, holotype), ex-type living culture CGMCC 3.24525; *ibid.*, QG62B (HKAS 128770, isotype), ex-isotype living culture CGMCC 3.24526.

GenBank numbers – CGMCC 3.24525: ITS = PV608612, LSU = PV607466, SSU = PV607353, *tef1-α* = PV626491; CGMCC 3.24526: ITS = PV608613, LSU = PV607467, SSU = PV607354, *tef1-α* = PV626492.

Notes – Based on the phylogenetic analysis of multiple genes, *Setophoma dactylidis* (CGMCC 3.24525 and CGMCC 3.24526) shares a close relationship with *S. caverna* (R150, ex-type) with 88% ML and 1.00 PP support values (Fig. 54). A pairwise nucleotide comparison showed that *Setophoma dactylidis* differs from *S. caverna* (R150) in 22/507 bp of ITS (4.34%, without gaps), 2/841 bp of LSU (0.24%). Morphologically, our collections share a different morphology from the holotype of *Setophoma caverna* (R150) in ascospores (21–33.5 × 4.5–6 µm,

L/W = 5.2, 7-septate vs. 17–28.5 × 3.5–6 µm, L/W = 4.8, 3-septate) (Crous et al. 2019b). Thus, we identified *Setophoma dactylidis* as a new species based on phylogenetic analyses and morphological characteristics.

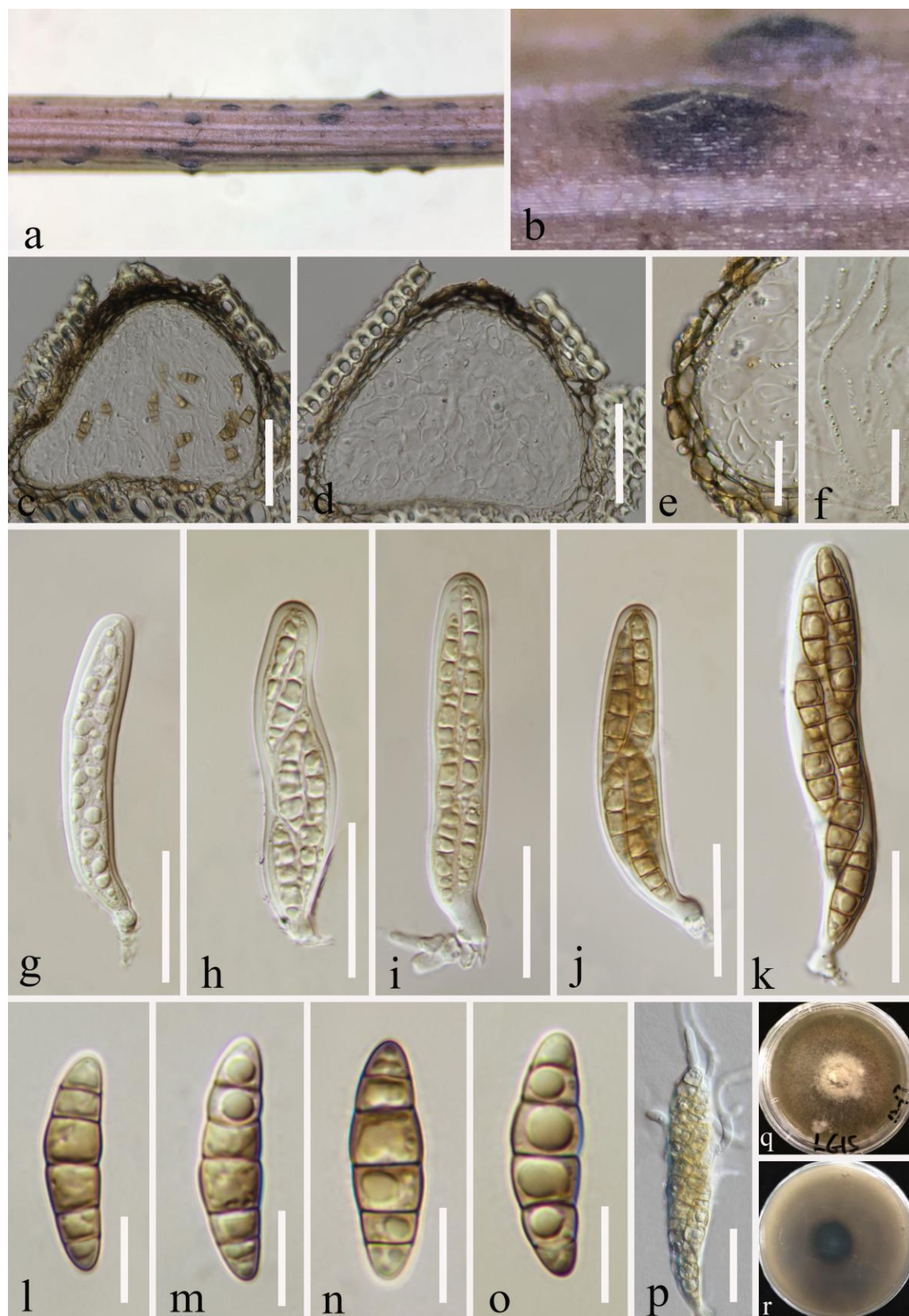


Figure 74 – *Septoriella zhaotongensis* (HKAS 132966, holotype). a, b Appearance of ascomata on the host substrate. c, d Sections of ascomata. e Peridium. f Pseudoparaphyses. g–k Asci. l–o

Ascospores. p A germinated ascus. q, r Colony on PDA (q: above, r: below). Scale bars: c, d = 50 μm , g–k, p = 30 μm , e, f = 20 μm , l–o = 10 μm .

Pleosporaceae Nitschke, Verh. Naturhist. Vereines Preuss. Rheinl.: 74 (1869)

Notes – Pleosporaceae was earlier placed in Pseudosphaeriaceae by Theissen & Sydow (1918). Lumbsch & Huhndorf (2010) confirmed the familial placement of Pleosporaceae with respect to other families in Pleosporales according to multigene phylogenetic studies (Lumbsch & Huhndorf 2010). Hongsanan et al. (2020b) and Hyde et al. (2024a) accept 28 genera in Pleosporaceae.

Comoclathris Clem., The genera of Fungi, 37, 173 (1909)

Notes – *Comoclathris* was established by Clements (1909) with *C. lanata* as the type species. Initially, this species was classified within the *Diademaceae* due to its ascomata featuring a flat, circular, lid-like opening (Shoemaker & Babcock 1992). Previously, *Comoclathris* was regarded as a synonym of *Platyspora* (Ariyawansa et al. 2014b) and was also associated with an asexual morph resembling that of *Alternaria*-like fungi (Simmons 1967). Consequently, based on these morphological traits, the genus was provisionally assigned to Pleosporaceae (Zhang et al. 2012, Woudenberg et al. 2013). *Comoclathris compressa* (CBS 157.53 and CBS 156.53) was analyzed as representative sequence, forming a well-supported clade within Pleosporaceae (Ariyawansa et al. 2014b). Eventually, integrating phylogenetic evidence with morphological characteristics, *Comoclathris* was formally placed within Pleosporaceae (Ariyawansa et al. 2015c, Thambugala et al. 2017, Wijayawardene et al. 2017, Wanasinghe et al. 2018). *Comoclathris* can be differentiated from *Pleospora*, *Pleoseptum*, and *Clathrospora* by its flattened, dark reddish-brown muriform ascospores, which possess a single longitudinal septum, as well as ascomata characteristics, such as a circular, lid-like opening. In contrast, species of *Clathrospora* typically exhibit two or more rows of longitudinal septa (Shoemaker & Babcock 1992, Zhang et al. 2012, Ariyawansa et al. 2014b, 2015c). There were 46 species accepted in the genus *Comoclathris* (Index Fungorum 2025); however, most lack molecular data. In this study, we introduce a new record species for *Comoclathris sedi*, with descriptions and illustrations (Fig. 77). An updated phylogenetic tree based on combined ITS, LSU, SSU, and *rpb2* sequence data is presented in Fig. 76.

Comoclathris sedi Wanas., Ariyaw., Camporesi & K.D. Hyde, Fungal Diversity 71: 105 (2015)
Fig. 77

Index Fungorum number: IF550955; Facesoffungi number: FoF00509

Saprobic on dead stems of *Dipsacus* sp. Sexual morph: *Ascomata* 160–200 high μm $\times$ 145–190 μm diam. ($\bar{x}$ = 190 $\times$ 175 μm , n = 10), globose to subglobose, superficial, scattered or aggregated, coriaceous, brown or black, covered with pale to dark brown setae, without a distinct ostiole. *Peridium* 13–28 μm wide ($\bar{x}$ = 19 μm , n = 30), relatively thick-walled cells of *textura angularis*, inner cells flattened, hyaline. *Hamathecium* comprises 2–3.5 μm wide ($\bar{x}$ = 2.8 μm , n = 30), filiform, dense, septate, branching pseudoparaphyses, embedded in a gelatinous matrix. *Asci* 90–155 $\times$ 21–28 μm ($\bar{x}$ = 110 $\times$ 24 μm , n = 20), 8-spored, cylindric-clavate to clavate, apically rounded, short pedicellate, bitunicate, fissitunicate, thick-walled, indistinct shallow ocular chamber. *Ascospores* 25–30 $\times$ 10–15 μm ($\bar{x}$ = 27 $\times$ 13 μm , n = 30), overlapping, fusiform, muriform, 5–7 transverse septa and 2–5 longitudinal septa, constricted at the middle septa, hyaline to reddish brown. Asexual morph: Undetermined.

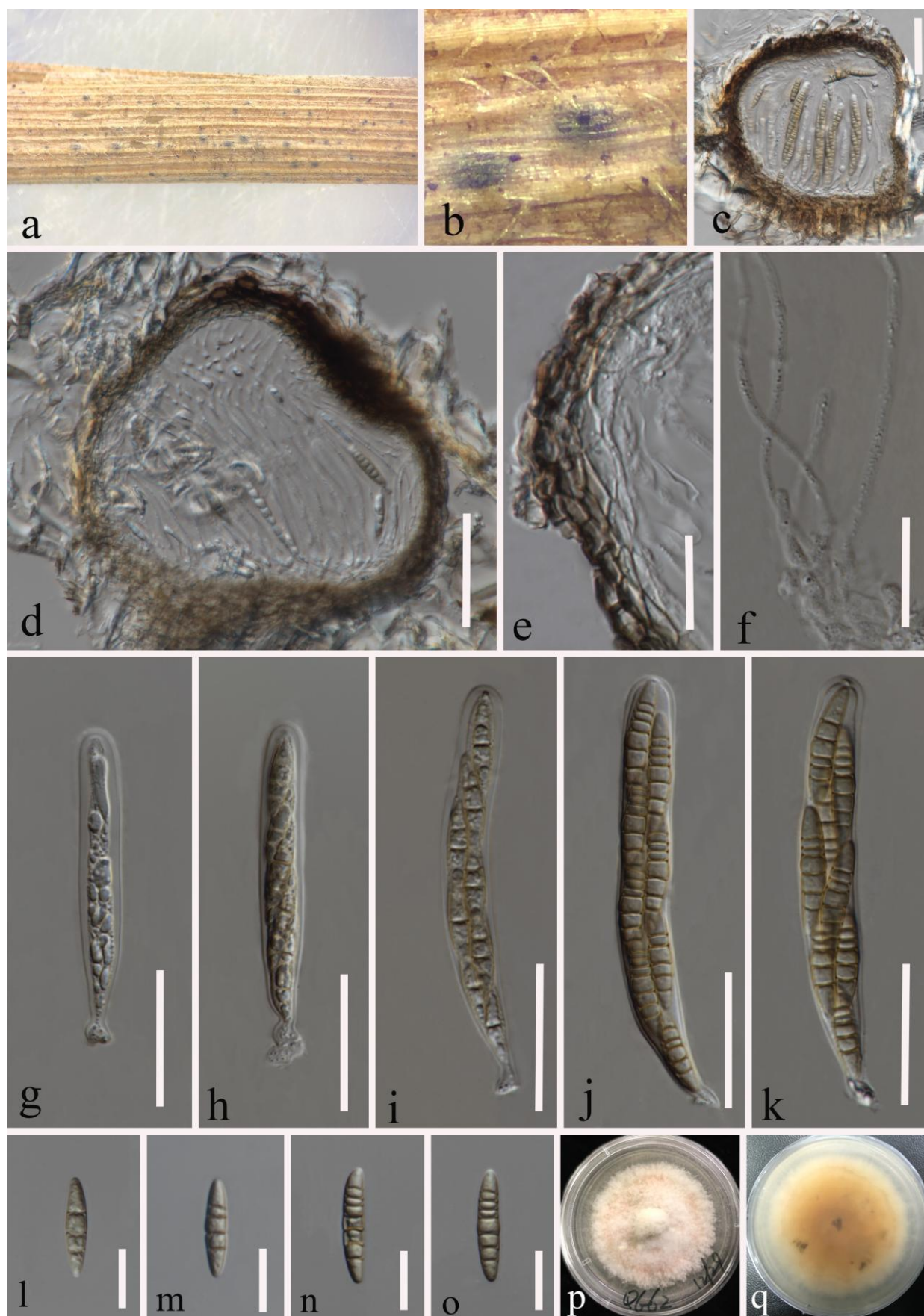


Figure 75 – *Setophoma dactylidis* (HKAS 128769, holotype). a, b Appearance of ascomata on the host substrate. c, d Sections of ascomata. e Peridium. f Pseudoparaphyses. g–k Asci. l–o Ascospores. p, q Colony on PDA (p: above, q: below). Scale bars: c, d = 50 μ m, g–k = 30 μ m, e, f = 20 μ m, l–o = 15 μ m.

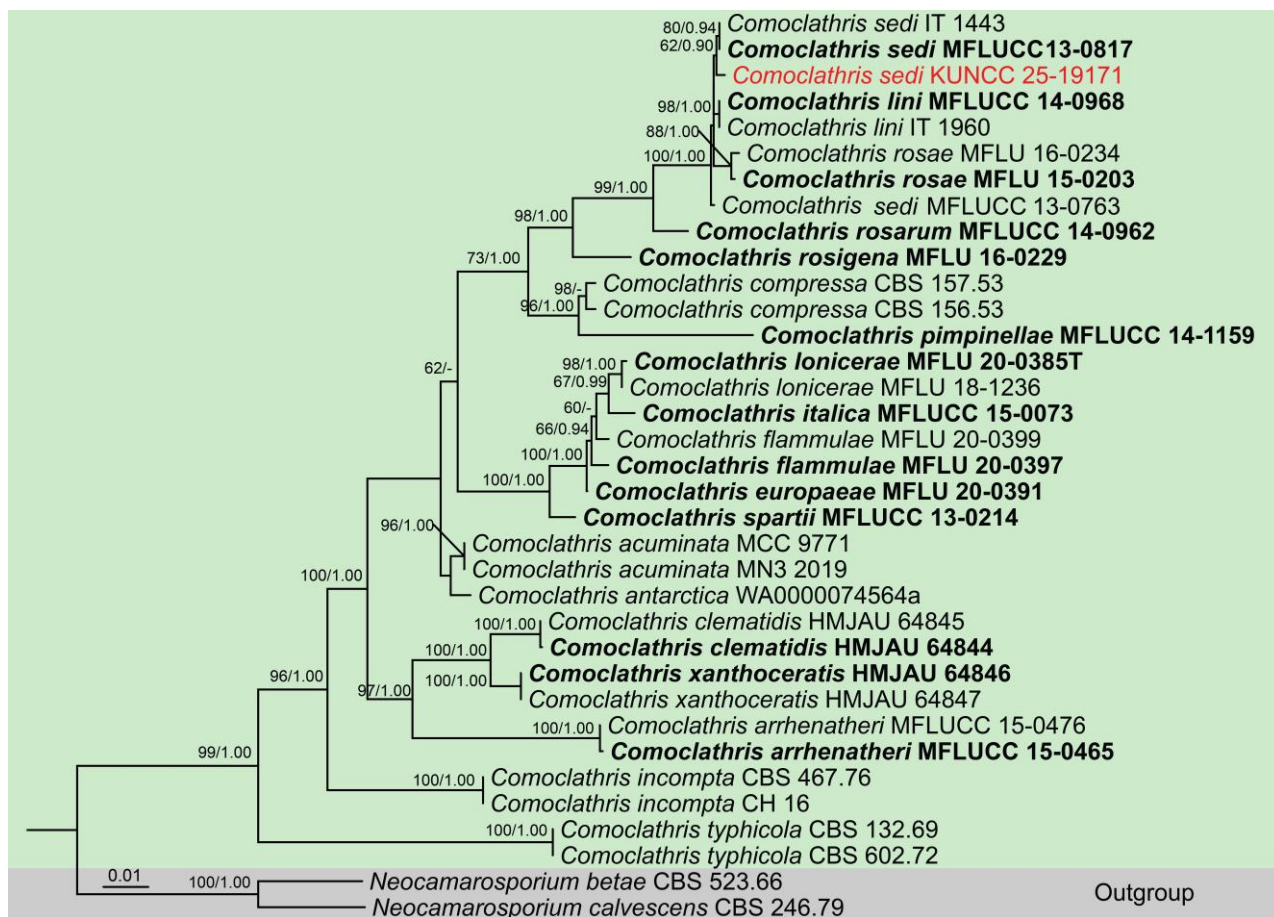


Figure 76 – RAxML phylogram generated from a combined dataset of partial ITS, LSU, SSU, and *rpb2* DNA sequence analyses for *Comoclathris*. Related sequences are obtained following Xu et al. (2024b). Thirty-five strains were included in the combined analyses, which comprised 3,274 characters in the combined ITS, LSU, SSU, and *rpb2* alignment. *Neocamarosporium betae* (CBS 523.66) and *Neocamarosporium calvescens* (CBS 246.79) were used as the outgroup taxa. The best-scoring RAxML tree with a final likelihood value of -11601.110756 is presented. The matrix contained 767 distinct alignment patterns, with 21.27% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.254941, C = 0.225063, G = 0.267816, T = 0.252181; substitution rates AC = 1.968875, AG = 4.392666, AT = 1.474791, CG = 0.984114, CT = 7.716225, GT = 1.000000. The tree topology of the ML analysis is similar to the Bayesian analysis. Bootstrap values for ML equal to or greater than 60% and PP values greater than 0.90 (rounding values to 2 decimal places) are labelled on the nodes. Strains of the newly described species are in orange, while type strains are in bold. (ITS: 539 bp, LSU: 851 bp, SSU: 1019 bp, *rpb2*: 865).

Culture characteristics – Ascospores germinated within 48 h on PDA. 5 cm diam. after three weeks at 27°C. Colony from above, dense, circular, low convex, surface smooth, with edge entire, white; from below, white at the edge, pale yellow at the center.

Material examined – China, Yunnan Province, Zhaotong grassland, on dead stems of *Dipsacus* sp. (Caprifoliaceae) found on the grassland, 27 August 2022, Y. Gao, QG41A (HKAS 135357), living culture KUNCC 25-19171.

Known hosts and distribution – on stems of *Sedum* sp. (Crassulaceae), *Clematis vitalba* (Ranunculaceae), *Rosa* sp. (Rosaceae) in Italy (Ariyawansa et al. 2015c), on dead stems of *Dipsacus* sp. (Caprifoliaceae) in Yunnan Province, China (This study).

GenBank numbers – KUNCC 25-19171: ITS = PV608614, LSU = PV607468, SSU = PV607355.

Notes – *Comoclathris sedi* was introduced by Ariyawansa et al. (2015c). The phylogenetic tree shows that *C. sedi* grouped with *C. lini* and *C. rosae* (Fig. 76). *C. sedi* (MFLUCC 13-0817, ex-type) differs from *C. lini* (MFLUCC 14-0968, ex-type) in ascospore (conically rounded ends vs. broadly rounded ends) (Wanasinghe et al. 2015). The ascospore dimensions of *Comoclathris sedi* (MFLUCC 13-0817) are comparatively smaller than those of *C. rosae* (MFLU 15-0203, holotype) (Wanasinghe et al. 2018). Our collection (KUNCC 25-19171) differs from *Comoclathris sedi* (MFLUCC 13-0817, ex-type) in having comparatively larger asci ($90\text{--}155 \times 21\text{--}28\text{ }\mu\text{m}$, L/W = 5.0 vs. $80\text{--}110 \times 16\text{--}18\text{ }\mu\text{m}$, L/W = 5.6) and different ascospore ($25\text{--}30 \times 10\text{--}15\text{ }\mu\text{m}$, L/W = 2.2, 5–7-transverse septa, 2–5-longitudinal septa, constricted at the middle septa vs. $19\text{--}20 \times 8\text{--}10\text{ }\mu\text{m}$, L/W = 2.1, 4–5-transverse septa and 1–2-longitudinal septa, not constricted at the septa) (Ariyawansa et al. 2015c, Wanasinghe et al. 2015). But, our collection (KUNCC 25-19171) was grouped with *Comoclathris sedi* (MFLUCC 13-0817 and IT 1443) (Fig. 76). Therefore, we introduce our collection as a new host and a new geographical record of *Comoclathris sedi* in China.

Teichosporaceae M.E. Barr, Mycotaxon 82: 374 (2002)

Notes – Teichosporaceae was established by Barr (2002) to accommodate eight genera, with *Teichospora* as the type genus. This family is characterised by having immersed or semi-immersed, erumpent to superficial, dark brown to black, pyriform or globose to subglobose, with papillate to elongate ostiolate ascomata; composed of several layers of lightly pigmented to dark brown to black, *textura angularis* cells peridium; branching, septate, anastomosing, cellular or trabeculate pseudoparaphyses; fissitunicate, bitunicate, cylindrical to oblong or sub-clavate, pedicellate, with small ocular chamber asci; hyaline or brown, ellipsoid to oblong or fusiform, cylindric-fusiform or oblong to elliptical, ovoid to clavate, symmetric or asymmetric, 1–3-septate or muriform ascospores (Barr 2002, Hongsanan et al. 2020a, Tennakoon et al. 2021b). Asexual morphs are coelomycetous and characterized by pycnidial, brown septate or brown, rarely hyaline, aseptate conidia (Hongsanan et al. 2020a). There are 17 genera accepted in this family (Hyde et al. 2024a). An updated phylogenetic tree based on combined ITS, LSU, SSU, *tef1- α* , and *rpb2* sequence data is presented in Fig. 78.

Floricola Kohlm. & Volkm.-Kohlm., Botanica Marina 43 (4): 385 (2000)

Notes – *Floricola* was established to accommodate the coelomycetous species *F. striata* as the type species. This genus is characterized by immersed to erumpent, scattered, pycnidial, conidiomata, conidiophores reduced to conidiogenous cells, conidiogenous cells with annellations, enteroblastic, phialidic, discrete, determinate, elongate ellipsoidal to cylindrical, 3-distoseptate, pale brown to dark brown conidia (Thambugala et al. 2015). In this study, we introduce a new record for *Floricola sulcata*, with descriptions and illustrations (Fig. 79).

Floricola sulcata (Marinc., M.J. Wingf. & Crous) Crous & Osieck, Fungal Systematics and Evolution 10: 47 (2022) Fig. 79

Index Fungorum number: IF844284; Facesoffungi number: FoF18355

Saprobic on dead stems of *Dactylis glomerata*. Sexual morph: Undetermined. Asexual morph: Coelomycetous. *Conidiomata* $120\text{--}150\text{ }\mu\text{m}$ diam. $\times$ $90\text{--}135\text{ }\mu\text{m}$ high ($\bar{x} = 135 \times 115\text{ }\mu\text{m}$, $n = 10$), globose or subglobose, superficial, scattered, solitary, uni-loculate, dark brown to black, without ostioles. *Conidiomata wall* $8\text{--}20\text{ }\mu\text{m}$ wide ($\bar{x} = 16\text{ }\mu\text{m}$, $n = 30$), uniform, outer layer composed of reddish-brown cells of *textura angularis*, lined with a thin, hyaline layer bearing conidiogenous cells. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* $3\text{--}4 \times 4\text{--}8.5\text{ }\mu\text{m}$ ($\bar{x} = 3.5 \times 6.5\text{ }\mu\text{m}$, $n = 20$), enteroblastic, phialidic or subglobose, determinate, discrete, truncate or doliiform, hyaline. *Conidia* $12.5\text{--}17 \times 5\text{--}7\text{ }\mu\text{m}$ ($\bar{x} = 15 \times 6\text{ }\mu\text{m}$, $n = 30$), broad oblong or ellipsoid, subtruncate at base, 3-septate, hyaline when immature, reddish brown at maturity, with prominent longitudinal striations.

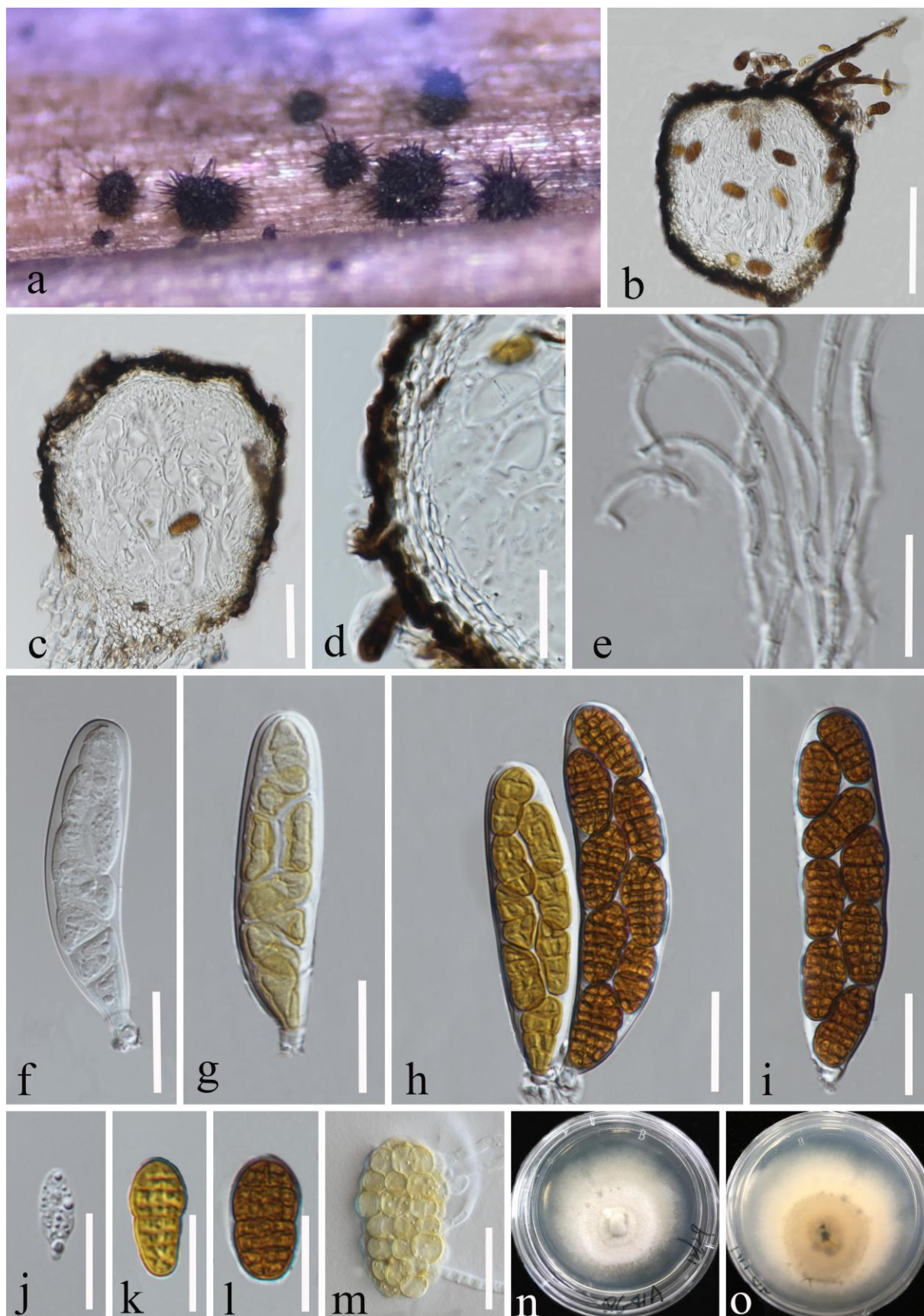


Figure 77 – *Comoclathris sedi* (HKAS 135357, a new host and a new geographical record). a Appearance of ascomata on the host substrate. b, c Sections of ascomata. d Peridium. e Pseudoparaphyses. f–i Asci. j–l Ascospores. m A germinated ascospore. n, o Colony on PDA (n: above, o: below). Scale bars: b = 100 μ m, c = 50 μ m, f–i = 30 μ m, d, e, j–m = 20 μ m.

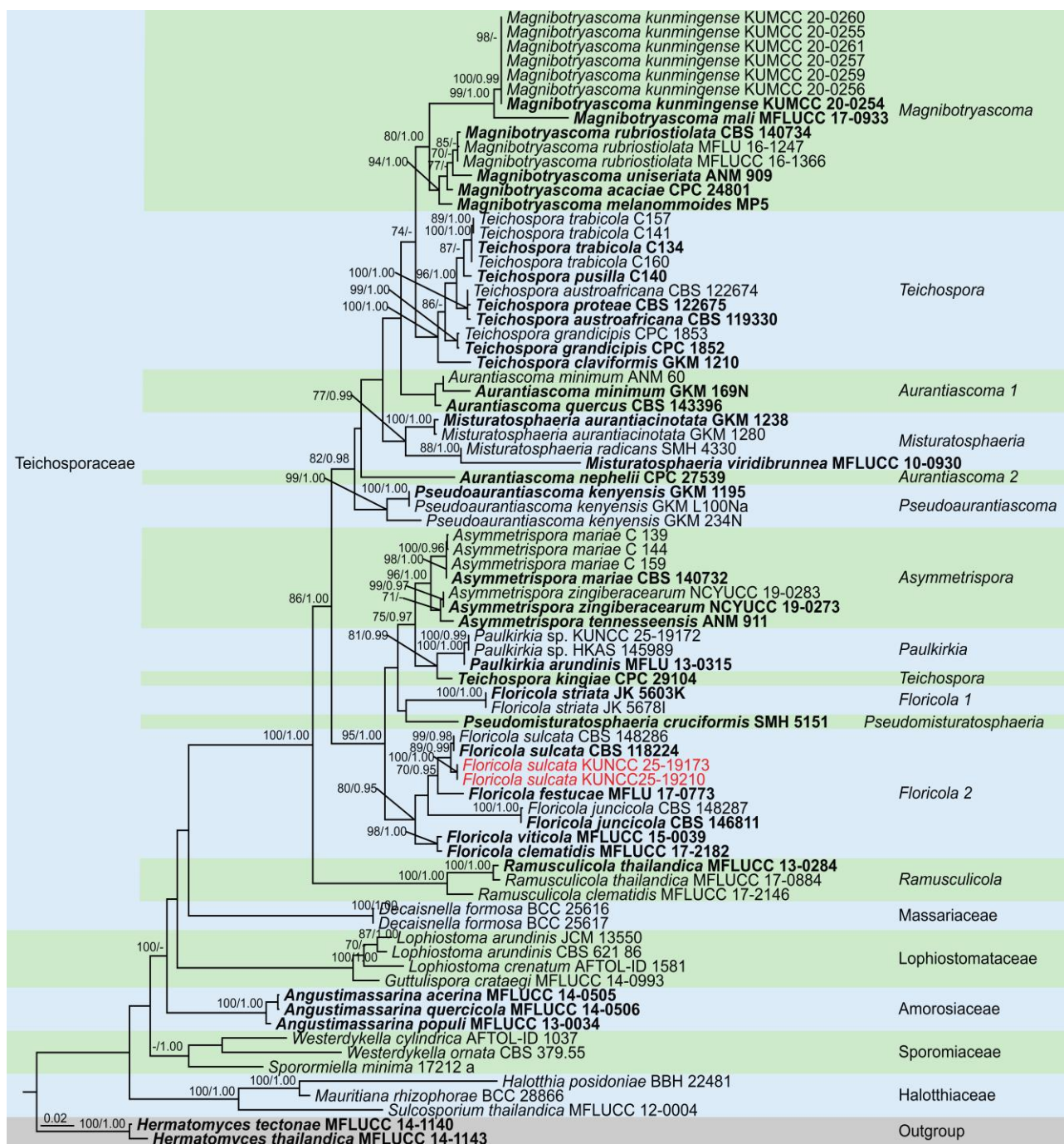


Figure 78 – RAxML phylogram generated from a combined dataset of partial ITS, LSU, SSU, *tef1- α* , and *rpb2* DNA sequence analyses for Teichosporaceae. Related sequences are obtained following Tennakoon et al. (2021b). Seventy-nine strains were included in the combined analyses, which comprised 4,109 characters in the combined ITS, LSU, SSU, *tef1- α* , and *rpb2* alignment. *Hermatomyces tectonae* (MFLUCC 14-1140) and *Hermatomyces thailandica* (MFLUCC 14-1143) were used as the outgroup taxa. The best-scoring RAxML tree with a final likelihood value of -24630.037475 is presented. The matrix contained 1518 distinct alignment patterns, with 42.12% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.243299, C = 0.252995, G = 0.278947, T = 0.224759; substitution rates AC = 1.224581, AG = 3.205102, AT = 1.678381, CG = 1.166123, CT = 8.372474, GT = 1.000000. The tree topology of the ML analysis is similar to the Bayesian analysis. Bootstrap values for ML equal to or greater than 60% and PP values greater than 0.90 (rounding values to 2 decimal places) are labelled on the nodes. Strains of the newly described species are in orange, while type strains are in bold. (ITS: 548 bp, LSU: 866 bp, SSU: 985 bp, *tef1- α* : 746 bp, *rpb2*: 964).

Culture characteristics – Colonies on PDA reaching 30 mm diam. after three weeks. Colony from above, dense, circular, low convex, surface smooth, with edge entire, with off-white, forming zonate greyish yellow, white to cream margin, brown at the center; from below, white at the edge, black at the center.

Material examined – China, Yunnan Province, Zhaotong grassland, on dead stems of *Dactylis glomerata* (Poaceae), 27 August 2022, Y. Gao, QG104A (HKAS 132990), living culture KUNCC 25-19173. *ibid.*, QG104B (HKAS 145984), living culture KUNCC25-19210.

Known hosts and distribution – From culm litter of *Restio subverticellatus* (Restionaceae) in South Africa (Krisai-Greilhuber et al. 2017), on dead culm of *Juncus effusus* (Juncaceae) in the Netherlands (Crous et al. 2022b), on dead stems of *Dactylis glomerata* (Poaceae) in Yunnan Province, China (this study).

GenBank numbers – KUNCC 25-19173: ITS = PV608617, LSU = PV607471, SSU = PV607358, *tef1*- α = PV626493; KUNCC25-19210: ITS = PV608618, LSU = PV607472, SSU = PV607359, *tef1*- α = PV626494.

Notes – *Sclerostagonospora sulcata* was described from culm litter of *Ischyrolepis subverticellata* (Restionaceae) in South Africa (Krisai-Greilhuber et al. 2017). Later, *Sclerostagonospora sulcata* was accommodated in the genus *Floricola* as *F. sulcata* (Crous et al. 2022b). Our collections (KUNCC 25-19173 and KUNCC25-19210) were grouped with *Floricola sulcata* (CBS 118224 and CBS 148286) (Fig. 78). A pairwise nucleotide comparison showed that our collections (KUNCC 25-19173 and KUNCC25-19210) differ from *F. sulcata* (CBS 118224, ex-type) in 6/544 bp of ITS (1.1%, without gaps), 3/835 bp of LSU (0.36%). Morphologically, our collections are similar to *F. sulcata* (CBS 118224) (Krisai-Greilhuber et al. 2017, Crous et al. 2022b). This finding represents a new and geographical record of *Floricola sulcata* from *Dactylis glomerata* in China and provides sequence data (SSU and *tef1*- α) for the species.

Torulaceae Corda, Deutschlands Flora, Abt. III. Die Pilze Deutschlands 2: 71 (1829)

Notes – Torulaceae was introduced by Corda (Sturm 1829) with *Torula* as the type genus. Torulaceae is known only by asexual characteristics, such as effuse and powdery colony; immersed mycelia; erect and subcylindrical, micro- or macronematous conidiophores; clavate or doliiform to ellipsoid, cupulate, smooth to verruculose and mono- to polyblastic conidiogenous cells; subcylindrical, acrogenous, phragmosporous, smooth to verrucose, brown conidia (Crous et al. 2015a, Hyde et al. 2016, Su et al. 2016). Torulaceae includes seven genera: *Cylindrotorula*, *Dendryphon*, *Neotorula*, *Rostriconidium*, *Rutola*, *Sporidesmioides*, and *Torula* (Hyde et al. 2024a).

Torula Pers., Ann. Bot. (Usteri) 15: 25 (1794)

Notes – *Torula* was established by Persoon (1795), with *T. herbarum* designated as the type species. Species in *Torula* are hyphomycetous asexual morphs, characterized by superficial dark colonies, branched chains, dark brown conidia (Su et al. 2018, Tibpromma et al. 2018a, Li et al. 2020b, Yang et al. 2022b). There were 342 species accepted in the genus *Torula* (Index Fungorum 2025). Only 35 species have molecular data (He et al. 2025, Li et al. 2025, Zhang et al. 2025), though morphological descriptions and molecular data are lacking for most species. In this study, we introduce two new records for *Torula chromolaenae* and *T. fici*, with descriptions and illustrations (Figs. 81, 82). An updated phylogenetic tree based on combined ITS, LSU, SSU, *tef1*- α , and *rpb2* sequence data is presented in Fig. 80.

Torula chromolaenae J.F. Li, Phookamsak, Mapook & K.D. Hyde, Mycological Progress 16 (4): 454 (2017) Fig. 81

Index Fungorum number: IF819536; Facesoffungi number: FoF02713.

Saprobic on dead stems of *Dactylis glomerata*. Sexual morph: Undetermined. Asexual morph: Colonies are discrete on the host, black, powdery. *Conidiophores* 7–14.5 μ m long $\times$ 2.5–6 μ m diam. ($\bar{x}$ = 11.5 $\times$ 4 μ m, n = 20), macronematous, mononematous, solitary, erect, light brown,

verruculose, thick-walled, consisting of one cell, without apical branches, ellipsoid to subglobose, arising from hypha. *Conidiogenous cells* 4.3–6.5 μm long $\times$ 4–6 μm diam. ($\bar{x}$ = 5.2 $\times$ 4.9 μm , n = 25), subglobose or doliiform, polyblastic, terminal, smooth to minutely verruculose, light brown to brown, paler at the apex. *Conidia* 10.7–17 $\times$ 4.3–6.3 μm ($\bar{x}$ = 14.5 $\times$ 5.5 μm , n = 30), subcylindrical, catenated, acrogenous, simple, phragmosporous, 2–3-septate, slightly constricted at some septa, light brown to brown, smooth to minutely verruculose, rounded at both ends, often paler at apex. Conidial secession schizolytic.



Figure 79 – *Floricola sulcata* (HKAS 132990, a new host and a geographical record). a, b Appearance of conidiomata on the host substrate. c, d Sections of conidiomata. e Conidiomata wall. f–k Conidiogenous cells and Conidia. l Conidia. m A germinated conidium. n, o Culture characters on PDA (n: above, o: below). Scale bars: c, d = 50 μm , e, l = 20 μm , m = 15 μm , f–k = 10 μm .

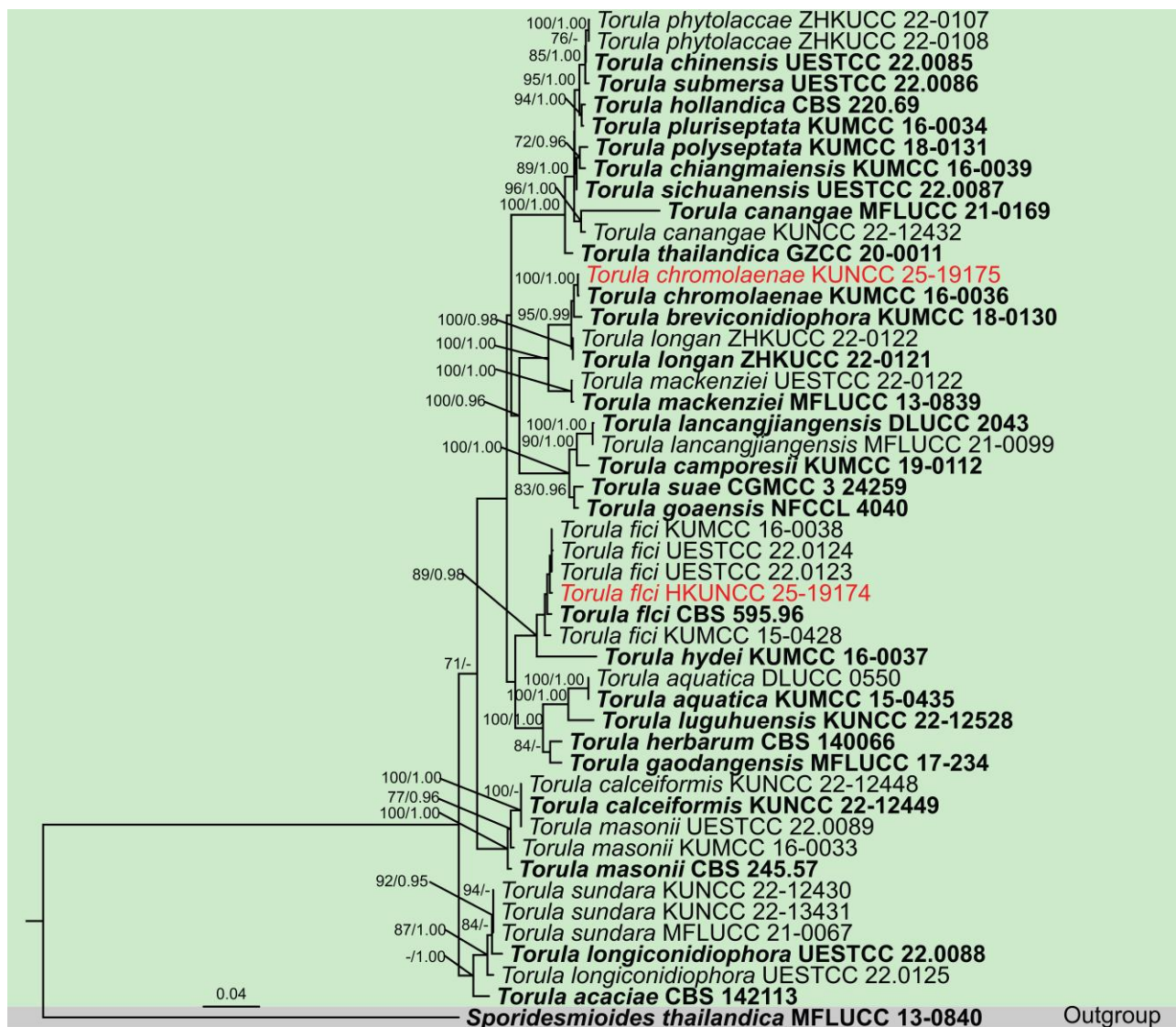


Figure 80 – RAxML phylogram generated from a combined dataset of partial ITS, LSU, SSU, *tef1*- α , and *rpb2* DNA sequence analyses for *Torula*. Related sequences are obtained following Tian et al. (2023). Forty-eight strains were included in the combined analyses, which comprised 4,154 characters in the combined ITS, LSU, SSU, *tef1*- α , and *rpb2* alignment. *Sporidesmioides thailandica* (MFLUCC 13-0840) was used as the outgroup taxon. The best-scoring RAxML tree with a final likelihood value of -16274.912356 is presented. The matrix contained 1,038 distinct alignment patterns, with 23.86% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.246318, C = 0.260993, G = 0.269688, T = 0.223000; substitution rates AC = 1.799472, AG = 3.895546, AT = 1.516684, CG = 1.107865, CT = 9.306890, GT = 1.000000. The tree topology of the ML analysis is similar to the Bayesian analysis. Bootstrap values for ML equal to or greater than 70% and PP values greater than 0.95 (rounding values to 2 decimal places) are labelled on the nodes. Strains of the newly described species are in orange, while type strains are in bold. (ITS: 523 bp, LSU: 835 bp, SSU: 1004 bp, *tef1*- α : 868 bp, *rpb2*: 924).

Culture characteristics – Colonies on PDA reaching 15 mm diam. after two weeks. Colony from above, dense, circular, low convex, surface smooth, with edge entire, white at the edge, dark green at the margin, white at the center; from below, white at the edge, dark green at the center.

Material examined – China, Yunnan Province, Xishuangbanna, on dead stems of unidentified grass (Poaceae), 25 November 2020, Y. Gao, BNGY8 (HKAS 145985), living culture KUNCC 25-19175.

Known hosts and distribution – on a dead branch of *Chromolaena odorata* (Asteraceae) in Thailand (Li et al. 2017a), on dead stems of grass (Poaceae) in Yunnan Province, China (This study).

GenBank numbers – KUNCC 25-19175: ITS = PV608620, LSU = PV607474, SSU = PV607361, *tef1-α* = PV626496, *rpb2* = PV655527.

Notes – Phylogenetic analyses showed that our collection (KUNCC 25-19175) grouped within *Torula chromolaenae* (KUMCC 16-0036, holotype) with 100% ML and 1.00 PP support values (Fig. 80). A comparison of the ITS, LSU, SSU, *tef1-α*, and *rpb2* nucleotide base pair indicates that our collection is identical to the type strain of *T. chromolaenae* (KUMCC 16-0036), which is not significantly different (521/526 bp in ITS, 846/846 bp in LSU, 840/841 bp in SSU, 872/872 bp in *tef1-α*, 818/818 bp in *rpb2*). Our collection (KUNCC 25-19175) with *T. chromolaenae* (KUMCC 16-0036) is also similar in morphology, having doliiform conidiogenous cells and 2–3-septate conidia. (Li et al. 2017a). Based on morphological and phylogenetic support, we introduce our collection as a new record of *Torula chromolaenae* from grass in China.

Torula fici Crous, IMA Fungus 6 (1): 192 (2015)

Fig. 82

Index Fungorum number: IF816154; Facesoffungi number: FoF02712

Saprobic on dead stems of grass. Sexual morph: Undetermined. Asexual morph: Colonies discrete on a host, black, powdery. *Conidiophores* 7.4–14 μm long × 2.3–5.8 μm diam. ($\bar{x}$ = 12 × 4 μm, n = 15), macronematous, mononematous, solitary, erect, light brown, verruculose, thick-walled, first cell from the bottom is pale brown to sub-hyaline, wide at the base and narrow at the apex, conidiophore arising from prostrate hypha. *Conidiogenous cells* 4–6.5 μm long × 4.2–7 μm diam. ($\bar{x}$ = 5.5 × 5.2 μm, n = 20), subglobose, polyblastic, terminal, smooth to minutely verruculose, brown to dark brown, paler or subhyaline at apex. *Conidia* 11–25 × 4.2–6.3 μm ($\bar{x}$ = 15.5 × 5.5 μm, n = 30), subcylindrical, catenated, acrogenous, simple, phragmosporous, 3–9-septate, slightly constricted at some septa, light yellow to dark brown, smooth to minutely verruculose, rounded at both ends, often paler at the apex. Conidial secession schizolytic.

Culture characteristics – Colonies on PDA reaching 45 mm diam. after three weeks. Colony from above, dense, circular, low convex, surface smooth, with edge entire, pale yellow at the margin, white at the center; from below, white to cream at the edge, yellow-brown at the center, producing pigmentation on PDA media.

Material examined – China, Yunnan Province, Kunming, on dead stems of unidentified grass (Poaceae), 25 March 2021, Y. Gao, GY55 (HKAS 135325), living culture KUNCC 25-19174.

Known hosts and distribution – *Chromolaena odorata* (Asteraceae), *Ficus septica*, *Ficus religiosa* (Moraceae), *Garcinia* sp. (Clusiaceae), *Magnolia grandiflora* (Magnoliaceae), *Olea europaea* (Oleaceae), *Pandanus* sp. (Pandanaceae), *Musa* sp. (Musaceae) from China (Taiwan), Cuba, South Africa, Thailand (Crous et al. 2015a, b, c, Li et al. 2017a, b, Tibpromma et al. 2018b, Jayasiri et al. 2019, Mapook et al. 2020, Samarakoon et al. 2021, Tennakoon et al. 2021a, Jayawardena et al. 2022), on dead stems of grass (Poaceae) in Yunnan Province, China (This study).

GenBank numbers – KUNCC 25-19174: ITS = PV608619, LSU = PV607473, SSU = PV607360, *tef1-α* = PV626495, *rpb2* = PV655526.

Notes – In our phylogenetic analyses, combined ITS, LSU, SSU, *tef1-α*, and *rpb2* sequence data show our collection (KUNCC 25-19174) grouped with *Torula fici* (KUMCC 16-0038, UESTCC 22-0124, UESTCC 22-0123, KUMCC 15-0428, CBS 595.96) (Fig. 80). Morphological comparisons revealed that our collection is similar to *T. fici* (CBS 595.96, ex-type) (Crous et al. 2015a, b, c). Hence, we introduce *Torula fici* (KUNCC 25-19174) as a new host record from grass (Poaceae) in China based on morphology and phylogeny.

Sordariomycetes O.E. Erikss. & Winka, Myconet 1: 10 (1997)

Amphisphaeriales D. Hawksw. & O.E. Erikss., Systema Ascomycetum 5: 177 (1986)

Sporocadaceae Corda, Icones fungorum hucusque cognitorum 5: 34 (1842)

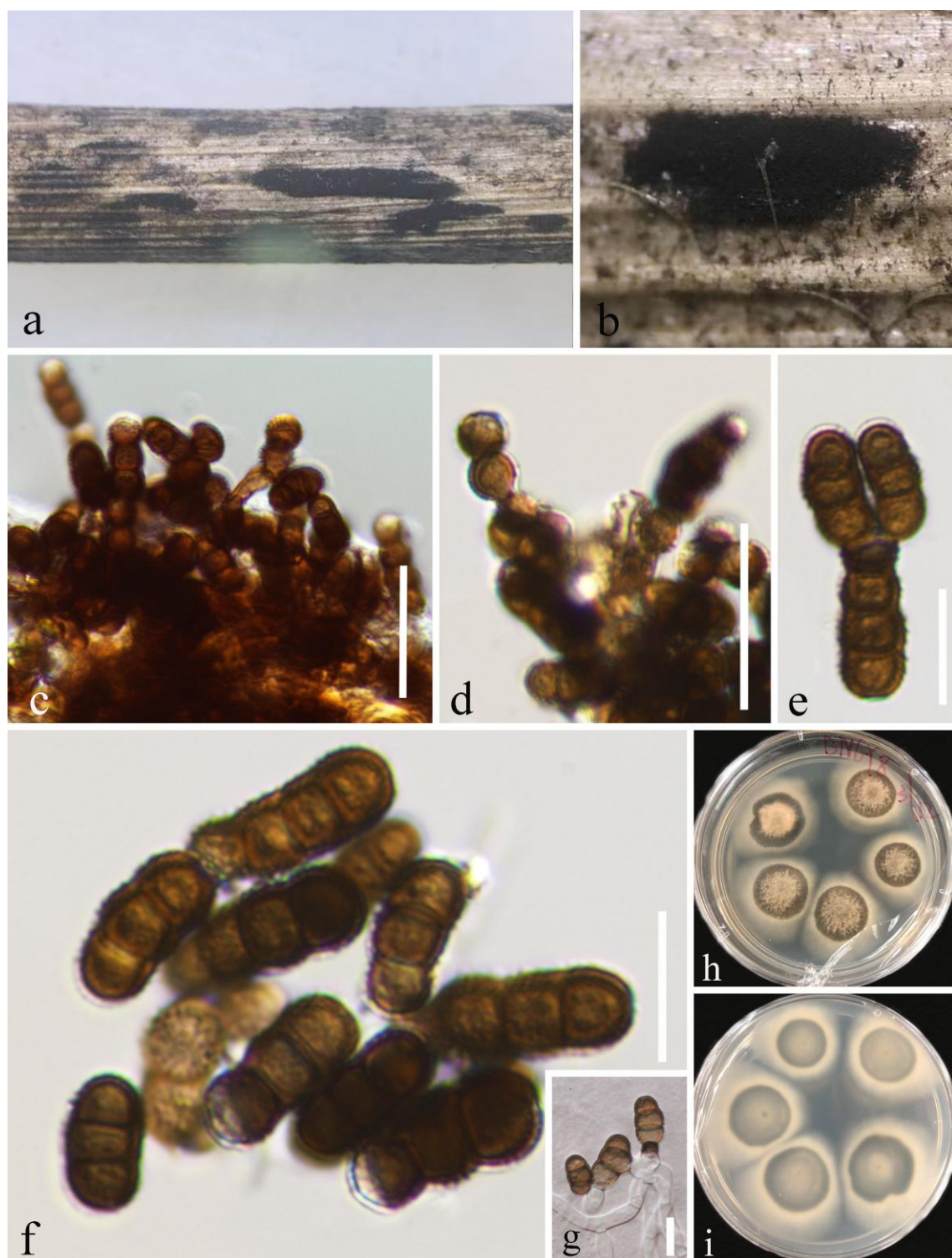


Figure 81 – *Torula chromolaenae* (HKAS 145985, a new host and a new geographical record). a, b Colonies on the host substrate. c, d Conidiophores with conidiogenous cells. e Branched chains of conidia. f Conidia in catenated chain and conidia. g Germinated conidia. h, i Culture characters on PDA (h: above, i: below). Scale bars: c, d = 20 μ m, e–g = 10 μ m.

Notes – Sporocadaceae was established by Corda (1842), with *Sporocadus* as the type genus. Species of Sporocadaceae are saprobic, endophytic, plant pathogenic, parasitic on humans and animals, and associated with a wide range of host plants (Maharachchikumbura et al. 2013, Jayawardena et al. 2015, Liu et al. 2019, Zhang et al. 2022). The family comprises 35 genera (Hyde et al. 2024a). The majority of genera exhibit multi-septate, somewhat fusiform conidia, often

bearing appendages at one or both extremities, commonly containing melanized cells. These fungi, referred to as pestalotioid, closely resemble *Pestalotia* (Liu et al. 2019). An updated phylogenetic tree based on combined ITS, LSU, *tub2*, *tef1-α*, and *rpb2* sequence data is presented in Fig. 83.

Discosia Lib., Plantae Cryptogamae, quas in Arduenna collegit Fasc. 4: no. 346 (1837)

Notes – *Discosia* was established by Libert (1837) with *D. artocreas* designated as the type species. *Discosia* is cosmopolitan and includes species of plant pathogens, saprobes, endophytes, and rarely biotrophs (Sutton 1980, Tanaka et al. 2011, Jiang et al. 2021c, Tennakoon et al. 2021a, Razaghi et al. 2024). Species of *Discosia* that exhibit a sexual form were formerly categorized under *Adisciso* and were distinguished by unitunicate asci containing a subapical ring that reacts either J⁺ or J[−] in Melzer's reagent, along with eight biseriate ascospores. In accordance with the "one fungus, one name" principle (Hawksworth et al. 2011), *Adisciso* was later synonymized with *Discosia* (Liu et al. 2019). Most species of *Discosia* have been reported as asexual, with only four as sexual (Yamamoto et al. 2012, Liu et al. 2019, Razaghi et al. 2024). In this study, we introduce a new host and geographical record for *Discosia macrozamia*, with descriptions and illustrations (Fig. 84). An updated phylogenetic tree based on combined ITS, LSU, *tub2*, *tef1-α*, and *rpb2* sequence data is presented in Fig. 83.

Discosia macrozamia Crous, Persoonia 40: 379 (2018)

Fig. 84

Index Fungorum number: IF825435; Facesoffungi number: FoF18356

Saprobic on a dead blade of *Photinia* × *fraseri*. Sexual morph: Undetermined. Asexual morph: Coelomycetous. *Conidiomata* 250–380 µm diam. × 70–90 µm high ($\bar{x}$ = 342 × 78 µm, n = 15), rounded, flattened, or concave at the center with a convex margin and a relatively thin stromatic base, conspicuous, stromatic, pycnidial, amphigenous, scattered or aggregated, black, epidermal, glabrous, unilocular or multilocular, ostiolate. *Ostiole* circular, papillate. *Conidiomatal wall* 20–30 µm wide ($\bar{x}$ = 22 µm, n = 30, conidiomatal wall at base), comprises several layers of small, flattened, brown to dark brown pseudoparenchymatous cells, light brown to brown, arranged in a *textura angularis*, fusing and indistinguishable from the host tissues; 7–13 µm wide ($\bar{x}$ = 10 µm, n = 30, conidiomatal wall at top), black. *Conidiophores* reduced to conidiogenous cells, arising from the upper cells of the basal stroma. *Conidiogenous cells* 5–8 × 1.5–4 µm ($\bar{x}$ = 6 × 2.5 µm, n = 30), holoblastic to phialidic, integrated, ampulliform, smooth-walled, hyaline. *Conidia* 24–30 × 3–5 µm ($\bar{x}$ = 26.5 × 4 µm, n = 30), fusiform to cylindrical, thick-walled, straight or slightly curved, hyaline, slightly constricted at one septum at apex, with cells of equal width, basal cell obconic, with a truncate base, apical cell subconical with a rounded apex, 3-septate, unbranched, filiform, flexuous or straight appendage; the presence of both ends, apical and basal appendages 6.5–11 × 0.5–1.2 µm ($\bar{x}$ = 9 × 0.9 µm, n = 25).

Culture characteristics – Conidia germinated on PDA reaching 50 mm diam. after three weeks at 27°C, colonies from above, circular, with the undulate edge, gray at the center, white at the margin; from below, pale yellow at the margin, white at the edge, dark brown at the center.

Material examined – China, Yunnan Province, Kunming, 10 October 2022, on the decaying leaf blade of *Photinia* × *fraseri* (Rosaceae), Y. Gao, KG4 (HKAS 132970), living culture KUNCC 25-19195.

Known hosts and distribution – on leaves of *Macrozamia miquelii* (Zamiaceae) in Australia (Crous et al. 2018), on the decaying leaf blade of *Photinia* × *fraseri* (Rosaceae) in Yunnan Province, China (This study).

GenBank numbers – KUNCC 25-19195: ITS = PV608642, LSU = PV607491, *tub2* = PV613327.

Notes – In the multigene phylogenetic analyses, our collection (KUNCC 25-19195) grouped with *Discosia macrozamia* (CBS 144436, CPC 32113) (Fig. 83). In addition, the nucleotides of our collection (KUNCC 25-19195) are not different from *D. macrozamia* (CBS 144436, ex-type). Our collection (HKAS 132970) is morphologically similar to *D. macrozamia* (CBS 144436) by its

conidiogenous cells, conidia, apical and basal appendages (Crous et al. 2018). Thus, this is a new host and a geographical record of *Discosia macrozamia* on *Photinia × fraseri* in China.

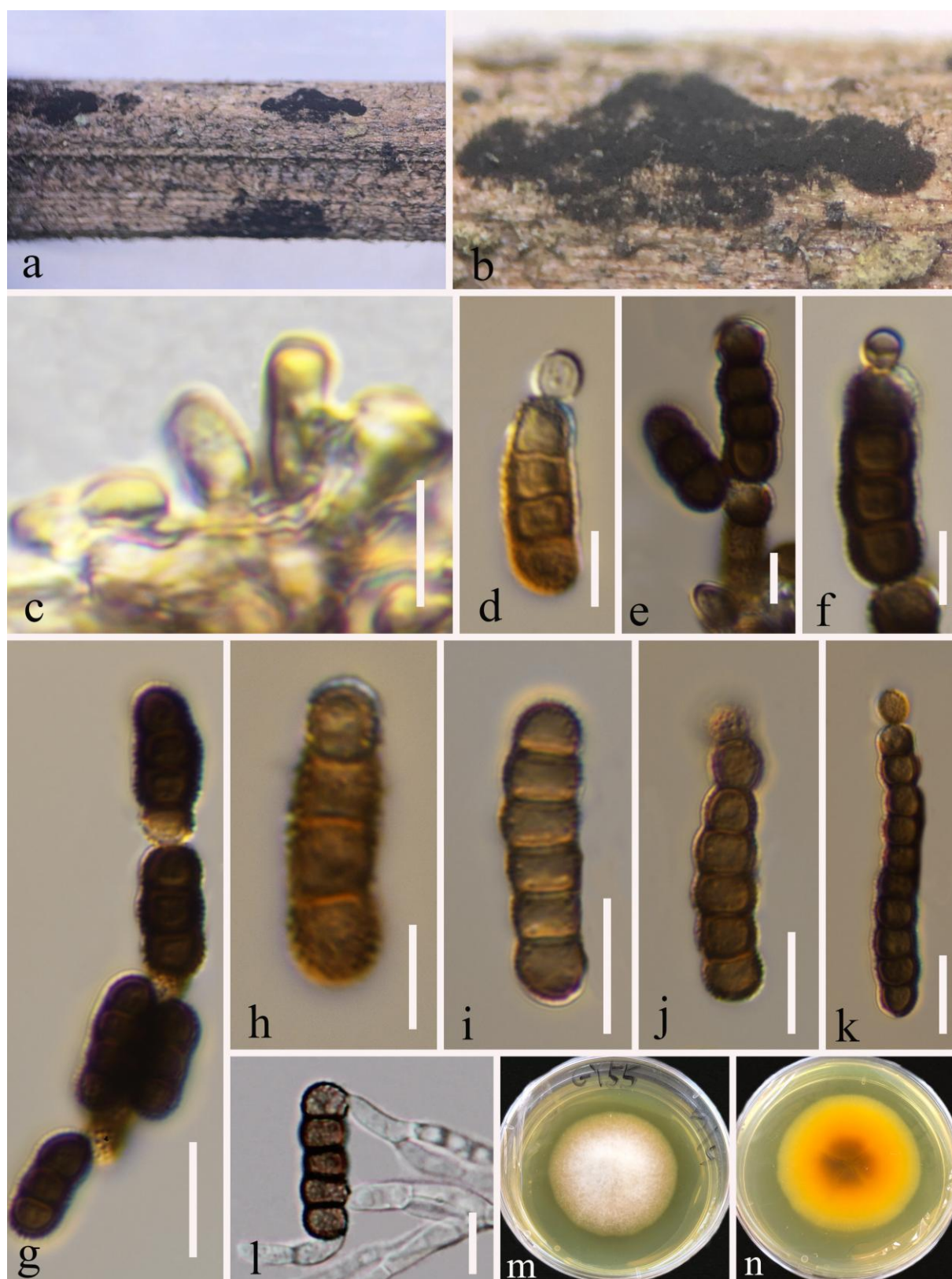


Figure 82 – *Torula fici* (HKAS 135325, a new host record). a, b Colonies on the host substrate. c Conidiogenous cells and Conidia. d–k Conidia in catenated chain and conidia. l A germinated conidium. m, n Culture characters on PDA (m: above, n: below). Scale bars: g, i–l = 10 μm, c, d–f, h = 5 μm.

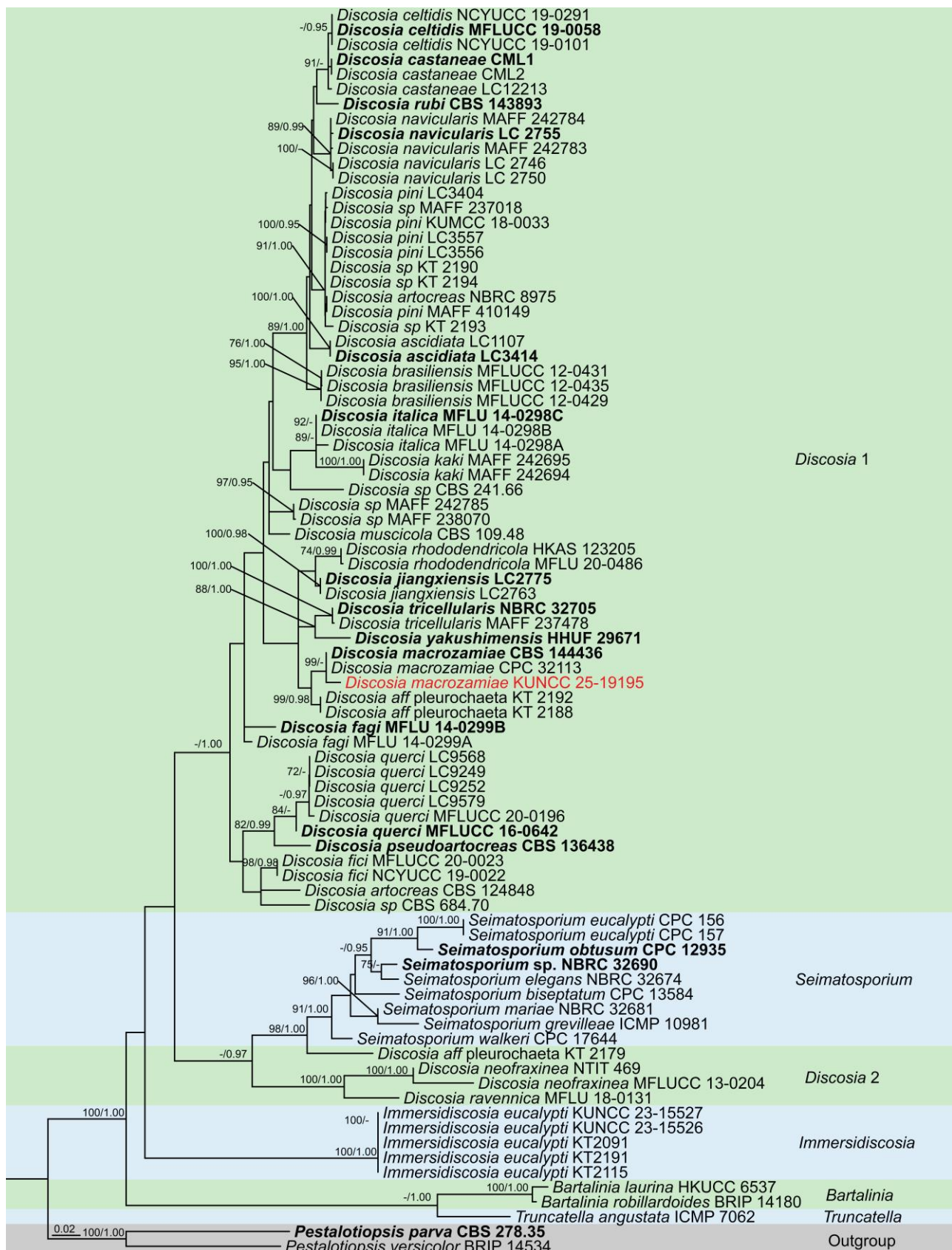


Figure 83 – RAxML phylogram generated from a combined dataset of partial ITS, LSU, *tub2*, *tef1-α*, and *rpb2* DNA sequence analyses for *Discosia*. Related sequences are obtained following Liu et al. (2019). Eighty-four strains were included in the combined analyses, which comprised 3,188 characters in the combined ITS, LSU, *tub2*, *tef1-α*, and *rpb2* alignment. *Pestalotiopsis parva* (CBS 278.35) and *Pestalotiopsis versicolor* (BRIP 14534) were used as the outgroup taxa. The best-

scoring RAxML tree with a final likelihood value of -15048.719579 is presented. The matrix contained 992 distinct alignment patterns, with 38.02% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.248883, C = 0.240013, G = 0.250202, T = 0.260903; substitution rates AC = 1.666628, AG = 4.331795, AT = 1.652257, CG = 1.266557, CT = 8.879328, GT = 1.000000. The tree topology of the ML analysis is similar to the Bayesian analysis. Bootstrap values for ML equal to or greater than 60% and PP values greater than 0.90 (rounding of values to 2 decimal places) are labelled on the nodes. Strains of the newly described species are in orange, while type strains are in bold. (ITS: 533 bp, LSU: 831 bp, *tub2*: 439 bp, *tef1- α* : 524 bp, *rpb2*: 861 bp).

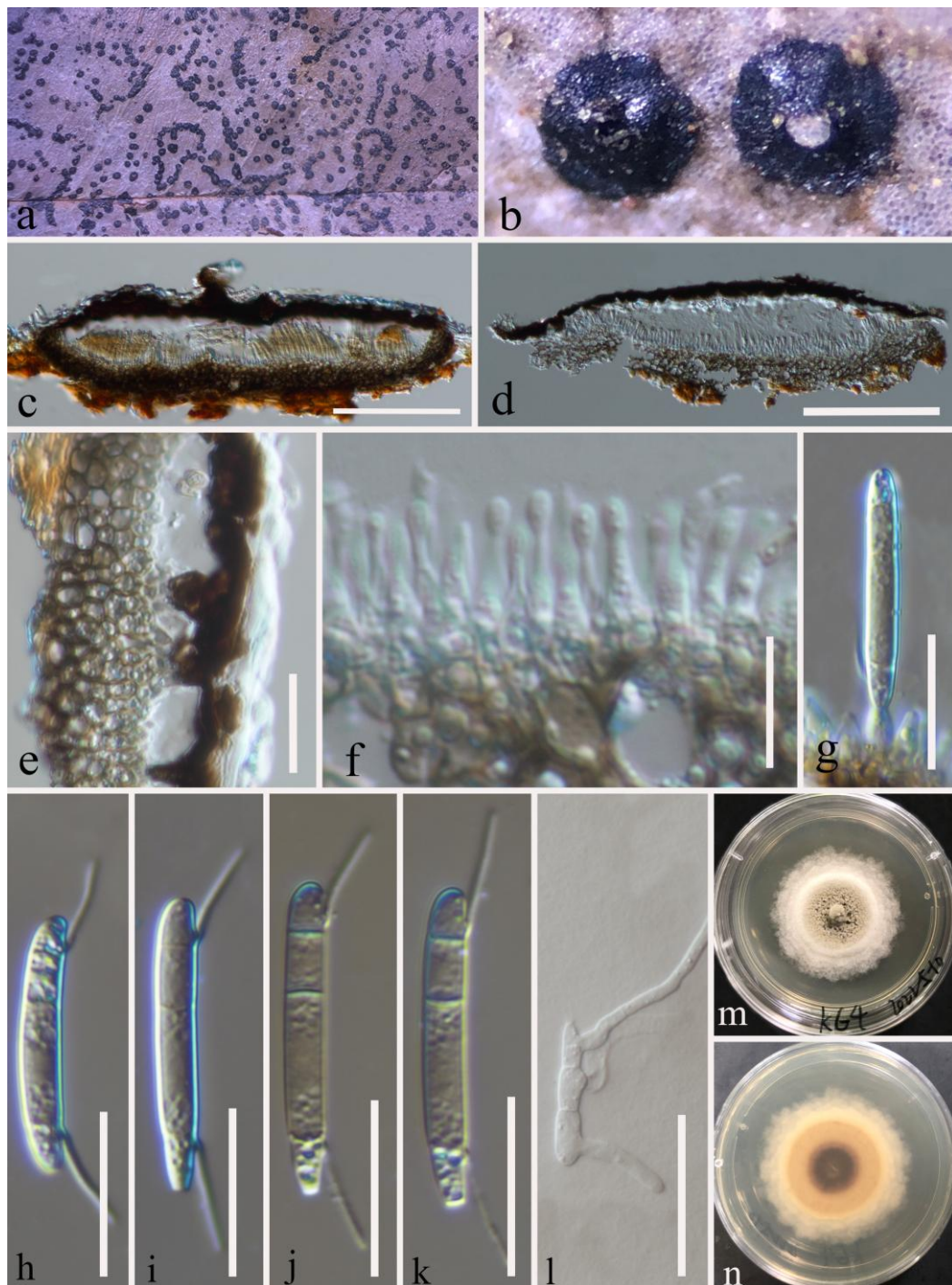


Figure 84 – *Discosia macrozamia* (HKAS 132970, a new host and a geographical record). a, b Appearance of conidiomata on host substrate. c, d Sections of conidiomata. e Conidiomatal wall. f, g Conidiogenous with developing conidia. h–k Conidia. l A germinated conidium. m, n Petri dishes with fungal cultures.

m, n Culture characters on PDA (m: above and n: below). Scale bars: c, d = 100 µm, l = 30 µm, e = 20 µm, g–k = 15 µm, f = 10 µm.

Truncatella Steyaert, Bull. Jard. bot. État Brux. 19: 293 (1949)

Notes – *Truncatella* was established by Steyaert (1949) with *T. truncata* designated as the type species. The taxonomic placement of *Truncatella* has changed multiple times over the years, initially assigned to Amphisphaeriaceae, it was later associated with Xylariales and Bartaliniaceae (Jeewon et al. 2003, Lumbsch & Huhndorf 2010, Senanayake et al. 2015). However, it is now recognized as belonging to Sporocadaceae (Hyde et al. 2020b). Species of *Truncatella* are distinguished by 3-septate, verruculose, pigmented conidia (Steyaert 1949, Jeewon et al. 2002, Maharachchikumbura et al. 2012, 2015, Dissanayake et al. 2024). They primarily act as endophytes and saprobes, though some species are also known as destructive pathogens responsible for diseases in several economically significant crops (Maharachchikumbura et al. 2016b). In this study, we introduce a new record for *Truncatella angustata*, with descriptions and illustrations (Fig. 86).

Truncatella angustata (Pers.) S. Hughes, Canad. J. Bot. 36 (6): 822 (1958)

Fig. 86

Index Fungorum number: IF307155; Facesoffungi number: FoF04092

Saprobic on dead stems of Poaceae sp. Sexual morph: Undetermined. Asexual morph: Coelomycetous. *Conidiomata* 115–130 µm diam. × 90–100 µm high ($\bar{x}$ = 121 × 93.5 µm, n = 10), immersed to erumpent, globose to subglobose, uni-loculate, solitary, coriaceous, brown to dark brown with ostiole. *Conidiomatal wall* 12–25 µm wide ($\bar{x}$ = 19 µm, n = 15), comprises several layers of hyaline to brown cells of *textura angularis* to *textura globulosa*. *Conidiophores* reduced to conidiogenous cells, cylindrical, hyaline, smooth-walled. *Conidiogenous cells* 5–10 × 1–3 µm ($\bar{x}$ = 8.5 × 2 µm, n = 20), cylindrical or phialidic, hyaline, smooth, percurrently proliferating. *Conidia* 15.5–20 × 6–8.5 µm ($\bar{x}$ = 17 × 6.8 µm, n = 30), ellipsoid or fusiform, straight to slightly curved, 3-septate, granulate, basal cell conic to obconic with a truncate base, single, cylindrical, unbranched, hyaline to brown, 4–7 apical appendages 20–30 × 0.5–1.5 µm ($\bar{x}$ = 23 × 1 µm, n = 15), centric, attenuated, flexuous, branched.

Culture characteristics – Conidia germinated on PDA reaching 60 mm diam. after two months at 27°C, colonies from above, raised with entire edge, dense papillate surface, a colony from above initially white, becoming white with gray at some regions, exuding olivaceous brown to black conidial masses, acervular; from below, white with black dots. *Conidiomata* semi-immersed or immersed, scattered to gregarious, stromatic, black on PDA. *Conidiophores* septate and branched, hyaline, and smooth. *Conidiogenous cells* discrete or integrated, hyaline, cylindrical to lageniform, and smooth. *hyphae* 1–3 µm wide ($\bar{x}$ = 2 µm, n = 30), branched, hyaline, septate. *Conidia* 13–20 × 5.5–7 µm ($\bar{x}$ = 17 × 6.8 µm, n = 30), fusiform, straight or occasionally slightly curved, 3-septate, pale brown to brown, 1–2 apical appendages 13.5–25 × 1–1.5 µm ($\bar{x}$ = 18.5 × 1.2 µm, n = 15), flexuous, centric, attenuated, branched.

Material examined – China, Yunnan Province, Zhaotong grassland, 25 September 2022, on the decaying stems of *Dactylis glomerata* (Poaceae), Y. Gao, LG2 (HKAS 132963), living culture KUNCC 25-19194.

Known hosts and distribution – On *Prunus armeniaca* (Rosaceae) in the US, on *Gevuina avellana* (Proteaceae) necrotic spots on leaves in Chile, on diseased branches of unidentified host in China, on *Picea abies* (Pinaceae) in Germany, on *Vitis vinifera* “Prunelard” (Vitaceae) rootstock in France, on *Lupinus* (Fabaceae) leaf, on *Prunus laurocerasus* (Rosaceae) fallen leaves, on food in Netherlands, on decaying bark in Spain, on *Heterodera carotae* cyst egg mas on *Daucus carota*, on *Pyrus malus* (Rosaceae, diseased apple tree) in Switzerland, from soil, on rhizosphere of

Gossypium sp. (Malvaceae) in Turkey, on *Picea abies* (Pinaceae) in the UK, from soil in the USA, on *Prunus* (Rosaceae) wood from unknown location, on *Salix* sp. (Salicaceae) or *Thuja* sp. (Cupressaceae) (Liu et al. 2019, Dissanayake et al. 2024), on the decaying stems of *Dactylis glomerata* (Poaceae) in Yunnan Province, China (This study).

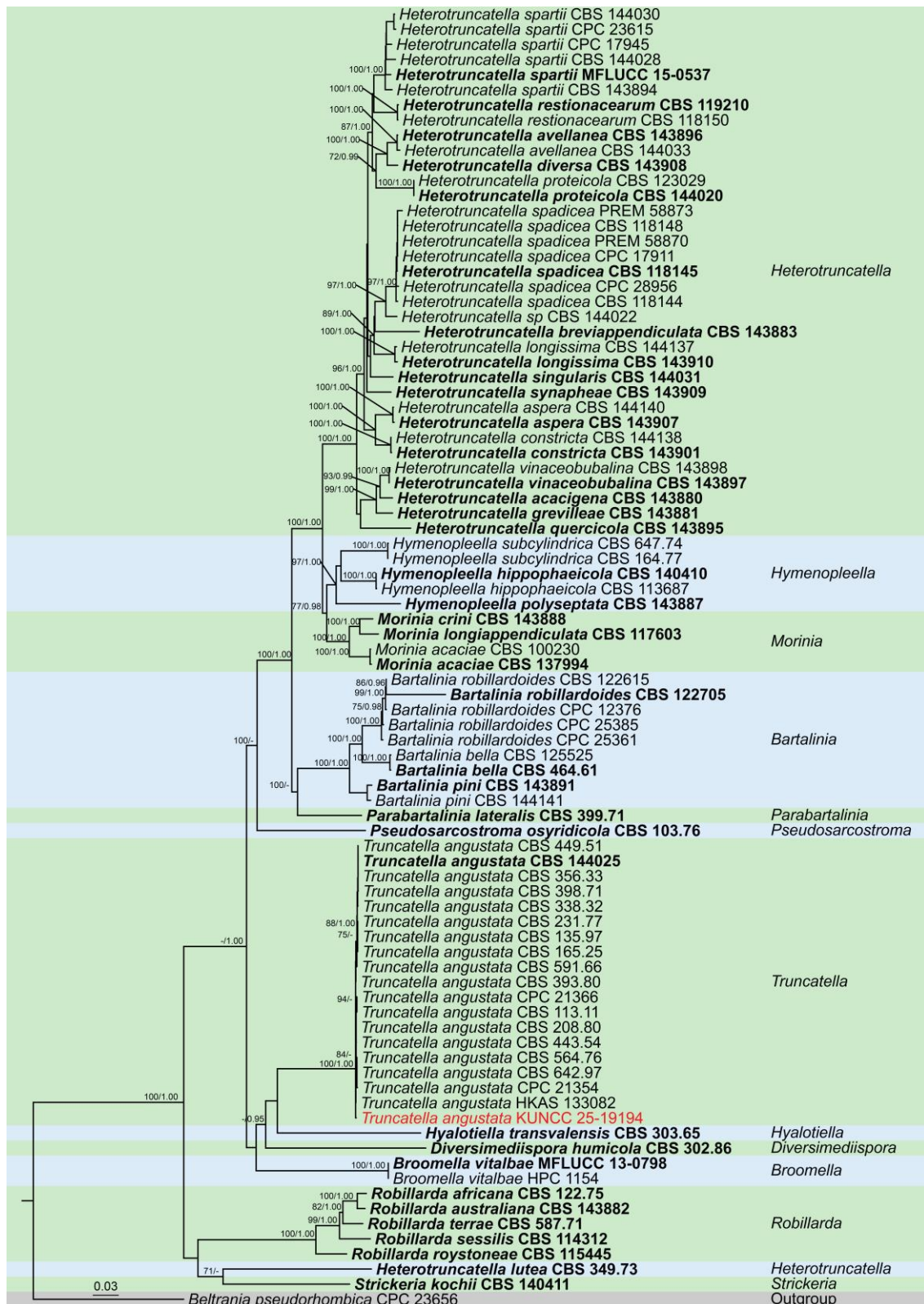


Figure 85 – RAxML phylogram generated from a combined dataset of partial ITS, LSU, *tub2*, *tef1-α*, and *rpb2* DNA sequence analyses for Sporocadaceae. Related sequences are obtained following

Liu et al. (2019). Eighty-six strains were included in the combined analyses, which comprised 3,347 characters in the combined ITS, LSU, *tub2*, *tef1-α*, and *rpb2* alignment. *Beltrania pseudorhombica* (CPC 23656) was used as the outgroup taxon. The best-scoring RAxML tree with a final likelihood value of -34968.699746 is presented. The matrix contained 1,591 distinct alignment patterns, with 7.89% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.251992, C = 0.253967, G = 0.240517, T = 0.253524; substitution rates AC = 1.496492, AG = 4.185489, AT = 1.261335, CG = 1.095786, CT = 6.512162, GT = 1.000000. The tree topology of the ML analysis is similar to the Bayesian analysis. Bootstrap values for ML equal to or greater than 60% and PP values greater than 0.90 (rounding of values to 2 decimal places) are labelled on the nodes. Strains of the newly described species are in orange, while type strains are in bold. (ITS: 496 bp, LSU: 828 bp, *tub2*: 667 bp, *tef1-α*: 524 bp, *rpb2*: 832 bp).

GenBank numbers – KUNCC 25-19194: ITS = PV608641, LSU = PV607497, *tub2* = PV613326.

Notes – *Stilbospora angustata* was initially described by Persoon (1801) lack of morphological characteristics and no additional collection records. Subsequently, it was reclassified under *Truncatella* by Hughes (1958). The holotype, likely collected by Persoon in Europe, is presumed to be housed in the herbarium L (L910264-703, Nag Raj 1993), however, it could not be located. And, to ensure the stable application of the generic type species *Truncatella angustata*, Liu et al. (2019) designated strain (CBS H-23508) as the neotype. This decision is based on its morphological resemblance to the original description, as well as the detailed description and illustrations of *Truncatella Angustata* provided by Nag Raj (1993), which align with the commonly accepted concept of this genus. Moreover, Liu et al. (2019) considered *Pestalotia hartigii*, *Pestalotia ramulosa*, *Monochaetia rosenwaldii*, *Truncatella truncata* with *Truncatella angustata* as synonyms because their type species are grouped with *Truncatella angustata*. In our multigene phylogenetic analyses, our collection (KUNCC 25-19194) grouped with *Truncatella angustata* (CBS 449.51, CBS 144025, CBS 356.33, CBS 398.71, CBS 338.32, CBS 231.77, CBS 135.97, CBS 165.25, CBS 591.66, CBS 393.80, CPC 21366, CBS 113.11, CBS 208.80, CBS 443.54, CBS 564.76, CBS 642.97, CPC 21354, HKAS 133082) (Fig. 85). We provide asexual forms of *Stilbospora angustata* (KUNCC 25-19194) from specimens and culture media. Morphologically, *Stilbospora angustata* (KUNCC 25-19194) shares similar morphology to other species of *Truncatella angustata* (Liu et al. 2019). Therefore, we identify our collection as *Truncatella angustata*, a new host record on *Dactylis glomerata* in China.

Chaetosphaeriales Huhndorf, A.N. Mill. & F.A. Fernández, Mycologia 96 (2): 378 (2004)

Neoleptosporaceae J.F. Zhang, Y.Y. Chen & Jian K. Liu, Fungal Diversity 122: 110 (2023)

Notes – Neoleptosporaceae was established to accommodate *Neoleptospora* species. The members of this family are saprophytes on the culm of herbaceous plants. Neoleptosporaceae is characterized by immersed, solitary, brown to black, ostiolate, coriaceous, subglobose to depressed globose, clypeate ascomata; composed of dark brown to black cells of *textura angularis* that emerge with the host epidermal cells outwardly peridium; cellular, numerous, septate, branched, paraphyses hamathecium. broadly cylindrical, unitunicate, pedicellate, with a J-, wedge-shaped, subapical ring asci; fasciculate, fusiform, C-shaped or sigmoid, aseptate, ends acute, guttulate ascospores (Groenewald et al. 2023, Zhang et al. 2023). Neoleptosporaceae includes only one genus. An updated phylogenetic tree based on combined ITS and LSU sequence data is presented in Fig. 87.

Neoleptospora Phukhams. & K.D. Hyde, Fungal Diversity 102: 147 (2020)

Notes – *Neoleptospora* was established by Phukhamsakda et al. (2020) with *N. clematidis* designated as the type species. *Neoleptospora* was initially regarded as morphologically similar to *Leptospora*, however, phylogenetic analyses have shown that it forms a distinct lineage and cannot be placed within any established family in Chaetosphaeriales (Phukhamsakda et al. 2020). *Neoleptospora camporesiana* (Hyde et al. 2020a), *N. fusiformispora* (Zhang et al. 2023), and *N. palmae* (Zhang et al. 2024b) were subsequently introduced into this genus. In this study, we introduce two new records for *N. camporesiana* and *N. fusiformispora*, with descriptions and illustrations (Figs. 88, 89).

Neoleptospora camporesiana R.H. Perera & K.D. Hyde, Fungal Diversity 100: 219 (2020) Fig. 88

Index Fungorum number: IF556898; Facesoffungi number: FoF06962

Saprobic on dead stalks of grasses. Sexual morph: *Ascomata* 260–340 × 205–230 µm ($\bar{x}$ = 300 × 225 µm, n = 10), immersed, solitary or gregarious, subglobose or conical, only black short papillate visible, coriaceous, uni-loculate, ostiolate. *Peridium* 7–18 µm ($\bar{x}$ = 12 µm, n = 30), composed of thin-walled, brown to dark brown cells of *textura angularis*, outer cells merging with the host epidermal cells. *Paraphyses* 2–4 µm ($\bar{x}$ = 2.8 µm, n = 30), branched, hyaline, septate, border at the base, tapering to the ends. *Asci* 65–70 × 14–18 µm ($\bar{x}$ = 68 × 16 µm, n = 25), 8-spored, broad cylindrical, thin-walled wall and frangible. *Ascospores* 56–80 × 2–5 µm ($\bar{x}$ = 66 × 3 µm, n = 30), fasciculate, narrowly fusiform, C-shaped, straight or curved, guttulate, hyaline, aseptate, ends rounded, with polar mucilaginous appendage at the apex, guttulate or verrucose. Asexual morph: Undetermined.

Culture characteristics – Ascospores germinated on PDA reaching 35 mm diam. after three weeks at 27°C, colonies from above, circular, brown at the center, light yellow at the margin with white mycelium; from below, white at the edge, pale brown at the center.

Material examined – China, Yunnan Province, Kunming, on decaying dead stalks on unidentified grass (Poaceae), 25 May 2021, Y. Gao, HLT9 (HKAS 126580), living culture KUNCC 25-19187.

Known hosts and distribution – on dead stalks of unidentified grass in Thailand (Hyde et al. 2020a), on dead stems of *Heteropanax fragrans* (Roxb.) Seem. in China (Manawasinghe et al. 2022), on the decaying stalks of grass (Poaceae) in Yunnan Province, China (This study).

GenBank numbers – KUNCC 25-19187: ITS = PV649817, SSU = PV607362, *tef1-α* = PV626505.

Notes – Our phylogenetic analysis revealed that the collection KUNCC 25-19187 is clustered with *Neoleptospora camporesiana* (MFLUCC 15-1016, ZHKUCC 22-0218, KUMCC 21-0014) group with 95/0.99 ML/PP (Fig. 87). Morphologically, our collection (HKAS 126580) has a similar size to *N. camporesiana* (KUMCC 21-0014) in ascomata (300 × 225 µm vs. 303 × 267 µm), peridium (12 µm vs. 12 µm), asci (68 × 16 µm vs. 98 × 12 µm), and ascospores (66 × 3 µm vs. 70 × 3 µm) (Manawasinghe et al. 2022). Based on morphological and phylogenetic studies, we introduced our collection as a new host record from grass in China.

Neoleptospora fusiformispora J.F. Zhang, Y.Y. Chen & Jian K. Liu, Fungal Diversity 122: 113 (2023) Fig. 89

Index Fungorum number: IF900739; Facesoffungi number: FoF14594

Saprobic on dead stems of grasses. Sexual morph: *Ascomata* 210–350 µm diam. × 190–330 µm high ($\bar{x}$ = 295 × 293 µm, n = 10), immersed, subglobose to depressed-globose, only black shiny ostioles visible, coriaceous, uni-loculate, solitary or gregarious, short papillate. *Ostiole* long,

hyaline periphyses lining the ostiolar canal. *Peridium* 23–44 μm wide ($\bar{x}$ = 29 μm , n = 30), composed of several layers of brown to dark brown, thick-walled, pseudoparenchymatous cells of *textura angularis* that merge with the host epidermal cells, becoming hyaline, elongated, thin-walled cells of *textura angularis* inwardly. *Paraphyses* 2–3.5 μm wide ($\bar{x}$ = 3 μm , n = 30), hyaline, branched, septate, border at the base, tapering to the end. *Asci* 100–145 $\times$ 10–17 μm ($\bar{x}$ = 120 $\times$ 13 μm , n = 30), 8-spored, cylindrical, unitunicate, with a J- in Melzer's reagent, wedge-shaped, subapical ring, with a long-pedicellate, thin wall. *Ascospores* 60–73 $\times$ 2.5–4 μm ($\bar{x}$ = 64 $\times$ 3.3 μm , n = 25), overlapping, fasciculate, narrowly fusiform, C-shaped, straight or curved, guttulate, 1-septate, hyaline, with drop-shaped appendages at both ends. Asexual morph: Undetermined.

Material examined – China, Yunnan Province, Kunming, on decaying stems of unidentified grass (Poaceae), 13 June 2022, Y. Gao, DG4 (HKAS 128736).

Known hosts and distribution – on dead culm of unidentified herbaceous plant in China (Zhang et al. 2023), on the decaying stems of grass (Poaceae) in Yunnan Province, China (This study).

GenBank numbers – HKAS 128736: ITS = PV649816, LSU = PV607490.

Notes – In the phylogenetic analysis, our collection (HKAS 128736) is related to the *Neoleptospora fusiformispora* (GZCC 20-0158, ex-type) with 100% ML and 1.00 PP support (Fig. 87). In morphology, our collection (HKAS 128736) resembles *N. fusiformispora* (GZCC 20-0158) in having immersed ascomata which are globose to depressed-globose, wedge-shaped asci, J- in Melzer's reagent, with fusiform ascospores (Zhang et al. 2023). Hence, based on morphological and phylogenetic evidence, we introduced our collection as a new host record for grass from China.

Sordariales Chadeff. ex D. Hawksw. & O.E. Erikss., Systema Ascomycetum 5: 182 (1986)

Schizotheciaceae Y. Marin & Stchigel, Microorganisms 8 (9, no. 1430): 24 (2020)

Notes – Schizotheciaceae was introduced by Marin-Felix et al. (2020) to accommodate lasiosphaeriaceous taxon, with *Schizothecium* as the type genus. Fourteen genera were accepted in Schizotheciaceae (Marin-Felix et al. 2020, Hyde et al. 2024a). The Schizotheciaceae are characterized by the production of ornate, ostiolate ascomata with various shapes (globose to subglobose, pyriform, pyriform-conical, ovoid or obpyriform) (Marin-Felix et al. 2020). An updated phylogenetic tree based on combined ITS, LSU, *tub2*, and *rpb2* sequence data is presented in Fig. 90.

Schizothecium Corda, Icones fungorum hucusque cognitorum 2: 29 (1838)

Notes – *Schizothecium* was introduced by Corda (1838) with *S. fimicola* as the type species. *Schizothecium* presents short, swollen agglutinated hairs or prominent, protruding ascomatal wall cells (Marin-Felix et al. 2020). Huang et al. (2021) introduced *Neoschizothecium*, characterized solely by its sexual morph, to classify ten species. This classification was supported by morphological traits and phylogenetic analyses within the Sordariomycetes. The genus, typified by *Neoschizothecium curvisporum*, was created to include *Schizothecium* species not belonging to the Podosporaceae. Furthermore, *Neoschizothecium* was designated as the type genus of the newly proposed family Neoschizotheciaceae by Huang et al. (2021). However, according to Marin-Felix & Miller (2022), the establishment of *Neoschizothecium* to reclassify former *Schizothecium* species is considered unnecessary. Further investigation is required before reassigning this species to *Schizothecium*. The nine new combinations under *Neoschizothecium* for former *Schizothecium* species are also deemed unnecessary, aligning with the argument that Neoschizotheciaceae is invalid (Marin-Felix & Miller 2022, Hyde et al. 2024a). And Marin-Felix & Miller (2022) resurrected the generic name *Schizothecium* in Schizotheciaceae, Sordariales, Sordariomycetes. In

this study, we introduce a new species, *Schizothecium dactylidis*, with descriptions and illustrations (Fig. 91).

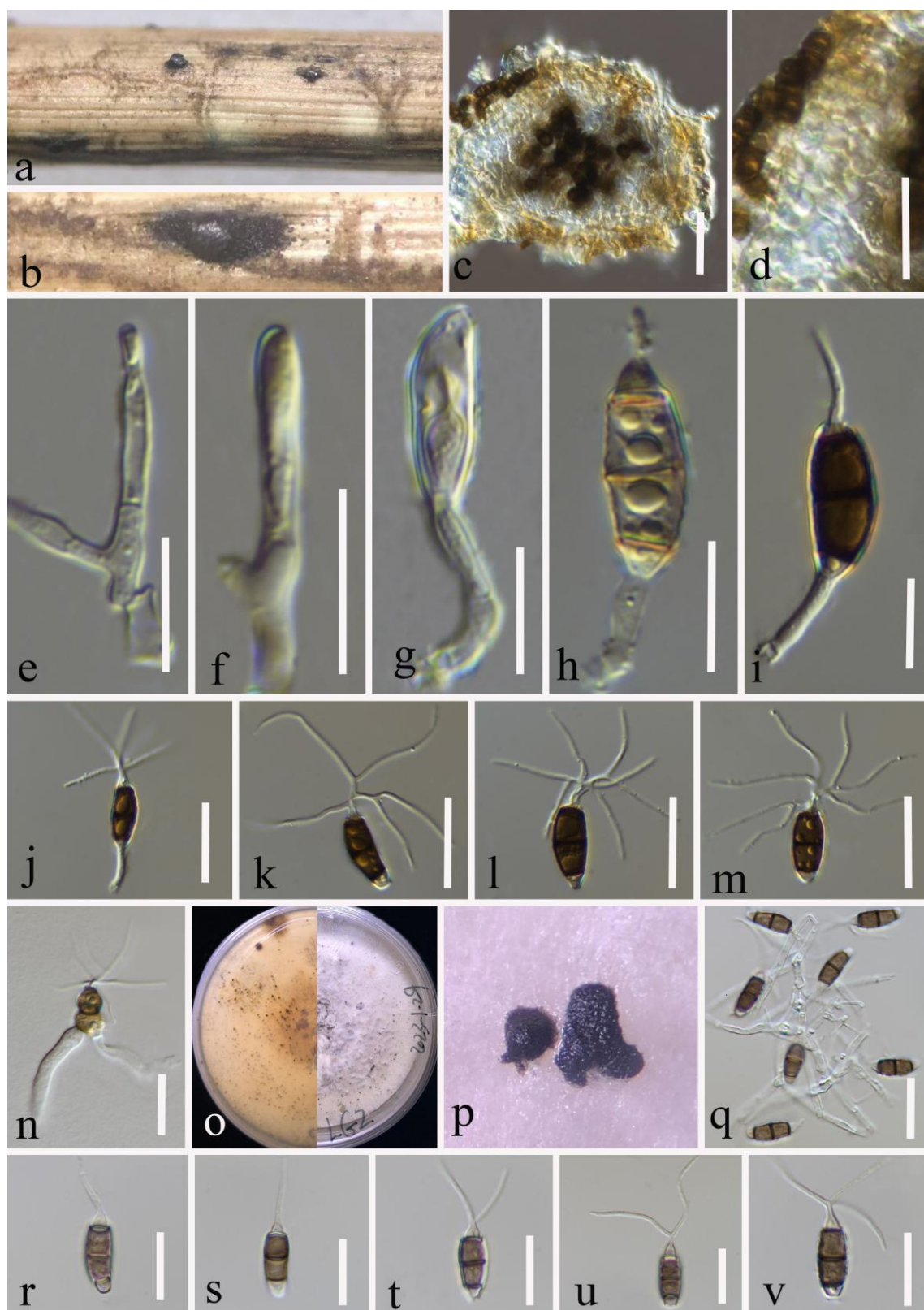


Figure 86 – *Truncatella angustata* (HKAS 132963, a new host record). a, b Conidiomata on the host substrate. c A section of a conidioma. d Conidiomatal wall. e–i Conidiogenous with conidia. j–m Conidia. n A germinated conidium. o Cultural characters on PDA (left: below, right: above).

p Conidiomata on PDA. q Conidiogenous cells and conidia from PDA. r–v Conidia from PDA. Scale bars: c = 30 μ m, d, j–n, q = 20 μ m, r–v = 15 μ m, e–i = 10 μ m.

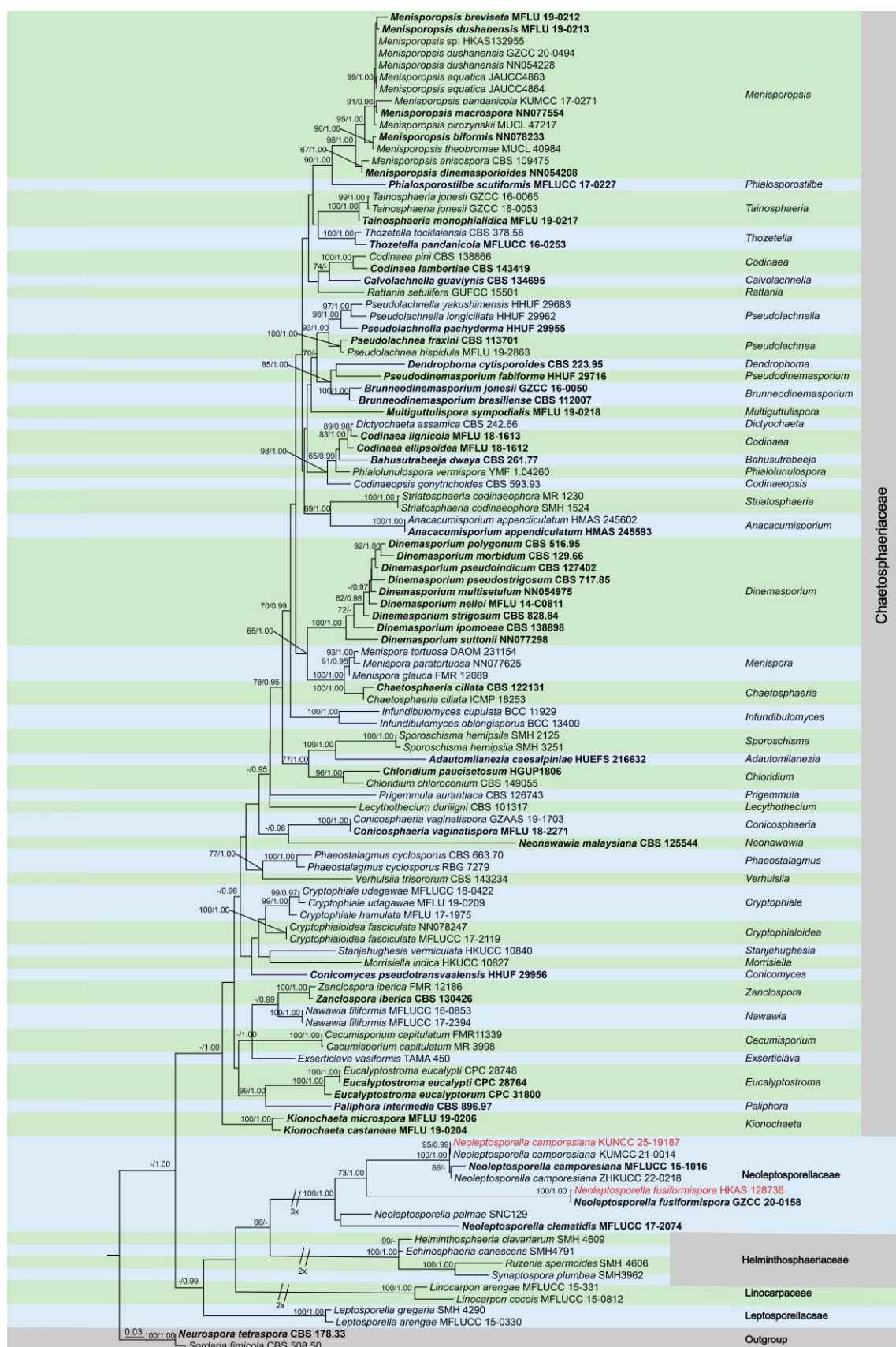


Figure 87 – RAxML phylogram generated from a combined dataset of partial ITS and LSU DNA sequence analyses for Chaetosphaeriales. Related sequences are obtained following Zhang et al.

(2023). One hundred and twelve strains were included in the combined analyses, which comprised 1,345 characters in the combined ITS and LSU alignment. *Neurospora tetraspora* (CBS 178.33) and *Sordaria fimicola* (CBS 508.50) were used as the outgroup taxa. The best-scoring RAxML tree with a final likelihood value of -21532.861071 is presented. The matrix contained 807 distinct alignment patterns, with 11.55% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.224599, C = 0.272677, G = 0.309842, T = 0.192882; substitution rates AC = 1.385837, AG = 1.917554, AT = 1.339246, CG = 0.881162, CT = 5.756928, GT = 1.000000. The tree topology of the ML analysis is similar to the Bayesian analysis. Bootstrap values for ML equal to or greater than 60% and PP values greater than 0.95 (rounding of values to 2 decimal places) are labelled on the nodes. Strains of the newly described species are in orange, while type strains are in bold. (ITS: 501 bp, LSU: 844 bp).

Schizothecium dactylidis Y. Gao, H. Gui & K.D. Hyde, sp. nov.

Fig. 91

Index Fungorum number: IF903841; Facesoffungi number: FoF17715

Holotype – HKAS 132985

Etymology: The specific epithet is derived from the genus *Dactylis* (Poaceae), which the holotype was found.

Saprobic on dead stems of *Dactylis glomerata*. Sexual morph: Undetermined. Asexual morph: dark brown to black spore masses visible on host substrates. *Conidiophores* are reduced to conidiogenous cells. *Conidiogenous cells* 3.5–5 × 3–4 µm ($\bar{x}$ = 4.3 × 3.5 µm, n = 20), globose to subglobose or phialidic, hyaline, aseptate, discrete, smooth-walled. *Conidia* 20–22 × 12–15 µm ($\bar{x}$ = 22 × 14 µm, n = 20, immature conidia), 37–44 × 24–30 µm ($\bar{x}$ = 40.5 × 27 µm, n = 20, mature conidia), ellipsoidal or subglobose to oval, pale brown to dark brown, smooth-walled, aseptate, germ pore at one end, with gelatinous sheath.

Culture characteristics – Conidia germinated on PDA, reaching 15 mm diam. after three weeks at 27°C, colonies from above, irregular, pale gray to olive-gray in the middle, surface rough, umbonate, dull; from below, dark brown to grey in the center, grey at the margin.

Material examined – China, Yunnan Province, Zhaotong grassland, on decaying leaves of *Dactylis glomerata* (Poaceae), 25 September 2022, Y. Gao, QG63A (HKAS 132985), living culture (KUNCC 25-19192).

GenBank numbers – KUNCC 25-19192: ITS = PV608640, LSU = PV607496, *rpb2* = PV631997.

Notes – In the multigene phylogenetic analyses, *Schizothecium dactylidis* (KUNCC 25-19192) grouped as a sister taxon to *S. glutinans* (CBS 134.83) with 100% ML and 1.00 PP support values (Fig. 90). Based on the recommendations of Jeewon & Hyde (2016), and Chethana et al. (2021) the nucleotide comparisons showed that *S. dactylidis* (KUNCC 25-19192) is significantly different from *S. glutinans* (CBS 134.83) in ITS 8.26% (48/581, with 15 gaps) and LSU 1.21% (10/826, without gaps). Bell & Mahoney (1995) provided a sexual morphological analysis of *Schizothecium glutinans* on rabbit dung in the United States. Therefore, we identified the *Schizothecium dactylidis* as a new species from *Dactylis glomerata* in China.

Xylariales Nannf., Nova Acta Regiae Societatis Scientiarum Upsaliensis Ser. IV. 8 (2): 66 (1932)

Apiosporaceae K.D. Hyde, J. Fröhl., Joanne E. Taylor & M.E. Barr, Sydowia 50 (1): 23 (1998)

Notes – Apiosporaceae was introduced by Hyde et al. (1998) to accommodate the genera *Appendicospora* and *Apiospora*, with *Apiospora* as the type genus. Apiosporaceae is closely related to Amphisphaeriaceae within Amphisphaeriales (Crous & Groenewald 2013). The Apiosporaceae includes four genera: *Apiospora*, *Arthrimum*, *Nigrospora*, and *Neoarthrinium* (dos Santos et al. 2024, Hyde et al. 2024a).

Apiospora Sacc., Conspectus generum pyrenomycetum italicorum systemate carpologico dispositum: 9 (1875)

Notes – *Apiospora* was introduced by Saccardo (1875), with *A. montagnei* as the type species (Saccardo et al. 1931). The sexual morph of *Apiospora* is characterized by perithecial, multi-locular stromata, hyaline ascospores with a thick gelatinous sheath (Senanayake et al. 2015, Dai et al. 2016, Pintos & Alvarado 2021). The asexual morph in basauxic conidiogenesis, globose to sub-globose, or obovoid to fusiform, pale brown to brown conidia (Hyde et al. 1998, 2024a, Dai et al. 2016). Members of *Apiospora* can be saprobes, endophytes, phytopathogens, some are associated with air, lichens, soil-borne or animal tissues (Sharma et al. 2014, Dai et al. 2017, Goodenough et al. 2017, Wang et al. 2017a, 2018, Hyde et al. 2020b, Senanayake et al. 2020b, Tang et al. 2020, Pintos & Alvarado 2021, Yin et al. 2021). In this study, we introduce three new records for *Apiospora arundinis*, *A. locuta-pollinis*, *A. rasikravindrae*, a new species, *A. poacearum*, with descriptions and illustrations (Figs. 93–96). An updated phylogenetic tree based on combined ITS, LSU, *tub2*, and *rpb2* sequence data is presented in Fig. 92.

***Apiospora arundinis* (Corda) Pintos & P. Alvarado, Fungal Systematics and Evolution 7: 205 (2021)** Fig. 93

Index Fungorum number: IF837742; Facesoffungi number: FoF13417

Saprobic on dead culms of Poaceae sp. Sexual morph: Undetermined. Asexual morph: Colonies are compact, round, dark brown to black. *Conidiophores* indistinct, often reduced to conidiogenous cells. *Conidiogenous cells* 2–5 × 2–6 µm ($\bar{x}$ = 3.5 × 4 µm, n = 20), monoblastic or polyblastic, determinate, terminal or intercalary, globose to ellipsoidal, hyaline to brown, smooth. *Conidia* 5.5–7.5 × 5–7 µm ($\bar{x}$ = 6.2 × 6 µm, n = 30), globose to ovoid or ellipsoidal, aseptate, smooth-walled, pale brown to brown.

Culture characteristics – Conidia germinated on PDA within 24 hours. Colonies on PDA reached 60 mm in three weeks at room temperature (27°C). Colony from above, with an undulate edge, white, sparse aerial mycelium on the surface; from below, white to pale yellow to light brown.

Material examined – China, Yunnan Province, Zhaotong grassland, on decaying culms of bamboo (Poaceae), 21 August 2021 Y. Gao, ZG9 (HKAS 126576), living culture KUNCC 25-19184; China, Yunnan Province, Kunming, on decaying stems of unidentified grass (Poaceae), 20 June 2021, Y. Gao, CCSG25 (HKAS 133003), living culture KUNCC 25-19185, *ibid.* CCSG27 (HKAS 133004), living culture KUNCC 25-19186.

Known hosts and distribution – *Apiospora arundinis* has been collected on *Brunfelsia brasiliensis*, *Castanea mollissima*, *Phyllostachys praecox*, *Polygonatum cyrtonema*, *Saccharum officinarum* in China (Chen et al. 2014, Jiang & Tian 2021, Liao et al. 2022, Li et al. 2023, Dissanayake et al. 2024), on decaying stems of grass (Poaceae) in Yunnan Province, China (This study).

GenBank numbers – KUNCC 25-19184: ITS = PV608633, LSU = PV607487, *tef1-α* = PV626502; KUNCC 25-19185: ITS = PV608634, LSU = PV607488, *tef1-α* = PV626503; KUNCC 25-19186: ITS = PV608635, LSU = PV607489, *tef1-α* = PV626504.

Notes – Our phylogenetic analysis revealed that our collections (KUNCC 25-19184, KUNCC 25-19185, KUNCC 25-19186) are grouped within the *Apiospora arundinis* (KUMCC 21-0697, KUMCC 21-0698, KUNCC 23-15560, CBS 133509, CBS 124788, CBS 449.92) (Fig. 92). From a morphological perspective, our collections (KUNCC 25-19184, KUNCC 25-19185, KUNCC 25-19186) align closely with the characteristics of *A. arundinis* as described by Liu et al. (2023c), particularly in the comparable size of the conidia to those documented in earlier research (Chen et al. 2014, Jiang et al. 2021a, Liao et al. 2022). Therefore, we identified that our collections are *Apiospora arundinis*, which represents a new host record.

Apiospora locuta-pollinis (F. Liu & L. Cai) Pintos & P. Alvarado, Fungal Systematics and Evolution 7: 206 (2021) Fig. 94

Synonyms: *Arthrinium pseudomarii* T.Z. Chen, Yong Wang bis & K.D. Hyde, Mycotaxon 136 (1): 191 (2021)

Basionym: *Arthrinium locutum-pollinis* F. Liu & L. Cai, Mycosphere 9 (6): 1094 (2018)

Index Fungorum number: IF834523; Facesoffungi number: FoF05221

Saprobic on dead stems of grasses. Sexual morph: Undetermined. Asexual morph: *Colonies* on the natural substrate are velvety, dry, dull, dark brown to black, with a sterile mycelial outer zone and a round, abundantly sporulating, where conidia are readily liberated upon disturbance. *Mycelium* branched, superficial, septate, hyaline to dark brown, smooth-walled, hyphae. *Conidiophores* are reduced to conidiogenous cells, grouped to form sporodochia. *Conidiogenous cells* $2-7 \times 2-5.5 \mu\text{m}$ ($\bar{x} = 3.8 \times 3.5 \mu\text{m}$, $n = 15$), globose to subglobose or cylindrical, monoblastic or polyblastic, hyaline to brown, aggregated, smooth. *Conidia* $6-8.5 \mu\text{m}$ ($\bar{x} = 7 \mu\text{m}$, $n = 35$), globose in the surface view, with a central scar, straight germ slit spore length, brown to dark brown.

Culture characteristics – Conidia germinated on PDA, reaching 60 mm diam. after two weeks at 27°C, colonies from above, white, filiform, flat, woolly, spreading, with abundant aerial mycelia; from below, off-white to yellow.

Material examined – China, Yunnan Province, Kunming, on decaying stems of unidentified grass (Poaceae), 01 March 2022, Y. Gao, XG2 (HKAS 132969), living culture KUNCC 25-19177; China, Yunnan Province, Kunming, on decaying stems of unidentified grass (Poaceae), 21 April 2021, Y. Gao, GY40 (HKAS 132995), living culture KUNCC 25-19178; China, Yunnan Province, Zhaotong grassland, on decaying stems of unidentified grass (Poaceae), 27 August 2022, Y. Gao, QG66 (HKAS 146007), living culture KUNCC 25-19179.

Known hosts and distribution – on leaves of *Aristolochia debilis* (Aristolochiaceae) in China (Chen et al. 2021, as *Arthrinium pseudomarii*), on *Brassica campestris* (Brassicaceae) in China (Tian et al. 2021), on dead culms of bamboos in China (Dissanayake et al. 2024), on decaying stems of grass (Poaceae) in Yunnan Province, China (This study).

GenBank numbers – KUNCC 25-19177: ITS = PV608625, LSU = PV607479, *tub2* = PV613316, *tef1-α* = PV626411; KUNCC 25-19178: ITS = PV608626, LSU = PV607480, *tub2* = PV613317, *tef1-α* = PV626412; KUNCC 25-19179: ITS = PV608627, LSU = PV607481, *tub2* = PV613318, *tef1-α* = PV626413.

Notes – Our phylogenetic analyses showed that our collections (KUNCC 25-19177, KUNCC 25-19178, KUNCC 25-19179) group within the lineage of *Apiospora locuta-pollinis* (GUCC 10228, KUNCC 22-12408, KUNCC 24-17551, KUNCC 24-17550, KUMCC 21-0694, KUMCC 21-0693, LC11683) (Fig. 92). Chen et al. (2021) originally described *Arthrinium pseudomarii* (GUCC 10228) from the leaves of *Aristolochia debilis* in Yunnan Province, China. Later, Tian et al. (2021) found that *Arthrinium pseudomarii* was phylogenetically and morphologically similar to *Apiospora locuta-pollinis*, leading them to synonymize *Arthrinium pseudomarii* under *Apiospora locuta-pollinis*. Our multigene phylogenetic results show that *Apiospora marii* (KUMCC 21-0693, KUMCC 21-0694) groups with *Apiospora locuta-pollinis* (LC11683, holotype) but not with *Apiospora marii* (CBS 497.90, ex-type). Therefore, we recommend that collections (KUMCC 21-0693, KUMCC 21-0694) be transferred to *Apiospora locuta-pollinis* (KUMCC 21-0693, KUMCC 21-0694). Morphologically, our collections are closely related to *Apiospora locuta-pollinis* (LC11683), with colonies abundantly sporulating, a sterile mycelial outer zone and round conidiogenous cells monoblastic or polyblastic, hyaline to brown, aggregated; conidia are globose,

with a central scar. Hence, our collections are identified as *Apiospora locuta-pollinis*, a new host record on grass.

Apiospora poacearum Y. Gao, H. Gui & K.D. Hyde, sp. nov.

Fig. 95

Index Fungorum number: IF903842; Facesoffungi number: FoF17716

Holotype – HKAS 133006

Etymology – The specific epithet is derived from the host family Poaceae, which the holotype was found.

Saprobic on dead stems of grasses. Sexual morph: Undetermined. Asexual morph: Colonies velvety, dark brown to black, dry, dull, they have a sterile outer zone of mycelial cells and a spherical, heavily sporulating surface on which conidia are easily released when disturbed. *Mycelium* branching, smooth-walled, superficial, septate, hyaline to dark brown, hyphae. *Conidiophores* are reduced to conidiogenous cells, grouped to form sporodochia. *Conidiogenous cells* $4\text{--}8 \times 3\text{--}6\ \mu\text{m}$ ($\bar{x} = 6 \times 5\ \mu\text{m}$, $n = 15$), subglobose or cylindrical, monoblastic or polyblastic, aggregated, hyaline to brown, smooth. *Conidia* $8\text{--}11 \times 7\text{--}10\ \mu\text{m}$ ($\bar{x} = 10 \times 8.5\ \mu\text{m}$, $n = 25$), ellipsoidal or globose in the surface view, without a central scar, smooth, pale brown to dark brown.

Culture characteristics – Conidia germinated on PDA, reaching 60 mm diam. after two weeks at 27°C, colonies from above, orange-red with red spots, filiform, spreading, flat, woolly, with abundant aerial mycelia; from below, orange-red, producing pigmentation on agar medium.

Material examined – China, Yunnan Province, Kunming, on decaying stems of unidentified grass (Poaceae), 27 June 2021, Y. Gao, CCSG34 (HKAS 133006, holotype), living culture KUNCC 25-19180; Y. Gao, CCSG14 (HKAS 132986), living culture KUNCC 25-19207;

GenBank numbers – KUNCC 25-19180: ITS = PV608629, LSU = PV607483, *tub2* = PV613320, *tef1- α* = PV626498; KUNCC 25-19207: ITS = PV608628, LSU = PV607482, *tub2* = PV613319, *tef1- α* = PV626497.

Notes – In the phylogenetic analyses, *Apiospora poacearum* (KUNCC 25-19180 and KUNCC 25-19207) formed a distinct lineage and basal to *A. sphaerosperma* (CBS 114314, CBS 114317, CBS 114318), *Apiospora serenensis* (ATCC 76309 and IMI 326869) with 74% ML and 0.90 PP statistical supports (Fig. 92). Morphologically, *Apiospora poacearum* (KUNCC 25-19180) is different from *A. sphaerosperma* (CBS 114314, ex-type) in having smaller conidia ($7\text{--}10\ \mu\text{m}$ vs. $9\text{--}12\ \mu\text{m}$ diam., conidia without equatorial slit vs. with pale equatorial slit), subglobose or cylindrical conidiogenous cells vs. ampulliform (Crous & Groenewald 2013). *Apiospora poacearum* (KUNCC 25-19180) is distinct from *A. serenensis* (IMI 326869, holotype) in conidiophores consisting of spherical or ampulliform cells, brown or olive-brown, large or ascending, straight or curved, with numerous transverse septa (Larrondo & Calvo 1990). Both phylogenetic analyses and morphological characteristics supported our collections as a species. In addition, cultural characterization revealed that the production of an orange-red pigment on the growth medium, indicating its potential for future applications.

Apiospora rasikravindrae (Shiv M. Singh, L.S. Yadav, P.N. Singh, Rahul Sharma & S.K. Singh) Pintos & P. Alvarado, Fungal Systematics and Evolution 7: 207 (2021)

Fig. 96

Index Fungorum number: IF837716; Facesoffungi number: FoF14321

Saprobic on dead stems of grasses. Sexual morph: Undetermined. Asexual morph: *Conidiomata* pycnidial, immersed in the substrate, erumpent when mature, scattered, ellipsoidal or fusiform, with a long axis, broken at the top by one crack, dark brown to black. *Conidiogenous cells* $2\text{--}4 \times 4\text{--}6\ \mu\text{m}$ ($\bar{x} = 3 \times 4\ \mu\text{m}$, $n = 15$), monoblastic or polyblastic, terminal or intercalary, determinate, cylindrical, hyaline to brown, smooth, aggregated. *Conidia* $8\text{--}11.5 \times 7\text{--}10\ \mu\text{m}$ ($\bar{x} = 10$

$\times 8.5 \mu\text{m}$, $n = 25$), globose to ovoid, occasionally elongated to ellipsoidal in surface view, smooth-walled, with a central scar and straight germ slit spore length, brown to dark brown.



Figure 88 – *Neoleptosporella camporesiana* (HKAS 126580, a new host record). a, b Ascomata on the host substrate. c, d Vertical sections through ascomata. e Paraphyses. f Peridium. g–i Asci. j–o Ascospores (k Arrows indicate basal cell appendages). p Germinated ascospores. q, r Colonies on PDA (q: above, r: below). Scale bars: c, d = 100 μm , p = 50 μm , g–i = 30 μm , e, f, j–o = 20 μm .

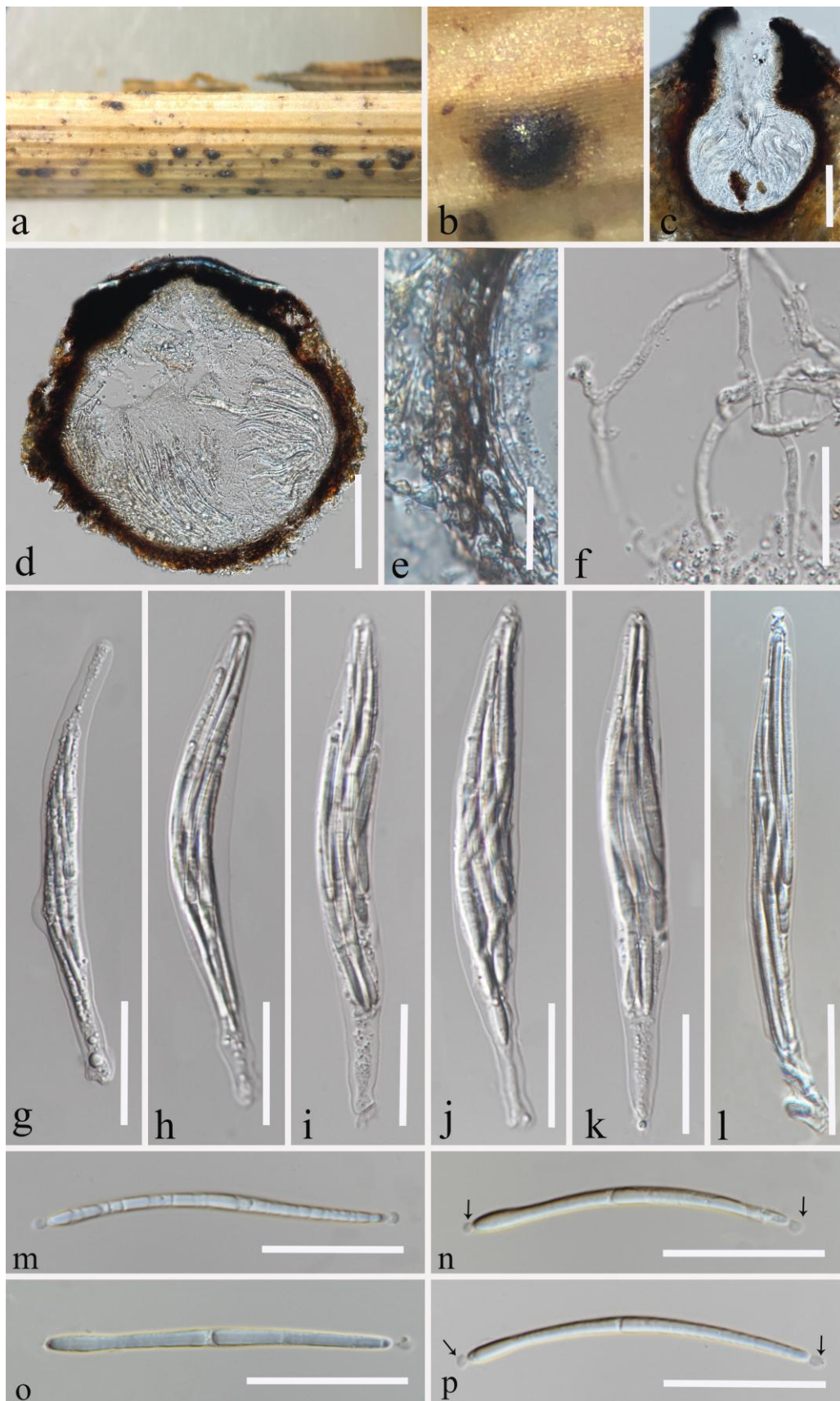


Figure 89 – *Neoleptospora fusiformispora* (HKAS 128736, a new host record). a, b Ascomata on the host substrate. c, d Vertical sections through ascomata. e Peridium. f Paraphyses. g–l Asci. m–p Ascospores (n, p Arrows indicate basal cell appendages). Scale bars: c, d = 100 μm , e–p = 30 μm .

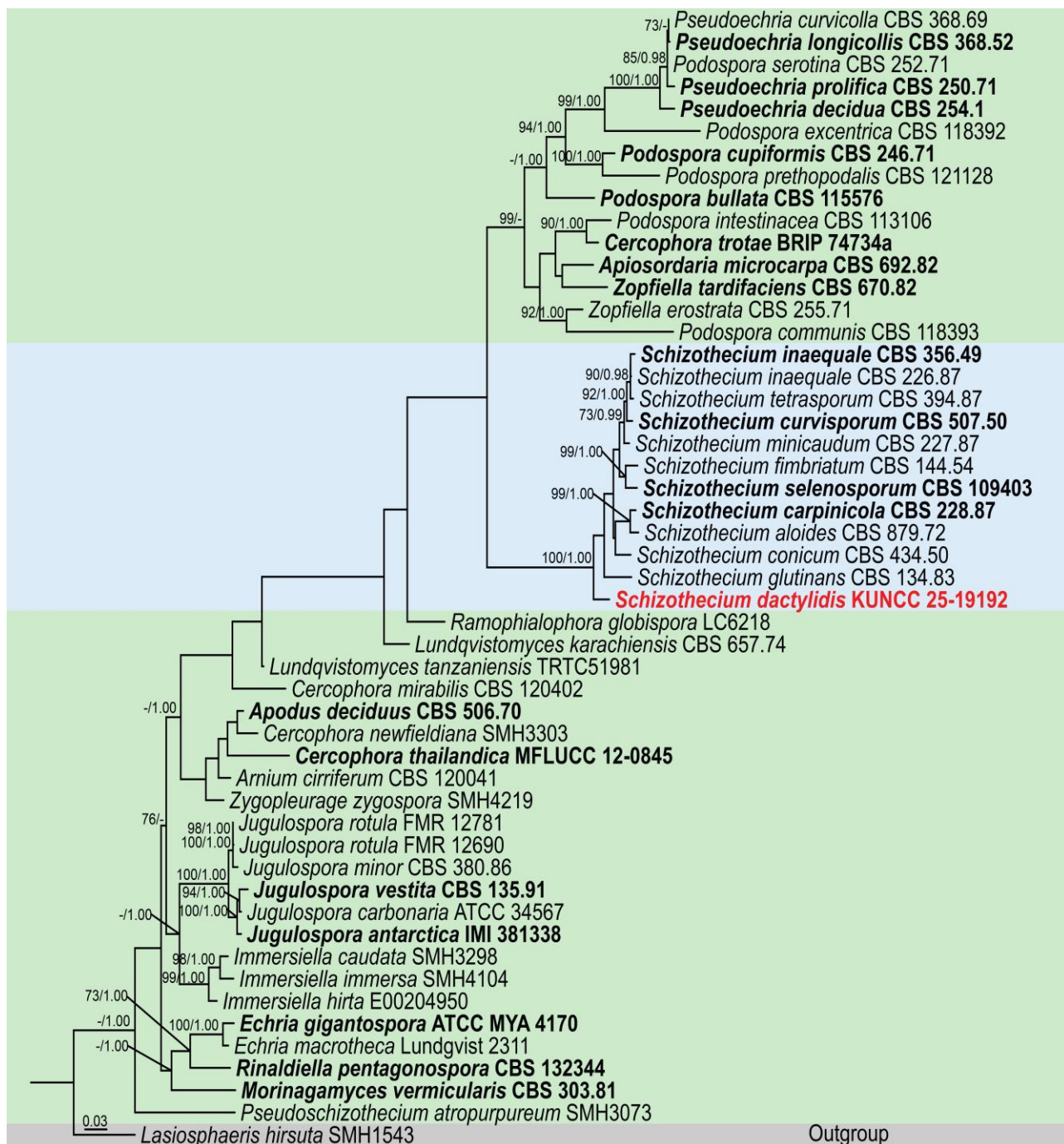


Figure 90 – RAxML phylogram generated from a combined dataset of partial ITS, LSU, *tub2*, and *rpb2* DNA sequence analyses for Schizotheciaceae. Related sequences are obtained following Huang et al. (2021) and Marin-Felix & Miller (2022). Fifty-one strains were included in the combined analyses, which comprised 3,009 characters in the combined ITS, LSU, *tub2*, and *rpb2* alignment. *Lasio-sphaeria hirsuta* (SMH1543) was used as the outgroup taxon. The best-scoring RAxML tree with a final likelihood value of -25186.452473 is presented. The matrix contained 1419 distinct alignment patterns, with 35.29% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.236859, C = 0.265713, G = 0.280739, T = 0.216690; substitution rates AC = 1.217387, AG = 2.651342, AT = 1.388673, CG = 1.169226, CT = 5.232365, GT = 1.000000. The tree topology of the ML analysis is similar to the Bayesian analysis. Bootstrap values for ML equal to or greater than 60% and PP values greater than 0.90 (rounding of values to 2 decimal places) are labelled on the nodes. Strains of the newly described species are in orange, while type strains are in bold. (ITS: 542 bp, LSU: 850 bp, *tub2*: 552 bp, *rpb2*: 1065 bp).

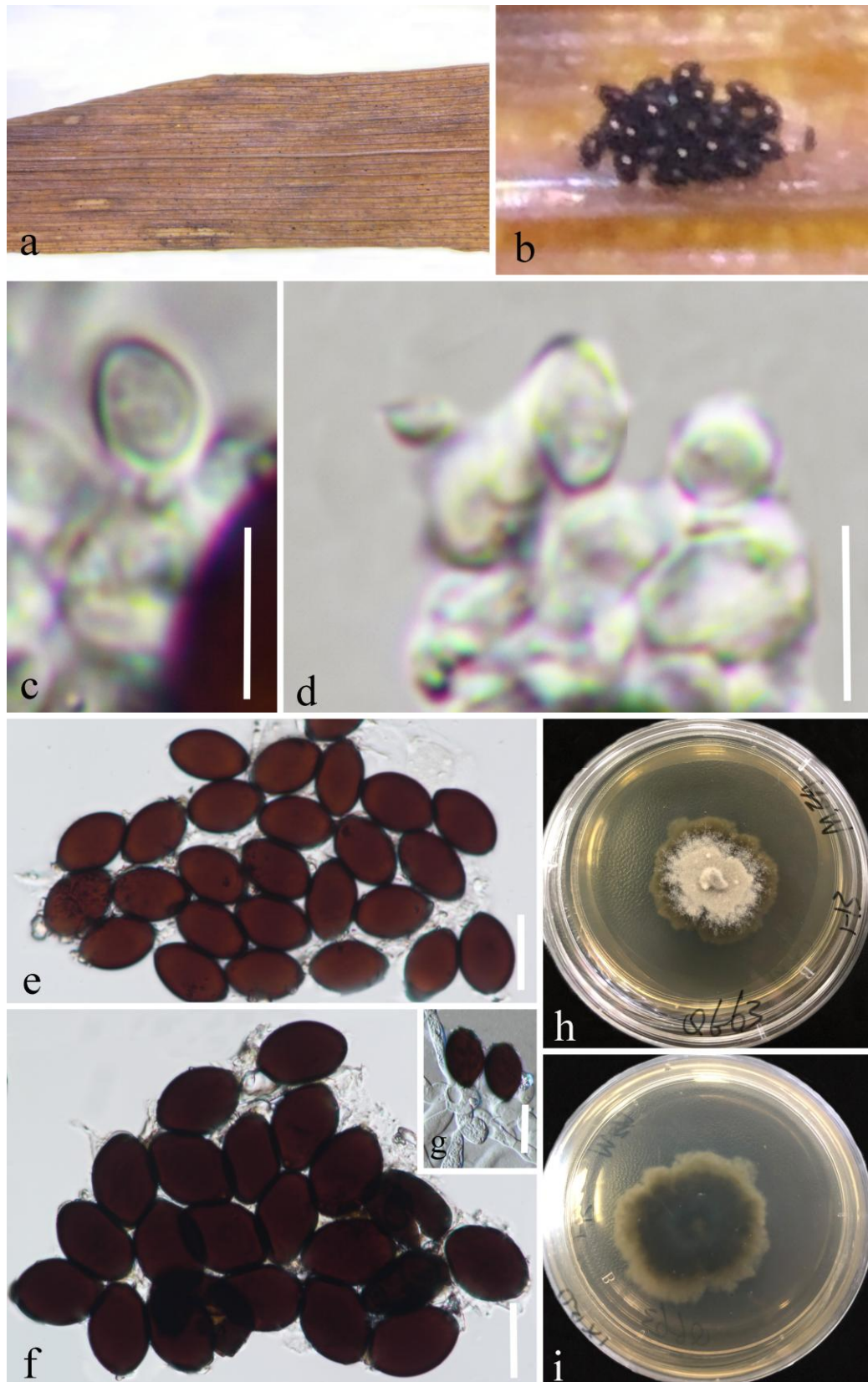


Figure 91 – *Schizothecium dactylidis* (HKAS 132985, holotype). a, b Group of conidia on the host surface. c, d Conidiogenous with conidia. e, f Conidia. g Germinated conidia. h, i Culture characters on PDA (h: above, i: below). Scale bars: f = 30 μ m, e, g = 20 μ m, c, d = 5 μ m.

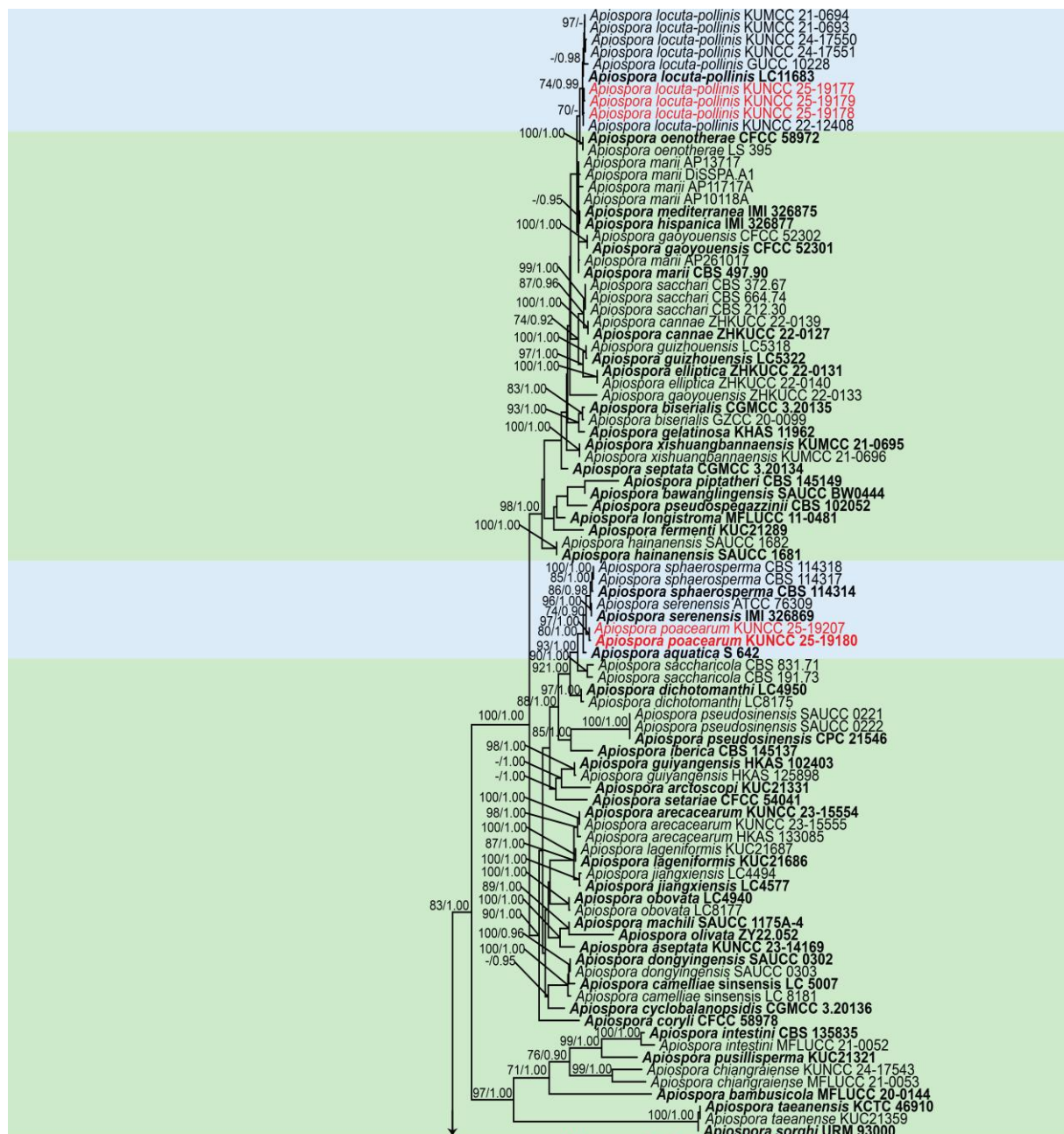


Figure 92 – RAxML phylogram generated from a combined dataset of partial ITS, LSU, *tub2*, and *tef1-α* DNA sequence analyses for *Apiospora*. Related sequences are obtained following Dissanayake et al. (2024), Liu et al. (2024), Tian et al. (2024), Yan & Zhang (2024) and Zhao et al. (2024). Two hundred and seven strains were included in the combined analyses, which comprised 2,454 characters in the combined ITS, LSU, *tub2*, and *tef1-α* alignment. *Nigrospora vesicularis* (CGMCC 3.18128) and *Nigrospora osmanthi* (CGMCC 3.18126) were used as the outgroup taxa. The best-scoring RAxML tree with a final likelihood value of -31162.925996 is presented. The matrix contained 1,326 distinct alignment patterns, with 18.12% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.237259, C = 0.250184, G = 0.256559, T = 0.255999; substitution rates AC = 1.293672, AG = 3.280185, AT = 1.147564, CG = 0.907520, CT = 4.996740, GT = 1.000000. The tree topology of the ML analysis is similar to the Bayesian analysis. Bootstrap values for ML equal to or greater than 60% and PP values greater than 0.90 (rounding of values to 2 decimal places) are labelled on the nodes. Strains of the newly described species are in orange, while type strains are in bold. (ITS: 555 bp, LSU: 837 bp, *tub2*: 634 bp, *tef1-α*: 429 bp).

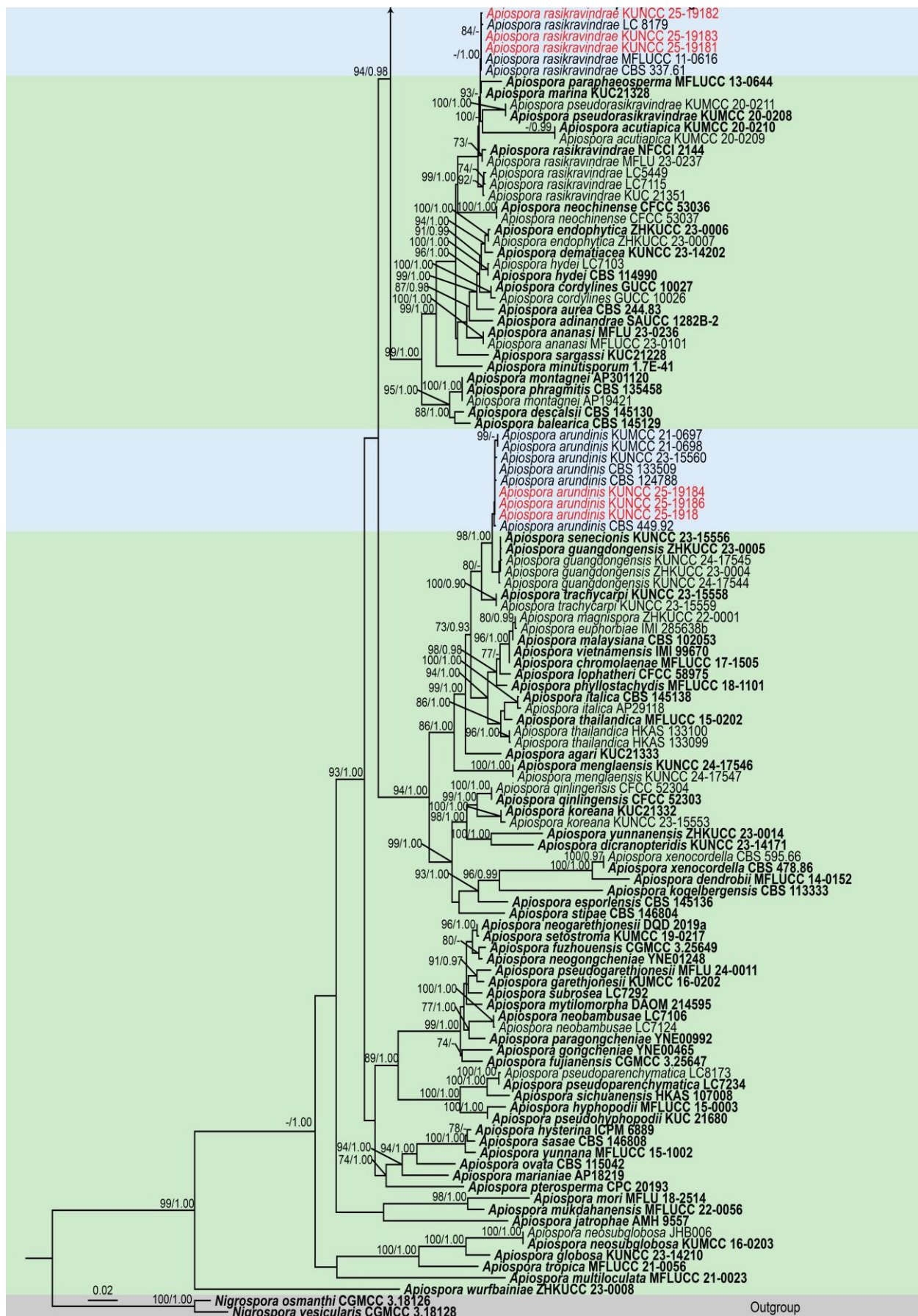


Figure 92 – Continued.

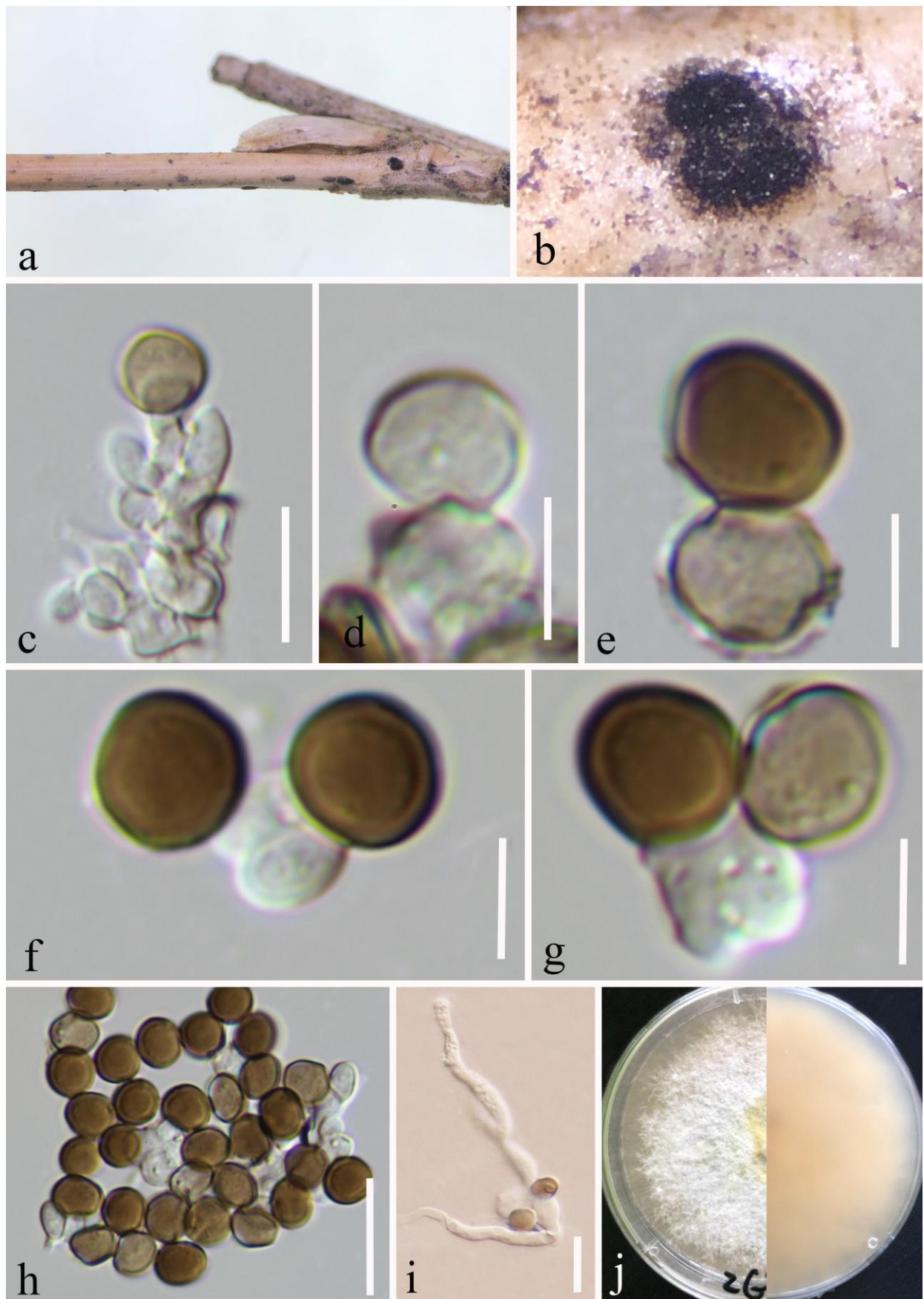


Figure 93 – *Apiospora arundinis* (HKAS 126576, a new host record). a, b Colony on the host substrate. c conidiophore d–g Conidiogenous cells bearing conidia. h Conidia. i Germinated conidia. j Culture characters on PDA (left: above, right: below). Scale bars: h, i = 15 μ m, c = 10 μ m, d–g = 5 μ m.

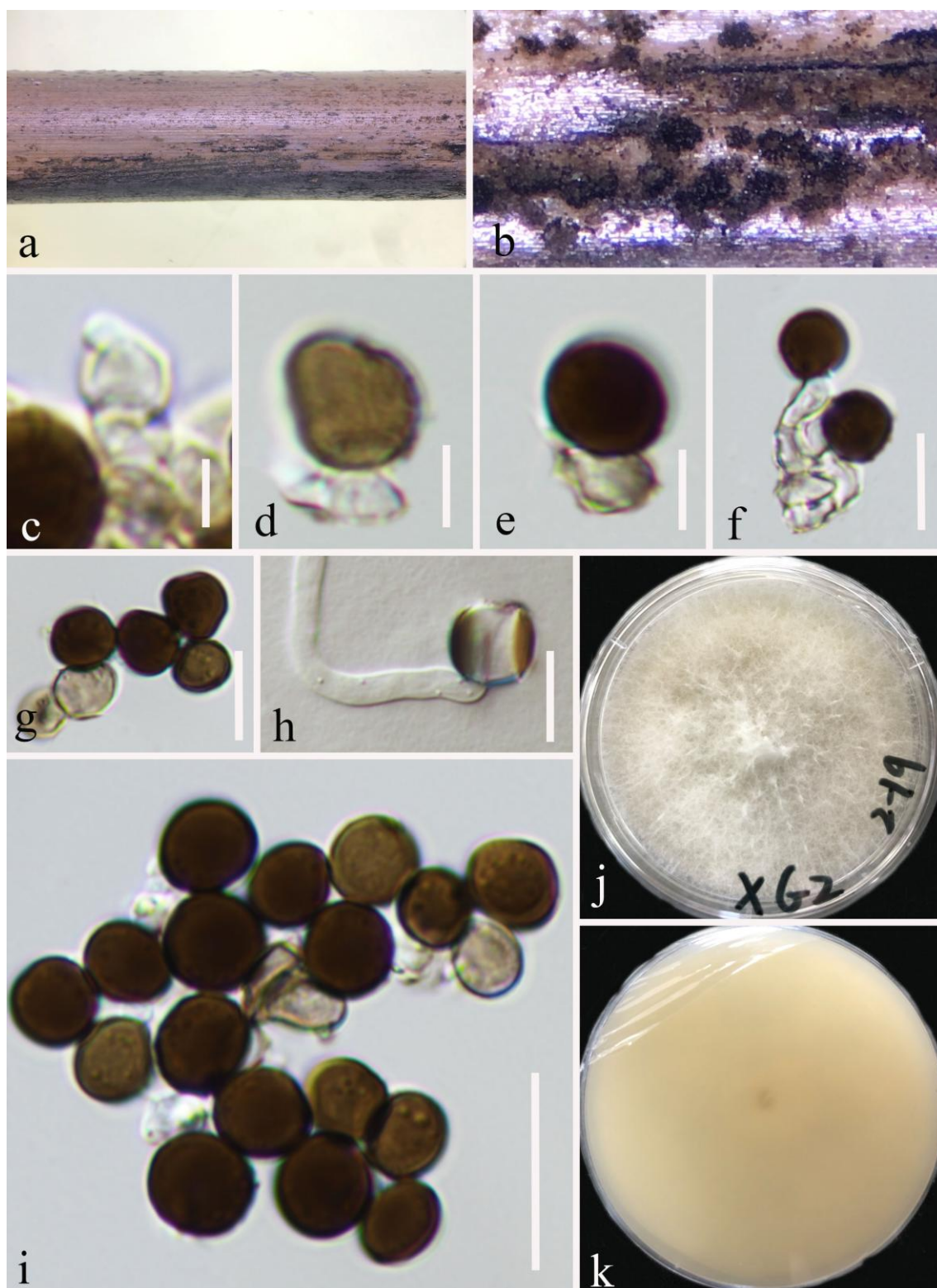


Figure 94 – *Apiospora locuta-pollinis* (HKAS 132969, a new host record). a, b Appearance of the fungus on the dead host substrate. c–e Conidiogenous cells bearing conidia. f Conidia with conidiophores. g, i Conidia. h A germinated conidium. j, k Culture characters on PDA (j: above, k: below). Scale bars: i = 15 µm, f–h = 10 µm, c–e = 5 µm.

Culture characteristics – Colonies on PDA reaching 60 mm diam. after two weeks at 27°C, colonies from above, circular, velvety, appressed with entire margins, dense, white, flat; from below, pale yellow. After incubation for three months on PDA, *Hyphae* 1.5–3 µm ($\bar{x}$ = 2.5 µm, n = 30), hyaline, branched, septate, constricted at the septum. *Conidiophores* are cylindrical, septate,

verrucose, flexuous, and sometimes reduced to conidiogenous cells. *Conidiogenous cells* are ellipsoidal or subglobose, erect, branched, blastic, aggregated in clusters on hyphae, hyaline to pale brown, smooth. *Conidia* $7\text{--}11 \times 5\text{--}10 \mu\text{m}$ ($\bar{x} = 9 \times 8 \mu\text{m}$, $n = 25$), globose to ellipsoid, with a central scar and straight germ slit spore length, brown to black.

Material examined – China, Yunnan Province, Kunming, on decaying stems of unidentified grass (Poaceae), 01 March 2022, Y. Gao, XG5 (HKAS 132967), living culture KUNCC 25-19181. *ibid.*, GY35 (HKAS 145999, KUNCC 25-19182), *ibid.*, HLT2 (HKAS 145991, KUNCC 25-19183).

Known hosts and distribution – on *Cissus* sp. in the Netherlands and on rice in Thailand (Crous & Groenewald 2013), From soil in Svalbard (Singh et al. 2013), on bamboo in China (Wang et al. 2018), on *Phyllostachys aurea* in Spain (Pintos et al. 2019), on dead culms of bamboo in Thailand (Tian et al. 2022a), from egg masses of *Arctoscopus japonicus* in Korea (Kwon et al. 2022), on dead leaves of *Ananas comosus* in Thailand (Tian et al. 2024), on decaying stems grass (Poaceae) in Yunnan Province, China (This study).

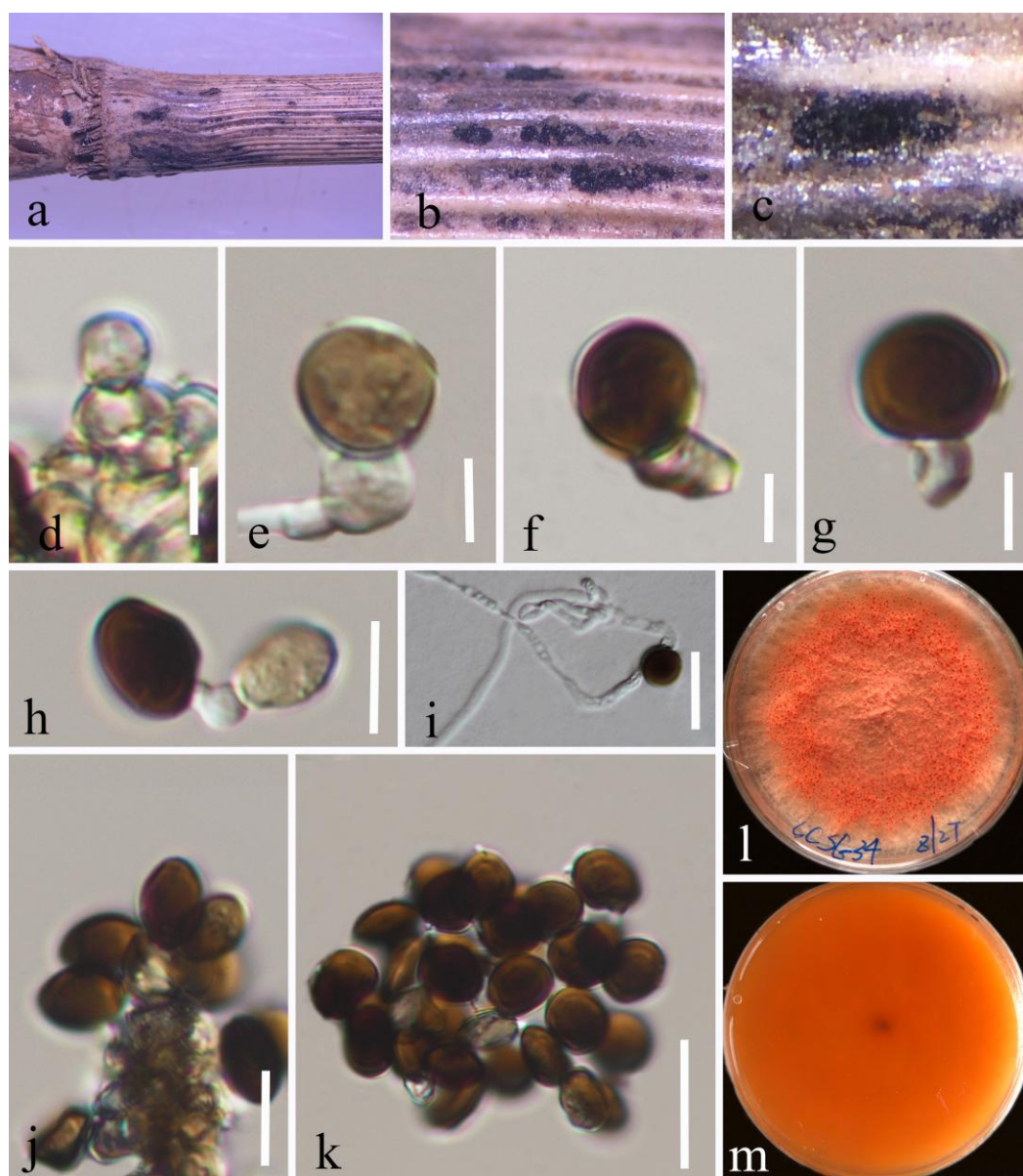


Figure 95 – *Apiospora poacearum* (HKAS 133006, holotype). a–c Appearance of the fungus on dead host substrate. d–h Conidiogenous cells bearing conidia. j Conidia with conidiophores. i A germinated conidium. k Conidia. l, m Culture characters on PDA (l: above, m: below). Scale bars: i = $15 \mu\text{m}$, f–h = $10 \mu\text{m}$, c–e = $5 \mu\text{m}$.

GenBank numbers – KUNCC 25-19181: ITS = PV608630, LSU = PV607484, *tub2* = PV613321, *tefl*- α = PV626499; KUNCC 25-19182: ITS = PV608631, LSU = PV607485, *tub2* = PV613322, *tefl*- α = PV626500; KUNCC 25-19183: ITS = PV608632, LSU = PV607486, *tub2* = PV613323, *tefl*- α = PV626501.

Notes – Our phylogenetic analyses showed that our collections (KUNCC 25-19181, KUNCC 25-19182, KUNCC 25-19183) grouped with *Apiospora rasikravindrae* (LC 8179, MFLUCC 11-0616, CBS 337.61) (Fig. 92). Morphologically, our new collections are closely related to *A. rasikravindrae* (LC 8179, MFLUCC 11-0616) in having lenticular, globose to ovoid, occasionally elongated to ellipsoidal, smooth-walled, brown to black, germ-slit conidia and mononematous, micro-semi-macronematous, unbranched, flexuous or straight, smooth and hyaline, thin-walled, conidiophores (Tian et al. 2024). Hence, our collections are identified as *Apiospora rasikravindrae*, a new host record on grass.

Nigrospora Zimm., Centralbl. Bakteriell. Parasitenk. 8: 220 (1902)

Notes – Seifert et al. (2011) revised *Nigrospora* and identified *Khuskia* as its sexual morph. Later, Maharachchikumbura et al. (2016a) classified *Nigrospora* within Sordariomycetes under genera *incertae sedis*. This genus is a widely distributed dematiaceous ascomycete known for its broad host range. Members of *Nigrospora* have been documented as pathogens, saprobes, and endophytes across diverse hosts (Rashmi et al. 2019). The asexual morph of *Nigrospora* is characterized by branched semimacronematous or micronematous conidiophores, sphaerical to subsphaerical, monoblastic conidiogenous cells, globose to subglobose, black, aseptate, shiny conidia and sexual morph comprises perithecial ascomata, short-stalked asci, biseriate ascospores (Seifert et al. 2011, Wang et al. 2017b, Rashmi et al. 2019, Raza et al. 2019). 53 species are listed in Index Fungorum (2025). In this study, we introduce a new species, *Nigrospora dactylidis*, based on morphology and molecular data, together with descriptions and illustrations (Fig. 98). An updated phylogenetic tree based on combined ITS, LSU, *tub2*, and *tefl*- α sequence data is presented in Fig. 97.

Nigrospora dactylidis Y. Gao, H. Gui & K.D. Hyde, sp. nov.

Fig. 98

Index Fungorum number: IF903843; Facesoffungi number: FoF17717

Holotype – HKAS 132965

Etymology – The specific epithet is derived from the genus of *Dactylis* (Poaceae), which the holotype was found.

Saprobic on dead stems of *Dactylis glomerata*. Sexual morph: Undetermined. Asexual morph: *Sporulate* dark brown to black spore masses visible on host substrates. *Conidiophores* 35–75 $\times$ 5–7 μ m ($\bar{x}$ = 60 $\times$ 6 μ m, n = 15), straight, pale brown, unbranched, septate. *Conidiogenous cells* 5.5–12 $\times$ 5–9 μ m ($\bar{x}$ = 9.5 $\times$ 6.5 μ m, n = 25), cylindrical, holoblastic, monoblastic, straight, hyaline, aseptate, discrete, smooth-walled. *Conidia* 15–19 $\times$ 11–19 μ m ($\bar{x}$ = 17 $\times$ 15 μ m, n = 25), globose to subglobose, pale brown to dark brown, smooth-walled, without longitudinal germ slits.

Culture characteristics – Conidia germinated on PDA, reaching 60 mm diam. after three weeks at 27°C, colonies from above, circular, gray, with white mycelium on the surface, flat, woolly; from below, black.

Material examined – China, Yunnan Province, Zhaotong grassland, on decaying stems of *Dactylis glomerata* (Poaceae), 25 September 2022, Y. Gao, LG10A (HKAS 132965, holotype), living culture KUNCC 25-19190, *ibid.*, LG10B (HKAS 145993), living culture KUNCC 25-19191.

GenBank numbers – KUNCC 25-19190: ITS = PV608638, LSU = PV607494, *tub2* = PV613324, *tefl*- α = PV626507; KUNCC 25-19191: ITS = PV608639, LSU = PV607495, *tub2* = PV613325, *tefl*- α = PV626508.

Notes – *Nigrospora dactylidis* (KUNCC 25-19190 and KUNCC 25-19191) was found to be phylogenetically grouped with *N. manihoticola* (URM8461, ex-type) (Fig. 97). Nucleotide base pair comparisons across ITS 10/495 (2.02%). *Nigrospora dactylidis* (HKAS 132965) differs from *N. manihoticola* (URM8461) in having large conidiogenous cells (5.5–12 $\times$ 5–9 μ m, L/W = 1.3 vs.

3.7–15×3.7–12.5 μm , L/W = 1.2, with cylindrical shape and hyaline vs. globose to subglobose to ovoid shape and pale brown or dark brown) (De Queiroz et al. 2023). Based on both morphology and phylogeny, *Nigrospora dactylidis* is introduced as a new species.

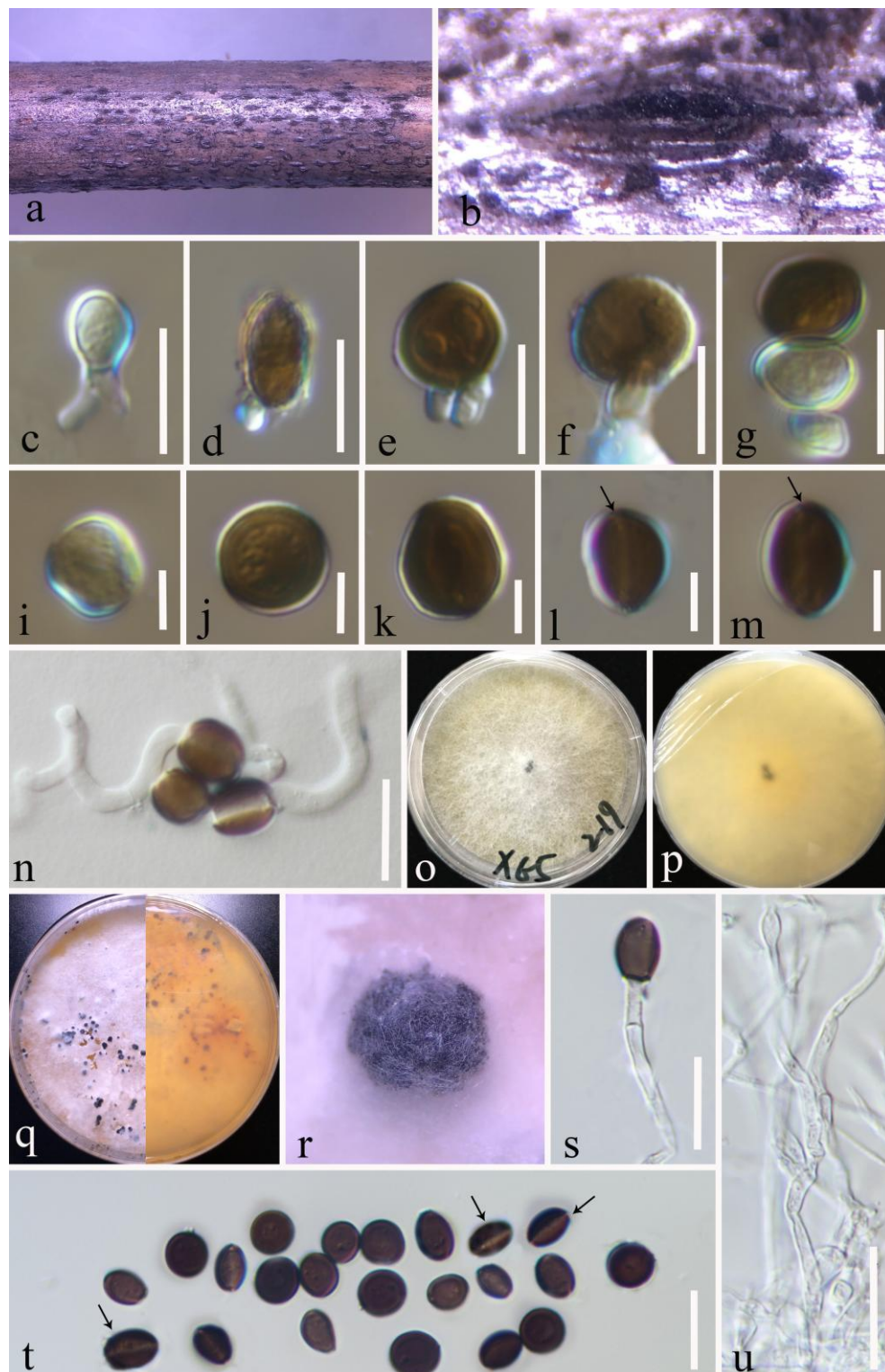


Figure 96 – *Apiospora rasikravindrae* (HKAS 132967, a new host record). a, b Conidiomata on the host substrate. c–g Conidiogenous cells bearing conidia. i–m Conidia. n Germinated conidia. o, p Culture characters on PDA (o: above, p: below). q Colony after incubation for three months on PDA (left: above, right: below). r Conidiomata formed in culture. s Conidia with conidiophores in culture. t Conidia in culture (Conidia in ventral view showing the germ slit in arrows). u Hyphae in culture. Scale bars: u = 20 μm , n, s, t = 15 μm , c–g = 10 μm , i–m = 5 μm .



Figure 97 – RAXML phylogram generated from a combined dataset of partial ITS, LSU, *tub2*, and *tef1-α* DNA sequence analyses for *Nigrospora*. Related sequences are obtained following de Queiroz Brito et al. (2023), Wang et al. (2024b), Zhang et al (2024a). Eighty-five strains were included in the combined analyses, which comprised 2,251 characters in the combined ITS, LSU, *tub2*, and *tef1-α* alignment. *Apiospora malaysiana* (CBS 102053) and *Apiospora pseudoparenchymatica* (LC7234) were used as the outgroup taxa. The best-scoring RAXML tree with a final likelihood value of -15945.658373 is presented. The matrix contained 856 distinct alignment patterns, with 29.13% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.222452, C = 0.283550, G = 0.254205, T = 0.239793; substitution rates AC = 1.118103, AG = 3.178664, AT = 1.019953, CG = 1.152853, CT = 5.250662, GT = 1.000000. The tree topology of the ML analysis is similar the Bayesian analysis. Bootstrap values for ML equal to or greater than 70% and PP values greater than 0.95 (rounding of values to 2 decimal places) are

labelled on the nodes. Strains of the newly described species are in orange, while type strains are in bold. (ITS: 525 bp, LSU: 843 bp, *tef1*- α : 480bp, *tub2*: 403 bp)

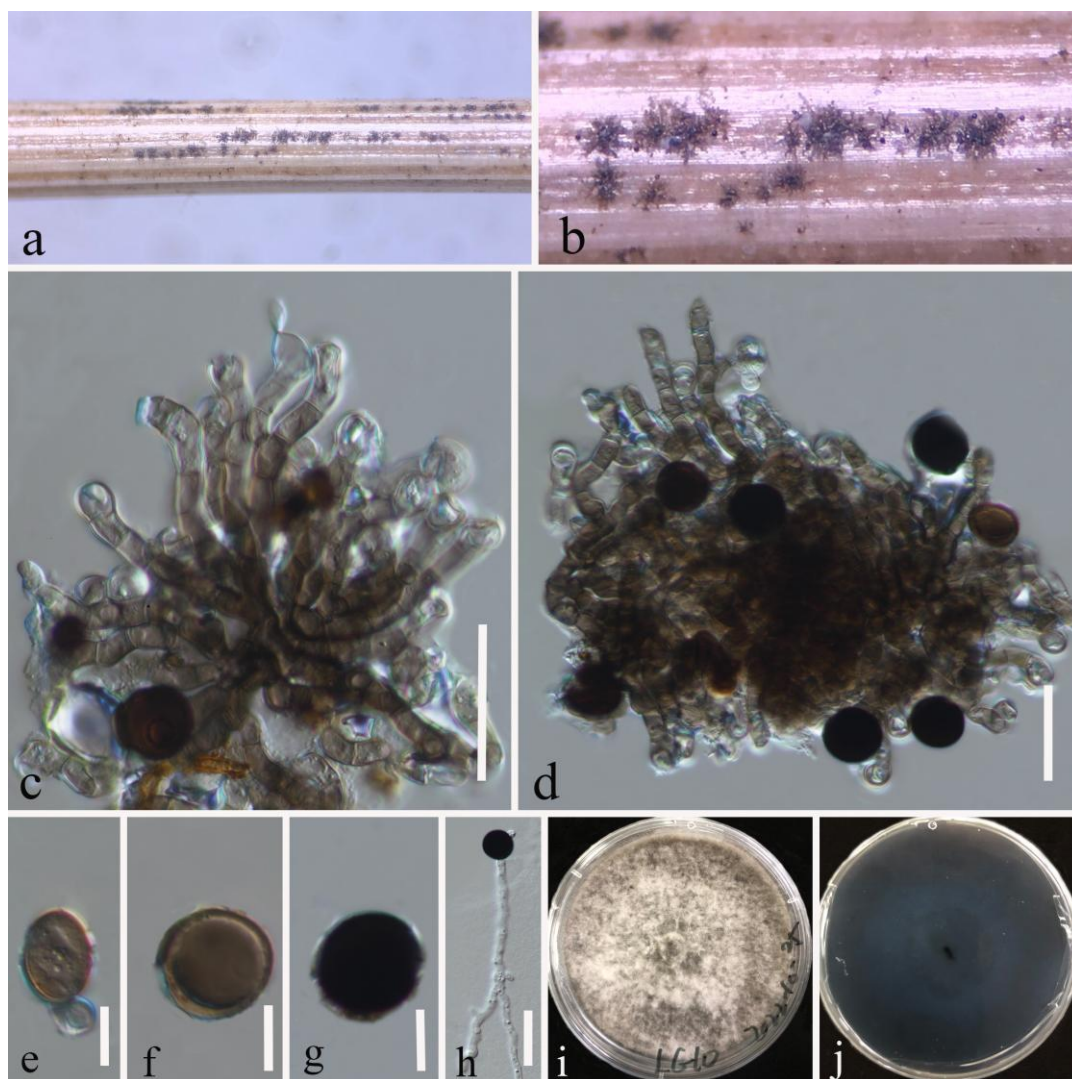


Figure 98 – *Nigrospora dactylidis* (HKAS 132965, holotype). a, b Conidial mass on the host substrate. c, d Conidiophores. e–g Conidia. h A germinated conidium. i, j Culture characters on PDA (i: above, j: from below). Scale bars: c, d, h = 30 μ m, e–g = 10 μ m.

Chaetosphaeriaceae Réblová, M.E. Barr & Samuels, Sydowia 51: 56 (1999)

Notes – Chaetosphaeriaceae was introduced by Réblová et al. (1999) with *Chaetosphaeria* as the type genus. There are 107 genera accepted in this family (Wu & Diao 2022, Hyde et al. 2024a). The sexual morphs of Chaetosphaeriaceae are characterized by having globose to subglobose, ovoid, immersed, dark brown to black, carbonaceous, coriaceous, or membranaceous, with papillate ascomata; clavate to cylindrical, unitunicate, long or shortly pedicellate, with J-, apical ring asci; cylindrical to ellipsoid or fusiform, hyaline or brown or dark, with guttules, sheath or appendages, 0–3-septate ascospores. The asexual morphs of Chaetosphaeriaceae are either coelomycetous or hyphomycetous. Coelomycetous members are characterized by superficial, cupuliform or globose, with setose, unilocular conidiomata; ovoid to cylindrical, black to brown, septate, multi-septate setae; cylindrical, brown, unbranched, 4–6-septate conidiophores; phialidic, subcylindrical to lageniform, holoblastic or enteroblastic, brown, conidiogenous cells; fusiform to allantoid, globose to subglobose or ellipsoid, hyaline to brown, aseptate conidia. Hyphomycetous fungi exhibit dark brown or colorless, septate conidiophores accompanied by short surrounding collar hyphae; their conidiogenous cells are colorless and feature a noticeable funnel-shaped collarette. The conidia,

which can be continuous or mucilaginous, range from aseptate to multi-septate and vary in shape from fusiform and allantoid to cylindrical or doliiform, with colors spanning from hyaline to dark brown. (Hyde et al. 2020b).

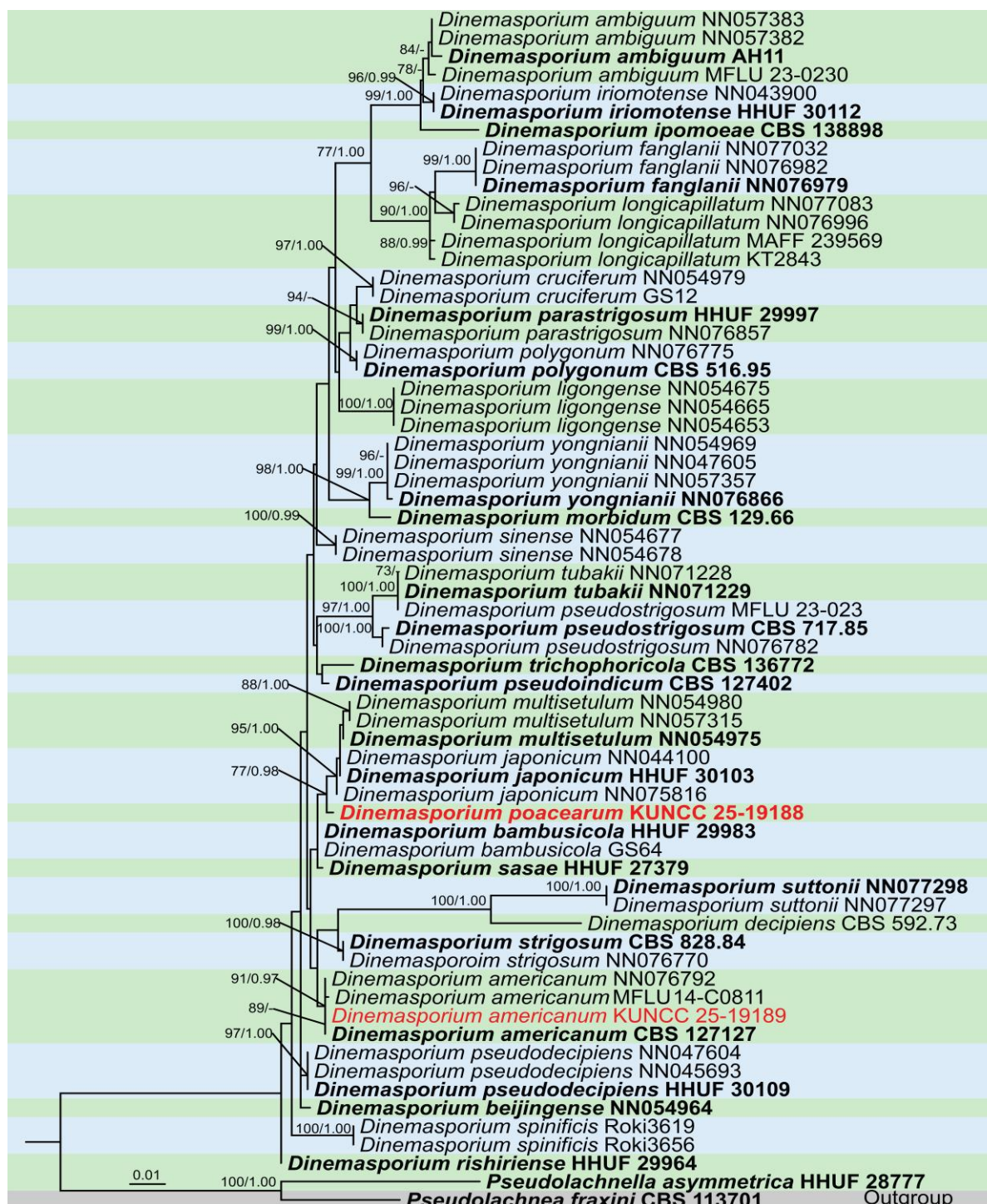


Figure 99 – RAxML phylogram generated from a combined dataset of partial ITS and LSU DNA sequence analyses for *Dinemasporium*. Related sequences are obtained following Wu & Diao (2022) and Tian et al. (2024). Sixty-five strains were included in the combined analyses, which comprised 1,306 characters in the combined ITS and LSU alignment. *Pseudolachnea fraxini* (CBS 113701) and *Pseudolachnella asymmetrica* (HHUF 28777) were used as the outgroup taxa. The best-scoring RAxML tree with a final likelihood value of -4219.886567 is presented. The matrix contained 232 distinct alignment patterns, with 24.68% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.220197, C = 0.276340, G = 0.300689, T =

0.202775; substitution rates AC = 1.335694, AG = 4.391788, AT = 3.847512, CG = 1.316419, CT = 12.313114, GT = 1.000000. The tree topology of the ML analysis is similar to the Bayesian analysis. Bootstrap values for ML equal to or greater than 70% and PP values greater than 0.95 (rounding of values to 2 decimal places) are labelled on the nodes. Strains of the newly described species are in orange, while type strains are in bold. (ITS: 460 bp, LSU: 846 bp).

Dinemasporium Lév., Ann. Sci. Nat., Bot. sér. 3, 5: 274 (1846)

Notes – *Dinemasporium* was identified by Lévillé (1846) with *D. strigosum* as the type species. *Dinemasporium* is characterized by superficial, with setae conidiomata, “phialidic” conidiogenous cells, fusiform, hyaline to pale brown, aseptate conidia with a single, unbranched, filiform, cellular appendage at each end (not separated from the body via septa), lateral appendages present or absent (Duan et al. 2007, Crous et al. 2012). Duan et al. (2007) initially revised *Dinemasporium*, recognizing 14 accepted species. Wu & Diao (2022) identified 24 species of *Dinemasporium*, including seven new species, and provided a key to the species. In this study, we introduce a new record for *Dinemasporium americanum* and a new species, *D. poacearum*, based on morphology and molecular data, together with descriptions and illustrations (Figs. 100, 101). An updated phylogenetic tree based on combined ITS and LSU sequence data is presented in Fig. 99.

Dinemasporium americanum Crous & Tuthill, Persoonia 28: 131 (2012)

Fig. 100

Index Fungorum number: IF585306; Facesoffungi number: FoF18357

Saprobic on dead stems of *Stipa capillata*. Sexual morph: Undetermined. Asexual morph: *Conidiomata* superficial, scattered or grouped, irregular, cupulate, unilocular, with stroma cells of *textura angularis* at the base and a lateral excipulum of *textura porrecta* or *textura intricata* of pale to dark brown cells, dark brown to black. *Conidiomatal setae* 4.5–11 µm wide ($\bar{x}$ = 8 µm, n = 35), up to 585 µm long, arising from the basal stroma or surrounding, straight, smooth, unbranched, thick-walled, brown to black but pale at the apex, tapering towards an acute apex. *Conidiophores* lining the basal stroma, smooth, septate, cylindrical, thick-walled, hyaline, arising from basal and periclinal wall cells. *Conidiogenous cells* 6.5–17.5 × 2–3 µm ($\bar{x}$ = 12 × 2.5 µm, n = 25), cylindrical or phialidic, hyaline, smooth, tapering toward the apex. *Conidia* 11–14.5 × 2.5–3.5 µm ($\bar{x}$ = 13 × 3 µm, n = 30), naviculate or ellipsoid, blastic-phialidic, slightly truncate at the base, obtuse at the apex, guttulate, unicellular, smooth-walled, hyaline, bearing a single unbranched appendage at each end. *Appendage* 10–14 µm ($\bar{x}$ = 12 µm, n = 25) hyaline, filamentous, straight or curved.

Culture characteristics – Conidia germinated on PDA, reaching 15 mm diam. after two weeks at 27°C, colonies from above, circular, white, raised at the center, flat, woolly; from below, white, without producing pigmentation on agar medium.

Material examined – China, Yunnan Province, Kunming, on decaying stems of *Stipa capillata* (Poaceae), 15 March 2022, Y. Gao, GY169 (HKAS 135328), living culture KUNCC 25-19189.

Known hosts and distribution – From the soil in the United States (Crous et al. 2012), on dead leaves, culm, the seed of unidentified grass in China (Wu & Diao 2022), on the decaying stems of *Stipa capillata* (Poaceae) in Yunnan Province, China (This study).

GenBank numbers – KUNCC 25-19189: ITS = PV608637, LSU = PV607493.

Notes – Our phylogenetic analysis revealed that the collection (KUNCC 25-19189) is grouped with *Dinemasporium americanum* (NN076792, CBS 127127) and *D. nelloi* (MFLU 14-0811, holotype) lineage (Fig. 99). Liu et al. (2015) introduced *D. nelloi*, which shared morphological similarities with *D. americanum* (CBS 127127, ex-type) based on molecular and morphological data. Liu et al. (2015) reported that conidia of *D. nelloi* (MFLU 14-0811) are longer than those of *D. americanum* (CBS 127127) (10–20 × 2.5–3.5 µm, L/W = 5 vs. 9–16 × 2.5–3 µm, L/W = 4.5; Crous et al. 2012). However, sequence comparisons showed that *D. nelloi* (MFLU 14-0811) and *D. americanum* (CBS 127127) are identical in ITS (486/486 bp, 100%) and identical in LSU (847/848 bp, 100%). Therefore, we synonymize *Dinemasporium nelloi* under *D. americanum*. In this study, our collection is similar to *D. americanum* based on both phylogeny and morphology

(Crous et al. 2012, Wu & Diao 2022). Therefore, we report a new host record of *D. americanum* on *Stipa capillata* in China.

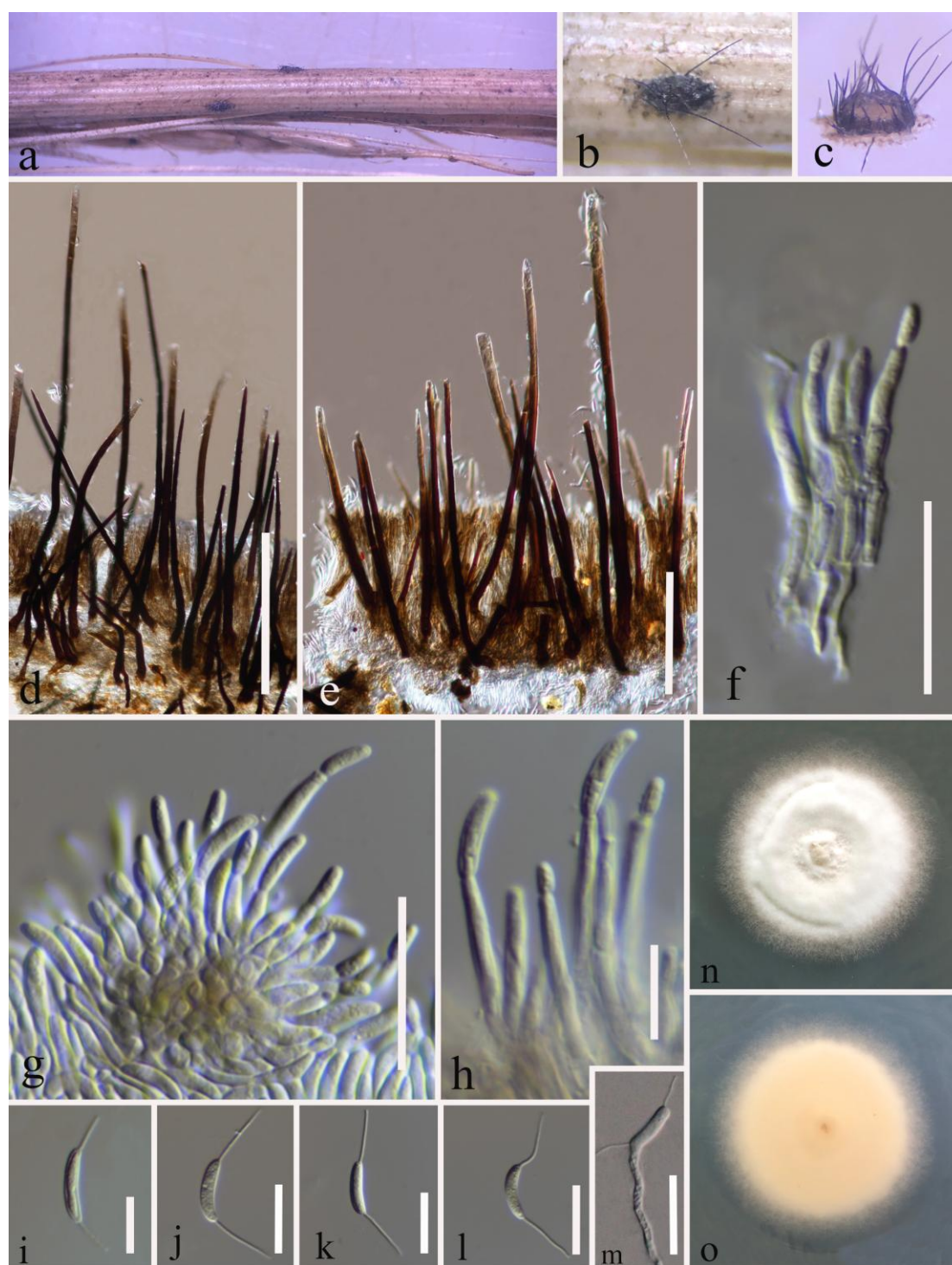


Figure 100 – *Dinemasporium americanum* (HKAS 135328, a new host record). a–c Conidiomata on the host substrate. d, e Conidiomatal setae. f–h Conidiogenous cells bearing conidia. i–l Conidia. m A germinated conidium. n, o Culture characters on PDA (n: above, o: below). Scale bars: d = 200 µm, e = 100 µm, f, g = 20 µm, j–m = 15 µm, h, i = 10 µm.

Dinemasporium poacearum Y. Gao, H. Gui & K.D. Hyde, sp. nov.

Index Fungorum number: IF903844; Facesoffungi number: FoF17718

Holotype – HKAS 133001

Fig. 101

Etymology – The specific epithet is derived from the host family Poaceae, which the holotype was found.

Saprobic on dead stems of grasses. Sexual morph: Undetermined. Asexual morph: Coelomycetous. *Conidiomata* 180–205 μm high, 140–185 μm diam. ($\bar{x}$ = 197 $\times$ 157 μm , n = 15), superficial, scattered or grouped, cupulate, globose or subglobose, unilocular, with orange to brown conidial mass in the center, dark brown to black. *Conidiomatal setae* 9–11 μm wide ($\bar{x}$ = 10 μm , n = 15), up to 570 μm long, arising from the basal stroma or surrounding, straight, smooth, thick-walled, unbranched, brown to black but pale at the apex. *Excipulum* 12–30 μm ($\bar{x}$ = 19 μm , n = 25), composed of rectangular brown cells. *Conidiophores* lining the basal stroma, smooth, septate, cylindrical, simple or branched, hyaline. *Conidiogenous cells* 11–20 $\times$ 2–3 μm ($\bar{x}$ = 14.5 $\times$ 2.2 μm , n = 25), cylindrical to lageniform, phialidic, hyaline, smooth. *Conidia* 11–14.5 $\times$ 2.5–3.5 μm ($\bar{x}$ = 12.5 $\times$ 3 μm , n = 30), naviculate or ellipsoid, slightly truncate at the base, obtuse at the apex, guttulate, unicellular, smooth, hyaline, bearing a single unbranched appendage at each end. *Appendage* 10–15 μm ($\bar{x}$ = 13 μm , n = 30) hyaline, filamentous, straight or curved.

Culture characteristics – Conidia germinated on PDA, reaching 30 mm diam. after three weeks at 27°C, colonies from above, circular, white, raised at the center, flat, woolly; from below, white at the edge, golden yellow at the center, without producing pigmentation on agar medium.

Material examined – China, Yunnan Province, Kunming, on decaying stems of unidentified grass (Poaceae), 27 June 2021, Y. Gao, CCSG9 (HKAS 133001, holotype), living culture KUNCC 25-19188.

GenBank numbers – KUNCC 25-19188: ITS = PV608636, LSU = PV607492, *tef1- α* = PV626506.

Notes – Our phylogenetic analyses showed that *Dinemasporium poacearum* (KUNCC 25-19188) grouped sister to *D. japonicum* (HHUF 30103, NN075816, NN044100) with 77% ML and 0.98 PP support values (Fig. 99). Morphologically, *D. poacearum* (KUNCC 25-19188) differs from *D. japonicum* (HHUF 30103, holotype) in having conidiomata with long setae (570 μm vs. 210 μm) and larger conidia (11–14.5 $\times$ 2.5–3.5 μm , L/W = 4.3 vs. 7–11 $\times$ 2–3 μm , L/W = 3.6) (Hashimoto et al. 2014). Both phylogenetic analyses and morphological characteristics supported our collection as a new species.

Xylariaceae Tul. & C. Tul., *Selecta Fungorum Carpologia*, Tomus Secundus. Xylariei - Valsei - Sphaeriei 2: 3 (1863)

Notes – Xylariaceae was established by Tulasne & Tulasne (1863), with *Xylaria* as its type genus, and is found across tropical, subtropical, and temperate zones (Dennis 1957, Whalley 1985, 1996, Rogers 2000, Suwannasai et al. 2013, Koyani et al. 2016). Members of this family are primarily recognized as saprobes (Rogers 1979, 2000, Pažoutová et al. 2010), though some act as plant pathogens, inflicting damage on economically important crops (Edwards et al. 2003, Husbands & Aime 2018, Garcia-Aroca et al. 2021). Additionally, certain species function as endophytes that may transition to pathogenic roles under host stress conditions (Whalley 1996, Okane et al. 2008). Many species within Xylariaceae are notable for their production of unique bioactive compounds and secondary metabolites (Stadler et al. 2005, Bitzer et al. 2008, Song et al. 2014, Helaly et al. 2018, Liang et al. 2025, Zhao et al. 2025). Consequently, these organisms are of significant interest due to their ecological and economic importance. Recent taxonomic revisions have recognized 42 genera within Xylariaceae (Hyde et al. 2024a). An updated phylogenetic tree based on combined ITS, LSU, *tub2*, *rpb2*, and *act* sequence data is presented in Fig. 102.

Astrocystis Berk. & Broome, J. Linn. Soc., Bot. 14 (73 & 74): 123 (1875)

Notes – *Astrocystis* was identified by Berkeley & Broome (1873) with *A. mirabilis* as the type species. Species of *Astrocystis* primarily inhabit monocotyledonous plants, and are characterized by developing uni- or occasionally multi-peritheciate stromata, typically beneath the host cuticle or on its surface, with relatively short stipe asci, while the ascus apical apparatus is small, amyloid, stopper-shaped (Smith et al. 2003). Over 22 species have been recorded worldwide,

with five documented in China (Taylor & Hyde 2003, Hyde et al. 2019, Wu et al. 2021, Li et al. 2022). Li et al. (2024) significantly expanded knowledge of *Astrocystis* in China, reporting four newly described species and documenting a new occurrence in the genus. In this study, we introduce a new record for *Astrocystis sublimbata*, based on morphology and molecular data, together with descriptions and illustrations (Fig. 103).

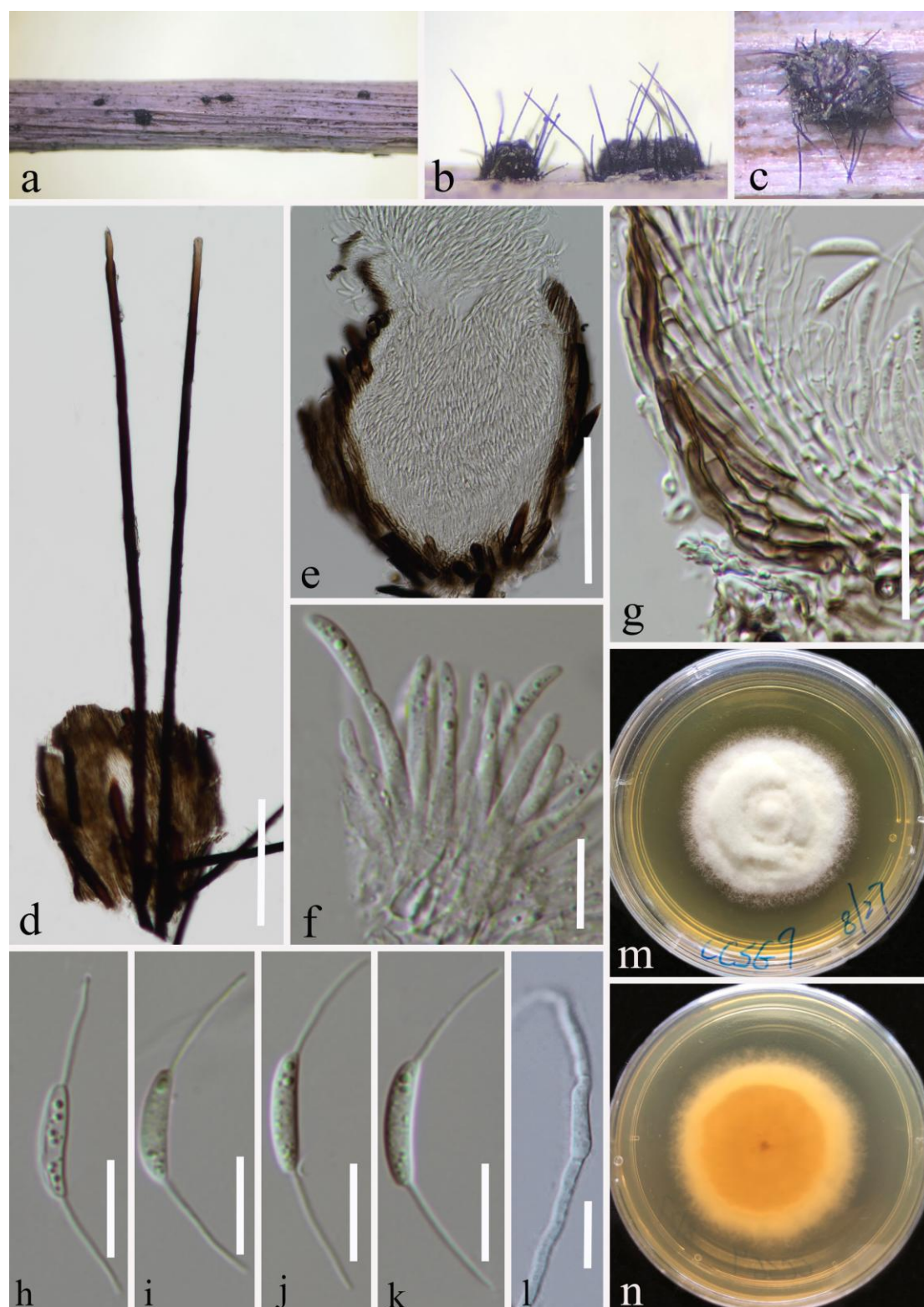


Figure 101 – *Dinemasporium poacearum* (HKAS 133001, holotype). a–c Conidiomata on the host substrate. d Conidiomatal setae. e Conidioma in longitudinal section f Conidiogenous cells bearing

conidia. g Conidiomata wall. h–k Conidia. l A germinated conidium. m, n Culture characters on PDA (m: above, n: below). Scale bars: d, e = 100 μ m, g = 20 μ m, f, h–l = 10 μ m.

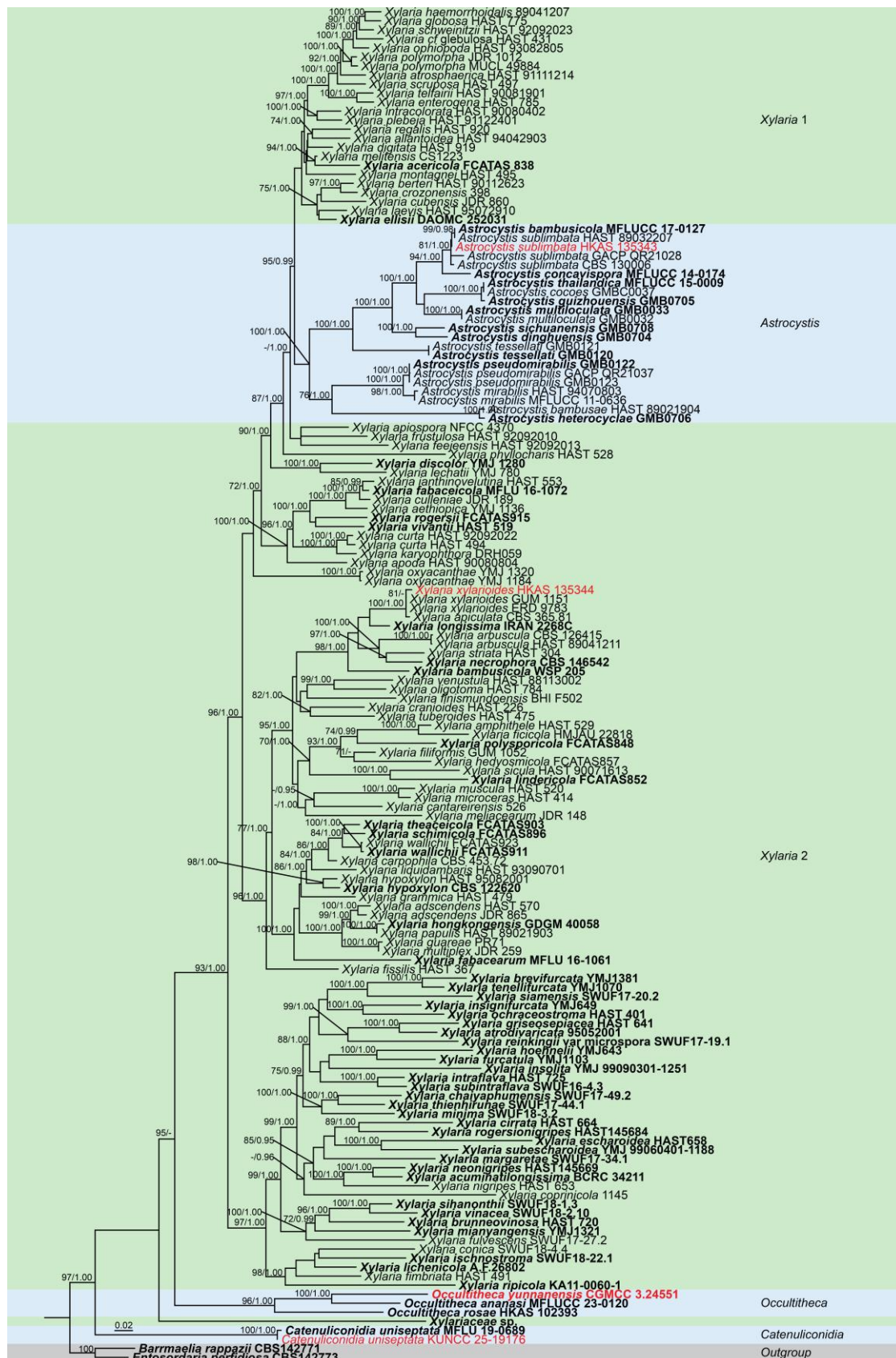


Figure 102 – RAxML phylogram generated from a combined dataset of partial ITS, LSU, *tub2*, *rpb2*, and *act* DNA sequence analyses for Xylariaceae. Related sequences are obtained following

Yuan et al. (2020), Li et al. (2022), Samarakoon et al. (2022), Li et al. (2024), Tian et al. (2024). One hundred and fifty strains were included in the combined analyses, which comprised 4,415 characters in the combined ITS, LSU, *tub2*, *rpb2*, and *act* alignment. *Entosordaria perfidiosa* (CBS 142773) and *Barrmaelia rappazii* (CBS 142771) were used as the outgroup taxa. The best-scoring RAxML tree with a final likelihood value of -120380.123701 is presented. The matrix contained 2,555 distinct alignment patterns, with 33.92% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.233306, C = 0.276313, G = 0.244558, T = 0.245823; substitution rates AC = 1.366566, AG = 5.383059, AT = 1.237841, CG = 1.108038, CT = 7.694992, GT = 1.000000. The tree topology of the ML analysis is similar to the Bayesian analysis. Bootstrap values for ML equal to or greater than 70% and PP values greater than 0.95 (rounding of values to 2 decimal places) are labelled on the nodes. Strains of the newly described species are in orange, while type strains are in bold. (ITS: 571 bp, LSU: 827 bp, *tub2*: 1534 bp, *rpb2*: 1191 bp, *act*: 292 bp).

Astrocystis sublimbata (Durieu & Mont.) G.C. Hughes, Mycol. Pap. 50: 9 (1953)

Fig. 103

Index Fungorum number: IF293531; Facesoffungi number: FoF18358

Saprobic on a dead stalk of grasses. Sexual morph: *Stromata* superficial, visible as black dots on the host, semi-globose to conical, solitary or sometimes clustered, carbonaceous, black. *Ostiole* faintly pronounced to papillate. *Paraphyses* 3–5 μm ($\bar{x}$ = 4.5 μm , n = 25), wider at the base, filamentous, septate, guttulate. *Asci* 90–135 $\times$ 7–11 μm ($\bar{x}$ = 110 $\times$ 9.5 μm , n = 20), 8-spored, cylindrical-clavate, apically rounded, uniseriate, short-pedicellate, with a J⁺ apical ring in Melzer's reagent, square-shaped apical apparatus. *Ascospores* 16–20 $\times$ 7–9 μm ($\bar{x}$ = 18 $\times$ 8.2 μm , n = 25), uniseriate, fusiform or ellipsoidal and strongly inequilateral with the flattened side flat to slightly concave, smooth-walled, occasionally slightly beaked at one end dark brown, with a short gelatinous appendage at one or both ends and more with a prominent gelatinous sheath. Asexual morph: Undetermined.

Culture characteristics – Colonies on PDA reaching 60 mm diam. after four weeks at 27°C, colonies from above, circular, velvety, appressed with entire margins, dense, white, umbonate, flat; from below, white.

Material examined – China, Yunnan Province, Kunming, on a decaying stalk of unidentified grass (Poaceae), 27 July 2021, Y. Gao, GY148 (HKAS 135343). DNA was extracted directly from stromata.

Known hosts and distribution – Known to inhabit *Arundo* (Poaceae), bamboo (Bambuseae, Arundinariinae) in Ireland, France, Portugal, the United Kingdom, Sudan, Venezuela, Guizhou Province, China (Li et al. 2022), on decaying stalks of grasses (Poaceae) in Yunnan Province, China (This study).

GenBank numbers – HKAS 135343: ITS = PV608624, LSU = PV607478.

Notes – In the present study, the multigene phylogeny indicates that our collection (HKAS 135343) and other existing strains of *Astrocystis sublimbata* (CBS130006, HAST 89032207, GACP QR21028), *A. bambusicola* (MFLUCC 17-0127, ex-type) group together and form a monophyletic clade with 81% ML and 1.00 PP support values (Fig. 102). Our collection (HKAS 135343) shows no significant differences from *Astrocystis sublimbata* (GACP QR21028) in morphological analyses (Li et al. 2022). Additionally, our phylogenetic analyses show *Astrocystis sublimbata* (HAST 89032207) is closely related to *A. bambusicola* (MFLUCC 17-0127) (Hyde et al. 2017), however, *A. sublimbata* (HAST 89032207) differs from *A. bambusicola* by its superficial stromata (vs. erumpent), and ascospores (15.7–18.4 $\times$ 7–8 μm , L/W = 2.0 vs. 12–16 $\times$ 6.1–7 μm , L/W = 2.1) (Hyde et al. 2017, 2019). Based on morphological characteristics and phylogenetic analyses, we report our collection as a new record of *Astrocystis sublimbata* from the decaying stalk of grasses in Yunnan, China.

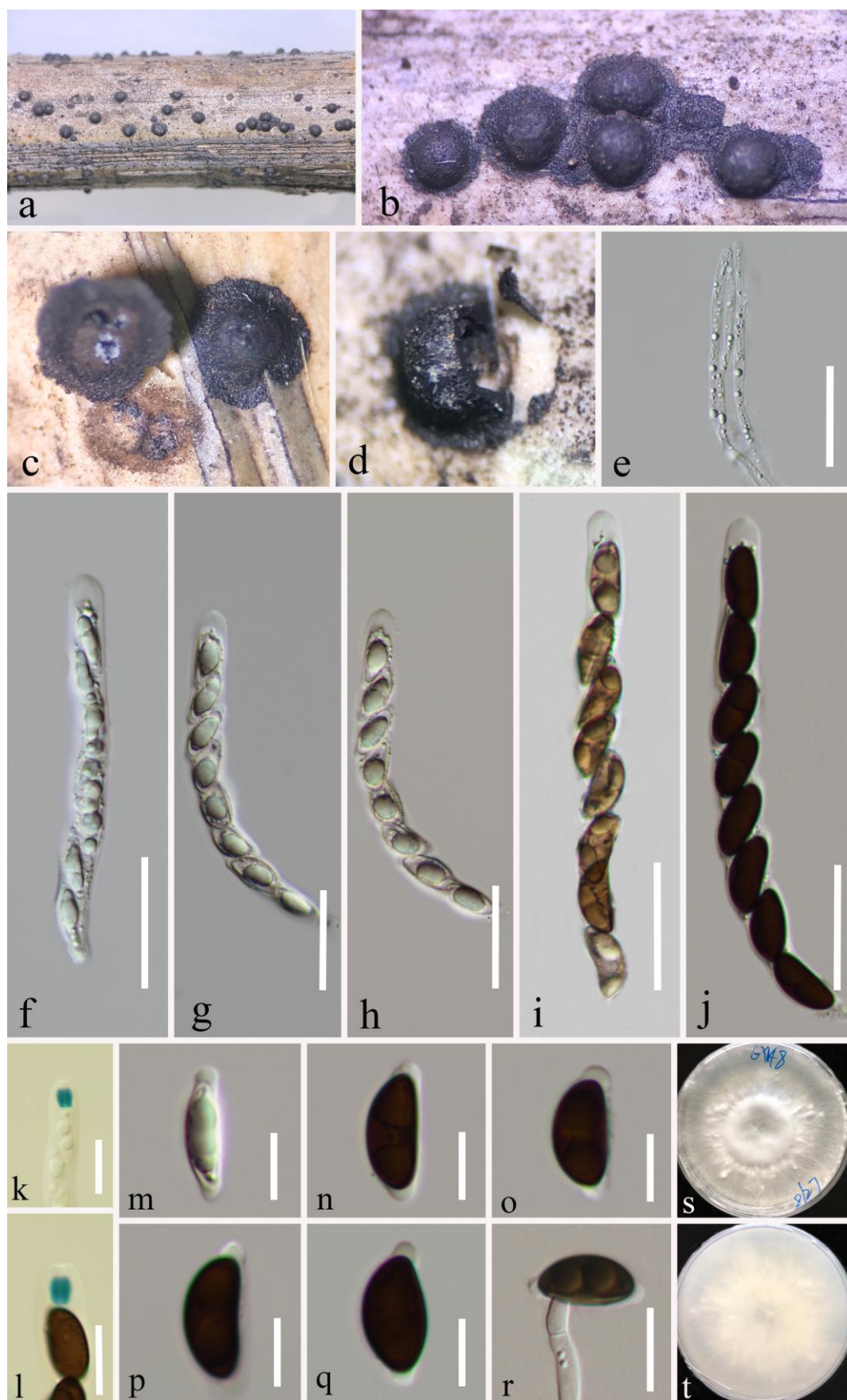


Figure 103 – *Astrocystis sublimbata* (HKAS 135343, a new host record). a–d Stromata on the host substrate. e Paraphyses. f–j Asci. k, l J^+ apical ring in Melzer's reagent. m–q Ascospores in side view showing the basal cellular appendage. r A germinated ascospore. s, t Culture characters on PDA (s: above, t: below). Scale bars: e = 50 μm , f–j = 30 μm , k, l, r = 15 μm , m–q = 10 μm .

Catenuliconidia N.G. Liu & K.D. Hyde, Fungal Diversity 104: 97 (2020)

Notes – *Catenuliconidia* was established by Yuan et al. (2020) with *C. uniseptata* as the type species. There is only one species listed in Index Fungorum (2025). In this study, we introduce a new record for *Catenuliconidia uniseptata*, based on morphology and molecular data, together with descriptions and illustrations (Fig. 104).

Catenuliconidia uniseptata N.G. Liu & K.D. Hyde, Fungal Diversity 104: 97 (2020) Fig. 104

Index Fungorum number: IF556465; Facesoffungi number: FoF06117

Saprobic on dead stems of *Jasminum nudiflorum*. Sexual morph: Undetermined. Asexual morph: Colonies on natural substrate effuse, velvety, and black. Mycelium immersed, branched, and composed of septate, hyaline to pale brown hyphae. Conidiophores macronematous, mononematous, in groups, erect, cylindrical, straight or broadly curved, brown to dark brown, septate, unbranched, thick-walled, smooth. Conidiogenous cells cylindrical, terminal, blastic, and integrated, brown. Conidia 17–26 × 6–9 µm ($\bar{x}$ = 21 × 8 µm, n = 35), ellipsoid to cylindrical, catenate, developing in acropetal chains, 1-septate, septum darkened, constricted at the septum, truncate at both ends, subhyaline to olive green when immature, brown to black when mature.

Material examined – China, Yunnan Province, Kunming, on a decaying stem of *Jasminum nudiflorum* (Oleaceae), 11 November 2020, Y. Gao, GY19 (HKAS 145990), living culture KUNCC 25-19176.

Known hosts and distribution – on decaying wood of unknown host in China (Yuan et al. 2020), on a decaying stem of *Jasminum nudiflorum* (Oleaceae) in Yunnan Province, China (This study).

GenBank numbers – KUNCC 25-19176: ITS = PV608621, LSU = PV607475.

Notes – Our collection (KUNCC 25-19176) obtained from dead woody twigs of *Jasminum nudiflorum* is identified as *Catenuliconidia uniseptata* from phylogeny with 100% ML and 1.00 PP support values (Fig. 102). Morphologically, our collection most resembles *C. uniseptata* (MFLU 19-0689, holotype) in having superficial, effuse, velvety, black colonies and macronematous, mononematous, septate, unbranched conidiophores, ellipsoid to cylindrical, catenate, developing in acropetal chains of conidia (Yuan et al. 2020). Based on the known host of *Catenuliconidia uniseptata*, our collection (KUNCC 25-19176) is reported as a new host on *Jasminum nudiflorum* in Yunnan, China.

Occultitheca J.D. Rogers & Y.M. Ju, Sydowia 55: 359 (2003)

Notes – *Occultitheca* was established by Rogers & Ju (2003) with *O. costaricensis* as the type species. It was isolated from a decaying wood in Costa Rica. *Occultitheca rosae* was introduced as the second species collected on a dead branch of *Rosa* sp. (Rosaceae) in China (Samarakoon et al. 2022). Tian et al. (2024) reported a third species, *Occultitheca ananasi*, isolated from dead leaves of *Ananas comosus* in Thailand. Species within *Occultitheca* are distinguished by their immersed ascomata, short pedicellate asci with a J⁺ apical ring, brown ascospores with hyaline dwarf cells and a straight germ slit (Rogers & Ju 2003, Samarakoon et al. 2022, Tian et al. 2024). In this study, we introduce a new species, *Occultitheca yunnanensis*, based on morphology and molecular data, together with descriptions and illustrations (Fig. 105).

Occultitheca yunnanensis Y. Gao, H. Gui & K.D. Hyde, sp. nov.

Fig. 105

Index Fungorum number: IF903845; Facesoffungi number: FoF17719

Holotype – HKAS 128756

Etymology – The specific epithet “yunnanensis” refers to the Yunnan Province, where the holotype was found.

Saprobic on dead stems of unidentified grass. Sexual morph: Ascomata 280–385 µm high × 255–360 µm diam. ($\bar{x}$ = 330 × 310 µm, n = 10), subglobose to globose, immersed to erumpent through the host surface, solitary, scattered, uni-loculate, black. Clypeus carbonaceous, short, black, comprising host epidermal cells and dark fungal hyphae. Ostiole centric, with ostiolar canal

periphysate. *Peridium* 20–40 μm wide ($\bar{x}$ = 27 μm , n = 35), thin inner layer, composed of hyaline, thin-walled cells of *textura angularis*, outer layer thick, comprising brown to dark brown, thick-walled cells of *textura angularis*. *Paraphyses* 3–5 μm wide ($\bar{x}$ = 4 μm , n = 30), wider at the base, filamentous, septate, guttulate, constricted at the septa, embedded in a gelatinous matrix. *Asci* 80–130 $\times$ 7–10 μm ($\bar{x}$ = 110 $\times$ 8.5 μm , n = 25), 8-spored, clavate to cylindrical-clavate, apically rounded, unitunicate, short pedicellate, rectangular to slightly obconic, with a J^+ apical ring in Melzer's reagent. *Ascospores* 9–11 $\times$ 5–8 μm ($\bar{x}$ = 10.5 $\times$ 6.5 μm , n = 30), uniseriate, inequilaterally oblong-ellipsoidal, rounded at apex, hyaline when young, pale brown to brown when mature, aseptate, smooth, with guttulate. Asexual morph: Undetermined.

Culture characteristics – Colonies on PDA reaching 50 mm diam. after four weeks at 27°C, colonies from above, circular, dense, white, umbonate, papillate with fluffy; from below, pale yellow to cream.

Material examined – China, Yunnan Province, Kunming, on a decaying stem of unidentified grass (Poaceae), 13 May 2021, Y. Gao, GY57A (HKAS 128756, holotype), ex-type living culture CGMCC 3.24551.

GenBank numbers – CGMCC 3.24551: ITS = PV608622, LSU = PV607476, *tub2* = PV613314, *rpb2* = PV655528.

Notes – *Occultitheca yunnanensis* is introduced as a new species based on its distinct morphology and phylogenetic analysis of combined ITS, LSU, *tub2*, *rpb2*, and *act* sequence data. *Occultitheca yunnanensis* (CGMCC 3.24551) is closely related to *O. ananasi* (MFLUCC 23-0120, ex-type) with 100% ML and 1.00 PP support values (Fig. 102). *Occultitheca yunnanensis* differs from *O. ananasi* (MFLUCC 23-0120) in having long asci (82–130 $\times$ 7–10 μm , L/W = 12.5 vs. 70–90 $\times$ 5–10 μm , L/W = 10.5) and wider ascospores (9–11 $\times$ 5–8 μm , L/W = 1.5 vs. 10–12.5 $\times$ 3.5–4.5 μm , L/W = 2.8) (Tian et al. 2024). The nucleotide differences in the ITS, LSU, *tub2*, and *rpb2* gene regions between our collection and *O. ananasi* are 8.06% (39/484), 1.79% (14/784), 17.54% (259/1477), and 15.19% (143/941), respectively. Therefore, based on the polyphasic approach recommended for species boundary delimitation (Jayawardena et al. 2021, Maharachchikumbura et al. 2021a), we introduce *Occultitheca yunnanensis* as a novel taxon.

Xylaria Hill ex Schrank, Baiersche Flora 1: 200 (1789)

Notes – *Xylaria* was established by Schrank (1789) with *X. hypoxylon* as the type species. The majority of *Xylaria* species are saprotrophic, though some exhibit parasitic behavior, while others establish symbiotic relationships with plants as endophytes (Martín 1970, Rogers 1979, Deshmukh et al. 2022). These fungi are widely distributed across temperate, subtropical, and tropical regions (Ma et al. 2022). *Xylaria* species are commonly referred to as “dead man's fingers” (Deshmukh et al. 2022). Species of *Xylaria* possess distinctive survival adaptations, with melanin production forming both a physical and chemical barrier that prevents colonization by competing fungi. This adaptation also enables them to expel excess water in highly humid environments, allowing them to thrive in extreme conditions (Rajtar et al. 2023). Recently, Pan et al. (2025) described two new *Xylaria* species and established a key to 46 *Xylaria* species associated with fallen leaves and petioles worldwide. In this study, we introduce a new record for *Xylaria xylarioides*, based on morphology and molecular data, together with descriptions and illustrations (Fig. 106).

Xylaria xylarioides (Speg.) Hladki & A.I. Romero, Fungal Diversity 42: 86 (2010)

Fig. 106

Index Fungorum number: IF512724; Facesoffungi number: FoF18359

Saprobic on dead twigs of a Fagaceae host. Sexual morph: *Stromata* 960–1150 μm diam. $\times$ 640–800 μm high ($\bar{x}$ = 1100 $\times$ 760 μm , n = 10), superficial, capitate, depressed-capitate or obconical at fertile part, often with a pointed apex, upright or prostrate, solitary or sometimes clustered, carbonaceous, multilocular, black. *Ostioles* faintly pronounced to papillate. *Paraphyses* 2–5 μm wide ($\bar{x}$ = 3.5 μm , n = 30), wider at the base, filamentous, septate, guttulate, constricted at the septa. *Asci* 105–180 $\times$ 8–12 μm ($\bar{x}$ = 140 $\times$ 9.5 μm , n = 20), 8-spored, clavate to cylindrical-

clavate, apically rounded, uniseriate, long stipitate, with J⁺ apical ring in Melzer's reagent, inverted hat-shaped to more or less rectangular. *Ascospores* 20–23 × 7–9 μm ($\bar{x}$ = 20.5 × 8 μm, n = 30), uniseriate, inequilaterally naviform-ellipsoid or fusiform, with narrowly rounded to subacute or slightly pinched ends, lower end with a small hemispherical refractive cellular appendage, hyaline when young, pale brown to brown when mature, aseptate, smooth, with guttulate, with a straight to nearly spore-length germ slit. Asexual morph: Undetermined.

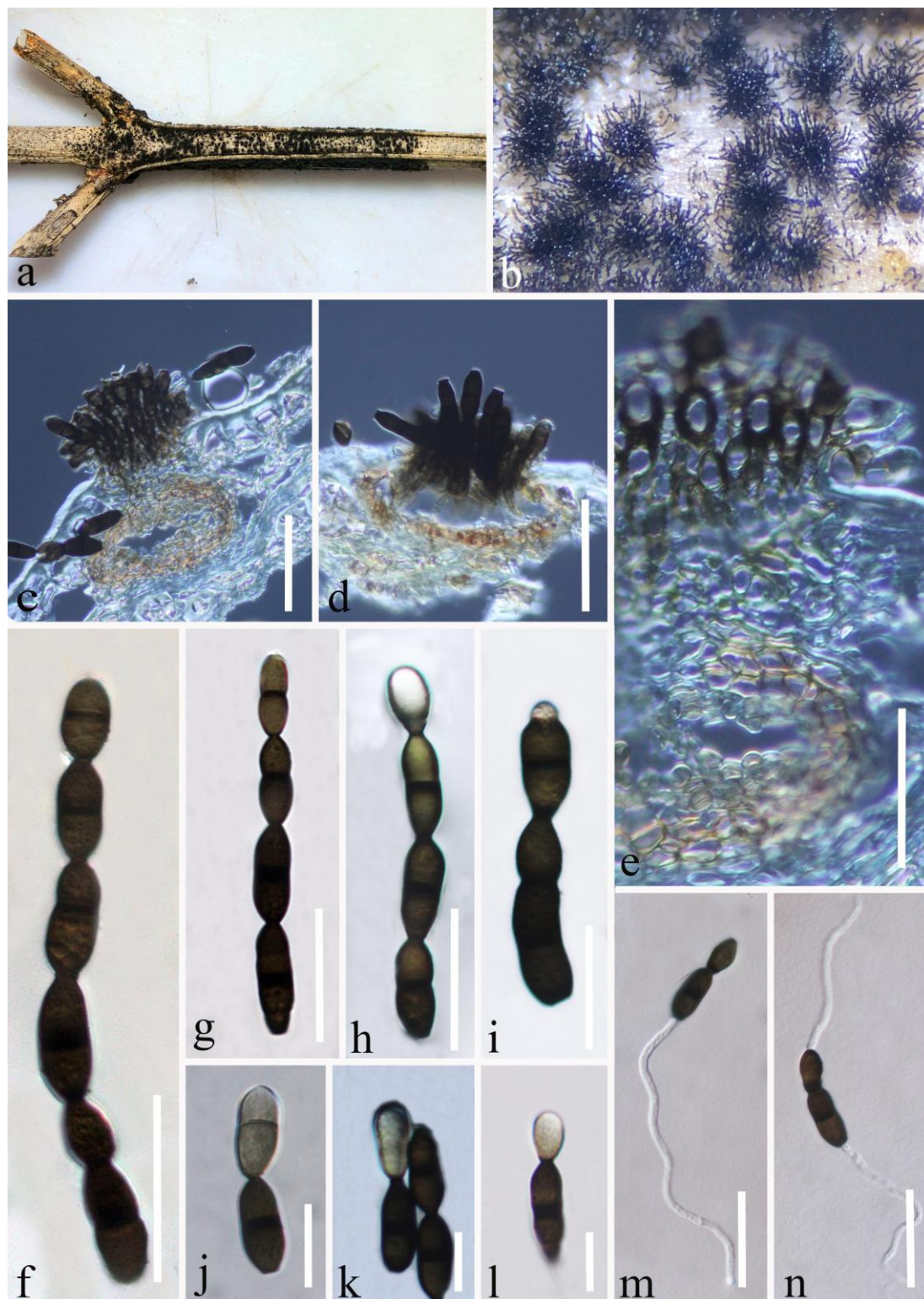


Figure 104 – *Catenuliconidia uniseptata* (HKAS 145990, a new host record). a, b Colonies on the host. c, d Sporodochium. e Peridium. f–i Conidial chains. j–l conidia. m, n Germinated conidia. Scale bars: c, d = 50 μm, e–h, m, n = 30 μm, i = 20 μm, j–l = 15 μm.

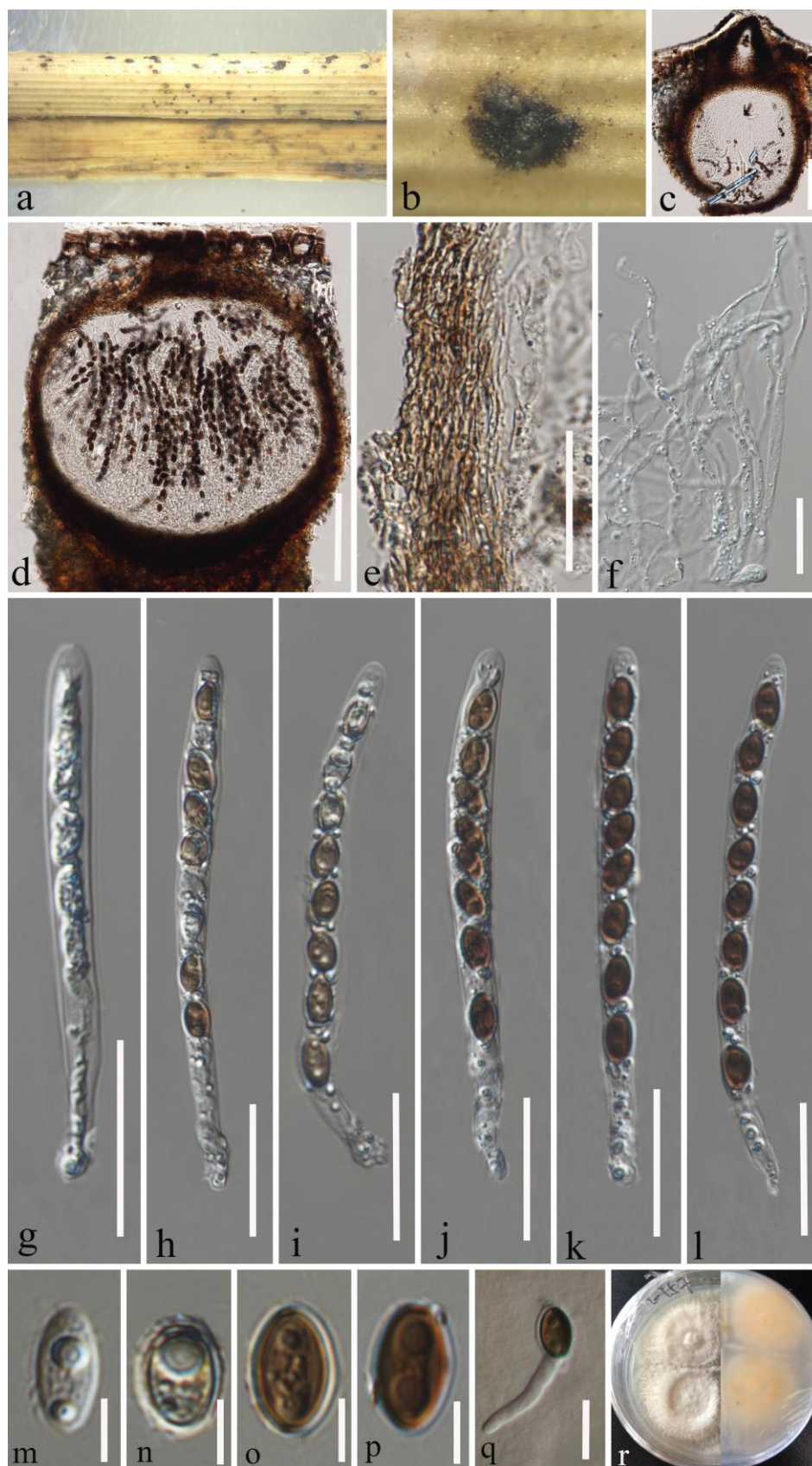


Figure 105 – *Occultitheca yunnanensis* (HKAS 128756, holotype). a, b Ascomata on the host substrate. c, d Cross sections through ascomata. e Peridium. f Paraphyses. g–l Asci. m–p Ascospores. q A germinated ascospore. r Culture characters on PDA (left: above, right: below). Scale bars: c, d = 100 μ m, e–l = 30 μ m, q = 10 μ m, m–p = 5 μ m.



Figure 106 – *Xylaria xylarioides* (HKAS 135344, a new host and a geographical record). a, d Stromata on the host substrate. c, d Sections of stromata. e Peridium. f Paraphyses. g–k Asci. l Ascospores (Ascospores in ventral view showing the germ slit in arrows). m, n J^+ Apical ring in

Melzer's reagent. o Germinated ascospores. p, q Culture characters on PDA (p: above, q: below).
Scale bars: d = 300 μ m, e = 100 μ m, f = 50 μ m, g–l = 30 μ m, o = 20 μ m, n, m = 10 μ m.

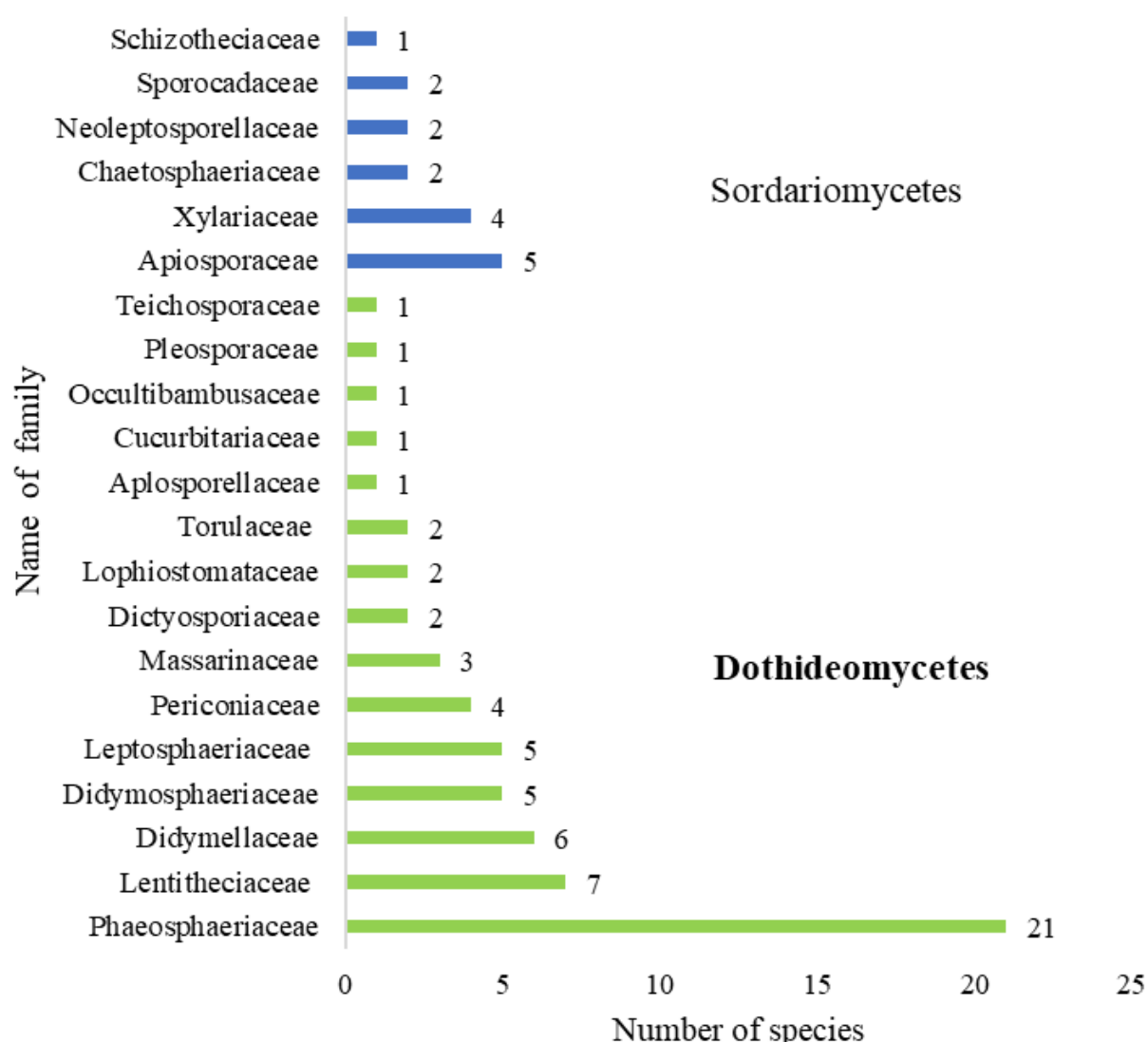


Figure 107 – The overview of fungal species in each family of in Dothideomycetes and Sordariomycetes (Axis X is fungal number and axis Y is fungal family).

DISCUSSION

This study delves into the saprobic ascomycetes associated with grassland vegetation, primarily collected in Yunnan, China. Through morphological comparisons and multigene phylogenetic analyses, we introduced a new genus, 31 new species, and 47 new records. Our findings across 21 families and 46 genera, with Dothideomycetes emerging as the dominant class, representing 80% of the species, and Sordariomycetes at 20%. Ascomycota is the most speciose and complex phylum of fungi (Thiyagaraja et al. 2025). Dothideomycetes represents the largest and most diverse class within Ascomycota, encompassing approximately 20,000 species distributed across 50 orders, 223 families, and 1,941 genera (Pem et al. 2024). The Phaeosphaeriaceae (Dothideomycetes) was identified as the dominant family (Fig. 107). Notably, we report 42 species in their sexual forms, 33 in their asexual forms, and three with both forms. In this study, we clarify several previously incomplete life-cycle records. We document *Pseudocyclothyriella lolii* as the first sexual morph known for the genus *Pseudocyclothyriella*. While the asexual morph of *Phaeosphaeriopsis grevilleae* was reported by Marin-Félix et al. (2019), we provide its sexual morph here. For taxa with earlier reports lacking one morph viz. *Neoascochyta humicola* (Hou et al.

2020), *Keissleriella gloeospora* (sexual morph in Tanaka et al. 2015), *Paraphaeosphaeria michotii* (Zhuang & Li 2009), and *Stagonospora poaceicola* (Brahmanage et al. 2020), we report their asexual morphs. Together, these findings reduce the number of asexual–sexual gaps within several genera and strengthen species-level concepts. Beyond filling life-history gaps, our results expand a previously monotypic genus (*Pseudocyclothyriella*), underscoring how the addition of new species improves taxonomic resolution, refines generic boundaries and enables more accurate ecological and biodiversity assessments. Given the vast proportion of fungal diversity that remains undescribed, systematically augmenting sparsely populated genera is a practical route to closing knowledge gaps. The establishment of *Pseudocyclothyriella* as monotypic and its subsequent expansion with *P. lolii* exemplify the dynamic, iterative nature of fungal taxonomy and discovery (Wanasinghe et al. 2022).

The vegetation of Zhaotong grassland was composed of 20 plant families, with Asteraceae, Caryophyllaceae, Gramineae, and Rosaceae being the most prevalent (Zhu et al. 2022). We identified and characterized a total of 138 fungal collections. We found 107 collections of fungal isolates from Poaceae, 16 from unidentified hosts, six from Asteraceae, four from Caprifoliaceae, and one collection each from Araliaceae, Iridaceae, Oleaceae, Orobanchaceae, and Rosaceae. Most fungal (107 collections) were associated with Poaceae (grasses), suggesting a remarkable and impressive specialization or adaptation to this dominant plant family in grasslands. A few collections from Asteraceae, Caprifoliaceae, and other families indicate potential host flexibility among some species.

The highest number of fungi was isolated from Zhaotong (75 collections) (elevation: 2950 m), followed by Kunming (46 collections) (elevation: 1990 m), Qujing (11 collections) (elevation: 2800 m), and Xishuangbanna (five collections) (elevation: 550). These variations may be attributed to differences in climatic conditions, soil composition, and vegetation cover, which can significantly influence fungal distribution. Zhaotong, characterized by a temperate climate and extensive grassland, may provide favorable conditions for fungal colonization and proliferation, whereas the lower fungal diversity recorded in Xishuangbanna may be attributed to differences in ecosystem structure and sampling limitations.

Among all the known fungal species worldwide, 10,233 species, belonging to 3 kingdoms, 13 phyla, 44 classes, 174 orders, 572 families, and 2,379 genera, were first discovered from China, occupying the second highest worldwide and accounting for 6.84% of global known fungal diversity (Wang & Cai 2023). Species discovered from the southwest (Guizhou, Sichuan, Tibet, Yunnan) and low-latitude tropical and subtropical regions (Guangdong, Taiwan) accounted for the highest proportion of China (Wang & Cai 2023). In recent years, Luo et al. (2025) mentioned that the fungal diversity in China has drawn the attention of taxonomists, and a total of 27,807 fungal species and subspecies have been recorded by the Catalogue of Life China 2024 Annual Checklist. Wang et al. (2021) reported that Yunnan was the province with the most newly discovered fungal species, accounting for about a quarter of the total number of new species discovered in China.

Yunnan takes up only 4.1% of the total land area of China, but includes more than half of the total plant species found and has various types of vegetation. Yunnan is biogeographically located at the junction where tropical Asia, East Asia, and the Himalayan subtropical-temperate zones meet. This results in Yunnan has a complicated geological history, a particular geography, a huge difference in elevations (76 m to 6740 m), and a complex topography, which have influenced the formation of various habitats of high biodiversity: 245 families; 2140 genera; 13,253 species and varieties of seed plants; more than 12 types of vegetation; and 167 plant formations, including tropical rain forests, tropical dry forests, subtropical evergreen broad-leaved forest, cold temperate coniferous forests, and alpine bushes and meadows (Zhu 2016, Zhu & Tan 2022). Many communities are rich in woody and herbaceous species, providing abundant hosts and substrates for fungi of varying trophic types (saprophytic, endophytic, and soil microfungi).

In Yunnan, China, grasslands are primarily distributed in the high-elevation mountainous regions of northwestern and northeastern Yunnan, where alpine meadows and subalpine meadows dominate them. Previous studies have mainly focused on how grassland degradation significantly

alters soil microbial communities and related ecological processes (Che et al. 2019, Liu et al. 2023d). Although microbial participation in litter decomposition is widely known within terrestrial soils, the role and significance of microorganisms during the aerial standing litter phase of decomposition remain poorly investigated (Lodato et al. 2021). In many grasses and grass-like plants, the shedding and collapse of plant organs (such as leaves and stems) onto the soil surface usually do not happen after senescence and death. As a result, large amounts of standing dead plant litter can accumulate in various ecosystems (Knapp & Seastedt 1986, Seastedt 1988, Biondini & Manske 1996, Asaeda et al. 2002, Lodato et al. 2021). Wang et al. (2017a) found that the standing litter of *Cleistogenes squarrosa* (Poaceae) experienced higher nighttime relative humidity than litter on the soil surface, which led to increased microbial respiratory activity, biomass accumulation, and faster decomposition rates compared to surface litter (Liu et al. 2015). Additionally, microbial preconditioning and transformation of the standing litter of *Cleistogenes squarrosa* resulted in a quicker decomposition rate once the litter collapsed to the soil surface, thereby enhancing the efficiency and rate of soil organic matter formation (Gliksman et al. 2018). Lodato et al. (2021) examined the fungi inhabiting the standing leaf litter of *Schizachyrium scoparium* and *Schizachyrium tenerum* (Poaceae) in a Longleaf Pine savanna ecosystem, and the results showed that as fungal biomass increased, there was a significant loss in the carbon quality of plant leaves. Grasslands are often overlooked in fungal diversity studies; however, these ecosystems host many fungal species that contribute to ecosystem functioning. Recording new species highlights the importance of conserving grassland habitats. The urgency of this conversation is underscored by the understanding that grasslands are vulnerable to climate change and land-use modifications. Studying their fungal communities can provide insights into ecosystem resilience and responses to environmental shifts, further emphasizing the need for conservation.

This study underscores the ecological significance of saprophytic and fungal diversity in grassland ecosystems. Studying grassland fungi presents several challenges, including their high diversity of grassland fungi and the difficulty of identifying many species, especially in the absence of distinguishing morphological features. The use of molecular techniques, such as DNA barcoding, while effective, can be time-consuming and costly (Lücking et al. 2020, Jayawardena et al. 2021, Maharachchikumbura et al. 2021a). The degradation of the grass plant material further complicates the precise identification of the host in this study. Despite these challenges, our study provides valuable insights into fungal diversity and its possible ecological functions. We assume that incorporating this information will better equip future research to address these challenges. The observed distribution patterns suggest that fungal species have adapted to specific hosts and environmental conditions. The discovery of new species and records underscores the need for continued research in underexplored habitats. This emphasis on exploration and discovery is crucial for expanding our knowledge of fungal biodiversity and ecosystem dynamics.

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DECLARATION ON CONFLICT OF INTEREST

The authors have declared that no competing interests exist.

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