





Unveiling fungi associated with *Castanopsis* woody litter in Yunnan Province, China: Insights into Pleosporales (Dothideomycetes) species

Guang-Cong Ren^{1,2}, Saowaluck Tibpromma³, Kai-Xuan Dong^{1,2}, Chen-Xi Gao^{1,2}, Chao-Shan Zhang^{1,2}, Samantha C. Karunaratna³, Abdallah M. Elgorban⁴, Heng Gui^{5,6}

1 School of Pharmacy, Guiyang Healthcare Vocational University, Guiyang 550081, China

2 Guizhou Provincial Engineering Research Center of Medical Resourceful Healthcare Products, Guiyang Healthcare Vocational University, Guiyang 550081, China

3 Center for Yunnan Plateau Biological Resources Protection and Utilization College of Biological Resource and Food Engineering, Qujing Normal University, Qujing, Yunnan 655011, China

4 Center of Excellence in Biotechnology Research (CEBR), King Saud University, Riyadh, Saudi Arabia

5 Center for Mountain Futures (CMF), Kunming Institute of Botany, Chinese Academy of Sciences, Kunming 650201, China

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

Corresponding author: Saowaluck Tibpromma (saowaluckfai@gmail.com)



This article is part of:

Exploring the Hidden Fungal Diversity: Biodiversity, Taxonomy, and Phylogeny of Saprobic Fungi

Edited by Samantha C. Karunaratna, Danushka Sandaruwan Tennakoon, Ajay Kumar Gautam

Academic editor:

Danushka Sandaruwan Tennakoon

Received: 15 May 2024

Accepted: 28 July 2024

Published: 22 August 2024

Citation: Ren G-C, Tibpromma S, Dong K-X, Gao C-X, Zhang C-S, Karunaratna SC, Elgorban AM, Gui H (2024) Unveiling fungi associated with *Castanopsis* woody litter in Yunnan Province, China: Insights into Pleosporales (Dothideomycetes) species. MycoKeys 108: 15–45. <https://doi.org/10.3897/mycokeys.108.127560>

Copyright: © Guang-Cong Ren et al. This is an open access article distributed under terms of the Creative Commons Attribution License (Attribution 4.0 International – CC BY 4.0).

Abstract

During a survey of the diversity of lignicolous fungi in Yunnan Province, China, we collected and identified five microfungi species from dead woody litters of *Castanopsis* trees in terrestrial habitats. Through both morphological comparisons and phylogenetic analyses of multi-gene sequences, we identified two taxa as new species and three collections as new host records within Pleosporales. *Pseudolophiostoma lincangense* **sp. nov.** is introduced as a sexual morph in Lophiostomataceae, *Pleopunctum baoshanense* **sp. nov.** is introduced as a hyphomycetous fungi in Phaeoseptaceae, and *Paraphoma aquatica* as a first report of sexual morph in *Paraphoma*. In addition, *Occultibambusa kunmingensis* and *Pleopunctum megalosporum* were isolated for the first time from the dead twigs of *Castanopsis delavayi* and *C. calathiformis*, respectively. Comprehensive morphological descriptions, illustrations, and phylogenetic analysis results are provided for the above-mentioned species.

Key words: Hyphomycetes, new species, phylogeny, sexual morph, taxonomy

Introduction

Castanopsis is an evergreen tree belonging to Fagaceae and represents one of the largest genera with approximately 134 species, predominantly distributed across tropical and subtropical regions of Asia (Tan et al. 2023). Notably, 58 species are native to China, with 30 being endemic. *Castanopsis* species are valued for their timber and edible nuts, contributing significantly to the economy (Huang et al. 1999; Tang et al. 2005). Fungal diversity associated with *Castanopsis* has been extensively documented across various countries, including China, Korea, India, Indonesia, Japan, Nepal, Papua New

Guinea, Thailand, and the United States (Crawford et al. 1987; Tang et al. 2005; Duong et al. 2008; Osono et al. 2020; Jayawardena et al. 2020). The presence of fungi on *Castanopsis* trees has been widely introduced, with approximately 360 records worldwide representing 220 species across 35 different *Castanopsis* species (Duong et al. 2008). Tang et al. (2005) reported 38 fungal taxa during a study on decaying leaves of *Castanopsis fissa* in Hong Kong, China highlighting the rich fungal diversity within this genus. These fungi encompass endophytes and saprobes found on different parts of *Castanopsis* trees, such as ectomycorrhizal, woody branches, fallen trunks, bark, and leaves (Inácio et al. 2005; Gao et al. 2016; Hyde et al. 2016; Ren et al. 2022; Pang et al. 2023).

Yunnan Province, located in southwestern China, boasts significant biological diversity attributed to its complex topography, highly variable climate, and lush vegetation (Feng and Yang 2018). This region covers an extensive area of 394,000 square with approximately 94% comprising mountainous terrain (Asian Development Bank 2012). Over the past decade, there has been a surge in interest in studying microfungi in Yunnan Province, with numerous studies focusing on leaf litter fungi and lignicolous freshwater fungi (Cai et al. 2002; Luo et al. 2018; Hapuarachchi et al. 2019; Dong et al. 2020). Recent discoveries have unveiled several new taxa from Dothideomycetes and Sordariomycetes inhabiting woody litter in terrestrial habitats, such as Diatrypaceae, Didymosphaeriaceae, Hermatomycetaceae, Hysteriaceae, Monoblastiaceae and Phaeoseptaceae (Maharachchikumbura et al. 2021; Mortimer et al. 2021; Ren et al. 2022; Wanasinghe and Mortimer et al. 2022). However, many studies lack proper identification and phylogenetic data, underscoring the need to re-evaluate various species in this region (Mortimer et al. 2021).

Pleosporales was established by Barr (1987) and is recognized as the largest order within the class Dothideomycetes, constituting a quarter of all species (Wijayawardene et al. 2022). This order has a remarkable diversity, comprising 91 families and 614 genera (Wijayawardene et al. 2022). Taxonomically, pleosporalean taxa exhibit versatility in ecological niches, being found as epiphytes, endophytes, parasites, hyperparasites, lichenized organisms, or saprobes across a wide range of habitats worldwide (Wanasinghe et al. 2020; Yang et al. 2023). Studies have highlighted the discovery of numerous new pleosporalean species from freshwater, marine, and terrestrial environments (Brahmanage et al. 2020). Morphologically, the sexual morph of Pleosporales is characterized by perithecial ascomata, typically with a papillate apex, ostiolate, cellular pseudoparaphyses, and bitunicate asci. The asexual morphs encompass both coelomycetes and hyphomycetes (Hong-sanan et al. 2020).

The present study aims to describe two novel fungal species and three new host records collected from dead woody litter in Baoshan and Lincang of Yunnan Province, China. This involves morphological illustrations and multi-gene phylogenetic analyses utilizing ML and BI methods to confirm the phylogenetic placement. The study aims to contribute to fungal diversity and ecology in Yunnan Province while providing valuable insights into the taxonomy and phylogenetics of woody litter fungi.

Materials and methods

Sample collection, observation, and isolation

Decayed woody samples were collected from mixed forest areas in China (Yunnan Province) during the rainy season (July) and brought to the laboratory in separate zip-lock plastic bags. Specimens were examined using a stereomicroscope (Olympus SZ61, Tokyo, Japan). Micro-morphological characteristics were photographed using a Canon EOS 600D (Tokyo, Japan) digital camera mounted on a Nikon ECLIPSE 80i (Tokyo, Japan) compound microscope. All microscopic measurements were taken using the Tarosoft (R) Image Frame Work v.09, and the measurements were reported as minimum–maximum values and average values. Images were processed with Adobe Photoshop CS6 software v.13 (Adobe Systems, San Jose, CA, USA). Single-spore isolation was used to obtain pure cultures, following the methods described by Ren et al. (2022). Herbarium materials were deposited at the Herbarium of Cryptogams Kunming Institute of Botany, Academia Sinica (HKAS), Kunming, China, and living cultures were deposited at the Kunming Institute of Botany Culture Collection (KUNCC), Kunming, China. Faces of fungi (Jayasiri et al. 2015) and Index Fungorum (2024) numbers were obtained for the new taxa.

DNA extraction, PCR amplification, and sequencing

Genomic DNA was extracted from the mycelium grown on PDA at 25 °C for four weeks using Biospin Fungus Genomic DNA Extraction Kit (BioFlux®) (Hangzhou, P.R. China). Five gene regions, including internal transcribed spacer region (ITS), large subunit nuclear ribosomal (LSU), small subunit ribosomal RNA (SSU), translation elongation factor 1-alpha gene (*tef1-α*), and RNA polymerase II second largest subunit (*rpb2*) were amplified with primers ITS5/ITS4 (White et al. 1990), LR0R/LR5 (Vilgalys and Hester 1990), NS1/NS4 (White et al. 1990), 983F/2218R (Rehner and Buckley 2005) and fRPB2-5F/fRPB2-7cR (Liu et al. 1999), respectively. The PCR thermal cycle programs for SSU, LSU, ITS, *tef1-α*, and *rpb2* were set as described in Wanasinghe et al. (2021). The quality of PCR products was checked on 1% agarose gel electrophoresis stained with ethidium bromide. The PCR products were sent for sequencing at Qingke Company, Kunming City, Yunnan Province, China. The sequences were deposited in GenBank.

Phylogenetic analyses

Sequences exhibiting high similarities (>90%) were identified through BLASTn searches to determine the closest match to the taxa. Representative sequences were individually blasted and the initial results from BLASTn searches show our five taxa belong to *Pseudolophiostoma* in Lophiostomataceae, *Occultibambusa* in Occultibambusaceae, *Pleopunctum* in Phaeoseptaceae, and *Paraphoma* in Phaeosphaeriaceae. Thus, four different datasets were prepared and analysed in this study based on recent publications (Gomzhina et al. 2020; Phukham-sakda et al. 2020; Magaña-Dueñas et al. 2021; Guarnaccia et al. 2022; Yu et al. 2022; Xu et al. 2023). The sequences were downloaded from GenBank (<http://www.ncbi.nlm.nih.gov/>) and the accession numbers are listed in Table 1.

Table 1. Names, strain numbers, and corresponding GenBank accession numbers of the taxa used in the phylogenetic analysis.

Taxon name	Strain number	GenBank accession numbers					
		SSU	ITS	LSU	tef1- α	rpb2	tub2
<i>Alpestrisphaeria jonesii</i>	GAAZ 54-1	KX687755	KX687757	KX687753	KX687759	NA	NA
<i>Alpestrisphaeria jonesii</i>	GAAZ 54-2	KX687756	KX687758	KX687754	KX687760	NA	NA
<i>Alpestrisphaeria terricola</i>	SC-12 ^T	JX985749	JN662930	JX985750	NA	NA	NA
<i>Angustimassarina acerina</i>	MFLUCC 14-0505 ^T	NG_063573	KP888637	NR_138406	KR075168	NA	NA
<i>Angustimassarina populi</i>	MFLUCC 13-0034 ^T	NG_061204	KP888642	KP899137	KR075164	NA	NA
<i>Biappendiculispora japonica</i>	KT 573 ^T	AB618686	LC001728	AB619005	LC001744	NA	NA
<i>Biappendiculispora japonica</i>	KT 794	AB618688	LC001730	AB619007	LC001746	NA	NA
<i>Biappendiculispora japonica</i>	KT 686	AB618687	LC001729	AB619006	LC001745	NA	NA
<i>Brunneofusispora clematidis</i>	MFLUCC 17-2070	MT226685	MT310615	MT214570	MT394692	MT394629	NA
<i>Brunneofusispora inclinatioستيولا</i>	CGMCC 3.20403	MZ964884	MZ964866	MZ964875	OK061075	OK061069	NA
<i>Brunneofusispora sinensis</i>	KUMCC 17-0030	MH393556	MH393558	MH393557	NA	MH395329	NA
<i>Capulatispora sagittiforme</i>	KT 1934 ^T	AB618693	AB369268	AB369267	LC001756	NA	NA
<i>Coelodictyosporium muriforme</i>	MFLUCC 13-0351 ^T	KP899127	KP899136	KP888641	KR075163	NA	NA
<i>Coelodictyosporium pseudodictyosporium</i>	MFLUCC 13-0451 ^T	NA	KR025858	KR025862	NA	NA	NA
<i>Crassiclypeus aquaticus</i>	KT 970 ^T	LC312472	LC312501	LC312530	LC312559	LC312588	NA
<i>Crassiclypeus aquaticus</i>	KH 104	LC312470	LC312499	LC312528	LC312557	LC312586	NA
<i>Decaisnella formosa</i>	BCC 25616	GQ925833	GQ925846	NA	GU479851	NA	NA
<i>Decaisnella formosa</i>	BCC 25617	GQ925834	GQ925847	NA	GU479850	NA	NA
<i>Desertiserpentica hydei</i>	SQUCC 15092 ^T	MW077163	MW077147	MW077156	MW075773	NA	NA
<i>Dimorphiopsis brachystegiae</i>	CPC 22679 ^T	NA	KF777160	KF777213	NA	NA	NA
<i>Ernakulamia krabiensis</i>	MFLUCC 18-0237	MK347880	MK347773	MK347990	NA	NA	NA
<i>Ernakulamia xishuangbannaensis</i>	KUMCC 17-0187	MH260354	MH275080	MH260314	NA	NA	NA
<i>Flabellascoma aquaticum</i>	KUMCC 15-0258	MN304832	MN304827	MN274564	MN328898	MN328895	NA
<i>Flabellascoma cycadicola</i>	KT 2034 ^T	LC312473	LC312502	LC312531	LC312560	LC312589	NA
<i>Flabellascoma fusiforme</i>	MFLUCC 18-1584	NA	MN304830	MN274567	MN328902	NA	NA
<i>Guttulispora crataegi</i>	MFLUCC 14-0993	KP899126	KP899135	KP888640	KR075162	NA	NA
<i>Guttulispora crataegi</i>	MFLUCC 13-0442 ^T	KP899125	KP899134	KP888639	KR075161	NA	NA
<i>Kiskunsagia ubrizsyi</i>	REF121 ^T	MK589351	JN859341	MK589359	MK599325	NA	NA
<i>Lentistoma aquaticum</i>	MFLUCC 18-1275	MT864320	MT627697	MN913723	MT954370	NA	NA
<i>Lentistoma bipolare</i>	KT 3056	LC312484	LC312513	LC312542	LC312571	LC312600	NA
<i>Lentistoma bipolare</i>	CBS 115375	LC312477	LC312506	LC312535	LC312564	LC312593	NA
<i>Leptoparies magnoliae</i>	MFLU 18-1291	ON870915	ON878077	ON870390	NA	NA	NA
<i>Leptoparies palmarum</i>	KT 1653 ^T	LC312485	LC312514	LC312543	LC312572	LC312601	NA
<i>Leptosphaeria heterospora</i>	AFTOL-ID 1036	NA	GQ203795	AY016369	DQ497609	DQ497615	NA
<i>Lignosphaeria fusispora</i>	MFLUCC 11-0377 ^T	NA	KP888646	NR_164233	NA	NA	NA
<i>Lophiohelichrysum helichrysi</i>	IT-1296 ^T	KT333437	KT333435	KT333436	KT427535	NA	NA
<i>Lophiopoacea paramacrostromum</i>	MFLUCC 11-0463 ^T	KP899122	NA	KP888636	NA	NA	NA
<i>Lophiopoacea winteri</i>	KT 740	AB618699	JN942969	AB619017	LC001763	JN993487	NA
<i>Lophiopoacea winteri</i>	KT 764	AB618700	JN942968	AB619018	LC001764	JN993488	NA
<i>Lophiostoma multiseptatum</i>	CBS 623.86	GU296163	NA	GU301833	NA	GU371791	NA
<i>Lophiostoma multiseptatum</i>	KT 604/JCM17668 ^T	AB618684	LC001726	AB619003	LC001742	NA	NA
<i>Lophiostoma semiliberum</i>	KT 622	AB618694	JN942966	AB619012	LC001757	JN993483	NA
<i>Lophiostoma semiliberum</i>	KT 652	AB618695	JN942967	AB619013	LC001758	JN993485	NA
<i>Neoocultibambusa chiangraiensis</i>	MFLUCC 12-0559	KU712458	KU712442	KU764699	NA	KU872761	NA

Taxon name	Strain number	GenBank accession numbers					
		SSU	ITS	LSU	tef1- α	rpb2	tub2
<i>Neooccultibambusa kaiyangensis</i>	CGMCC 3.20404	MZ964886	MZ964868	MZ964877	OK061077	OK061071	NA
<i>Neooccultibambusa trachycarpi</i>	CGMCC 3.20405	MZ964888	MZ964870	MZ964879	OK061079	OK061073	NA
<i>Neopaucispora rosae-ecae</i>	MFLUCC 17-0807 ^T	MG829139	MG828924	MG829033	MG829217	NA	NA
<i>Neotrematosphaeria biappendiculatum</i>	KTC 975	GU205254	NA	GU205228	NA	NA	NA
<i>Neotrematosphaeria biappendiculatum</i>	KTC 1124 ^T	GU205256	NA	GU205227	NA	NA	NA
<i>Neovaginatisspora clematidis</i>	MFLUCC 17-2149	MT226676	MT310606	MT214559	MT394738	NA	NA
<i>Neovaginatisspora fuckelii</i>	MFLUCC 17-1334	MN304833	MN304828	MN274565	MN328899	MN328896	NA
<i>Neovaginatisspora fuckelii</i>	KT 634	AB618690	LC001732	AB619009	LC001750	NA	NA
<i>Occultibambusa aquatica</i>	MFLUCC 11-0006	KX698112	KX698114	KX698110	NA	NA	NA
<i>Occultibambusa bambusae</i>	MFLUCC 13-0855	KU872116	KU940123	KU863112	KU940170	KU940193	NA
<i>Occultibambusa chiangraiensis</i>	MFLUCC 16-0380	KX655551	NA	KX655546	KX655566	KX655561	NA
<i>Occultibambusa fuispora</i>	MFLUCC 11-0127	NA	KU940125	KU863114	KU940172	KU940195	NA
<i>Occultibambusa hongheensis</i>	KUMCC 21-0020	MZ329029	MZ329037	MZ329033	NA	MZ325467	NA
<i>Occultibambusa jonesii</i>	GZCC 16-0117	KY628324	NA	KY628322	KY814758	KY814756	NA
<i>Occultibambusa kunmingensis</i>	HKAS 102151	MT864342	MT627716	MN913733	MT878453	MT954407	NA
<i>Occultibambusa kunmingensis</i>	KUNCC 21-0506	PP779901	PP779906	PP779897	PP778371	NA	NA
<i>Occultibambusa maolanensis</i>	GZCC 16-0116	KY628325	NA	KY628323	KY814759	KY814757	NA
<i>Occultibambusa pustula</i>	MFLUCC 11-0502	KU872118	KU940126	KU863115	NA	NA	NA
<i>Occultibambusa sichuanensis</i>	CGMCC 3.20938	NA	ON332913	ON332931	ON383989	ON381181	NA
<i>Occultibambusa sichuanensis</i>	UESTCC 22.0004	NA	ON332914	ON332932	ON383990	ON381182	NA
<i>Parapaucispora pseudoarmatispora</i>	KT 2237	LC100018	LC100021	LC100026	LC100030	NA	NA
<i>Paraphoma aquatica</i>	FMR 16956 ^T	NA	OU612361	OU612360	OU612357	OU612356	OU612355
<i>Paraphoma aquatica</i>	KUNCC 21-0523	NA	PP779905	PP779896	PP778370	NA	NA
<i>Paraphoma chlamydocopiosa</i>	UMPC01	NA	KU999072	NA	NA	KU999080	KU999084
<i>Paraphoma chrysanthemicola</i>	CBS 172.70	NA	KF251165	KF251669	KF252173	KF253123	KF252660
<i>Paraphoma chrysanthemicola</i>	CBS 522.66 ^T	NA	KF251166	KF251670	KF252174	KF253124	KF252661
<i>Paraphoma convolvuli</i>	MF-9.222	NA	MG764055	MG764069	NA	NA	NA
<i>Paraphoma convolvuli</i>	MF-9.265	NA	MG764062	MG764071	MG779467	NA	MG779457
<i>Paraphoma convolvuli</i>	MF-9.298.1	NA	MG764057	MG764074	MG779468	NA	MG779459
<i>Paraphoma convolvuli</i>	MF-9.300.1	NA	MG764064	MG764066	MG779469	NA	MG779460
<i>Paraphoma convolvuli</i>	MF-9.301.1	NA	MG764060	MG764075	MG779470	KF253126	MG779461
<i>Paraphoma dioscoreae</i>	CPC 11361	NA	KF251169	KF251673	KF252177	KF253127	KF252664
<i>Paraphoma dioscoreae</i>	CBS 135100	NA	KF251167	KF251671	KF252175	NA	KF252662
<i>Paraphoma fimeti</i>	CBS 170.70 ^T	NA	KF251170	KF251674	KF252178	KF253128	KF252665
<i>Paraphoma fimeti</i>	CBS 368.91	NA	KF251171	KF251675	KF252179	KF253129	KF252666
<i>Paraphoma garibaldii</i>	CBS 148459	NA	OL435708	NA	NA	OL449256	OL449254
<i>Paraphoma garibaldii</i>	CBS 148460	NA	OL435709	NA	NA	OL449257	OL449255
<i>Paraphoma ledniceana</i>	CBS 146533	NA	MT371091	MT371396	MT372655	MT372654	MT372661
<i>Paraphoma melnikiae</i>	MF-9.88	NA	MG764063	MG764065	MG779466	NA	MG779456
<i>Paraphoma melnikiae</i>	MF-9.95	NA	MG764054	MG764067	MG779462	NA	NA
<i>Paraphoma melnikiae</i>	MF-9.182.1	NA	MG764058	MG764068	MG779463	NA	MG779454
<i>Paraphoma melnikiae</i>	MF-9.240	NA	MG764061	MG764070	MG779464	NA	MG779453
<i>Paraphoma melnikiae</i>	MF-9.296.1	NA	MG764056	NA	MG779465	NA	MG779458
<i>Paraphoma pye</i>	UMPP04; BRIP 65171	NA	KU999075	NA	NA	NA	KU999087
<i>Paraphoma pye</i>	UMPP02	NA	KU999073	NA	NA	KU999081	KU999085
<i>Paraphoma radicina</i>	CBS 111.79	NA	KF251172	KF251676	KF252180	KF253130	KF252667

Taxon name	Strain number	GenBank accession numbers					
		SSU	ITS	LSU	tef1- α	rpb2	tub2
<i>Paraphoma radicina</i>	CBS 102875 ^T	NA	KF251173	KF251677	KF252181	KF253131	KF252668
<i>Paraphoma raphiolepidis</i>	CBS 142524 ^T	NA	KY979758	KY979813	KY979851	KY979896	KY979924
<i>Paraphoma salicis</i>	CBS 146797	NA	MW883437	MW883829	MW890069	NA	MW890140
<i>Paraphoma variabilis</i>	CBS 147695 ^T	NA	LR993310	LR993311	LR993313	NA	LR993314
<i>Paraphoma vinacea</i>	UMPV004	NA	KU176887	KU176891	NA	NA	KU176895
<i>Paucispora kunmingense</i>	MFLUCC 17-0932 ^T	MF173430	MF173432	MF173428	MF173434	MF173436	NA
<i>Paucispora quadrispora</i>	KT 843 ^T	AB618692	LC001734	AB619011	LC001755	NA	NA
<i>Phaeoseptum aquaticum</i>	CBS 123113 ^T	NA	JN644072	KY940803	NA	NA	NA
<i>Phaeoseptum carolshearerianum</i>	NFCCI-4221 ^T	MK307816	MK307813	MK307810	MK309874	MK309877	NA
<i>Phaeoseptum carolshearerianum</i>	NFCCI-4384	MK307818	MK307815	MK307812	MK309876	MK309879	NA
<i>Phaeoseptum hydei</i>	MFLUCC 17-0801 ^T	MT240624	MT240623	MT240622	MT241506	NA	NA
<i>Phaeoseptum mali</i>	HKAS122916	ON009082	ON009098	ON009114	ON009257	ON009282	NA
<i>Phaeoseptum mali</i>	HKAS122917	ON009083	ON009099	ON009115	ON009258	ON009283	NA
<i>Phaeoseptum mali</i>	MFLUCC 17-2108 ^T	NA	MK625197	MK659580	MK647990	NA	NA
<i>Phaeoseptum manglicola</i>	NFCCI-4666 T	MK307817	MK307814	MK307811	MK309875	MK309878	NA
<i>Phaeoseptum terricola</i>	MFLUCC 10-0102 ^T	MH105780	MH105779	MH105778	MH105781	NA	NA
<i>Platystomum crataegi</i>	MFLUCC 14-0925 ^T	KT026113	KT026117	KT026109	KT026121	NA	NA
<i>Platystomum rosae</i>	MFLUCC 15-0633 ^T	KT026115	KT026119	KT026111	NA	NA	NA
<i>Platystomum salicicola</i>	MFLUCC 15-0632 ^T	KT026114	KT026118	KT026110	NA	NA	NA
<i>Pleopunctum baoshanense</i>	KUNCC 21-0494^T	PP779898	PP779902	PP779893	PP778367	PP778372	NA
<i>Pleopunctum clematidis</i>	MFLUCC 17-2091	NA	MT214573	MT310618	MT394632	MT394693	NA
<i>Pleopunctum ellipsoideum</i>	MFLUCC 19-0390 ^T	MK804514	MK804517	MK804512	MK828510	NA	NA
<i>Pleopunctum ellipsoideum</i>	MFLUCC 21-0064	NA	OM258687	OM250079	NA	NA	NA
<i>Pleopunctum guizhouense</i>	GZCC 23-0595	NA	OR091332	OR098710	NA	NA	NA
<i>Pleopunctum heveae</i>	MFLUCC 21-0146	NA	OL782070	OL780491	NA	NA	NA
<i>Pleopunctum megalosporum</i>	KUNCC 10785 ^T	NA	OQ146985	ON261162	OQ943186	NA	NA
<i>Pleopunctum megalosporum</i>	KUNCC 10442	NA	OQ146986	OQ135180	OQ943187	NA	NA
<i>Pleopunctum megalosporum</i>	KUNCC 21-0622	PP779899	PP779903	PP779894	PP778368	PP778373	NA
<i>Pleopunctum menglaense</i>	KUMCC 21-0026 ^T	ON009087	ON009103	ON009119	ON009262	ON009287	NA
<i>Pleopunctum menglaense</i>	KUMCC 21-0025	ON009086	ON009102	ON009118	ON009261	ON009286	NA
<i>Pleopunctum multicellularum</i>	KUNCC 10789 ^T	NA	OQ146989	ON261166	OQ943190	NA	NA
<i>Pleopunctum multicellularum</i>	KUNCC 10781	NA	OQ146981	ON261158	OQ943189	NA	NA
<i>Pleopunctum multicellularum</i>	KUNCC 10778	NA	OQ146978	ON261155	NA	NA	NA
<i>Pleopunctum pseudoellipsoideum</i>	MFLUCC 19-0391 ^T	NA	MK804518	MK804513	MK828511	NA	NA
<i>Pleopunctum pseudoellipsoideum</i>	HKAS122915	ON009085	ON009101	ON009117	ON009260	ON009285	NA
<i>Pleopunctum rotundatum</i>	KUNCC 10787 ^T	NA	OQ146987	ON261164	OQ943194	NA	NA
<i>Pleopunctum rotundatum</i>	KUNCC 10780	NA	OQ146980	ON261157	OQ943193	NA	NA
<i>Pleopunctum thailandicum</i>	MFLUCC 21-0039 ^T	NA	MZ198896	MZ198894	MZ172461	NA	NA
<i>Pleopunctum pseudoellipsoideum</i>	KUMCC 21-0820	ON009084	ON009100	ON009116	ON009259	ON009284	NA
<i>Pseudocapulatispora clematidis-subumbellatae</i>	MFLUCC 17-2063	MT226677	MT310607	MT214560	MT394739	MT394687	NA
<i>Pseudocapulatispora longiappendiculatum</i>	MFLUCC 17-1452 ^T	MT214415	MT214368	MT214462	MT235783	NA	NA
<i>Pseudocapulatispora longiappendiculatum</i>	MFLUCC 17-1457	MT214416	MT214369	MT214463	MT235784	MT235821	NA
<i>Pseudolophiostoma chiangraiense</i>	MFLUCC 17-2076 ^T	MT226678	MT310608	MT214561	MT394740	MT394688	NA
<i>Pseudolophiostoma clematidis</i>	MFLUCC 17-2081	MT226679	MN393004	MT214562	MT394741	MT394689	NA
<i>Pseudolophiostoma cornisporum</i>	KH 322 ^T	LC312486	LC312515	LC312544	LC312573	LC312602	NA
<i>Pseudolophiostoma lincangense</i>	KUNCC 21-0606^T	PP779900	PP779904	PP779895	PP778369	PP778374	NA
<i>Pseudolophiostoma mangiferae</i>	MFLUCC 17-2651 ^T	MG931028	MG931031	MG931025	NA	NA	NA

Taxon name	Strain number	GenBank accession numbers					
		SSU	ITS	LSU	<i>tef1-α</i>	<i>rpb2</i>	<i>tub2</i>
<i>Pseudolophiostoma mangiferae</i>	MFLUCC 17-2653	MG931029	MG931032	MG931026	NA	NA	NA
<i>Pseudolophiostoma obtusisporum</i>	KT 3098	LC312490	LC312519	LC312548	LC312577	LC312606	NA
<i>Pseudolophiostoma obtusisporum</i>	KT 2838 ^T	LC312489	LC312518	LC312547	LC312576	LC312605	NA
<i>Pseudolophiostoma tropicum</i>	KH 352	LC312492	LC312521	LC312550	LC312579	LC312608	NA
<i>Pseudolophiostoma tropicum</i>	KT 3134 ^T	LC312493	LC312522	LC312551	LC312580	LC312609	NA
<i>Pseudolophiostoma vitigenum</i>	HH 26930 ^T	AB618697	LC001735	AB619015	LC001761	NA	NA
<i>Pseudolophiostoma vitigenum</i>	HH 26931	AB618698	LC001736	AB619016	LC001762	NA	NA
<i>Pseudopaucispora brunneospora</i>	KH 227 ^T	LC312494	LC312523	LC312552	LC312581	LC312610	NA
<i>Pseudoplatystomum scabridisporum</i>	BCC 22835	NA	NA	GQ925844	GU479857	GU479830	NA
<i>Pseudoplatystomum scabridisporum</i>	BCC 22836	NA	NA	GQ925845	GU479856	GU479829	NA
<i>Quintaria lignatilis</i>	CBS 117700	GU296188	NA	GU301865	NA	GU371761	NA
<i>Quintaria lignatilis</i>	BCC 17444	GU479764	NA	GU479797	GU479859	GU479832	NA
<i>Seriascoma bambusae</i>	KUMCC 21-0021	MZ329031	MZ329039	MZ329035	MZ325470	MZ325468	NA
<i>Seriascoma didymosporum</i>	MFLUCC 11-0179	KU872119	KU940127	KU863116	KU940173	KU940196	NA
<i>Seriascoma yunnanense</i>	MFLU 19-0690	MN174694	NA	MN174695	MN210324	MN381858	NA
<i>Setophoma terrestris</i>	CBS 335.29	NA	KF251246	NA	NA	KF253196	KF252729
<i>Sigarispora coronillae</i>	MFLUCC 14-0941 ^T	KT026116	KT026120	KT026112	NA	NA	NA
<i>Sigarispora junci</i>	MFLUCC 14-0938 ^T	MG829178	MG828966	MG829078	NA	NA	NA
<i>Sigarispora ravennicum</i>	MFLUCC 14-0005 ^T	KP698415	KP698413	KP698414	NA	NA	NA
<i>Sigarispora scrophulariicola</i>	MFLUCC 17-0689 ^T	NA	MG828969	MG829081	NA	NA	NA
<i>Teichospora rubriostiolata</i>	TR7	NA	KU601590	KU601590	KU601609	KU601599	NA
<i>Teichospora traticola</i>	C134	NA	KU601591	KU601591	KU601601	KU601600	NA
<i>Thyridaria macrostomoides</i>	GKM 224N	NA	GU385191	NA	GU327777	NA	NA
<i>Thyridaria macrostomoides</i>	GKM 1033	NA	GU385190	NA	GU327776	NA	NA
<i>Thyridaria macrostomoides</i>	GKM 1159	NA	GU385185	NA	GU327778	NA	NA
<i>Vaginatisspora appendiculata</i>	MFLUCC 13-0835 ^T	KY264749	NA	KY264745	NA	NA	NA
<i>Vaginatisspora aquatica</i>	MFLUCC 11-0083 ^T	KJ591575	KJ591577	KJ591576	NA	NA	NA
<i>Vaginatisspora scabrisspora</i>	KT 2443 ^T	LC312496	LC312525	LC312554	LC312583	LC312612	NA
<i>Versicolorisporium triseptatum</i>	JCM 14775	AB524501	AB365596	AB3330081	NA	NA	NA
<i>Versicolorisporium triseptatum</i>	UESTCC 21.0016	OL741381	OL741378	OL741318	NA	NA	NA

The newly generated sequences are indicated in bold. T refers to ex-type strains, and NA refers to "no data in GenBank".

The newly generated sequences were assembled by BioEdit 7.2.3 (Hall 1999). The individual gene regions were separately aligned in the MAFFT v.7 web server (<http://mafft.cbrc.jp/alignment/server/>) (Katoh et al. 2019). The alignments of each gene were improved by manually deleting the ambiguous regions plus gaps and combined using BioEdit 7.2.3. The final alignments were converted to NEXUS format (.nxs) using Clustal X version 1.81 (Thompson et al. 1997) and processed for Bayesian and maximum parsimony analysis. The FASTA format was changed into PHY format via the Alignment Transformation Environment (ALTER) online program (<http://www.sing-group.org/ALTER/>) and used for maximum likelihood (ML) analysis.

The maximum likelihood (ML) analysis was performed on the CIPRES Science Gateway v.3.3 (<http://www.phylo.org/portal2/>; Miller et al. 2010) using RAXML-HPC2 on XSEDE v.8.2.12 (Stamatakis 2014) with parameters adjusted for 1000 bootstrap iterations and the GTRGAMMA substitution model. Bayesian inference was performed in MrBayes v.3.2.7a (Ronquist et al. 2012) using Markov

chain Monte-Carlo sampling (BMCMC) to determine posterior probabilities (PPs) (Rannala and Yang 1996). The model of evolution for each gene was estimated using MrModeltest v.2.3 (Nylander et al. 2008) via PAUP v.4.0b10 (Ronquist and Huelsenbeck 2003). Six simultaneous Markov chains were run for 2,000,000 generations, with trees sampled at 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 and Adobe Illustrator® CS6 v.26.0 (Adobe Systems, San Jose, CA, USA). The newly produced sequences were deposited in the GenBank nucleotide database (Table 1).

Results

Phylogenetic analysis

Analyses 1, Lophiostomataceae phylogeny, was based on combined SSU, LSU, ITS, *tef1- α* , and *rpb2*. The final alignment contained 4,230 characters used for the phylogenetic analyses, including alignment gaps. The alignment contained 74 strains, and the tree was rooted with *Teichospora rubriostiolata* (TR7) and *T. trubicola* (C134). The RAxML analysis of the combined dataset yielded a best-scoring tree with a final ML optimization likelihood value of -29697.884081. The matrix had 1,584 distinct alignment patterns with 26.07% undetermined characters or gaps. The estimated base frequencies were as follows; A = 0.249681, C = 0.245034, G = 0.268293, T = 0.236992; substitution rates AC = 1.509197, AG = 3.725453, AT = 1.272039, CG = 1.297966, CT = 7.905766, GT = 1.0; gamma distribution shape parameter α = 0.192719 and tree-length = 0.192719. The tree topologies of combined sequence data obtained from ML and BI analyses were not significantly different. Our isolate, *Pseudolophiostoma lincangense* (KUNCC 21-0606), was closer and sister to *P. vitigenum* strains (HH 26930, HH 26931) but formed a separate lineage with 100% ML bootstrap and 1.00 BYPP support (Fig. 1).

Analyses 2, Occultibambusaceae phylogeny, was based on combined SSU, LSU, ITS, *tef1- α* , and *rpb2*. The final alignment contained 4,103 characters used for the phylogenetic analyses, including alignment gaps. The alignment contained 25 strains, and the tree was rooted with *Ernakulamia krabiensis* (MFLUCC 18-0237) and *E. xishuangbannaensis* (KUMCC 17-0187). The RAxML analysis of the combined dataset yielded a best-scoring tree with a final ML optimization likelihood value of -16329.806421. The matrix had 1,047 distinct alignment patterns with 24.1% undetermined characters or gaps. The estimated base frequencies were as follows; A = 0.243761, C = 0.253253, G = 0.274093, T = 0.228893; substitution rates AC = 2.182200, AG = 2.182200, AT = 1.737406, CG = 1.445194, CT = 9.965966, GT = 1.0; gamma distribution shape parameter α = 0.155054 and tree-length = 0.951813. The tree topologies of combined sequence data obtained from ML and BI analyses were not significantly different. Our new isolate (KUNCC 21-0506) was nested with *Occultibambusa kunmingensis* (HKAS 102151, type) and with 100% ML bootstrap and 1.00 BYPP support (Fig. 2).

Analyses 3, Phaeoseptaceae phylogeny, was based on combined SSU, LSU, ITS, *tef1- α* , and *rpb2*. The final alignment contained 3,195 characters used for the phylogenetic analyses, including alignment gaps. The alignment contained

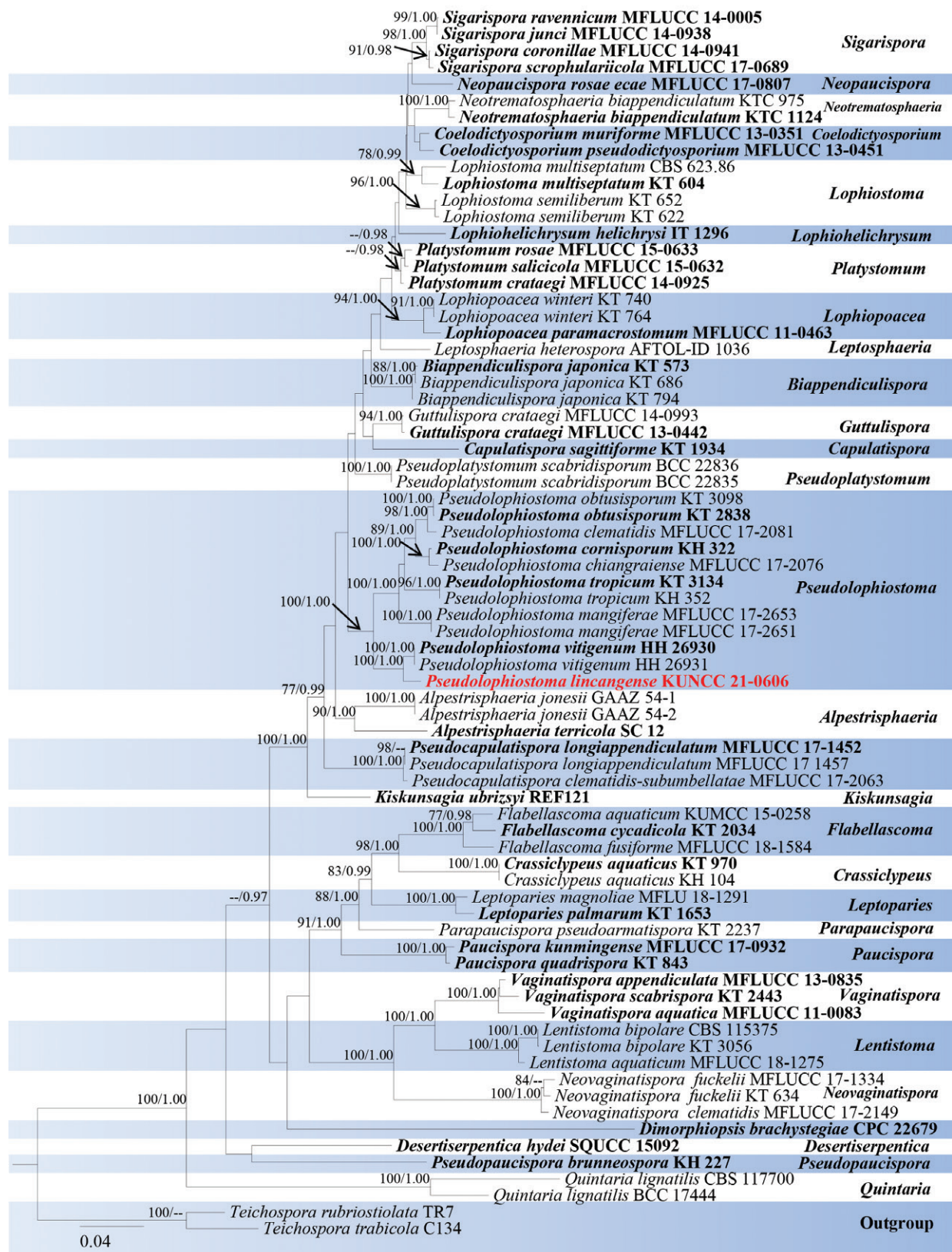


Figure 1. Phylogram generated from ML analysis based on SSU, LSU, ITS, *tef1*- α , and *rpb2* sequence data representing the family Lophiostomataceae. Related sequences were obtained from Phukhamsakda et al. (2020). Bootstrap values for ML are equal to or greater than 75%, and posterior probability values are equal to or greater than 0.95 from the BYPP analysis labelled on the nodes. Strains of the newly described species are in red, while type strains are in bold. The tree is rooted with *Teichospora rubriostiolata* (TR7) and *T. trabicola* (C134).

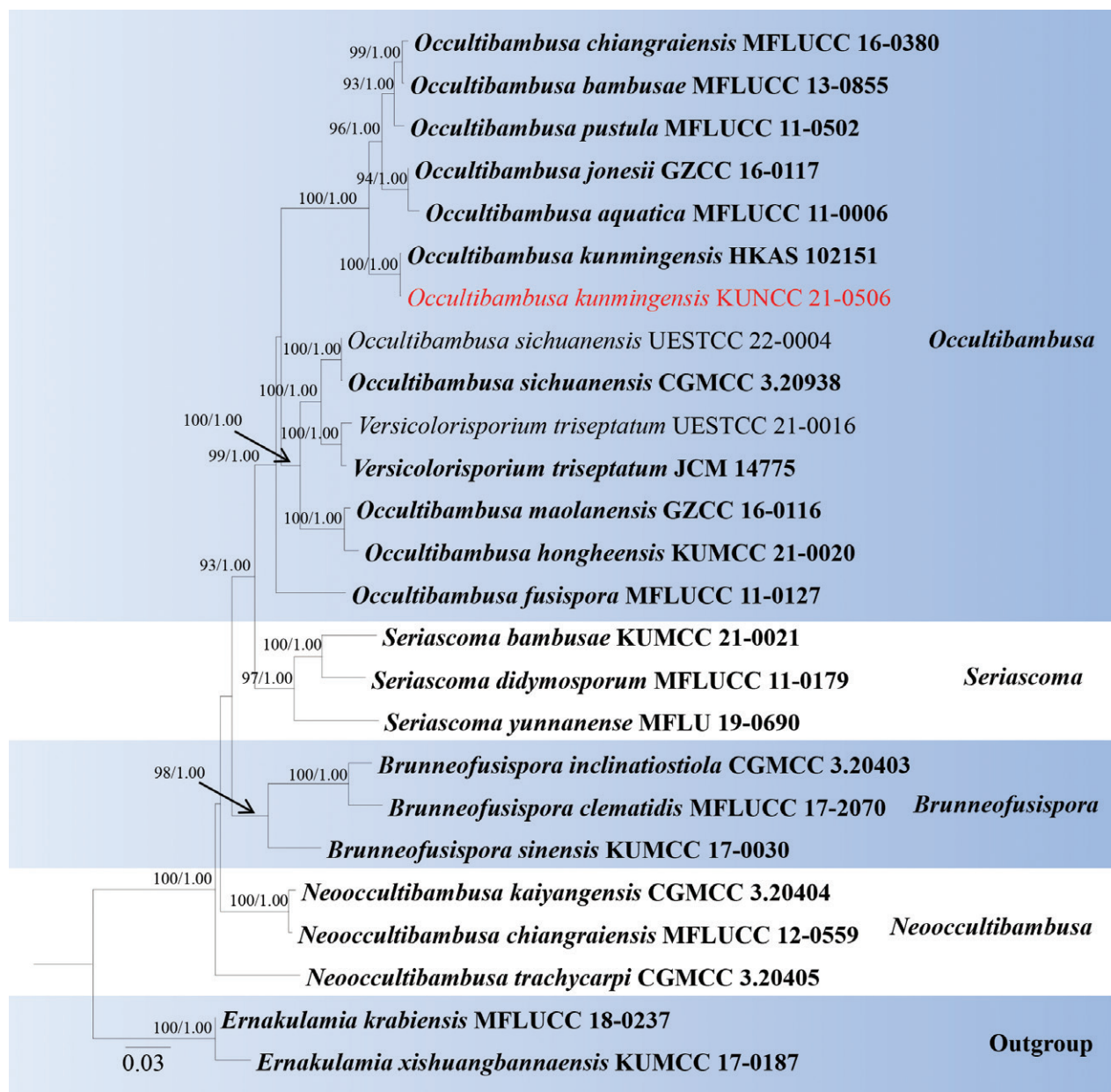


Figure 2. Phylogram generated from maximum likelihood analysis based on the combined SSU, LSU, ITS, *tef1- α* , and *rpb2* dataset of Occultibambusaceae species. Related sequences were obtained from Yu et al. (2022). Bootstrap values for ML are equal to or greater than 75%, and posterior probability values are equal to or greater than 0.95 from the BYPP analysis labelled on the nodes. Strains of the newly described species are in red, while type strains are in bold. The tree is rooted with *Ernakulamia krabiensis* (MFLUCC 18-0237) and *E. xishuangbannaensis* (KUMCC 17-0187).

37 strains, and the tree was rooted with *Angustimassarina acerina* (MFLUCC 14-0505) and *A. populi* (MFLUCC 13-0034). The RaxML analysis of the combined dataset yielded a best-scoring tree with a final ML optimization likelihood value of -12325.441217. The matrix had 882 distinct alignment patterns with 30.9% undetermined characters or gaps. The estimated base frequencies were as follows: A = 0.249369, C = 0.247445, G = 0.266516, T = 0.236670; substitution rates AC = 1.406931, AG = 4.076513, AT = 1.212607, CG = 1.303216, CT = 8.242374, GT = 1.000000; gamma distribution shape parameter α = 0.201687 and tree-length = 3.128705. The tree topologies of combined sequence data

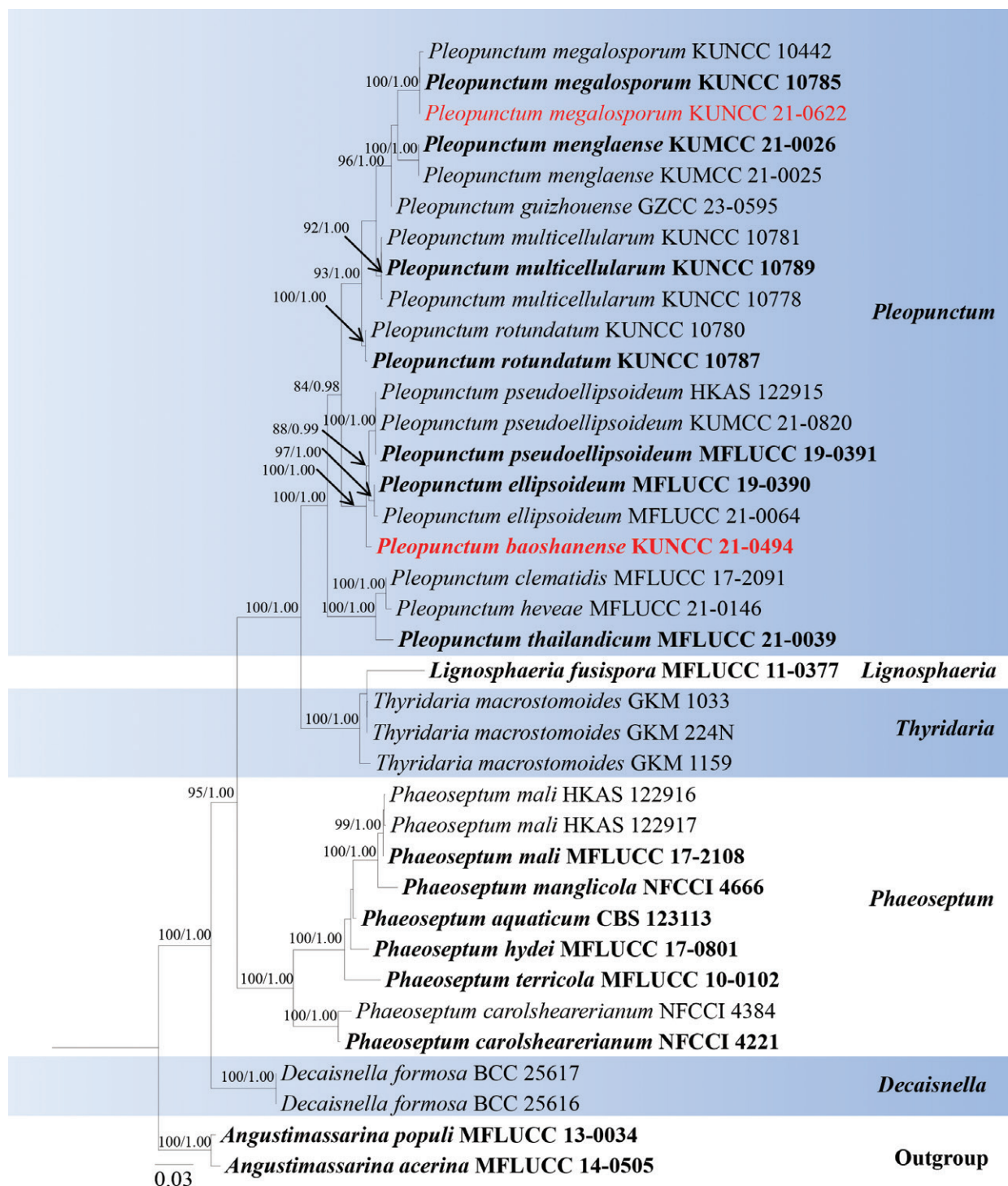


Figure 3. Phylogram generated from maximum likelihood analysis based on the combined SSU, LSU, ITS, *tef1*- α , and *rpb2* dataset of Phaeoseptaceae species. Related sequences were obtained from Xu et al. (2023). Bootstrap values for ML are equal to or greater than 75%, and posterior probability values are equal to or greater than 0.95 from the BYPP analysis labelled on the nodes. Strains of the newly described species are in red, while type strains are in bold. The tree is rooted with *Angustimassarina acerina* (MFLUCC 14-0505) and *A. populi* (MFLUCC 13-0034).

obtained from ML and BI analyses were not significantly different. Our isolate, *Pleopunctum baoshanense* (KUNCC 21-0494), constituted a strongly supported (100% ML and 1.00 BYPP) independent lineage basal to *P. pseudoellipsoideum*

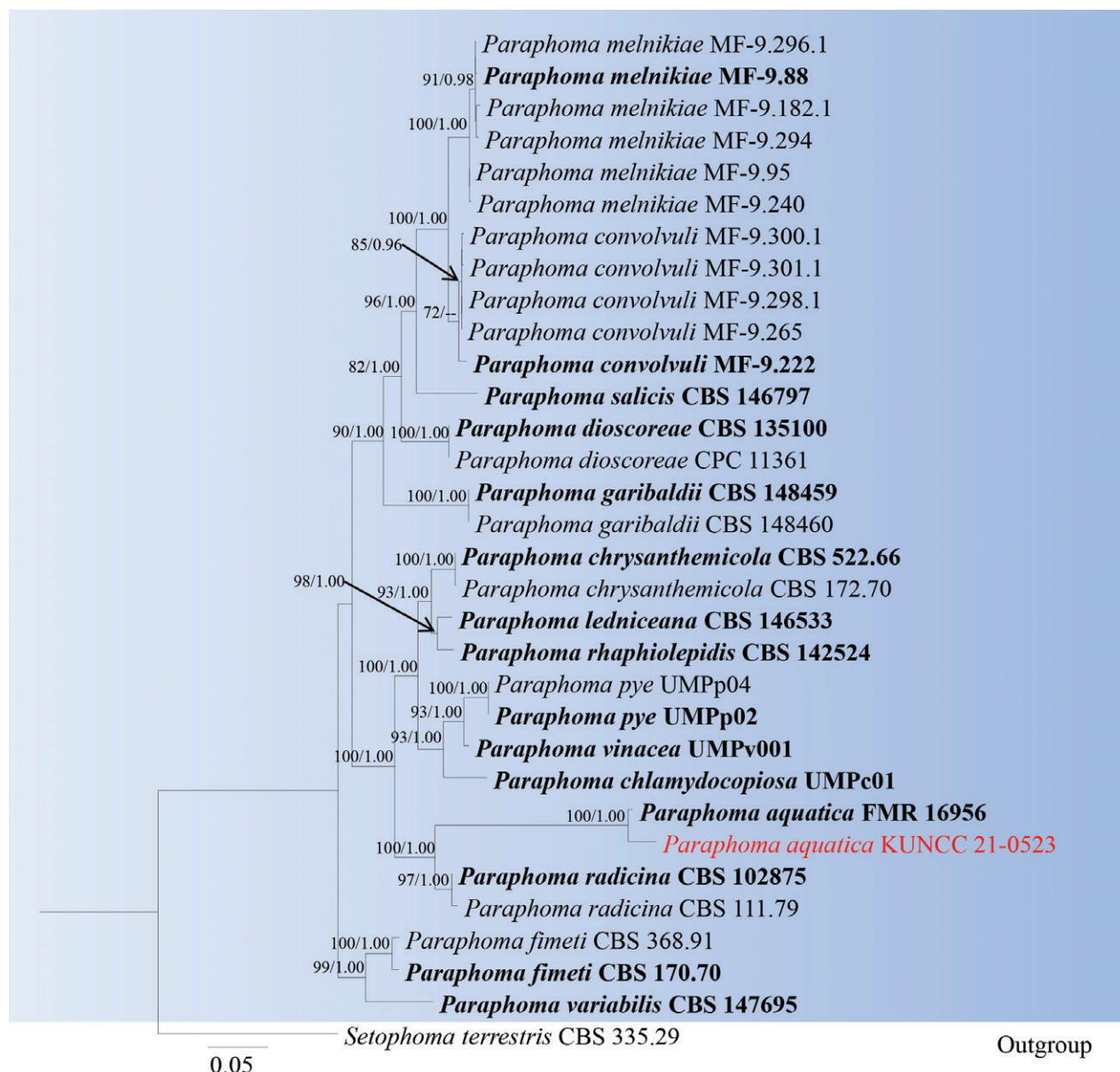


Figure 4. Phylogram generated from maximum likelihood analysis based on the combined LSU, ITS, *tef1- α* , *rpb2* and *tub2* dataset of *Paraphoma* species. Related sequences were obtained from previous publications (Magaña-Dueñas et al. 2021, Guarnaccia et al. 2022, and Gomzhina et al. 2020). Bootstrap values for ML are equal to or greater than 75%, and posterior probability values are equal to or greater than 0.95 from the BYPP analysis labelled on the nodes. Strains of the newly described species are in red, while type strains are in bold. The tree is rooted with *Setophoma terrestris* (CBS 335.29).

(MFLUCC 19-0391, KUMCC 21-0820, HKAS122915) and *P. ellipsoideum* (97% ML and 1.00 BYPP). While our other isolate (KUNCC 21-0622) was grouped together with *P. menglaense* strains (KUNCC 1442, KUNCC 10785) with 100% ML bootstrap and 1.00 BYPP support (Fig. 3).

Analyses 4, *Paraphoma* phylogeny, was based on combined LSU, ITS, *tef1- α* , *rpb2*, and *tub2*. The final alignment contained 3,351 characters used for the phylogenetic analyses, including alignment gaps. The alignment contained 32 strains, and the tree was rooted with *Setophoma terrestris* (CBS 335.29). The RAxML analysis of the combined dataset yielded a best-scoring tree with a final ML optimization likelihood value of -13609.051798. The matrix had 929

distinct alignment patterns with 37.21% undetermined characters or gaps. The estimated base frequencies were as follows; A = 0.238385, C = 0.250275, G = 0.266033, T = 0.245306; substitution rates AC = 1.198498, AG = 2.769971, AT = 1.326456, CG = 0.861230, CT = 5.288549, GT = 1.0; gamma distribution shape parameter α = 0.274993 and tree-length = 1.180712. The tree topologies of combined sequence data obtained from ML and BI analyses were not significantly different. Our isolate, *Paraphoma baoshanenses* (KUNCC 21-0523), forms a distinct branch close to *P. aquatica* (FMR 16956) and with 100% ML bootstrap and 1.00 BYPP support (Fig. 4).

Taxonomy

The present study introduces two new species and three new records. These taxa belong to the order Pleosporales and are described below.

***Pseudolophiostoma lincangense* G.C. Ren & Tibpromma, sp. nov.**

Index Fungorum: IF902122

Facesoffungi Number: FoF15842

Fig. 5

Etymology. The epithet refers to the location where the fungus was collected.

Holotype. HKAS 122880.

Description. **Saprobic** on dead twigs of *Castanopsis calathiformis* (Fagaceae) in terrestrial habitat. **Sexual morph: Ascomata** 280–330 μm high, 230–290 μm diam. (\bar{x} = 310 \times 260 μm , n = 5), solitary or gregarious, immersed, papilla erumpent through host surface, subglobose, single or two locular, coriaceous, brown to dark brown, ostiolate. **Ostioles** 110–160 μm long, 80–90 μm diam., carbonaceous, mostly central, with crest-like opening, filled with hyaline periphyses. **Peridium** 10–20 μm wide, comprising 4–9 layers, composed of dark brown outer layers, inner layers comprising hyaline, flattened, angular, thick-walled cells of **textura angularis**. **Hamathecium** composed of numerous, 1–2 μm wide, filamentous, septate, branched, cellular pseudoparaphyses. **Asci** 80–100 \times 15–20 μm (\bar{x} = 94 \times 16 μm , n = 20), 8-spored, bitunicate, fission-tunicate, cylindrical, with pedicel, apically rounded, with a minute ocular chamber. **Ascospores** 32–40 \times 5–5.8 μm (\bar{x} = 35 \times 5.3 μm , n = 30), 1–2-seriate, fusiform, hyaline, straight or slightly curved, 1-septate, becoming 3-septate when germinated, constricted at the septa, narrower towards both end cells, upper cell longer than lower cell, guttulate, smooth-walled, with mucilaginous sheath. **Asexual morph:** Undetermined.

Culture characteristics. Ascospores germinated on PDA within 24 h at room temperature (25 °C). Germ tubes produced from the apical or the second cell of ascospore. **Colonies** on PDA, reaching 25 mm diameter after two weeks at 20–25 °C, mycelia superficial, circular, flat, fimbriate, undulate edge, gray with white gray at the center; reverse, dark green, pale yellow at the center.

Material examined. CHINA, Yunnan Province, Lincang (24°5'30"N, 100°5'33"E, elevation: 1557.49 m) on dead woody twigs of *Castanopsis calathiformis* (Fagaceae), 12 July 2020, G.C. Ren, LC25 (HKAS 122880, holotype), ex-type living culture KUNCC 21-0606.

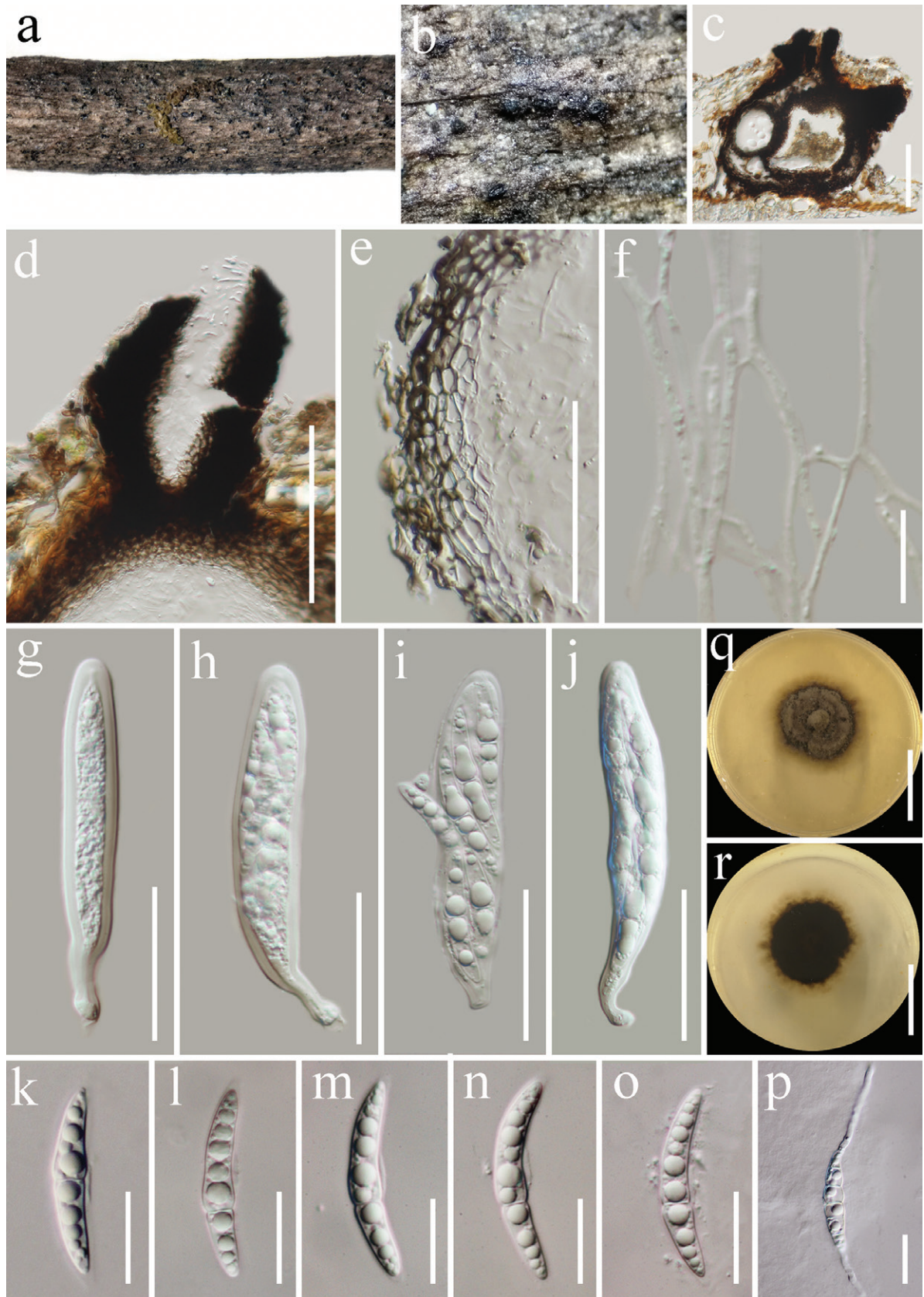


Figure 5. *Pseudolophiostoma lincangense* (HKAS 122880, holotype) **a, b** appearance of ascomata on the host surface **c** section of ascoma **d** ostiole **e** peridium **f** pseudoparaphyses **g–j** asci **k–o** ascospores **p** germinated ascospore **q, r** culture characters on PDA (**q** = from above, **r** = from below). Scale bars: 100 μm (**c, d**); 50 μm (**e**); 10 μm (**f**); 30 μm (**g–j**); 15 μm (**k–p**); 30 mm (**q, r**).

Notes. Multi-loci phylogenetic analyses based on a concatenated SSU, LSU, ITS, *tef1*- α , and *rpb2* sequence dataset show that our new collection (KUNCC 21-0606) clusters sister to strains of *Pseudolophiostoma vitigenum* (HH 26930 and HH 26931) with 100% ML and 1.00 BYPP support (Fig. 1). Sequence comparison for the ITS region between *Pseudolophiostoma lincangense* (KUNCC 21-0606) and *P. vitigenum* (HH 26930, type) showed a 2.67% (14/524 bp) base pair difference, 0.24% (2/848 bp) base pair difference for LSU region, 1.97% (17/863 bp) base pair difference for *tef1*- α region, but we were unable to compare *rpb2* gene of *P. vitigenum* as there was no sequence data. Comparatively, the morphological characterization of *Pseudolophiostoma lincangense* is similar to *P. vitigenum* in having immersed ascomata with papilla; carbonaceous ostiole with crest-like opening, and filled with hyaline periphyses; cylindrical asci with a short truncate pedicel and a minute ocular chamber; fusiform, hyaline, constricted at the septa, 1-septate ascospores (Thambugala et al. 2015). However, our new collection differs from *P. vitigenum* in having single or two locular ascomata, peridium consists of two layer cells of *textura angularis*, smaller asci ($94 \times 16 \mu\text{m}$ vs. $129.8 \times 20.1 \mu\text{m}$) and ascospores ($35 \times 5.3 \mu\text{m}$ vs. $38.5 \times 10.5 \mu\text{m}$), and of the upper cell of the ascospores is longer than the lower cell (Thambugala et al. 2015). Therefore, we identify our collection as a new species from Yunnan Province, China.

***Occultibambusa kunmingensis* C.X. Liu, H. Zhang & K.D. Hyde, Fungal Diversity 105: 471.**

Index Fungorum: IF557930

Facesoffungi Number: FoF09272

Fig. 6

Description. *Saprobic* on dead twigs of *Castanopsis delavayi* (Fagaceae) in terrestrial habitat. **Sexual morph:** **Ascomata** 160–180 μm high, 160–240 μm diam. ($\bar{x} = 175 \times 195 \mu\text{m}$, $n = 5$), dark brown to black, solitary or gregarious, semi-immersed to superficial, coriaceous, subglobose, with a short papillate, ostiolate. **Ostioles** 50–65 μm long, 35–40 μm diam., black, short. **Peridium** 20–35 μm thick, thin at the base and becoming wider laterally, composed of several layers of brown to dark brown, thick-walled cells of *textura angularis*. **Hamathecium** 2.5–3.5 μm wide, hyphae-like, septate, cellular pseudoparaphyses, embedded in a gelatinous matrix. **Asci** (60)74–107(–116) \times 12–14 μm ($\bar{x} = 82 \times 13 \mu\text{m}$, $n = 20$), 8-spored, bitunicate, fissitunicate, clavate or cylindrical-clavate, narrowly rounded at the apex, with a short truncate pedicel, apically rounded, with a minute ocular chamber. **Ascospores** 30–40 \times 4–6 μm ($\bar{x} = 35.6 \times 5.3 \mu\text{m}$, $n = 20$), overlapping 1–2-seriate, fusiform, straight or slightly curved, 1-septate, brown, constricted at the septa, guttulate, thin and smooth-walled, without mucilaginous sheaths and appendages. **Asexual morph:** Undetermined.

Culture characteristics. Ascospores germinated on PDA within 24 h at room temperature (25 °C). Germ tubes produced from the basal and apical cells of ascospore. **Colonies** on PDA, reaching 25 mm diameter after 2 weeks at 20–25 °C, mycelia superficial, dense, circular, raised, entire edge, velvety, flossy; reverse black.

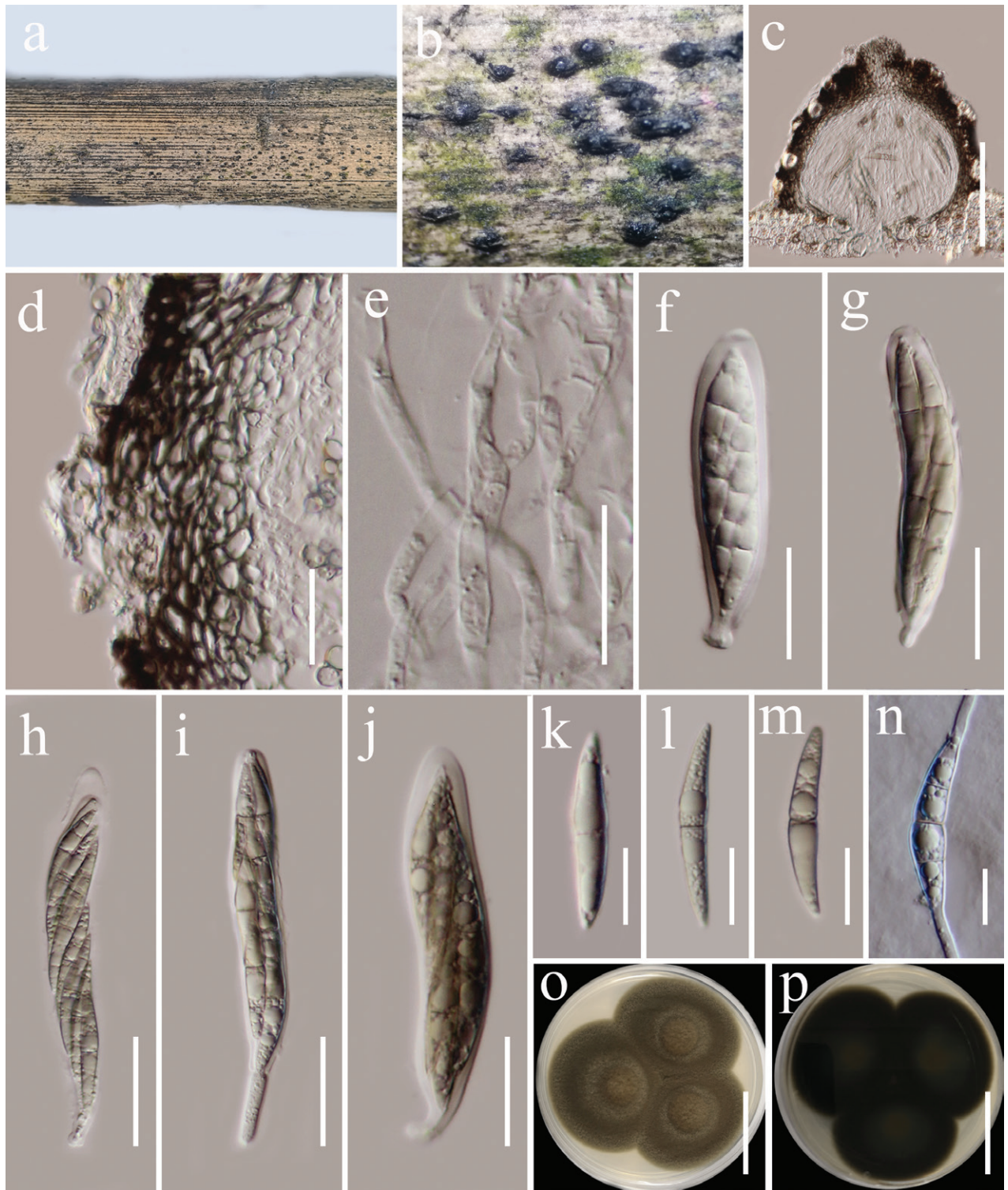


Figure 6. *Occultibambusa kunmingensis* (HKAS 122706) **a** host **b** ascomata on host surface **c** vertical section of ascoma **d** peridium **e** pseudoparaphyses **f–j** asci **k–m** ascospores **n** germinated ascospore **o, p** colonies on PDA (**o** = from above, **p** = from below). Scale bars: 100 μ m (**c**); 20 μ m (**d–j**); 10 μ m (**k–n**); 20 mm (**o, p**).

Material examined. CHINA, Yunnan Province, Baoshan (25°18'48"N, 99°09'50"E) on dead woody twigs of *Castanopsis delavayi* (Fagaceae), 12 July 2020, G.C. Ren, BS17 (HKAS 122706), living culture KUNCC 21-0506.

Known host, habitats, and distribution. Bamboo and *Castanopsis delavayi* from freshwater and terrestrial in China (Dong et al. 2020; Jiang et al. 2021; this study).

Notes. According to the multi-gene phylogenetic analyses of combined SSU, LSU, ITS, *tef1- α* , and *rpb2* sequence dataset, our new isolate (KUNCC 21-0506) nested with *Occultibambusa kunmingensis* (HKAS 102151), which was isolated from decaying bamboo submerged in freshwater in China (Dong et al. 2020) with 100% ML and 1.00 BYPP bootstrap support (Fig. 2). Our new isolate fits well with the morphological characteristics of the holotype of *O. kunmingensis* in having semi-immersed to superficial ascomata with short papillate, clavate or cylindrical-clavate asci, fusiform, 1-septate, brown ascospores without mucilaginous sheaths and appendages (Dong et al. 2020). Sequence comparison for the ITS and *tef1- α* region between our isolates (KUNCC 21-0506) and *O. kunmingensis* (HKAS 102151) showed no significant base pair differences. Therefore, we identified our taxon as a new host record of *O. kunmingensis* from *Castanopsis delavayi* (Fagaceae) in China, and it is the first record from woody litter.

***Pleopunctum baoshanense* G.C. Ren & Tibpromma, sp. nov.**

Index Fungorum: IF902123

Facesofungi Number: FoF15843

Fig. 7

Etymology. The specific epithet “*baoshanense*” reflects the location “Baoshan” where the holotype was collected.

Holotype. HKAS 134936.

Description. **Saprobic** on decaying wood of *Castanopsis calathiformis* (Fagaceae) in terrestrial habitat. **Sexual morph:** Undetermined. **Asexual morph:** Hyphomycetous. **Colonies** on natural substrate sporodochial, superficial, black, scattered, gregarious. **Mycelium** immersed in the substratum, composed of septate hyphae. **Conidiophores** 3–5 μm wide (\bar{x} = 3.8 μm , n = 15), macronematous, mononematous, cylindrical, unbranched, septate, hyaline and smooth-walled. **Conidiogenous cells** monoblastic, terminal, integrated, hyaline. **Conidia** 33–46 \times 22.5–27.6 μm (\bar{x} = 39 \times 25 μm , n = 40), acrogenous, solitary, muriform, oval to ellipsoidal, smooth-walled, broadly obtuse at apex and dark brown, truncate at base and paler brown, often with a hyaline, elliptical to globose basal cell, 10–14 \times 13–15 μm (\bar{x} = 12 \times 13 μm , n = 30).

Culture characteristics. Conidia germinated on PDA within 24 h at room temperature (25 °C). Germ tubes produced from the basal cells of conidia. **Colonies** on PDA, reaching 30 mm diameter after 2 weeks at 20–25 °C, mycelia superficial, irregular, umbonate at the center, fimbriate, undulate entire, grey, radially furrowed, with hyaline, glistening, rough, wrinkled, granular droplets of oil; reverse, grey, radially furrowed, grey white at the margin.

Material examined. CHINA, Yunnan Province, Baoshan (25°18'48"N, 99°09'50"E), on dead woody twigs of *Castanopsis calathiformis* (Fagaceae), 12 July 2020, G.C. Ren, B194 (HKAS 134936, holotype), ex-type living culture KUNCC 21-0494.

Notes. Multi-loci phylogenetic analyses based on a concatenated SSU, LSU, ITS, *tef1- α* , and *rpb2* sequence dataset show that our new collection (KUNCC

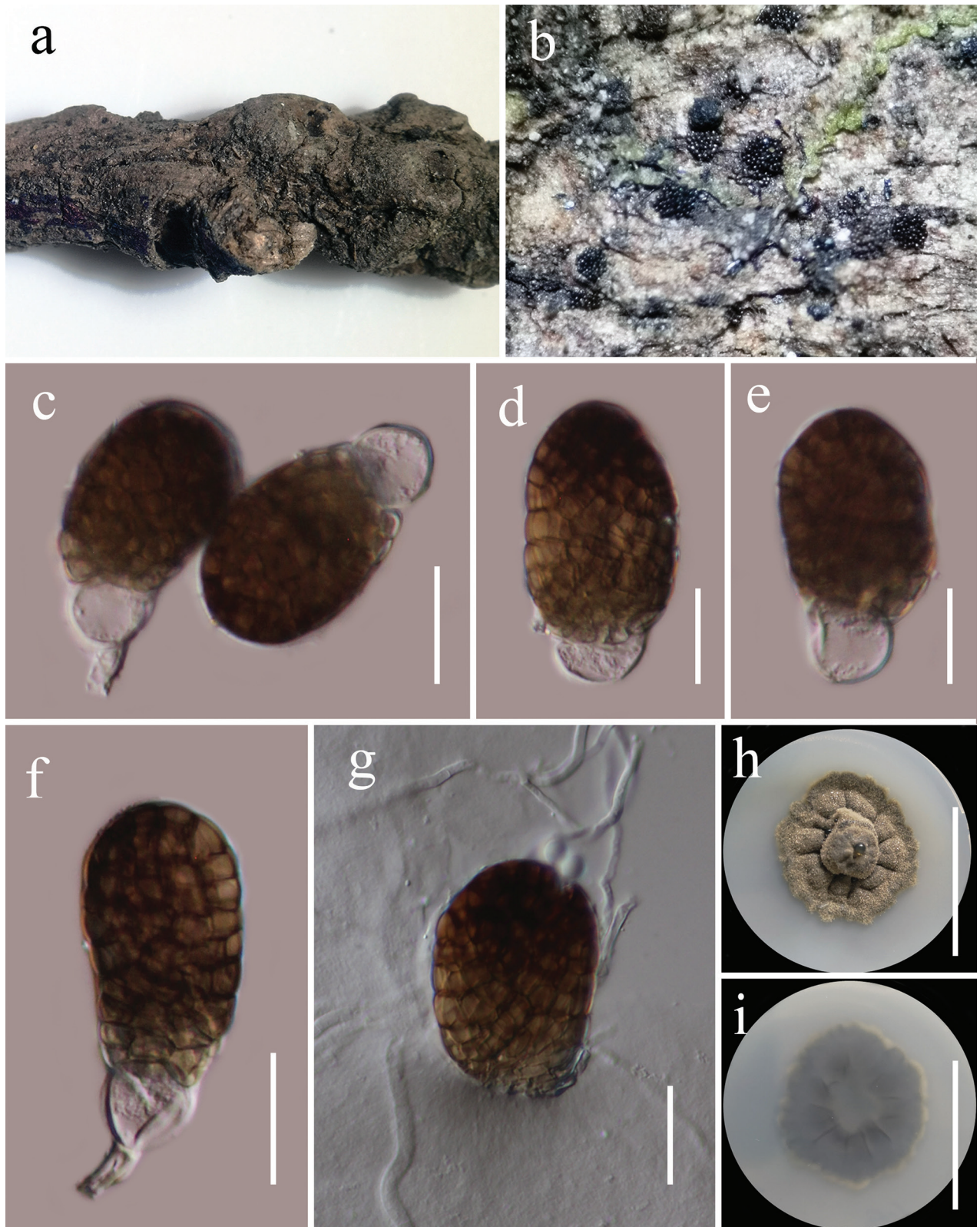


Figure 7. *Pleopunctum baoshanense* (HKAS 134936, holotype) **a** host **b** colonies on the host surface **c–f** conidia with basal hyaline cells **g** germinated conidium **h, i** colony on PDA (**h** = from above, **i** = from below). Scale bars: 20 μ m (**c–g**); 20 mm (**h, i**).

21-0494) clusters sister to strains of *Pleopunctum pseudoellipsoideum* (MFLUCC 19-0391, KUMCC 21-0820, HKAS 122915) and *P. ellipsoideum* (MFLUCC 19-0390, MFLUCC 21-0064) with solid support (100% ML and 1.00 BYPP, Fig. 3).

Sequence comparison for the ITS region between *Pleopunctum baoshanense* (KUMCC 21-0494) and *P. pseudoellipsoideum* (MFLUCC 19-0391) showed a 1.54% (8/520 bp, without the gaps) base pair difference, 2.26% (21/930 bp, without the gaps) base pair difference for the *tef1- α* region. Sequence comparison for the ITS region between *Pleopunctum baoshanense* (KUNCC 21-0494) and *P. ellipsoideum* (MFLUCC 19-0390) showed a 1.65% (8/486 bp, without the gaps) base pair difference, 1.81% (15/827 bp, without the gaps) base pair difference for *tef1- α* region. *Pleopunctum baoshanense*, *P. pseudoellipticum*, and *P. ellipsoideum* are morphologically similar, they have sporodochial conidiomata; septate hyphae mycelium; mononematous, cylindrical conidiophores; monoblastic, terminal, hyaline conidiogenous cells and muriform, oval to ellipsoidal conidia often with a hyaline, elliptical to globose basal cell, but can be distinguished from *P. pseudoellipsoideum* and *P. ellipsoideum* in having hyaline conidiophores and conidiogenous cells, different sizes of conidia (39 × 25 μm vs. 50 × 24 μm vs. 45 × 20 μm), while both of them have medium brown conidiophores and conidiogenous cells (Liu et al. 2019; Xu et al. 2023). Therefore, based on morphology and phylogenetic distinctiveness, we introduce *Pleopunctum baoshanense* as a new species.

***Pleopunctum megalosporum* R.J. Xu, Q. Zhao & Boonmee Journal of Fungi 9 (5, no. 560): 9 (2023)**

Index Fungorum: IF847826

Facesofungi Number: FoF14063

Fig. 8

Description. *Saprobic* on dead twigs of *Castanopsis calathiformis* (Fagaceae) in terrestrial habitat. **Sexual morph:** Undetermined. **Asexual morph:** Hyphomycetous. **Colonies** on host, sporodochial, superficial, light brown, scattered, and punctiform. **Mycelium** immersed in the substratum, composed of septate, branched, sub hyaline to light brown hyphae. **Conidiophores** 13–66 × 2.6–4.2 μm (\bar{x} = 37.7 × 3.5, n = 20), macronematous, mononematous, hyaline to light brown, cylindrical, unbranched, septate, smooth-walled. **Conidiogenous cells** 3.9–5.5 × 3.6–4.7 μm (\bar{x} = 4.6 × 4 μm , n = 20), monoblastic, terminal, light brown. The conidia are dimorphic, acrogenous, and solitary. **α conidia** 30–40 × 10–15 μm (\bar{x} = 33 × 12.5 μm , n = 30), hyaline to light brown, muriform, oblong to obovate, constricted at septa, slightly obtuse to rounded at apex. **β conidia** 48–60 × 24–31 μm (\bar{x} = 54.7 × 27.3 μm , n = 30), brown, muriform, oval to long elliptical, slightly constricted at septa, often with a hyaline, elliptical to globose, 0–multiple-basal cells, 12.5–17.6 × 7.7–11 μm (\bar{x} = 14.7 × 9.2 μm , n = 20).

Culture characteristics. Conidia germinated on PDA within 24 h at room temperature (25 °C). Germ tubes produced from the basal cells of conidia. **Colonies** on PDA, reaching 30 mm diameter after 2 weeks at 20–25 °C, mycelia superficial, irregular, slightly umbonate at the center, fimbriate, undulate edge, grey at the margin, grey white at the center, with hyaline, glistening, granular droplets of oil; reverse, atrovirens, notably radially furrowed, golden brown at the margin.

Material examined. CHINA, Yunnan Province, Lincang (24°5'30"N, 100°5'33"E, elevation: 1557.49 m), on dead woody twigs of *Castanopsis calathiformis* (Fagaceae), 12 July 2020, G.C. Ren, LC62 (HKAS 134935), living culture KUNCC 21-0622.

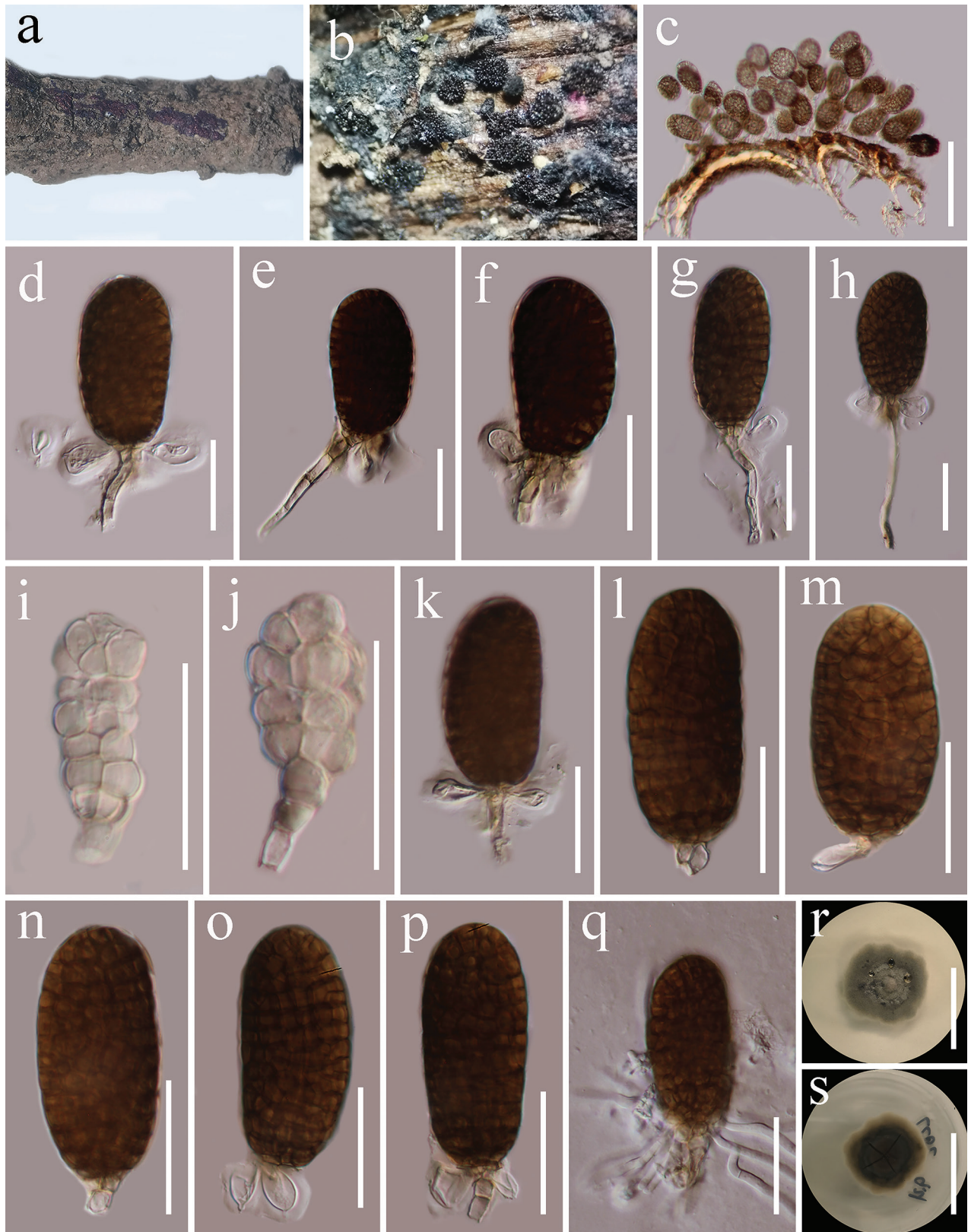


Figure 8. *Pleopunctum megalosporum* (HKAS 134935) **a** host **b** colonies on the host surface **c** conidia on substrate **d–h**, **k–p** conidia with basal cells and conidiophores **i, j** conidia showing remnant of conidiogenous cells at base **q** germinated conidium **r, s** colony on PDA (**r** = from above, **s** = from below). Scale bars: 100 μ m (**c**); 30 μ m (**d–q**); 20 mm (**s, r**).

Known host, habitats, and distribution. *Cryptocarya acutifolia*, freshwater and terrestrial, China (Xu et al. 2023; this study).

Notes. *Pleopunctum megalosporum* was introduced by Xu et al. (2023) from submerged decaying wood in a freshwater stream in China. Our collection (KUMCC 21-0622) resembles *P. megalosporum* (KUMCC22-10799) in having sporodochial conidiomata; septate, subhyaline to light brown mycelium; mononematous, cylindrical, light brown conidiophores; monoblastic, terminal, light brown conidiogenous cells and muriform, oval to long elliptical conidia often with a hyaline, elliptical to globose, 0–multiple-basal cell (Xu et al. 2023). Multi-loci phylogenetic analyses based on a concatenated SSU, LSU, ITS, *tef1-α*, and *rpb2* sequence dataset show that our new collection (KUNCC 21-0622) clusters with *Pleopunctum megalosporum* (KUNCC 10785, KUNCC 10442) with strong support (100% ML and 1.00 BYPP, Fig. 3). Sequence comparison for the ITS and *tef1-α* region between our isolate (KUNCC 21-0622) and *Pleopunctum megalosporum* (KUNCC 10785) showed no significant base pair differences. Therefore, we introduce our collection as the first record of *P. megalosporum* from *Castanopsis calathiformis* (Fagaceae) in China.

***Paraphoma aquatica* Magaña-Dueñas, Stchigel & Cano-Lira Journal of Fungi 7(12, no. 1102): 9 (2021)**

Index Fungorum number: IF841364

FacesofFungi number: FoF15844

Fig. 9

Description. *Saprobic* on dead woody twigs of *Castanopsis delavayi* (Fagaceae). **Sexual morph: Ascumata** 110–130 × 120–130 μm (\bar{x} = 122 × 126 μm, n = 5), solitary, scattered, erumpent to immersed, uni-loculate, globose to subglobose, black. **Ostioles** central. **Peridium** 7–12 μm wide, thin, comprising 3–4 layers of light brown to brown cells of *textura prismatica*. **Hamathecium** 1.5–2.5 μm wide, cylindrical, filiform, hyaline, septate, branched, cellular pseudoparaphyses, embedded in a gelatinous matrix. **Asci** 45–63 × 9–11 μm (\bar{x} = 55 × 9.5 μm, n = 20), 8-spored, bitunicate, fissitunicate, clavate, slightly broad at center, apically rounded, with short and rounded pedicel, minute ocular chamber. **Ascospores** 19–22 × 4–4.6 μm (\bar{x} = 20.7 × 4.2 μm, n = 30), overlapping, biseriate, hyaline, narrowly fusiform, straight or slightly curved, with 3 transverse septa, enlarged at the second cell, constricted at the septa, smooth-walled, guttulate, without a mucilaginous sheath. **Asexual morph:** see Magaña-Dueñas et al. (2021).

Culture characteristics. Ascospores germinated on PDA within 24 h at room temperature (25 °C). Germ tubes produced from the basal and apical cells of ascospore. **Colonies** on PDA, reaching 25 mm diameter after 2 weeks at 20–25 °C, mycelia superficial, medium density mycelia, entire margin, umbonate at center, band, rough surface, velvety, raised, grayish yellow, white mycelium attached to the central surface; reverse atrovirens.

Material examined. CHINA, Yunnan Province, Baoshan (25°18'48"N, 99°09'50"E), on dead woody twigs of *Castanopsis delavayi* (Fagaceae), 12 July 2020, G.C. Ren, BS42 (HKAS 122713), living culture KUNCC 21-0523.

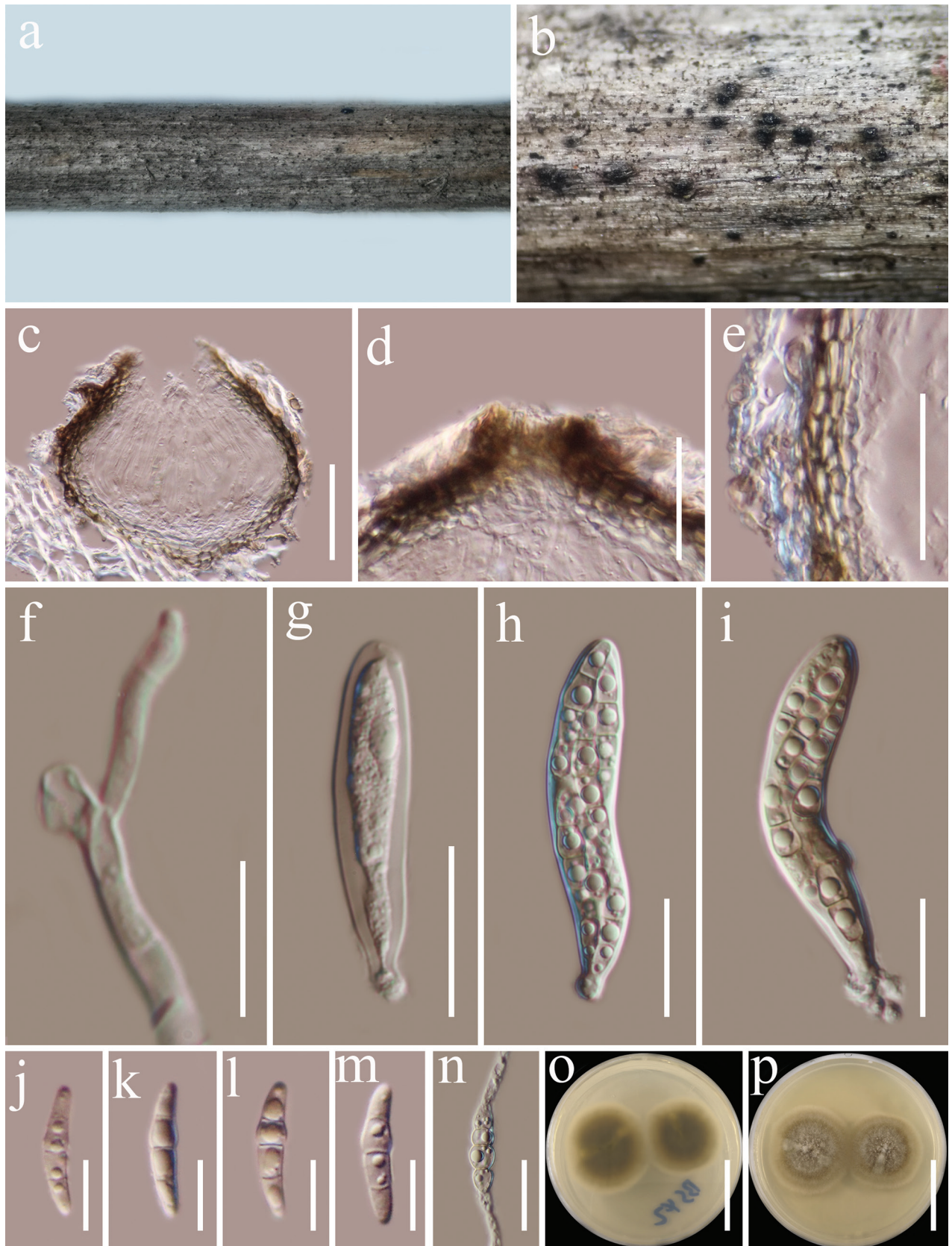


Figure 9. *Paraphoma aquatica* (HKAS 122713) **a** host **b** ascomata on the host surface **c** vertical section of ascoma **d** ostiole **e** peridium **f** pseudoparaphyses **g**–**i** asci **j**–**m** ascospores **n** germinated ascospore **o**, **p** culture characters on PDA (**o** = from above, **p** = from below). Scale bars: 50 μ m (**c**); 30 μ m (**d**, **e**); 10 μ m (**f**, **j**–**n**); 20 μ m (**g**–**i**); 20 mm (**o**, **p**).

Known host, habitats, and distribution. Capafonts and *Castanopsis delavayi*, freshwater submerged plant debris and terrestrial, China and Spain (Magaña-Dueñas et al. 2021; this study).

Notes. Multi-loci phylogenetic analyses based on a concatenated LSU, ITS, *tef1- α* , *rpb2*, and *tub2* sequence dataset show that our new collection (KUNCC 21-0523) formed a sister lineage to the ex-type strain of *Paraphoma aquatica* (FMR 16956) with solid support (100% ML and 1.00 BYPP, Fig. 4). Sequence comparison for the ITS region between *Paraphoma baoshanenses* (KUNCC 21-0523) and *P. aquatica* (FMR 16956) showed a 6.17% (30/486 bp) base pair difference, 0.12% (2/848 bp) base pair difference for LSU region, 2.06% (9/437 bp) base pair difference for the *tef1- α* region. Unfortunately, the morphology could not be compared as *Paraphoma aquatica* was reported in its asexual morph with no information on its sexual morph (Magaña-Dueñas et al. 2021). The species of *Paraphoma* were introduced from its asexual morph (Morgan-Jones and White 1983; de Gruyter et al. 2010; Quaedvlieg et al. 2013; Moslemi et al. 2016, 2018; Crous et al. 2017, 2021a, 2021b; Gomzhina et al. 2020; Magaña-Dueñas et al. 2021; Guarnaccia et al. 2022), while we introduced our new collection from its sexual morph. Therefore, we could not compare our new collection with other *Paraphoma* species. However, based on the phylogenetic distinctiveness, we introduce our collection as the first record of *P. aquatica* from *Castanopsis delavayi* (Fagaceae) in China, and our species is the first sexual morph recorded in this genus.

Discussion

This study introduces two new species of woody litter fungi: *Pseudolophiostoma lincangense*, and *Pleopunctum baoshanense* from Yunnan Province, China. We also report new host records of *Occultibambusa kunmingensis* on *Castanopsis delavayi*, *Pleopunctum megalosporum* on *Castanopsis calathiformis* for the first time in China, and *Paraphoma aquatica* is the first sexual morph of *Paraphoma* on *Castanopsis delavayi*.

Pseudolophiostoma was introduced by Thambugala et al. (2015), with *P. vitigenum* designated as the type species. Currently, this genus comprises seven accepted species (Species Fungorum 2024). *Pseudolophiostoma* species are typically saprobes found on various herbaceous, woody, or vine plants such as *Bidens pilosa* var. *radiata*, *Clematis fulvicoma*, *Livistona boninensis*, *Stachytarpheta jamaicensis*, and *Vitis coignetiae*, and are distributed across China (Taiwan), Japan, and Thailand (Thambugala et al. 2015; Hashimoto et al. 2018; Tennakoon et al. 2018; Phukhamsakda et al. 2020). *Pseudolophiostoma* species are known only by their sexual morph, and their asexual morph has not been discovered yet (Thambugala et al. 2015). Therefore, the asexual morph of *Pseudolophiostoma* remains uncertain and thus, further studies with additional collections are needed to understand the asexual morph.

Occultibambusa, introduced by Dai et al. (2017) with *O. bambusae* as the type species, is commonly found on bamboo culms. These species have a wide distribution, particularly in China and Thailand, where they inhabit both freshwater and terrestrial habitats (Hyde et al. 2016; Dai et al. 2017; Zhang et al. 2017; Dong et al. 2020; Jiang et al. 2021; Yu et al. 2022). Currently, Species

Fungorum (2024) recognizes 10 *Occultibambusa* species. Most of these species have been reported based on their sexual morphs, with only *O. fusispora* known from its holomorph, and the coelomycetous asexual morph discovered in culture (Dai et al. 2017; Jiang et al. 2021). In this study, our collection also reports sexual morph and thus, further studies are needed to understand the asexual morph with additional fresh collections.

Pleopunctum was introduced as the first hyphomycetous genus in Phaeocephalaceae by Liu et al. (2019) to include two species: *P. ellipsoideum* and *P. pseudoellipticum*. Subsequently, nine *Pleopunctum* species viz. *P. bauhiniae*, *P. clematidis*, *P. guizhouense*, *P. heveae*, *P. megalosporum*, *P. menglaense*, *P. multicellularum*, *P. rotundatum* and *P. thailandicum* were accepted (Phukhamsakda et al. 2020; Boonmee et al. 2021; Koukol and Delgado 2021; Senwanna et al. 2021; Wanasinghe et al. 2021; Xu et al. 2023; Zhang et al. 2023). Currently, eleven *Pleopunctum* species are accepted in Species Fungorum (2024) and all have been reported in their asexual morph (Liu et al. 2019). *Pleopunctum* species distributed in China and Thailand and saprobic on dead wood of *Bauhinia variegata* (Fabaceae), *Clematis sikkimensis* (Ranunculaceae), *Hevea brasiliensis* (Euphorbiaceae) and some unknown woody litter in freshwater and terrestrial habitats (Hyde et al. 2019; Phukhamsakda et al. 2020; Senwanna et al. 2021; Xu et al. 2023). *Pleopunctum bauhiniae*, *P. clematidis*, *P. heveae*, *P. megalosporum*, and *P. menglaense* have dimorphic conidia on the natural substrate (Hyde et al. 2019; Phukhamsakda et al. 2020; Senwanna et al. 2021; Wanasinghe et al. 2021; Xu et al. 2023). However, *P. ellipsoideum*, *P. guizhouense*, *P. multicellularum*, *P. pseudoellipticum*, *P. rotundatum* and *P. thailandicum* are characterized by one conidium type and share very similar morphological characteristics (Liu et al. 2019; Boonmee et al. 2021; Koukol and Delgado 2021; Xu et al. 2023). The phenotypic variation among strains, influenced by environmental factors, can make morphological differentiation challenging (Hyde et al. 2020). However, our research has shown that molecular sequence data are a reliable tool for identifying *Pleopunctum* species. This confidence-inspiring finding, supported by previous publications and our study (Boonmee et al. 2021; Koukol and Delgado 2021; Xu et al. 2023).

Paraphoma was established in 1983 with *P. radicina* as the type species (Morgan-Jones and White 1983). Subsequently, fourteen species are accepted in *Paraphoma*. Currently, fifteen *Paraphoma* species are accepted in Species Fungorum (2024). *Paraphoma* species are widely distributed worldwide, for instance in Australia, China, Czech Republic, Italy, the Netherlands, New Zealand, Russia, South Korea, Spain, Switzerland, Ukraine, the United Kingdom and the United States. These species include endophytes, pathogens, and saprobes on the plant of *Atractylodes lancea*, *Buxus sempervirens*, *Chrysanthemum morifolium*, *Campanula rapunculoides*, Convolvulaceae sp., *Dioscorea tokoro*, *Juniperus communis*, *Paraphoma vinacea*, *Rhaphiolepis indica*, *Strawberry*, *Salix* cf. *alba*, *Tanacetum cinerariifolium*, soil and dung (de Gruyter et al. 2010; Bensch et al. 2012; Quaedvlieg et al. 2013; Crous et al. 2017, 2021b; Moslemi et al. 2018; Gomzhina et al. 2020; Guarnaccia et al. 2022). Currently, only asexual morph has been reported from *Paraphoma* species (Quaedvlieg et al. 2013; Gomzhina et al. 2020). However, we have discovered the sexual morph of *Paraphoma aquatica*, which is saprobic on dead wood of *Castanopsis calathiformis* (Fagaceae), and this is the first sexual morph recorded in *Paraphoma*.

Additional information

Conflict of interest

The authors have declared that no competing interests exist.

Ethical statement

No ethical statement was reported.

Funding

Saowaluck Tibpromma and Samantha C. Karunarathna thank the Yunnan Revitalization Talents Support Plan (High-End Foreign Experts Program) and the Key Laboratory of Yunnan Provincial Department of Education of the Deep-Time Evolution on Biodiversity from the Origin of the Pearl River for their support. The authors extend their appreciation to the Deputyship for Research and Innovation, "Ministry of Education" in Saudi Arabia for funding this research (IFKSUOR3-299-17).

Author contributions

Conceptualization: GCR, Data curation: GCR, Investigation: GCR, ST, SCK, Project administration: GCR, ST, SCK, Software: GCR, Supervision: ST, SCK, Writing – review and editing: GCR, ST, KXD, CXG, CSZ, SCK, AME, HG.

Author ORCIDs

Guang-Cong Ren  <https://orcid.org/0000-0001-9923-2626>

Saowaluck Tibpromma  <https://orcid.org/0000-0002-4706-6547>

Samantha C. Karunarathna  <https://orcid.org/0000-0001-7080-0781>

Abdallah M. Elgorban  <https://orcid.org/0000-0003-3664-7853>

Data availability

All of the data that support the findings of this study are available in the main text.

References

- Asian Development Bank (2012) Greater Mekong Subregion Atlas of the Environment (2nd edn). Asian Development Bank. <http://hdl.handle.net/11540/92>
- Barr ME (1987) Prodrum to class Loculoascomycetes. Amherst. University of Massachusetts, Massachusetts.
- Bensch K, Braun U, Groenewald JZ, Crous PW (2012) The genus *Cladosporium*. Studies in Mycology 72: 1–401. <https://doi.org/10.3114/sim0003>
- Boonmee S, Wanasinghe DN, Calabon MS, Huanraluek N, Chandrasiri SKU, Jones GEB, Rossi W, Leonardi M, Singh SK, Rana S, Singh PN, Maurya DK, Lagashetti AC, Choudhary D, Dai Y-C, Zhao C-L, Mu Y-H, Yuan H-S, He S-H, Phookamsak R, Jiang H-B, Martín MP, Dueñas M, Telleria MT, Kafucka IL, Jagodziński AM, Liimatainen K, Pereira DS, Phillips AJL, Suwannarach N, Kumla J, Khuna S, Lumyong S, Potter TB, Shivas RG, Sparks AH, Vaghefi N, Abdel-Wahab MA, Abdel-Aziz FA, Li G-J, Lin W-F, Singh U, Bhatt RP, Lee HB, Nguyen TTT, Kirk PM, Dutta AK, Acharya K, Sarma VV, Niranjana M, Rajeshkumar KC, Ashtekar N, Lad S, Wijayawardene NN, Bhat DJ, Xu R-J, Wijesinghe SN, Shen H-W, Luo Z-L, Zhang J-Y, Sysouphanthong P, Thongklang N, Bao D-F, Aluthmuhandiram JVS, Abdollahzadeh J, Javadi A, Dovana F, Usman M, Khalid AN, Dissanayake AJ, Telagathoti A, Probst M, Peintner U, Garrido-Benavent I, Bóna L, Merényi Z, Boros L, Zoltán B, Stielow JB, Jiang N,

- Tian C-M, Shams E, Dehghanizadeh F, Pordel A, Javan-Nikkhah M, Denchev TT, Denchev CM, Kemler M, Begerow D, Deng C-Y, Harrower E, Bozorov T, Kholmuradova T, Gafforov Y, Abdurazakov A, Xu J-C, Mortimer PE, Ren G-C, Jeewon R, Maharachchikumbura SSN, Phukhamsakda C, Mapook A, Hyde KD (2021) Fungal diversity notes 1387–1511: Taxonomic and phylogenetic contributions on genera and species of fungal taxa. *Fungal Diversity* 111(1): 1–335. <https://doi.org/10.1007/s13225-021-00489-3>
- Brahmanage RS, Dayarathne MC, Wanasinghe DN, Thambugala KM, Jeewon R, Chethana KWT, Samarakoon MC, Tennakoon DS, De Silva NI, Camporesi E, Raza M, Yan JY, Hyde KD (2020) Taxonomic novelties of saprobic *Pleosporales* from selected dicotyledons and grasses. *Mycosphere: Journal of Fungal Biology* 11(1): 2481–2541. <https://doi.org/10.5943/mycosphere/11/1/15>
- Cai L, Tsui CKM, Zhang KQ, Hyde KD (2002) Aquatic fungi from Lake Fuxian, Yunnan, China. *Fungal Diversity* 9: 57–70. <https://fungaldiversity.org/fdp/sfdp/9-4.pdf>
- Crawford RH, Carpenter SE, Mayfield J, Martin RE (1987) Fungi from foliage of *Arctostaphylospatula*, *Castanopsis chrysophylla*, and *Ceanothus velutinus*. US Department of Agriculture, Forest Service, Pacific Northwest Research Station. <https://doi.org/10.5962/bhl.title.70795>
- Crous PW, Wingfield MJ, Burgess TI, Hardy GESTJ, Barber PA, Alvarado P, Barnes CW, Buchanan PK, Heykoop M, Moreno G, Thangavel R et al. (2017) Fungal Planet description sheets: 558–624. *Persoonia* 38: 240–384. <https://doi.org/10.3767/003158517X698941>
- Crous PW, Osieck ER, Jurjević Ž, Boers J, van Iperen AL, Starink-Willemse M, Dima B, Balashov S, Bulgakov TS, Johnston PR, Morozova OV, Pinruan U, Sommai S, Alvarado P, Decock CA, Lebel T, McMullan-Fisher S, Moreno G, Shivas RG, Zhao L, Abdollahzadeh J, Abrinbana M, Ageev DV, Akhmetova G, Alexandrova AV, Altés A, Amaral AGG, Angelini C, Antonín V, Arenas F, Asselman P, Badali F, Baghela A, Bañares A, Barreto RW, Baseia IG, Bellanger JM, Berraf-Tebbal A, Biketova AYU, Bukharova NV, Burgess TI, Cabero J, Câmara MPS, Cano-Lira JF, Ceryngier P, Chávez R, Cowan DA, de Lima AF, Oliveira RL, Denman S, Dang QN, Dovana F, Duarte IG, Eichmeier A, Erhard A, Esteve-Raventós F, Fellin A, Ferisin G, Ferreira RJ, Ferrer A, Finy P, Gaya E, Geering ADW, Gil-Durán C, Glässnerová K, Glushakova AM, Gramaje D, Guard FE, Guarnizo AL, Haelewaters D, Halling RE, Hill R, Hirooka Y, Hubka V, Iliushin VA, Ivanova DD, Ivanushkina NE, Jangsantear P, Justo A, Kachalkin AV, Kato S, Khamsuntorn P, Kirtsideli IY, Knapp DG, Kochkina GA, Koukol O, Kovács GM, Kruse J, Kumar TKA, Kušan I, Læssøe T, Larsson E, Lebeuf R, Levicán G, Loizides M, Marinho P, Luangsa-ard JJ, Lukina EG, Magaña-Dueñas V, Maggs-Kölling G, Malysheva EF, Malysheva VF, Martín B, Martín MP, Matočec N, McTaggart AR, Mehrabi-Koushki M, Mešić A, Miller AN, Mironova P, Moreau P-A, Morte A, Müller K, Nagy LG, Nanu S, et al. (2021a) Fungal Planet description sheets: 1284–1382. *Persoonia* 47: 178–374. <https://doi.org/10.3767/persoonia.2021.47.06>
- Crous PW, Hernández-Restrepo M, Schumacher RK, Cowan DA, Maggs-Kölling G, Marais E, Wingfield MJ, Yilmaz N, Adan OCG, Akulov A, Duarte E, Berraf-Tebbal A, Bulgakov TS, Carnegie AJ, de Beer ZW, Decock C, Dijksterhuis J, Duong TA, Eichmeier A, Hien LT, Houbraken JAMP, Khanh TN, Liem NV, Lombard L, Lutzoni FM, Miadlikowska JM, Nel WJ, Pascoe IG, Roets F, Roux J, Samson RA, Shen M, Spetik M, Thangavel R, Thanh HM, Thao LD, van Nieuwenhuijzen EJ, Zhang JQ, Zhang Y, Zhao LL, Groenewald JZ (2021b) New and Interesting Fungi. 4. *Fungal Systematics and Evolution* 7(1): 255–343. <https://doi.org/10.3114/fuse.2021.07.13>
- Dai DQ, Phookamsak R, Wijayawardene NN, Li WJ, Bhat DJ, Xu JC, Taylor JE, Hyde KD, Chukeatirote E (2017) Bambusicolous fungi. *Fungal Diversity* 82: 1–105. <https://doi.org/10.1007/s13225-016-0367-8>

- de Gruyter J, Woudenberg JHC, Aveskamp MM, Verkley GJM, Groenewald JZ, Crous PW (2010) Systematic reappraisal of species in *Phoma* section *Paraphoma*, *Pyrenochaeta* and *Pleurophoma*. *Mycologia* 102(5): 1066–1081. <https://doi.org/10.3852/09-240>
- Dong W, Wang B, Hyde KD, McKenzie EHC, Raja HA, Tanaka K, Abdel-Wahab MA, Abdel-Aziz FA, Doilom M, Phookamsak R, Hongsanan S, Wanasinghe DN, Yu XD, Wang GN, Yang H, Yang J, Thambugala KM, Tian Q, Luo ZL, Yang JB, Miller AN, Fournier J, Boonmee S, Hu DM, Nalumpang S, Zhang H, Fournier J, Boonmee S, Hu DM, Nalumpang S, Zhang H (2020) Freshwater Dothideomycetes. *Fungal Diversity* 105(1): 319–575. <https://doi.org/10.1007/s13225-020-00463-5>
- Duong LM, McKenzie EHC, Lumyong S, Hyde KD (2008) Fungal succession on senescent leaves of *Castanopsis diversifolia* in Doi Suthep-Pui National Park, Thailand. *Fungal Diversity* 30: 23–36.
- Feng B, Yang Z (2018) Studies on diversity of higher fungi in Yunnan, southwestern China: A review. *Plant Diversity* 40(4): 165–171. <https://doi.org/10.1016/j.pld.2018.07.001>
- Gao Y, Liu F, Cai L (2016) Unravelling *Diaporthe* species associated with *Camellia*. *Systematics and Biodiversity* 14(1): 102–117. <https://doi.org/10.1080/14772000.2015.1101027>
- Gomzhina MM, Gasich EL, Khlopunova LB, Gannibal PB (2020) *Paraphoma* species associated with Convolvulaceae. *Mycological Progress* 19(3): 185–194. <https://doi.org/10.1007/s11557-020-01558-8>
- Guarnaccia V, Martino I, Tabone G, Crous PW, Gullino ML (2022) *Paraphoma garibaldii* sp. nov. causing leaf spot disease of *Campanula rapunculoides* in Italy. *Fungal Systematics and Evolution* 9(1): 19–26. <https://doi.org/10.3114/fuse.2022.09.03>
- Hall TA (1999) BioEdit: A user-friendly biological sequence alignment editor and analysis program for Windows 95/98/NT. *Nucleic Acids Symposium Series* 41: 95–98.
- Hapuarachchi KK, Karunaratna SC, Phengsintham P, Yang HD, Kakumyan P, Hyde KD, Wen TC (2019) Ganodermataceae (Polyporales): Diversity in Greater Mekong Subregion countries (China, Laos, Myanmar, Thailand, and Vietnam). *Mycosphere* 10(1): 221–309. <https://doi.org/10.5943/mycosphere/10/1/6>
- Hashimoto A, Hirayama K, Takahashi H, Matsumura M, Okada G, Chen CY, Huang JW, Kakishima M, Ono T, Tanaka T (2018) Resolving the *Lophiostoma bipolare* complex: Generic delimitations within Lophiostomataceae. *Studies in Mycology* 90(1): 161–189. <https://doi.org/10.1016/j.simyco.2018.03.001>
- Hongsanan S, Hyde KD, Phookamsak R, Wanasinghe DN, McKenzie EHC, Sarma VV, Boonmee S, Lücking R, Bhat DJ, Liu NG (2020) Refined families of Dothideomycetes: Dothideomycetidae and Pleosporomycetidae. *Mycosphere* 11(1): 1553–2107. <https://doi.org/10.5943/mycosphere/11/1/13>
- Huang CC, Zhang YT, Bartholomew B (1999) Fagaceae. In: Wu ZY, Raven PH (Eds) *Flora of China*, vol. 4. Science Press, Beijing & Missouri Botanical Garden Press, St. Louis, 314–400.
- Hyde KD, Hongsanan S, Jeewon R, Bhat DJ, McKenzie EHC, Jones EBG, Phookamsak R, Ariyawansa HA, Boonmee S, Zhao Q, Abdel-Aziz FA, Abdel-Wahab MA, Banmai S, Chomnunti P, Cui BK, Daranagama DA, Das K, Dayarathne MC, de Silva NI, Dissanayake AJ, Doilom M, Ekanayaka AH, Gibertoni TB, Go'es-Neto A, Huang SK, Jayasiri SC, Jayawardena RS, Konta S, Lee HB, Li WJ, Lin CG, Liu JK, Lu YZ, Luo ZL, Manawasinghe IS, Manimohan P, Mapook A, Niskanen T, Norphanphoun C, Papizadeh M, Perera RH, Phukhamsakda C, Richter C, Santiago ALCMA, Drechsler-Santos ER, Senanayake IC, Tanaka K (2016) Fungal diversity notes 367–490: Taxonomic and phylogenetic contributions to fungal taxa. *Fungal Diversity* 80: 1–270. <https://doi.org/10.1007/s13225-016-0373-x>
- Hyde KD, Tennakoon DS, Jeewon R, Bhat DJ, Maharachchikumbura SSN, Rossi W, Leonardi M, Lee HB, Mun HY, Houbraken J, Nguyen TTT, Jeon SJ, Frisvad JC, Wanasinghe DN,

- Lücking R, Aptroot A, Cáceres MES, Karunarathna SC, Hongsanan S, Phookamsak R, de Silva NI, Thambugala KM, Jayawardena RS, Senanayake IC, Boonmee S, Chen J, Luo Z-L, Phukhamsakda C, Pereira OL, Abreu VP, Rosado AWC, Bart B, Randrianjohany E, Hofstetter V, Gibertoni TB, Soares AMS, Plautz Jr HL, Sotão HMP, Xavier WKS, Bezerra JDP, de Oliveira TGL, de Souza-Motta CM, Magalhães OMC, Bundhun D, Harishchandra D, Manawasinghe IS, Dong W, Zhang S-N, Bao D-F, Samarakoon MC, Pem D, Karunarathna A, Lin C-G, Yang J, Perera RH, Kumar V, Huang S-K, Dayarathne MC, Ekanayaka AH, Jayasiri SC, Xiao Y, Konta S, Niskanen T, Liimatainen K, Dai Y-C, Ji X-H, Tian X-M, Mešić A, Singh SK, Phutthacharoen K, Cai L, Sorvongxay T, Thiyagaraja V, Norphanphoun C, Chaiwan N, Lu Y-Z, Jiang H-B, Zhang J-F, Abeywickrama PD, Aluthmuhandiram JVS, Brahmanage RS, Zeng M, Chethana T, Wei D, Réblová M, Fournier J, Nekvindová J, do Nascimento Barbosa R, dos Santos JEF, de Oliveira NT, Li G-J, Ertz D, Shang Q-J, Phillips AJL, Kuo C-H, Camporesi E, Bulgakov TS, Lumyong S, Jones EBG, Chomnunti P, Gentekaki E, Bungartz F, Zeng X-Y, Fryar S, Tkalčec Z, Liang J, Li G, Wen T-C, Singh PN, Gafforov Y, Promputtha I, Yasanthika E, Goonasekara ID, Zhao R-L, Zhao Q, Kirk PM, Liu J-K, Yan JY, Mortimer PE, Xu J, Doilom M (2019) Fungal diversity notes 1036–1150: Taxonomic and phylogenetic contributions on genera and species of fungal taxa. *Fungal Diversity* 96(1): 1–242. <https://doi.org/10.1007/s13225-019-00429-2>
- Hyde KD, Jeewon R, Chen YJ, Bhunjun CS, Calabon MS, Jiang HB, Lin CG, Norphanphoun C, Sysouphanthong P, Pem D, Tibpromma S, Zhang Q, Doilom M, Jayawardena RS, Liu JK, Maharachchikumbura SSN, Phukhamsakda C, Phookamsak R, Al-Sadi AM, Naritsada Thongklang N, Wang Y, Gafforov Y, Jones EBG, Lumyong S (2020) The numbers of fungi: Is the descriptive curve flattening? *Fungal Diversity* 103(1): 219–271. <https://doi.org/10.1007/s13225-020-00458-2>
- Inácio CA, Cannon PF, Ferry BF (2005) Revision of the genus *Placostromella* and inclusion of *Palawaniella castanopsis* as a third species. *Mycological Progress* 4(2): 133–137. <https://doi.org/10.1007/s11557-006-0116-6>
- Index Fungorum (2024) Index Fungorum. <http://www.indexfungorum.org/names/Names.asp>
- Jayasiri SC, Hyde KD, Ariyawansa HA, Bhat J, Buyck B, Cai L, Dai YC, Abd-Elsalam KA, Ertz D, Hidayat I, Jeewon R, Jones EBG, Bahkali AH, Karunarathna SC, Liu J-K, Luangsa-ard JJ, Lumbsch HT, Maharachchikumbura SSN, McKenzie EHC, Moncalvo J-M, Ghobad-Nejhad M, Nilsson H, Pang K-L, Pereira OL, Phillips AJL, Raspé O, Rollins AW, Romero AI, Etayo J, Selçuk F, Stephenson SL, Suetrong S, Taylor JE, Tsui CKM, Vizzini A, Abdel-Wahab MA, Wen T-C, Boonmee S, Dai DQ, Daranagama DA, Dissanayake AJ, Ekanayaka AH, Fryar SC, Hongsanan S, Jayawardena RS, Li W-J, Perera RH, Phookamsak R, de Silva NI, Thambugala KM, Tian Q, Wijayawardene NN, Zhao R-L, Zhao Q, Kang J-C, Promputtha I (2015) The Faces of Fungi database: Fungal names linked with morphology, phylogeny and human impacts. *Fungal Diversity* 74(1): 3–18. <https://doi.org/10.1007/s13225-015-0351-8>
- Jayawardena RS, Hyde KD, Chen YJ, Papp V, Palla B, Papp D, Bhunjun CS, Hurdeal VG, Senwana C, Manawasinghe IS, Harischandra DL, Gautam AK, Avasthi S, Chuankid B, Goonasekara ID, Hongsanan S, Zeng XY, Liyanage KK, Liu NG, Karunarathna A, Hapuarachchi KK, Luangharn T, Raspé O, Brahmanage R, Doilom M, Lee HB, Mei L, Jeewon R, Huanraluek N, Chaiwan N, Stadler M, Wang Y (2020) One stop shop IV: taxonomic update with molecular phylogeny for important phytopathogenic genera: 76–100 (2020). *Fungal Diversity* 103: 87–218. <https://doi.org/10.1007/s13225-020-00460-8>
- Jiang HB, Phookamsak R, Hyde KD, Mortimer PE, Xu JC, Kakumyan P, Karunarathna SC, Kumla J (2021) A taxonomic appraisal of bambusicolous fungi in *Occultibambusa*

- ceae (Pleosporales, Dothideomycetes) with new collections from Yunnan Province, China. *Life* (Basel, Switzerland) 11(9): 932. <https://doi.org/10.3390/life11090932>
- Katoh K, Rozewicki J, Yamada KD (2019) MAFFT online service: Multiple sequence alignment, interactive sequence choice and visualization. *Briefings in Bioinformatics* 20(4): 1160–1166. <https://doi.org/10.1093/bib/bbx108>
- Koukol O, Delgado G (2021) Why morphology matters: The negative consequences of hasty descriptions of putative novelties in asexual ascomycetes. *IMA Fungus* 12(1): 1–8. <https://doi.org/10.1186/s43008-021-00073-z>
- Liu YJ, Whelen S, Hall BD (1999) Phylogenetic relationships among ascomycetes: Evidence from an RNA polymerase II subunit. *Molecular Biology and Evolution* 16(12): 1799–1808. <https://doi.org/10.1093/oxfordjournals.molbev.a026092>
- Liu NG, Hyde KD, Bhat DJ, Jumpathong J, Liu JK (2019) Morphological and phylogenetic studies of *Pleopunctum* gen. nov. (Phaeoseptaceae, Pleosporales) from China. *Mycosphere* 10(1): 757–775. <https://doi.org/10.5943/mycosphere/10/1/17>
- Luo Z, Hyde KD, Bhat DJ, Jeewon R, Maharachchikumbura SSN, Bao DF, Li WL, Su XJ, Yang XY, Su HY (2018) Morphological and molecular taxonomy of novel species Pleurotheciaceae from freshwater habitats in Yunnan, China. *Mycological Progress* 17(5): 511–530. <https://doi.org/10.1007/s11557-018-1377-6>
- Magaña-Dueñas V, Cano-Lira JF, Stchigel AM (2021) New Dothideomycetes from freshwater habitats in Spain. *Journal of Fungi* (Basel, Switzerland) 7(12): 1102. <https://doi.org/10.3390/jof7121102>
- Maharachchikumbura SSN, Wanasinghe DN, Cheewangkoon R, Al-Sadi AM (2021) Uncovering the hidden taxonomic diversity of fungi in Oman. *Fungal Diversity* 106(1): 229–268. <https://doi.org/10.1007/s13225-020-00467-1>
- Miller MA, Pfeiffer W, Schwartz T (2010) Creating the CIPRES Science Gateway for inference of large phylogenetic trees. *Proceedings of the Gateway Computing Environments Workshop (GCE)*. New Orleans, LA, 1–8. <https://doi.org/10.1109/GCE.2010.5676129>
- Morgan-Jones G, White JF (1983) Studies in the genus *Phoma*. iii: *Paraphoma*, a new genus to accommodate *Phoma radicina* 1983. *Mycotaxon* 18: 57–65.
- Mortimer PE, Jeewon R, Xu JC, Lumyong S, Wanasinghe DN (2021) Morpho-phylo taxonomy of novel dothideomycetous fungi associated with dead woody twigs in Yunnan Province, China. *Frontiers in Microbiology* 12: 654683. <https://doi.org/10.3389/fmicb.2021.654683>
- Moslemi A, Ades PK, Groom T, Crous PW, Nicolas ME, Taylor PWJ (2016) *Paraphoma* crown rot of pyrethrum (*Tanacetum cinerariifolium*). *Plant Disease* 100(12): 2363–2369. <https://doi.org/10.1094/PDIS-05-16-0628-RE>
- Moslemi A, Ades PK, Crous PW, Groom T, Scott JB, Nicolas ME, Taylor PWJ (2018) *Paraphoma chlamydocopiosa* sp. nov. and *Paraphoma pye* sp. nov., two new species associated with leaf and crown infection of pyrethrum. *Plant Pathology* 67(1): 124–135. <https://doi.org/10.1111/ppa.12719>
- Nylander JAA, Wilgenbusch JC, Warren DL, Swofford DL (2008) AWTY: A system for graphical exploration of MCMC convergence in Bayesian phylogenetics. *Bioinformatics* (Oxford, England) 24(4): 581–583. <https://doi.org/10.1093/bioinformatics/btm388>
- Osono T, Matsuoka S, Hirose D (2020) Diversity and geographic distribution of ligninolytic fungi associated with *Castanopsis sieboldii* leaf litter in Japan. *Frontiers in Microbiology* 11: 595427. <https://doi.org/10.3389/fmicb.2020.595427>
- Pang W, Zhang P, Zhang Y, Zhang X, Huang Y, Zhang T, Liu B (2023) The ectomycorrhizal fungi and soil bacterial communities of the five typical tree species in the Junzifeng national nature reserve, Southeast China. *Plants* 12(22): 3853. <https://doi.org/10.3390/plants12223853>

- Phukhamsakda C, McKenzie EHC, Phillips AJL, Jones EBG, Bhat DJ, Marc S, Bhunjun CS, Wanasinghe DN, Thongbai B, Camporesi E, Ertz D, Jayawardena RS, Perera RH, Ekanayake AH, Tibpromma S, Doilom M, Xu J, Hyde KD (2020) Microfungi associated with *Clematis* (Ranunculaceae) with an integrated approach to delimiting species boundaries. *Fungal Diversity* 102(1): 1–203. <https://doi.org/10.1007/s13225-020-00448-4>
- Quaedvlieg W, Verkley GJM, Shin HD, Barreto RW, Alfenas AC, Swart WJ, Groenewald JZ, Crous PW (2013) Sizing up septoria. *Studies in Mycology* 75: 307–390. <https://doi.org/10.3114/sim0017>
- Rambaut A (2012) FigTree version 1.4.0. <http://tree.bio.ed.ac.uk/software/figtree>
- Rannala B, Yang Z (1996) Probability distribution of molecular evolutionary trees: A new method of phylogenetic inference. *Journal of Molecular Evolution* 43(3): 304–311. <https://doi.org/10.1007/BF02338839>
- Rehner SA, Buckley E (2005) A *Beauveria* phylogeny inferred from nuclear ITS and EF1- α sequences: Evidence for cryptic diversification and links to *Cordyceps* teleomorphs. *Mycologia* 97(1): 84–98. <https://doi.org/10.3852/mycologia.97.1.84>
- Ren G, Wanasinghe DN, de Farias ARG, Hyde KD, Yasanthika E, Xu J, Balasuriya A, Chethana KWT, Gui H (2022) Taxonomic novelties of woody litter fungi (Didymosphaeriaceae, Pleosporales) from the Greater Mekong Subregion. *Biology (Basel)* 11(11): 1660. <https://doi.org/10.3390/biology11111660>
- Ronquist F, Huelsenbeck JP (2003) MrBayes 3: Bayesian phylogenetic inference under mixed models. *Bioinformatics (Oxford, England)* 19(12): 1572–1574. <https://doi.org/10.1093/bioinformatics/btg180>
- Ronquist F, Teslenko M, van der Mark P, Ayres DL, Darling A, Höhna S, Larget B, Liu L, Suchard MA, Huelsenbeck JP (2012) MrBayes 3.2: Efficient Bayesian phylogenetic inference and model choice across a large model space. *Systematic Biology* 61(3): 539–542. <https://doi.org/10.1093/sysbio/sys029>
- Senwana C, Mapook A, Samarakoon MC, Karunarathna A, Wang Y, Tang AMC, Haituk S, Suwannarach N, Hyde KD, Cheewangkoon R (2021) Ascomycetes on Para rubber (*Hevea brasiliensis*). *Mycosphere: Journal of Fungal Biology* 12(1): 1334–1512. <https://doi.org/10.5943/mycosphere/12/1/18>
- Species Fungorum (2024) Species Fungorum. <https://www.speciesfungorum.org/Names/Names.asp> [Accessed on May 15, 2024]
- Stamatakis A (2014) RAxML Version 8: A tool for Phylogenetic Analysis and Post-Analysis of Large Phylogenies. *Bioinformatics (Oxford, England)* 30(9): 1312–1313. <https://doi.org/10.1093/bioinformatics/btu033>
- Tan WH, Ong L, Strijk JS (2023) *Castanopsis corallocarpus* (Fagaceae), a new species from Royal Belum (Perak) in Peninsular Malaysia. *PhytoKeys* 219: 1–10. <https://doi.org/10.3897/phytokeys.219.95991>
- Tang AMC, Jeewon R, Hyde KD (2005) Succession of microfungal communities on decaying leaves of *Castanopsis fissa*. *Canadian Journal of Microbiology* 51(11): 967–974. <https://doi.org/10.1139/w05-086>
- Tennakoon DS, Kuo CH, Jeewon R, Thambugala KM, Hyde KD (2018) Saprobic Lophiostomataceae (Dothideomycetes): *Pseudolophiostoma mangiferae* sp. nov. and *Neovaginatipora fuckelii*, a new record from *Mangifera indica*. *Phytotaxa* 364(2): 157–171. <https://doi.org/10.11646/phytotaxa.364.2.3>
- Thambugala KM, Hyde KD, Tanaka K, Tian Q, Wanasinghe DN, Ariyawansa HA, Jayasiri SC, Boonmee S, Camporesi E, Hashimoto A, Hirayama K, Schumacher RK, Promputtha I, Liu ZY (2015) Towards a natural classification and backbone tree for

- Lophiostomataceae, Floricolaceae, and Amorosiaceae fam. nov. *Fungal Diversity* 74(1): 199–266. <https://doi.org/10.1007/s13225-015-0348-3>
- Thompson JD, Gibson TJ, Plewniak F, Jeanmougin F, Higgins DG (1997) The ClustalX windows interface: Flexible strategies for multiple sequence alignment aided by quality analysis tools. *Nucleic Acids Research* 24(24): 4876–4882. <https://doi.org/10.1093/nar/25.24.4876>
- Vilgalys R, Hester M (1990) Rapid genetic identification and mapping of enzymatically amplified ribosomal DNA from several *Cryptococcus* species. *Journal of Bacteriology* 172(8): 4238–4246. <https://doi.org/10.1128/jb.172.8.4238-4246.1990>
- Wanasinghe DN, Mortimer PE (2022) Taxonomic and phylogenetic insights into novel Ascomycota from forest woody litter. *Biology (Basel)* 11(6): 889. <https://doi.org/10.3390/biology11060889>
- Wanasinghe DN, Mortimer PE, Senwannan C, Cheewangkoon R (2020) Saprobic Dothideomycetes in Thailand: *Phaeoseptum hydei* sp. nov., a new terrestrial ascomycete in Phaeoseptaceae. *Phytotaxa* 449(2): 149–163. <https://doi.org/10.11646/phytotaxa.449.2.3>
- Wanasinghe DN, Mortimer PE, Xu JC (2021) Insight into the systematics of microfungi colonizing dead woody twigs of *Dodonaea viscosa* in Honghe (China). *Journal of Fungi (Basel, Switzerland)* 7(3): 180. <https://doi.org/10.3390/jof7030180>
- White TJ, Bruns T, Lee S, Taylor JW (1990) Amplification and direct sequencing of fungal ribosomal RNA genes for phylogenetics. *PCR protocols: A Guide to Methods and Applications*. Academic Press, 315–322. <https://doi.org/10.1016/B978-0-12-372180-8.50042-1>
- Wijayawardene NN, Hyde KD, Dai DQ, Sánchez-García M, Goto BT, Saxena RK, Erdoğdu M, Selçuk F, Rajeshkumar KC, Aptroot A, Błaszczowski J, Boonyuen N, da Silva GA, de Souza FA, Dong W, Ertz D, Haelewaters D, Jones EBG, Karunaratna SC, Kirk PM, Kukwa M, Kumla J, Leontyev DV, Lumbsch HT, Maharachchikumbura SSN, Marguno F, Martínez-Rodríguez P, Mešić A, Monteiro JS, Oehl F, Pawłowska J, Pem D, Pfliegler WP, Phillips AJL, Pošta A, He MQ, Li JX, Raza M, Sruthi OP, Suetrong S, Suwannarach N, Tedersoo L, Thiyagaraja V, Tibpromma S, Tkalčec Z, Tokarev YS, Wanasinghe DN, Wijesundara DSA, Wimalaseana SDMK, Madrid H, Zhang GQ, Gao Y, Sánchez-Castro I, Tang LZ, Stadler M, Yurkov A, Thines M (2022) Outline of Fungi and fungus-like taxa – 2021. *Mycosphere* 13(1): 53–453. <https://doi.org/10.5943/mycosphere/13/1/2>
- Xu RJ, Zhu YA, Liu NG, Boonmee S, Zhou DQ, Zhao Q (2023) Taxonomy and phylogeny of hyphomycetous muriform conidial taxa from the Tibetan Plateau, China. *Journal of Fungi (Basel, Switzerland)* 9(5): 560. <https://doi.org/10.3390/jof9050560>
- Yang J, Liu LL, Jones EBG, Hyde KD, Liu ZY, Bao DF, Liu NG, Li WL, Shen HW, Yu XD, Liu JK (2023) Freshwater fungi from karst landscapes in China and Thailand. *Fungal Diversity* 119(1): 1–212. <https://doi.org/10.1007/s13225-023-00514-7>
- Yu XD, Zhang SN, Liu JK (2022) Morpho-phylogenetic evidence reveals novel Pleosporalean taxa from Sichuan Province, China. *Journal of Fungi (Basel, Switzerland)* 8(7): 720. <https://doi.org/10.3390/jof8070720>
- Zhang JF, Liu JK, Hyde KD, Yang W, Liu ZY (2017) Fungi from Asian Karst formations II. Two new species of *Occultibambusa* (Occultibambusaceae, Dothideomycetes) from karst landforms of China. *Mycosphere: Journal of Fungal Biology* 8(4): 550–559. <https://doi.org/10.5943/mycosphere/8/4/4>
- Zhang YZ, Chen QL, Ma J, Lu YZ, Chen HB, Liu NG (2023) Morphological and multigene phylogenetic analyses reveal five new hyphomycetes from freshwater habitats. *Frontiers in Microbiology* 14: 1253239. <https://doi.org/10.3389/fmicb.2023.1253239>