

ARTICLE

Culturable Mycobiota from Guizhou Wildlife Park in China

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Citation – Zhang ZY, Pan H, Tao G, Li X, Han YF, Feng Y, Tong SQ, Ding CY 2024 – Culturable Mycobiota from Guizhou Wildlife Park in China. *Mycosphere* 15(1), 654–763, Doi 10.5943/mycosphere/15/1/5

Abstract

Wildlife parks play a positive role in strengthening the publicity and education of wildlife protection, rational utilization of wildlife resources, and socio-economic development. Due to anthropogenic influences, wildlife parks are characterized by highly heterogeneous environments, which inevitably harbor a great diversity of fungal taxa. Few systematic surveys of soil fungal taxa in wildlife parks have been reported. We investigated fungal taxa in the soil of Guizhou Wildlife Park, China, using culture-dependent methods to enrich the information on fungal diversity in such habitats. Preliminary internal transcribed spacer (ITS) analyses showed that 223 taxa were obtained in this study. Such taxa belonged to 126 genera, 10 undefined genera, 12 classes, and three phyla. This study identifies and describes one new order, one new family, two new genera, 21 new species, two new combinations, one new record from China and one asexual morph based on morphological and phylogenetic distinctions. *Tuberculiformaceae* is introduced as a new family, in the new order *Tuberculiformales* with *Tuberculiforma* as the type genus. In addition, a new genus, *Paragongromeriza*, with *Paragongromeriza sinensis* as the type species is introduced. Taxonomic novelties: New section, *Guizhouorum* is introduced in *Penicillium*. The novel species identified in this study are *Amorocoelophoma sinensis*, *Aphanoascus guizhouensis*, *Apiospora olivata*, *Bisifusarium sinense*, *Idriella longispora*, *Marquandomyces sinensis*, *Nigrograna guizhouensis*, *Paragongromeriza sinensis*, *Parasarocladium sinense*, *Penicillium guizhouense*, *Phaeodothis sinensis*, *Pseudogymnoascus wildlifiparkensis*, *Quasiconcha sinensis*, *Scolecobasidium guizhouense*, *Scolecobasidium inverellipsoidisporum*, *Scolecobasidium parahumicola*, *Talaromyces longistipes*, *Talaromyces parapalmae*, *Tuberculiforma sinensis*, *Volutella sinensis*, *Yunnanomyces sexualis*. New combinations, *Keithomyces echinosporus* and *Tuberculiforma catenatus*. New record in China, *Scolecobasidium longiphorum* and the asexual morph of *Nemania rubi* are given as the first reports. This work further demonstrated that wildlife park encompasses a high fungal diversity, including many previously unknown species which enhances our comprehension of soil fungal diversity within urban environments.

Keywords – Ascomycota – new taxa – *Paragongromeriza* – soil fungi – *Tuberculiforma* – *Tuberculiformaceae* – *Tuberculiformales*

INTRODUCTION

Fungi represent one of the most diverse groups of organisms on the planet and play an essential role in ecosystem processes and functioning (Hyde 2022, Niego et al. 2023). Such high

Submitted: 29 November 2023; **Accepted:** 24 April 2024; **Published:** 30 May 2024

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Accepted by: Ishara S. Manawasinghe

fungal diversity is partly because many are cosmopolitan, with a wider geographical distribution than plants and other organisms (Hernández-Restrepo et al. 2017). Additionally, many habitats and substrates remain unexplored as far as fungi are concerned and might support many undescribed species (Hernández-Restrepo et al. 2017). The number of fungi has always been intriguing (Hyde 2022). In recent years, new DNA sequencing technologies have revolutionized studies of fungal taxonomy and diversity, leading to changes in the estimates of fungal species numbers ranging from 2.2 to 3.8 based on host association (Hawksworth & Lücking 2017) and 11.7 to 13.2 million species using culture-independent methods such as metabarcoding and metagenomics (Cheek et al. 2020, Hawksworth & Lücking 2017, Nilsson et al. 2019, Peay et al. 2016, Tedersoo et al. 2014). These studies highlight the gap between the formally described fungal taxa and the estimated diversity, suggesting that only 5%–10% of all fungal species have been described (James et al. 2020). As far as fungal taxonomy, pure culture methods are still fundamental. Pure cultures of fungi make studying many aspects of their biology possible, which will help us understand their function in natural ecosystems. More importantly, cultures are valuable for linking sexual and asexual morphs and understanding functional guilds and can be preserved as isolates (as dry and living) in reference collections (Yasanthika et al. 2022). Unfortunately, to date, many fungal taxa do not have pure cultures. Researchers have worked hard on this and have developed many new fungi isolation methods. For example, Yasanthika et al. (2022) systematically reviewed various methods for isolating fungi from soil, such as baiting and dilution plate methods.

Numerous studies have shown that fungi are found in marine, cave, forest, volcanic, mountain, desert, freshwater aquatic systems, lake, grassland, and indoor environments (Hyde et al. 2022). However, the composition of fungi in environments closely related to human life and health (e.g., in hospitals, campuses, and wildlife parks) has not received enough attention. Guizhou Wildlife Park is located within the Lengshuigou sub-field of the Zhazuo Forestry Farm of Guizhou Province in Zhazuo Town, Xiwen County, Guiyang City, covering an area of about 5,000 acres. This is a part animals and forest landscape display viewing as the main line. In addition, in Guizhou Wildlife Park wildlife relocation, protection, popularization of science education, breeding and scientific research, is for the public to provide excursions and sightseeing, rest, and recreation of the comprehensive wildlife park. There are 536 wild animal species in Guizhou Wildlife Park, many of which are under national protection. In addition, the topography of the park is changeable, with gentle slopes, mountain cols, broad valleys, mountain peaks, stone forests, karst caves, and other karst landforms, and the soil heterogeneity is exceptionally high. The fungal diversity and resources in wildlife parks are of great significance. Therefore, the purposes of this study were as follows: (1) To investigate the diversity and composition of soil fungi in wildlife park. (2) To provide the description and illustration of the new fungal taxa.

MATERIALS AND METHODS

Sample collection and Fungal isolation

Soil samples were collected from the green belts of Guizhou Wildlife Park in southwest China on July 17, 2022. Samples were collected 3–10 cm below the soil surface, placed in Ziploc plastic bags preserved at 4 °C, brought back to the laboratory, and processed immediately. Three different modified media were used to maximize the number of fungi isolated: Martin's medium (KH_2PO_4 1 g/L, MgSO_4 0.5 g/L, peptone 5 g/L, glucose 2 g/L, agar 20 g/L, 1% Bengal red aqueous solution 3.3 mL/L), Sabouraud's dextrose agar (SDA; peptone 10 g/L, dextrose 40 g/L, agar 20 g/L, 1% Bengal red aqueous solution 3.3 mL/L), and Sabouraud's dextrose agar yeast extract (SDAY; peptone 10 g/L, dextrose 40 g/L, agar 20 g/L, yeast extract 2 g/L, 1% Bengal red aqueous solution 3.3 mL/L).

Fungi were isolated following the dilution plate method (Zhang et al. 2023a). A total of 2 g of each collected sample was suspended in 20 ml of sterile water in a 50 ml sterile conical flask. The conical flasks were thoroughly shaken using a Vortex vibration meter. The suspension was then diluted to a concentration of 10^{-4} . Then, 1 ml of the diluted sample was transferred to a sterile Petri

dish, and Martin's medium, SDA, SDAY containing 50 mg/L penicillin and 50 mg/L streptomycin, was added and mixed. Three replicates of each medium. The plates were incubated at 25 °C for 1–2 weeks, and single colonies were selected from the plates and inoculated into new potato dextrose agar (PDA, potato 200 g/L, dextrose 20 g/L, agar 20 g/L) plates.

Additionally, according to the description of Li et al. (2022), the soil was treated with the baiting technique, followed by the isolation of fungi to obtain more taxa. Briefly, clean and sterile chicken feathers were placed in a sterile petri dish after adding the soil sample, wetted with distilled water, and incubated at room temperature for one month (Zhang et al. 2021a). Then, the strains were isolated using the same methods and media described above.

DNA extraction, PCR amplification and sequencing

Total genomic DNA was extracted from fungal mycelia using a 5% chelex-100 solution. The internal transcribed spacer (ITS) sequences of all isolates were amplified and sequenced. According to Zhang et al. (2021b), the isolates whose ITS sequences are less than 97% similar to the closest strain were recognized as potential new species, and more of their loci were amplified for phylogenetic analysis. However, different loci are often required in the phylogenetic analysis of different taxa, so this study also amplified different loci for different taxa, as shown in Table 1. The amplification reactions were performed in 25 µl final volumes consisting of a 2 µl DNA template (10 ng/µl), 1 µl forward primer (10 µM), 1 µl reverse primer (10 µM), 12.5 µl 2 × SanTaq PCR Master Mix (containing Taq polymerase, dNTP, and Mg²⁺; Sangon Biotech Co., Ltd, Shanghai, China), and 8.5 µl sterile water (Zhang et al. 2023a). The PCR was run using a T100 thermal cycler (Bio-Rad, California, USA), and the resulting amplified PCR products were sequenced in both directions using PCR primers. The PCR products were visualized on a 1% agarose gel stained with ethidium bromide, and the positive PCR products were then sent for sequencing to Sangon Biotech (Shanghai, China). All new sequences generated were deposited to GenBank (Table 2).

Morphological observation

Fungi cultures were cultivated on fresh malt extract agar (MEA), oatmeal agar (OA), potato dextrose agar (PDA), and synthetic nutrient-poor agar (SNA) and incubated at 25 °C in the dark for 3–5 weeks. Colony diameter and characteristics were measured after 14 days of incubation. The cultures were observed micro morphologically after they produced reproductive structures. The characterization and measurement of fungal microscopic characteristics were performed in 25% clear lactic acid. The observations were performed with an OLYMPUS BX53 compound microscope with differential interference contrast (DIC) optics. Photomicrographs and measurements were taken with an OLYMPUS DP73 high-definition color digital camera using cellSens v.1.18.

Descriptions of novelties and taxonomic recombination were deposited in MycoBank and Facesoffungi, and the type strains for the novel taxa represented by living cultures were deposited at the China General Microbiological Culture Collection Center (CGMCC), China. Additionally, type collections (dried at 50 °C) and all living cultures of the novel taxa were deposited in the College of Eco-Environmental Engineering, Guizhou Minzu University, China.

Phylogenetic analyses

DNASTAR Lasergene SeqMan Pro v. 7.1.0 (44.1) was used to edit ambiguous bases at both ends of the raw forward and reverse reads and to assemble them. The collation of sequences (including name simplification and renaming) was performed using TBtools software (Chen et al. 2020). Sequence alignments were generated with MAFFT v. 7 using the default settings (Katoh & Standley 2013) and manually edited in MEGA v. 7.0.21 (Kumar et al. 2015). The “Concatenate Sequence” function in PhyloSuite v.1.2.3 (Xiang et al. 2023) was used to concatenate the loci.

The maximum likelihood (ML) and Bayesian inference (BI) methods were used for phylogenetic inferences of each concatenated alignment. The best substitution evolution model for each data partition was estimated using ModelFinder v2.2.0 (Kalyaanamoorthy et al. 2017) in

PhyloSuite v.1.2.3 (Xiang et al. 2023) before the ML and BI analyses. ML analyses were performed using IQ-TREE v2.2.0 (Nguyen et al. 2015) with ultrafast bootstrapping (UFBoot2; Hoang et al. 2018) in PhyloSuite v.1.2.3 (Xiang et al. 2023). Bayesian analyses were performed using MrBayes v. 3.2.6 (Ronquist et al. 2012). Markov chain Monte Carlo sampling (MCMC) analyses of four chains were started in parallel using a random tree topology. Four simultaneous Markov chains were run for 10 M generations. Trees were sampled every 1,000 generations or until the run was stopped automatically when the average standard deviation of split frequencies fell below 0.01. The first 25% of the trees were discarded as the burn-in phase of each analysis, and the remaining trees were used to calculate the posterior probabilities (PP). The resulting trees were plotted using FigTree v. 1.4.2 (<http://tree.bio.ed.ac.uk/software/figtree>) and edited using Microsoft Paint. Alignments derived from this study were uploaded to Figshare (Doi: 10.6084/m9.figshare.24495265).

RESULTS

Ten samples were collected from Guizhou Wildlife Park, and 223 fungal taxa were isolated (Supplementary Table 1). By conducting a BLASTn search in GenBank using the ITS sequences, in conjunction with assessments of morphology and phylogeny, it was determined that these taxa were belonged to 126 genera, 10 undefined genera, 12 classes, and three phyla (Supplementary Table 1).

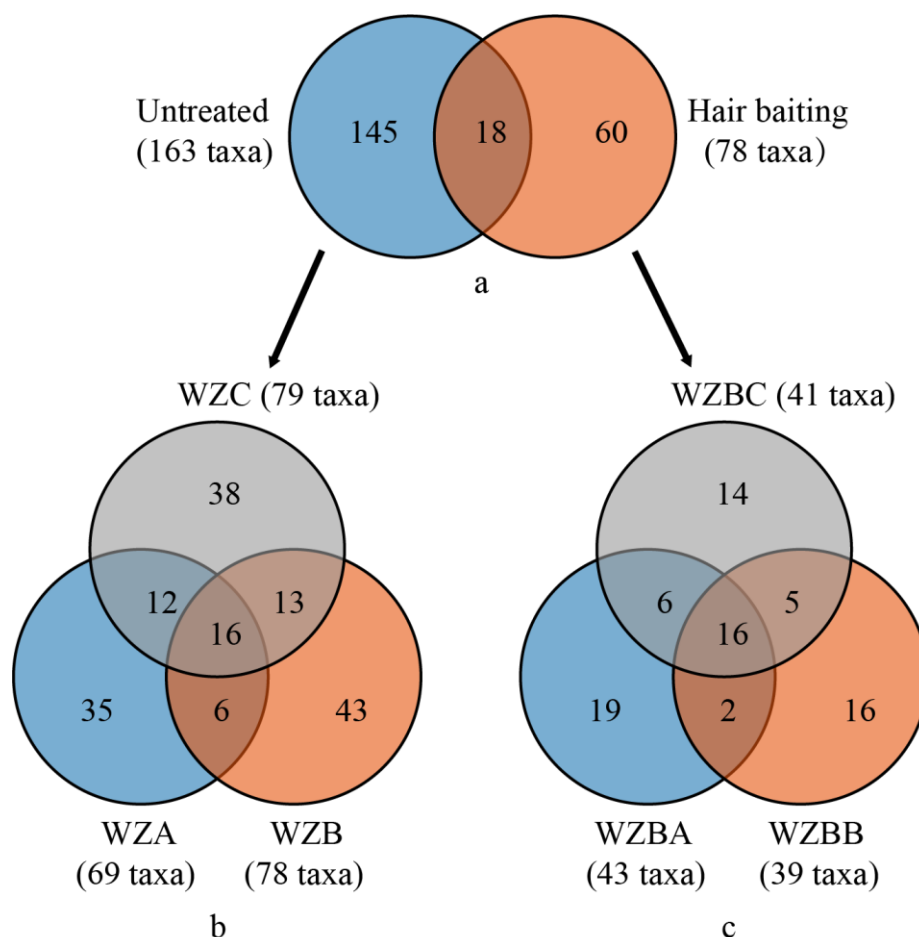


Figure 1 – Venn diagram of fungal taxa numbers obtained from different treatments and mediums in this study. a) Venn diagrams showing shared and unique taxa numbers in untreated soils, WZA, WZB, and WZC indicate taxa obtained from untreated soils using Martin's, SDA, and SDAY medium, respectively. b) Venn diagrams showing shared and unique taxa numbers in feather treatment soils, WZBA, WZBB, and WZCB indicate taxa obtained from untreated soils using Martin's, SDA, and SDAY medium, respectively.

Table 1 Details of genes/loci with PCR primers used in different taxa.

Genera name	Genes/loci	Primers	References
<i>Amorocoelophoma</i> , <i>Aphanoascus</i> , <i>Nigrograna</i> , <i>Parasarocladium</i> , <i>Quasiconcha</i> , <i>Tuberculiforma</i> , <i>Volutella</i>	SSU	NS1/NS4	White et al. (1990)
	ITS	ITS1/ITS4	White et al. (1990)
	LSU	LR0R/LR7	Vilgalys & Hester (1990), Moncalvo et al. (2000)
	<i>EF1A</i>	EF1-983F/EF1-2218R	Rehner & Buckley (2005)
	<i>RPB2</i>	RPB2-5f/RPB2-7cR	Liu et al. (1999)
	<i>TUB</i>	Bt-2a/Bt-2b	Glass & Donaldson (1995)
<i>Apiospora</i> , <i>Scolecobasidium</i> , <i>Yunnanomyces</i>	SSU	NS1/NS4	White et al. (1990)
	ITS	ITS1/ITS4	White et al. (1990)
	LSU	LR0R/LR7	Vilgalys & Hester (1990), Moncalvo et al. (2000)
	<i>EF1A</i>	EF1-728F/EF2	Carbone & Kohn (1999), O'Donnell et al. (1998)
	<i>RPB2</i>	RPB2-5f/RPB2-7cR	Liu et al. (1999)
	<i>TUB</i>	Bt-2a/Bt-2b	Glass & Donaldson (1995)
<i>Bisifusarium</i>	SSU	NS1/NS4	White et al. (1990)
	ITS	ITS1/ITS4	White et al. (1990)
	LSU	LR0R/LR7	Vilgalys & Hester (1990), Moncalvo et al. (2000)
	<i>EF1A</i>	EF1/EF2	O'Donnell et al. (1998)
	<i>RPB2</i>	RPB2-5f/RPB2-7cR	Liu et al. (1999)
	<i>TUB</i>	Bt-2a/Bt-2b	Glass & Donaldson (1995)
<i>Idriella</i>	SSU	NS1/NS4	White et al. (1990)
	ITS	ITS1/ITS4	White et al. (1990)
	LSU	LR0R/LR7	Vilgalys & Hester (1990), Moncalvo et al. (2000)
	<i>EF1A</i>	EF1-983F/EF1-2218R	Rehner & Buckley (2005)
	<i>RPB2</i>	RPB2-5f/RPB2-7cR	Liu et al. (1999)
	<i>TUB</i>	Btub526F/Btub1332R	Jewell & Hsiang (2013)
<i>Keithomyces</i> , <i>Marquandomyces</i> , <i>Phaeodothis</i>	SSU	NS1/NS4	White et al. (1990)
	ITS	ITS1/ITS4	White et al. (1990)
	LSU	LR0R/LR7	Vilgalys & Hester (1990), Moncalvo et al. (2000)
	<i>EF1A</i>	EF1-983F/EF1-2218R	Rehner & Buckley (2005)
	<i>RPB2</i>	RPB2-5f/RPB2-7cR	Liu et al. (1999)
<i>Nemania</i>	SSU	NS1/NS4	White et al. (1990)
	ITS	ITS1/ITS4	White et al. (1990)

Table 1 Continued.

Genera name	Genes/loci	Primers	References
	LSU	LR0R/LR7	Vilgalys & Hester (1990), Moncalvo et al. (2000)
	<i>RPB2</i>	RPB2-5f/RPB2-7cR	Liu et al. (1999)
	<i>TUB</i>	Bt-2a/Bt-2b	Glass & Donaldson (1995)
<i>Paragongromeriza</i>	SSU	NS1/NS4	White et al. (1990)
	ITS	ITS4/ITS5	White et al. (1990)
	LSU	LR0R/LR7	Vilgalys & Hester (1990), Moncalvo et al. (2000)
	<i>EF1A</i>	EF1-983F/EF1-2218R	Rehner & Buckley (2005)
	<i>RPB2</i>	RPB2-5f/RPB2-7cR	Liu et al. (1999)
	<i>TUB</i>	Bt-T1/Bt-2b	O'Donnell & Cigelnik (1997), Glass & Donaldson (1995)
<i>Penicillium, Talaromyces</i>	SSU	NS1/NS4	White et al. (1990)
	ITS	ITS1/ITS4	White et al. (1990)
	LSU	LR0R/LR7	Vilgalys & Hester (1990), Moncalvo et al. (2000)
	<i>EF1A</i>	EF1-983F/EF1-2218R	Rehner & Buckley (2005)
	<i>RPB2</i>	RPB2-5f/RPB2-7cR	Liu et al. (1999)
	<i>TUB</i>	Bt-2a/Bt-2b	Glass & Donaldson (1995)
	<i>CaM</i>	CF1d/CF4	Peterson (2004)
<i>Pseudogymnoascus</i>	ITS	ITS1/ITS4	White et al. (1990)
	LSU	LR0R/LR7	Vilgalys & Hester (1990), Moncalvo et al. (2000)
	<i>EF1A</i>	EF1-983F/EF1-2218R	Rehner & Buckley (2005)
	<i>MCM7</i>	Mcm7-709f/Mcm7-1348r	Schmitt et al. (2009)

Table 2 Isolates and sequence accession numbers of new taxa in this study.

Species	Isolates	GenBank accession numbers							
		SSU	ITS	LSU	<i>RPB2</i>	<i>EF1A</i>	<i>TUB</i>	<i>CaM</i>	<i>McM7</i>
<i>Quasiconcha sinensis</i>	CGMCC 3.25498 = ZY22.011 T	OR680859	OR680490	OR680557	OR842907	OR865892	OR843197		
<i>Quasiconcha sinensis</i>	ZY22.012	OR680860	OR680491	OR680558	OR842908	OR865893	OR843198		
<i>Quasiconcha sinensis</i>	ZY22.013	OR680861	OR680492	OR680559	OR842909	OR865894	OR843199		
<i>Amorocoelophoma sinensis</i>	CGMCC 3.25499 = ZY22.014 T	OR680862	OR680493	OR680560	OR842910	OR858892	OR843200		

Table 2 Continued.

Species	Isolates	GenBank accession numbers							
		SSU	ITS	LSU	<i>RPB2</i>	<i>EF1A</i>	<i>TUB</i>	<i>CaM</i>	<i>McM7</i>
<i>Amorocoelophoma sinensis</i>	ZY22.015	OR680863	OR680494	OR680561	OR842911	OR858893	OR843201		
<i>Amorocoelophoma sinensis</i>	ZY22.016	OR680864	OR680495	OR680562	OR842912	OR858894	OR843202		
<i>Phaeodothis sinensis</i>	CGMCC 3.25500 = ZY22.017 T	OR680865	OR680496	OR680563	OR842913	OR858895			
<i>Phaeodothis sinensis</i>	ZY22.018	OR680866	OR680497	OR680564	OR842914	OR858896			
<i>Nigrograna guizhouensis</i>	CGMCC 3.25501 = ZY22.019 T	OR680867	OR680498	OR680565	OR842915	OR858897	OR843203		
<i>Nigrograna guizhouensis</i>	ZY22.020	OR680868	OR680499	OR680566	OR842916	OR858898	OR843204		
<i>Nigrograna guizhouensis</i>	ZY22.021	OR680869	OR680500	OR680567	OR842917	OR858899	OR843205		
<i>Scolecobasidium guizhouense</i>	CGMCC 3.25502 = ZY22.022 T	OR680870	OR680501	OR680568	OR842918	OR858900	OR843206		
<i>Scolecobasidium guizhouense</i>	ZY22.023	OR680871	OR680502	OR680569	OR842919	OR858901	OR843207		
<i>Scolecobasidium guizhouense</i>	ZY22.024	OR680872	OR680503	OR680570	OR842920	OR858902	OR843208		
<i>Scolecobasidium parahumicola</i>	CGMCC 3.25503 = ZY22.025 T	OR680873	OR680504	OR680571	OR842921	OR858903	OR843209		
<i>Scolecobasidium parahumicola</i>	ZY22.026	OR680874	OR680505	OR680572	OR842922	OR858904	OR843210		
<i>Scolecobasidium inverellipsoidisporum</i>	CGMCC 3.25504 = ZY22.027 T	OR680875	OR680506	OR680573	OR842923	OR858905	OR843211		
<i>Scolecobasidium inverellipsoidisporum</i>	ZY22.028	OR680876	OR680507	OR680574	OR842924	OR858906	OR843212		
<i>Scolecobasidium inverellipsoidisporum</i>	ZY22.029	OR680877	OR680508	OR680575	OR842925	OR858907	OR843213		
<i>Scolecobasidium inverellipsoidisporum</i>	ZY22.030	OR680878	OR680509	OR680576	OR842926	OR858908	OR843214		
<i>Scolecobasidium tshawytschae</i>	CGMCC 3.25506 = ZY22.031	OR680879	OR680510	OR680577	OR842927	OR858909	OR843215		
<i>Scolecobasidium longiphorum</i>	CGMCC 3.25505 = ZY22.032	OR680880	OR680511	OR680578	OR842928	OR858910	OR843216		

Table 2 Continued.

Species	Isolates	GenBank accession numbers							
		SSU	ITS	LSU	<i>RPB2</i>	<i>EF1A</i>	<i>TUB</i>	<i>CaM</i>	<i>McM7</i>
<i>Yunnanomyces sexualis</i>	CGMCC 3.25507 = ZY22.033 T		OR680512	OR680579	OR842929	OR858911	OR843217		
<i>Yunnanomyces sexualis</i>	ZY22.034		OR680513	OR680580	OR842930	OR858912	OR843218		
<i>Penicillium guizhouense</i>	CGMCC 3.25508 = ZY22.035 T	OR680881	OR680514	OR680581	OR842931	OR858913	OR843219	OR828450	
<i>Penicillium guizhouense</i>	ZY22.036	OR680882	OR680515	OR680582	OR842932	OR858914	OR843220	OR828451	
<i>Penicillium guizhouense</i>	ZY22.037	OR680883	OR680516	OR680583	OR842933	OR858915	OR843221	OR828452	
<i>Penicillium guizhouense</i>	ZY22.038	OR680884	OR680517	OR680584	OR842934	OR858916	OR843222	OR828453	
<i>Talaromyces longistipes</i>	CGMCC 3.25509 = ZY22.039 T	OR680885	OR680518	OR680585	OR842935	OR865895	OR843223	OR828454	
<i>Talaromyces longistipes</i>	ZY22.040	OR680886	OR680519	OR680586	OR842936	OR865896	OR843224	OR828455	
<i>Talaromyces parapalmae</i>	CGMCC 3.25510 = ZY22.041 T		OR680520	OR680587	OR842937	OR865897	OR843225	OR828456	
<i>Talaromyces parapalmae</i>	ZY22.042		OR680521	OR680588	OR842938	OR865898	OR843226	OR828457	
<i>Talaromyces parapalmae</i>	ZY22.043		OR680522	OR680589	OR842939	OR865899	OR843227	OR828458	
<i>Aphanoascus guizhouensis</i>	CGMCC 3.25511 = ZY22.044 T	OR680887	OR680523	OR680590	OR842940	OR858917	OR843228		
<i>Aphanoascus guizhouensis</i>	ZY22.045	OR680888	OR680524	OR680591	OR842941	OR858918	OR843229		
<i>Tuberculiforma sinensis</i>	CGMCC 3.25512 = ZY22.046 T	OR680889	OR680525	OR680592	OR842942	OR858919	OR843230		
<i>Tuberculiforma sinensis</i>	ZY22.047	OR680890	OR680526	OR680593	OR842943	OR858920	OR843231		
<i>Tuberculiforma sinensis</i>	ZY22.048	OR680891	OR680527	OR680594	OR842944	OR858921	OR843232		
<i>Tuberculiforma sinensis</i>	ZY22.049	OR680892	OR680528	OR680595	OR842945	OR858922	OR843233		
<i>Pseudogymnoascus wildlifiparkensis</i>	CGMCC 3.25513 = ZY22.050 T		OR680529	OR680596		OR858923			OR820946
<i>Pseudogymnoascus wildlifiparkensis</i>	ZY22.051		OR680530	OR680597		OR858924			OR820947
<i>Apiospora olivata</i>	CGMCC 3.25514 = ZY22.052 T	OR680893	OR680531	OR680598	OR842946	OR858925	OR843234		
<i>Apiospora olivata</i>	ZY22.053	OR680894	OR680532	OR680599	OR842947	OR858926	OR843235		
<i>Apiospora olivata</i>	ZY22.054	OR680895	OR680533	OR680600	OR842948	OR858927	OR843236		
<i>Apiospora olivata</i>	ZY22.055	OR680896	OR680534	OR680601	OR842949	OR858928	OR843237		

Table 2 Continued.

Species	Isolates	GenBank accession numbers							
		SSU	ITS	LSU	<i>RPB2</i>	<i>EF1A</i>	<i>TUB</i>	<i>CaM</i>	<i>McM7</i>
<i>Paragongromeriza sinensis</i>	CGMCC 3.25515 = ZY22.056 T	OR680897	OR680535	OR680602	OR842950	OR858929	OR843238		
<i>Paragongromeriza sinensis</i>	ZY22.057	OR680898	OR680536	OR680603	OR842951	OR858930	OR843239		
<i>Paragongromeriza sinensis</i>	ZY22.058	OR680899	OR680537	OR680604	OR842952	OR858931	OR843240		
<i>Paragongromeriza sinensis</i>	ZY22.059	OR680900	OR680538	OR680605	OR842953	OR858932	OR843241		
<i>Paragongromeriza sinensis</i>	ZY22.060	OR680901	OR680539	OR680606	OR842954	OR858933	OR843242		
<i>Marquandomyces marquandii</i>	CGMCC 3.25516 = ZY22.061	OR680902	OR680540	OR680607	OR842955	OR858934			
<i>Marquandomyces marquandii</i>	ZY22.062	OR680903	OR680541	OR680608	OR842956	OR858935			
<i>Keithomyces echinosporus</i>	CGMCC 3.25517 = ZY22.063	OR680904	OR680542	OR680609	OR842957	OR858936			
<i>Marquandomyces sinensis</i>	CGMCC 3.25518 = ZY22.064 T	OR680905	OR680543	OR680610	OR842958	OR858937			
<i>Marquandomyces sinensis</i>	ZY22.065	OR680906	OR680544	OR680611	OR842959	OR858938			
<i>Bisifusarium sinense</i>	CGMCC 3.25519 = ZY22.066 T	OR680907	OR680545	OR680612	OR842960	OR858939	OR843243		
<i>Bisifusarium sinense</i>	ZY22.067	OR680908	OR680546	OR680613	OR842961	OR858940	OR843244		
<i>Bisifusarium sinense</i>	ZY22.068	OR680909	OR680547	OR680614	OR842962	OR858941	OR843245		
<i>Volutella sinensis</i>	CGMCC 3.25520 = ZY22.069 T	OR680910	OR680548	OR680615	OR842963	OR858942	OR843246		
<i>Volutella sinensis</i>	ZY22.070	OR680911	OR680549	OR680616	OR842964	OR858943	OR843247		
<i>Parasarocladium sinense</i>	CGMCC 3.25521 = ZY22.071 T	OR680912	OR680550	OR680617	OR842965	OR865900	OR843248		
<i>Parasarocladium sinense</i>	ZY22.072	OR680913	OR680551	OR680618	OR842966	OR865901	OR843249		
<i>Idriella longispora</i>	CGMCC 3.25522 = ZY22.073 T	OR755847	OR680552	OR680619	OR842967	OR858944	OR843250		
<i>Idriella longispora</i>	ZY22.074	OR755848	OR680553	OR680620	OR842968	OR858945	OR843251		
<i>Idriella longispora</i>	ZY22.075	OR755849	OR680554	OR680621	OR842969	OR858946	OR843252		
<i>Nemania rubi</i>	CGMCC 3.25523 = ZY22.076	OR680914	OR680555	OR680622	OR842970		OR843253		
<i>Nemania rubi</i>	ZY22.077	OR680915	OR680556	OR680623	OR842971		OR843254		

Ex-type strains are indicated with **T**.

A total of 163 taxa were isolated from the untreated soil samples, and they belonged to 99 genera, 12 classes, three phyla, one undefined genus in Lecanoromycete, three undefined genera in Sordariomycetes, and four undefined genera in Fungi (Supplementary Table 1). A total of 78 taxa were obtained from the feather-enriched soil, and they belonged to 52 genera, seven classes, three phyla, and one undefined genus in fungi (Supplementary Table 1). Significantly more of the former than the latter, showing that baits function as environmental stressors that specifically enrich holobionts with specific functions (Yasanthika et al. 2022) but reduce the diversity of many taxa with a wide range of nutrient sources, and thus the composition of the fungal communities in the samples.

A comparison of the isolation effects of different mediums revealed no significant difference in the number of fungal taxa isolated using the three mediums (Martin's medium, SDA, SDAY), both from untreated soil and from feather-enriched treated soil. Still, some endemic taxa were isolated using each medium (Fig. 1). There are vast treasures of fungi in the natural environment that have not been purely cultured or formally described. Different tools (media with different compositions) can lead to more fruitful digging.

Taxonomy

In this study, each novel taxon was treated using the latest and most comprehensive publications of that particular taxa. Based on morphological and phylogenetic distinctions, this study identifies and describes 21 new species, two new combinations, one new record from China, and adds the asexual morph of the known species, *Nemania rubi*.

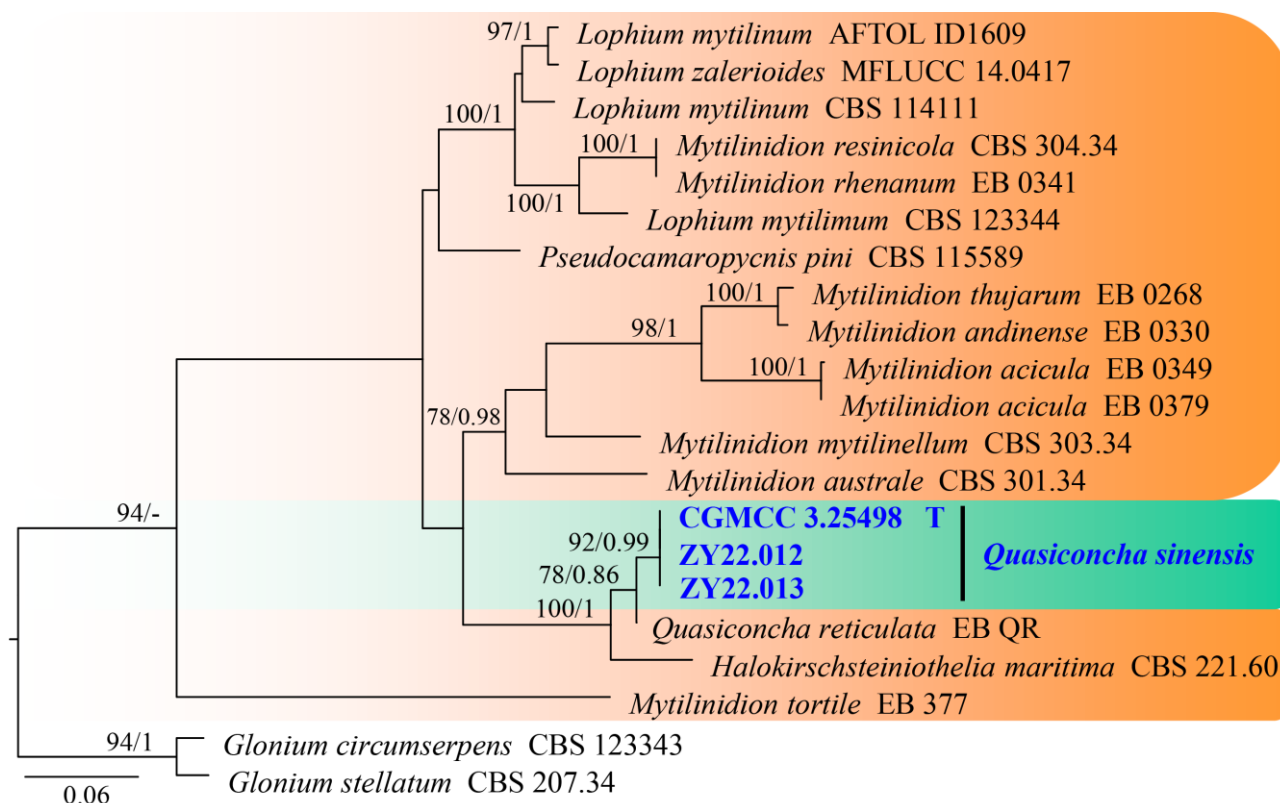


Figure 2 – Phylogram generated from maximum likelihood analysis based on combined SSU, ITS, LSU, *RPB2*, and *EF1A* sequence data. Estimated base frequencies were as follows; A = 0.256, C = 0.228, G = 0.264, T = 0.252; substitution rates AC = 1.14377, AG = 6.57495, AT = 3.94689, CG = 1.12724, CT = 13.85930, GT = 1.00000; gamma distribution shape parameter α = 0.335. The tree topology of ML analysis is similar to BI analysis. Bootstrap support values for MLBS $\geq$ 70% and BYPP $\geq$ 0.7 are defined as BS/PP above the nodes. Hyphens (-) represent support values less than 70% in ML and 0.7 in BI. Newly generated sequences are in blue and “T” indicates type strain.

Phylum *Ascomycota* Caval.-Sm.

Class *Dothideomycetes* O.E. Erikss. & Winka.

Mytilinidiales E. Boehm, C.L. Schoch & Spatafora

Mytilinidiaceae Kirschst.

Quasiconcha M.E. Barr & M. Blackw.

Based on the dataset combined SSU, ITS, LSU, *RPB2*, and *EF1A* sequences, the phylogeny of *Quasiconcha sinensis* and its related taxa were studied. *Glonium circumserpens* (CBS 123343) and *G. stellatum* (CBS 207.34) were used as the outgroup for the phylogenetic analysis. The concatenated sequences included 21 taxa and consisted of 4,018 nucleotides (SSU, 829 bp; ITS, 638 bp; LSU, 809 bp; *RPB2*, 815 bp; and *EF1A*, 927 bp) with inserted gaps. The phylogenetic trees showed that three new isolates, CGMCC 3.25498, ZY 22.012, and ZY 22.013 clustered into a single clade with a high support value (92% BS support [BS]/0.99 posterior probability [PP]). In addition, *Q. sinensis* and *Q. reticulata* clustered with moderate support value (78/0.86) (Fig. 2).

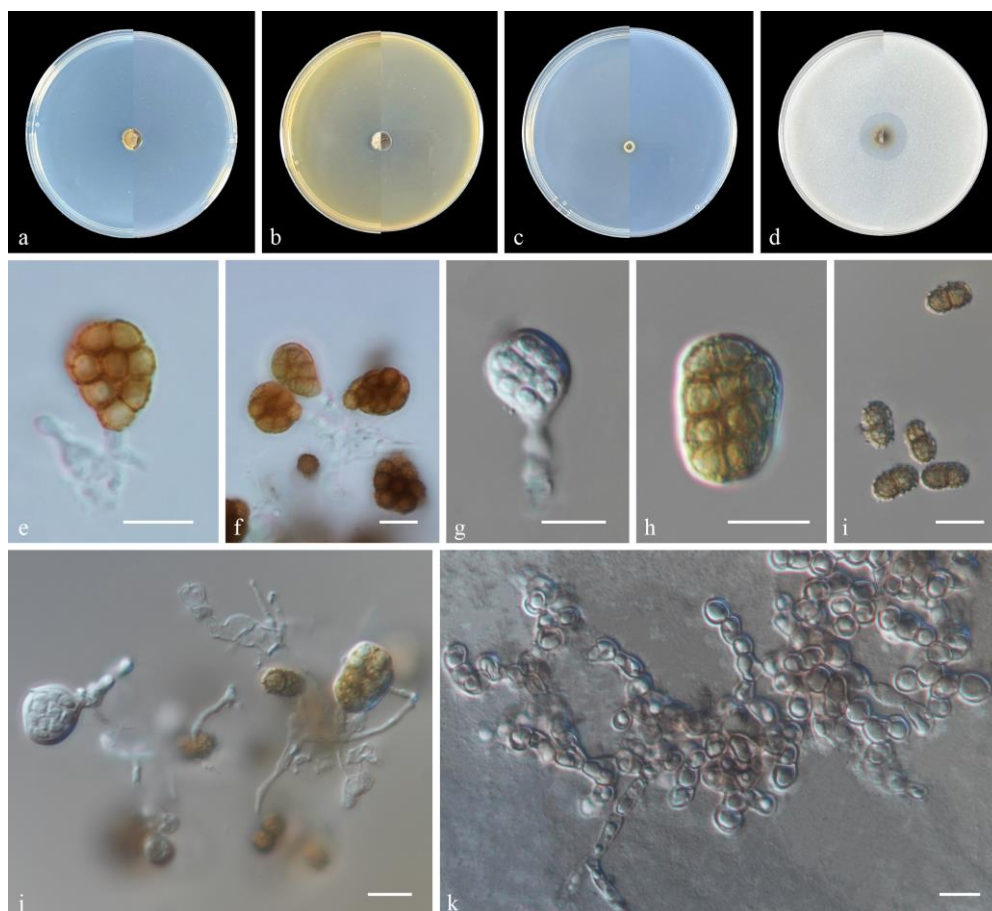


Figure 3 – *Quasiconcha sinensis* (CGMCC 3.25498). a–d Upper and reverse views of cultures on PDA, MEA, SNA, and OA 14 d after inoculation. e–h, j Asci. i Ascospores. k Conidia. Scale bars: e–k = 10 µm.

Quasiconcha sinensis Zhi Y. Zhang & Y. F. Han, sp. nov.

Fig. 3

Mycobank number: MB850364; Facesoffungi number: FoF15073

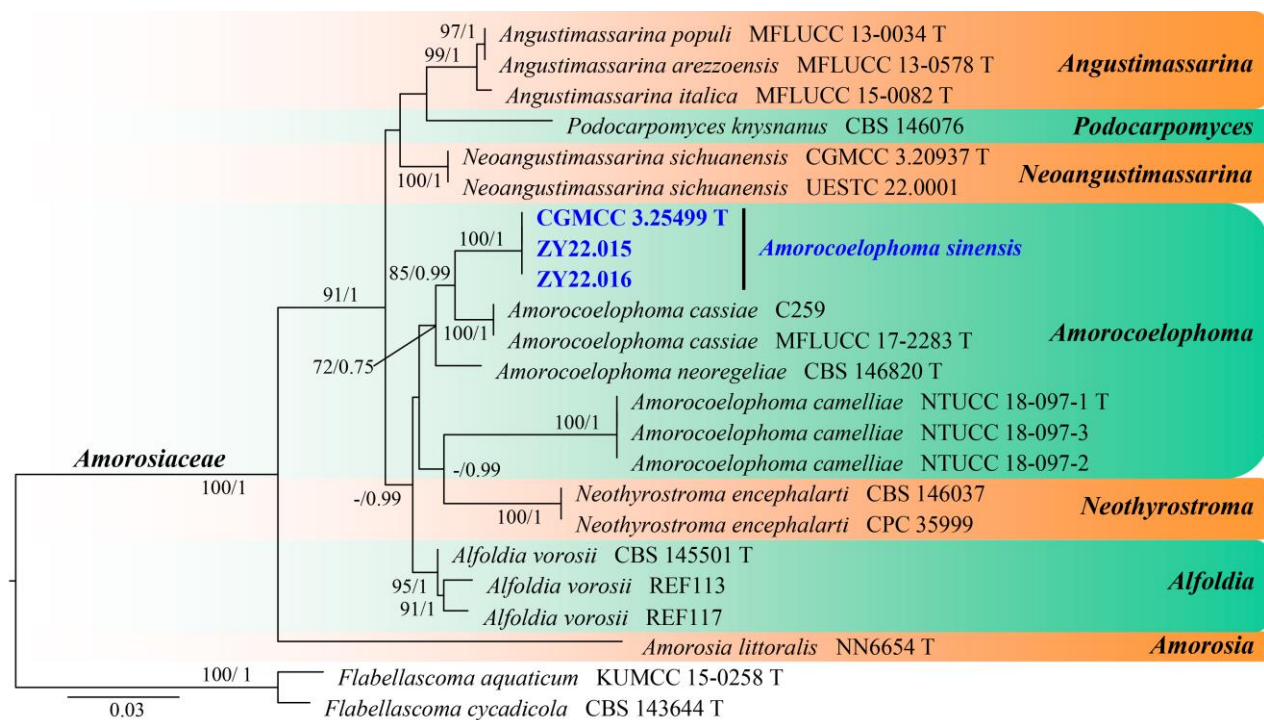
Etymology – Named after the location China, where the holotype was collected.

Holotype – ZY H-22.011

Description – *Hyphae* branched, septate, hyaline, smooth, 1–3 µm diam. Sexual morph *Ascomata* rare, superficial, black. *Asci* 14–16.5 × 11.5–12.5 µm (av. 15.3 × 11.9 µm, n = 30), 8-spored, obovate, pyriform to subglobose, abundant, thin-walled at maturity; paraphyses not seen. *Ascospores* 8.5–10.5 × 4.5–6 µm (av. 9.6 × 5.2 µm, n = 30), brown, broadly ellipsoid, symmetric, one septate, slightly constricted at septum; coarsely reticulate in surface view, in side view tips of

ridges protruding as low echinulations, surrounded by a delicate outer layer when immature; uniseriate, straight, oblique or transverse in the ascus. Asexual morph conidiophores simple or absent, cylindrical, smooth, hyaline. *Conidiogenous cells* solitary on aerial hyphae, cylindrical to ampulliform, straight or slightly curved, smooth, hyaline. *Conidia* irregularly chained, subglobose to globose, hemispherical, pyriform, oval, or irregular, smooth, hyaline, $4-8 \times 4.5-7 \mu\text{m}$ (av. $6.1 \times 5.7 \mu\text{m}$, $n = 30$).

Material examined – China, Guizhou Province, Guiyang City, Xiuwen County, Zhazuo Town, soil collected from the green belts of Guizhou Wildlife Park, 106.69 E, 26.85 N, 25 May 2022, Zhi-Yuan Zhang (holotype, ZY H-22.011), ex-type CGMCC 3.25498 = ZY 22.011; *ibid.* ZY 22.012 and ZY 22.013.



G = 0.270, T = 0.241; substitution rates AC = 0.94803, AG = 2.10070, AT = 1.67042, CG = 0.77655, CT = 9.62980, GT = 1.00000; gamma distribution shape parameter α = 0.279. The tree topology of ML analysis is similar to BI analysis. Bootstrap support values for MLBS $\geq$ 70% and BYPP $\geq$ 0.7 are defined as BS/PP above the nodes. Hyphens (-) represent support values less than 70% in ML and 0.7 in BI. Newly generated sequences are in blue and “T” indicates type strain.

Pleosporales Luttr. ex M.E. Barr

Amorosiaceae Thambug. & K.D. Hyde

Amorocoelophoma Jayasiri, E.B.G. Jones & K.D. Hyde

Based on the dataset combined SSU, ITS, LSU, and *EF1A* sequences, the phylogeny of *Amorocoelophoma sinensis* and its related taxa were studied. *Flabellascoma cycadicola* (CBS 143644) and *F. aquaticum* (KUMCC 15-0258) were used as the outgroup for the phylogenetic analysis. The concatenated sequences included 23 taxa and consisted of 2,914 nucleotides (SSU, 862 bp; ITS, 503 bp; LSU, 823 bp; and *EF1A*, 726 bp) with inserted gaps. The phylogenetic trees showed that genera of *Amorosiaceae* clustered into a group with a high support value (100/1, Fig. 4). The new isolates, CGMCC 3.25499, ZY 22.015, and ZY 22.016 clustered into a single clade with a high support value (100/1) and close relationships with *A. cassiae* and *A. neoregeliae* (Fig. 4). In addition, three isolates of *A. camelliae* clustered into a single clade and separated from *A. cassiae*, *A. neoregeliae*, and *A. sinensis* (Fig. 4), which is consistent with Yu et al. (2022) results. Therefore, the genus *Amorocoelophoma* should be polyphyletic.

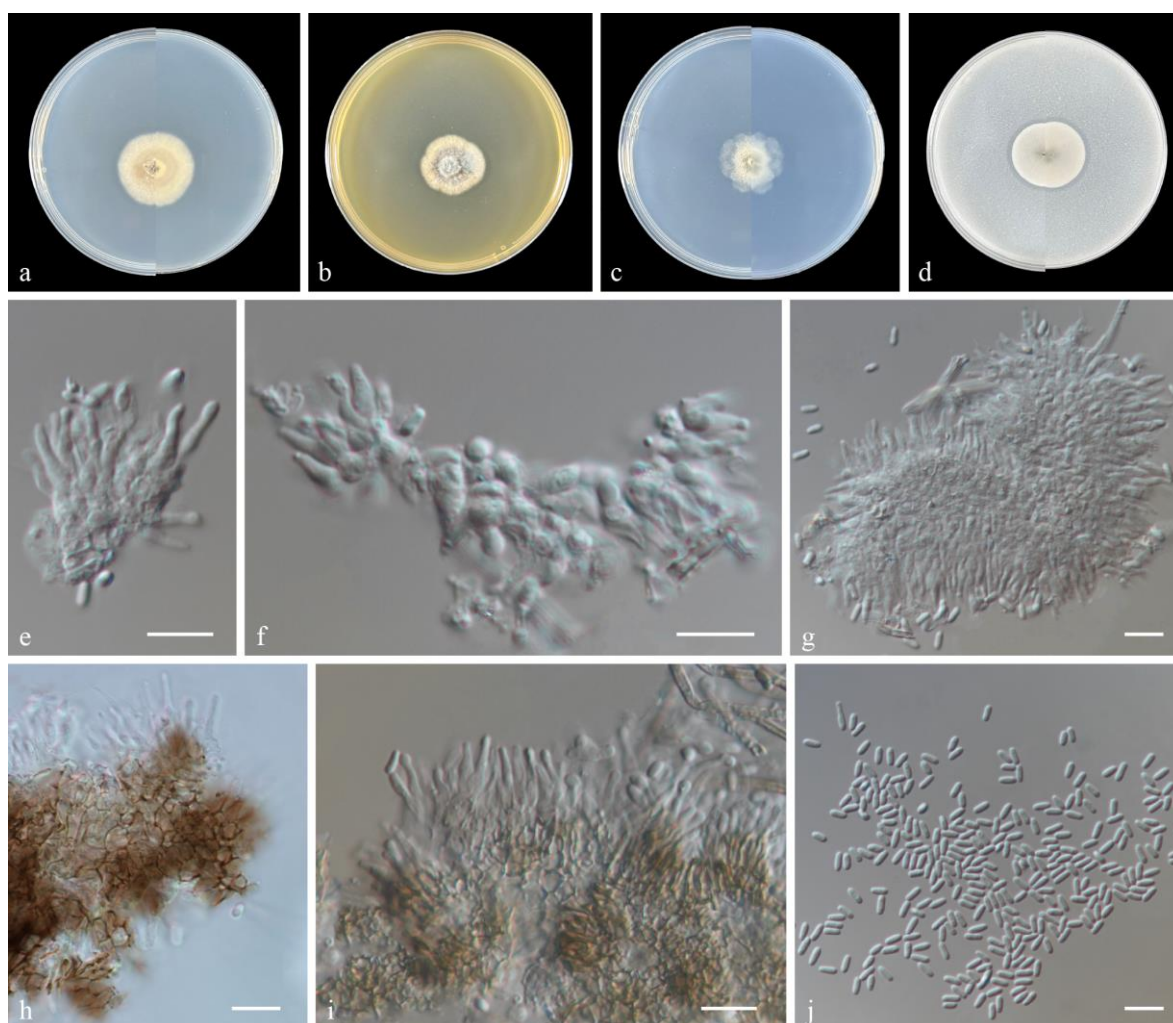


Figure 5 – *Amorocoelophoma sinensis* (CGMCC 3.25499). a–d Upper and reverse views of cultures on PDA, MEA, SNA, and OA 14 d after inoculation. e–g Conidiogenous cells and conidia. h–i Conidioma wall. j Conidia. Scale bars: e–j = 10 µm.

Amorocoelophoma sinensis Zhi Y. Zhang & Y. F. Han, sp. nov.

Fig. 5

Mycobank number: MB850365; Facesoffungi number: FoF15074

Etymology – Named after the location China, where the holotype was collected.

Holotype – ZY H-22.014

Description – *Hyphae* branched, septate, hyaline, smooth, 1–2 µm diam. Sexual morph: Not observed. Asexual morph: Coelomycetous. *Conidiomata* pycnidial, solitary to gregarious, ovoid to globose, brown, covered with hyaline to pale brown, septate, branched hyphal growth as an outer brown layer. *Conidiomata* wall, two-layered, inner hyaline textura angularis, outer layer textura angularis brown. *Conidiogenous cells* 6.5–11.5 × 1–2.5 µm (av. 9.2 × 1.7 µm, n = 30), phialidic, ampulliform, doliform, curved, hyaline, smooth. *Conidia* 3–5.5 × 1.5–2 µm (av. 4.1 × 1.9 µm, n = 30), hyaline, aseptate, cylindrical, smooth- and thin-walled.

Culture characteristics (14 d at 25 °C) – Colony on PDA 25–28 mm, flocculent, pure white, nearly round, margin regular; reverse pure white. Colony on MEA 22–24 mm, fluffy, papyrus white at the centre, pure white at the margin, margin regular; reverse pure white. Colony on SNA 20–24 mm, flocculent, petaloid, pure white, margin undulated; reverse pure white. Colony on OA 22–23 mm, fluffy, pure white, flat, compact, sectorization; reverse pure white.

Material examined – China, Guizhou Province, Guiyang City, Xiuwen County, Zhazuo Town, soil collected from the green belts of Guizhou Wildlife Park, 106.69 E, 26.85 N, 25 May 2022, Zhi-Yuan Zhang (holotype, ZY H-22.014), ex-type CGMCC 3.25499 = ZY 22.014; *ibid.* ZY 22.015. China, Guizhou Province, Guiyang City, Xiuwen County, Zhazuo Town, soil collected from the green belts of Guizhou Wildlife Park, 106.69 E, 26.85 N, 25 May 2022, Zhi-Yuan Zhang ZY 22.016.

Notes – In the phylogenetic analyses, *Amorocoelophoma sinensis* formed a distinct clade separated from *A. cassiae* and *A. neoregeliae* (Fig. 4). However, *A. sinensis* differs from *A. cassiae* in its presence of ampulliform conidiogenous cells, and smaller conidia (3–5.5 × 1.5–2 µm in *A. sinensis*; 9–11 × 2–3 µm in *A. cassiae*) (Jayasiri et al. 2019). *Amorocoelophoma sinensis* can be distinguished from *A. neoregeliae* by its solitary to gregarious conidiomata and two-layered conidiomata wall (Crous et al. 2021). In addition, they can be distinguished by their low sequence similarities. In a comparison of SSU, ITS, LSU, and *EF1A* nucleotides, *A. sinensis* (Type strain CGMCC 3.25499) has 99.6%, 95.4%, 94.5%, and 96.2% similarity, in SSU (1027/1031 bp, one gap), ITS (440/461 bp, three gaps), LSU (817/864 bp, 37 gaps), and *EF1A* (880/914 bp, no gap), which is different from *A. cassiae* (Type strain MFLUCC 17-2283). In a comparison of ITS, LSU, and *EF1A* nucleotides, *A. sinensis* (CGMCC 3.25499) has 92.9%, 94.3%, and 95.5% similarity, in ITS (344/370 bp, eight gaps), LSU (803/851 bp, 37 gaps), and *EF1A* (867/907 bp, no gap), which is different from *A. neoregeliae* (Type strain CBS 146820).

Didymosphaeriaceae Munk

Phaeodothis Syd. & P. Syd.

Based on the dataset combined SSU, ITS, and LSU sequences, the phylogeny of *Phaeodothis sinensis* and its related taxa were studied. *Tremateia arundicola* (MFLU 16-1275) and *T. guiyangensis* (GZAAS01) were used as the outgroup for the phylogenetic analysis. The concatenated sequences included 41 taxa and consisted of 2,233 nucleotides (SSU, 940 bp; ITS, 465 bp; and LSU, 828 bp) with inserted gaps. The phylogenetic trees showed that genera of *Didymosphaeriaceae* are clustered into a group with a high support value (100/1). Additionally, our two new isolates, CGMCC 3.25500 and ZY 22.018 clustered into a single clade with a high support value (99/0.99) and close relationship with *P. winteri* (Fig. 6).

Phaeodothis sinensis Zhi Y. Zhang & Y. F. Han, sp. nov.

Fig. 7

Mycobank number: MB850366; Facesoffungi number: FoF15075

Etymology – Named after the location China, where the holotype was collected.

Holotype – ZY H-22.017

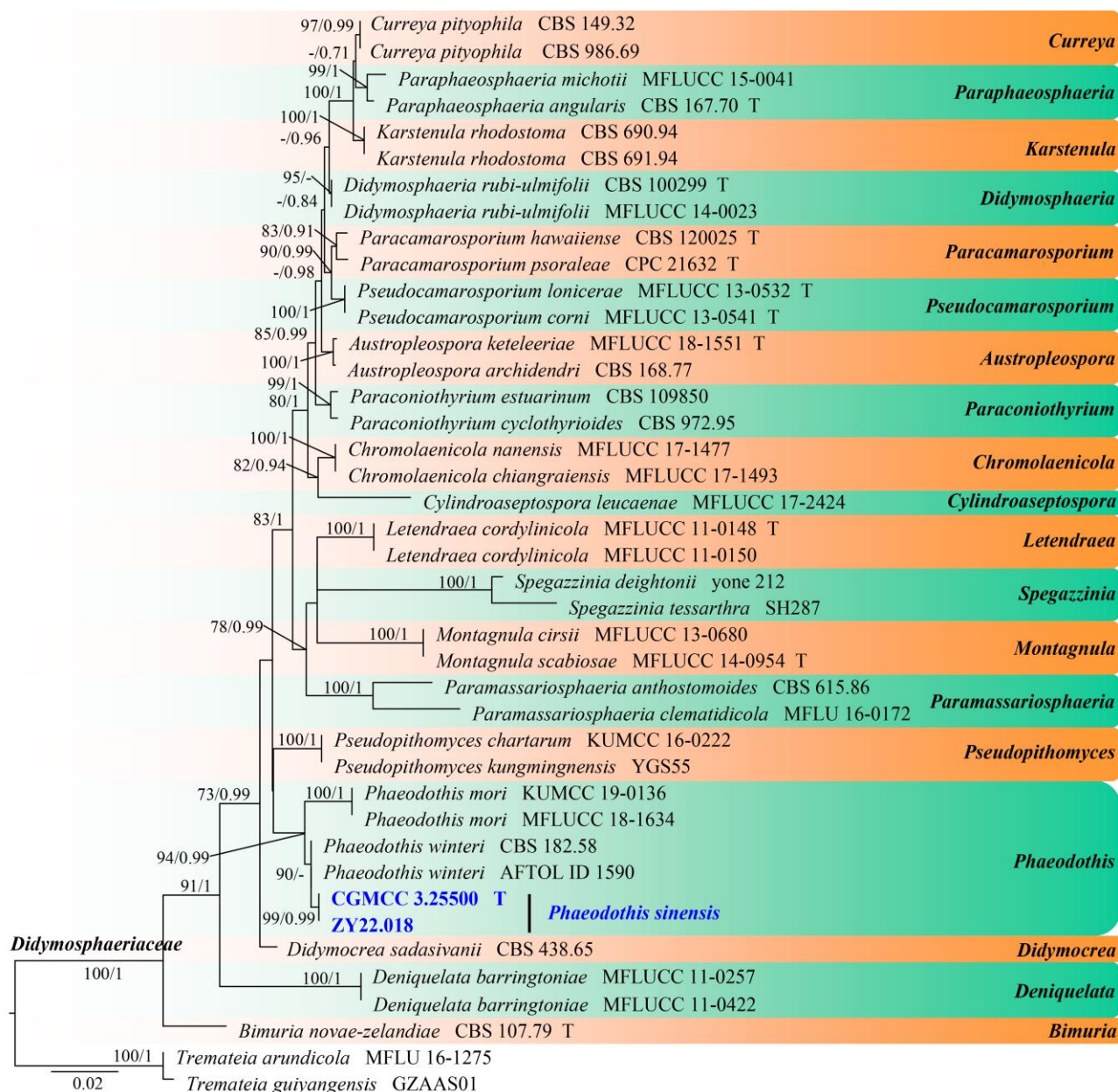


Figure 6 – Phylogram generated from maximum likelihood analysis based on combined SSU, ITS, and LSU sequence data. Estimated base frequencies were as follows; A = 0.245, C = 0.228, G = 0.278, T = 0.249; substitution rates AC = 1.77319, AG = 2.22177, AT = 1.61533, CG = 1.02611, CT = 7.49524, GT = 1.00000; gamma distribution shape parameter α = 0.254. The tree topology of ML analysis is similar to BI analysis. Bootstrap support values for MLBS $\geq$ 70% and BYPP $\geq$ 0.7 are defined as BS/PP above the nodes. Hyphens (-) represent support values less than 70% in ML and 0.7 in BI. Newly generated sequences are in blue and “T” indicates type strain.

Description – *Hyphae* branched, septate, hyaline, smooth, 1–2.5 μ m diam. Sexual morph: *Ascomata* dark brown to black, subglobose to globose. *Peridium* composing several layers of irregular cells arranged in a textura angularis, cells towards the inside hyaline, at the outside, light brown, thick-walled, somewhat flattened. *Asci* 45.5–52 $\times$ 6–8.5 μ m (av. 49.1 $\times$ 6.9 μ m, n = 30), 8-spored, bitunicate, cylindrical to cylindric-clavate, short pedicellate with furcate to obtusely ends, apically rounded with an indistinct ocular chamber. *Ascospores* 8.5–14 $\times$ 3–4 μ m (av. 11.8 $\times$ 3.5 μ m, n = 30), overlapping biseriate, yellowish brown, subfusoid, septate at the centre, strongly constricted at the septum, straight or slightly curved, enlarged near the septum at the upper cell, non-surrounded by the thin mucilaginous sheath, smooth-walled. Asexual morph: Not observed.

Culture characteristics (14 d at 25 °C) – Colony on PDA 56–59 mm, flocculent, exudates hyaline, pure white, margin slightly undulated; reverse pure white. Colony on MEA 51–54 mm, fluffy, flat, pure white, margin slightly undulated; reverse rape yellow. Colony on SNA 37–44 mm, flocculent, white, aerial mycelium sparse, zonate with different sectors, margin serrated; reverse white. Colony on OA 61–64 mm, fluffy to velvety, pure white, flat, margin slightly undulated; reverse pure white.

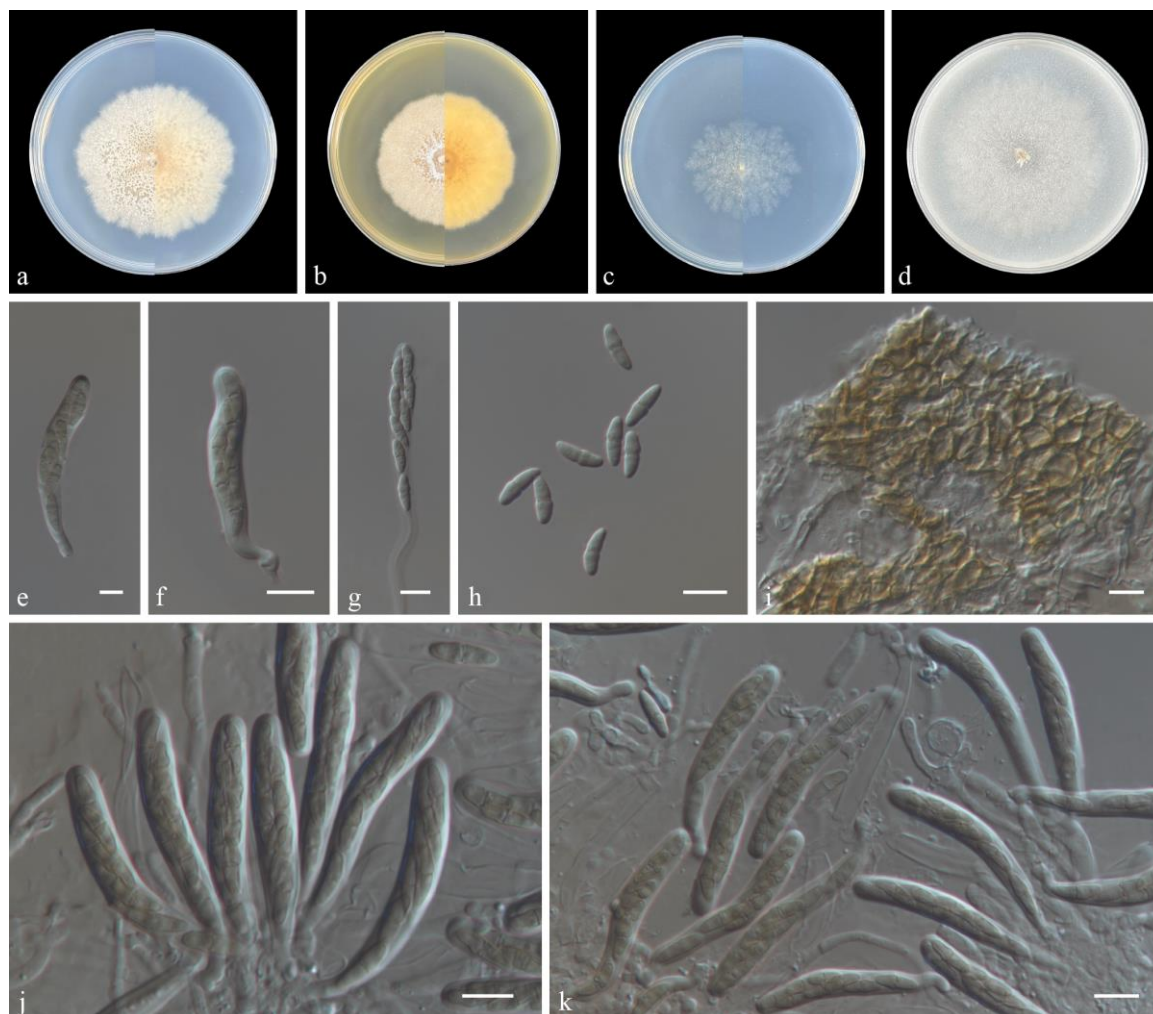


Figure 7 – *Phaeodothis sinensis* (CGMCC 3.25500). a–d Upper and reverse views of cultures on PDA, MEA, SNA, and OA 14 d after inoculation. e–g, j–k Asci. h Ascospores. i Ascoma wall. Scale bars: e–k = 10 µm.

Material examined – China, Guizhou Province, Guiyang City, Xiuwen County, Zhazuo Town, soil collected from the green belts of Guizhou Wildlife Park, 106.69 E, 26.85 N, 25 May 2022, Zhi-Yuan Zhang (holotype, ZY H-22.017), ex-type CGMCC 3.25500 = ZY 22.017; *ibid.* ZY 22.018.

Notes – According to the multi-locus phylogenetic analyses, *Phaeodothis sinensis* formed a single clade nested in the genus *Phaeodothis* and is closely related to *P. winteri* (a synonym of *Didymosphaeria winteri*) (Fig. 6). However, our novel species, *P. sinensis* can be distinguished from *P. winteri* in having small asci (45.5–52 × 6–8.5 µm), whereas *P. winteri* has larger asci (60–80 × 10–12 µm) (Niessl 1875). Furthermore, the GenBank database (March 2024) contains only 12 records of *P. winteri*. Within these records, certain strains are represented by only one sequences, whereas the strains selected for phylogenetic analysis, CBS 182.58 and AFTOL ID 1590, possess both SSU and LSU sequences. It is worth noting that CBS 162.31 is characterized by an ITS sequence exclusively. Despite the high similarity of *P. sinensis* (Type strain CGMCC 3.25500) to

the SSU and LSU sequences of CBS 182.58 and AFTOL ID 1590, the resemblance to the ITS sequence of CBS 162.31 (MH855163) is considerably lower (84.3% similarity, 78 bp difference with 20 gaps).

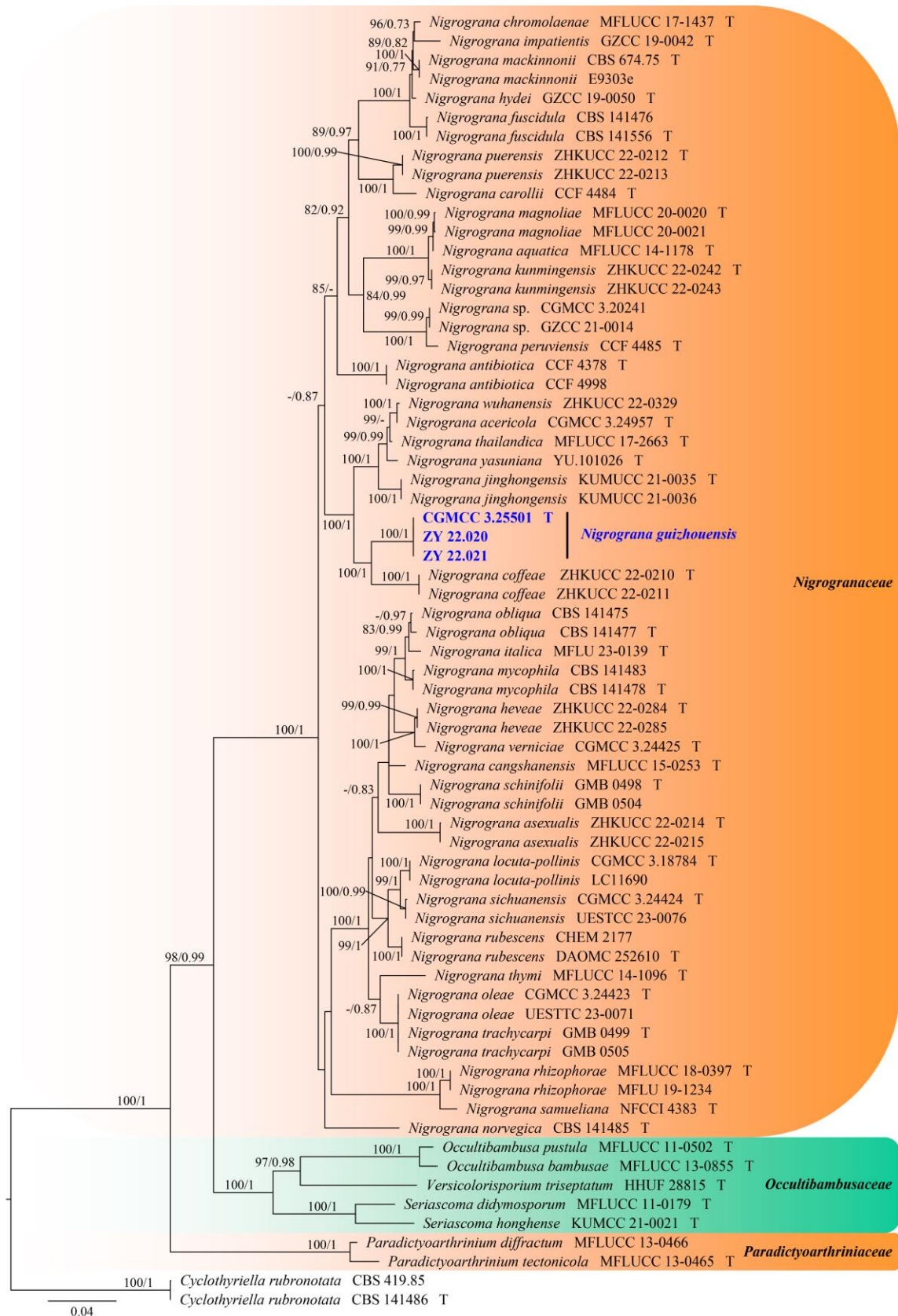


Figure 8 – Phylogram generated from maximum likelihood analysis based on combined SSU, ITS, LSU, *RPB2*, and *EF1A* sequence data. Estimated base frequencies were as follows; A = 0.247, C =

0.247, G = 0.268, T = 0.238; substitution rates AC = 1.52552, AG = 4.01441, AT = 1.55613, CG = 0.93046, CT = 10.14103, GT = 1.00000; gamma distribution shape parameter α = 0.349. The tree topology of ML analysis is similar to BI analysis. Bootstrap support values for MLBS $\geq$ 70% and BYPP $\geq$ 0.7 are defined as BS/PP above the nodes. Hyphens (-) represent support values less than 70% in ML and 0.7 in BI. Newly generated sequences are in blue and “T” indicates type strain.

***Nigrogranaceae* Jaklitsch & Voglmayr**

***Nigrograna* Gruyter, Verkley & Crous**

Based on the dataset combined SSU, ITS, LSU, *RPB2*, and *EF1A* sequences, the phylogeny of *Nigrograna sinensis* and its related taxa were studied. Two strains, CBS 419.85 and CBS 141486 of *Cyclothyriella rubronotata* were used as the outgroup for the phylogenetic analysis. The concatenated sequences included 68 taxa and consisted of 3,734 nucleotides (SSU, 984 bp; ITS, 462 bp; LSU, 829 bp; *RPB2*, 755 bp; and *EF1A*, 704 bp) with inserted gaps. The phylogenetic trees showed that members of the family *Nigrogranaceae* are clustered into a group with a high support value (100/1). Additionally, our three new isolates, CGMCC 3.25501, ZY 22.020, and ZY22.021 clustered into a single clade with a high support value (100/1) and close relationship with *N. coffeae* (Fig. 8).

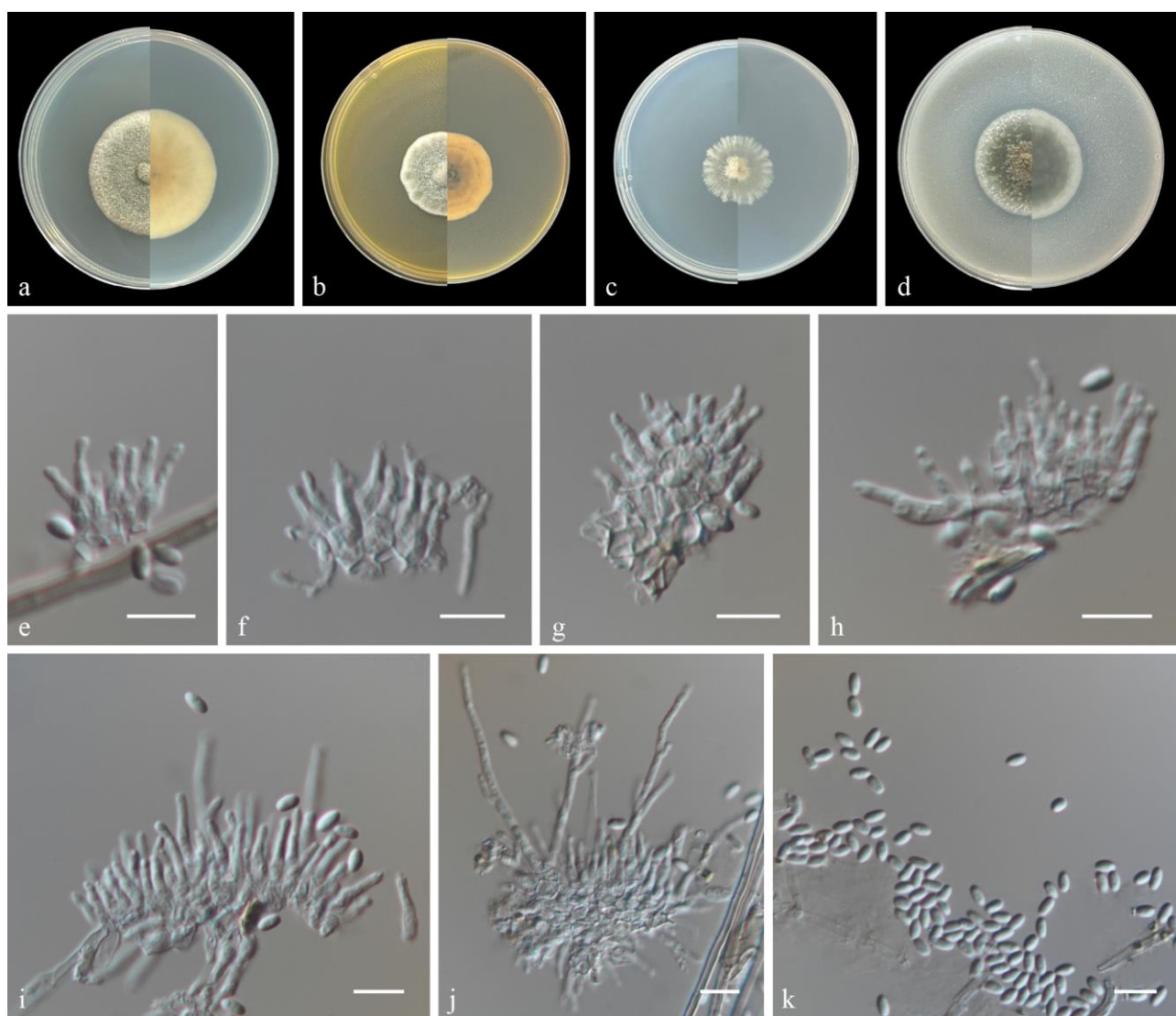


Figure 9 – *Nigrograna guizhouensis* (CGMCC 3.25501). a–d Upper and reverse views of cultures on PDA, MEA, SNA, and OA 14 d after inoculation. e–j Conidiogenous cells and conidia. k Conidia. Scale bars: e–k = 10 μ m.

Nigrograna guizhouensis Zhi Y. Zhang, Heng Pan & Y. F. Han, sp. nov.

Fig. 9

Mycobank number: MB850367; Facesoffungi number: FoF15076

Etymology – Named after the location Guizhou, where the holotype was collected.

Holotype – ZY H-22.019

Description – *Hyphae* branched, septate, hyaline, smooth, 1–2 µm diam. Sexual morph: Not observed. Asexual morph: Coelomycetous. *Pycnidia* globose to subglobose, or pyriform, solitary, unilocular, dark brown. *Pycnidial wall* brown, the wall with pseudoparenchymatous cells. *Conidiophores* absent, or simple. *Phialides* 9–15 × 2–3.5 µm (av. 12.9 × 2.7 µm, n = 30), subcylindrical to cylindrical, ampulliform, lageniform, straight or slightly curved. *Conidia* 3.5–6 × 2–3 µm (av. 4.7 × 2.6 µm, n = 30), subcylindrical to cylindrical, ellipsoidal, unicellular, aseptate, granules absent, hyalin, smooth-walled.

Culture characteristics (14 d at 25 °C) – Colony on PDA 42–43 mm, flocculent to fluffy, papyrus white to white from centre to margin, nearly round, margin regular; reverse grey white. Colony on MEA 30–33 mm, fluffy, papyrus white to white from centre to the margin; reverse light ivory. Colony on SNA 24–25 mm, flocculent, white, margin undulated; reverse white. Colony on OA 35–36 mm, aerial mycelium dense, flocculent, reed green to white from centre to margin, margin regular; reverse reed green to white from centre to margin.

Material examined – China, Guizhou Province, Guiyang City, Xiuwen County, Zhazuo Town, soil collected from the green belts of Guizhou Wildlife Park, 106.69 E, 26.85 N, 25 May 2022, Zhi-Yuan Zhang (holotype, ZY H-22.019), ex-type CGMCC 3.25501 = ZY 22.019; *ibid.* ZY 22.020. China, Guizhou Province, Guiyang City, Xiuwen County, Zhazuo Town, soil collected from the green belts of Guizhou Wildlife Park, 106.69 E, 26.85 N, 25 May 2022, Zhi-Yuan Zhang ZY 22.021.

Notes – In the phylogenetic analyses, *Nigrograna guizhouensis* formed a distinct clade and close relationship with *N. coffeae* (Fig. 8). However, *N. guizhouensis* produces an asexual morph, which is not observed in *N. coffeae* (Lu et al. 2022). Additionally, they can be distinguished by their low sequence similarity (75% similarity, 337 gaps in 1338 base pairs (bp) of SSU; 96% similarity, 21 bp differences in 503 bp of ITS; 98% similarity, 16 bp differences in 855 bp of LSU; 89% similarity, 100 bp differences in 899 bp of *RPB2*; 96% similarity, 35 bp differences in 954 bp of *EF1A*).

Venturiales Y. Zhang ter, C.L. Schoch & K.D. Hyde

Sympoventuriaceae Y. Zhang ter, C.L. Schoch & K.D. Hyde

Scolecobasidium E.V. Abbott

Based on the dataset combined SSU, ITS, LSU, *TUB*, and *EF1A* sequences, the phylogeny of *Scolecobasidium* was studied. *Pseudosigmoidea excentrica* (CBS 469.59) and *Sympoventuria capensis* (CBS 120136) were used as the outgroup for the phylogenetic analysis. The concatenated sequences included 78 taxa and consisted of 3,600 nucleotides (SSU, 973 bp; ITS, 814 bp; LSU, 830 bp; *TUB*, 412 bp; and *EF1A*, 571 bp) with inserted gaps. The phylogenetic trees showed that members of *Scolecobasidium* are clustered into a group with a high support value (100/1). Additionally, our three new isolates (CGMCC 3.25502, ZY 22.023, and ZY 22.024) of *S. guizhouense* clustered into a single clade with a high support value (100/1) and closely related to *S. terrestre* and *S. constrictum* (Fig. 10). Two new isolates (CGMCC 3.25503 and ZY 22.026) of *S. parahumicola* clustered into a single clade with a high support value (100/1) and closely related to *S. humicola* and *S. podocarp*i (Fig. 10), and four new isolates (CGMCC 3.25504, ZY 22.028, ZY 22.029, and ZY 22.030) of *S. inverellipsoidisporum* clustered into a single clade with a high support value (100/1) and closely related to *S. echinulatum* (Fig. 10). In addition, the new isolates CGMCC 3.25506 and CGMCC 3.25505 were belongs to *S. tshawytschae* and *S. longiphorum*, respectively (Fig. 10).

Scolecobasidium guizhouense Zhi Y. Zhang & Y. F. Han, sp. nov.

Fig. 11

Mycobank number: MB850368; Facesoffungi number: FoF15077

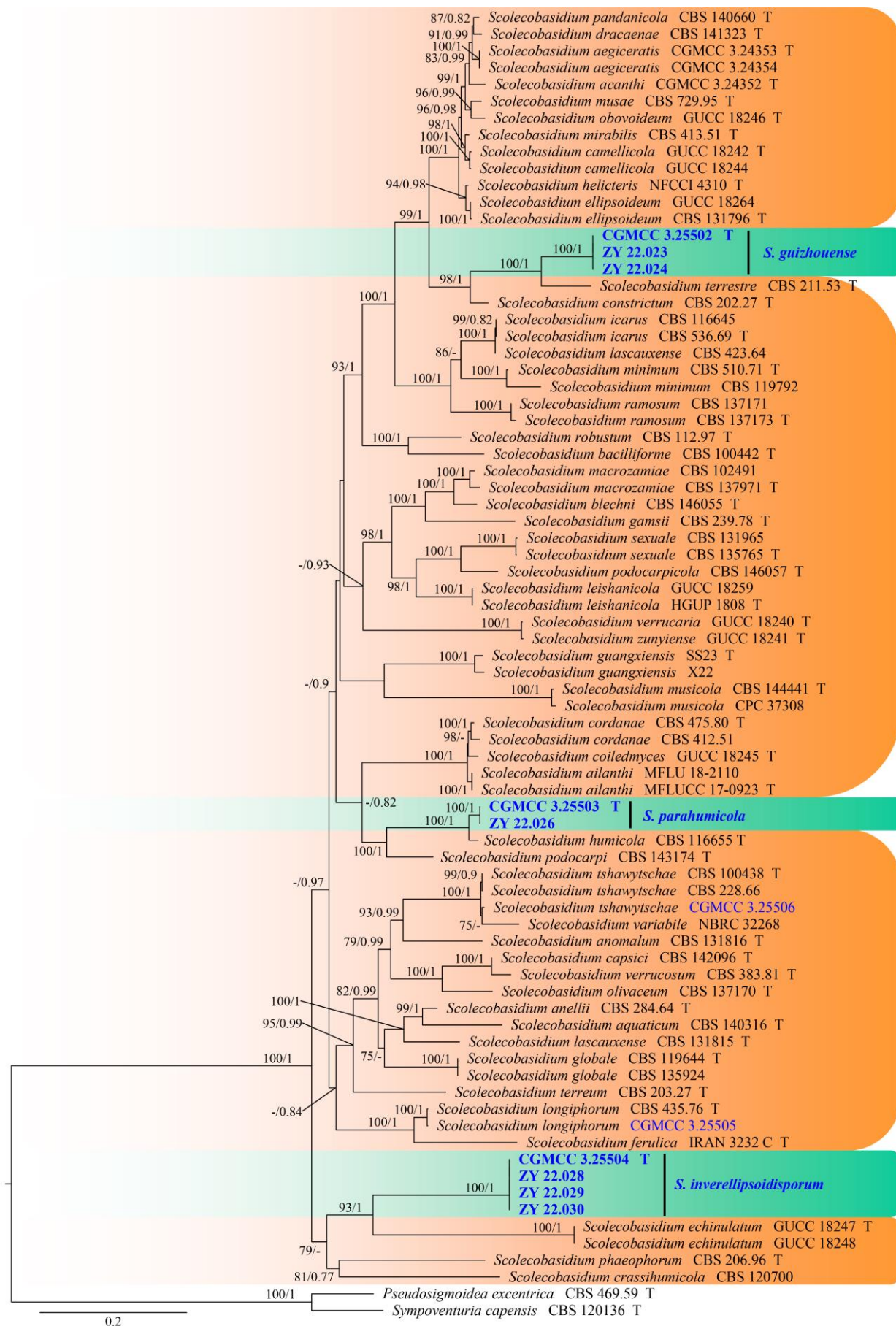


Figure 10 – Phylogram generated from maximum likelihood analysis based on combined SSU, ITS, LSU, *TUB*, and *EF1A* sequence data. Estimated base frequencies were as follows; A = 0.241, C =

0.242, G = 0.292, T = 0.226; substitution rates AC = 0.95877, AG = 1.89661, AT = 0.92859, CG = 0.89348, CT = 3.51585, GT = 1.00000; gamma distribution shape parameter α = 0.443. The tree topology of ML analysis is similar to BI analysis. Bootstrap support values for MLBS $\geq$ 70% and BYPP $\geq$ 0.7 are defined as BS/PP above the nodes. Hyphens (-) represent support values less than 70% in ML and 0.7 in BI. Newly generated sequences are in blue and “T” indicates type strain.



Figure 11 – *Scolecobasidium guizhouense* (CGMCC 3.25502). a–d Upper and reverse views of cultures on PDA, MEA, SNA, and OA 14 d after inoculation. e–i Conidiophores and conidiogenous cells bearing conidia. j–l Hyphal coil and conidiogenous cells bearing conidia. Scale bars: e–l = 10 μ m.

Etymology – Named after the location Guizhou, where the holotype was collected.

Holotype – ZY H-22.022

Description – *Hyphae* branched, septate, hyaline to pale brown, smooth-walled, 0.5–2 μ m diam. Sexual morph: Not observed. Asexual morph: *Conidiophores* subcylindrical to cylindrical, arising from the aerial hyphae or hyphal ropes, continuous or septate, usually reduced to conidiogenous cells. *Conidiogenous cells* 0–2-septate, solitary, hyaline to pale brown, smooth, clavate, sometimes subcylindrical, straight to geniculous-sinuous, with single or several sympodial apical loci with rhexolytic conidiogenesis, 3.5–13 $\times$ 2–3 μ m (av. 6.8 $\times$ 2.3 μ m, n = 30). *Conidia* echinulate to verruculose, subhyaline to pale brown, cylindrical, sometimes ellipsoidal, usually constricted at the septum, ends obtusely rounded, 7.5–11 $\times$ 2–3 μ m (av. 9.2 $\times$ 2.6 μ m, n = 30).

Culture characteristics (14 d at 25 °C) – Colony on PDA 18–19 mm, flocculent, broom yellow, flat; reverse brown beige. Colony on MEA 17–18 mm, flocculent, light ivory, nearly round,

margin regular; reverse ochre brown. Colony on SNA 13–15 mm, flocculent, aerial mycelium sparse, light ivory; reverse light ivory. Colony on OA 22–23 mm, compact, flat, flocculent, green brown; reverse quartz grey.

Material examined – China, Guizhou Province, Guiyang City, Xiuwen County, Zhazuo Town, soil collected from the green belts of Guizhou Wildlife Park, 106.69 E, 26.85 N, 25 May 2022, Zhi-Yuan Zhang (holotype, ZY H-22.022), ex-type CGMCC 3.25502 = ZY 22.022; *ibid.* ZY 22.023. China, Guizhou Province, Guiyang City, Xiuwen County, Zhazuo Town, soil collected from the green belts of Guizhou Wildlife Park, 106.69 E, 26.85 N, 25 May 2022, Zhi-Yuan Zhang ZY 22.024.

Notes – In the phylogenetic analyses, *Scolecobasidium guizhouensis* formed a distinct clade and separated from *S. terrestre* and *S. constrictum* (Fig. 10). Although *S. guizhouensis* has a similar morphology to *S. terrestre* and *S. constrictum*. Still, the conidia sizes and shapes of *S. guizhouensis* are significantly different. *Scolecobasidium guizhouensis* differs from *S. terrestre* by echinulate to verruculose conidia and the number of septa (0–3 vs. 0–1) in the conidia (Song et al. 2023). Additionally, *S. guizhouensis* differs from *S. constrictum* in the shape of its conidia (cylindrical vs. broadly ellipsoidal to cylindrical) (Song et al. 2023, Wei et al. 2022). In addition, they can be distinguished by their low sequence similarities. In a comparison of SSU, ITS, LSU, *TUB*, and *EF1A* nucleotides, *S. guizhouensis* (Type strain CGMCC 3.25502) has 100%, 71.7%, 99.1%, 76.5%, and 87.8% similarity, in SSU (955/955 bp, one gap), ITS (554/772 bp, 123 gaps), LSU (789/796 bp, three gaps), *TUB* (363/474 bp, 14 gaps), and *EF1A* (324/369 bp, no gap), which is different from *S. terrestre* (Type strain CBS 211.53). In a comparison of SSU, ITS, LSU, *TUB*, and *EF1A* nucleotides, *S. guizhouensis* (CGMCC 3.25502) has 100%, 73.8%, 99%, 77.7%, and 68.6% similarity, in SSU (955/955 bp, one gap), ITS (530/718 bp, 114 gaps), LSU (863/871 bp, no gap), *TUB* (367/472 bp, 14 gaps), and *EF1A* (261/380 bp, 50 gaps), which is different from *S. constrictum* (Type strain CBS 202.27).

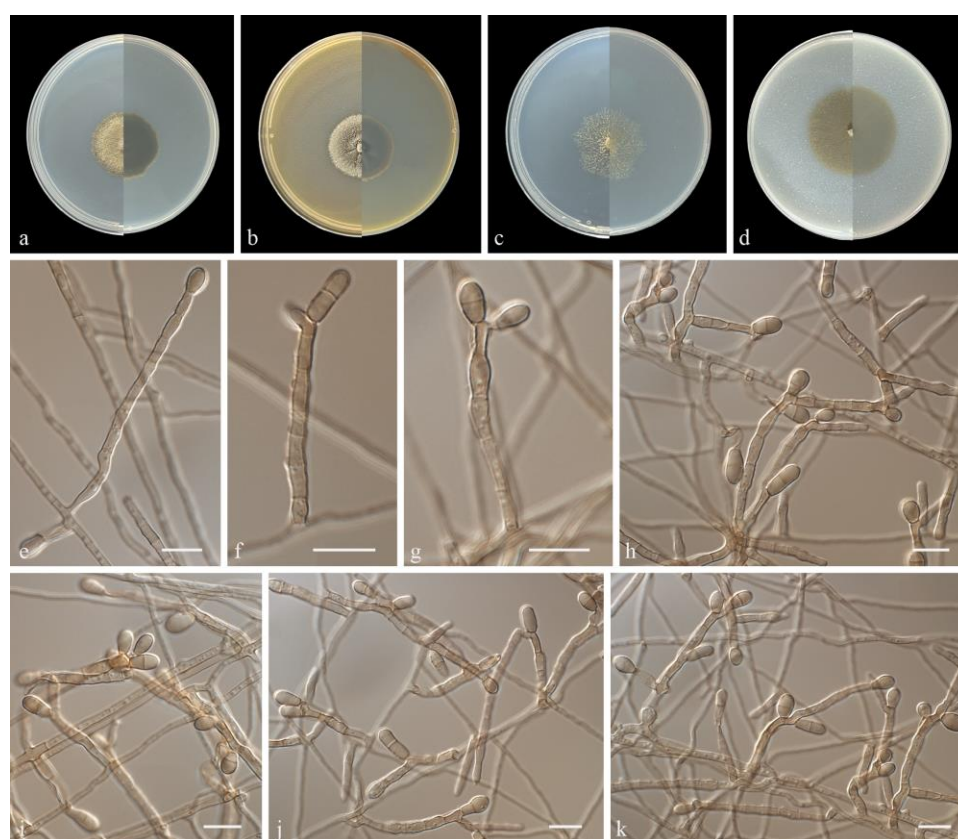


Figure 12 – *Scolecobasidium parahumicola* (CGMCC 3.25503). a–d Upper and reverse views of cultures on PDA, MEA, SNA, and OA 14 d after inoculation. e–k Conidiophores, conidiogenous cells and conidia. Scale bars: e–k = 10 μ m.

Scolecobasidium parahumicola Zhi Y. Zhang & Y. F. Han, sp. nov.

Fig. 12

Mycobank number: MB850369; Facesoffungi number: FoF15078

Etymology – Based on its close phylogenetic relationship to *Scolecobasidium humicola*.

Holotype – ZY H-22.025

Description – *Hyphae* branched, septate, hyaline to pale brown, 1–2 μm diam. Sexual morph: Not observed. Asexual morph: *Conidiophores* 0–7-septate, branched, straight to irregularly curved, subcylindrical to cylindrical, hyaline to pale brown, arising from the aerial hyphae. *Conidiogenous cells* polyblastic, sympodial, terminal or intercalary, subhyaline to brown, smooth, subcylindrical to cylindrical, straight or curved, $3.5\text{--}10.5 \times 1.5\text{--}3.5 \mu\text{m}$ (av. $6.9 \times 2.2 \mu\text{m}$, $n = 30$), with 1–2 terminal or lateral conidia. *Conidia* 0–1-septate, smooth-walled, subhyaline to pale brown, cylindrical with rounded ends, pyriform, rarely ellipsoidal, $4\text{--}11.5 \times 3\text{--}4 \mu\text{m}$ (av. $7.2 \times 3.58 \mu\text{m}$, $n = 30$).

Culture characteristics (14 d at 25 °C) – Colony on PDA 29–31 mm, flocculent, yellow-brown, flat; reverse green grey. Colony on MEA 27–28 mm, flocculent to felty, reed green to grey white from centre to margin, nearly round; reverse dusty grey. Colony on SNA 30–34 mm, flat, grey white, aerial mycelia sparse; reverse grey white. Colony on OA 35–36 mm, flat, felty, beige grey; reverse beige grey.

Material examined – China, Guizhou Province, Guiyang City, Xiuwen County, Zhazuo Town, soil collected from the green belts of Guizhou Wildlife Park, 106.69 E, 26.85 N, 25 May 2022, Zhi-Yuan Zhang (holotype, ZY H-22.025), ex-type CGMCC 3.25503 = ZY 22.025; *ibid.* ZY 22.026.

Notes – In the phylogenetic analyses, *Scolecobasidium parahumicola* formed a distinct clade separated from *S. humicola* and *S. podocarpi* (Fig. 10). Although *Scolecobasidium parahumicola* has similar morphological characteristics to *S. humicola* and *S. podocarpi*, conidiophores and conidia shapes of *S. parahumicola* are significantly different (Barron & Bush 1962, Crous et al. 2017). *Scolecobasidium parahumicola* differs from *S. humicola* in its conidia shape (cylindrical, pyriform, smooth-walled vs. ovoid to short cylindric, finely echinulate) (Barron & Bush 1962). *Scolecobasidium parahumicola* differs from *S. podocarpi* by the conidiophores (0–7-septate, branched, straight to irregularly curved vs. 1-septate, erect, unbranched), and conidia (cylindrical, pyriform, smooth-walled vs. fusoidellipsoid to subcylindrical, verruculose) (Crous et al. 2017). In addition, they can be distinguished by their low sequence similarities. In a comparison of SSU, ITS, LSU, *TUB*, and *EF1A* nucleotides, *S. parahumicola* (Type strain CGMCC 3.25503) has 99.8%, 95.4%, 99.1%, 95.3% and 93.1% similarity, in SSU (942/943 bp, one gap), ITS (626/656 bp, 7 gaps), LSU (773/780 bp, no gap), *TUB* (413/433 bp, no gap), and *EF1A* (352/378 bp, six gaps), which is different from *S. humicola* (Type strain CBS 116655). In a comparison of ITS and LSU nucleotides, *S. guizhouensis* (CGMCC 3.25502) has 76.6% and 96.8% similarity, in ITS (579/755 bp, 65 gaps) and LSU (810/836 bp, 114 gaps), which is different from *S. podocarpi* (Type strain CBS 143174).

Scolecobasidium inverellipsoidisporum Zhi Y. Zhang & Y. F. Han, sp. nov.

Fig. 13

Mycobank number: MB850371; Facesoffungi number: FoF15079

Etymology – Referring to its inverted ellipsoidal conidia.

Holotype – ZY H-22.027

Description – *Hyphae* branched, septate, hyaline to pale brown, 0.5–2.5 μm diam. Sexual morph: Not observed. Asexual morph: *Conidiophores* simple, solitary, erect, smooth, subcylindrical to cylindrical, often reduced to conidiogenous cells. *Conidiogenous cells* integrated, terminal, polyblastic, sympodial, cylindrical tapering towards the apex, sometimes apical 1–3 branches, continued growth or sporulation, subhyaline to pale brown, $9\text{--}26.5 \times 1.5\text{--}2.5 \mu\text{m}$ (av. $13.7 \times 2 \mu\text{m}$, $n = 30$). *Conidia* solitary, inverted ellipsoidal, rarely cylindrical, constricted at the septum, the upper cells slightly wider than the lower ones, subhyaline to pale brown, 0–1-septate, smooth or somewhat verrucose, constricted at the septum, $6.5\text{--}17 \times 3\text{--}5.5 \mu\text{m}$ (av. $9.9 \times 4.1 \mu\text{m}$, $n = 30$).

Culture characteristics (14 d at 25 °C) – Colony on PDA 14–16 mm, flocculent to fluffy, dark ivory; reverse reed green. Colony on MEA 9–10 mm, raised, flocculent, olive grey; reverse granite grey. Colony on SNA 13–15 mm, flat, flocculent, olive grey, aerial mycelia sparse; reverse beige grey. Colony on OA 13–15 mm, flat, flocculent, beige grey, reverse green grey.

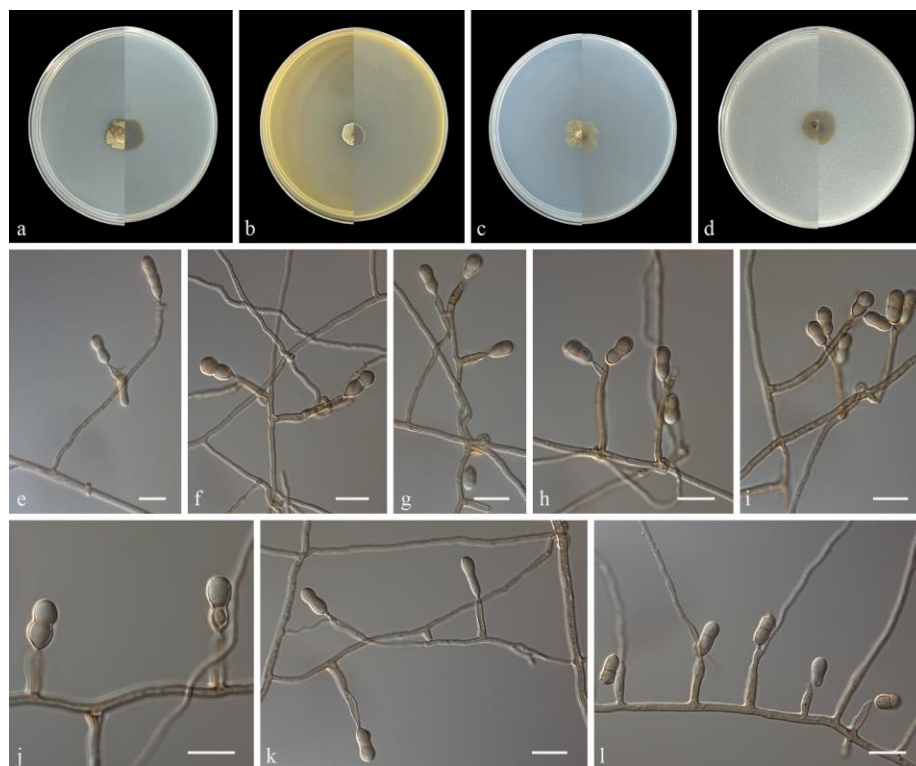


Figure 13 – *Scolecobasidium inverellipsoidisporum* (CGMCC 3.25504). a–d Upper and reverse views of cultures on PDA, MEA, SNA, and OA 14 d after inoculation. e–l Conidiophores, conidiogenous cells and conidia. Scale bars: e–l = 10 μ m.

Material examined – China, Guizhou Province, Guiyang City, Xiuwen County, Zhazuo Town, soil collected from the green belts of Guizhou Wildlife Park, 106.69 E, 26.85 N, 25 May 2022, Zhi-Yuan Zhang (holotype, ZY H-22.027), ex-type CGMCC 3.25504 = ZY 22.027; *ibid.* ZY 22.028. China, Guizhou Province, Guiyang City, Xiuwen County, Zhazuo Town, soil collected from the green belts of Guizhou Wildlife Park, 106.69 E, 26.85 N, 25 May 2022, Zhi-Yuan Zhang ZY 22.029; *ibid.* ZY 22.030.

Notes – In the phylogenetic analyses, *Scolecobasidium inverellipsoidisporum* formed a distinct clade separated from *S. echinulatum* (Fig. 10). However, the conidiophores and conidia of *S. inverellipsoidisporum* are significantly different. Conidiophores are simple in *S. inverellipsoidisporum*, which is differentiated in *S. echinulatum*, and conidia inverted ellipsoidal in *S. inverellipsoidisporum*, which is ellipsoidal to cylindrical in *S. echinulatum* (Wei et al. 2022). In addition, they can be distinguished by their low sequence similarities. In a comparison of SSU, ITS, LSU, *TUB*, and *EF1A* nucleotides, *S. inverellipsoidisporum* (Type strain CGMCC 3.25504) has 93.3%, 74.3%, 90.5%, 70.7% and 62.3% similarity, in SSU (942/1,009 bp, three gaps), ITS (545/733 bp, 65 gaps), LSU (780/861 bp, nine gaps), *TUB* (317/448 bp, 30 gaps), and *EF1A* (255/409 bp, 78 gaps), which is different from *S. echinulatum* (Type strain GUCC 18247).

Scolecobasidium longiphorum Matsush., *Icones Microfungorum a Matsushima lectorum*, Kobe, p. 127, 1975. Fig. 14

Description – *Hyphae* branched, septate, subhyaline to pale brown, 1–2.5 μ m diam. Sexual morph: Not observed. Asexual morph: *Conidiophores* arising from aerial hyphae, brown, solitary, branched, simple, 1–2-septate, straight or curved. *Conidiogenous cells* integrated, terminal, lateral,

polyblastic, subcylindrical to cylindrical, straight or slightly curved, subhyaline to pale brown, $11.5\text{--}31.5 \times 2.5\text{--}4.5 \mu\text{m}$ (av. $18.2 \times 3.2 \mu\text{m}$, $n = 30$). *Conidia* subcylindrical to cylindrical, rounded at both ends, 1–3-septate, not or slightly constricted at the septum, smooth or verruculose, $12.5\text{--}24 \times 5.5\text{--}9 \mu\text{m}$ (av. $18.3 \times 7.5 \mu\text{m}$, $n = 30$), crowded, pale brown.

Culture characteristics (14 d at 25 °C) – Colony on PDA 14–15 mm, flocculent to fluffy, light Ivory; reverse brown beige. Colony on MEA 6–8 mm, raised, flocculent, pure white; reverse clay brown. Colony on SNA 10–12 mm, flat, flocculent, powdery, light Ivory, aerial mycelia sparse; reverse grey beige. Colony on OA 12–13 mm, flat, flocculent, felty, sand yellow; reverse curry.

Material examined – China, Guizhou Province, Guiyang City, Xiuwen County, Zhazuo Town, soil collected from the green belts of Guizhou Wildlife Park, 106.69 E, 26.85 N, 25 May 2022, Zhi-Yuan Zhang ZY 22.032 = CGMCC 3.25505.



Figure 14 – *Scolecobasidium longiphorum* (CGMCC 3.25505). a–d Upper and reverse views of cultures on PDA, MEA, SNA, and OA 14 d after inoculation. e–m Conidiophores, conidiogenous cells and conidia. Scale bars: e–m = 10 μm .

Notes – *Scolecobasidium longiphorum* was introduced by Matsushima (1975). In this study, one newly collected isolate clustered with *S. longiphorum* was fully phylogenetically supported (Fig. 10). The comparison of the morphological characteristics of the two strains found them to be similar (Matsushima 1975, Samerpitak et al. 2014). Notably, the ex-type culture (CBS 435.76) of *S. longiphorum* had the following nucleotide similarities with the sequences of our newly collected strain (ZY 22.032). On SSU, ITS, LSU, *TUB*, and *EF1A*, respectively: 949/949 (100%, no gap), 613/615 (99.6%, no gap), 776/776 (100%, no gap), 450/450 (100%, no gap), and 318/321 (99%,

including one gap). Therefore, we identified our isolate as *S. longiphorum* and illustrated it, representing a new record from China.

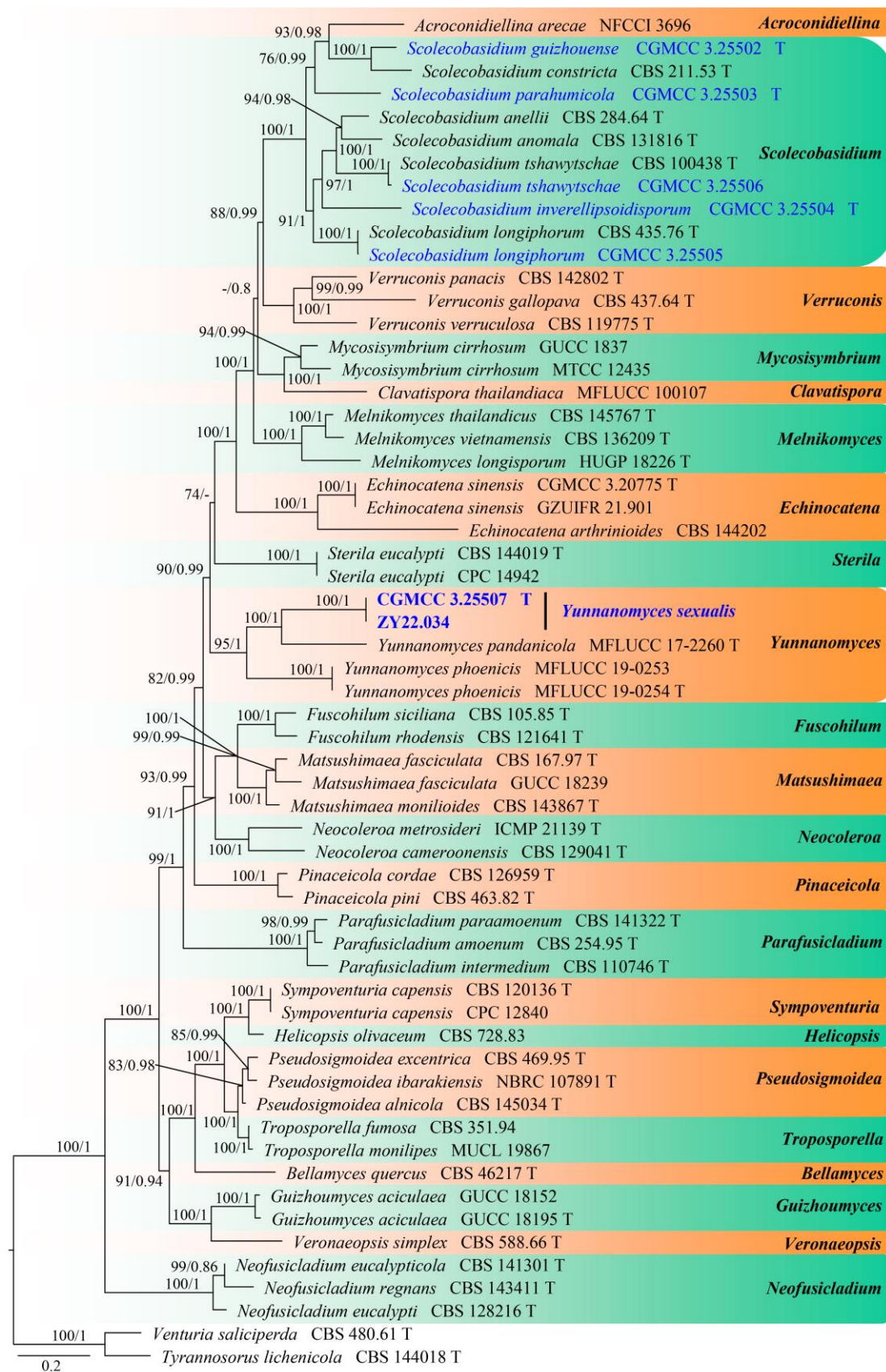


Figure 15 – Phylogram generated from maximum likelihood analysis based on combined ITS, LSU, EF1A, TUB, and RPB2 sequence data. Estimated base frequencies were as follows; A = 0.241,

C = 0.254, G = 0.289, T = 0.216; substitution rates AC = 1.44873, AG = 2.75029, AT = 1.48756, CG = 1.12302, CT = 5.67486, GT = 1.00000; gamma distribution shape parameter α = 0.889. The tree topology of ML analysis is similar to BI analysis. Bootstrap support values for MLBS $\geq$ 70% and BYPP $\geq$ 0.7 are defined as BS/PP above the nodes. Hyphens (-) represent support values less than 70% in ML and 0.7 in BI. Newly generated sequences are in blue and “T” indicates type strain.

***Yunnanomyces* Tibpromma & K.D. Hyde**

Based on the dataset combined ITS, LSU, *EF1A*, *TUB*, and *RPB2* sequences, the phylogeny of *Sympoventuriaceae* was studied. *Venturia saliciperda* (CBS 480.61) and *Tyrannosorus lichenicola* (CBS 144018) were used as the outgroup for the phylogenetic analysis. The concatenated sequences included 59 taxa and consisted of 3,389 nucleotides (ITS, 769 bp; LSU, 812 bp; *EF1A*, 686 bp; *TUB*, 340 bp; and *RPB2*, 782 bp) with inserted gaps. The phylogenetic trees showed that members of the genus *Yunnanomyces* clustered into a single group with a high support value (95/1) (Fig. 15). Additionally, our two new isolates (CGMCC 3.25507 and ZY 22.034) of *Y. sexualis* clustered into a single clade with a high support value (100/1) and closely related to *Y. pandanicola* and *Y. phoenicis* (Fig. 15). *Sympoventuriaceae* genera sections in the phylogenetic tree were followed by Wei et al. (2022).

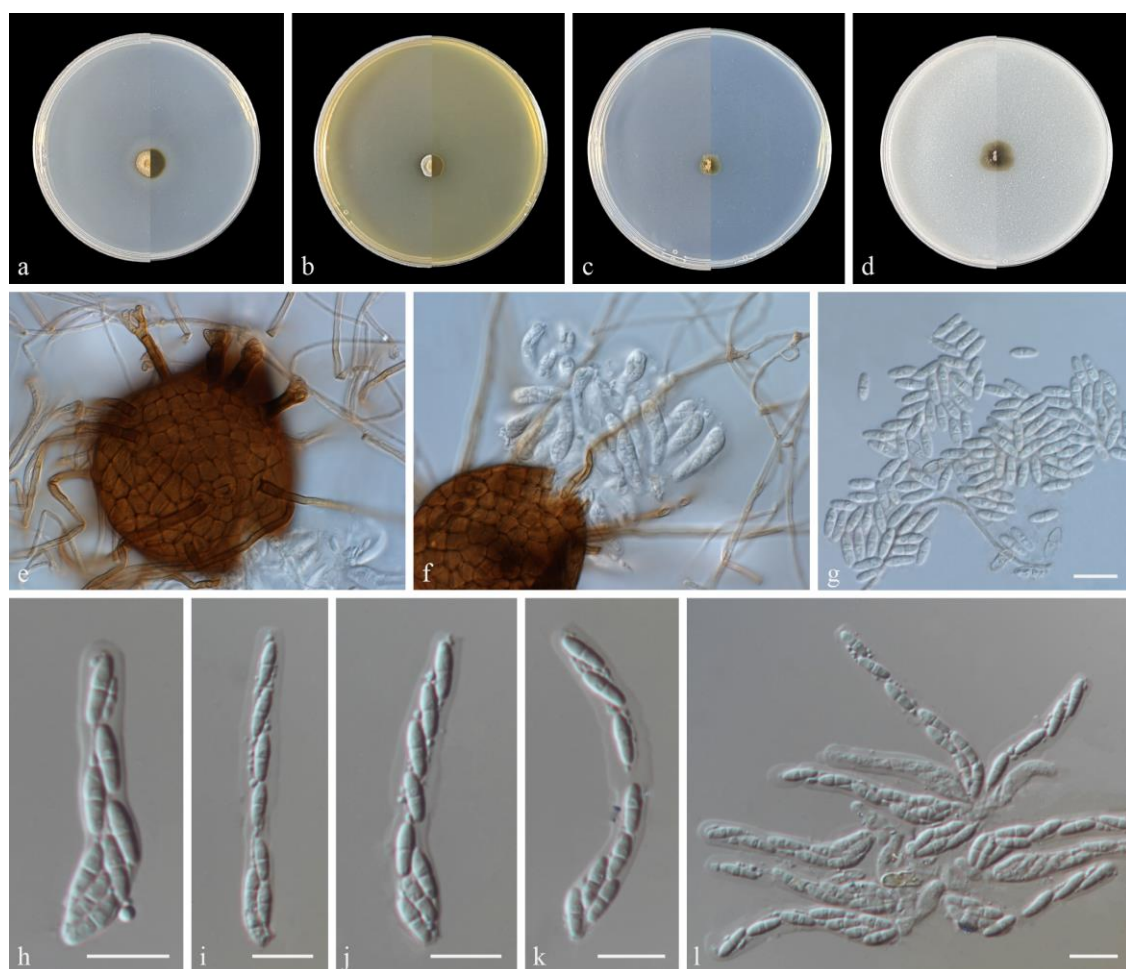


Figure 16 – *Yunnanomyces sexualis* (CGMCC 3.25507). a–d Upper and reverse views of cultures on PDA, MEA, SNA, and OA 14 d after inoculation. e–f Ascomata. g Ascospores. h–l Asci. Scale bars: g–l = 10 μ m.

Yunnanomyces sexualis Zhi Y. Zhang, Heng Pan & Y. F. Han, sp. nov.
Mycobank number: MB850372; Facesoffungi number: FoF15080
Etymology – Named after the present sexual morph.

Fig. 16

Holotype – ZY H-22.033

Description – *Hyphae* branched, septate, hyaline, smooth, 1–2.5 µm diam. Sexual morph: *Ascomata* superficial, guttulate to ellipsoidal, 33–46 µm high, 29–40 µm diam. *Ascomata* wall orange-brown, of textura epidermoidea in surface view. Hairs arcuate or flexuous, subhyaline to brown, septate. *Asci* 36–46 × 5.5–7 µm (av. 41.6 × 6.1 µm, n = 30), numerous, 8-spored, bitunicate, broadly cylindrical to somewhat obclavate, straight or curved, with a short, knob-like pedicel or pedicel lacking, each with an inconspicuous ocular chamber. *Ascospores* 6–8.5 × 2–2.5 µm (av. 7.2 × 2.2 µm, n = 30), narrowly fusiform, subhyaline to hyaline, overlapping to biseriate, 1-septate, the upper cells wider and longer than the lower ones, smooth-walled. Asexual morph: Not observed.

Culture characteristics (14 d at 25 °C) – Colony on PDA 11–12 mm, flocculent, beige; reverse brown curry. Colony on MEA 8–10 mm, flocculent, dark ivory to oyster white from centre to margin; reverse curry. Colony on SNA 6–9 mm, flocculent, felty, rape yellow; reverse curry. Colony on OA 11–13 mm, flat, aerial mycelia sparse, flocculent, grey beige; reverse curry.

Material examined – China, Guizhou Province, Guiyang City, Xiuwen County, Zhazuo Town, soil collected from the green belts of Guizhou Wildlife Park, 106.69 E, 26.85 N, 25 May 2022, Zhi-Yuan Zhang (holotype, ZY H-22.033), ex-type CGMCC 3.25507 = ZY 22.033; *ibid.* ZY 22.034.

Notes – In phylogenetic analyses, *Yunnanomyces sexualis* nests in the genus *Yunnanomyces* and is the sibling to *Y. pandanicola* and *Y. phoenicis* (Fig. 16). However, *Y. sexualis* produces a sexual morph, which is not observed in *Y. pandanicola* and *Y. phoenicis* (Tibpromma et al. 2018, Zhang et al. 2019). In addition, they can be distinguished by their low sequence similarities. In a comparison of ITS, LSU, and *RPB2* nucleotides, *S. sexualis* (Type strain CGMCC 3.25507) has 79.4%, 98.2% and 73.6% similarity, in ITS (372/468 bp, 15 gaps), LSU (787/801 bp, no gap), and *RPB2* (753/1,022 bp, 13 gaps), which is different from *S. pandanicola* (Type strain MFLUCC 17-2260). In a comparison of LSU and *RPB2* nucleotides, *S. sexualis* (CGMCC 3.25507) has 95% and 74.1% similarity, in LSU (784/825 bp, three gaps) and *RPB2* (756/1,019 bp, nine gaps), which is different from *S. phoenicis* (Type strain MFLUCC 19-0254).

Class **Eurotiomycetes** O.E. Erikss. & Winka

Eurotiales G.W. Martin ex Benny & Kimbr.

Aspergillaceae Link

Penicillium Link

Based on the dataset combined ITS, *TUB*, *CaM*, and *RPB2* sequences, the phylogeny of subgenus *Aspergilloides* of *Penicillium* was studied. *Aspergillus glaucus* (CBS 516.65) and *Hamigera avellanea* (CBS 295.48) were used as the outgroup for the phylogenetic analysis. The concatenated sequences included 109 taxa and consisted of 2,642 nucleotides (ITS, 609 bp; *TUB*, 482 bp; *CaM*, 671 bp; and *RPB2*, 880 bp) with inserted gaps. The phylogenetic trees showed that members of each section of subgenus *Aspergilloides* of *Penicillium* are clustered into separate branches with high support values (Fig. 17). Additionally, our four new isolates (CGMCC 3.25508, ZY 22.036, ZY 22.037, and ZY22.038) of *Penicillium guizhouense* clustered into a single clade with a high support value (100/1) and closely related to sections *Aspergilloides*, *Sclerotium*, *Charlesia*, *Eremophila*, and *Griseola* (Fig. 17). In addition, Houbraken et al. (2020) defined *Penicillium thiersii* as a series (i.e., *Thiersiorum*) in section *Aspergilloides*, subgenus *Aspergilloide*, but the phylogenetic tree they constructed showed low support for this result (77%/-). In this study, *Penicillium thiersii* formed a single clade, which may be a distinctive section in the subgenus *Aspergilloides*. *Penicillium* sections in the phylogenetic tree (Fig. 17) were followed by Houbraken et al. (2020).

Section **Guizhouorum** Zhi Y. Zhang & Y. F. Han, sp. nov. sect. nov.

MycoBank number: MB850373

Etymology – Named after the type species of the series, *Penicillium guizhouense*.

Type species – *Penicillium guizhouense*

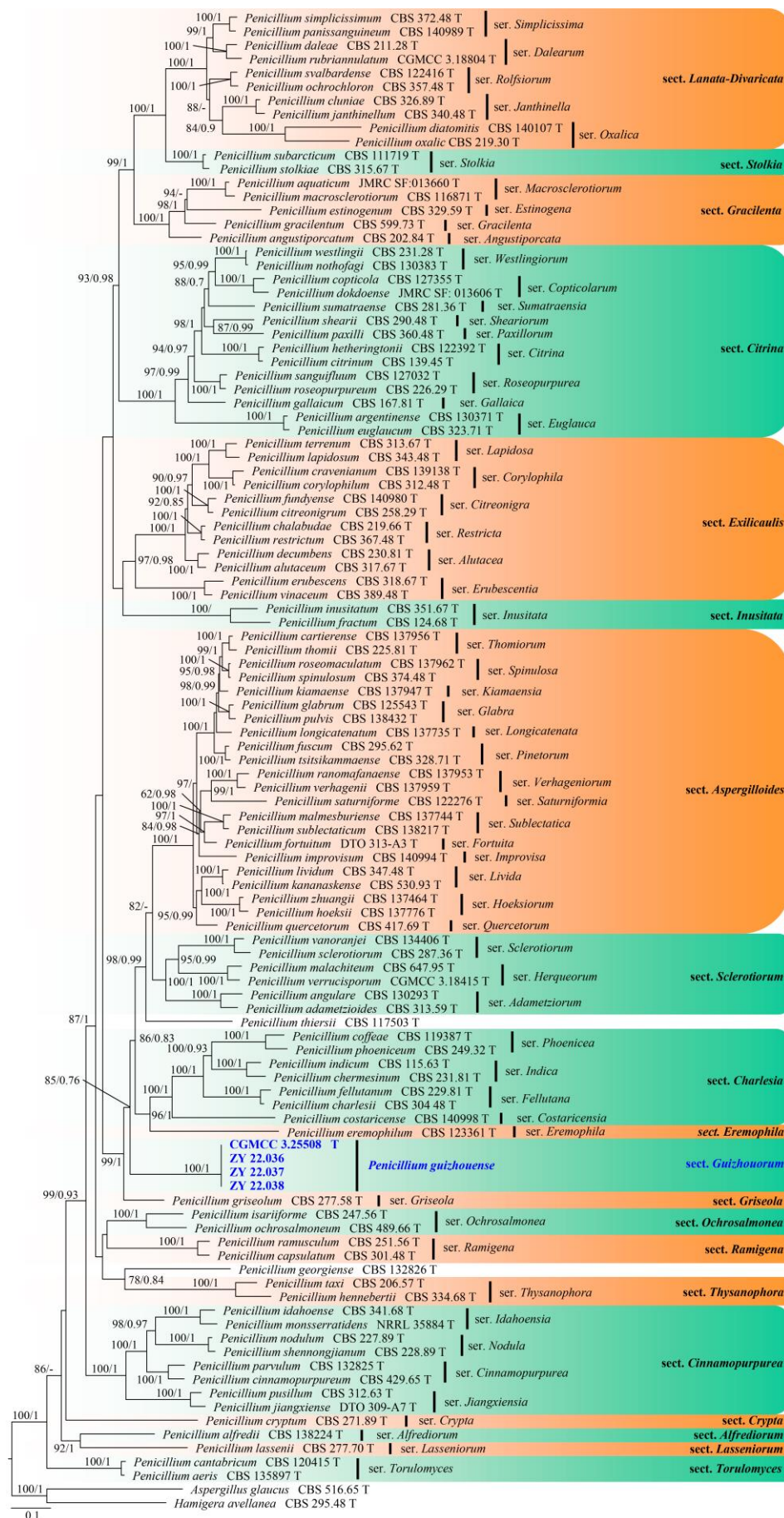


Figure 17 – Phylogram generated from maximum likelihood analysis based on combined ITS, *TUB*, *CaM*, and *RPB2* sequence data. Estimated base frequencies were as follows; A = 0.226, C = 0.273,

G = 0.271, T = 0.230; substitution rates AC = 1.13471, AG = 3.20290, AT = 1.36830, CG = 0.78656, CT = 5.78072, GT = 1.00000; gamma distribution shape parameter α = 0.858. The tree topology of ML analysis is similar to BI analysis. Bootstrap support values for MLBS $\geq$ 70% and BYPP $\geq$ 0.7 are defined as BS/PP above the nodes. Hyphens (-) represent support values less than 70% in ML and 0.7 in BI. Newly generated sequences are in blue and “T” indicates type strain.

Description – *Hyphae* branched, septate, hyaline, smooth. Sexual morph: Not observed. Asexual morph: *Sclerotia* absent. *Stipes* vesiculate finely rough walled, monoverticillate. *Phialides* ampulliform to subcylindrical, 4–20 per stipe. *Conidia* in moderately long chains, ellipsoidal, globose to subglobose, smooth or rough.

Notes – *Phylogeny*: Section *Guizhouorum* belongs to the subgenera *Aspergilloides* and is phylogenetically most closely related to the sect. *Aspergilloides*, *Sclerotium*, *Charlesia*, *Eremophila*, and *Griseola* (Fig. 17). *Morphology*: of these sections, only all members of the sect. *Eremophila* produced sexual morphs; some members of the sect. *Aspergilloides* produced sexual morphs, and none of the members in the remaining sections produced sexual morphs (Houbraken & Samson 2011, Houbraken et al. 2014, Houbraken et al. 2020). In addition, members of sections *Sclerotium* and *Charlesia* have monoverticillate conidiophores, biverticillate conidiophores, or both (Houbraken & Samson 2011, Peterson et al. 2005, Visagie et al. 2013). Furthermore, members of the sect. *Griseola* are conspicuously echinulate, with conspicuous connective conidia (Houbraken et al. 2020), a different sect. *Guizhouorum*.

Penicillium guizhouense Zhi Y. Zhang & Y. F. Han, sp. nov.

Fig. 18

MycoBank number: MB850374; Facesoffungi number: FoF15081

Etymology – Named after the location Guizhou, where the holotype was collected.

Holotype – ZY H-22.035

Description – *Hyphae* branched, septate, hyaline, smooth, 1–4 μ m diam. Sexual morph: Not observed. Asexual morph: *Sclerotia* absent. *Conidiophores* 60–150 μ m long, stipes vesiculate up to 10 μ m diam, finely rough walled, monoverticillate. *Phialides* ampulliform to subcylindrical, 4–20 per stipe, 14–19.5 $\times$ 3–5 μ m (av. 16.9 $\times$ 4.1 μ m, n = 30). *Conidia* in moderately long chains, ellipsoidal, globose to subglobose, smooth or rough, 4–6 $\times$ 3–5.5 μ m (av. 4.9 $\times$ 4.2 μ m, n = 30).

Culture characteristics (14 d at 25 °C) – Colony on PDA 32–40 mm, good sporulation; conidia dull green to greyish green, texture velutinous and floccose, low; mycelium white; exudate absent; soluble pigment not produced; margin low, wide, entire; reverse greenish white. Colony on MEA 38–43 mm, good sporulation, texture floccose, velvety at the edge; conidia pure green or pure to dull green; exudate absent; soluble pigment not produced; reverse light yellow to greyish yellow. Colony on SNA 26–29 mm, sporulation moderately dense; mycelium sparse; texture floccose; conidia greenish white to greyish green; exudate absent; soluble pigment not produced; reverse greenish white. Colony on OA 30–31 mm, good sporulation; conidia dull green to greyish green, texture velutinous and floccose, low; exudate absent; soluble pigment not produced; reverse greenish white.

Material examined – China, Guizhou Province, Guiyang City, Xiuwen County, Zhazuo Town, soil collected from the green belts of Guizhou Wildlife Park, 106.69 E, 26.85 N, 25 May 2022, Zhi-Yuan Zhang (holotype, ZY H-22.035), ex-type CGMCC 3.25508 = ZY 22.035; *ibid.* ZY 22.036. China, Guizhou Province, Guiyang City, Xiuwen County, Zhazuo Town, soil collected from the green belts of Guizhou Wildlife Park, 106.69 E, 26.85 N, 25 May 2022, Zhi-Yuan Zhang ZY 22.037; *ibid.* ZY 22.038.

Notes – Based on multi-locus phylogenies, the four new isolates formed a single clade and separated from members in the sect. *Aspergilloides*, *Sclerotium*, *Charlesia*, *Eremophila*, and *Griseola* (Fig. 17). Of these sections, only all members of the sect. *Eremophila* produced sexual morphs; some members of the sect. *Aspergilloides* produced sexual morphs, and none of the members in the remaining sections produced sexual morphs (Houbraken & Samson 2011, Houbraken et al. 2014, Houbraken et al. 2020). Additionally, members of sections *Sclerotium*

and *Charlesia* have monoverticillate conidiophores, biverticillate conidiophores, or both (Houbraken & Samson 2011, Peterson et al. 2005, Visagie et al. 2013). Furthermore, members of the sect. *Griseola* are conspicuously echinulate, with conspicuous connective conidia, which differs from *P. guizhouense* (Houbraken et al. 2020). In addition, they can be distinguished by their low sequence similarities. In a comparison of ITS, *TUB*, *CaM*, and *RPB2* nucleotides, *P. guizhouense* (Type strain CGMCC 3.25508) has 92.6%, 77.7%, 73.8%, and 85.5% similarity, in ITS (505/545 bp, 12 gaps), *TUB* (345/444 bp, 23 gaps), *CaM* (528/715 bp, 46 gaps), and *RPB2* (819/957 bp, three gaps), which is different from *P. griseolum* (Type strain CBS 277.58) type species of section *Griseola*. *Penicillium guizhouense* (CGMCC 3.25508) has 87.1%, 65%, 64.3%, and 84.1% similarity, in ITS (497/570 bp, 17 gaps), *TUB* (266/409 bp, 70 gaps), *CaM* (302/469 bp, 79 gaps), and *RPB2* (819/973 bp, no gap), which is different from *P. eremophilum* (Type strain CBS 123361) type species of section *Eremophila*. *Penicillium guizhouense* (CGMCC 3.25508) has 92.1%, 73.9%, 69.2%, and 82.3% similarity, in ITS (507/550 bp, nine gaps), *TUB* (321/434 bp, 13 gaps), *CaM* (504/728 bp, 74 gaps), and *RPB2* (788/957 bp, three gaps), which is different from *P. charlesii* (Type strain CBS 304.48) type species of section *Charlesia*. *Penicillium guizhouense* (CGMCC 3.25508) has 93.5%, 69.1%, 68.4%, and 82.8% similarity, in ITS (509/544 bp, eight gaps), *TUB* (343/496 bp, 67 gaps), *CaM* (354/517 bp, 73 gaps), and *RPB2* (756/912 bp, no gap), which is different from *P. sclerotiorum* (Type strain CBS 287.36) type species of section *Sclerotiorum*. *Penicillium guizhouense* (CGMCC 3.25508) has 94.4%, 73.1%, 71.9%, and 84.2% similarity, in ITS (511/541 bp, four gaps), *TUB* (322/440 bp, 23 gaps), *CaM* (367/510 bp, 45 gaps), and *RPB2* (821/975 bp, no gap), which is different from *P. glabrum* (Type strain CBS 125543) type species of section *Aspergilloides*.

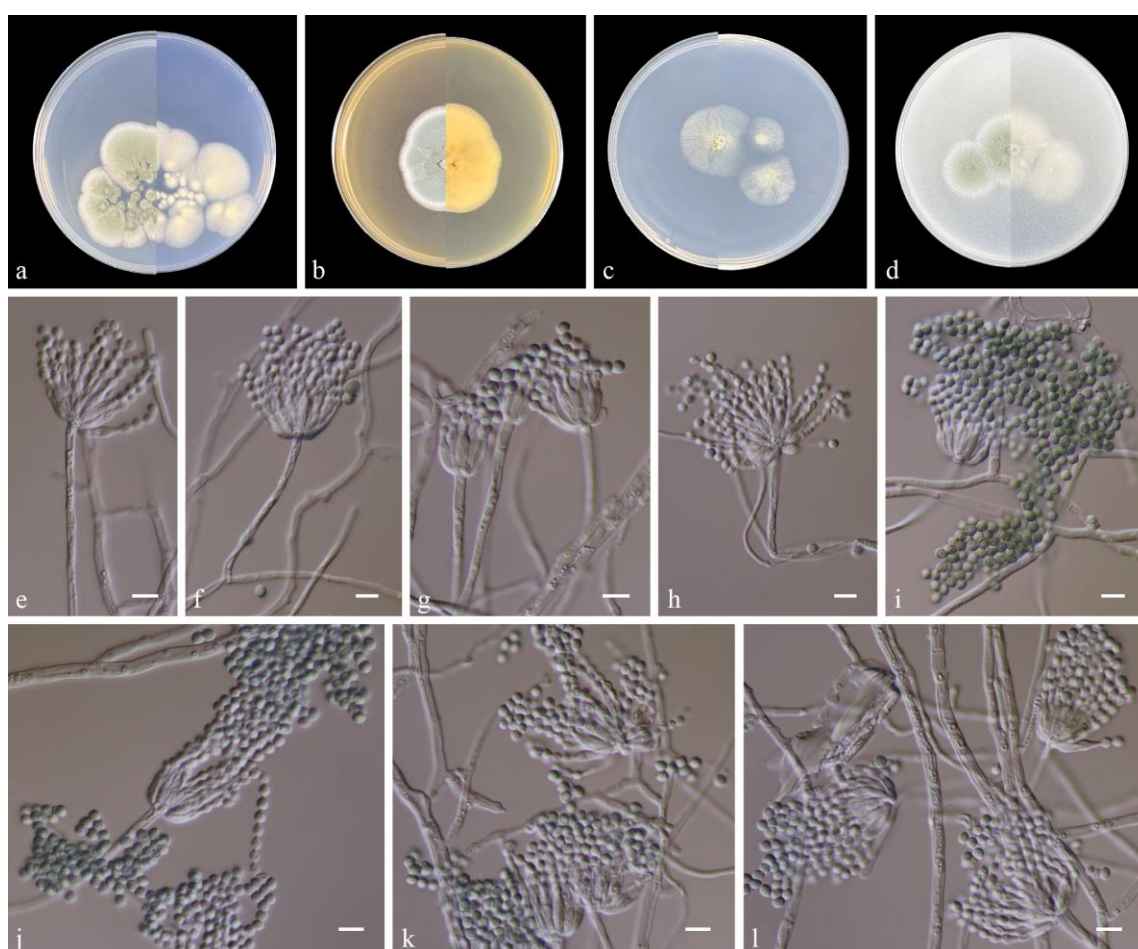


Figure 18 – *Penicillium guizhouense* (CGMCC 3.25508). a–d Upper and reverse views of cultures on PDA, MEA, SNA, and OA 14 d after inoculation. e–l Conidiophores, conidial heads and conidia. Scale bars: e–l = 10 μ m.

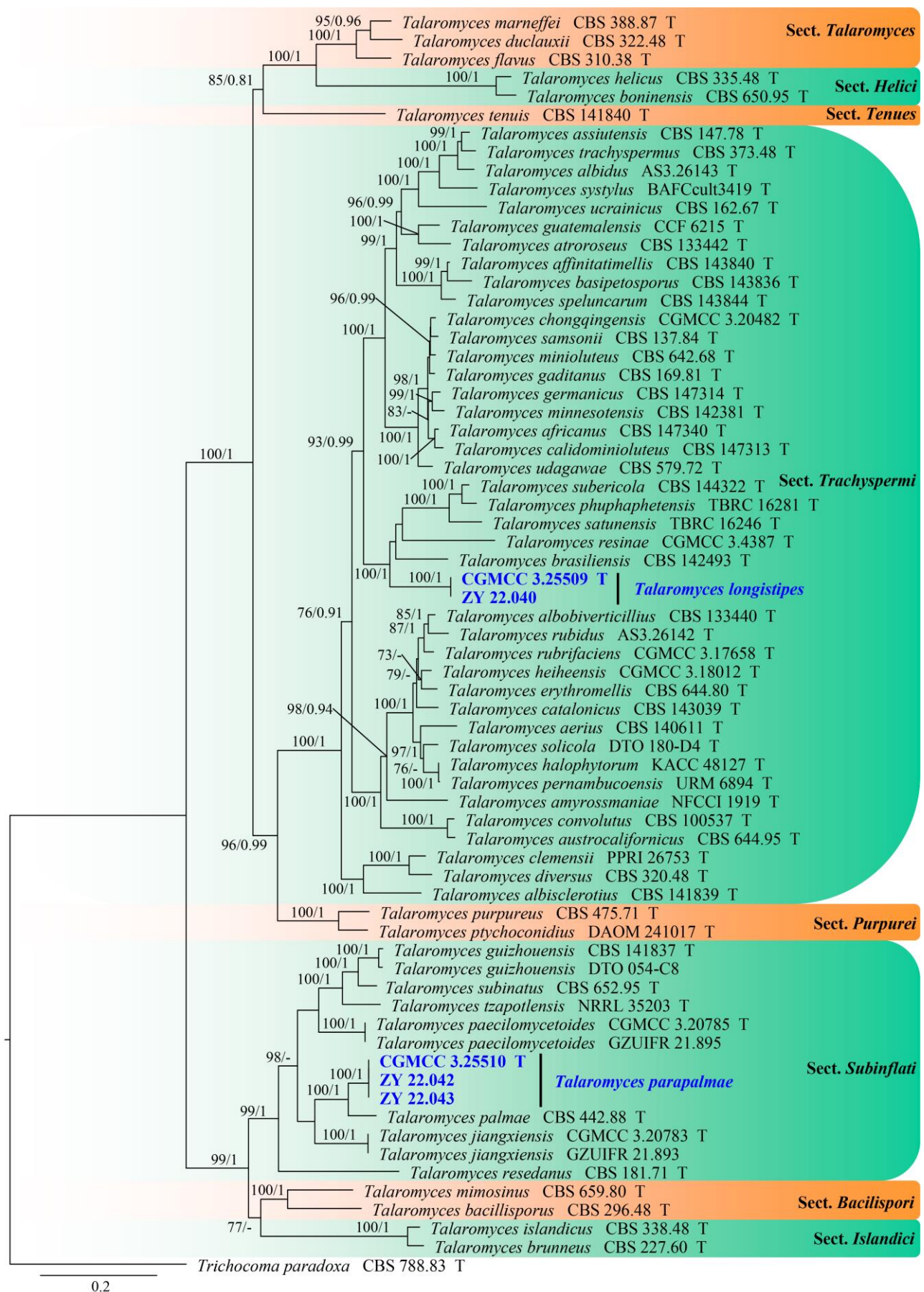


Figure 19 – Phylogram generated from maximum likelihood analysis based on combined ITS, *TUB*, *CaM*, and *RPB2* sequence data. Estimated base frequencies were as follows; A = 0.239, C = 0.257, G = 0.239, T = 0.265.

G = 0.267, T = 0.237; substitution rates AC = 1.40725, AG = 5.07808, AT = 1.42514, CG = 0.97933, CT = 6.45110, GT = 1.00000; gamma distribution shape parameter α = 1.033. The tree topology of ML analysis is similar to BI analysis. Bootstrap support values for MLBS $\geq$ 70% and BYPP $\geq$ 0.7 are defined as BS/PP above the nodes. Hyphens (-) represent support values less than 70% in ML and 0.7 in BI. Newly generated sequences are in blue and “T” indicates type strain.

***Talaromyces* C.R. Benj.**

Based on the dataset combined ITS, *TUB*, *CaM*, and *RPB2* sequences, the phylogeny of *Talaromyces* was studied. *Trichocoma paradoxa* (CBS 788.83) was used as the outgroup for the phylogenetic analysis. The concatenated sequences included 68 taxa and consisted of 2,465 nucleotides (ITS, 516 bp; *TUB*, 494 bp; *CaM*, 560 bp; and *RPB2*, 895 bp) with inserted gaps. The phylogenetic trees showed that two new isolates (CGMCC 3.25509 and ZY22.040) of *T. longistipes* clustered into a single clade with a high support value (100/1) and nested in the section *Trachyspermi*, and closely related to species *T. brasiliensis* and *T. resiniae* (Fig. 19). In addition, three new isolates (CGMCC 3.25510, ZY 22.042, and ZY22.043) of *T. parapalmae* clustered into a single clade with a high support value (100/1) and nested in the section *Subinflati*, and closely related to species *T. palmae* (Fig. 19). *Talaromyces* sections in the phylogenetic tree were followed by Houbraeken et al. (2020) and Sun et al. (2020).

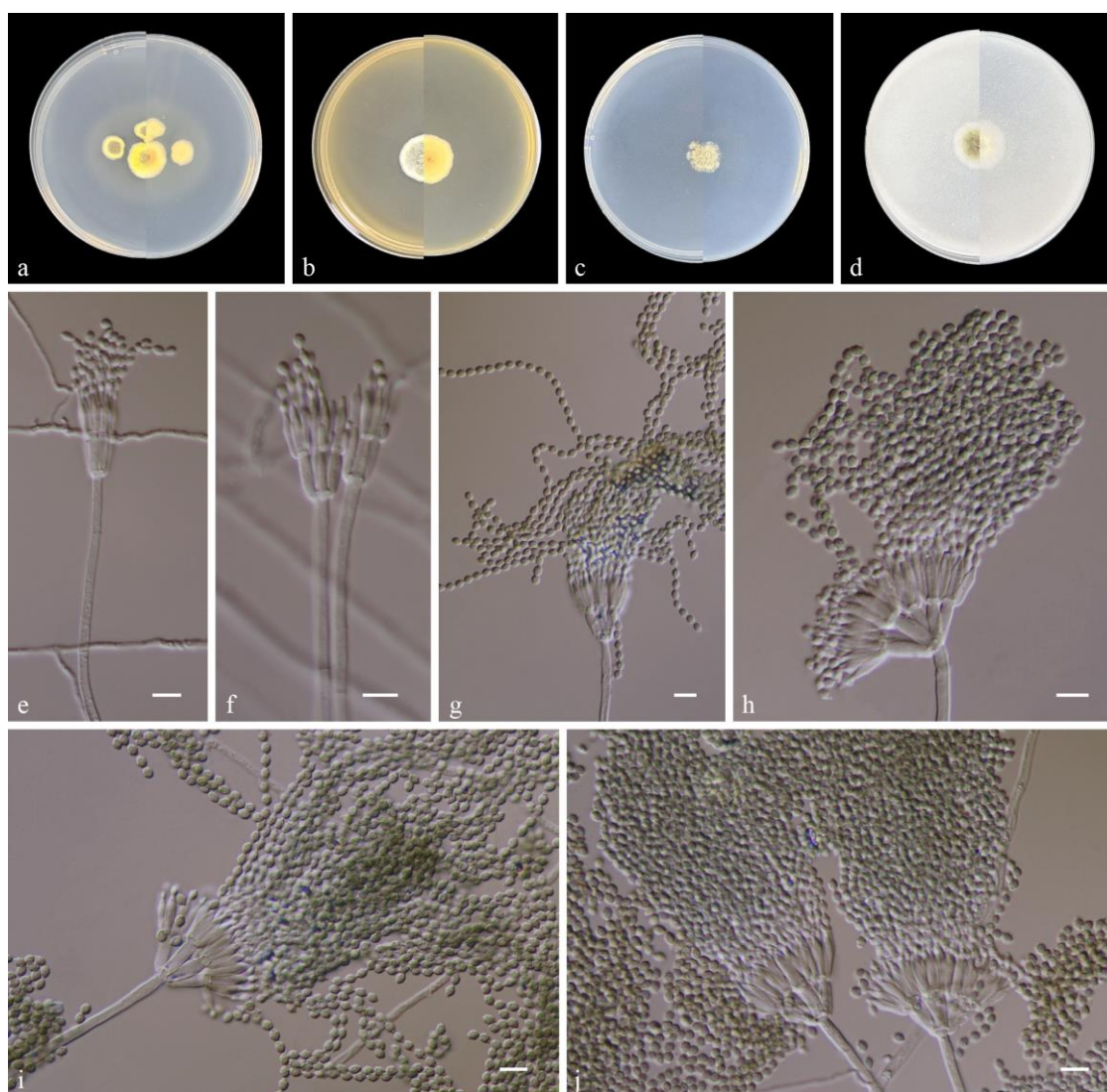


Figure 20 – *Talaromyces longistipes* (CGMCC 3.25509). a–d Upper and reverse views of cultures on PDA, MEA, SNA, and OA 14 d after inoculation. e–j Phialides, conidia and conidia chain. Scale bars: e–j = 10 μm.

Talaromyces longistipes Zhi Y. Zhang & Y. F. Han, sp. nov.

Fig. 20

Mycobank number: MB850375; Facesoffungi number: FoF15082

Etymology – Referring to its longer stipes.

Holotype – ZY H-22.039

Description – *Hyphae* branched, septate, hyaline, smooth, 1–5 µm diam. Sexual morph: Not observed. Asexual morph: *Sclerotia* absent. *Conidiophores* biverticillate, stipes smooth-walled, non-vesiculate, 50–200 × 3–4.5 µm; metulae 2–6 per stipe, 12–19 × 3.5–5.5 µm. *Phialides* acerose, tapering into very thin neck, 2–5 per metulae, 13.5–18 × 2.5–4 µm. *Conidia* in long chains, ellipsoidal to broad fusiform, rough, pale green, 3.5–6 × 3–4 µm (av. 4.7 × 3.4 µm, n = 30).

Culture characteristics (14 d at 25 °C) – Colony on PDA 14–15 mm, moderately deep, plane; margin entire; sporulation moderately dense; conidia *en masse* greyish green; mycelium greenish yellow; colony texture floccose; exudates absent; soluble pigments greenish yellow; reverse greenish yellow. Colony on MEA 18–20 mm, moderately deep, margin entire; sporulation strong; conidia *en masse* greyish green; mycelium light yellow to grey white; colony texture floccose; exudates absent; soluble pigments absent; reverse greenish yellow. Colony on SNA 12–13 mm, plane; margin irregular; sporulation moderate; conidia *en masse* greenish yellow; mycelium grey yellow to grey white; colony texture floccose; exudates absent; soluble pigments absent; reverse greenish yellow. Colony on OA 18–20 mm, flat, margin entire; sporulation strong; conidia *en masse* greenish yellow; mycelium grey yellow; exudates absent; soluble pigments absent; reverse grey white.

Material examined – China, Guizhou Province, Guiyang City, Xiuwen County, Zhazuo Town, soil collected from the green belts of Guizhou Wildlife Park, 106.69 E, 26.85 N, 25 May 2022, Zhi-Yuan Zhang (holotype, ZY H-22.039), ex-type CGMCC 3.25509 = ZY 22.039; *ibid.* ZY 22.040.

Notes – Phylogenetically, *Talaromyces longistipes* falls into a terminal clade of section *Trachyspermi*, including species *T. brasiliensis*, *T. phuphaphetensis*, *T. resinae*, *T. satunensi*, and *T. subericola* (Fig. 19). *Talaromyces brasiliensis*, *T. longisporu*, *T. resinae*, and *T. subericola* have smooth-walled stipes and conidial ornamentation, whereas *T. phuphaphetensis* and *T. satunensis* can be differentiated as having tuberculate stipes and smooth-walled conidia (Barbosa et al. 2018, Rodríguez-Andrade et al. 2020, Nuankaew et al. 2022, Qi & Kong 1982). *Talaromyces longistipes* differs from *T. resinae* in having biverticillate conidiophore (most biverticillate and monoverticillate symmetric in *T. resinae*) (Qi & Kong 1982). *Talaromyces longistipes* differs from *T. brasiliensis* in having longer stipes (12–19 × 3.5–5.5 µm in *T. longistipes* vs. 8–11 × 2.5–3.5 µm in *T. brasiliensis*), and larger conidia (5–6 × 3–4 µm in *T. longistipes* vs. 2–3 µm) (Barbosa et al. 2018). *Talaromyces longistipes* differs from *T. subericola* in its conidia shape (ellipsoidal to broad fusiform vs. ellipsoidal to globose) (Rodríguez-Andrade et al. 2020). In addition, they can be distinguished by their low sequence similarities. In a comparison of ITS, *TUB*, *CaM*, and *RPB2* nucleotides, *T. longistipes* (Type strain CGMCC 3.25509) has 93.1%, 87.5%, 78.7%, and 91.8% similarity, in ITS (410/440 bp, two gaps), *TUB* (303/346 bp, 18 gaps), *CaM* (401/509 bp, 24 gaps), and *RPB2* (916/997 bp, no gap), which is different from *T. brasiliensis* (Type strain CBS 142493). *Talaromyces longistipes* (CGMCC 3.25509) has 92.1%, 84.3%, 73.3%, and 89.2% similarity, in ITS (493/535 bp, eight gaps), *TUB* (392/465 bp, 21 gaps), *CaM* (386/526 bp, 50 gaps), and *RPB2* (886/993 bp, no gap), which is different from *T. resinae* (Type strain CGMCC 3.4387). *Talaromyces longistipes* (CGMCC 3.25509) has 88.8%, 81.8%, and 76.2% similarity, in ITS (480/540 bp, 12 gaps), *TUB* (371/453 bp, 17 gaps), and *CaM* (401/526 bp, 26 gaps), which is different from *T. satunensis* (Type strain TBRC 16246). *Talaromyces longistipes* (CGMCC 3.25509) has 88.6%, 82.8%, 78.3%, and 89.2% similarity, in ITS (475/536 bp, 10 gaps), *TUB* (378/456 bp, 17 gaps), *CaM* (410/523 bp, 22 gaps), and *RPB2* (943/1,057 bp, no gap), which is different from *T. phuphaphetensis* (Type strain TBRC 16281). *Talaromyces longistipes* (CGMCC 3.25509) has 89.1%, 86.9%, 79.2%, and 90.6% similarity, in ITS (418/469 bp, nine gaps), *TUB* (287/330 bp, six gaps), *CaM* (370/467 bp, 27 gaps), and *RPB2* (772/852 bp, no gap), which is different from *T. subericola* (Type strain CBS 144322).

Talaromyces parapalmae Zhi Y. Zhang & Y. F. Han, sp. nov.

Fig. 21

Mycobank number: MB850376; Facesoffungi number: FoF15083

Etymology – Based on its close phylogenetic relationship to *Talaromyces palmae*.

Holotype – ZY H-22.041

Description – *Hyphae* branched, septate, hyaline, smooth, 1–6 μm diam. Sexual morph: Not observed. Asexual morph: *Conidiophores* biverticillate with a minor proportion having subterminal branches, sometimes monoverticillate. *Stipes* smooth walled, 20–80 $\times$ 3–5 μm , branches 23–57 μm . *Metulae* 1–4 per stipe, divergent, 10–25 $\times$ 2.5–5.5 μm . *Phialides* acerose, 1–5 per metulae, 11–29 $\times$ 2–4.5 μm . *Conidia* smooth, chain, subglobose to ellipsoidal, 2.5–6(–8) $\times$ 2–4.5 μm (av. 3.8 $\times$ 2.8 μm , n = 30).

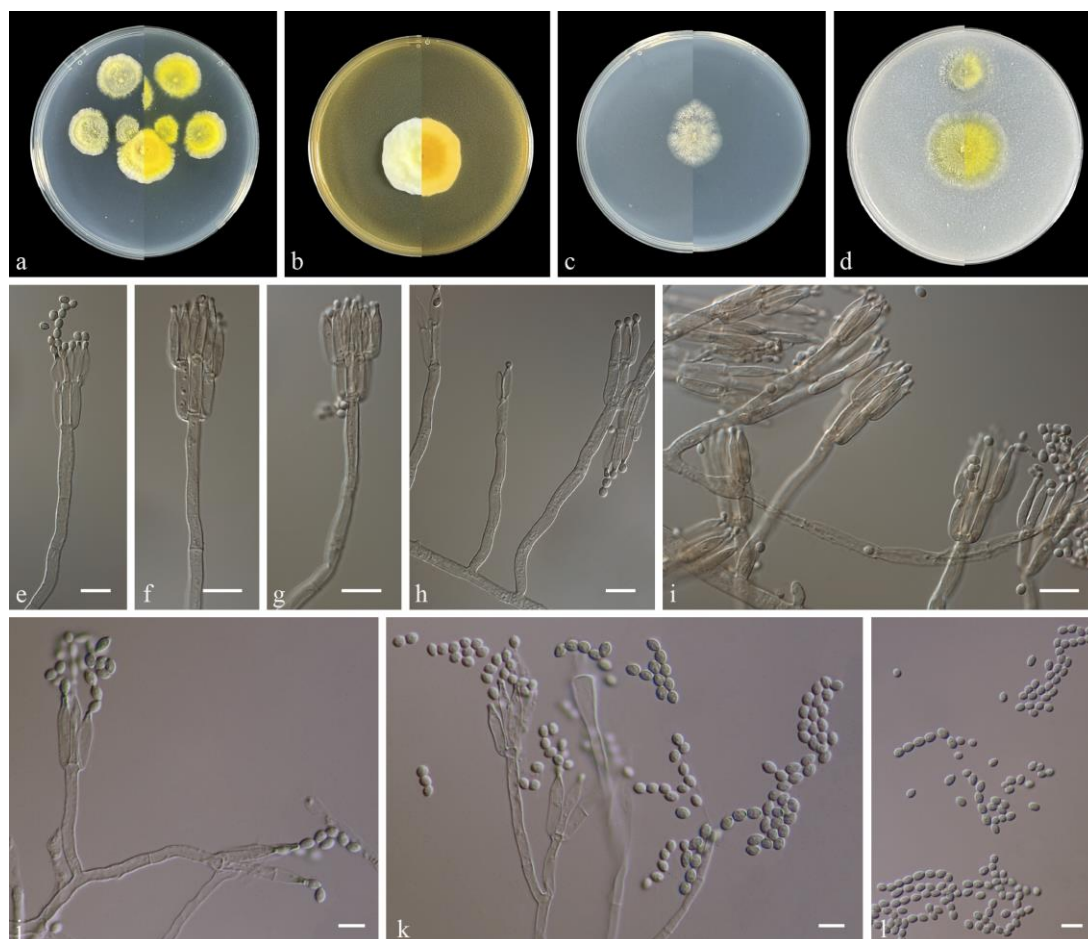


Figure 21 – *Talaromyces parapalmae* (CGMCC 3.25510). a–d Upper and reverse views of cultures on PDA, MEA, SNA, and OA 14 d after inoculation. e–k Phialides and conidia. l Conidia. Scale bars: e–l = 10 μm .

Culture characteristics – (14 d at 25 °C) – Colony on PDA 26–27 mm, raised at the centre, sulcate, margins low; mycelia white, yellow; sporulation absent; soluble pigments absent; exudates absent; reverse yellow. Colony on MEA 32–35 mm, slightly raised, fluffy; margins entire; mycelia white to grey yellow; texture floccose; sporulation absent; soluble pigments absent; exudates absent; reverse zinc yellow. Colony on SNA 23–28 mm, low, margins entire; mycelia grey white; texture floccose; sporulation absent; soluble pigments absent; exudates absent; reverse grey white. Colony on OA 25–27 mm, low, plane; margins plane, entire; mycelia white and grey yellow; texture velvety; sporulation strong in the centre, conidia *en masse* dark green; soluble pigments absent; exudates absent; reverse light yellow.

Material examined – China, Guizhou Province, Guiyang City, Xiuwen County, Zhazuo Town, soil collected from the green belts of Guizhou Wildlife Park, 106.69 E, 26.85 N, 25 May

2022, Zhi-Yuan Zhang (holotype, ZY H-22.041), ex-type CGMCC 3.25510 = ZY 22.041; *ibid.* ZY 22.042 *ibid.* ZY 22.043.

Notes – Currently, seven species are accepted in the section *Subinflati* (Houbraken et al. 2020, Sun et al. 2020, Zhang et al. 2023a). *Talaromyces parapalmae* is classified as a new lineage in the section *Subinflati*, forming a strongly supported clade (100/1) (Fig. 19). Phylogenetically, *T. parapalmae* is closely related to *T. palmae* (Fig. 19). Morphologically, *T. parapalmae* differs from *T. palmae* in having monoverticillate and biverticillate conidiophore (biverticillate in *T. palmae*). *Talaromyces palmae* produces synnemata, which is not observed in *T. parapalmae* (Yilmaz et al. 2014). In addition, they can be distinguished by their low sequence similarities. In a comparison of ITS, *TUB*, *CaM*, and *RPB2* nucleotides, *T. parapalmae* (Type strain CGMCC 3.25510) has 95.8%, 90.6%, 69.7%, and 95.3% similarity, in ITS (535/558 bp, five gaps), *TUB* (396/437 bp, six gaps), *CaM* (422/605 bp, 39 gaps), and *RPB2* (703/737 bp, no gap), which is different from *T. palmae* (Type strain CBS 442.88).

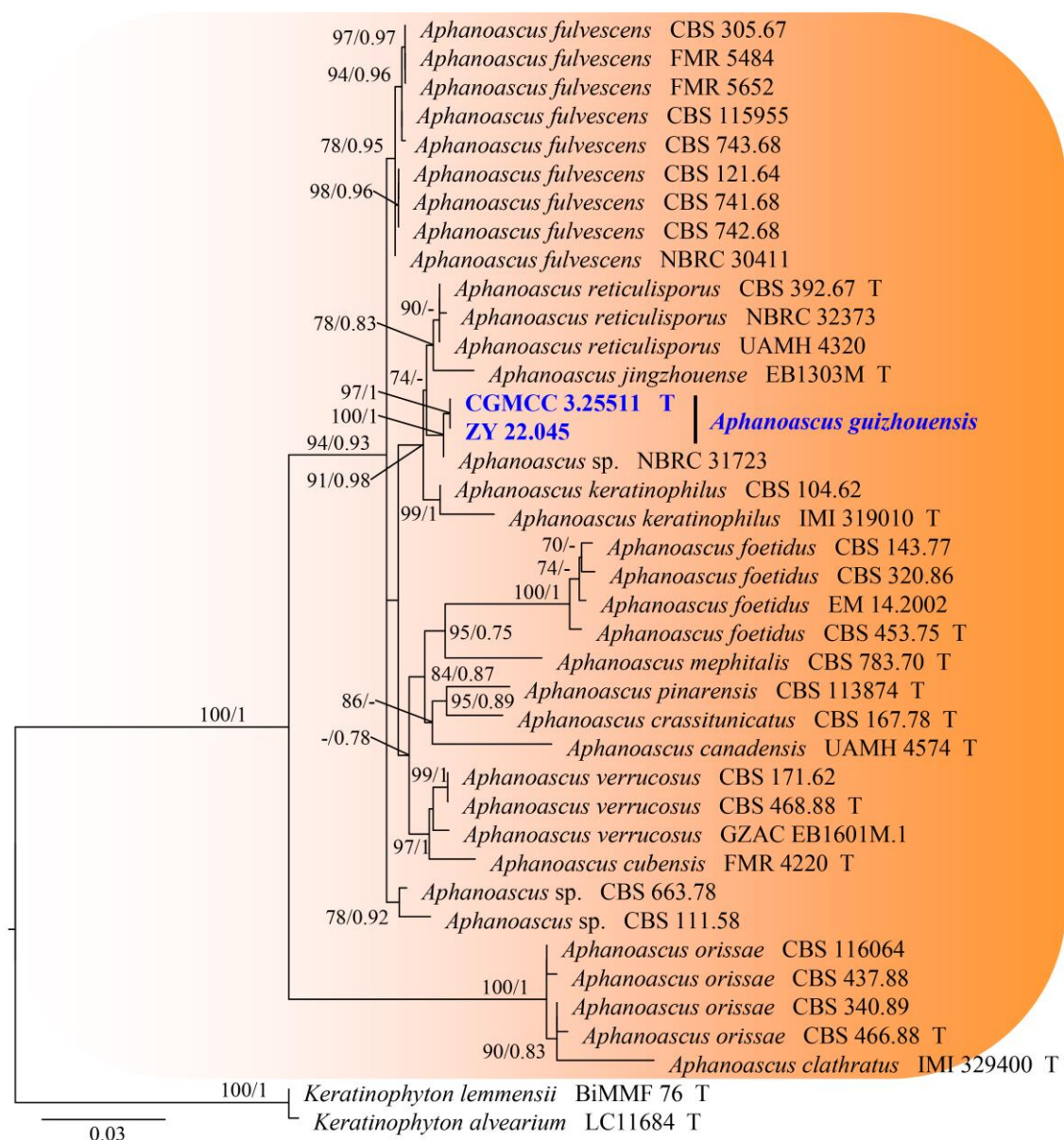


Figure 22 – Phylogram generated from maximum likelihood analysis based on combined ITS and LSU sequence data. Estimated base frequencies were as follows; A = 0.234, C = 0.235, G = 0.292, T = 0.239; substitution rates AC = 1.33380, AG = 3.50342, AT = 2.17538, CG = 0.80264, CT = 9.43457, GT = 1.00000; gamma distribution shape parameter $\alpha = 0.372$. The tree topology of ML analysis is similar to BI analysis. Bootstrap support values for MLBS $\geq 70\%$ and BYPP ≥ 0.7 are

defined as BS/PP above the nodes. Hyphens (-) represent support values less than 70% in ML and 0.7 in BI. Newly generated sequences are in blue and “T” indicates type strain.

Onygenales Cif. ex Benny & Kimbr.

Onygenaceae Berk.

Aphanoascus Zukal

Based on the dataset combined ITS and LSU sequences, the phylogeny of *Aphanoascus* was studied. *Keratinophyton lemmensii* (BiMMF 76) and *K. alvearium* (LC11684) were used as the outgroup for the phylogenetic analysis. The concatenated sequences included 39 taxa and consisted of 1,337 nucleotides (ITS, 514 bp; and LSU, 823 bp) with inserted gaps. The phylogenetic trees showed that members of the genus *Aphanoascus* clustered into a group with a high support value (100/1) (Fig. 22). Additionally, our two new isolates (CGMCC 3.25511 and ZY22.040) of *A. guizhouensis* clustered into a single clade with a high support value (97/1) and closely related to species *A. jingzhouense* and *A. reticulispurus* (Fig. 22). In this study, sequences data mostly from Kandemir et al. (2022), were downloaded from NCBI GenBank for molecular phylogenetic analyses.

Aphanoascus guizhouensis Zhi Y. Zhang, Heng Pan & Y. F. Han, sp. nov.

Fig. 23

Mycobank number: MB850377; Facesoffungi number: FoF15084

Etymology – Named after the location Guizhou, where the holotype was collected.

Holotype – ZY H-22.044

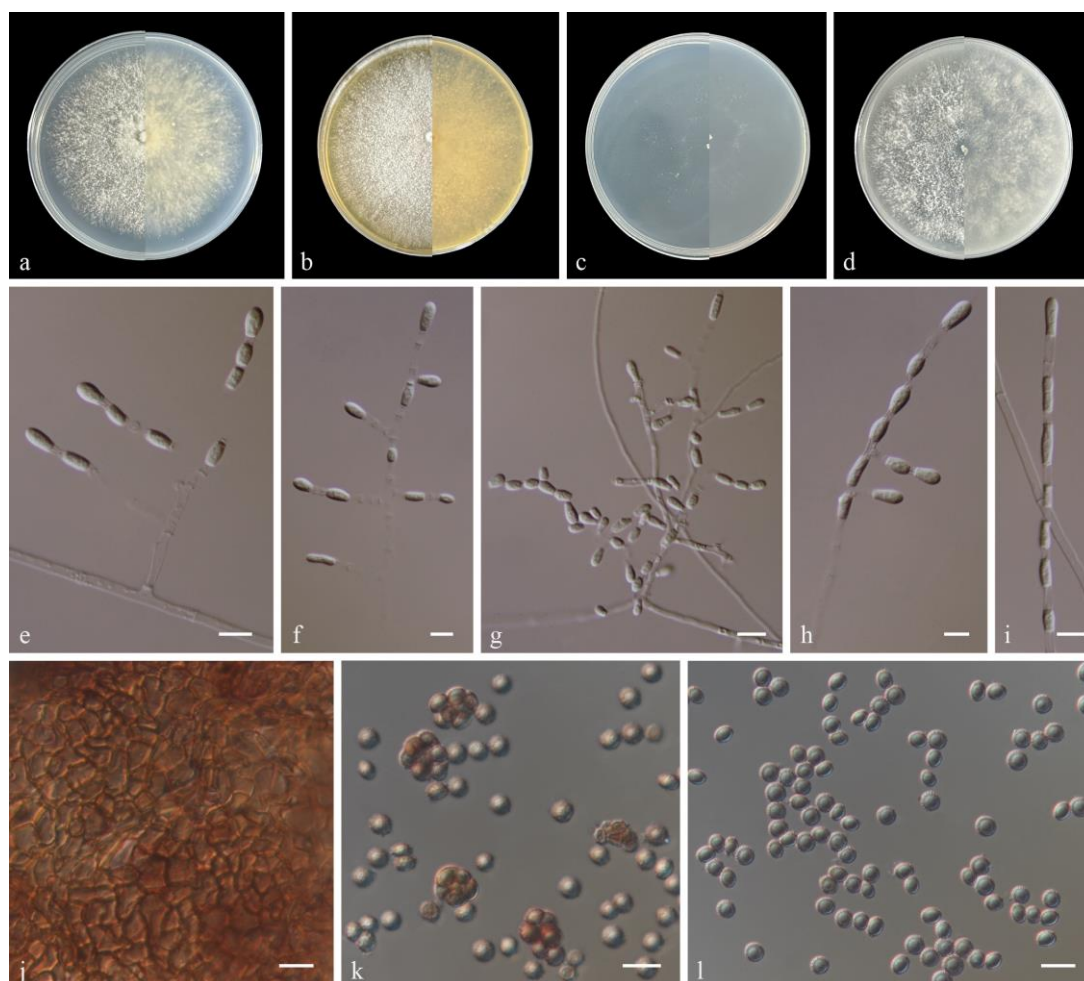


Figure 23 – *Aphanoascus guizhouensis* (CGMCC 3.25511). a–d Upper and reverse views of cultures on PDA, MEA, SNA, and OA 14 d after inoculation. e–g Terminal, lateral and intercalary conidia. h–i Arthroconidia. j Ascumata wall. k Asci. l Ascospores. Scale bars: e–l = 10 µm.

Description – *Hyphae* branched, septate, hyaline, smooth, 1–3 µm diam. Sexual morph: *Ascomata* superficial, spherical, non-ostiolate, light brown. *Asci* numerous, subglobose to ellipsoidal, 11.5–16 × 8–11 µm, 8-spored, evanescent. *Ascospores* globose to ellipsoidal, narrow-ridged reticulate-alveolate, with small verrucae in the pits, one-celled, pale-brown, 5–6.5 × 4–6 µm (av. 5.8 × 5 µm, n = 30). Asexual morph: *Conidia* terminal and lateral, sessile, on short protrusions, the short stalk or the side branches, solitary, hyaline, smooth, clavate, ellipsoidal, with a truncate base, 4.5–9.5 × 2.5–4 µm (av. 6.8 × 3.4 µm, n = 30). *Intercalary conidia* abundant, solitary, cylindrical, clavate to barrel, 6–13.5 × 4–6 µm (av. 9.6 × 5 µm, n = 30). *Arthroconidia* abundant, thin-walled, cylindrical, smooth, 8–13 × 3–4.5 µm (av. 10.9 × 3.9 µm, n = 30).

Culture characteristics (14 d at 25 °C) – Colony on PDA 78–79 mm, fluffy, flocculent, white, aerial mycelium dense; reverse white. Colony on MEA fast-growing, more than 90 mm, flocculent, granular, white, aerial mycelium dense; reverse grey yellow. Colony on SNA 55–60 mm, aerial mycelium very sparse, white; reverse white. Colony on OA fast-growing, more than 90 mm, fluffy, flocculent, white, aerial mycelium dense; reverse white.

Material examined – China, Guizhou Province, Guiyang City, Xiuwen County, Zhazuo Town, soil collected from the green belts of Guizhou Wildlife Park, 106.69 E, 26.85 N, 25 May 2022, Zhi-Yuan Zhang (holotype, ZY H-22.044), ex-type CGMCC 3.25511 = ZY 22.044; *ibid.* ZY 22.045.

Notes – Phylogenetically, *Aphanoascus guizhouensis* forms a distinct clade and is closely related to *A. jingzhouense*, *A. keratinophilus*, and *A. reticulisporus* (Fig. 22). Among these species, *A. jingzhouense* does not produce sexual morph, which is observed in *A. guizhouensis*, *A. keratinophilus*, and *A. reticulisporus* (Cano & Guarro 1990, Zhang et al. 2017a). *Aphanoascus guizhouensis* differs from *A. keratinophilus* in ascospore shape and size (globose to ellipsoidal, 5–6.5 × 4–6 µm in *A. guizhouensis* vs. globose to oblate, 6–8.5 × 4.5–6 µm in *A. keratinophilus*), and has intercalary conidia and arthroconidia, which is not observed in *A. keratinophilus* (Cano & Guarro 1990). *Aphanoascus guizhouensis* differs from *A. reticulisporus* in conidia shape and size (clavate, ellipsoidal, 4.5–9.5 × 2.5–4 µm in *A. guizhouensis* vs. clavate, 7–16 × 4–4.5 µm in *A. reticulisporus*) (Cano & Guarro 1990). In addition, they can be distinguished by their low sequence similarities. In a comparison of ITS and LSU nucleotides, *A. guizhouensis* (Type strain CGMCC 3.25511) has 97.3% and 99.4% similarity, in ITS (545/560 bp, four gaps) and LSU (856/861 bp, two gaps), which is different from *A. reticulisporus* (Type strain CBS 392.67). *Aphanoascus guizhouensis* (CGMCC 3.25511) has 97.1% similarity, in ITS (544/560 bp, no gap), which is different from *A. jingzhouense* (Type strain EB1303M). *Aphanoascus guizhouensis* (CGMCC 3.25511) has 93.7% similarity, in ITS (537/573 bp, 15 gaps), which is different from *A. keratinophilus* (Type strain IMI 319010).

Tuberculiformales Zhi Y. Zhang & Y. F. Han, ord. nov.

MycoBank number: MB850378

Etymology – Named after its tuberculiform-like conidiogenous structure.

Type family – *Tuberculiformaceae*

Description – *Hyphae* branched, septate. Sexual morph: Not observed. Asexual morph: *Conidiophores* are usually reduced to conidiogenous cells. *Conidiogenous cells* arise in clusters on intercalary or terminal, swollen, subglobose to inequilaterally ampulliform, cup-shaped, like tuberculiform. *Conidia* solitary or in chains.

Based on the dataset combined SSU, ITS, LSU, and *RPB2* sequences, the phylogeny of *Tuberculiforma sinensis* and its related taxa were studied. *Geoglossum nigrum* (OSC 100009) and *Trichoglossum hirsutum* (KH03232003-1) were used as the outgroup for the phylogenetic analysis. The concatenated sequences included 77 taxa and consisted of 3,668 nucleotides (SSU, 974 bp; ITS, 789 bp; LSU, 853 bp; and *RPB2*, 1,052 bp) with inserted gaps. The phylogenetic trees showed that four new isolates (CGMCC 3.25512, ZY 22.047, ZY 22.048, and ZY22.049) of *T. sinensis* clustered into a single clade with a high support value (100/1) and closely related to *T. catenata* and three beetle-associated isolate (INBio4503Q, INBio4513L, and INBio4513J) (Fig. 24).

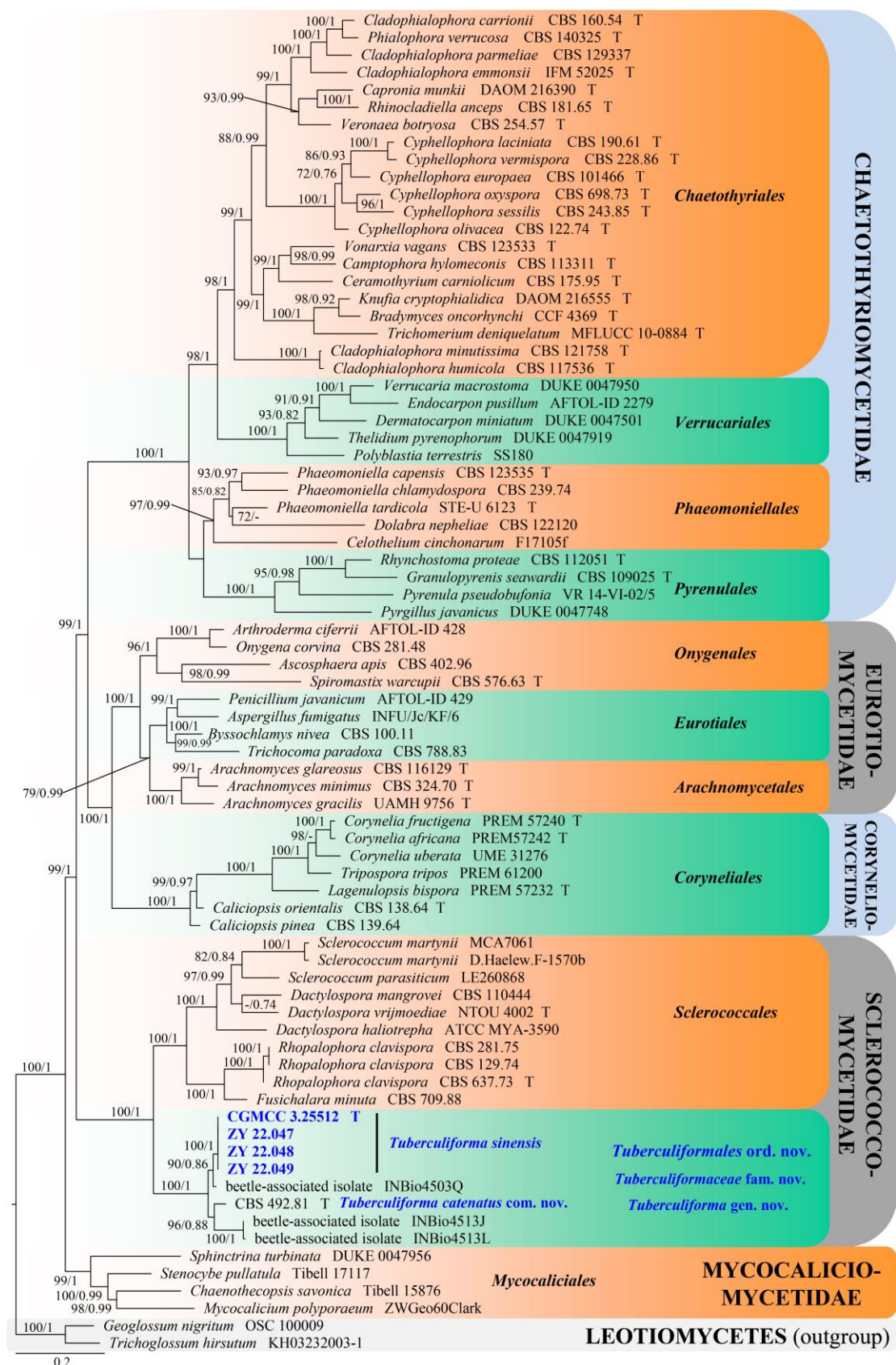


Figure 24 – Phylogram generated from maximum likelihood analysis based on combined SSU, ITS, LSU, and *RPB2* sequence data. Estimated base frequencies were as follows; A = 0.256, C = 0.227, G = 0.275, T = 0.242; substitution rates AC = 1.39013, AG = 2.72152, AT = 1.29109, CG = 0.99535, CT = 5.53269, GT = 1.00000; gamma distribution shape parameter α = 0.612. The tree topology of ML analysis is similar to BI analysis. Bootstrap support values for MLBS $\geq$ 70% and

BYPP ≥ 0.7 are defined as BS/PP above the nodes. Hyphens (-) represent support values less than 70% in ML and 0.7 in BI. Newly generated sequences are in blue and “T” indicates type strain.

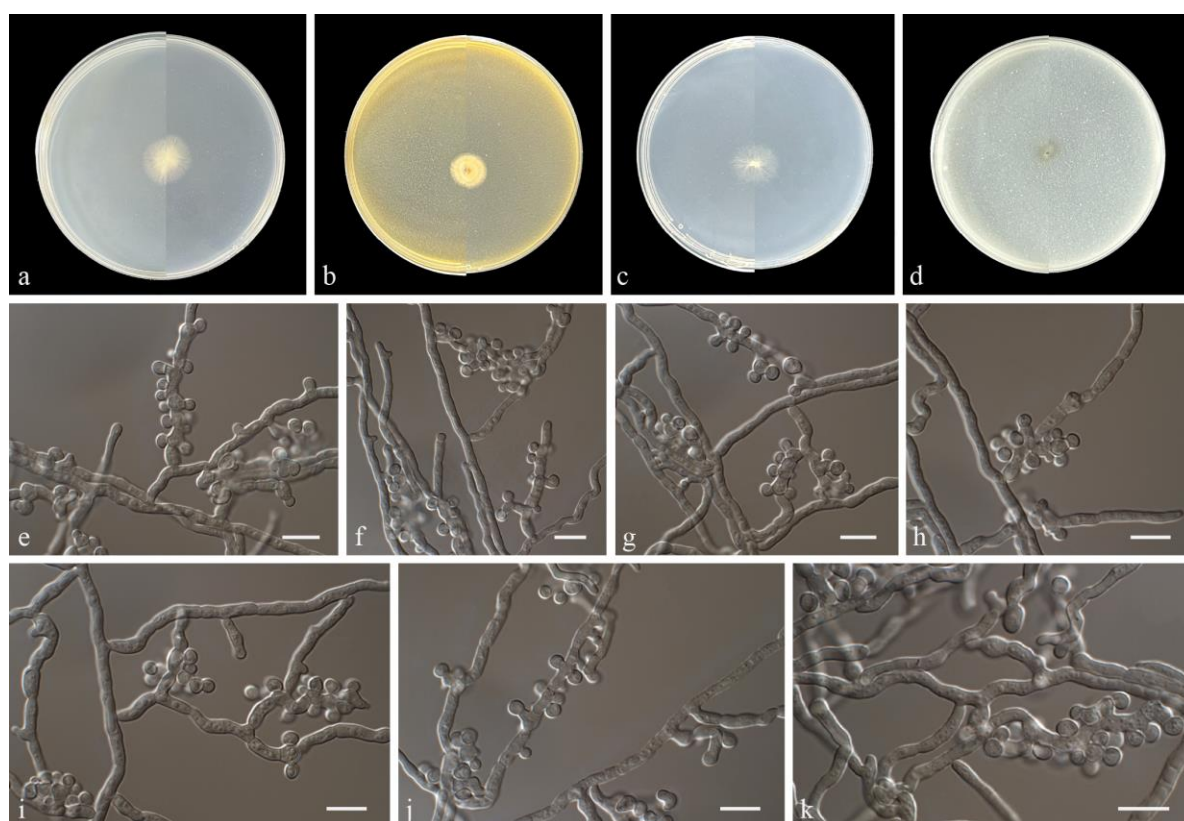


Figure 25 – *Tuberculiforma sinensis* (CGMCC 3.25512). a–d Upper and reverse views of cultures on PDA, MEA, SNA, and OA 14 d after inoculation. e–k Conidiogenous cells and conidia. Scale bars: e–l = 10 μm .

Notes – Réblová et al. (2017) created the subclass *Sclerococomycetidae* and the order *Sclerococcales* based on morphological diagnoses and molecular phylogenetic data. Réblová et al. (2017) may not have been aware of the species *Anthopsis catenata* (Van Oorschot & de Hoog 1982), the morphological characters of beetle-associated isolates (INBio4503Q, INBio4513J, and INBio4513L) are not recorded in the literature, and therefore incorrectly treated these isolates as taxa in *Sclerococcales* based on phylogenetic analyses. In this study, we proposed the new species *Tuberculiforma sinensis*, *A. catenata*, and three beetle-related isolates (INBio4503Q, INBio4513J, and INBio4513L) clustered into a single clade and separated from *Sclerococcales*. Although no sexual stage was observed for *T. sinensis* and *A. catenata* (Van Oorschot & de Hoog 1982), their asexual phenotypes are distinct from those of the *Sclerococcales*. Therefore, we propose a new order of *Tuberculiformales* by combining molecular phylogenetic data and morphological diagnoses.

Tuberculiformaceae Zhi Y. Zhang & Y. F. Han, fam. nov.

Mycobank number: MB850379

Etymology – Named after its tuberculiform-like conidiogenous structure.

Type genus – *Tuberculiform*

Description – *Hyphae* branched, septate. Sexual morph: Not observed. Asexual morph: *Conidiophores* are usually reduced to conidiogenous cells. *Conidiogenous cells* arise in clusters on intercalary or terminal, swollen, subglobose to inequilaterally ampulliform, cup-shaped, like tuberculiform. *Conidia* solitary or in chains, semicircular or ellipsoidal to subglobose, with truncate bases.

Tuberculiforma Zhi Y. Zhang & Y. F. Han, gen. nov.

Mycobank number: MB850380

Etymology – Named after its tuberculiform-like conidiogenous structure.

Type species – *Tuberculiforma sinensis*

Description – *Hyphae* branched, septate; fertile parts of hyphae aerial, lateral or terminal, with short lateral secondary branches consisting of subglobose cells. Sexual morph: Not observed. Asexual morph: *Conidiophores* are usually reduced to conidiogenous cells. *Conidiogenous cells* arise in clusters on intercalary or terminal, swollen, subglobose to inequilaterally ampulliform, cup-shaped, like tuberculiform. *Conidia* solitary or in chains, semicircular or ellipsoidal to subglobose, with truncate bases.

Tuberculiforma sinensis Zhi Y. Zhang & Y. F. Han, sp. nov.

Fig. 25

Mycobank number: MB850381; Facesoffungi number: FoF15085

Etymology – Named after the location China, where the holotype was collected.

Holotype – ZY H-22.046

Description – *Hyphae* branched, septate, hyaline, smooth, 1–4 µm diam; fertile parts of hyphae aerial, lateral or terminal, with short lateral secondary branches consisting of subglobose cells. Sexual morph: Not observed. Asexual morph: *Conidiophores* are usually reduced to conidiogenous cells. *Conidiogenous cells* arise in clusters on intercalary or terminal, usually swollen, subglobose to inequilaterally ampulliform, sometimes cup-shaped. *Conidia* solitary, smooth-walled, semicircular or ellipsoidal to subglobose, with truncate bases, 2.5–4.5 × 2.5–4 µm (av. = 3.1 × 3.2 µm).

Culture characteristics (14 d at 25 °C) – Colony on PDA 17–18 mm, fluffy, white, aerial mycelium sparse at the margin; reverse white. Colony on MEA 13–14 mm, fluffy, white, sulciform, aerial mycelium dense; reverse white. Colony on SNA 14–18 mm, fluffy, flat, white, aerial mycelium sparse; reverse white. Colony on OA 6–7 mm, fluffy, flat, silk grey, aerial mycelium sparse; reverse silk grey.

Material examined – China, Guizhou Province, Guiyang City, Xiuwen County, Zhazuo Town, soil collected from the green belts of Guizhou Wildlife Park, 106.69 E, 26.85 N, 25 May 2022, Zhi-Yuan Zhang (holotype, ZY H-22.046), ex-type CGMCC 3.25512 = ZY 22.046; *ibid.* ZY 22.047. China, Guizhou Province, Guiyang City, Xiuwen County, Zhazuo Town, soil collected from the green belts of Guizhou Wildlife Park, 106.69 E, 26.85 N, 25 May 2022, Zhi-Yuan Zhang ZY 22.048, *ibid.* ZY 22.049.

Notes – Phylogenetically, *Tuberculiforma sinensis* forms a distinct clade and is closely related to *A. catenata* and three beetle-associated isolates (INBio4503Q, INBio4513J, and INBio4513L) (Fig. 24). Morphologically, *T. sinensis* differs from *A. catenata* in its solitary conidia (Van Oorschot & de Hoog 1982). In addition, INBio4503Q, INBio4513J, and INBio4513L were obtained from the beetle gut content of Passalidae and their lack of morphological description (Vargas-Asensio et al. 2014). Thus, we did not compare the morphological characteristics between these isolates and *T. sinensis*. In addition, *T. sinensis* differs from *A. catenata* by their low sequence similarities. In a comparison of ITS and LSU nucleotides, *T. sinensis* (Type strain CGMCC 3.25512) has 93.6% and 87.4% similarity, in ITS (474/506 bp, nine gaps) and LSU (804/919 bp, 104 gaps), which is different from *A. catenata* (Type strain CBS 492.81).

Tuberculiforma catenatus (Oorschot, de Hoog & G. Schöler) Zhi Y. Zhang & Y. F. Han, com. nov.

≡ *Anthopsis catenata* Oorschot, de Hoog & G. Schöler, van Oorschot & de Hoog, Antonie van Leeuwenhoek 48(1): 63 (1982).

The genus *Anthopsis* was established in 1977, with the type species *A. deltoidea* (Marchisio et al. 1977). Recently, *Anthopsis deltoidei* was transferred to the genus *Cyphellophora*, named as *Cyphellophora deltoidea* (Crous et al. 2023). Additionally, in our phylogenetic study, *A. catenata* is

closely related to the new genus *Tuberculiforma*. Therefore, we propose a new combination for that species.

Class *Leotiomyces* O.E. Erikss. & Winka

Thelebolales Haeckel

Thelebolaceae Engl.

Pseudogymnoascus Raitio

Based on the dataset combined ITS, LSU, *MCM7*, *RPB2*, and *EF1A* sequences, the phylogeny of *Pseudogymnoascus* was studied. *Leuconeurospora pulcherrima* (CBS 343.76) and *Leuconeurospora* sp. (02NH04 and 15PA04) were used as the outgroup for the phylogenetic analysis. The concatenated sequences included 103 taxa and consisted of 4,021 nucleotides (ITS, 544 bp; LSU, 1,202 bp; *MCM7*, 596 bp; *RPB2*, 761 bp; and *EF1A*, 918 bp) with inserted gaps. The phylogenetic trees showed that members of the genus *Pseudogymnoascus* clustered into a group with a high support value (100/1) (Fig. 26). Additionally, our two new isolates (CGMCC 3.25513 and ZY 22.01) of *P. wildlifiparkensis* clustered into a single clade with a high support value (100/1) and closely related to *P. campensis* and 13 undescribed isolates (Fig. 26). Clades are identified using clade nomenclature (A to M) formally defined by Minnis and Lindner (2013).

Pseudogymnoascus wildlifiparkensis Zhi Y. Zhang & Y. F. Han, sp. nov.

Fig. 27

MycoBank number: MB850382; Facesoffungi number: FoF15086

Etymology – Named after the location of Guizhou Wildlife Park, where the holotype was collected.

Holotype – ZY H-22.050

Description – *Hyphae* branched, septate, hyaline, smooth, 1–2.5 µm diam. Sometimes lateral hyphae end in pyriform-shaped arthroconidia with a truncate base. Sexual morph: Not observed. Asexual morph: *Conidiophores* abundant, solitary, erect, arising in right or acute angles with the main axis, hyaline, smooth, usually bearing verticils of one to two branches arising from the stipe at an acute angle. *Aleurioconidia* solitary, pyriform or subglobose, with a broad truncated basal scar, 2.5–4 × 2–3 µm (av. 3.2 × 2.5, n = 30), in conidiophores separated by connective cells, smooth. *Intercalary conidia* pyriform to elongated, drum, cylindrical with slightly wider in the middle, or irregular, with a broad truncated scar at the base or both ends, 3.5–8 × 2.5–3.5 µm (av. 5.5 × 3.1 µm, n = 30), smooth. *Arthroconidia* not observed.

Culture characteristics (14 d at 25 °C) – Colony on PDA 16–18 mm, white to pale green, fluffy, flocculent, sectorization, sulcate, margin corrugated, exudates and diffusible pigments absent; reverse broom yellow to dahlia yellow. Colony on MEA 18–21 mm, white, fluffy, flocculent, sulcate, margin regular, exudates and diffusible pigments absent; reverse zinc yellow. Colony on SNA 22–24 mm, white, fluffy, flocculent, margin regular, exudates and diffusible pigments absent; reverse white. Colony on OA 18–19 mm, white, fluffy, exudates absent, producing a diffusible faint white pigment; reverse white.

Material examined – China, Guizhou Province, Guiyang City, Xiuwen County, Zhazuo Town, soil collected from the green belts of Guizhou Wildlife Park, 106.69 E, 26.85 N, 25 May 2022, Zhi-Yuan Zhang (holotype, ZY H-22.050), ex-type CGMCC 3.25513 = ZY 22.050; *ibid.* ZY 22.051.

Notes – Based on multi-locus phylogenetic analyses (Fig. 26) and morphological characteristics, *P. wildlifiparkensis* is proposed as a novel species belonging to clade A (Minnis & Lindner 2013). Clade A consists of *P. campensis* and several unidentified isolates (Minnis & Lindner 2013, Zhang et al. 2023b). Morphologically, *P. wildlifiparkensis* mainly differs from *P. campensis* in intercalary conidia shape and size (pyriform to elongated, drum, cylindrical with slightly wide in the middle, or irregular, av. 5.5 × 3.1 µm in *P. wildlifiparkensis* vs. barrel, reniform, pyriform to elongated or irregular, av. 4 × 2.6 µm in *P. campensis*) (Zhang et al. 2023b). In addition, *P. wildlifiparkensis* differs from *P. campensis* by their *MCM7* sequence similarities (97.7%, 597/611, no gap).

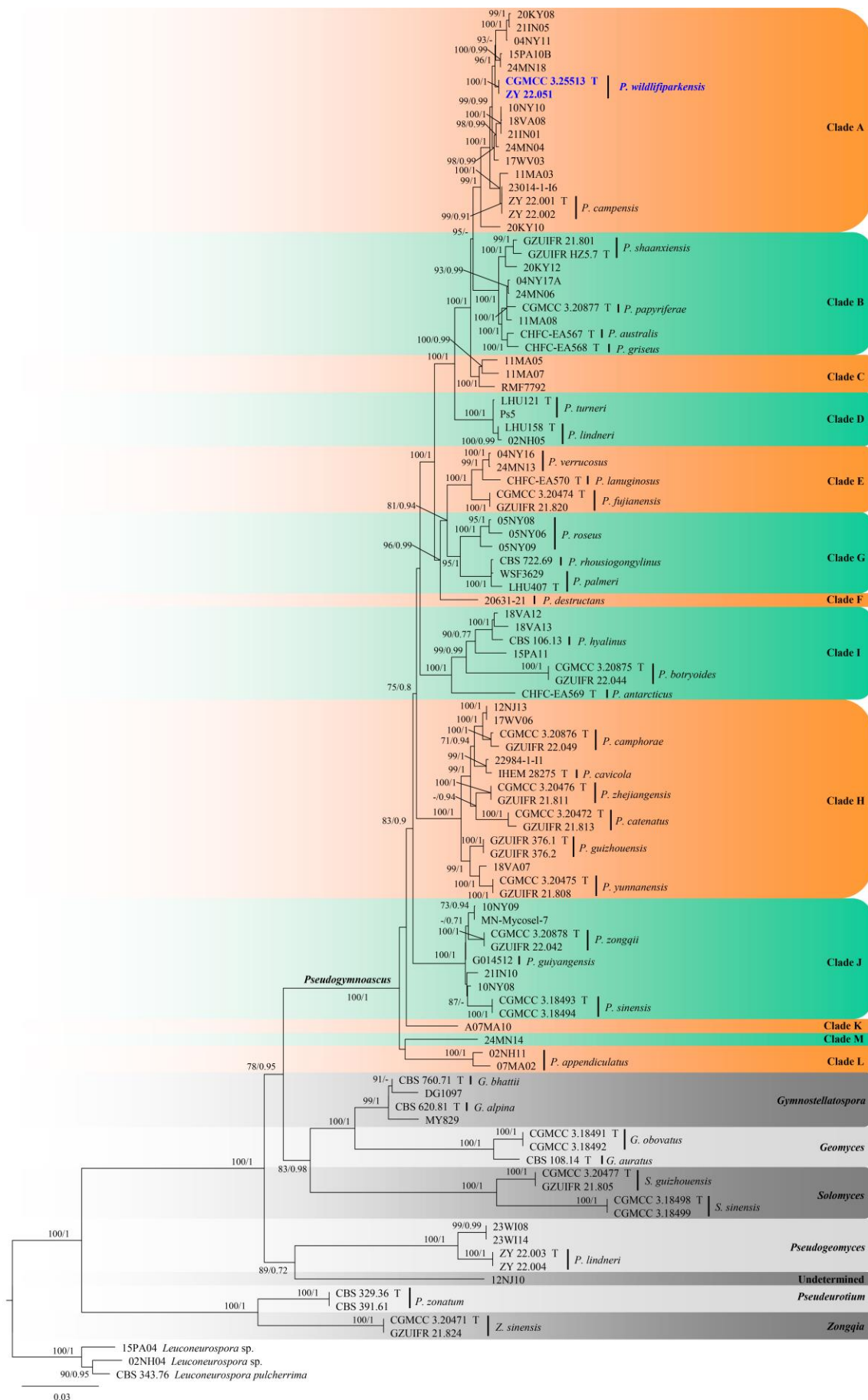


Figure 26 – Phylogram generated from maximum likelihood analysis based on combined ITS, LSU, MCM7, RPB2, and EF1A sequence data. Estimated base frequencies were as follows; A = 0.247,

C = 0.253, G = 0.262, T = 0.239; substitution rates AC = 1.25186, AG = 5.37492, AT = 1.41898, CG = 1.04073, CT = 7.88603, GT = 1.00000; gamma distribution shape parameter α = 0.519. The tree topology of ML analysis is similar to BI analysis. Bootstrap support values for MLBS $\geq$ 70% and BYPP $\geq$ 0.7 are defined as BS/PP above the nodes. Hyphens (-) represent support values less than 70% in ML and 0.7 in BI. Newly generated sequences are in blue and “T” indicates type strain.

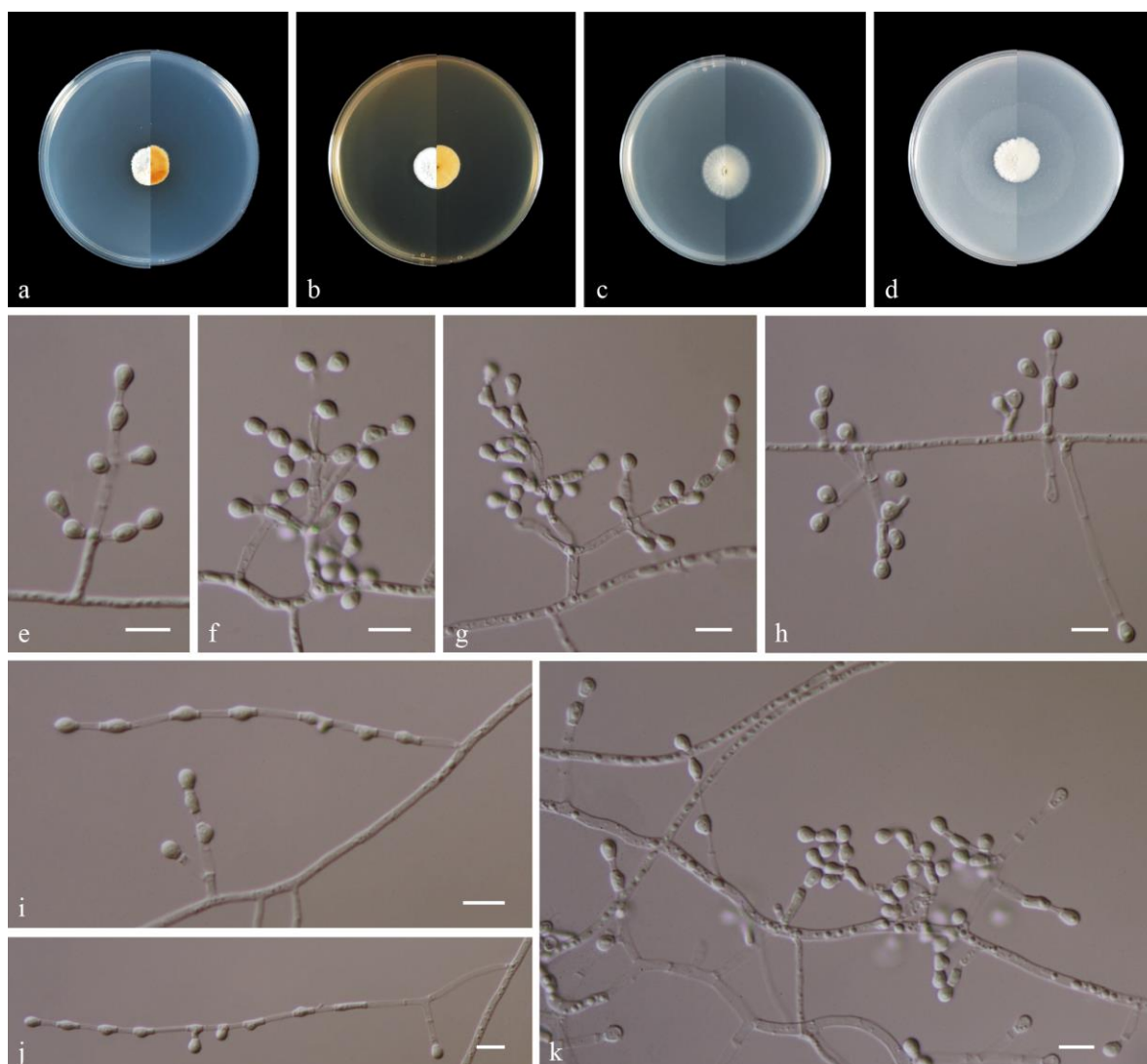


Figure 27 – *Pseudogymnoascus wildlifiparkensis* (CGMCC 3.25513). a–d Upper and reverse views of cultures on PDA, MEA, SNA, and OA 14 d after inoculation. e–h, k Conidiophore and conidia. i–j Intercalary conidia. Scale bars: e–k = 10 µm.

Class **Sordariomycetes** O.E. Erikss. & Winka

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

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

Apiospora Sacc.

Based on the dataset combined ITS, LSU, *EF1A*, and *TUB* sequences, the phylogeny of *Apiospora* was studied. *Nigrospora vesicularis* (CGMCC 3.18128) and *N. osmanthi* (CGMCC 3.18126) were used as the outgroup for the phylogenetic analysis. The concatenated sequences included 148 taxa and consisted of 2,705 nucleotides (ITS, 834 bp; LSU, 837 bp; *EF1A*, 445 bp; and *TUB*, 589 bp) with inserted gaps. The phylogenetic trees showed that four new isolates (CGMCC 3.25514, ZY 22.053, ZY 22.054, and ZY 22.055) of *A. olivata* clustered into a single clade with a high support value (100/1) and closely related to species *A. machili* (Fig. 28).

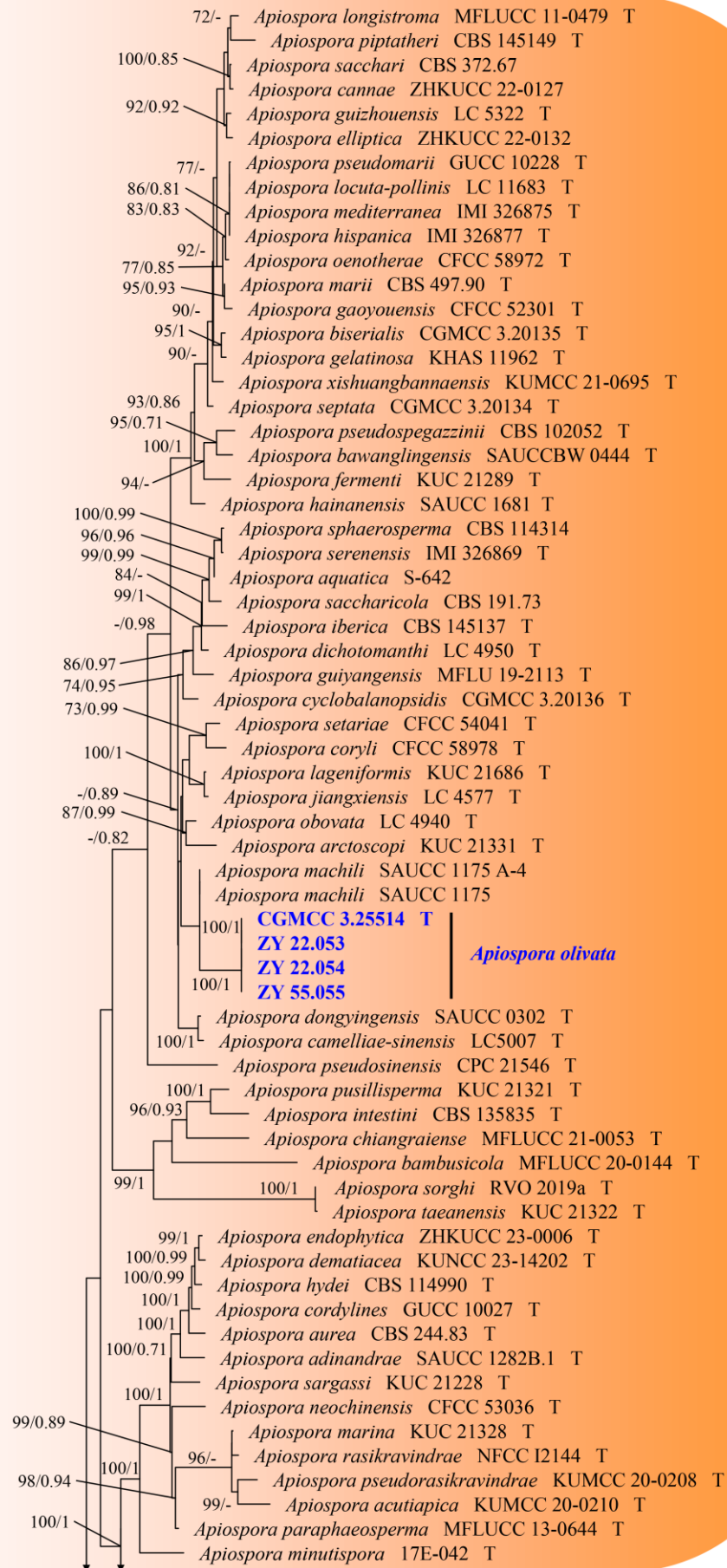


Figure 28 – Phylogram generated from maximum likelihood analysis based on combined ITS, LSU, *EF1A*, and *TUB* sequence data. Estimated base frequencies were as follows; A = 0.234, C = 0.250,

G = 0.258, T = 0.258; substitution rates AC = 1.31382, AG = 3.16922, AT = 1.03860, CG = 1.02028, CT = 4.88016, GT = 1.00000; gamma distribution shape parameter $\alpha = 0.467$. The tree topology of ML analysis is similar to BI analysis. Bootstrap support values for MLBS $\geq 70\%$ and BYPP ≥ 0.7 are defined as BS/PP above the nodes. Hyphens (-) represent support values less than 70% in ML and 0.7 in BI. Newly generated sequences are in blue and “T” indicates type strain.

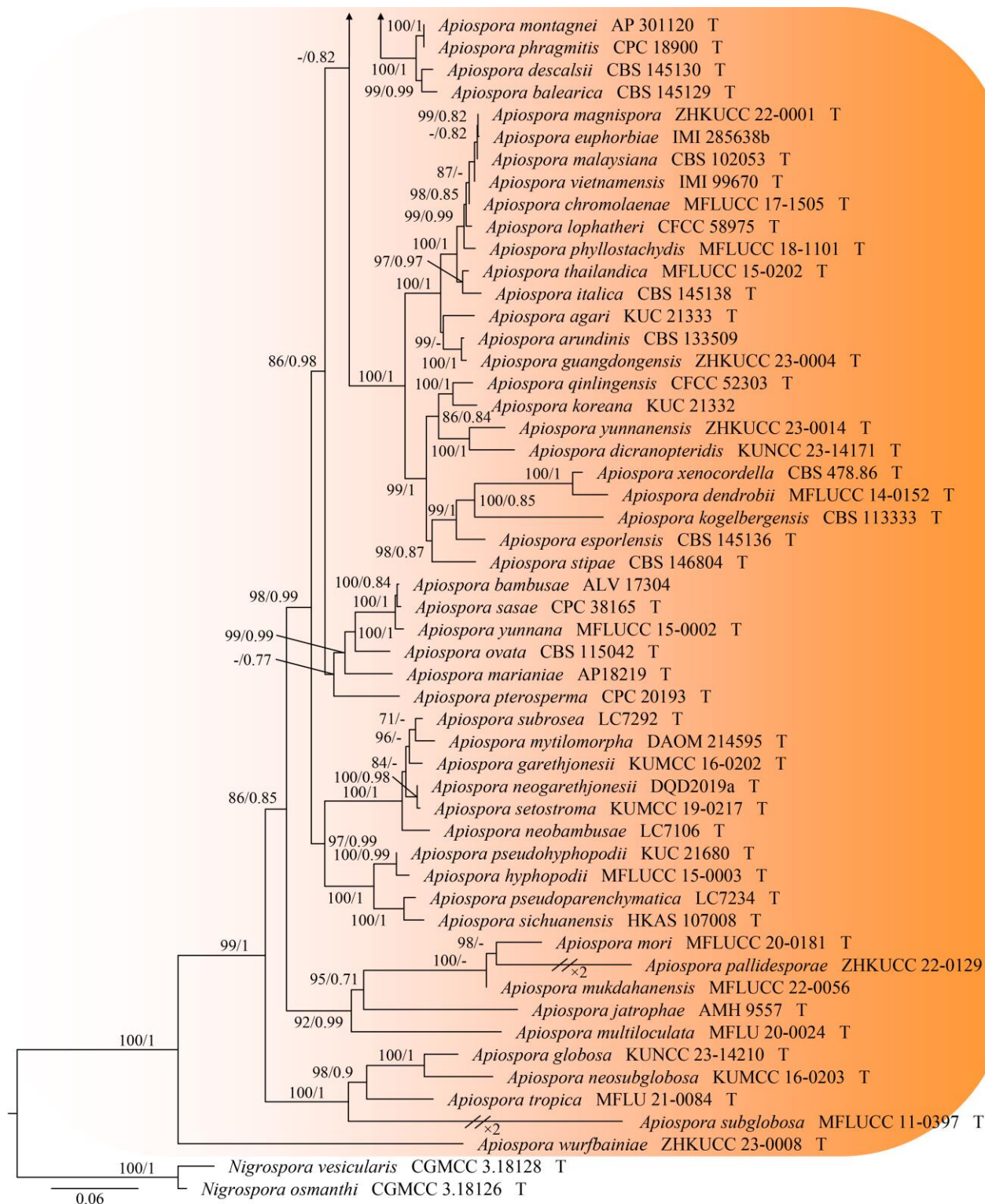


Figure 28 – Continued.

Apiospora olivata Zhi Y. Zhang & Heng Pan, sp. nov.

Mycobank number: MB850383; Facesoffungi number: FoF15087

Fig. 29

Etymology – Referring to the production of the olivary conidia.

Holotype – ZY H-22.052

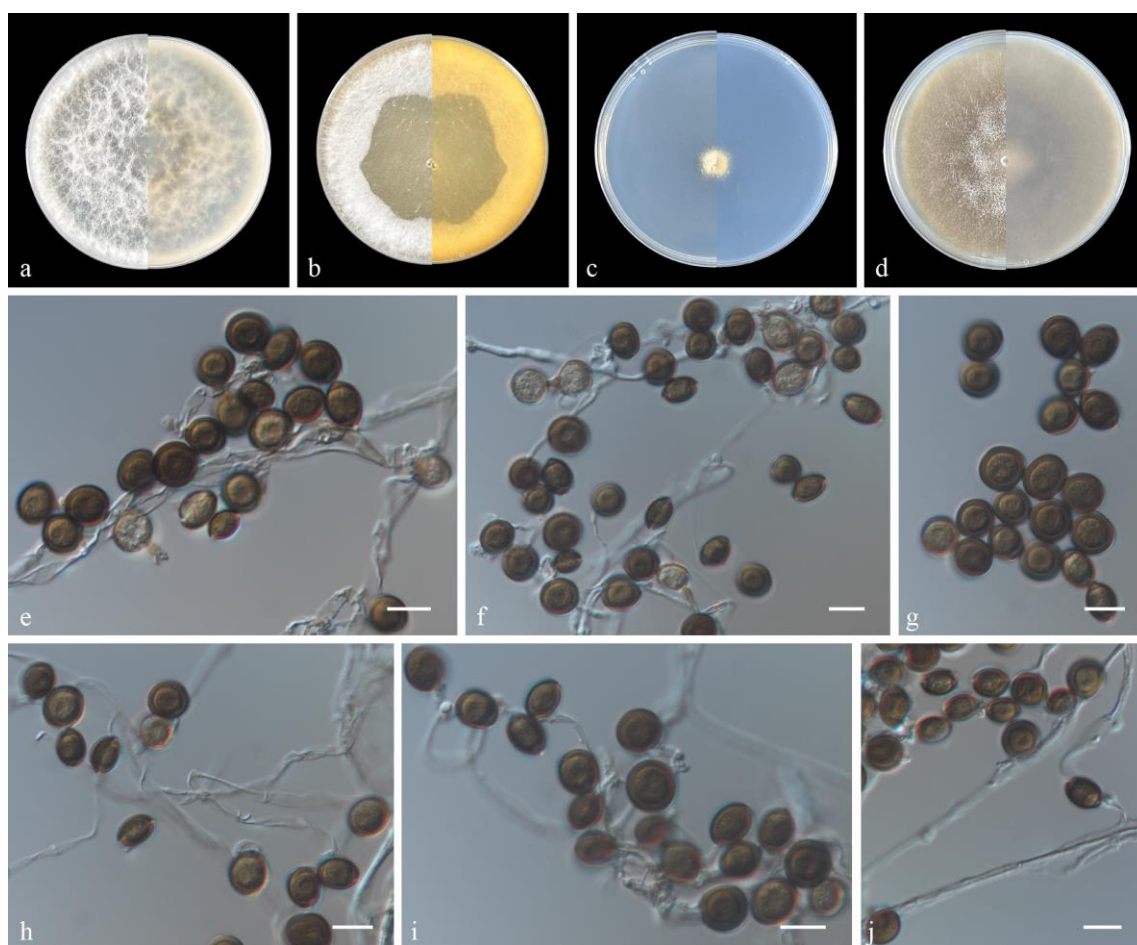


Figure 29 – *Apiospora olivata* (CGMCC 3.25514). a–d Upper and reverse views of cultures on PDA, MEA, SNA, and OA 14 d after inoculation. e–j Conidiophore, conidiogenous cells and conidia. Scale bars: e–j = 10 μ m.

Description – *Hyphae* branched, septate, hyaline, smooth, 1–3 μ m diam. Sexual morph: Not observed. Asexual morph: *Conidiophores* are reduced to conidiogenous cells. *Conidiogenous cells* aggregated in clusters on hyphae or solitary, smooth, hyaline, cylindrical, erect or curved. *Conidia* brown, finely roughened, granular, olivary with slightly bluntly rounded at both ends, 8–12 $\times$ 5.5–8 μ m (av. 10.2 $\times$ 6.7, n = 30), subglobose to globose, 8–11.5 μ m (av. = 9.7, n = 30).

Culture characteristics (14 d at 25 $^{\circ}$ C) – Colony on PDA fast-growing, more than 90 mm, flocculent, felty, margin circular, initially white, becoming curry on the surface; reverse pale green. Colony on MEA fast-growing, more than 90 mm, slightly thick, flat, mycelia white; reverse pale yellow. Colony on SNA 15–17 mm, fluffy, flocculent, margin irregular, white; reverse white. Colony on OA fast-growing, more than 90 mm, thick, concentrically spreading with aerial mycelium, white; reverse white.

Material examined – China, Guizhou Province, Guiyang City, Xiuwen County, Zhazuo Town, soil collected from the green belts of Guizhou Wildlife Park, 106.69 E, 26.85 N, 25 May 2022, Zhi-Yuan Zhang (holotype, ZY H-22.052), ex-type CGMCC 3.25514 = ZY 22.052; *ibid.* ZY 22.053. China, Guizhou Province, Guiyang City, Xiuwen County, Zhazuo Town, soil collected from the green belts of Guizhou Wildlife Park, 106.69 E, 26.85 N, 25 May 2022, Zhi-Yuan Zhang ZY 22.054 and ZY 22.055.

Notes – Phylogenetically, *Apiospora olivata* forms a distinct clade and is closely related to *A. machili* (Fig. 28). Morphologically, *A. olivata* differs from *A. machili* in conidiogenous cells and

conidia. *Apiospora machili* has the conidiogenous cells polyblastic, septate, verrucose and smaller conidia ($7.1\text{--}9.5 \times 5.6\text{--}8.8 \mu\text{m}$), whereas *A. olivata* conidiogenous cells cylindrical, erect or curved, smooth and bigger conidia ($8\text{--}12 \times 5.5\text{--}8 \mu\text{m}$) (Liu et al. 2024). In addition, they can be distinguished by their low ITS sequence similarities (79.7%, 531/666 bp, 117 gaps).

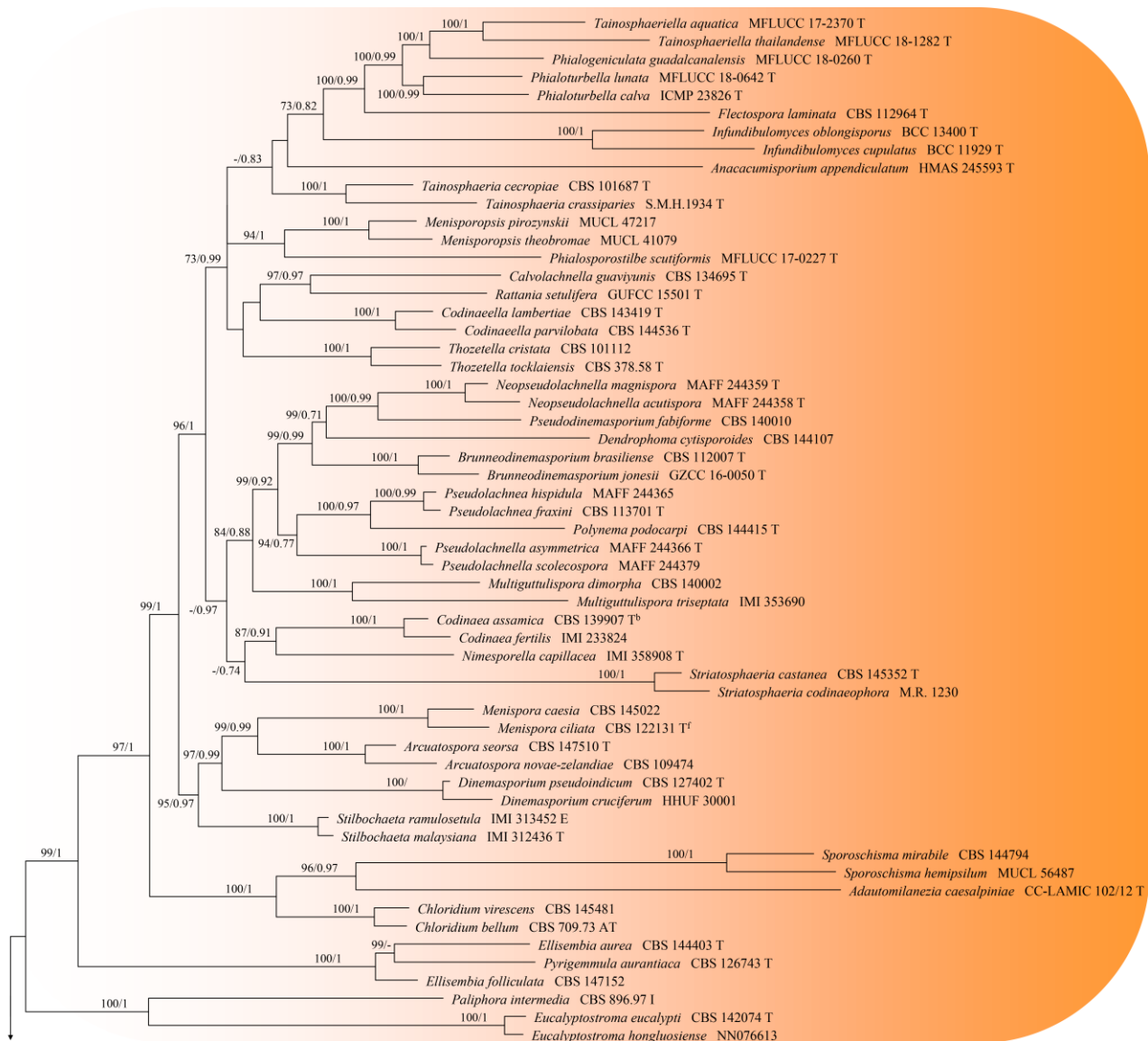


Figure 30 – Phylogram generated from maximum likelihood analysis based on combined ITS, LSU, and *EF1A* sequence data. Estimated base frequencies were as follows; A = 0.221, C = 0.291, G = 0.295, T = 0.193; substitution rates AC = 1.01770, AG = 1.75029, AT = 1.26725, CG = 0.85079, CT = 5.57638, GT = 1.00000; gamma distribution shape parameter $\alpha = 0.700$. The tree topology of ML analysis is similar to BI analysis. Bootstrap support values for MLBS $\geq 70\%$ and BYPP ≥ 0.7 are defined as BS/PP above the nodes. Hyphens (-) represent support values less than 70% in ML and 0.7 in BI. Newly generated sequences are in blue and “T” indicates type strain.

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

Chaetosphaeriaceae Réblová, M.E. Barr & Samuels

Based on the dataset combined ITS, LSU, and *EF1A* sequences, the phylogeny of *Paragongromeriza* and its related taxa were studied. *Tracylla eucalypti* (CBS 144429) and *T. aristata* (CBS 141404) were used as the outgroup for the phylogenetic analysis. The concatenated sequences included 140 taxa and consisted of 2,474 nucleotides (ITS, 712 bp; LSU, 848 bp; and *EF1A*, 914 bp) with inserted gaps. The phylogenetic trees showed that five new

Phylogenetic tree showing the relationships between various species, primarily focusing on the genus *Chaetosphaeria* and related genera. The tree is rooted at the bottom left. Bootstrap values are indicated at the nodes. The tree is color-coded: orange for *Chaetosphaeria* and related genera, green for *Paragongromeriza sinensis*, and blue for other genera.

Species listed (from top to bottom):

- Gongromeriza myriocarpa* CBS 141.53 T⁴
- Gongromeriza myriocarpa* CBS 264.76 N
- Gongromeriza pygmaea* CBS 144786
- Gongromeriza pygmaea* CBS 699.74 T⁴
- Phaeostagalagus cyclosporus* CBS 663.70
- Sporendoclada beijingensis* CGMCC 3.20738 T
- Sporendoclada fumosa* NN047731
- CGMCC 3.25515 T*
- ZY 22.057*
- ZY 22.058*
- ZY 22.059*
- ZY 22.060*
- Paragongromeriza sinensis* gen. et sp. nov.
- Chaetosphaeria guttulata* MFLUCC 17-1703 T
- Chaetosphaeria polygonalis* GZCC 20-0438 T
- Psilobotrys minutus* CBS 223.74
- Psilobotrys minutus* CBS 247.75
- Fusocatenula variegata* NN055332
- Fusocatenula submersa* MFLUCC 18-1342 T
- Chaetosphaeria mangrovei* MCD069 T
- Chaetosphaeria immurea* CBS 131270
- Chaetosphaeria immanis* CBS 145639
- Verhulstia bifurcata* NN077655
- Verhulstia trisorum* CBS 143234 T
- Gongromerizella lignicola* CBS 143.54 I
- Gongromerizella pini* CBS 146011 T
- Phialocephala fusca* CBS 301.85
- Caligiospora dilabens* CBS 734.83 E
- Caligiospora dilabens* CBS 735.83 T
- Caligiospora pannosa* CBS 551.80 T
- Caliciactrum bicolor* ICMP 15136
- Caliciactrum bicolor* PRA-21507 T
- Craspedodichthymum elatum* NN042874
- Papillospora hebetiseta* CBS 102340 T
- Papillospora hebetiseta* S.M.H. 2729
- Achrochaeta taiwanii* ICMP 15161
- Dictyochoeta callimorpha* ICMP 15130
- Dictyochoeta fuegiana* ICMP 15153 T²
- Fuschloridium cylindrosporum* CBS 101429 E
- Fuschloridium cylindrosporum* CBS 101430
- Capillissphaeria crustacea* CBS 144664
- Capillissphaeria crustacea* CBS 144665
- Spicatispora fennica* CBS 101641
- Paragaeumannomyces panamensis* S.M.H. 3596 T
- Paragaeumannomyces rubicundus* S.M.H. 3221 T
- Ericotrypha spinosa* S.M.H. 2754 T
- Kylinochaeta kylini* S.M.H. 3015 T
- Curvichaeta curvispora* ICMP 15115 T
- Curvichaeta curvispora* ICMP 15118
- Chaetosphaeria metallica* PDD 92539 T
- Chaetosphaeria metallica* PDD 92557
- Catenularia minor* PRM 900544 T²
- Catenularia angulosa* MFLUCC 18-1331
- Chalarodes obpyramidalis* PDD 119364
- Phaeodichloridium aquaticum* MFLUCC 18-1341 T
- Chaetosphaeria abietis* CBS 427.83
- Chaetosphaeria cylindrospora* S.M.H. 3568 T
- Chaetosphaeria coniosporis* S.M.H. 2183 T
- Cacumisporium capitatum* CBS 131690
- Cacumisporium acutatum* CBS 101315 T
- Naravaria filiformis* MFLUCC 17-2394
- Zanclospora novae-zelandiae* ICMP 15781 E
- Zanclospora ramifera* ICMP 22738 T
- Linkosia multiseptum* NN042961
- Linkosia rostrata* NN047479
- Morriisia indica* NN042908
- Aunstrupia nodipes* NN043149
- Ritsgaardia longispora* CGMCC 3.20794 T
- Ritsgaardia obclavata* CGMCC 3.20787 T
- Kionochaetiella ivoriensis* CBS 374.76 T
- Cryptophialoidea fasciculata* MFLU 18-1499
- Cryptophiale udagovae* GZCC 18-0047
- Paracryptophiale pirczynskii* NN044888
- Paraceratocladium sibiricum* NN055375
- Conicosomyces pseudotransvaalensis* HHUF 29956 T
- Paraceratocladiella polysetosa* NN044119
- Kionochaeta ramifera* MUCL 39164
- Kionochaeta microspora* GZCC 18-0036 T
- Eucalyptostromiella beijingensis* NN078016
- Pseudothozetella lunata* CGMCC 3.20661 T
- Geniculoseta preussii* CBS 262.76
- Geniculoseta preussii* CBS 263.75
- Tracylla eucalypti* CBS 144429 T
- Tracylla aristata* CBS 141404 E

Paragongromeriza Zhi Y. Zhang & Y. F. Han, gen. nov.

Etymology – Based on its close phylogenetic relationship to the genus *Gongromeriza*.

Description – *Hyphae* branched, septate, hyaline, smooth. Sexual morph: Not observed.

702

rounded base, pale brown to hyaline, aseptate, smooth. *Chlamydospores* mainly lateral, sessile or on a short stalk, sometimes terminal, rarely intercalary, solitary, globose, subglobose or pyriform, brown, thick-walled, smooth.

Notes – The genus *Paragongromeriza*, represented by *P. sinensis*, exhibits a close relationship with *Gongromeriza*, *Phaeostalagmus*, *Sporendocladia*, and *Chaetosphaeria* (*C. guttulate* and *C. polygonalis*) (Réblová et al. 2022, Réblová & Nekvindová 2023, Wu & Diao 2022). *Paragongromeriza* can be easily distinguished from other family members by its distinctive characteristics. One of the critical features is the absence of a sexual morph. Additionally, the apex of the conidiophores has collarettes. *Chlamydospores* are lateral, sessile, or have a short stalk.

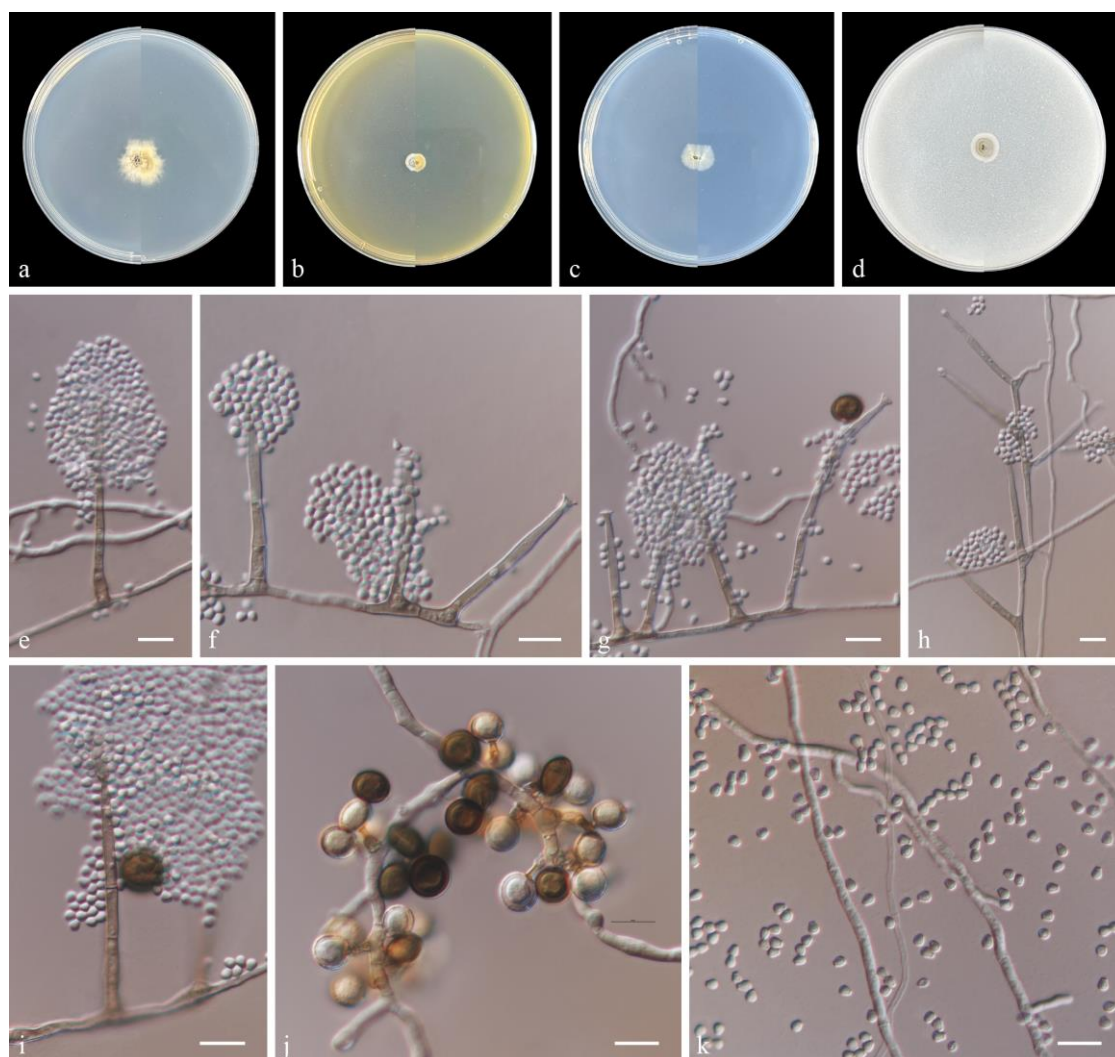


Figure 31 – *Paragongromeriza sinensis* (CGMCC 3.25515). a–d Upper and reverse views of cultures on PDA, MEA, SNA, and OA 14 d after inoculation. e–i Conidiophore and conidia. j Chlamydospores. k Conidia. Scale bars: e–k = 10 µm.

Paragongromeriza sinensis Zhi Y. Zhang & Y. F. Han, sp. nov.

Fig. 31

Mycobank number: MB850385; Facesoffungi number: FoF15088

Etymology – Named after the location China, where the holotype was collected.

Holotype – ZY H-22.056

Description – *Hyphae* branched, septate, hyaline, smooth, 1–3 µm diam. Sexual morph: Not observed. Asexual morph: The chloridium-type conidiophores 33.5–52.5 × 2–3.5 µm, macronematous, solitary, straight or slightly flexuous, unbranched, with none or 1–5 percurrent proliferations, septate, cylindrical or slightly tapering upwards, brown to hyaline, apex collarette, tapering to 1–2 µm below the collarette, collarettes 3–4.5 µm wide, 2–2.5 µm deep. *Conidiogenous*

cells 20–23 × 2.5–3 µm, tapering to 1–1.5 µm below the collarette, monophialidic, with a single conidiogenous locus, terminal, subcylindrical, slightly inflated in the base part, brown to hyaline, collarettes 3–3.5 µm wide, 2–2.5 µm deep, flaring, shortly funnel-shaped. *Conidia* 2–4 × 2–2.5 µm (av. 2.9 × 2.3 µm, n = 30), cuneiform to obovate with a broadly rounded base, pale brown to hyaline, aseptate, smooth. *Chlamydospores* 6.5–11.5 × 7.5–10 µm, mainly lateral, sessile or on a short stalk, sometimes terminal, rarely intercalary, solitary, globose, subglobose or pyriform, brown, thick-walled, smooth.

Culture characteristics (14 d at 25 °C) – Colony on PDA 14–20 mm, grey-white, fluffy, margin irregular; reverse white to grey. Colony on MEA 6–7 mm, caesious, slightly raised, margin regular; reverse grey. Colony on SNA 10–12 mm, white, flocculent, felty, margin irregular; reverse white. Colony on OA 9–10 mm, grey, flat, annular, margin regular; reverse grey.

Material examined – China, Guizhou Province, Guiyang City, Xiuwen County, Zhazuo Town, soil collected from the green belts of Guizhou Wildlife Park, 106.69 E, 26.85 N, 25 May 2022, Zhi-Yuan Zhang (holotype, ZY H-22.056), ex-type CGMCC 3.25515 = ZY 22.056; *ibid.* ZY 22.057. China, Guizhou Province, Guiyang City, Xiuwen County, Zhazuo Town, soil collected from the green belts of Guizhou Wildlife Park, 106.69 E, 26.85 N, 25 May 2022, Zhi-Yuan Zhang ZY 22.058, ZY 22.059, and ZY 22.060.

Notes – Phylogenetically, five new isolates, CGMCC 3.25515, ZY 22.057, ZY 22.058, ZY 22.059, and ZY 22.060, formed a single clade with a strongly supported value (Fig. 30), representing *Paragongromeriza sinensis*. However, *P. sinensis* can be easily distinguished morphologically from other family members due to its absent sexual morph (Réblová et al. 2022, Réblová & Nekvindová 2023, Wu & Diao 2022). The apex of the conidiophores has collarettes, and the chlamydospores are lateral, sessile, or have a short stalk (Réblová et al. 2022, Réblová & Nekvindová 2023, Wu & Diao 2022).

***Hypocreales* Lindau**

***Clavicipitaceae* Rogerson**

Based on the dataset combined SSU, ITS, LSU, *RPB2*, and *EF1A* sequences, the phylogeny of *Keithomyces*, *Marquandomyces* and its related taxa were studied. *Pleurocordyceps aurantiaca* (MFLUCC 17-2113) and *P. marginaliradians* (MFLU 17-1582) were used as the outgroup for the phylogenetic analysis. The concatenated sequences included 49 taxa and consisted of 3,953 nucleotides (SSU, 950 bp; ITS, 645 bp; LSU, 790 bp; *RPB2*, 715 bp; and *EF1A*, 853 bp) with inserted gaps. The phylogenetic trees showed that two new isolates (CGMCC 3.25518 and ZY 22.065) of *M. sinensis* clustered into a single clade with a high support value (100/1) and was closely related to *M. marquandii* (Fig. 32). The new isolates CGMCC 3.25517 and RCEF 4111 (type strain of *Paecilomyces echinosporus*) clustered into a single clade with a high support value (100/1) and nested in the genus *Keithomyces* (Fig. 32). In addition, the new isolates CGMCC 3.25516 and ZY 22.062 together with CBS 182.27 (type strain of *M. marquandii*) clustered into a single clade with a high support value (100/0.9) (Fig. 32).

***Keithomyces* Samson, Luangsa-ard & Houbraken**

Keithomyces echinosporus (M.J. Chen, G.H. Sung & B. Huang) Zhi Y. Zhang & Y. F. Han, com. nov. Fig. 33

≡ *Paecilomyces echinosporus* M.J. Chen, G.H. Sung & B. Huang, Mycotaxon 114: 28 (2010).

Mycobank number: MB850386; Facesoffungi number: FoF15089

Description – *Hyphae* branched, septate, hyaline, smooth, 1.5–3.5 µm diam. Sexual morph: Not observed. Asexual morph: *Conidiophores* mononematous unbranched arising laterally from aerial hyphae, smooth-walled, hyaline, simple, 40–95 × 2.5–3.5 µm. *Phialides* solitary, sometimes directly arising from aerial hyphae, or up to 5 in a whorl, acerose with elongated neck, straight to slightly tapered to-wards neck, smooth-walled, hyaline, 9–16 × 2–3 µm. *Conidia* one-celled, subglobose to ellipsoidal, fusiform, catenate, minutely echinulate, hyaline, 2.5–5 × 2–3 µm (av. 3.8 × 2.6 µm, n = 30). *Chlamydospores* not observed.

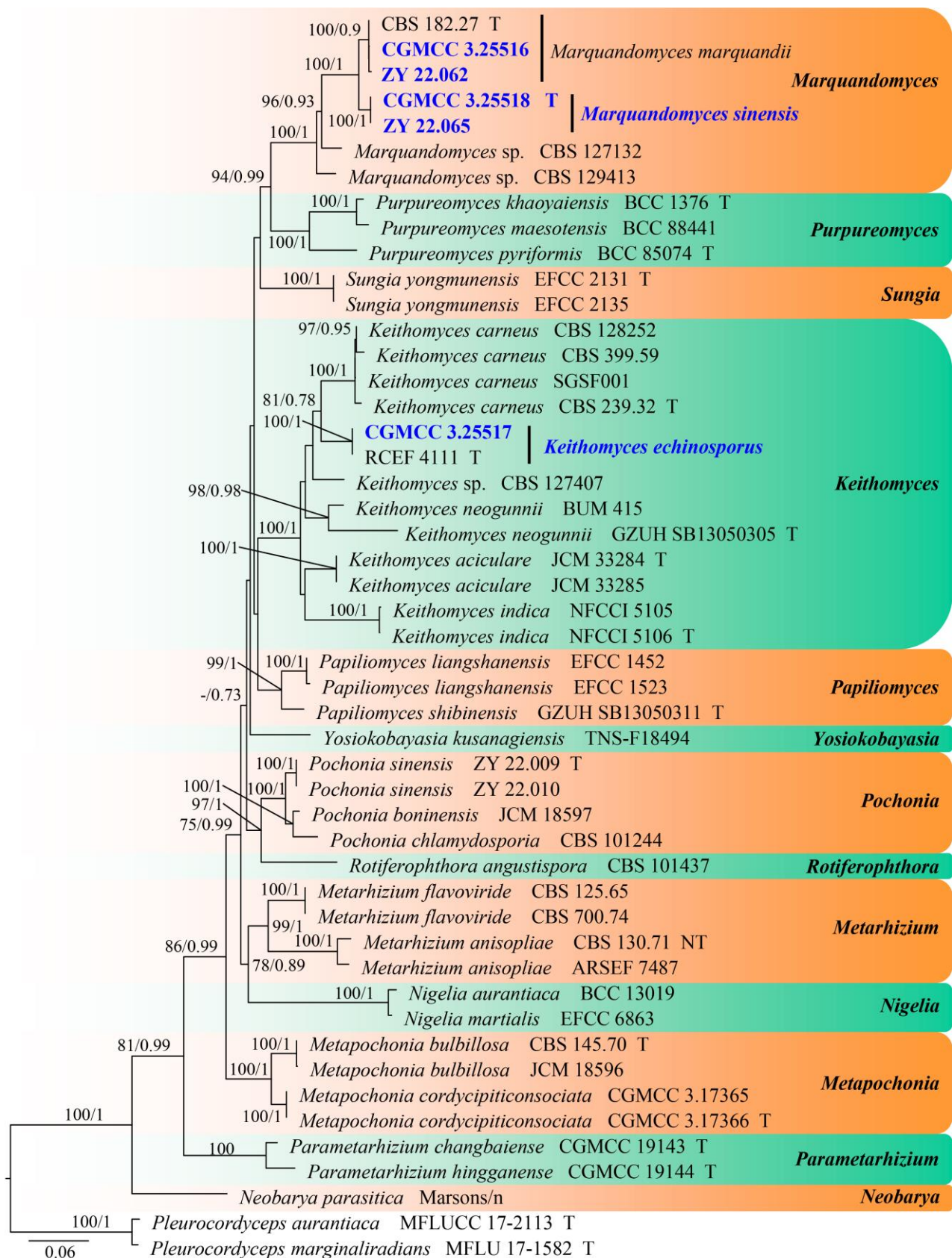


Figure 32 – Phylogram generated from maximum likelihood analysis based on combined SSU, ITS, LSU, *RPB2*, and *EF1A* sequence data. Estimated base frequencies were as follows; A = 0.243, C = 0.255, G = 0.271, T = 0.230; substitution rates AC = 1.74579, AG = 3.83882, AT = 1.32103, CG = 1.66440, CT = 7.85844, GT = 1.00000; gamma distribution shape parameter α = 0.357. The tree topology of ML analysis is similar to BI analysis. Bootstrap support values for MLBS $\geq$ 70% and

BYPP ≥ 0.7 are defined as BS/PP above the nodes. Hyphens (-) represent support values less than 70% in ML and 0.7 in BI. Newly generated sequences are in blue and “T” indicates type strain.

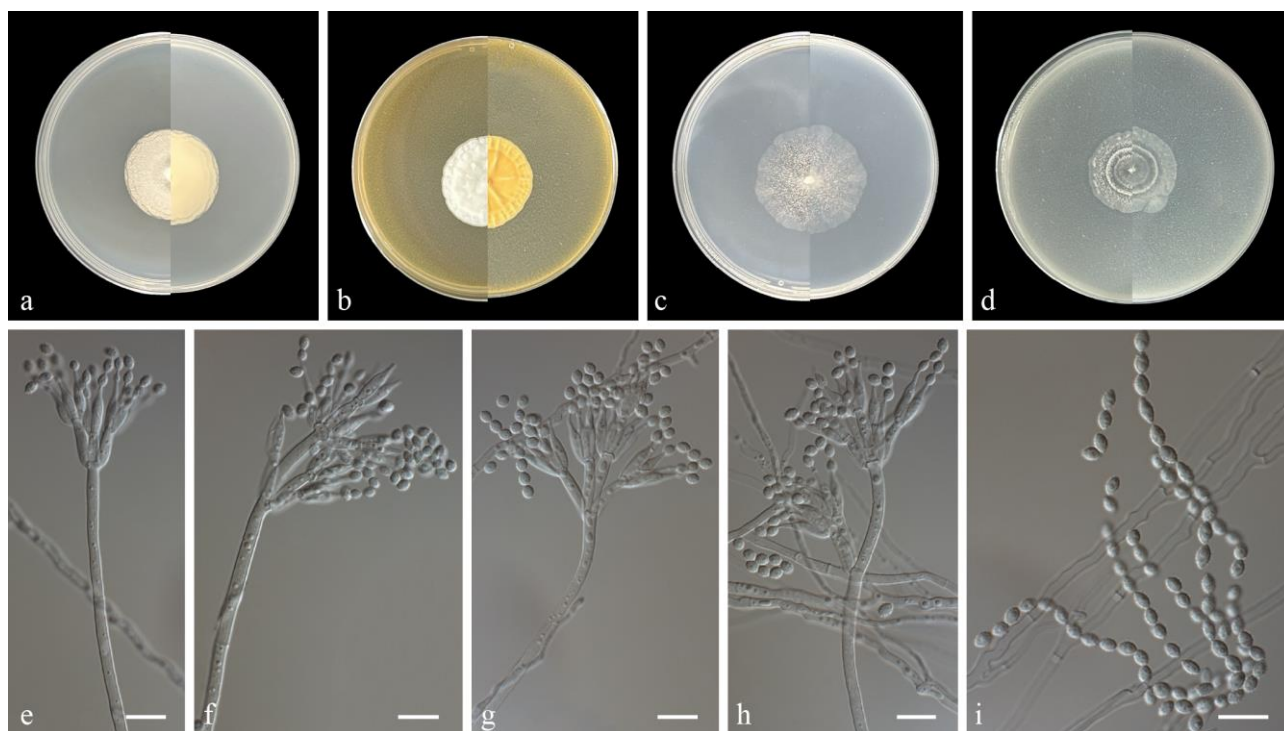


Figure 33 – *Keithomyces echinosporus* (CGMCC 3.25517). a–d Upper and reverse views of cultures on PDA, MEA, SNA, and OA 14 d after inoculation. e–h Conidiophore and conidia. i Conidia. Scale bars: e–i = 10 μ m.

Culture characteristics (14 d at 25 °C) – Colony on PDA 32–33 mm, fluffy, white, irregularly furrowed on the margins; reverse white. Colony on MEA 30–32 mm, fluffy, slightly ridged at the centre, white, margin slightly corrugated; reverse white. Colony on SNA 36–39 mm, powdery, flocculent, aerial hyphae sparse, margin irregular, white; reverse white. Colony on OA 26–29 mm, powdery, flocculent, aerial hyphae sparse, corrugated, margin irregular, white; reverse white.

Material examined – China, Guizhou Province, Guiyang City, Xiuwen County, Zhazuo Town, soil collected from the green belts of Guizhou Wildlife Park, 106.69 E, 26.85 N, 25 May 2022, Zhi-Yuan Zhang CGMCC 3.25517 = ZY 22.063.

Notes – *Paecilomyces echinosporus* was introduced by Chen et al. (2010). In this study, one newly collected isolate clustered with *P. echinosporus* and nested in the genus *Keithomyces* with strong support (100/1, Fig. 32). The comparison of the morphological characteristics of the two strains found them to be similar (Chen et al. 2010). Additionally, the ex-type culture (RCEF 4111) of *P. echinosporus* had high nucleotide similarities (ITS, 554/554, 100%) with the sequences of our newly collected strain (CGMCC 3.25517). Therefore, we identified our isolate as *P. echinosporus* and transferred it to the genus *Keithomyces* as *Keithomyces echinosporus*, as well as illustrated.

Marquandomyces Samson, Houbraken & Luangsa-ard

Marquandomyces sinensis Zhi Y. Zhang & Y. F. Han, sp. nov.

Fig. 34

MycoBank number: MB850387; Facesoffungi number: FoF15090

Etymology – Named after the location China, where the holotype was collected.

Holotype – ZY H-22.064

Description – *Hyphae* branched, septate, hyaline, smooth, 1–2.5 μ m diam. Sexual morph: Not observed. Asexual morph: *Conidiophores* mononematous arising laterally from aerial hyphae or formed as side branches on the aerial hyphae, smooth-walled, hyaline, simple, 24–57.5 $\times$ 1.5–3 μ m, consisting of single or verticillate branches with whorls of 2–4 phialides. *Phialides* solitary or up to

5 in a whorl, consisting of a short cylindrical to ellipsoidal basal portion, tapering into a distinct neck, $10\text{--}23 \times 2\text{--}4.5 \mu\text{m}$. *Conidia* one-celled, chains, ellipsoidal to fusiform, smooth-walled, hyaline, pale vinaceous en masse, $4\text{--}6.5 \times 2\text{--}4.5 \mu\text{m}$ (av. $5 \times 2.9 \mu\text{m}$, $n = 30$). *Chlamydospore*-like structures usually present solitary, thin-walled, subglobose to ellipsoidal, $14\text{--}17.5 \times 12.5\text{--}14.5 \mu\text{m}$.

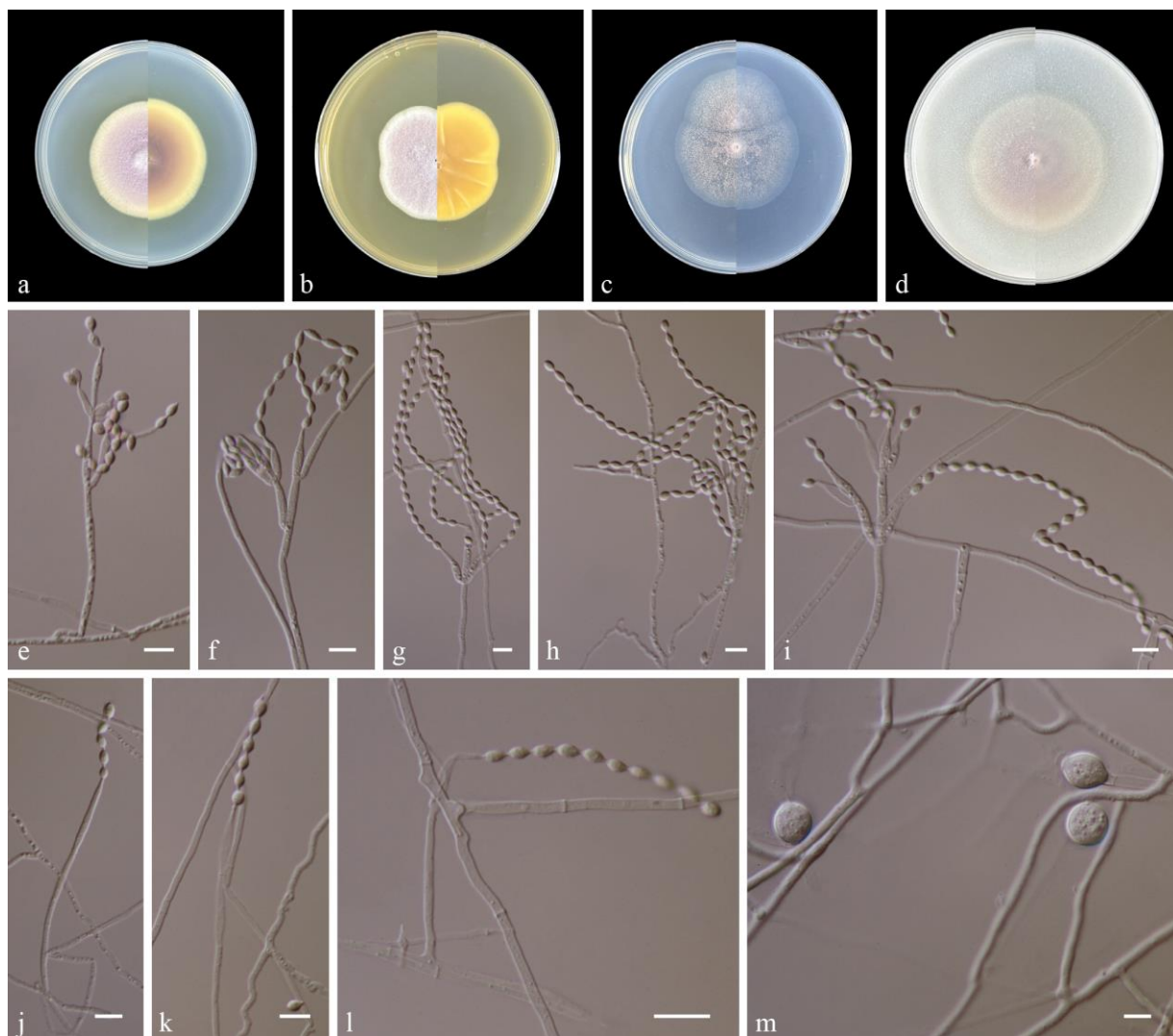


Figure 34 – *Marquandomyces sinensis* (CGMCC 3.25518). a–d Upper and reverse views of cultures on PDA, MEA, SNA, and OA 14 d after inoculation. e–l Conidiophore and conidia. m Chlamydospore-like structures. Scale bars: e–m = $10 \mu\text{m}$.

Culture characteristics (14 d at 25°C) – Colony on PDA 46–47 mm, flocculent, fluffy, antique pink to white from centre to margin, margin regular; reverse khaki grey to white from centre to margin. Colony on MEA 40–45 mm, flocculent, fluffy, pink-white to white, margin irregular, local invaginate; reverse sulfur yellow to rape yellow from centre to margin. Colony on SNA 46–47 mm, powdery, margin regular, pink; reverse white. Colony on OA 47–48 mm, felty, aerial hyphae sparse, pink to white, margin regular; reverse grey.

Material examined – China, Guizhou Province, Guiyang City, Xiuwen County, Zhazuo Town, soil collected from the green belts of Guizhou Wildlife Park, 106.69 E, 26.85 N, 25 May 2022, Zhi-Yuan Zhang (holotype, ZY H-22.064), ex-type CGMCC 3.25518 = ZY 22.064; *ibid.* ZY 22.065.

Notes – Phylogenetically, two new isolates, CGMCC 3.25518 and ZY 22.065, formed a single clade with a strongly supported value (100/1) and were nested in the genus *Marquandomyces* and closely related to *M. marquandii* (Fig. 32). However, morphologically, *M. sinensis* differs from

M. marquandii in the conidia size ($4\text{--}6.5 \times 2\text{--}4.5 \mu\text{m}$ in *M. sinensis* vs. $3\text{--}3.5 \times 2\text{--}2.2 \mu\text{m}$ in *M. marquandii*) and phialides size ($10\text{--}23 \times 2\text{--}4.5 \mu\text{m}$ in *M. sinensis* vs. $8\text{--}15 \times 1.5\text{--}2 \mu\text{m}$) (Samson 1974). In addition, *M. sinensis* differs from *M. marquandii* by their low ITS sequence similarities (95%, 504/530, 16 gaps).

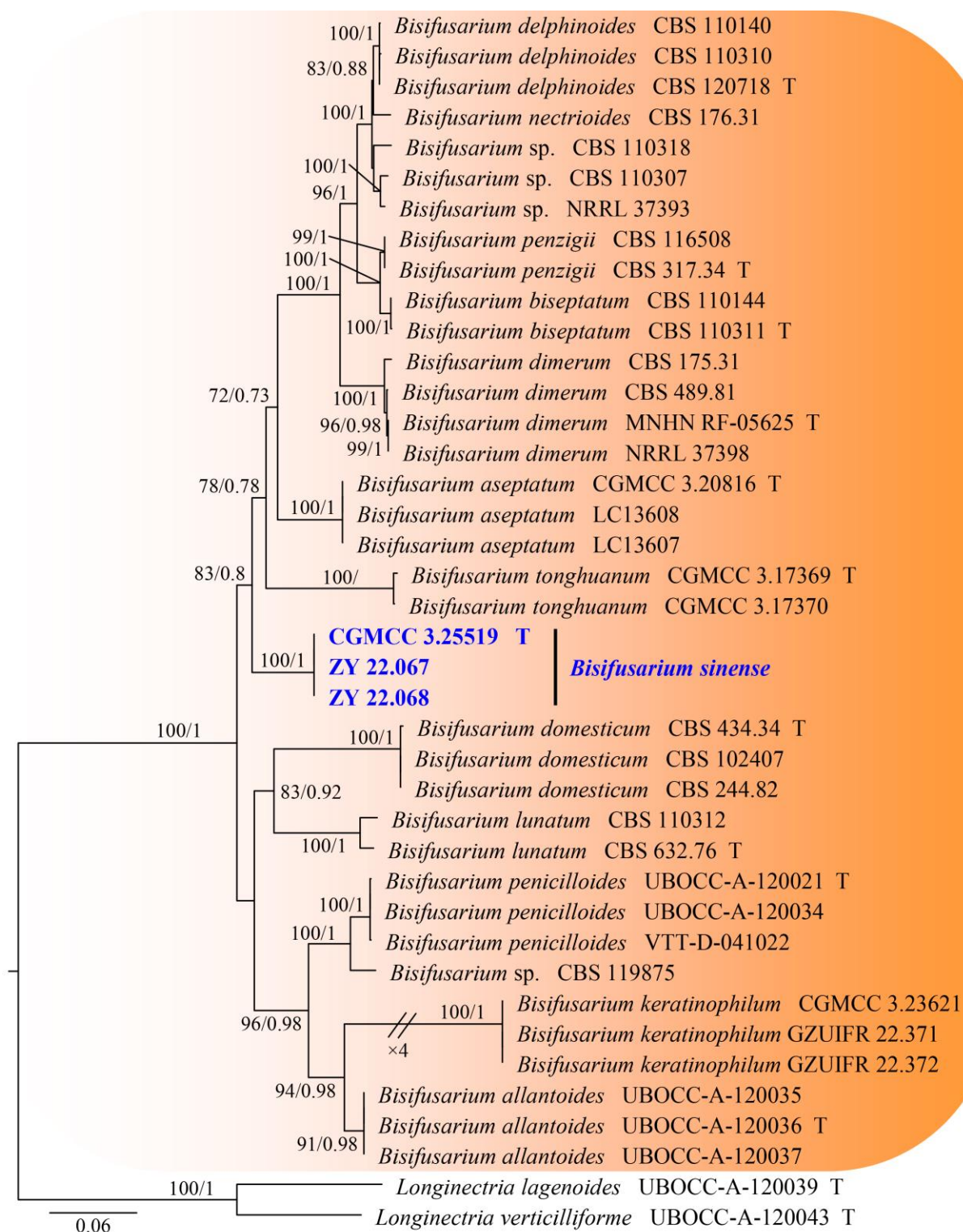


Figure 35 – Phylogram generated from maximum likelihood analysis based on combined ITS, LSU, EF1A, and TUB sequence data. Estimated base frequencies were as follows; A = 0.234, C = 0.275, G = 0.248, T = 0.244; substitution rates AC = 1.57765, AG = 3.51602, AT = 2.00400, CG = 1.14915, CT = 6.59522, GT = 1.00000; gamma distribution shape parameter $\alpha = 0.536$. The tree topology of ML analysis is similar to BI analysis. Bootstrap support values for MLBS $\geq 70\%$ and

BYPP ≥ 0.7 are defined as BS/PP above the nodes. Newly generated sequences are in blue and “T” indicates type strain.

Nectriaceae Tul. & C. Tul.

Bisifusarium L. Lombard, Crous & W. Gams

Based on the dataset combined ITS, LSU, *EF1A*, and *TUB* sequences, the phylogeny of *Bisifusarium* was studied. *Longinectria verticilliforme* (UBOCC-A-120043) and *L. lagenoides* (UBOCC-A-120039) were used as the outgroup for the phylogenetic analysis. The concatenated sequences included 49 taxa and consisted of 3,953 nucleotides (ITS, 513 bp; LSU, 514 bp; *EF1A*, 694 bp; and *TUB*, 599 bp) with inserted gaps. The phylogenetic trees showed that three new isolates (CGMCC 3.25519, ZY 22.067, and ZY 22.068) of *B. sinense* clustered into a single clade with a high support value (100/1) and separated from other taxa in the genus *Bisifusarium* (Fig. 35).

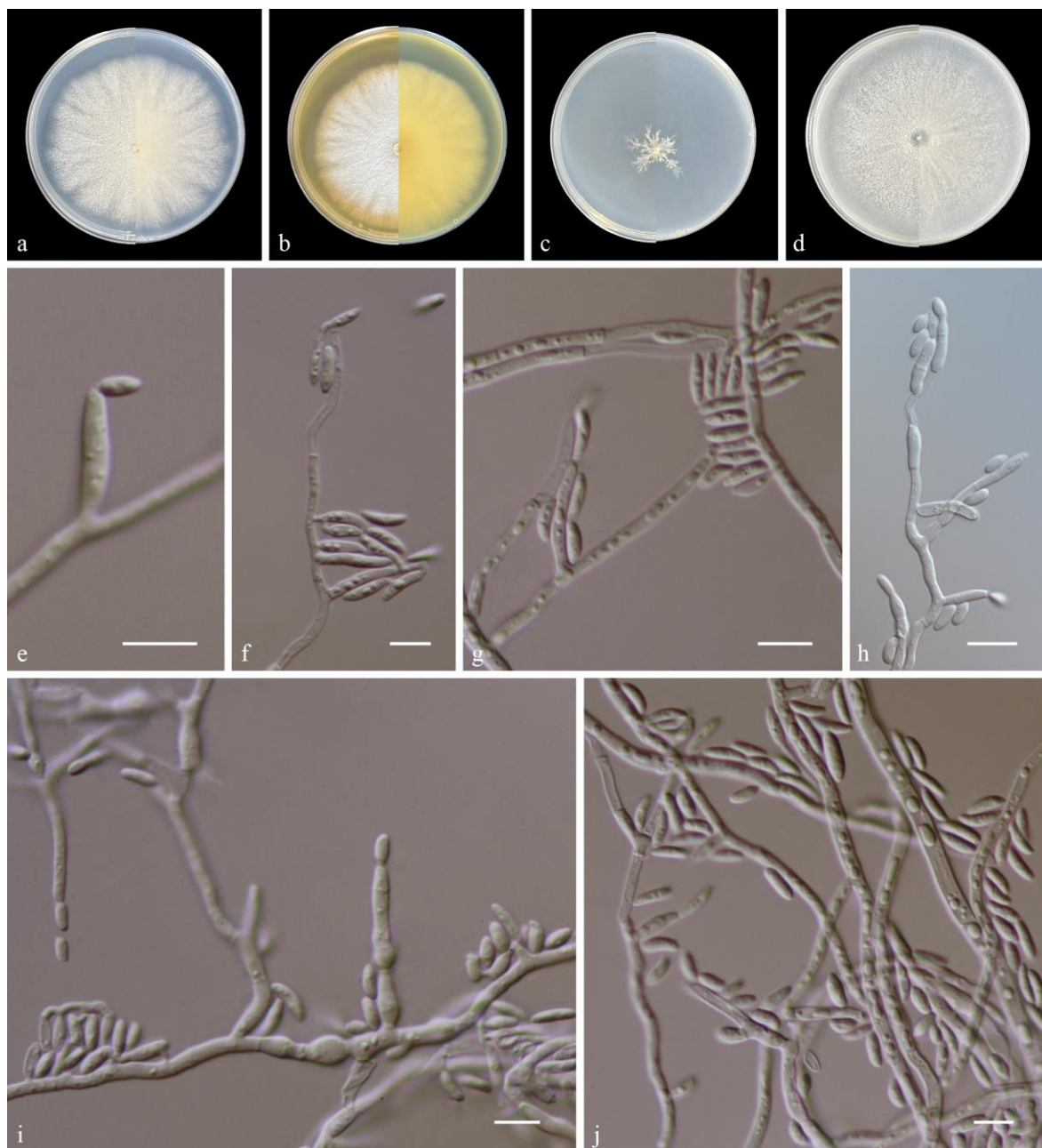


Figure 36 – *Bisifusarium sinense* (CGMCC 3.25519). a–d Upper and reverse views of cultures on PDA, MEA, SNA, and OA 14 d after inoculation. e–j Conidiophore and conidia. Scale bars: e–j = 10 μ m.

Bisifusarium sinense Zhi Y. Zhang & Y. F. Han, sp. nov.

Fig. 36

Mycobank number: MB850388; Facesoffungi number: FoF15091

Etymology – Named after the location China, where the holotype was collected.

Holotype – ZY H-22.066

Description – *Hyphae* branched, septate, hyaline, smooth, 1.5–4 µm diam. Sexual morph: Not observed. Asexual morph: *Phialides* were less abundant than in the other described *Bisifusarium* species. *Polyphialides* were not observed. *Monophialides* formed terminally or laterally on hyphae and were cylindrical, tapering toward the tip, straight or curved, 9–23 × 2–4 µm. *Microconidia* and macroconidia were difficult to distinguish. They were mostly aseptate, rarely 1-septate, fusiform, cylindrical with obtusely rounded ends, straight or curved, 3.5–13 × 2–4 µm (av. 8.4 × 2.6 µm, n = 30). *Chlamydospores* absent.

Culture characteristics (14 d at 25 °C) – Colony on PDA 74–77 mm, flocculent, felty, white, margin irregular; reverse white. Colony on MEA 69–70 mm, flocculent, felty, white, margin irregular; reverse white. Colony on SNA 19–29 mm, aerial hyphae sparse, white, margin irregular; reverse white. Colony on OA 72–73 mm, flocculent, powdery, white, margin regular; reverse white.

Material examined – China, Guizhou Province, Guiyang City, Xiuwen County, Zhazuo Town, soil collected from the green belts of Guizhou Wildlife Park, 106.69 E, 26.85 N, 25 May 2022, Zhi-Yuan Zhang (holotype, ZY H-22.066), ex-type CGMCC 3.25519 = ZY 22.066; *ibid.* ZY 22.067. China, Guizhou Province, Guiyang City, Xiuwen County, Zhazuo Town, soil collected from the green belts of Guizhou Wildlife Park, 106.69 E, 26.85 N, 25 May 2022, Zhi-Yuan Zhang ZY 22.068.

Notes – Phylogenetically, three new isolates, CGMCC 3.25519, ZY 22.067, and ZY 22.068, formed a single clade with a strongly supported value (100/1) and were nested in the genus *Bisifusarium* and close relationships with *B. aseptatum* and *B. tonghuanum* (Fig. 35). Morphologically, *B. sinense* can be differentiated from *B. aseptatum* and *B. tonghuanum* by its microconidia, macroconidia were difficult to distinguishable and are absent *Chlamydospores* (Sun et al. 2017, Wang et al. 2022). In addition, *B. sinense* differs from *B. aseptatum* and *B. tonghuanum* by their low sequence similarities. In a comparison of ITS, *EF1A*, *TUB*, and *RPB2* nucleotides, *B. sinense* (Type strain CGMCC 3.25519) has 94.2%, 87.2%, 90.6%, and 91.7% similarity, in ITS (472/501 bp, nine gaps), *EF1A* (574/658 bp, 26 gaps), *TUB* (301/332 bp, seven gaps), and *RPB2* (770/839 bp, no gap), which is different from *B. aseptatum* (Type strain CGMCC 3.20816). *Bisifusarium sinense* (CGMCC 3.25519) has 93.5%, 81.8%, 90.1%, and 90.5% similarity, in ITS (477/510 bp, three gaps), *EF1A* (518/633 bp, 23 gaps), *TUB* (301/334 bp, 12 gaps), and *RPB2* (749/827 bp, two gaps), which is different from *B. tonghuanum* (Type strain CGMCC 3.17369).

Volutella Tode

Based on the dataset combined ITS and LSU sequences, the phylogeny of *Volutella*, *Chaetopsina*, and *Atractium* were studied. *Pseudonectria buxi* (CBS 324.53) and *P. folicola* (CBS 123190) were used as the outgroup for the phylogenetic analysis. The concatenated sequences included 28 taxa and consisted of 1,286 nucleotides (ITS, 479 bp; and LSU, 807 bp) with inserted gaps. The phylogenetic trees showed that two new isolates (CGMCC 3.25520 and ZY 22.070) of *V. sinensis* clustered into a single clade with a high support value (100/1) and closely related to *V. aerea* (Fig. 37).

Volutella sinensis Zhi Y. Zhang & Y. F. Han, sp. nov.

Fig. 38

Mycobank number: MB850389; Facesoffungi number: FoF15092

Etymology – Named after the location China, where the holotype was collected.

Holotype – ZY H-22.069

Description – *Hyphae* branched, septate, hyaline, smooth, 1–3 µm diam. *Setae* and *sporodochia* not observed. *Verticillium*-like synasexual morph present. Sexual morph: Not observed. Asexual morph: *Conidiophores* on aerial hyphae, hyaline, branched, septate, cylindrical, straight or slightly curved, solitary, rarely verticillated, 15–40 × 1.5–2.0 µm, producing 1–4

phialides per node laterally or in whorls of 2–3 phialides terminally. *Phialides* hyaline, aseptate, slender, cylindrical, straight or slightly curved, slightly tapering towards the tip, 19–47.5 μm (av. 32.8 μm) long, 1–2 μm (av. 1.5 μm) wide at the base, 1–1.5 μm (av. 0.8 μm) near the aperture. *Conidia* hyaline, smooth, cylindrical, with obtuse ends, solitary, straight or slightly curved, smooth, 1-celled, 3.5–8.5 $\times$ 1–2 μm (av. 5.8 $\times$ 1.6 μm , $n = 30$).

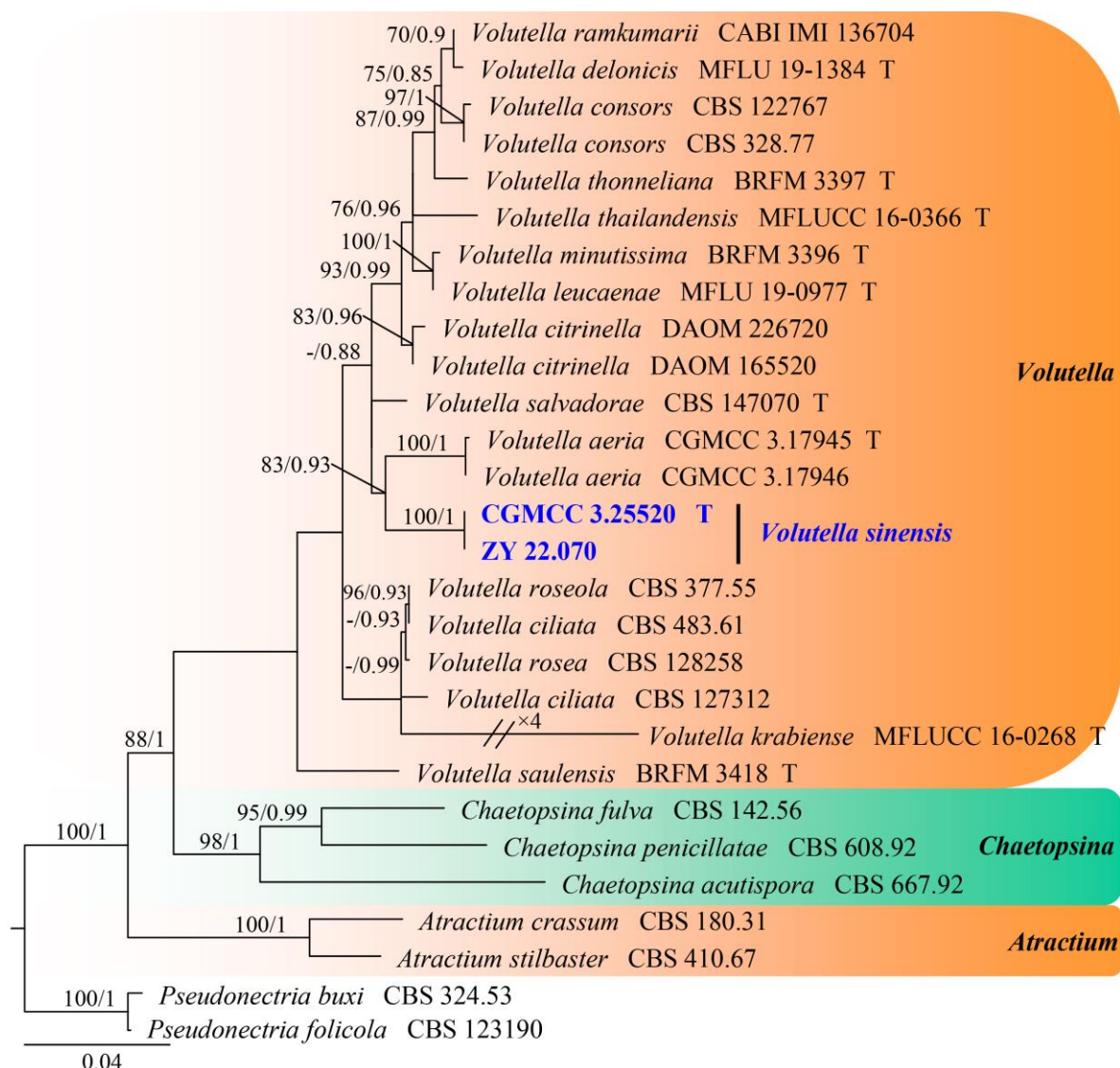


Figure 37 – Phylogram generated from maximum likelihood analysis based on combined ITS and LSU sequence data. Estimated base frequencies were as follows; A = 0.239, C = 0.238, G = 0.288, T = 0.235; substitution rates AC = 1.48228, AG = 2.13151, AT = 1.77998, CG = 0.80707, CT = 8.89247, GT = 1.00000; gamma distribution shape parameter $\alpha = 0.373$. The tree topology of ML analysis is similar to BI analysis. Bootstrap support values for MLBS $\geq 70\%$ and BYPP ≥ 0.7 are defined as BS/PP above the nodes. Hyphens (-) represent support values less than 70% in ML and 0.7 in BI. Newly generated sequences are in blue and "T" indicates type strain.

Culture characteristics (14 d at 25 °C) – Colony on PDA 26–28 mm, flocculent, aerial hyphae dense, white, margin irregular; reverse white. Colony on MEA 42–43 mm, flocculent, white, margin regular; reverse white. Colony on SNA 46–48 mm, flocculent, aerial hyphae sparse, white, margin regular; reverse white. Colony on OA 61–62 mm, flocculent, aerial hyphae sparse, white, margin regular; reverse white.

Material examined – China, Guizhou Province, Guiyang City, Xiuwen County, Zhazuo Town, soil collected from the green belts of Guizhou Wildlife Park, 106.69 E, 26.85 N, 25 May

2022, Zhi-Yuan Zhang (holotype, ZY H-22.069), ex-type CGMCC 3.25520 = ZY 22.069; *ibid.* ZY 22.070.

Notes – Phylogenetically, the new isolates, CGMCC 3.25520 and ZY 22.070, formed a single clade with a strongly supported value (100/1) and were nested in the genus *Volutella* and allied to *V. aerea* (Fig. 37). However, morphologically, *V. sinensis* can be differentiated from *V. aerea* by its smaller conidia ($3.5\text{--}8.5 \times 1\text{--}2\ \mu\text{m}$ in *V. sinensis* vs. $5.5\text{--}11.5 \times 2\text{--}3.5\ \mu\text{m}$ in *V. aerea*) (Zhang et al. 2017b). *Volutella sinensis* absent setae and sporodochia, which are observed in *V. aerea* (Zhang et al. 2017b). In addition, *V. sinensis* differs from *V. aerea* by their low sequence similarities. In a comparison of ITS and LSU nucleotides, *V. sinensis* (Type strain CGMCC 3.25520) has 92% and 98% similarity, in ITS (484/526 bp, 12 gaps) and LSU (807/823 bp, three gaps), which is different from *V. aerea* (Type strain CGMCC 3.17945).

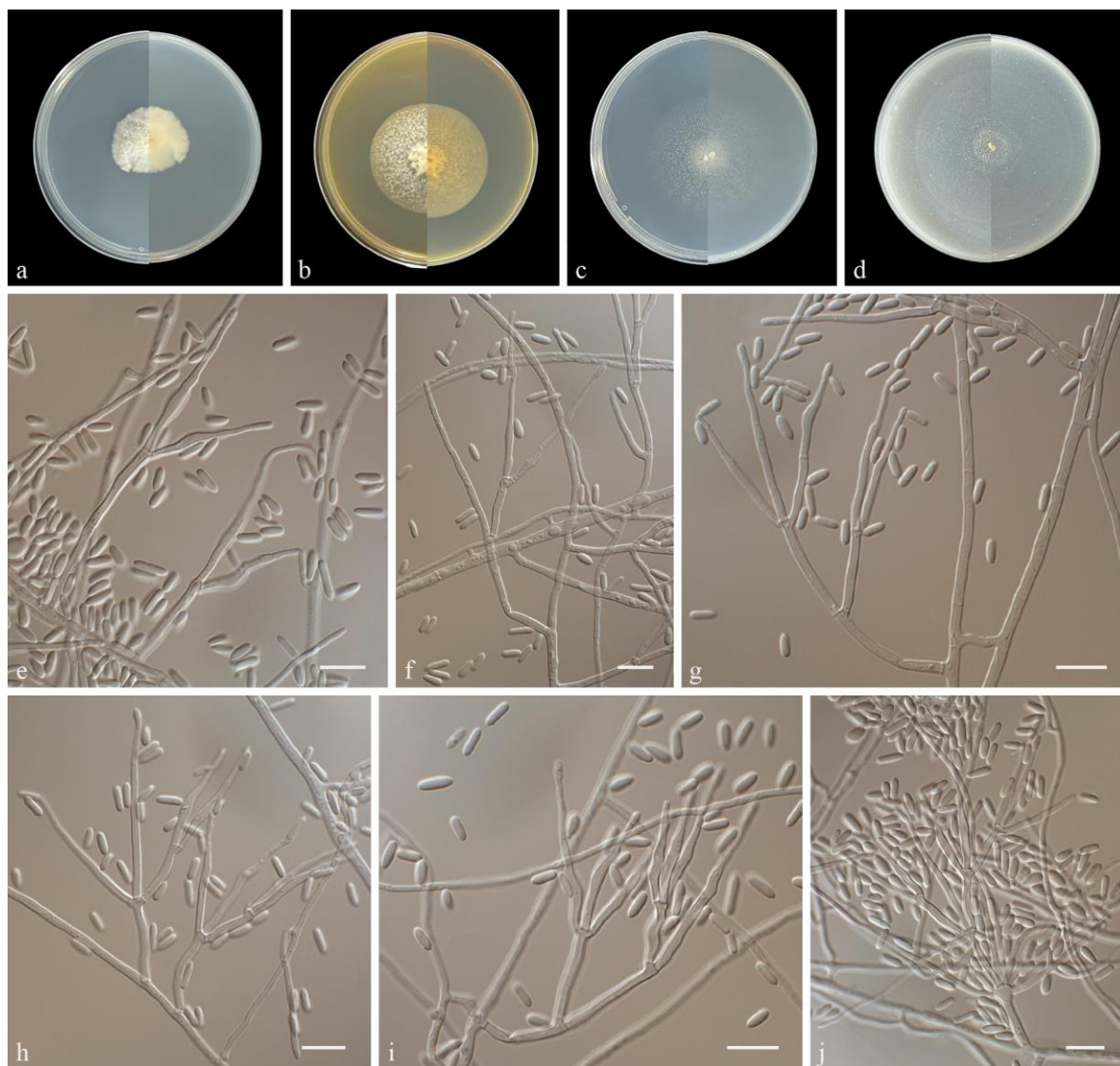


Figure 38 – *Volutella sinensis* (CGMCC 3.25520). a–d Upper and reverse views of cultures on PDA, MEA, SNA, and OA 14 d after inoculation. e–j Conidiophore and conidia. Scale bars: e–j = 10 μm .

***Sarocladiaceae* L. Lombard**

***Parasarocladium* Summerb., J.A. Scott, Guarro & Crous**

Based on the dataset combined ITS, LSU, *RPB2*, and *EF1A* sequences, the phylogeny of *Parasarocladium* was studied. *Sarocladium implicatum* (CBS 959.72) and *S. ochraceum* (CBS 428.67) were used as the outgroup for the phylogenetic analysis. The concatenated sequences

included 21 taxa and consisted of 2,790 nucleotides (ITS, 447 bp; LSU, 781 bp; *RPB2*, 754 bp; and *EF1A*, 808 bp) with inserted gaps. The phylogenetic trees showed that two new isolates (CGMCC 3.25521 and ZY22.072) of *P. sinense* clustered into a single clade with a high support value (100/0.9) and closely related to *P. gamsii* (Fig. 39).

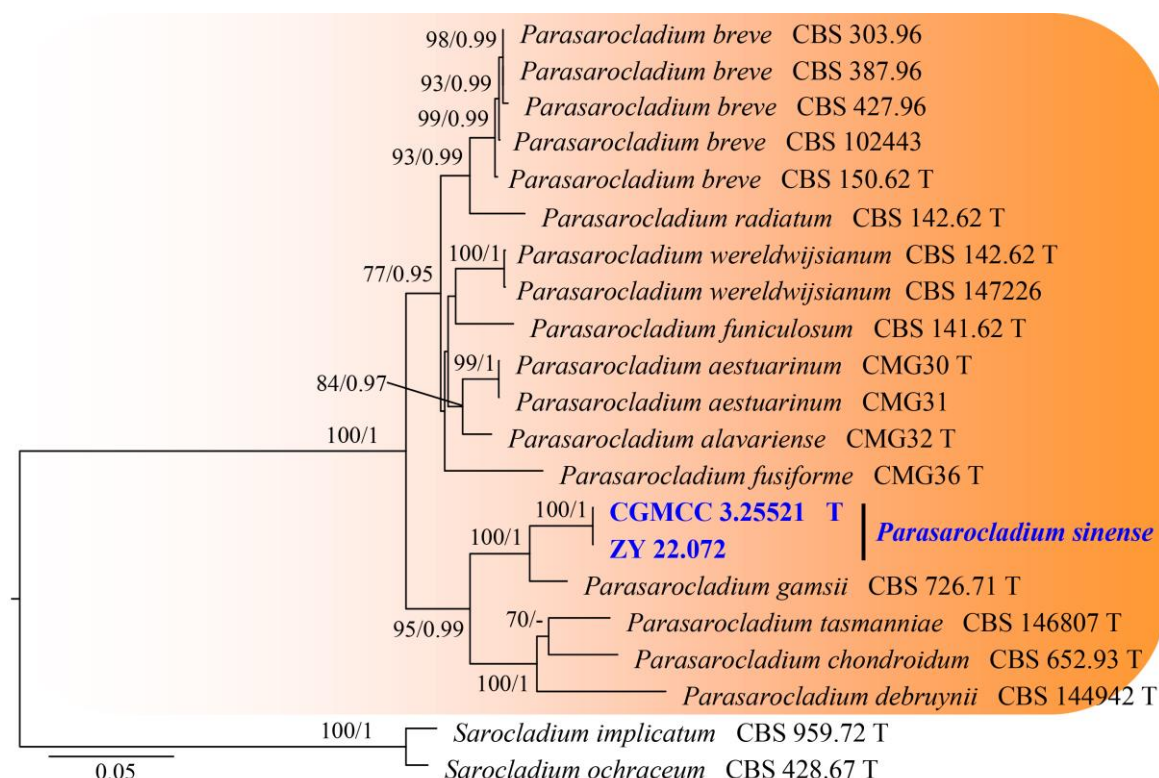


Figure 39 – Phylogram generated from maximum likelihood analysis based on combined ITS, LSU, *RPB2*, and *EF1A* sequence data. Estimated base frequencies were as follows; A = 0.226, C = 0.279, G = 0.281, T = 0.213; substitution rates AC = 1.84118, AG = 4.02202, AT = 1.69001, CG = 1.39118, CT = 14.53352, GT = 1.00000; gamma distribution shape parameter $\alpha = 0.351$. The tree topology of ML analysis is similar to BI analysis. Bootstrap support values for MLBS $\geq 70\%$ and BYPP ≥ 0.7 are defined as BS/PP above the nodes. Hyphens (-) represent support values less than 70% in ML and 0.7 in BI. Newly generated sequences are in blue and “T” indicates type strain.

Parasarocladium sinense Zhi Y. Zhang & Y. F. Han, sp. nov.

Fig. 40

Mycobank number: MB850390; Facesoffungi number: FoF15093

Etymology – Named after the location China, where the holotype was collected.

Holotype – ZY H-22.071

Description – *Hyphae* branched, septate, hyaline, smooth, occasionally inflated, chondroid, with abundant brown guttules, 1–3 μm diam. Sexual morph: Not observed. Asexual morph: *Conidiophores* scarce, solitary, erect, straight or irregularly curved, arising directly from aerial or substratal hyphae, unbranched, or occasionally branched, usually reduced to phialides, 6–20 $\times$ 2–3 μm . *Phialides* solitary, lateral or terminal, subcylindrical to cylindrical, tapering to the apex, straight or irregularly curved, hyaline, smooth-walled, 23–47.5 μm long, 1–2.5 μm wide at base; adelophialides not observed. *Conidia* aseptate, hyaline, smooth-walled, cylindrical or ellipsoidal, with both ends rounded, sometimes with a slightly apiculate base, 3.5–10.5 $\times$ 2–4 μm (av. 6.5 $\times$ 2.8 μm , $n = 30$), arranged in slimy heads. *Chlamydospores* not observed.

Culture characteristics (14 d at 25 $^{\circ}\text{C}$) – Colony on PDA 45–46 mm, flat, radially folded and rugose at centre, dusty, white, margin filiform, reverse white. Colony on MEA 57–59 mm, flocculent, cottony, white, margin regular; reverse white. Colony on SNA 12–20 mm, flat, aerial

hyphae sparse, white, margin irregular; reverse white. Colony on OA 44–46 mm, flat, dense, white, margin regular; reverse white.

Material examined – China, Guizhou Province, Guiyang City, Xiuwen County, Zhazuo Town, soil collected from the green belts of Guizhou Wildlife Park, 106.69 E, 26.85 N, 25 May 2022, Zhi-Yuan Zhang (holotype, ZY H-22.071), ex-type CGMCC 3.25521 = ZY 22.071; *ibid.* ZY 22.072.

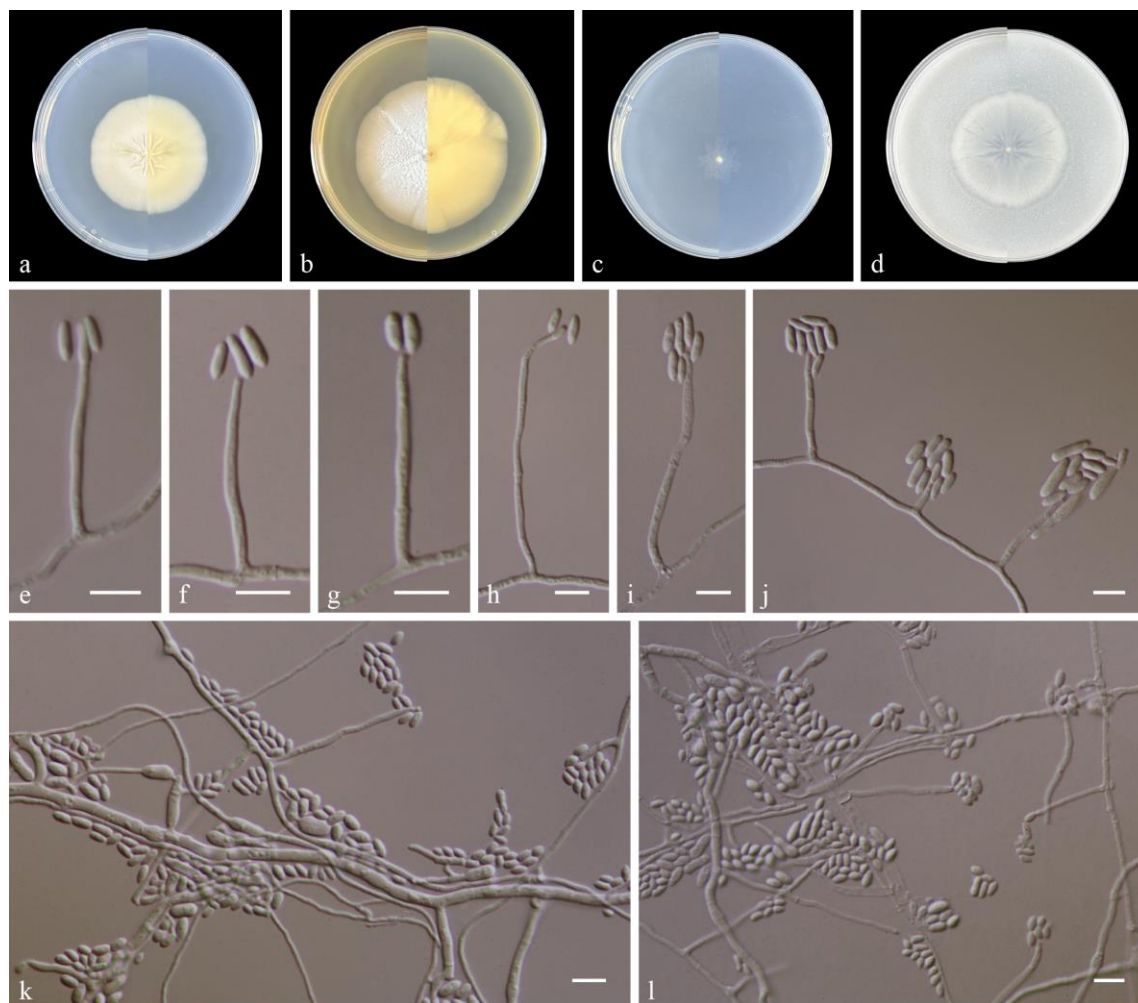


Figure 40 – *Parasarocladium sinense* (CGMCC 3.25521). a–d Upper and reverse views of cultures on PDA, MEA, SNA, and OA 14 d after inoculation. e–l Conidiophore and conidia. Scale bars: e–l = 10 μ m.

Notes – Phylogenetically, the new isolates CGMCC 3.25521 and ZY 22.072 formed a single clade with a strongly supported value (100/1) and were closely related to *Parasarocladium gamsii* (Fig. 39). Morphologically, *P. sinense* can be differentiated from *P. gamsii* by the conidia shape and size (cylindrical or ellipsoidal, $3.5\text{--}10.5 \times 2\text{--}4 \mu\text{m}$ in *P. sinense* vs. bacilliform to slightly fusiform, $(4\text{--})5\text{--}7\text{--}(12) \times 0.5\text{--}1 \mu\text{m}$ in *P. gamsii*) (Tichelaar 1972). In addition, *P. sinense* differs from *P. gamsii* by their low sequence similarities. In a comparison of ITS, LSU, *RPB2*, and *EF1A* nucleotides, *V. sinensis* (Type strain CGMCC 3.25520) has 97.2%, 99.6%, 92.4% and 91% similarity, in ITS (500/514 bp, seven gaps), LSU (776/779 bp, no gap), *RPB2* (698/755 bp, no gap), and *EF1A* (783/860 bp, 52 gaps), which is different from *P. gamsii* (Type strain CGMCC 3.17945).

Xylariales Nannf.

Microdochiaceae Hern.-Restr., Crous & J.Z. Groenew.

Idriella P.E. Nelson & S. Wilh.

Based on the dataset combined ITS, LSU, *TUB*, and *RPB2* sequences, the phylogeny of *Microdochiaceae* was studied. Two isolates, CBS 218.52 and CBS 217.52 of *Cryptostroma corticale* were used as the outgroup for the phylogenetic analysis. The concatenated sequences included 25 taxa and consisted of 2,848 nucleotides (ITS, 448 bp; LSU, 798 bp; *RPB2*, 764 bp; and *EF1A*, 838 bp) with inserted gaps. The phylogenetic trees showed that three new isolates (CGMCC 3.25522, ZY 22.074, and ZY22.075) of *Idriella longispora* clustered into a single clade with a high support value (100/0.9) and nested in the genus *Idriella*, and closely related to *I. multiformispora* (Fig. 41).

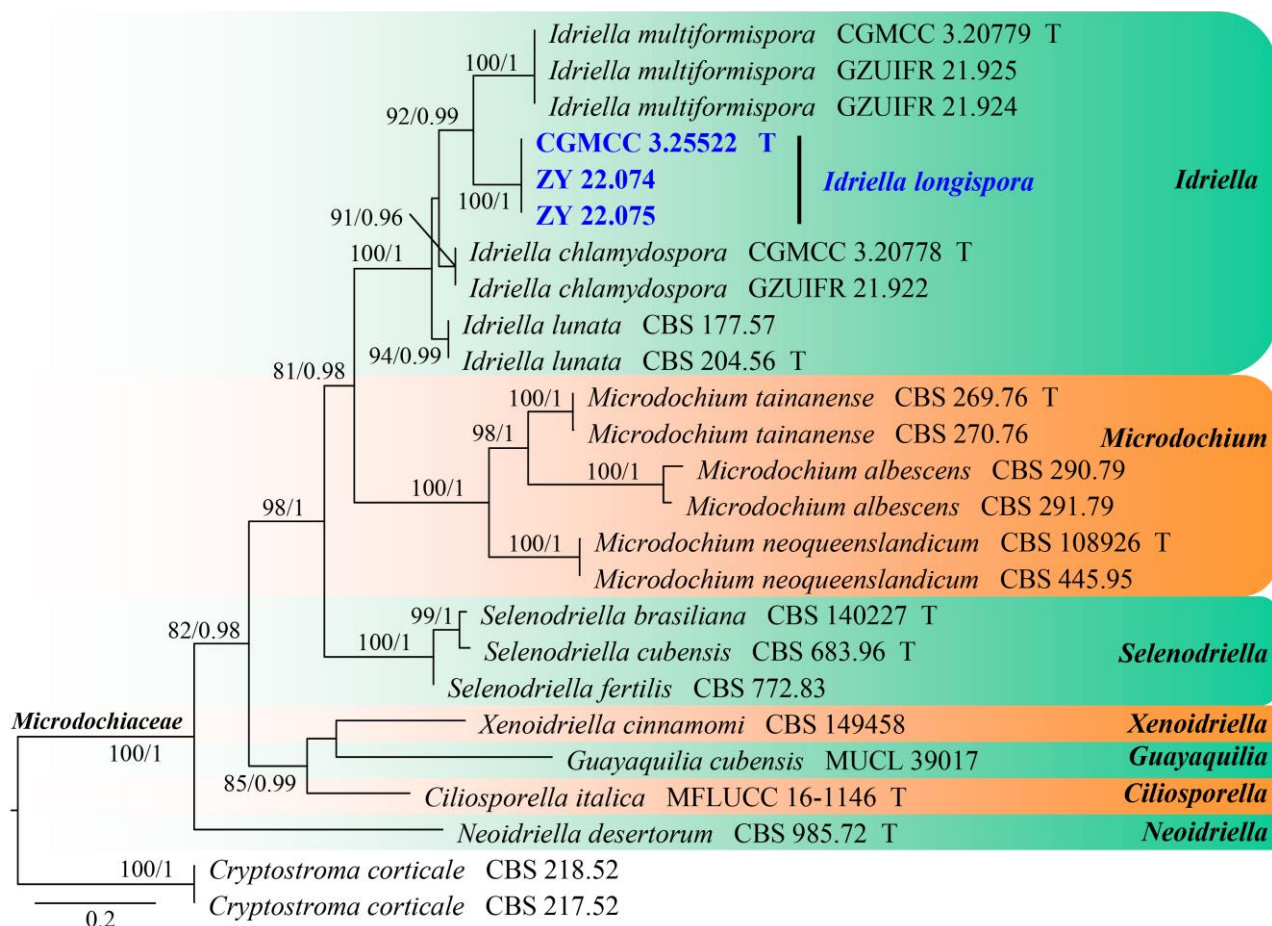


Figure 41 – Phylogram generated from maximum likelihood analysis based on combined ITS, LSU, *TUB*, and *RPB2* sequence data. Estimated base frequencies were as follows; A = 0.243, C = 0.249, G = 0.259, T = 0.248; substitution rates AC = 0.77920, AG = 2.40443, AT = 1.24981, CG = 0.54911, CT = 6.26913, GT = 1.00000; gamma distribution shape parameter $\alpha = 0.300$. The tree topology of ML analysis is similar to BI analysis. Bootstrap support values for MLBS $\geq 70\%$ and BYPP ≥ 0.7 are defined as BS/PP above the nodes. Newly generated sequences are in blue and “T” indicates type strain.

Idriella longispora Zhi Y. Zhang & Y. F. Han, sp. nov.

Fig. 42

Mycobank number: MB850391; Facesoffungi number: FoF15094

Etymology – Referring to its longer conidia than other species in this genus.

Holotype – ZY H-22.073

Description – *Hyphae* branched, septate, hyaline, smooth, 1–4 μm diam. Sexual morph: Not observed. Asexual morph: *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* numerous, borne on hyphae, solitary, erect, straight or irregularly curved, subcylindrical to cylindrical, 23.5–39 $\times$ 2.5–6 μm ; or sublageniform, 9.5–25.5 μm long, 1.5–3.5 μm wide at the base, 5.5–7 μm wide at the middle, 1–2 μm wide at the apex. *Conidia* acerose, pointed at each end, non-

septate, smooth-walled, gathered at the apex of conidiogenous cells, colourless, $14.5\text{--}28 \times 2.5\text{--}3.5 \mu\text{m}$ (av. $23.1 \times 3.1 \mu\text{m}$, $n = 30$). *Chlamydospores* are borne on hyphae, solitary, subglobose to globose, aseptate, brown, $8.5\text{--}21.5 \times 11\text{--}20.5 \mu\text{m}$ (av. $14.9 \times 15 \mu\text{m}$, $n = 30$).

Culture characteristics (14 d at 25°C) – Colony on PDA 30–32 mm, flocculent, felty, reed green to green beige from centre to margin, margin regular; reverse olive yellow to white from centre to margin. Colony on MEA 20–22 mm, flocculent, felty, grey white, margin partially convex; reverse beige grey. Colony on SNA, almost no growth. Colony on OA 22–26 mm, flocculent, felty, agate grey to basalt grey from centre to margin, margin irregular; reverse blue grey.

Material examined – China, Guizhou Province, Guiyang City, Xiuwen County, Zhazuo Town, soil collected from the green belts of Guizhou Wildlife Park, 106.69 E, 26.85 N, 25 May 2022, Zhi-Yuan Zhang (holotype, ZY H-22.073), ex-type CGMCC 3.25522 = ZY 22.073; *ibid.* ZY 22.074. China, Guizhou Province, Guiyang City, Xiuwen County, Zhazuo Town, soil collected from the green belts of Guizhou Wildlife Park, 106.69 E, 26.85 N, 25 May 2022, Zhi-Yuan Zhang ZY 22.075.

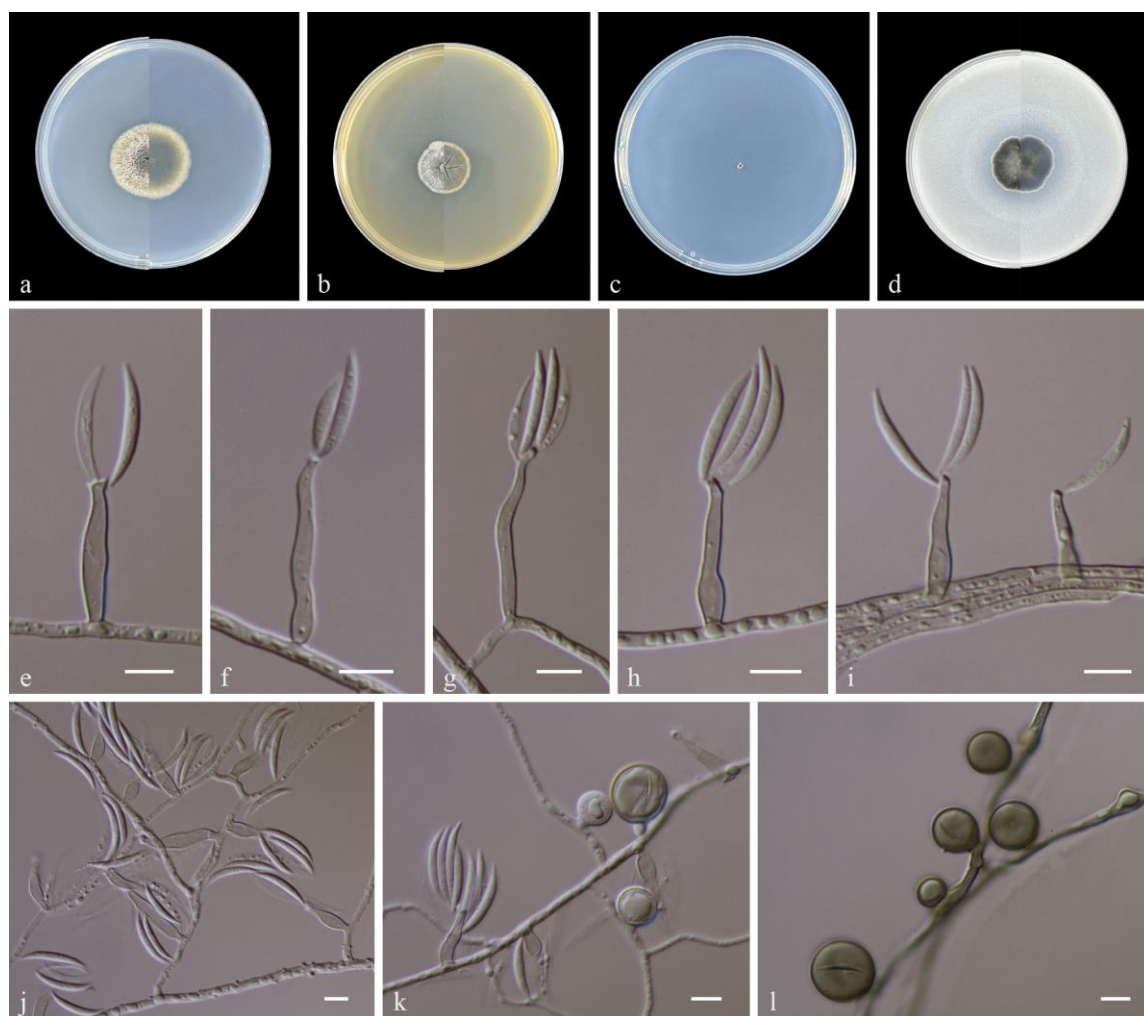


Figure 42 – *Idriella longispora* (CGMCC 3.25522). a–d Upper and reverse views of cultures on PDA, MEA, SNA, and OA 14 d after inoculation. e–j Conidiophore and conidia. k–l Chlamydospores. Scale bars: e–l = $10 \mu\text{m}$.

Notes – Phylogenetically, the new isolates, CGMCC 3.25522, ZY 22.074, and ZY 22.075, formed a single clade with a strongly supported value (100/1) and nested in the genus *Idriella* (Fig. 41). Morphologically, *I. longispora* can be differentiated from other members in the genus *Idriella* by its longer conidia, chlamydospores solitary, and aseptate (Castañeda-Ruiz & Kendrick 1991, Matsushima 1971, Rodrigues & Samuels 1992, Von Arx 1981, Zhang et al. 2023a). In addition,

I. longispora differs from *I. multiformispora* by their low sequence similarities. In a comparison of ITS, LSU, *TUB*, and *RPB2* nucleotides, *I. longispora* (Type strain CGMCC 3.25522) has 89%, 99.2%, 91.9%, and 85% similarity, in ITS (471/529 bp, 33 gaps), LSU (1,211/1,220 bp, no gap), *TUB* (738/803 bp, one gap), and *RPB2* (987/1161 bp, 19 gaps), which is different from *I. multiformispora* (Type strain CGMCC 3.20779).

Xylariaceae Tul. & C. Tul.

***Nemania* Gray**

Based on the dataset combined ITS, LSU, *RPB2*, and *TUB* sequences, phylogeny of *Nemania* was studied. *Kretzschmaria deusta* (MUCL 57705) and *K. hedjaroudei* (MUCL 57706) were used as the outgroup for the phylogenetic analysis. The concatenated sequences included 40 taxa and consisted of 3,100 nucleotides (ITS, 618 bp; LSU, 794 bp; *RPB2*, 997 bp; and *TUB*, 691 bp) with inserted gaps. The phylogenetic trees showed that our two new isolates (CGMCC 3.25523 and ZY22.077) and GMB0064 (type strain of *Nemania rubi*) were clustered into a single clade with a high support value (100/1) and separated from other taxa in the genus *Nemania* (Fig.43).

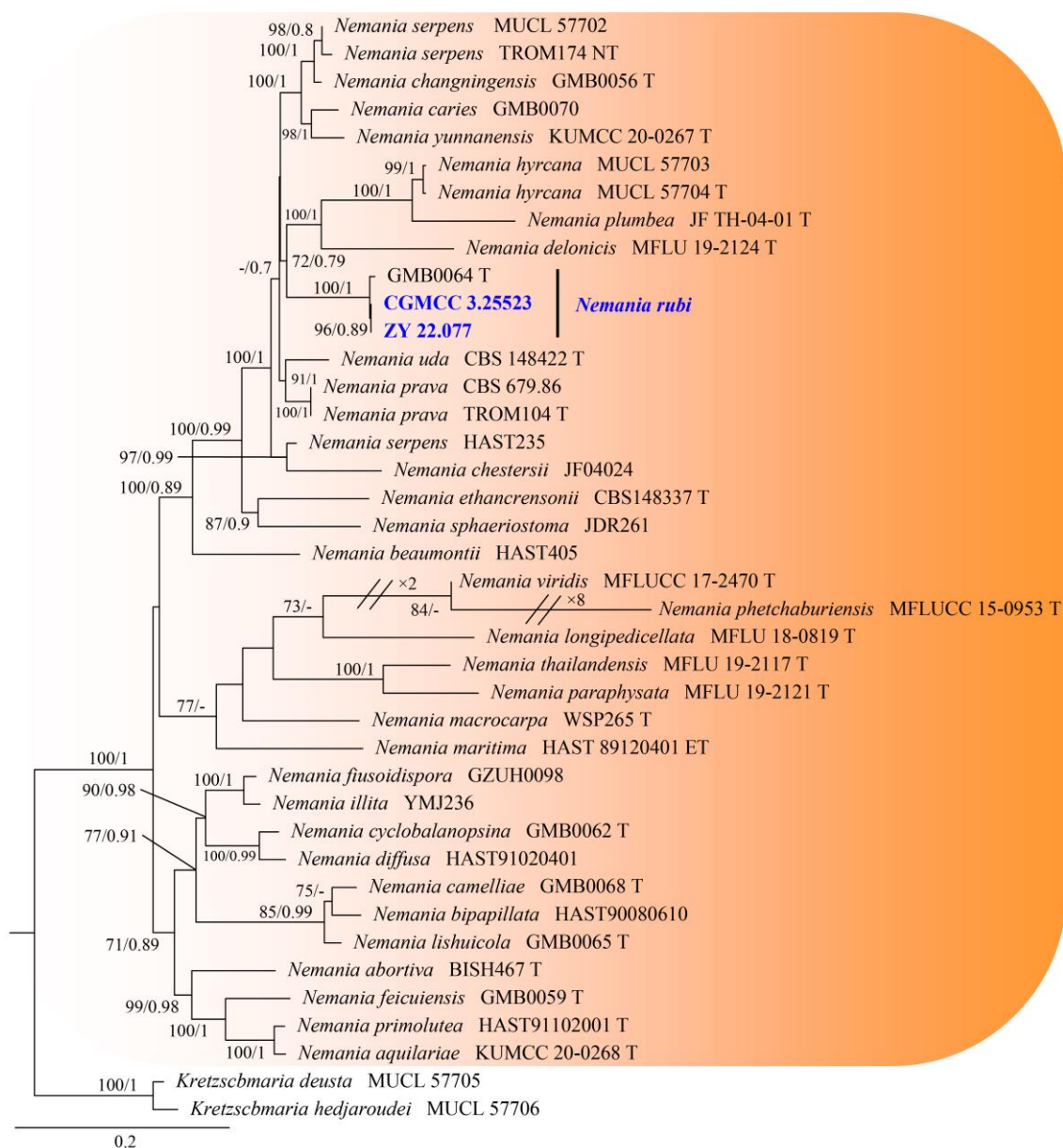


Figure 43 – Phylogram generated from maximum likelihood analysis based on combined ITS, LSU, *RPB2*, and *TUB* sequence data. Estimated base frequencies were as follows; A = 0.246, C = 0.259,

G = 0.263, T = 0.232; substitution rates AC = 1.34877, AG = 4.99360, AT = 0.99578, CG = 1.21621, CT = 7.97301, GT = 1.00000; gamma distribution shape parameter α = 0.439. The tree topology of ML analysis is similar to BI analysis. Bootstrap support values for MLBS $\geq$ 70% and BYPP $\geq$ 0.7 are defined as BS/PP above the nodes. Hyphens (-) represent support values less than 70% in ML and 0.7 in BI. Newly generated sequences are in blue and “T” indicates type strain.

Nemania rubi Y.H. Pi & Q.R. Li

Fig. 44

Description – *Hyphae* branched, septate, hyaline, smooth, 1–2.5 μ m diam. Sexual morph: Not observed. Asexual morph: geniculosporium-like. *Conidiophores* variables in length, hyaline to light brown. *Conidiogenous cells* up to 50 $\times$ 2–3.5 μ m, hyaline to light brown. *Conidia* hyaline, smooth, ellipsoid to subglobose with truncate base, 3–5.5 $\times$ 2.5–5 μ m (av. 4.1 $\times$ 3.3 μ m, n = 30).

Culture characteristics (14 d at 25 °C) – Colony on PDA 40–44 mm, flocculent, cottony, irregular wheel, margin irregular, white; reverse white. Colony on MEA 36–42 mm, flocculent, cottony, margin irregular, furrows, grey-white; reverse white. Colony on SNA 15–18 mm, flocculent, cottony, margin irregular, white; reverse white. Colony on OA 39–42 mm, flocculent, felty, margin ripple, white; reverse white.

Material examined – China, Guizhou Province, Guiyang City, Xiuwen County, Zhazuo Town, soil collected from the green belts of Guizhou Wildlife Park, 106.69 E, 26.85 N, 25 May 2022, Zhi-Yuan Zhang CGMCC 3.25523 = ZY 22.076; *ibid.* ZY 22.077.

Notes – Phylogenetically, the new isolates, CGMCC 3.25523, ZY 22.077, and GMB0064 (type strain of *Nemania rubi*), formed a single clade with a strongly supported value (Fig. 43). *Nemania rubi* was introduced by Pourmoghaddam et al. (2022) based on sexual morph. Unfortunately, Pourmoghaddam et al. (2022) did not observe an asexual morph of these species. Importantly, strain GMB0064 had the following nucleotide similarities with the sequences of our newly collected strain (ZY 22.076 and ZY 22.077). On ITS, LSU, *RPB2*, and *TUB*, respectively: 457/458 (99.7%, no gap), 801/801 (100%, no gap), 1078/1082 (99.6%, no gap), and 336/344 (97.6%, no gap). Therefore, we identified our isolates as *N. rubi* and provided its asexual morph.

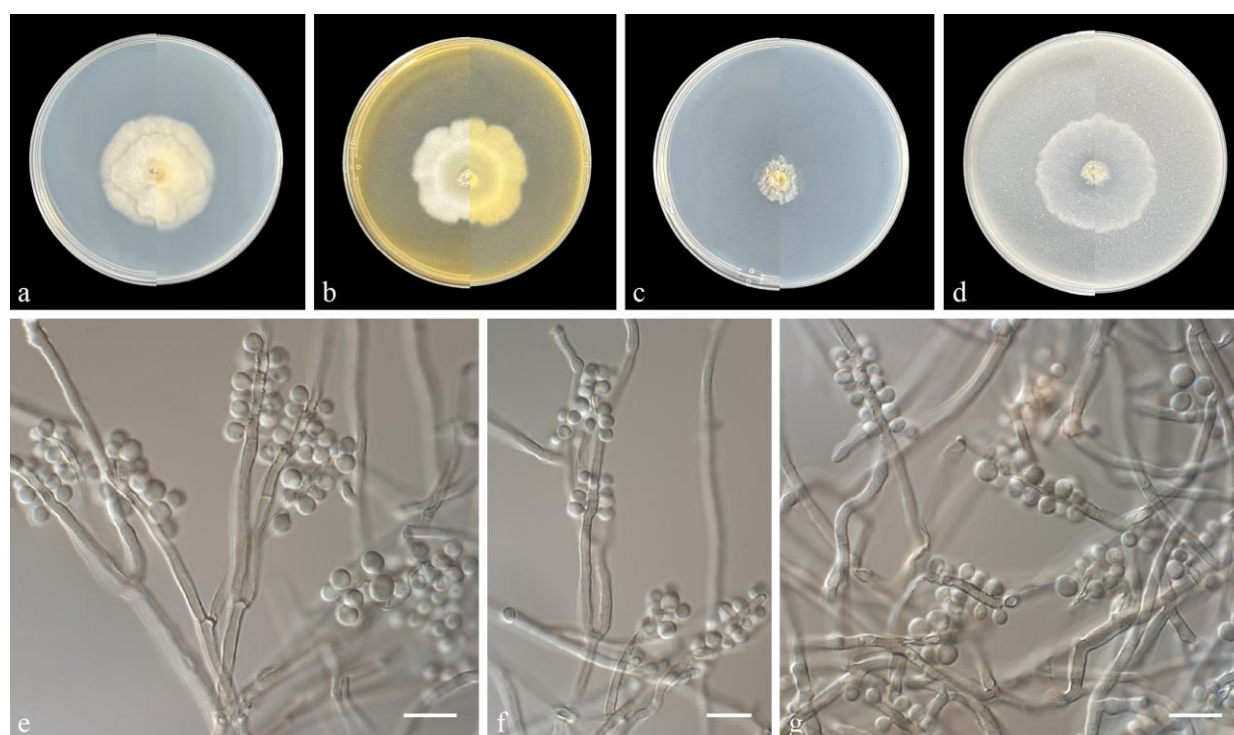


Figure 44 – *Nemania rubi* (CGMCC 3.25523). a–d Upper and reverse views of cultures on PDA, MEA, SNA, and OA 14 d after inoculation. e–g Conidiophores, conidiogenous cells and mature conidia. Scale bars: e–g = 10 μ m.

DISCUSSION

To date, the number of fungal species that have been described by mycologists remains limited, and numerous mycologists continue to struggle with it. However, mycologists seem to have “gone astray”. In recent years, they have either been particularly partial to exploring fungi in specialized habitats or keen to develop new techniques to explore fungi in nature. For example, Sun et al. (2024) investigated plant rust pathogens. Zhou et al. (2023) investigated fungal taxa associated with grapevine trunk diseases. Zhang et al. (2017b, 2021b) reported mycobiota in Chinese karst caves utilizing pure culture methods. Yang et al. (2023) conducted a comprehensive study on the freshwater fungi found in karst landscapes in China and Thailand. Li et al. (2023) designed the fungal enrichment culture method and fungal isolation chips and carried out the study using mangrove sediment samples as test subjects. The results showed that the new techniques had significant advantages in isolating uncultured and low-abundance fungal taxa and even obtained many taxa that were not detected by high-throughput sequencing. However, the composition of fungi in Urban soils has not received enough attention. Urbanization is an inevitable trend in humanity’s development and is an important symbol of the progress made in science and technology (Wang et al. 2018). Urbanization has swept across the globe over the last several decades (Berry 2008). The rate of urban expansion is currently at an unprecedented level, and the migration of people from rural to urban regions leads to increased anthropogenic changes to the urban environment, shaping the very high heterogeneity of urban soils. Therefore, studying and investigating the diversity of urban soil fungi can provide valuable scientific data for understanding their ecological functions and maintaining public health and safety (Zhang et al. 2023a). Currently, there is limited literature available regarding comprehensive investigations of fungal taxa in urban soil. Of course, this may be known taxa have not been given enough attention, and researchers have tended to publish new taxa separately when dealing with their findings. Fortunately, this situation is shifting. For instance, our group has reported many new taxa while ignoring known taxa during our investigations of keratinophilic fungal in urban soil in China since 2015 (Zhang et al. 2021a, Li et al. 2022, Zhang et al. 2023a). In this study, we investigated the mycobiota and keratinophilic fungi in urban soils in China using a wildlife park in Guizhou Province, China. We obtained 223 fungal taxa, including several undescribed taxa (Supplementary Table 1), from the collected soil samples using just three media of different compositions.

Traditionally, fungal species are commonly classified and described by morphological characteristics (Hawksworth 2001). However, morphological characteristics are often influenced by convergent evolution, which leads to difficulty in identifying and distinguishing some species based on morphological characteristics alone (Bickford et al. 2007, Otalora et al. 2017). The concept of integrated taxonomy, which utilizes a variety of novel methods to identify and characterize fungal species, is currently being embraced by the scientific community. Aime et al. (2021) propose that the publication of new fungal species should be supported by evidence drawn from more than one kind of data. In this study, the identification of new taxa was achieved through the integration of morphological characteristics and multilocus molecular phylogeny. However, we also observed some taxa (Undefined taxa in supplementary Table 1), which possibly represented new taxa based on phylogenetic analyses, did not sporulate on most of the culture media despite applying multiple strategies for stimulating sporulation. Soil serves as a vital habitat for a diverse array of fungi, supporting their survival and reproduction. Soil fungi are embedded in a network of soil organisms and do not exist in isolation, but interact with a variety of other fungi, bacteria and other organisms, whether this interaction is negative or positive. Consequently, numerous fungi that are capable of spore production in their natural habitats exhibit reduced or absent spore-producing capabilities when cultivated under controlled laboratory conditions. Although very difficult, mimicking natural environments to induce more spore production by fungi under laboratory conditions is an important task for all fungal taxonomists.

In conclusion, this study conducted a preliminary investigation of the fungal composition of urban soils, utilizing the Guizhou Wildlife Park as a case study to advance understanding in this field. In addition, we introduced 21 new species, two new combinations, and one new record from

China, and added the asexual morph of the known species, *Nemania rubi*, based on Morphological characterisation and multi-locus phylogenetic analyses. This study has important implications for the species diversity, taxonomy and geographic distribution of urban soil fungi.

ACKNOWLEDGEMENTS

This study was supported by the Guizhou Provincial Basic Research Program (Natural Science) (ZK [2023] 155), the National Natural Science Foundation of China (No. 32360007, 32060011), and “Hundred” Talent Projects of Guizhou Province (Qian Ke He [2020] 6005). We greatly appreciate Dr. Bensch for her advice on the new species names. We appreciate Charlesworth for the English language editing of the whole manuscript.

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Supplementary materials

Supplementary Table 1 List of fungal isolates in this study.

Fungal species	Untreated soil			Feather – baiting		
	WZA	WZB	WZC	WZBA	WZBB	WZBC
Ascomycota, Dothideomycetes						
<i>Aaosphaeria arxii</i>	Y		Y			
<i>Amorocoelophoma cassiae</i>		Y	Y			
<i>Amorocoelophoma sinensis</i>	Y	Y				
<i>Arthrographis longispora</i>			Y			
<i>Cladosporium aggregatocitricatum</i>				Y		Y
<i>Cladosporium anthropophilum</i>	Y	Y	Y	Y	Y	Y
<i>Cladosporium cladosporioides</i>	Y	Y	Y		Y	Y
<i>Cladosporium halotolerans</i>					Y	
<i>Cladosporium marinum</i>	Y		Y		Y	
<i>Cladosporium tenuissimum</i>	Y		Y			
<i>Didymella rosea</i>	Y		Y			
<i>Didymella segeticola</i>	Y	Y				
<i>Lophiostoma/Massarina</i> sp.	Y	Y	Y			
<i>Magnibotryascoma mali</i>	Y		Y			
<i>Minutisphaera</i> sp.						Y
<i>Mycosphaerella hedericola</i>					Y	
<i>Neopyrenochaeta acicola</i>	Y	Y				
<i>Neopyrenochaeta</i> sp.			Y			
<i>Neoramichloridium</i> sp.	Y					
<i>Nigrograna acericola</i>			Y			
<i>Nigrograna guizhouensis</i>			Y			
<i>Nigrospora chinensis</i>	Y					
<i>Paraconiothyrium brasiliense</i>			Y			
<i>Paraphaeosphaeria sporulosa</i>						Y
<i>Paraphoma ledniceana</i>	Y					
<i>Periconia macrospinoso</i>						Y
<i>Phaeodothis sinensis</i>		Y				
<i>Phaeosphaeria microscopica</i>		Y				
<i>Phomatodes nebulosa</i>			Y			
<i>Pleotrichocladium opacum</i>					Y	
<i>Preussia aemulans</i>		Y				

Supplementary Table 1 Continued.

Fungal species	Untreated soil			Feather – baiting		
	WZA	WZB	WZC	WZBA	WZBB	WZBC
<i>Pseudoshiraia conidialis</i>		Y				
<i>Pyrenochaeta gentianicola</i>			Y			
<i>Pyrenochaetopsis kuksensis</i>	Y		Y			
<i>Pyrenochaetopsis microspora</i>			Y			
<i>Pyrenochaetopsis</i> sp.			Y			
<i>Pyrenochaetopsis terricola</i>	Y		Y			
<i>Quasiconcha sinensis</i>	Y					
<i>Scolecobasidium guizhouense</i>	Y					
<i>Scolecobasidium</i> <i>inverellipsoidisporum</i>			Y			
<i>Scolecobasidium longiphorum</i>			Y			
<i>Scolecobasidium parahumicola</i>		Y				
<i>Scolecobasidium tshawytschae</i>			Y			
<i>Setophoma chromolaenae</i>		Y				
<i>Yunnanomyces sexualis</i>			Y			
Ascomycota, Eurotiomycetes						
<i>Aphanoascus foetidus</i>				Y		Y
<i>Aphanoascus guizhouensis</i>				Y	Y	Y
<i>Aphanoascus reticulisporus</i>				Y	Y	Y
<i>Aspergillus clavatonanicus</i>	Y	Y	Y	Y		Y
<i>Aspergillus fumigatus</i>				Y		
<i>Aspergillus japonicus</i>				Y		
<i>Aspergillus versicolor</i>		Y				
<i>Chrysosporium pseudomerdarium</i>	Y					
<i>Ctenomyces indicus</i>				Y	Y	Y
<i>Ctenomyces vellereus</i>				Y	Y	Y
<i>Keratinophyton alvearium</i>			Y			
<i>Keratinophyton evolceanui</i>				Y	Y	Y
<i>Keratinophyton hubeiense</i>				Y	Y	Y
<i>Keratinophyton minutisporosum</i>		Y				
<i>Keratinophyton terreum</i>				Y	Y	Y
<i>Knufia tsunedae</i>			Y			
<i>Nannizzia gypsea</i>				Y	Y	Y
<i>Onygenales</i> sp.		Y				
<i>Penicillium atramentosum</i>						Y
<i>Penicillium brevicompactum</i>	Y	Y	Y			
<i>Penicillium cainii</i>		Y	Y		Y	
<i>Penicillium chrysogenum</i>	Y					
<i>Penicillium crustosum</i>	Y	Y	Y			
<i>Penicillium daejeonium</i>	Y					
<i>Penicillium daleae</i>		Y				
<i>Penicillium fructuariae-cellae</i>			Y			
<i>Penicillium glabrum</i>	Y					
<i>Penicillium guanacastense</i>	Y	Y	Y			Y
<i>Penicillium guizhouense</i>	Y					
<i>Penicillium herquei</i>		Y				
<i>Penicillium jacksonii</i>	Y					
<i>Penicillium madriti</i>				Y		
<i>Penicillium malachiteum</i>			Y			
<i>Penicillium mexicanum</i>	Y			Y		Y
<i>Penicillium ochrochloron</i>		Y				
<i>Penicillium polonicum</i>						Y
<i>Penicillium steckii</i>					Y	

Supplementary Table 1 Continued.

Fungal species	Untreated soil			Feather – baiting		
	WZA	WZB	WZC	WZBA	WZBB	WZBC
<i>Penicillium sumatraense</i>			Y			
<i>Penicillium thomii</i>			Y			
<i>Penicillium viticola</i>		Y	Y			
<i>Talaromyces africanus</i>		Y				
<i>Talaromyces longistipes</i>		Y				
<i>Talaromyces neorugulosus</i>	Y					
<i>Talaromyces parapalmai</i>	Y	Y	Y			
<i>Talaromyces purpureogenus</i>					Y	
<i>Talaromyces rosarhiza</i>				Y		
<i>Tuberculiiforma sinensis</i>	Y					
Ascomycota, Lecanoromycete						
<i>Lecanoromycete</i> sp.	Y					
Ascomycota, Leotiomyces						
<i>Pseudogymnoascus pannorum</i>			Y			
<i>Pseudogymnoascus wildlifiparkensis</i>				Y	Y	Y
<i>Scytalidium sphaerosporum</i>			Y			
<i>Thelebolus stercoreus</i>					Y	Y
Ascomycota, Pezizomycetes						
<i>Scutellinia minutella</i>			Y			
Ascomycota, Saccharomycetes						
<i>Candida albicans</i>		Y				
<i>Galactomyces</i> sp.	Y					
<i>Zygosaccharomyces rouxii</i>	Y					
Ascomycota, Sordariomycetes						
<i>Albifimbria verrucaria</i>	Y	Y	Y	Y	Y	Y
<i>Apiospora arundinis</i>	Y					
<i>Apiospora dichotomanthi</i>	Y					
<i>Apiospora olivata</i>	Y					
<i>Bartalinia robillardoides</i>		Y	Y			
<i>Beauveria bassiana</i>		Y	Y	Y		
<i>Beauveria brongniartii</i>	Y	Y	Y			
<i>Bisifusarium sinense</i>	Y		Y			
<i>Botryotrichum verrucosum</i>			Y			
<i>Castanediella couratarii</i>	Y					
<i>Cercophora sparsa</i>				Y		
<i>Chaetomium globosum</i>					Y	Y
<i>Chloridium chloroconium</i>				Y		
<i>Chloridium fuscum</i>			Y			
<i>Clonostachys rogersoniana</i>					Y	Y
<i>Clonostachys rosea</i>				Y	Y	Y
<i>Codinaeella coryli</i>		Y				
<i>Cylindrocladiella nederlandica</i>				Y		
<i>Dactylonectria novozelandica</i>					Y	
<i>Diaporthe pseudooculi</i>	Y					
<i>Diaporthe sackstonii</i>					Y	
<i>Diaporthe unshiuensis</i>						Y
<i>Diaporthe velutina</i>						Y
<i>Emericellopsis microspora</i>				Y		
<i>Emericellopsis minima</i>	Y		Y			
<i>Eutypella</i> sp.	Y					
<i>Furcasterigmium furcatum</i>	Y		Y			
<i>Fusarium equiseti</i>		Y				
<i>Fusarium oxysporum</i>	Y		Y			

Supplementary Table 1 Continued.

Fungal species	Untreated soil			Feather – baiting		
	WZA	WZB	WZC	WZBA	WZBB	WZBC
<i>Fusarium solani</i>		Y	Y	Y	Y	Y
<i>Fusicolla aquaeductuum</i>		Y				
<i>Fusicolla merismoides</i>					Y	
<i>Graphium basitruncatum</i>	Y					
<i>Humicola nivea</i>				Y	Y	
<i>Hypocrea dichromospora</i>	Y	Y				
<i>Hypoxylon rogersii</i>						Y
<i>Idriella longispora</i>	Y					
<i>Immersidiscosia eucalypti</i>		Y	Y			
<i>Keithomyces echinosporus</i>		Y				
<i>Lasionectriopsis pteridii</i>	Y					
<i>Marquandomyces marquandii</i>		Y				
<i>Marquandomyces sinensis</i>			Y			
<i>Metacordyceps chlamydosporia</i>				Y		
<i>Metarhizium anisopliae</i>	Y	Y				
<i>Metarhizium gaoligongense</i>		Y				
<i>Microascus melanosporus</i>	Y					
<i>Microascus paisii</i>				Y		
<i>Nectriopsis microspora</i>	Y	Y	Y			
<i>Nemania rubi</i>		Y				
<i>Neocosmospora crassa</i>				Y		
<i>Paragongromeriza sinensis</i>		Y				
<i>Parasarocladium sinense</i>				Y		
<i>Parascedosporium putredinis</i>		Y				
<i>Parvothecium</i> sp.			Y			
<i>Peroneutypa scoparia</i>						Y
<i>Pestalotiopsis kenya</i>		Y	Y			
<i>Pestalotiopsis neglecta</i>		Y				
<i>Pestalotiopsis rosea</i>		Y				
<i>Pestalotiopsis trachycarpicola</i>			Y	Y		
<i>Pestalotiopsis unicolor</i>			Y			
<i>Phaeoacremonium</i>			Y			
<i>griseo-olivaceum</i>						
<i>Plectosphaerella cucumerina</i>			Y			
<i>Purpureocillium lilacinum</i>			Y			
<i>Ramophialophora petraea</i>		Y				
<i>Sarocladium strictum</i>		Y				
<i>Scedosporium apiospermum</i>				Y	Y	Y
<i>Scedosporium dehoogii</i>	Y			Y	Y	Y
<i>Sesquicillium essexcoheniae</i>				Y		
<i>Sesquicillium neerlandicum</i>		Y				
<i>Sesquicillium rossmaniae</i>	Y	Y	Y	Y	Y	Y
<i>Sordariomycetes</i> sp. 1			Y			
<i>Sordariomycetes</i> sp. 2		Y				
<i>Sordariomycetes</i> sp. 3		Y				
<i>Staphylotrichum acaciicola</i>		Y				
<i>Thelonectria discophora</i>	Y					
<i>Thyridium endophyticum</i>	Y	Y				
<i>Tolypocladium</i> sp.		Y				
<i>Trichoderma caribbaeum</i> var. <i>caribbaeum</i>					Y	
<i>Trichoderma polysporum</i>		Y				
<i>Trichoderma sichuanense</i>		Y	Y			

Supplementary Table 1 Continued.

Fungal species	Untreated soil			Feather – baiting		
	WZA	WZB	WZC	WZBA	WZBB	WZBC
<i>Varicosporellopsis</i> sp.		Y				
<i>Verruciconidia persicina</i>		Y				Y
<i>Volutella ciliata</i>	Y	Y	Y			
<i>Volutella consors</i>		Y				
<i>Volutella sinensis</i>	Y					
<i>Yunnania carbonaria</i>			Y	Y		
<i>Zygosporium masonii</i>					Y	
Ascomycota, Incertae sedis						
<i>Hormiactis candida</i>					Y	
Basidiomycota, Agaricomycetes						
<i>Bjerkandera adusta</i>				Y		Y
<i>Coprinellus aureogranulatus</i>			Y			
<i>Coprinellus xanthothrix</i>		Y				
<i>Coprinopsis urticicola</i>			Y			
<i>Fomitopsis pinicola</i>			Y			
<i>Irpex lacteus</i>		Y	Y			
<i>Kneiffiella microspora</i>		Y				
<i>Lentinus squarrosulus</i>			Y			
<i>Peniophora crassitunicata</i>		Y				
<i>Peniophora incarnata</i>	Y					
<i>Phaeophlebiopsis peniophoroides</i>						Y
<i>Phanerochaete concrescens</i>		Y	Y			
<i>Phanerochaete sordida</i>						Y
<i>Phlebia acerina</i>		Y	Y		Y	Y
<i>Phlebiopsis alba</i>	Y					
<i>Pleurotus pulmonarius</i>						Y
<i>Schizophyllum commune</i>		Y				
<i>Steccherinum tenuissimum</i>				Y		
Basidiomycota, Exobasidiomycetes						
<i>Eidernor doerrieniae</i>	Y					
Basidiomycota, Tremellomycetes						
<i>Apiotrichum akiyoshidainum</i>	Y					
<i>Apiotrichum laibachii</i>					Y	
<i>Apiotrichum scarabaeorum</i>	Y		Y		Y	
<i>Saitozyma podzolica</i>	Y	Y	Y			
<i>Tausonia pullulans</i>				Y		
Mucoromycota, Mucoromycetes						
<i>Cunninghamella echinulata</i>				Y	Y	
<i>Cunninghamella elegans</i>				Y		Y
<i>Mucor irregularis</i>		Y				
<i>Mucor minutus</i>	Y	Y	Y		Y	
Mucoromycota, Mortierellomycetes						
<i>Podila epicladia</i>		Y	Y			
Undetermined						
Fungi sp. 1		Y				
Fungi sp. 2			Y			
Fungi sp. 3				Y		
Fungi sp. 4	Y	Y	Y			
Fungi sp. 5	Y					

“Y” indicates that the fungus was isolated from soil using this medium.

Supplementary Table 2 The reference isolates and their GenBank accession numbers used for phylogenetic analysis in this study.

Fig. 3						
Species	Strains	GenBank accession numbers				
		SSU	ITS	LSU	<i>RPB2</i>	<i>EF1A</i>
<i>Glonium circumserpens</i>	CBS 123343	FJ161160		FJ161200	FJ161126	FJ161108
<i>Glonium stellatum</i>	CBS 207.34	FJ161140	MZ570257	FJ161179		FJ161095
<i>Halokirschsteiniiothelia maritima</i>	CBS 221.60			GU323203		GU349001
<i>Lophium mytilinum</i>	CBS 123344	FJ161163		FJ161203	FJ161128	FJ161110
<i>Lophium mytilinum</i>	AFTOL-ID 1609	DQ678030		DQ678081		DQ677926
<i>Lophium mytilinum</i>	CBS 114111	EF596818	EF596819	EF596819		
<i>Lophium zalerioides</i>	MFLUCC 14-0417	MF621592	MF621583	MF621587		
<i>Mytilinidion acicola</i>	EB 0379	GU397362		GU397346	GU397355	
<i>Mytilinidion acicola</i>	EB 0349	GU323185		GU323209	GU371757	
<i>Mytilinidion andinense</i>	EB 0330	FJ161159		FJ161199	FJ161125	FJ161107
<i>Mytilinidion australe</i>	CBS 301.34		MH855533	MH867035		
<i>Mytilinidion mytilinellum</i>	CBS 303.34	FJ161144	HM163570	MH867037	FJ161119	FJ161100
<i>Mytilinidion resinicola</i>	CBS 304.34	FJ161145	MH855535	MH867038	FJ161120	FJ161101
<i>Mytilinidion rhenanum</i>	EB 0341	GU323187		GU323207		
<i>Mytilinidion thujarum</i>	EB 0268	GU323188		GU323206		
<i>Mytilinidion tortile</i>	EB 377	GU323189		GU323205	FJ161127	FJ161109
<i>Pseudocamaropycnis pini</i>	CBS 115589		KU728518	KU728557		
<i>Quasiconcha reticulata</i>	EB QR			GU397349		
Fig. 5						
Species	Strains	GenBank accession numbers				
		SSU	ITS	LSU	<i>EF1A</i>	
<i>Amorosia littoralis</i>	NN 6654 T	AM292056	AM292047	AM292055		
<i>Amorocoelophoma camelliae</i>	NTUCC 18-097-1 T	MT071230	MT112303	MT071279	MT743271	
<i>Amorocoelophoma camelliae</i>	NTUCC 18-097-2	MT071231	MT112304	MT071280	MT743272	
<i>Amorocoelophoma camelliae</i>	NTUCC 18-097-3	MT071232	MT112305	MT071281	MT743273	
<i>Amorocoelophoma neoregeliae</i>	CBS 146820 T		MZ064410	NG_076726	MZ078247	
<i>Amorocoelophoma cassiae</i>	MFLUCC 17-2283 T	MK347847	MK347739	MK347956	MK360041	
<i>Amorocoelophoma cassiae</i>	C259	MK347847	MK347739	MK347956		
<i>Angustimassarina arezzoensis</i>	MFLUCC 13-0578 T	KY501113	KY496743	KY496722	KY514392	
<i>Angustimassarina italica</i>	MFLUCC15-0082 T	KY501124	KY496756	KY496736	KY514400	
<i>Angustimassarina populi</i>	MFLUCC 13-0034 T	KP899128	KP899137	KP888642	KR075164	
<i>Podocarpomyces knysnanus</i>	CBS 146076		MN562155	MN567662	MN556836	

Supplementary Table 2 Continued.

Species	Strains	GenBank accession numbers			
		SSU	ITS	LSU	<i>EF1A</i>
<i>Neoangustimassarina sichuanensis</i>	UESTC 22.0001	ON332918	ON332908	ON332926	ON381176
<i>Neoangustimassarina sichuanensis</i>	CGMCC 3.20937 T	ON332917	ON332907	ON332925	ON381175
<i>Alfoldia vorosii</i>	REF113	MK589345	JN859333	MK589353	MK599319
<i>Alfoldia vorosii</i>	REF117	MK589347	JN859337	MK589355	MK599321
<i>Alfoldia vorosii</i>	CBS 145501 T	MK589346	JN859336	MK589354	MK599320
<i>Neothyrostroma encephalarti</i>	CBS 146037		MN562104	MN567612	MN556830
<i>Neothyrostroma encephalarti</i>	CPC 35999		MN562105	MN567613	MN556831
<i>Flabellascoma aquaticum</i>	KUMCC 15-0258 T	MN304832	MN304827	MN274564	MN328898
<i>Flabellascoma cycadicola</i>	CBS 143644 T	LC312473	LC312502	LC312531	LC312560

Fig. 7

Species	Strains	GenBank accession numbers		
		SSU	ITS	LSU
<i>Austropleospora archidendri</i>	CBS 168.77		JX496049	JX496162
<i>Austropleospora keteleeriae</i>	MFLUCC 18-1551 T	MK347910	MK347802	MK348021
<i>Bimuria novae zelandiae</i>	CBS 107.79 T	AY016338	MH861181	AY016356
<i>Chromolaenicola chiangraiensis</i>	MFLUCC 17-1493	MN325011	MN325017	MN325005
<i>Chromolaenicola nanensis</i>	MFLUCC 17-1477	MN325008	MN325014	MN325002
<i>Curreya pityophila</i>	CBS 986.69		MH859500	MH871280
<i>Curreya pityophila</i>	CBS 149.32		MH855249	JX681087
<i>Cylindroaseptospora leucaenae</i>	MFLUCC 17-2424	MK347856	MK347749	MK347966
<i>Deniquelata barringtoniae</i>	MFLUCC 11-0422	JX254656	JX254654	JX254655
<i>Didymocrea sadasivanii</i>	CBS 438.65	DQ384066	MH858658	DQ384103
<i>Didymosphaeria rubi-ulmifolii</i>	CBS 100299 T	AY642523	JX496011	JX496124
<i>Didymosphaeria rubi-ulmifolii</i>	MFLUCC 14-0023	KJ436588		KJ436586
<i>Karstenula rhodostoma</i>	CBS 690.94	GU296154	OM337539	GU301821
<i>Karstenula rhodostoma</i>	CBS 691.94	AB797241		AB807531
<i>Letendraea cordylinicola</i>	MFLUCC 11-0148 T	KM214001	KM213995	KM213998
<i>Letendraea cordylinicola</i>	MFLUCC 11-0150	KM214002	KM213996	KM213999
<i>Montagnula cirsii</i>	MFLUCC 13-0680	KX274255	KX274242	KX274249
<i>Montagnula scabiosae</i>	MFLUCC 14-0954 T	KT443905	KT443907	KT443903
<i>Paracamarosporium hawaiiense</i>	CBS 120025 T	EU295655	JX496027	JX496140
<i>Paracamarosporium psoraleae</i>	CPC 21632 T		KF777143	KF777199
<i>Paraconiothyrium cyclothyrioides</i>	CBS 972.95	AY642524	JX496119	JX496232

Supplementary Table 2 Continued.

Species	Strains	GenBank accession numbers		
		SSU	ITS	LSU
<i>Paraconiothyrium estuarinum</i>	CBS 109850	AY642522	JX496016	JX496129
<i>Paramassariosphaeria anthostomoides</i>	CBS 615.86	GU205246	MH862005	GU205223
<i>Paramassariosphaeria clematidicola</i>	MFLU 16-0172	KU743208	KU743206	KU743207
<i>Paraphaeosphaeria angularis</i>	CBS 167.70 T		JX496047	JX496160
<i>Paraphaeosphaeria michotii</i>	MFLUCC 15-0041	MG829148	MG828933	MG829042
<i>Phaeodothis mori</i>	MFLUCC 18-1634	MN356452	MN356454	MN356450
<i>Phaeodothis mori</i>	KUMCC 19-0136	MN356453	MN356455	MN356451
<i>Phaeodothis winteri</i>	CBS 182.58	GU296183		GU301857
<i>Phaeodothis winteri</i>	AFTOL-ID 1590	DQ678021		DQ678073
<i>Pseudocamarosporium corni</i>	MFLUCC 13-0541 T	KJ819946	KJ747048	KJ813279
<i>Pseudocamarosporium loniceriae</i>	MFLUCC 13-0532 T	KJ819947	KJ747047	KJ813278
<i>Pseudopithomyces chartarum</i>	KUMCC 16-0222	MF173606	MF173607	MF173605
<i>Pseudopithomyces kungmingnensis</i>	YG S55	MK347906	MK347798	MK348017
<i>Spegazzinia deightonii</i>	yone 212	AB797292		AB807582
<i>Spegazzinia tessarthra</i>	SH 287	AB797294	JQ673429	AB807584
<i>Tremateia arundicola</i>	MFLU 16-1275	KX274254	KX274241	KX274248
<i>Tremateia guiyangensis</i>	GZAAS01	KX274253	KX274240	KX274247

Fig. 9

Species	Strains	GenBank accession numbers				
		SSU	ITS	LSU	<i>RPB2</i>	<i>EF1A</i>
<i>Cyclothyriella rubronotata</i>	CBS 141486 T	KX650507	KX650544		KX650574	KX650519
<i>Cyclothyriella rubronotata</i>	CBS 419.85			GU301875	GU371728	GU349002
<i>Nigrograna acericola</i>	CGMCC 3.24957 T		OR253153	OR253312		OR263572
<i>Nigrograna antibiotica</i>	CCF 4378 T	KF925328	JX570932	KF925327		JX570934
<i>Nigrograna antibiotica</i>	CCF 4998		LT221894	LT221895		
<i>Nigrograna aquatica</i>	MFLUCC 14-1178 T	MF415394	MF399065	MF415392		MF498582
<i>Nigrograna asexualis</i>	ZHKUCC 22-0214 T	OP450979	OP450965	OP450971	OP432241	OP432245
<i>Nigrograna asexualis</i>	ZHKUCC 22-0215	OP450980	OP450966	OP450972	OP432242	OP432246
<i>Nigrograna cangshanensis</i>	MFLUCC 15-0253 T	KY511065	KY511063	KY511064		
<i>Nigrograna carollii</i>	CCF 4484 T	LN626674	LN626657	LN626682	LN626662	LN626668
<i>Nigrograna chromolaenae</i>	MFLUCC 17-1437 T		MT214379	MT214473		MT235801
<i>Nigrograna coffeae</i>	ZHKUCC 22-0210 T	OP450981	OP450967	OP450973	OP432243	OP432247
<i>Nigrograna coffeae</i>	ZHKUCC 22-0211	OP450982	OP450968	OP450974	OP432244	OP432248

Supplementary Table 2 Continued.

Species	Strains	GenBank accession numbers				
		SSU	ITS	LSU	<i>RPB2</i>	<i>EF1A</i>
<i>Nigrograna fuscidula</i>	CBS 141556 T		KX650550			KX650525
<i>Nigrograna fuscidula</i>	CBS 141476	KX650509	KX650547		KX650576	KX650522
<i>Nigrograna heveae</i>	ZHKUCC 22-0284 T	OP584492	OP584490	OP584488	OP750374	OP750372
<i>Nigrograna heveae</i>	ZHKUCC 22-0285	OP584493	OP584491	OP584489	OP750375	OP750373
<i>Nigrograna hydei</i>	GZCC 19-0050 T		MN387225	MN387227		MN389249
<i>Nigrograna impatientis</i>	GZCC 19-0042 T		MN387226	MN387228		MN389250
<i>Nigrograna italica</i>	MFLU 23-0139 T		OR538590	OR538591	OR531365	OR531366
<i>Nigrograna jinghongensis</i>	KUMUCC 21-0035 T	MZ493289	MZ493303	MZ493317	MZ508421	MZ508412
<i>Nigrograna jinghongensis</i>	KUMUCC 21-0036	MZ493290	MZ493304	MZ493318	MZ508422	MZ508413
<i>Nigrograna kunmingensis</i>	ZHKUCC 22-0242 T	OP456382	OP456214	OP456379		OP471608
<i>Nigrograna kunmingensis</i>	ZHKUCC 22-0243	OP456383	OP484334	OP456380		OP471609
<i>Nigrograna locuta-pollinis</i>	CGMCC 3.18784 T		MF939601	MF939583	MF939610	MF939613
<i>Nigrograna locuta-pollinis</i>	LC11690		MF939603	MF939584	MF939611	MF939614
<i>Nigrograna mackinnonii</i>	CBS 674.75 T	GQ387552	KF015654	KF015612	KF015703	KF407986
<i>Nigrograna mackinnonii</i>	E9303e	LN626678	JN545759	LN626681	LN626666	LN626673
<i>Nigrograna magnoliae</i>	MFLUCC 20-0020 T	MT159634	MT159628	MT159622	MT159611	MT159605
<i>Nigrograna magnoliae</i>	MFLUCC 20-0021	MT159635	MT159629	MT159623	MT159612	MT159606
<i>Nigrograna mycophila</i>	CBS 141478 T		KX650553			KX650526
<i>Nigrograna mycophila</i>	CBS 141483	KX650510	KX650555		KX650577	KX650528
<i>Nigrograna norvegica</i>	CBS 141485 T	KX650511	KX650556		KX650578	
<i>Nigrograna obliqua</i>	CBS 141477 T		KX650560		KX650580	KX650531
<i>Nigrograna obliqua</i>	CBS 141475	KX650512	KX650558		KX650579	KX650530
<i>Nigrograna oleae</i>	CGMCC 3.24423 T		OR253080	OR253232		OR262140
<i>Nigrograna oleae</i>	UESTCC 23.0071		OR253089	OR253241		OR262145
<i>Nigrograna peruviensis</i>	CCF 4485 T	LN626677	LN626658	LN626683	LN626665	LN626671
<i>Nigrograna puerensis</i>	ZHKUCC 22-0212 T	OP450983	OP450969	OP450975		OP432249
<i>Nigrograna puerensis</i>	ZHKUCC 22-0213	OP450984	OP450970	OP450976		OP432250
<i>Nigrograna rhizophorae</i>	MFLUCC 18-0397 T		MN047085		MN431489	MN077064
<i>Nigrograna rhizophorae</i>	MFLU 19-1234			MN017845	MN431490	MN077063
<i>Nigrograna rubescens</i>	DAOMC 252610 T		OQ400924	OQ400934	OQ413082	OQ413077
<i>Nigrograna rubescens</i>	CHEM 2177		OQ400922	OQ400932	OQ413086	OQ413078
<i>Nigrograna samueliana</i>	NFCCI-4383 T	MK358810	MK358817	MK358812	MK330939	MK330937
<i>Nigrograna schinifolii</i>	GMB0498 T		OR120434			OR150022

Supplementary Table 2 Continued.

Species	Strains	GenBank accession numbers				
		SSU	ITS	LSU	<i>RPB2</i>	<i>EF1A</i>
<i>Nigrograna schinifolii</i>	GMB0504		OR120441			OR150023
<i>Nigrograna sichuanensis</i>	CGMCC 3.24424 T		OR253096	OR253248		OR251058
<i>Nigrograna sichuanensis</i>	UESTCC 23.0076		OR253100	OR253252		OR251059
<i>Nigrograna thailandica</i>	MFLUCC 17-2663 T	MK762704	MK762709	MK762716		
<i>Nigrograna thymi</i>	MFLUCC 14-1096 T	KY775574	KY775576	KY775573		KY775578
<i>Nigrograna trachycarpi</i>	GMB0499 T		OR120437			OR150024
<i>Nigrograna trachycarpi</i>	GMB0505		OR120440			OR150025
<i>Nigrograna</i> sp.	CGMCC 3.20241	OR853576	OR853552	OR853564	PP084035	PP111473
<i>Nigrograna</i> sp.	GZCC 21-0014	OR853577	OR853553	OR853565	PP084036	PP111474
<i>Nigrograna verniciae</i>	CGMCC 3.24425 T		OR253116	OR253275		OR251168
<i>Nigrograna wuhanensis</i>	ZHKUCC 22-0329 T	OQ061465	OP941389	OP941390		OP947079
<i>Nigrograna yasuniana</i>	YU.101026 T	LN626676	HQ108005	LN626684	LN626664	LN626670
<i>Occultibambusa bambusae</i>	MFLUCC 13-0855 T		KU940123	KU863112	KU940170	KU940193
<i>Occultibambusa pustula</i>	MFLUCC 11-0502 T		KU940126	KU863115		
<i>Paradictyoarthrinium diffractum</i>	MFLUCC13-0466	KP753960	KP744455	KP744498	KX437764	
<i>Paradictyoarthrinium tectonicola</i>	MFLUCC 13-0465 T	NG_063571	NR_155647	NG_059558	KX437763	
<i>Seriascoma didymosporum</i>	MFLUCC 11-0179 T		KU940127	KU863116	KU940173	KU940196
<i>Seriascoma honghense</i>	KUMCC 21-0021 T		MZ329039	MZ329035	MZ325470	MZ325468
<i>Versicolorisporium triseptatum</i>	HHUF 28815 T	NG_060995	NR_119392	NG_042318		
Fig. 14						
Species	Strains	GenBank accession numbers				
		SSU	ITS	LSU	<i>TUB</i>	<i>EF1A</i>
<i>Scolecobasidium acanthi</i>	CGMCC 3.24352 T		OQ448957	OQ448949	OQ442218	OQ442215
<i>Scolecobasidium aegiceratis</i>	CGMCC 3.24353 T		OQ448958	OQ448950	OQ442219	OQ442216
<i>Scolecobasidium aegiceratis</i>	CGMCC 3.24354		OQ448959	OQ448951	OQ442220	OQ442217
<i>Scolecobasidium ailanthi</i>	MFLU 18-2110	MK347839	MK347731		MK412881	
<i>Scolecobasidium ailanthi</i>	MFLUCC 17-0923 T	MK347838	MK347730	MK347947	MK412883	
<i>Scolecobasidium anellii</i>	CBS 284.64 T	KF156070	FR832477	KF156138	KF156184	KF155995
<i>Scolecobasidium anomalum</i>	CBS 131816 T	KF156065	HE575201	KF156137	KF156194	KF155986
<i>Scolecobasidium aquaticum</i>	CBS 140316 T	KX668260	KX668258	KX668259		
<i>Scolecobasidium bacilliforme</i>	CBS 100442 T	KP798638	KP798632	KP798635	KT272059	KT272070
<i>Scolecobasidium blechni</i>	CBS 146055 T		MN562134	MN567641	MN556843	MN556826
<i>Scolecobasidium camellicola</i>	GUCC 18242 T	MZ503654	MZ503728	MZ503761	MZ546907	MZ546874

Supplementary Table 2 Continued.

Species	Strains	GenBank accession numbers				
		SSU	ITS	LSU	<i>RPB2</i>	<i>EF1A</i>
<i>Scolecobasidium camellicola</i>	GUCC 18244	MZ503656	MZ503730	MZ503763	MZ546909	MZ546876
<i>Scolecobasidium capsici</i>	CBS 142096 T		KY173427	KY173518		
<i>Scolecobasidium coiledmyces</i>	GUCC 18245 T	MZ503657	MZ503731	MZ503764	MZ546910	MZ546877
<i>Scolecobasidium constrictum</i>	CBS 202.27 T	KF156072	MH854929	MH866423	KF156161	KF156003
<i>Scolecobasidium cordanae</i>	CBS 412.51	KF156056	HQ667540	KF156123	KF156200	KF155980
<i>Scolecobasidium cordanae</i>	CBS 475.80 T	KF156058	KF156022	KF156122	KF156197	KF155981
<i>Scolecobasidium crassihumicola</i>	CBS 120700	KJ867431	KJ867429	KJ867430	KJ867433	KJ867428
<i>Scolecobasidium dracaenae</i>	CBS 141323 T		KX228283	KX228334		KX228377
<i>Scolecobasidium echinulatum</i>	GUCC 18247 T	MZ503659	MZ503733	MZ503766	MZ546912	MZ546879
<i>Scolecobasidium echinulatum</i>	GUCC 18248	MZ503660	MZ503734	MZ503767	MZ546913	MZ546880
<i>Scolecobasidium ellipsoideum</i>	CBS 131796 T		MN077367			
<i>Scolecobasidium ellipsoideum</i>	GUCC 18264	MZ503676	MZ503750	MZ503783	MZ546929	MZ546896
<i>Scolecobasidium ferulica</i>	IRAN3232C T		MF186874	MH400207		
<i>Scolecobasidium gamsii</i>	CBS 239.78 T	KF156088	KF156019	KF156150	KF156190	KF155982
<i>Scolecobasidium globale</i>	CBS 119644 T	KF961108	KF961086	KF961097	KF961065	KF961075
<i>Scolecobasidium globale</i>	CBS 135924	KF961107	KF961092	KF961104	KF961070	KF961079
<i>Scolecobasidium guangxiensis</i>	SS23 T	MK929277	MK934570	MK956169		
<i>Scolecobasidium guangxiensis</i>	X22	MK961269	MK961215	MK961247		
<i>Scolecobasidium helicteris</i>	NFCCI 4310 T		MK014833		MK321318	
<i>Scolecobasidium humicola</i>	CBS 116655 T	KF156068	HQ667521	KF156124	KF156195	KF155984
<i>Scolecobasidium icarus</i>	CBS 116645	KF156083	HQ667525		LM644604	
<i>Scolecobasidium icarus</i>	CBS 536.69 T	KF156084	HQ667524	KF156132	KF156174	KF156009
<i>Scolecobasidium lascauxense</i>	CBS 131815 T	KF156069	FR832474	KF156136	KF156183	KF155994
<i>Scolecobasidium lascauxense</i>	CBS 423.64	KF156085	HQ667523	KF156131	KF156173	KF156008
<i>Scolecobasidium leishanicola</i>	GUCC 18259	MZ503671	MZ503745	MZ503778	MZ546924	MZ546891
<i>Scolecobasidium leishanicola</i>	HGUP1808 T	MK377071	MK377301	MK377073		
<i>Scolecobasidium longiphorum</i>	CBS 435.76 T	KF156060	KF156038	KF156135	KF156182	KF155978
<i>Scolecobasidium macrozambiae</i>	CBS 137971 T		KJ869123	KJ869180		
<i>Scolecobasidium macrozambiae</i>	CBS 102491	KF156092	KF156021	KF156152	KF156191	KF155983
<i>Scolecobasidium minimum</i>	CBS 510.71 T	KF156087	HQ667522	KF156134	KF156172	KF156007
<i>Scolecobasidium minimum</i>	CBS 119792	KF156086	KF156027	KF156133	KF156175	KT272073
<i>Scolecobasidium mirabilis</i>	CBS 413.51 T	KF156076	HQ667536	KF156140	KF156164	KF156001
<i>Scolecobasidium musae</i>	CBS 729.95 T	KF156082	KF156029	KF156144	KF156171	KF155999

Supplementary Table 2 Continued.

Species	Strains	GenBank accession numbers				
		SSU	ITS	LSU	<i>RPB2</i>	<i>EF1A</i>
<i>Scolecobasidium musicola</i>	CBS 144441 T		MH327824	MH327860	MH327898	MH327887
<i>Scolecobasidium musicola</i>	CPC 37308		MW063428		MW071116	MW071096
<i>Scolecobasidium obovoideum</i>	GUCC 18246 T	MZ503658	MZ503732	MZ503765	MZ546911	MZ546878
<i>Scolecobasidium olivaceum</i>	CBS 137170 T	LM644548	LM644521	LM644564	LM644605	KT272067
<i>Scolecobasidium pandanicola</i>	CBS 140660 T		KT950850	KT950864		
<i>Scolecobasidium phaeophorum</i>	CBS 206.96 T	KP798637	KP798631	KP798634	KT272062	KT272098
<i>Scolecobasidium podocarpi</i>	CBS 143174 T		MG386032	MG386085		
<i>Scolecobasidium podocarpicola</i>	CBS 146057 T		MN562138	MN567645		
<i>Scolecobasidium ramosum</i>	CBS 137171	LM644549	LM644522	LM644565	LM644606	KT272068
<i>Scolecobasidium ramosum</i>	CBS 137173 T	LM644551	LM644524	LM644567	MZ546928	KT272069
<i>Scolecobasidium robustum</i>	CBS 112.97 T	KP798639	KP798633	KP798636	KT272060	KT272071
<i>Scolecobasidium sexuale</i>	CBS 131965	KF156090	KF156017	KF156119	KF156188	KF155977
<i>Scolecobasidium sexuale</i>	CBS 135765 T	KF156089	KF156018	KF156118	KF156189	KF155976
<i>Scolecobasidium terrestre</i>	CBS 211.53 T	KF156073	HQ667519	KF156148	KF156187	KF156005
<i>Scolecobasidium terreum</i>	CBS 203.27 T		HQ667544		HQ877665	
<i>Scolecobasidium tshawytschae</i>	CBS 100438 T	KF156062	HQ667562	KF156126	KF156180	KF155990
<i>Scolecobasidium tshawytschae</i>	CBS 228.66	KF156064	KF156016	KF156128	KF156179	KF155992
<i>Scolecobasidium variable</i>	NBRC 32268	EU107353	DQ307334	EU107310		DQ307356
<i>Scolecobasidium verrucaria</i>	GUCC 18240 T	MZ503652	MZ503726	MZ503759	MZ546905	MZ546872
<i>Scolecobasidium verrucosum</i>	CBS 383.81 T	KF156067	KF156015	KF156129	KF156185	KT272099
<i>Scolecobasidium zunyiense</i>	GUCC 18241 T	MZ503653	MZ503727	MZ503760	MZ546906	MZ546873
<i>Sympoventuria capensis</i>	CBS 120136 T	KF156094	MK810921	MK810808	MK926481	MK888745
<i>Pseudosigmoidea excentrica</i>	CBS 469.59 T	KF156096	HQ667543	KF282669	MK926478	KF155975

Fig. 16

Species	Strains	GenBank accession numbers				
		ITS	LSU	<i>EF1A</i>	<i>TUB</i>	<i>RPB2</i>
<i>Acroconidiellina arecae</i>	NFCCI 3696	KX306747	KX306776			
<i>Bellamyces quercus</i>	CBS 46217 T	MK810901	MK810788	MK888726		MK887796
<i>Clavatispora thailandiaca</i>	MFLUCC 100107	MH065721	KF770458			
<i>Echinocatena arthrinioides</i>	CBS 144202	MH107890	MH107937			
<i>Echinocatena sinensis</i>	CGMCC 3.20775 T	OL897006	OL897048	ON568898	ON569026	ON568948
<i>Echinocatena sinensis</i>	GZUIFR 21.901	OL897007	OL897049	ON568899	ON569027	ON568949
<i>Fuscohilum rhodensis</i>	CBS 121641 T	MK810909	MK810796	MK888733	MK926471	MK887802

Supplementary Table 2 Continued.

Species	Strains	GenBank accession numbers				
		ITS	LSU	EF1A	TUB	RPB2
<i>Fuscohilum siciliana</i>	CBS 105.85 T	MK810910	MK810797	MK888734	MK926472	MN091924
<i>Guizhoumyces aciculaea</i>	GUCC 18195 T	MZ503724	MZ503757	MZ546870	MZ546903	MZ546866
<i>Guizhoumyces aciculaea</i>	GUCC 18152	MZ503723	MZ503756	MZ546869	MZ546902	MZ546865
<i>Helicopsis olivaceum</i>	CBS 728.83	MH861681	MH873393			
<i>Matsushimaea fasciculata</i>	CBS 167.97 T	LT962397	LT962402			
<i>Matsushimaea fasciculata</i>	GUCC 18239	MZ503725	MZ503758	MZ546871	MZ546904	MZ546867
<i>Matsushimaea monilioides</i>	CBS 143867 T	LT883468	LT883469			
<i>Melnikomyces longisporum</i>	HUGP 18226 T	MT731290	MT731291	MT739516	MT739515	
<i>Melnikomyces thailandicus</i>	CBS 145767 T	MN794374	MN794351			
<i>Melnikomyces vietnamensis</i>	CBS 136209 T	KJ869156	KJ869213			
<i>Mycosisymbrium cirrhosum</i>	MTCC12435	KR259883	KR259884			KR349124
<i>Mycosisymbrium cirrhosum</i>	GUCC 1837	MZ503722	MZ503755	MZ546868	MZ546901	MZ546864
<i>Neocoleroa cameroonensis</i>	CBS 129041 T	MK810902	MK810789	MK888727	MN078219	MK887797
<i>Neocoleroa metrosideri</i>	ICMP 21139 T	KU131678	KU131677			
<i>Neofusicladium eucalypti</i>	CBS 128216 T	MK810903	MK810790	MK888728	MK926468	MK887798
<i>Neofusicladium eucalypticola</i>	CBS 141301 T	MK810904	MK810791	MK888729		MK887799
<i>Neofusicladium regnans</i>	CBS 143411 T	MG386066	MG386119		MG386169	
<i>Parafusicladium amoenum</i>	CBS 254.95 T	MK810906	MK810793	MK888730	MK926469	
<i>Parafusicladium intermedium</i>	CBS 110746 T	MK810907	MK810794	MK888731	MK926470	MK887800
<i>Parafusicladium paraamoenum</i>	CBS 141322 T	MK810908	MK810795	MK888732		MK887801
<i>Pinaceicola cordae</i>	CBS 126959 T	MK810911	MK810798	MK888735	MK926473	
<i>Pinaceicola pini</i>	CBS 463.82 T	MK810915	MK810802	MK888739	MK926477	MK887804
<i>Pseudosigmoidea alnicola</i>	CBS 145034 T	MK442620	MK442556			
<i>Pseudosigmoidea excentrica</i>	CBS 469.95 T	HQ667543	KF282669	KF155975	MK926478	
<i>Pseudosigmoidea ibarakiensis</i>	NBRC 107891 T	LC146758	LC146759			
<i>Scolecobasidium anellii</i>	CBS 284.64 T	FR832477	KF156138	KF155995	KF156184	KF282684
<i>Scolecobasidium anomala</i>	CBS 131816 T	HE575201	KF156137	KF155986	KF156194	HE575205
<i>Scolecobasidium constricta</i>	CBS 211.53 T	HQ667519	KF156148	KF156005	KF156187	KF282686
<i>Scolecobasidium longiphorum</i>	CBS 435.76 T	KF156038	KF156135	KF155978	KF156182	
<i>Scolecobasidium tshawytschae</i>	CBS 100438 T	HQ667562	KF156126	KF155990	KF156180	KF282697
<i>Sterila eucalypti</i>	CBS 144019 T	MK810918	MK810805	MK888742		MK887807
<i>Sterila eucalypti</i>	CPC 14942	MK810916	MK810803	MK888740		MK887805
<i>Sympoventuria capensis</i>	CBS 120136 T	MK810921	MK810808	MK888745	MK926481	MK887810

Supplementary Table 2 Continued.

Species	Strains	GenBank accession numbers				
		ITS	LSU	EF1A	TUB	RPB2
<i>Symptoventuria capensis</i>	CPC 12840	MK810923	MK810810	MK888747	MK926483	MK887812
<i>Troposporella fumosa</i>	CBS 351.94	MK810924	MH874121			
<i>Troposporella monilipes</i>	MUCL 19867	DQ351723	AY856871			
<i>Veronaeopsis simplex</i>	CBS 588.66 T	EU041820	EU041877			MN091925
<i>Verruconis gallopava</i>	CBS 437.64 T	HQ667553	KF156112	KF155968	KF156203	KF282689
<i>Verruconis panacis</i>	CBS 142802 T	MF536882	MF536880	MF536881	MF536883	
<i>Verruconis verruculosa</i>	CBS 119775 T	KF156014	KF156106	KF155974	KF156193	
<i>Yunnanomyces pandanicola</i>	MFLUCC 17-2260 T	MH388369	MH376743			MH412736
<i>Yunnanomyces phoenicis</i>	MFLUCC 19-0254 T		MK976738			MK986484
<i>Yunnanomyces phoenicis</i>	MFLUCC 19-0253		MK976737			MK986483
<i>Tyrannosorus lichenicola</i>	CBS 144018 T	MK810953	MK810838	MK888775	MK926509	MK887840
<i>Venturia saliciperda</i>	CBS 480.61 T	MK811007	MK810891	MK888825	MK926558	MK887886

Fig. 18

Species	Strains	GenBank accession numbers			
		ITS	TUB	CaM	RPB2
<i>Penicillium simplicissimum</i>	CBS 372.48 T	GU981588	GU981632	MN969297	JN121507
<i>Penicillium panissanguineum</i>	CBS 140989 T	KT887862	KT887823	KT887784	MN969182
<i>Penicillium svalbardense</i>	CBS 122416 T	GU981603	DQ486644	KC346338	KF296457
<i>Penicillium ochrochloron</i>	CBS 357.48 T	GU981604	GU981672	MN969280	KF296445
<i>Penicillium daleae</i>	CBS 211.28 T	GU981583	GU981649	MN969251	KF296427
<i>Penicillium rubriannulatum</i>	CGMCC 3.18804 T	KY495029	KY495138	MN969336	KY495080
<i>Penicillium cluniae</i>	CBS 326.89 T	MN431386	MN969376	MN969246	KF296424
<i>Penicillium janthinellum</i>	CBS 340.48 T	GU981585	GU981625	MN969268	JN121497
<i>Penicillium diatomitis</i>	CBS 140107 T	FJ430748	HE651133	LT970912	LT797560
<i>Penicillium oxalicum</i>	CBS 219.30 T	AF033438	KF296462	MN969283	JN121456
<i>Penicillium stolckiae</i>	CBS 315.67 T	AF033444	JN617717	AF481135	JN121488
<i>Penicillium subarcticum</i>	CBS 111719 T	AF481120	JN617716	AF481141	MN969139
<i>Penicillium aquaticum</i>	JMRC SF:013660 T	KY587453	KY587450	KY587447	KY587449
<i>Penicillium macrosclerotiorum</i>	CBS 116871 T	KJ834511	KJ834469	DQ911123	JN121432
<i>Penicillium estinogenum</i>	CBS 329.59 T	MN431388	MN969381	MN969255	
<i>Penicillium gracilentum</i>	CBS 599.73 T	KC411768	KJ834453	MN969260	JN121537
<i>Penicillium angustiporcatum</i>	CBS 202.84 T	KC411690	KJ834431	MN969235	JN406617
<i>Penicillium nothofagi</i>	CBS 130383 T	JN617712	JN606732	JN606507	MN969129

Supplementary Table 2 Continued.

Species	Strains	GenBank accession numbers			
		ITS	TUB	CaM	RPB2
<i>Penicillium westlingii</i>	CBS 231.28 T	GU944601	JN606718	MN969312	JN606625
<i>Penicillium dokdoense</i>	JMRC:SF:013606 T	MG906868	MH243037	MH243031	
<i>Penicillium copticola</i>	CBS 127355 T	JN617685	JN606817	JN606553	JN606599
<i>Penicillium sumatraense</i>	CBS 281.36 T	GU944578	JN606639	MN969301	EF198541
<i>Penicillium shearii</i>	CBS 290.48 T	GU944606	JN606840	EU644068	JN121482
<i>Penicillium paxilli</i>	CBS 360.48 T	GU944577	JN606844	JN606566	JN606610
<i>Penicillium citrinum</i>	CBS 139.45 T	AF033422	GU944545	MN969245	JF417416
<i>Penicillium hetheringtonii</i>	CBS 122392 T	GU944558	GU944538	MN969263	JN606606
<i>Penicillium euglaucum</i>	CBS 323.71 T	JN617699	JN606856	JN606564	JN606594
<i>Penicillium argentinense</i>	CBS 130371 T	JN831361	JN606815	JN606549	MN969105
<i>Penicillium roseopurpureum</i>	CBS 226.29 T	GU944605	JN606838	JN606556	JN606613
<i>Penicillium sanguifluum</i>	CBS 127032 T	JN617681	JN606819	JN606555	MN969135
<i>Penicillium gallaicum</i>	CBS 167.81 T	JN617690	JN606837	JN606548	JN606609
<i>Penicillium lapidosum</i>	CBS 343.48 T	MN431392	KJ834465	FJ530984	JN121500
<i>Penicillium terrenum</i>	CBS 313.67 T	AM992111	KJ834496	KP016808	JN406577
<i>Penicillium corylophilum</i>	CBS 312.48 T	AF033450	JX141042	KP016780	KP064631
<i>Penicillium cravenianum</i>	CBS 139138 T	JX140900	JX141076	JX157418	KP064636
<i>Penicillium restrictum</i>	CBS 367.48 T	AF033457	KJ834486	KP016803	JN121506
<i>Penicillium chalabudae</i>	CBS 219.66 T	KP016811	KP016748	KP016767	KP064572
<i>Penicillium alutaceum</i>	CBS 317.67 T	AF033454	KJ834430	KP016768	JN121489
<i>Penicillium decumbens</i>	CBS 230.81 T	AY157490	KJ834446	KP016782	JN406601
<i>Penicillium citreonigrum</i>	CBS 258.29 T	AF033456	EF198621	EF198628	JN121474
<i>Penicillium fundyense</i>	CBS 140980 T	KT887853	KT887814	KT887775	MN969176
<i>Penicillium erubescens</i>	CBS 318.67 T	AF033464	HQ646566	EU427281	JN121490
<i>Penicillium vinaceum</i>	CBS 389.48 T	AF033461	HQ646575	HQ646586	JN406555
<i>Penicillium thomii</i>	CBS 225.81 T	KM189560	KM088799	KM089184	KM089571
<i>Penicillium cartierense</i>	CBS 137956 T	KM189564	KM088804	KM089189	KM089576
<i>Penicillium spinulosum</i>	CBS 374.48 T	AF033410	KJ834493	GQ367524	JN406558
<i>Penicillium roseomaculatum</i>	CBS 137962 T	KM189755	KM089004	KM089391	KM089778
<i>Penicillium kiamaense</i>	CBS 137947 T	KM189506	KM088743	KM089128	KM089515
<i>Penicillium glabrum</i>	CBS 125543 T	GU981567	GU981619	KM089152	JF417447
<i>Penicillium pulvis</i>	CBS 138432 T	KM189632	KM088876	KM089263	KM089650
<i>Penicillium fuscum</i>	CBS 295.62 T	AF033411	GQ367513	GQ367539	JN121483

Supplementary Table 2 Continued.

Species	Strains	GenBank accession numbers			
		ITS	TUB	CaM	RPB2
<i>Penicillium tsitsikammaense</i>	CBS 328.71 T	KM189451	KM088675	KM089060	KM089447
<i>Penicillium longicatenatum</i>	CBS 137735 T	KM189636	KM088880	KM089267	KM089654
<i>Penicillium ranomafanaense</i>	CBS 137953 T	KM189541	KM088779	KM089164	KM089551
<i>Penicillium verhagenii</i>	CBS 137959 T	KM189708	KM088955	KM089342	KM089729
<i>Penicillium saturniforme</i>	CBS 122276 T	EU644081	EU644080	EU644062	JN121439
<i>Penicillium improvisum</i>	CBS 140994 T	KT887867	KT887828	KT887789	MN969169
<i>Penicillium sublectaticum</i>	CBS 138217 T	KM189761	KM089010	KM089397	KM089784
<i>Penicillium malmesburiense</i>	CBS 137744 T	KM189676	KM088921	KM089308	KM089695
<i>Penicillium fortuitum</i>	DTO 313-A3 T	MF803942	MF803836	MF803932	MN969206
<i>Penicillium lividum</i>	CBS 347.48 T	KM189582	KM088825	KM089211	KM089598
<i>Penicillium kananaskense</i>	CBS 530.93 T	KM189780	KM089030	KM089417	KM089804
<i>Penicillium hoeksii</i>	CBS 137776 T	KM189707	KM088954	KM089341	KM089728
<i>Penicillium zhuangii</i>	CBS 137464 T	KF769435	KF769411	KF769422	MN969145
<i>Penicillium quercetorum</i>	CBS 417.69 T	KM189556	KM088795	KM089180	KM089567
<i>Penicillium thiersii</i>	CBS 117503 T	AF125936	KJ834497	AY741726	JN121434
<i>Penicillium sclerotiorum</i>	CBS 287.36 T	JN626132	JN626001	JN626044	JN406585
<i>Penicillium vanoranjei</i>	CBS 134406 T	KC695696	KC695686	KC695691	
<i>Penicillium adametzioides</i>	CBS 313.59 T	JN686433	JN799642	JN686387	JN406578
<i>Penicillium angulare</i>	CBS 130293 T	AF125937	KC773779	KC773804	JN406554
<i>Penicillium malachiteum</i>	CBS 647.95 T	KC773838	KC773794	KC773820	MN969125
<i>Penicillium verrucisporum</i>	CGMCC 3.18415 T	KX885069	KX885049	KX885059	KX885040
<i>Penicillium griseolum</i>	CBS 277.58 T	EF422848	EF506213	EF506232	JN121480
<i>Penicillium phoeniceum</i>	CBS 249.32 T	KC411711	KJ834483	AY741729	JN406597
<i>Penicillium coffeae</i>	CBS 119387 T	AY742702	KJ834443	AY741747	JN121436
<i>Penicillium charlesii</i>	CBS 304.48 T	AF033400	JX091508	AY741727	JN121486
<i>Penicillium fellutanum</i>	CBS 229.81 T	AF033399	KJ834450	AY741753	JN121460
<i>Penicillium indicum</i>	CBS 115.63 T	AY742699	EU427263	AY741744	JN406640
<i>Penicillium chermesinum</i>	CBS 231.81 T	AY742693	KJ834441	AY741728	MN969111
<i>Penicillium costaricense</i>	CBS 140998 T	MN431396	KT887834	KT887795	MN969173
<i>Penicillium eremophilum</i>	CBS 123361 T	GU733341	KY709170	KY611931	KY611970
<i>Penicillium ramusculum</i>	CBS 251.56 T	EF433765	EU427269	EU427278	JN121472
<i>Penicillium capsulatum</i>	CBS 301.48 T	AF033429	MN969375	KP735539	JN406582
<i>Penicillium georgiense</i>	CBS 132826 T	EF422852	EF506223	EF506239	KM089734

Supplementary Table 2 Continued.

Species	Strains	GenBank accession numbers			
		ITS	TUB	CaM	RPB2
<i>Penicillium taxi</i>	CBS 206.57 T	KJ834517	KJ834495	MN969302	JN121454
<i>Penicillium hennebertii</i>	CBS 334.68 T	KJ834507	KJ834454	MN969262	JN121493
<i>Penicillium isariiforme</i>	CBS 247.56 T	AF454077	KJ834459	MN969266	JN121470
<i>Penicillium ochrosalmoneum</i>	CBS 489.66 T	EF626961	EF506212	EF506237	JN121524
<i>Penicillium idahoense</i>	CBS 341.68 T	KC411747	EF626953	EF626954	JN121499
<i>Penicillium monsserratidens</i>	NRRL 35884 T	KF932962	KF932930	KF932947	KF933001
<i>Penicillium nodulum</i>	CBS 227.89 T	KC411703	KJ834475	KJ867003	JN406603
<i>Penicillium shennongjianum</i>	CBS 228.89 T	KC411705	KJ834491	AY678561	JN121458
<i>Penicillium cinnamopurpureum</i>	CBS 429.65 T	EF626950	EF626948	EF626949	JN406533
<i>Penicillium parvulum</i>	CBS 132825 T	EF422845	EF506218	EF506225	MN969131
<i>Penicillium jiangxiense</i>	DTO 309-A7 T	KJ890411	KJ890409	KJ890407	MN969122
<i>Penicillium pusillum</i>	CBS 312.63 T	EF626951	KF932925	KF932941	KF932995
<i>Penicillium aeris</i>	CBS 135897 T	KF303654	KF303614	KF303627	KF303681
<i>Penicillium cantabricum</i>	CBS 120415 T	KF303655	KF303615	KF303646	KF303682
<i>Penicillium cryptum</i>	CBS 271.89 T	KF303647	KF303608	KF303628	JN121478
<i>Penicillium lassenii</i>	CBS 277.70 T	KF303648	KF303607	KF303629	JN121481
<i>Penicillium alfredii</i>	CBS 138224 T	KJ775684	KJ775177	KJ775411	KJ834520
<i>Penicillium fractum</i>	CBS 124.68 T	KC411674	KJ834452	MN969256	JN121441
<i>Penicillium inusitatum</i>	CBS 351.67 T	AF033431	KJ834458	MN969265	JN121503
<i>Hamigera avellanea</i>	CBS 295.48 T	AF454075	EU021664	EU021682	EU021627
<i>Aspergillus glaucus</i>	CBS 516.65 T	EF652052	EF651887	EF651989	EF651934
Fig. 21					
Species	Strains	GenBank accession numbers			
		ITS	TUB	CaM	RPB2
<i>Talaromyces albidus</i>	AS3.26143 T	OQ746343	OQ746324	OQ746326	OQ746328
<i>Talaromyces rubidus</i>	AS3.26142 T	OQ746342	OQ746323	OQ746325	OQ746327
<i>Talaromyces mimosinus</i>	CBS 659.80 T	JN899338	KJ865726	KJ885272	MN969149
<i>Talaromyces bacillisporus</i>	CBS 296.48 T	KM066182	AY753368	KJ885262	JF417425
<i>Talaromyces boninensis</i>	CBS 650.95 T	JN899356	KJ865721	KJ885263	KM023276
<i>Talaromyces helicus</i>	CBS 335.48 T	JN899359	KJ865725	KJ885289	KM023273
<i>Talaromyces brunneus</i>	CBS 227.60 T	JN899365	KJ865722	KJ885264	KM023272
<i>Talaromyces islandicus</i>	CBS 338.48 T	KF984885	KF984655	KF984780	KF985018
<i>Talaromyces ptychoconidius</i>	DAOM 241017 T	FJ160266	GU385733	JX140701	KM023278

Supplementary Table 2 Continued.

Species	Strains	GenBank accession numbers			
		<i>ITS</i>	<i>TUB</i>	<i>CaM</i>	<i>RPB2</i>
<i>Talaromyces purpureus</i>	CBS 475.71 T	JN899328	GU385739	KJ885292	JN121522
<i>Talaromyces palmae</i>	CBS 442.88 T	JN899396	HQ156947	KJ885291	KM023300
<i>Talaromyces subinflatus</i>	CBS 652.95 T	JN899397	MK450890	KJ885280	KM023308
<i>Talaromyces tzapotlensis</i>	NRRL 35203 T	KX946902	KX946884	KX946893	KX946922
<i>Talaromyces resedanus</i>	CBS 181.71 T	MN431413	MN969436	MN969355	MN969214
<i>Talaromyces guizhouensis</i>	CBS 141837 T	MN864277	MN863346	MN863323	MN863335
<i>Talaromyces guizhouensis</i>	DTO 054-C8	MN864278	MN863347	MN863324	MN863336
<i>Talaromyces jiangxiensis</i>	CGMCC 3.20783 T	OL897029	ON569042	ON568888	ON568961
<i>Talaromyces jiangxiensis</i>	GZUIFR 21.893	OL897030	ON569043	ON568889	ON568962
<i>Talaromyces paecilomycetoides</i>	CGMCC 3.20785 T	OL897033	ON569044	ON568890	ON568963
<i>Talaromyces paecilomycetoides</i>	GZUIFR 21.895	OL897034	ON569045	ON568891	ON568964
<i>Talaromyces duclauxii</i>	CBS 322.48 T	JN899342	JX091384	KF741955	JN121491
<i>Talaromyces marneffei</i>	CBS 388.87 T	JN899344	JX091389	KF741958	KM023283
<i>Talaromyces flavus</i>	CBS 310.38 T	JN899360	JX494302	KF741949	JF417426
<i>Talaromyces tenuis</i>	CBS 141840 T	MN864275	MN863344	MN863321	MN863333
<i>Talaromyces solicola</i>	DTO 180-D4 T	FJ160264	GU385731	KJ885279	KM023295
<i>Talaromyces albobiverticillius</i>	CBS 133440 T	HQ605705	KF114778	KJ885258	KM023310
<i>Talaromyces assiutensis</i>	CBS 147.78 T	JN899323	KJ865720	KJ885260	KM023305
<i>Talaromyces convolutus</i>	CBS 100537 T	JN899330	KF114773	MN969316	JN121414
<i>Talaromyces minioluteus</i>	CBS 642.68 T	JN899346	MN969409	KJ885273	JF417443
<i>Talaromyces udagawae</i>	CBS 579.72 T	JN899350	KF114796	KX961260	MN969148
<i>Talaromyces trachyspermus</i>	CBS 373.48 T	JN899354	KF114803	KJ885281	JF417432
<i>Talaromyces austrocalifornicus</i>	CBS 644.95 T	JN899357	KJ865732	KJ885261	MN969147
<i>Talaromyces erythromellis</i>	CBS 644.80 T	JN899383	HQ156945	KJ885270	KM023290
<i>Talaromyces ucrainicus</i>	CBS 162.67 T	JN899394	KF114771	KJ885282	KM023289
<i>Talaromyces atroroseus</i>	CBS 133442 T	KF114747	KF114789	KJ775418	KM023288
<i>Talaromyces diversus</i>	CBS 320.48 T	KJ865740	KJ865723	KJ885268	KM023285
<i>Talaromyces systylus</i>	BAFCcult 3419 T	KP026917	KR233838	KR233837	
<i>Talaromyces rubrifaciens</i>	CGMCC 3.17658 T	KR855658	KR855648	KR855653	KR855663
<i>Talaromyces aerius</i>	CBS 140611 T	KU866647	KU866835	KU866731	KU866991
<i>Talaromyces heiheensis</i>	CGMCC 3.18012 T	KX447526	KX447525	KX447532	KX447529
<i>Talaromyces pernambucoensis</i>	URM 6894 T	LR535947	LR535945	LR535946	LR535948
<i>Talaromyces minnesotensis</i>	CBS 142381 T	LT558966	LT559083	LT795604	LT795605

Supplementary Table 2 Continued.

Species	Strains	GenBank accession numbers			
		<i>ITS</i>	<i>TUB</i>	<i>CaM</i>	<i>RPB2</i>
<i>Talaromyces catalonicus</i>	CBS 143039 T	LT899793	LT898318	LT899775	LT899811
<i>Talaromyces basipetosporus</i>	CBS 143836 T	LT906542	LT906563		LT906545
<i>Talaromyces affinitatimellis</i>	CBS 143840 T	LT906543	LT906552	LT906549	LT906546
<i>Talaromyces subericola</i>	CBS 144322 T	LT985888	LT985899	LT985904	LT985909
<i>Talaromyces speluncarum</i>	CBS 143844 T	LT985890	LT985901	LT985906	LT985911
<i>Talaromyces brasiliensis</i>	CBS 142493 T	MF278323	LT855560	LT855563	MN969198
<i>Talaromyces halophytorum</i>	KACC 48127 T	MH725786	MH729367	MK111426	MK111427
<i>Talaromyces gaditanus</i>	CBS 169.81 T	MH861318	OK338775	OK338802	OK338827
<i>Talaromyces samsonii</i>	CBS 137.84 T	MH861709	OK338798	OK338824	OK338844
<i>Talaromyces amyrossmaniae</i>	NFCCI 1919 T	MH909062	MH909064	MH909068	MH909066
<i>Talaromyces clemensii</i>	PPRI 26753 T	MK951940	MK951833	MK951906	MN418451
<i>Talaromyces guatemalensis</i>	CCF 6215 T	MN322789	MN329687	MN329688	MN329689
<i>Talaromyces albisclerotius</i>	CBS 141839 T	MN864276	MN863345	MN863322	MN863334
<i>Talaromyces resiniae</i>	CGMCC 3.4387 T	MT079858	MN969442	MT066184	MN969221
<i>Talaromyces chongqingensis</i>	CGMCC 3.20482 T	MZ358001	MZ361343	MZ361350	MZ361357
<i>Talaromyces africanus</i>	CBS 147340 T	OK339610	OK338782	OK338808	OK338833
<i>Talaromyces calidominioluteus</i>	CBS 147313 T	OK339612	OK338786	OK338817	OK338837
<i>Talaromyces germanicus</i>	CBS 147314 T	OK339619	OK338799	OK338812	OK338845
<i>Talaromyces phuphaphetensis</i>	TBRC 16281 T	ON692803	ON706960	ON706962	ON706964
<i>Talaromyces satunensis</i>	TBRC 16246 T	ON692804	ON706961	ON706963	
<i>Trichocoma paradoxa</i>	CBS 788.83 T	MH860643	JF417469	JF417506	JN121417

Fig. 23

Species	Strains	GenBank accession numbers	
		<i>ITS</i>	<i>LSU</i>
<i>Aphanoascus canadensis</i>	UAMH 4574 T	AJ439435	
<i>Aphanoascus clathratus</i>	IMI 329400 T	AJ439436	
<i>Aphanoascus crassitunicatus</i>	CBS 167.78 T	KT155812	MH872884
<i>Aphanoascus cubensis</i>	FMR 4220 T	AJ439432	
<i>Aphanoascus foetidus</i>	CBS 453.75 T	KT155907	KT155252
<i>Aphanoascus foetidus</i>	EM14.2002	KT948765	
<i>Aphanoascus foetidus</i>	CBS 143.77	NR_145206	KT155141
<i>Aphanoascus foetidus</i>	CBS 320.86	NR_145207	NG_064142
<i>Aphanoascus fulvescens</i>	CBS 115955	KT155718	KT155038

Supplementary Table 2 Continued.

Species	Strains	GenBank accession numbers	
		ITS	LSU
<i>Aphanoascus fulvescens</i>	FMR 5652	AJ439437	
<i>Aphanoascus fulvescens</i>	NBRC 30411	JN943432	JN941547
<i>Aphanoascus fulvescens</i>	CBS 121.64	MH858383	MH870012
<i>Aphanoascus fulvescens</i>	CBS 305.67	MH858976	MH870669
<i>Aphanoascus fulvescens</i>	CBS 741.68	KT155965	KT155310
<i>Aphanoascus fulvescens</i>	CBS 742.68	MH859218	MH870943
<i>Aphanoascus fulvescens</i>	CBS 743.68	MH859219	MH870944
<i>Aphanoascus fulvescens</i>	FMR 5484	AJ131785	
<i>Aphanoascus jingzhouense</i>	EB1303M T	NR_158334	
<i>Aphanoascus keratinophilus</i>	IMI 319010 T	AJ133436	
<i>Aphanoascus keratinophilus</i>	CBS 104.62	NR_145205	NG_064030
<i>Aphanoascus mephitalis</i>	CBS 783.70 T	NR_154665	NG_056949
<i>Aphanoascus orissae</i>	CBS 466.88 T	KT155649	AB075357
<i>Aphanoascus orissae</i>	CBS 340.89	AJ390393	MZ435803
<i>Aphanoascus orissae</i>	CBS 116064	KT155721	KT155041
<i>Aphanoascus orissae</i>	CBS 437.88	KT155898	NG_058858
<i>Aphanoascus pinarensis</i>	CBS 113874 T	KT155619	
<i>Aphanoascus reticulisporus</i>	CBS 392.67 T	MH859002	MH870704
<i>Aphanoascus reticulisporus</i>	NBRC 32373	JN943435	JN941550
<i>Aphanoascus reticulisporus</i>	UAMH 4320	AJ007841	
<i>Aphanoascus</i> sp.	NBRC 31723	JN943451	JN941548
<i>Aphanoascus</i> sp.	CBS 111.58	KT155687	KT155004
<i>Aphanoascus</i> sp.	CBS 663.78	KT155957	KT155302
<i>Aphanoascus verrucosus</i>	CBS 468.88 T	NR_131309	NG_057011
<i>Aphanoascus verrucosus</i>	GZAC EB1601M.1	NR_154812	
<i>Aphanoascus verrucosus</i>	CBS 171.62	NR_131267	KT155150
<i>Keratinophyton alvearium</i>	LC11684 T	MF939598	MF939580
<i>Keratinophyton lemmensii</i>	BiMM F76 T	MN633082	MT874998

Fig. 25

Species	Strains	GenBank accession numbers			
		ITS	LSU	SSU	RPB2
<i>Arachnomyces glareosus</i>	CBS 116129 T		FJ358273	FJ358341	
<i>Arachnomyces gracilis</i>	UAMH 9756 T	AY123779		AF525307	

Supplementary Table 2 Continued.

Species	Strains	GenBank accession numbers			
		ITS	LSU	SSU	RPB2
<i>Arachnomyces minimus</i>	CBS 324.70 T		FJ358274	FJ358342	
<i>Arthroderma ciferrii</i>	AFTOL-ID 428		EF413625	EF413624	EF413626
<i>Ascosphaera apis</i>	CBS 402.96	MH862580	FJ358275	FJ358343	
<i>Aspergillus fumigatus</i>	INFU/Jc/KF/6, F-A, Af293		FM179606	GU980961	XM_741647
<i>Bradomyces oncorhynchi</i>	CCF 4369 T		HG426063	HG426064	
<i>Byssochlamys nivea</i>	CBS 100.11		FJ358279	FJ358345	JF417414
<i>Caliciopsis orientalis</i>	CBS 138.64 T	KP881690	DQ470987	DQ471039	DQ470939
<i>Caliciopsis pinea</i>	CBS 139.64	KP881691	DQ678097	DQ678043	
<i>Camptophora hylomeconis</i>	CBS 113311 T	KC455241	EU035415	KC455295	KC455285
<i>Capronia munkii</i>	DAOM 216390 T	AF050250	EF413604	EF413603	EF413606
<i>Celothelium cinchonarum</i>	F 17105 f		DQ329020		
<i>Ceramothyrium carniolicum</i>	CBS 175.95 T	KC978733	KC455251	KC455294	
<i>Cladophialophora carrionii</i>	CBS 160.54 T	MH857278	FJ358234	FJ358302	
<i>Cladophialophora emmonsii</i>	IFM 52025 T	AB109184	AB100682	KF155193	
<i>Cladophialophora humicola</i>	CBS 117536 T	EU035408	KC809987	KJ636038	
<i>Cladophialophora minutissima</i>	CBS 121758 T	MH863155	KJ636047	EF016370	
<i>Cladophialophora parmeliae</i>	CBS 129337	JQ342180	JQ342182		
<i>Corynelia africana</i>	PREM 57242 T	NR_153901	KP881714	KP881719	
<i>Corynelia fructigena</i>	PREM 57240 T	NR_153902	KP881716	KP881720	
<i>Corynelia uberata</i>	UME 31276			AF242262	
<i>Cyphellophora laciniata</i>	CBS 190.61 T	MH858019	FJ358239	FJ358307	KC455286
<i>Cyphellophora europaea</i>	CBS 101466 T	KC455246	KC455259	KC455303	
<i>Cyphellophora olivacea</i>	CBS 122.74 T	KC455247	KC455260		
<i>Cyphellophora oxyspora</i>	CBS 698.73 T	KC455249	KC455262	KC455305	
<i>Cyphellophora sessilis</i>	CBS 243.85 T	MH861875	EU514700	KC455308	KC455288
<i>Cyphellophora vermisporea</i>	CBS 228.86 T	MH861947	KC455257	KC455301	KC455291
<i>Dactylospora haliotrepha</i>	ATCC MYA-3590		FJ176855	FJ176802	FJ238344
<i>Dactylospora mangrovei</i>	CBS 110444		FJ176890	FJ176836	FJ238375
<i>Dactylospora vrijmoediae</i>	NTOU 4002 T	NR_138396	KC692153	KC692152	KC692154
<i>Dermatocarpon miniatum</i>	DUKE 0047501	DQ782837	AY584644	AY584668	DQ782863
<i>Dolabra nepheliae</i>	CBS 122120		GU332517		
<i>Endocarpon pusillum</i>	AFTOL-ID 2279		EF643754	EF689837	
<i>Fusichalara minuta</i>	CBS 709.88	KX537754	KX537758	KX537773	KX537770

Supplementary Table 2 Continued.

Species	Strains	GenBank accession numbers			
		ITS	LSU	SSU	RPB2
<i>Geoglossum nigrum</i>	OSC 100009		AY544650	AY544694	
<i>Granulopyrenis seawardii</i>	CBS 109025 T		EF411062	EF411059	EF411065
<i>Chaenothecopsis savonica</i>	Tibell 15876	AY795868	AY796000	U86691	
<i>Knufia cryptophialidica</i>	DAOM 216555 T	JN040501		EF137364	
<i>Lagenulopsis bispora</i>	PREM 57232 T	KP881709	KP881717	KP881721	
<i>Mycocalicium polyporaum</i>	ZWGeo60Clark	AY789363	AY789362	AY789361	
<i>Onygena corvina</i>	CBS 281.48		FJ358287	FJ358352	
<i>Penicillium javanicum</i>	AFTOL-ID 429	KT232212	EF413621	EF413620	EF413622
<i>Phaeomoniella capensis</i>	CBS 123535 T	MH863300	MH874824		
<i>Phaeomoniella chlamydospora</i>	CBS 239.74	MH860847	MH872585		
<i>Phaeomoniella tardicola</i>	STE-U 6123 T	MH863154	GQ154619	GQ154640	
<i>Phialophora verrucosa</i>	CBS 140325 T	NR_146242	KJ930073	KM658059	
<i>Polyblastia terrestris</i>	SS 180		EU697703		
<i>Pyrenula pseudobufonia</i>	VR 14-VI-02/5		AY640962	AY641001	AY641068
<i>Pyrgillus javanicus</i>	DUKE 0047748	DQ826741	DQ823103	DQ823110	DQ842009
<i>Rhinocladiella anceps</i>	CBS 181.65 T	MH858534	EU041862	AY554292	DQ840564
<i>Rhopalophora clavispora</i>	CBS 129.74	KX537751	KX537755		KX537767
<i>Rhopalophora clavispora</i>	CBS 281.75	KX537752	KX537756	KX537771	KX537768
<i>Rhopalophora clavispora</i>	CBS 637.73 T	KX537753	KX537757	KX537772	KX537769
<i>Rhynchostoma proteae</i>	CBS 112051 T	EU552154	MN861683		
<i>Sclerococcum parasiticum</i>	LE 260868		MK759892	MK759888	
<i>Sclerococcum martynii</i>	MCA 7061	MZ221610	MZ221619	MZ221215	
<i>Sclerococcum martynii</i>	D. Haelew. F-1570b	MZ221616	MZ221623		MZ229309
<i>Sphinctrina turbinata</i>	DUKE 0047956		EF413632	U86693	EF413633
<i>Spiromastix warcupii</i>	CBS 576.63 T	MH858362	DQ782909	AB015768	DQ782870
<i>Stenocybe pullatula</i>	Tibell 17117	AY795878	AY796008	U86692	
<i>Thelidium pyrenophorum</i>	DUKE 0047919		EF643782		
<i>Trichocoma paradoxa</i>	CBS 788.83	JN899398	FJ358290	FJ358354	JN121550
<i>Trichoglossum hirsutum</i>	KH 03232003-1	DQ491494	AY544653	AY544697	DQ470881
<i>Trichomerium deniquelatum</i>	MFLUCC10-0884 T	JX313654	JX313660		
<i>Tripodopora tripod</i>	PREM 61200	KP881712	KP881718		
<i>Veronaea botryosa</i>	CBS 254.57 T	MH857711	EU041873	JN856021	
<i>Verrucaria macrostoma</i>	DUKE 0047950		EF643799	EF689874	

Supplementary Table 2 Continued.

Species	Strains	GenBank accession numbers				
		ITS	LSU	SSU	RPB2	
<i>Vonarxia vagans</i>	CBS 123533 T	FJ839636	FJ839672	KC455310	KC455293	
beetle-associated isolate	INBio 4503Q	KM242300	KM242300			
beetle-associated isolate	INBio 4513J	KM242356	KM242356			
beetle-associated isolate	INBio 4513L	KM242358	KM242358			
<i>Anthopsis catenata</i>	CBS 492.81 T	MH861371	MH873124			
Fig. 27						
Species	Strains	GenBank accession numbers				
		ITS	LSU	MCM7	RPB2	EF1A
<i>Geomyces auratus</i>	CBS 108.14 T	KF039895	KF017864	KF017690	KF017746	KF017805
<i>Geomyces obovatus</i>	CGMCC 3.18491 T	MT509362	MT509376	MT534202	MT534216	MT534227
<i>Geomyces obovatus</i>	CGMCC 3.18492	MT509363	MT509377	MT534203	MT534217	MT534228
<i>Gymnostellatospora alpina</i>	CBS620.81 T	MH861383	MH873132			
<i>Gymnostellatospora bhattii</i>	CBS760.71 T	MH860337	MH872092			
<i>Gymnostellatospora</i> sp.	DG1097	ON261539	ON361440	ON456965	ON457091	ON510835
<i>Gymnostellatospora</i> sp.	MY829	ON259518	ON361493	ON457027	ON457134	ON510895
<i>Leuconeurospora pulcherrima</i>	CBS 343.76	KF049206	FJ176884		FJ238367	FJ238409
<i>Leuconeurospora</i> sp.	02NH04	JX270349	KF017817	KF017648	KF017702	KF017757
<i>Leuconeurospora</i> sp.	15PA04	JX270479	KF017841	KF017669	KF017725	KF017781
<i>Pseudeurotium zonatum</i>	CBS 329.36 T	AY129286	DQ470988		DQ470940	DQ471112
<i>Pseudeurotium zonatum</i>	CBS 391.61	MH858096	MH869666			
<i>Pseudogeomyces lindneri</i>	ZY 22.003 T	OP796797	OP796792	OP781436		OP781431
<i>Pseudogeomyces lindneri</i>	ZY 22.004	OP796798	OP796793	OP781437		OP781432
<i>Pseudogeomyces</i> sp.	23WI08	JX270598	KF017858			KF017799
<i>Pseudogeomyces</i> sp.	23WI14	JX270604		KF017684		
<i>Pseudogymnoascus antarcticus</i>	CHFC-EA 569 T	JX845280	MN417282	MN432493	MN418135	MN418131
<i>Pseudogymnoascus appendiculatus</i>	02NH11	JX270356	KF017819	KF017650	KF017704	KF017759
<i>Pseudogymnoascus appendiculatus</i>	07MA02	JX270402	KF017827	KF017658	KF017712	KF017767
<i>Pseudogymnoascus australis</i>	CHFC-EA 567 T	MN417287	MN417284	MN432491	MN418137	MN418133
<i>Pseudogymnoascus botryoides</i>	CGMCC 3.20875 T	ON365910	ON366337		ON568967	ON568902
<i>Pseudogymnoascus botryoides</i>	GZUIFR 22.044	ON365911	ON366338		ON568968	ON568903
<i>Pseudogymnoascus campensis</i>	ZY 22.001 T	OP796795	OP796790	OP781434		OP781429
<i>Pseudogymnoascus campensis</i>	ZY 22.002	OP796796	OP796791	OP781435		OP781430
<i>Pseudogymnoascus camphorae</i>	CGMCC 3.20876 T	ON365914	ON366341	ON568921	ON568971	ON568906

Supplementary Table 2 Continued.

Species	Strains	GenBank accession numbers				
		ITS	LSU	MCM7	RPB2	EF1A
<i>Pseudogymnoascus camphorae</i>	GZUIFR 22.049	ON365915	ON366342	ON568922	ON568972	ON568907
<i>Pseudogymnoascus catenatus</i>	GZUIFR 21.813	MZ444078	MZ444105	MZ490760	MZ488543	MZ488520
<i>Pseudogymnoascus catenatus</i>	CGMCC 3.20472 T	MZ444080	MZ444107	MZ490762	MZ488545	MZ488522
<i>Pseudogymnoascus cavicola</i>	IHEM 28275 T	OU989484	OU641157			OU641535
<i>Pseudogymnoascus destructans</i>	20631-21	EU884921	KF017865	KF017691	KF017747	KF017806
<i>Pseudogymnoascus fujianensis</i>	CGMCC 3.20474 T	MZ444084	MZ444111	MZ490766	MZ488549	MZ488526
<i>Pseudogymnoascus fujianensis</i>	GZUIFR 21.820	MZ444085	MZ444112	MZ490767	MZ488550	MZ488527
<i>Pseudogymnoascus griseus</i>	CHFC-EA 568 T	MN417288	MN417285	MN432492	MN418138	MN418134
<i>Pseudogymnoascus guiyangensis</i>	G014512 T	KM925045				
<i>Pseudogymnoascus guizhouensis</i>	GZUIFR 376.1 T	MT509369	MT509383	MT534209	MT534223	MT534234
<i>Pseudogymnoascus guizhouensis</i>	GZUIFR 376.2	MT509370	MT509384	MT534210	MT534224	MT534235
<i>Pseudogymnoascus hyalinus</i>	CBS 106.13 T	OR475795	OR733547	OR734802	OR734803	OR473058
<i>Pseudogymnoascus lanuginosus</i>	CHFC-EA 570 T	MN417286	MN417283	MN418139	MN418136	MN418132
<i>Pseudogymnoascus lindneri</i>	02NH05	JX270350	KF017818	KF017649	KF017703	KF017758
<i>Pseudogymnoascus lindneri</i>	LHU158 T	MN542212			MN541384	MN541383
<i>Pseudogymnoascus palmeri</i>	WSF 3629	KF039897	KF017870	KF017696	KF017751	KF017811
<i>Pseudogymnoascus palmeri</i>	LHU407 T	MT988150			MW054468	MW054467
<i>Pseudogymnoascus papyriferae</i>	CGMCC 3.20877 T	ON365916	ON366343	ON568923	ON568973	ON568908
<i>Pseudogymnoascus rhouxiogongylinus</i>	CBS 722.69 T	OR736258	OR736259	OR734800	OR734801	OR734799
<i>Pseudogymnoascus roseus</i>	05NY06	JX270385	KF017824	KF017655	KF017709	KF017764
<i>Pseudogymnoascus roseus</i>	05NY08	JX270387	KF017825	KF017656	KF017710	KF017765
<i>Pseudogymnoascus roseus</i>	05NY09	JX270388	KF017826	KF017657	KF017711	KF017766
<i>Pseudogymnoascus shaanxiensis</i>	GZUIFR HZ5.7 T	MT509366	MT509380	MT534206	MT534220	MT534231
<i>Pseudogymnoascus shaanxiensis</i>	GZUIFR 21.801	MZ444066	MZ444093	MZ490748	MZ488531	MZ488508
<i>Pseudogymnoascus sinensis</i>	CGMCC 3.18493 T	MT509364	MT509378	MT534204	MT534218	MT534229
<i>Pseudogymnoascus sinensis</i>	CGMCC 3.18494	MT509365	MT509379	MT534205	MT534219	MT534230
<i>Pseudogymnoascus</i> sp.	04NY11	JX270375	KF017821	KF017652	KF017706	KF017761
<i>Pseudogymnoascus</i> sp.	04NY17A	JX270378	KF017823	KF017654	KF017708	KF017763
<i>Pseudogymnoascus</i> sp.	10NY08	JX270432	KF017829	KF017659	KF017714	KF017769
<i>Pseudogymnoascus</i> sp.	10NY09	JX270433	KF017830	KF017660	KF017715	KF017770
<i>Pseudogymnoascus</i> sp.	10NY10	JX270434	KF017831		KF017716	KF017771
<i>Pseudogymnoascus</i> sp.	11MA03	JX270438	KF017832	KF017661	KF017717	KF017772
<i>Pseudogymnoascus</i> sp.	11MA05	JX270440	KF017833	KF017662	KF017718	KF017773

Supplementary Table 2 Continued.

Species	Strains	GenBank accession numbers				
		ITS	LSU	MCM7	RPB2	EF1A
<i>Pseudogymnoascus</i> sp.	11MA07	JX270442	KF017834	KF017663	KF017719	KF017774
<i>Pseudogymnoascus</i> sp.	11MA08	JX270443	KF017835	KF017664	KF017720	KF017775
<i>Pseudogymnoascus</i> sp.	12NJ13	JX270459	KF017838	KF017667	KF017722	KF017778
<i>Pseudogymnoascus</i> sp.	15PA11	JX270486	KF017843	KF017671	KF017727	KF017783
<i>Pseudogymnoascus</i> sp.	17WV03	JX270510	KF017844	KF017672	KF017728	KF017784
<i>Pseudogymnoascus</i> sp.	17WV06	JX270513		KF017673	KF017729	KF017785
<i>Pseudogymnoascus</i> sp.	18VA07	JX270527	KF017847	KF017675		KF017788
<i>Pseudogymnoascus</i> sp.	18VA08	JX270528	KF017848	KF017676	KF017731	KF017789
<i>Pseudogymnoascus</i> sp.	18VA12	JX270532	KF017849		KF017732	KF017790
<i>Pseudogymnoascus</i> sp.	18VA13	JX270533	KF017850		KF017733	KF017791
<i>Pseudogymnoascus</i> sp.	20KY08	JX270562	KF017851	KF017677	KF017734	KF017792
<i>Pseudogymnoascus</i> sp.	20KY10	JX270563	KF017852	KF017678	KF017735	KF017793
<i>Pseudogymnoascus</i> sp.	20KY12	JX270565	KF017853	KF017679	KF017736	KF017794
<i>Pseudogymnoascus</i> sp.	21IN01	JX270568	KF017854	KF017680	KF017737	KF017795
<i>Pseudogymnoascus</i> sp.	21IN05	JX270572	KF017855	KF017681	KF017738	KF017796
<i>Pseudogymnoascus</i> sp.	21IN10	JX270577	KF017856	KF017682	KF017739	KF017797
<i>Pseudogymnoascus</i> sp.	24MN04	JX270612	KF017859	KF017685	KF017741	KF017800
<i>Pseudogymnoascus</i> sp.	24MN06	JX270614	KF017860	KF017686	KF017742	KF017801
<i>Pseudogymnoascus</i> sp.	24MN14	JX270622	KF017862	KF017688	KF017744	KF017803
<i>Pseudogymnoascus</i> sp.	24MN18	JX270626	KF017863	KF017689	KF017745	KF017804
<i>Pseudogymnoascus</i> sp.	22984-1-I1	JX415262	KF017866	KF017692		KF017807
<i>Pseudogymnoascus</i> sp.	23014-1-I6	JX512256	KF017867	KF017693	KF017748	KF017808
<i>Pseudogymnoascus</i> sp.	A07MA10	KF039893	KF017828		KF017713	KF017768
<i>Pseudogymnoascus</i> sp.	15PA10B	KF039894	KF017842	KF017670	KF017726	KF017782
<i>Pseudogymnoascus</i> sp.	RMF 7792	KF039898	KF017871	KF017697	KF017752	KF017812
<i>Pseudogymnoascus</i> sp.	MN-Mycosel-7	KF039899	KF017872	KF017698	KF017753	KF017813
<i>Pseudogymnoascus turneri</i>	LHU 121 T	MN542213			MN541380	MN541379
<i>Pseudogymnoascus turneri</i>	Ps5	MN542214			MN541382	MN541381
<i>Pseudogymnoascus verrucosus</i>	04NY16	JX270377	KF017822	KF017653	KF017707	KF017762
<i>Pseudogymnoascus verrucosus</i>	24MN13	JX270621	KF017861	KF017687	KF017743	KF017802
<i>Pseudogymnoascus yunnanensis</i>	CGMCC 3.20475 T	MZ444072	MZ444099	MZ490754	MZ488537	MZ488514
<i>Pseudogymnoascus yunnanensis</i>	GZUIFR 21.808	MZ444073	MZ444100	MZ490755	MZ488538	MZ488515
<i>Pseudogymnoascus zhejiangensis</i>	CGMCC 3.20476 T	MZ444075	MZ444102	MZ490757	MZ488540	MZ488517

Supplementary Table 2 Continued.

Species	Strains	GenBank accession numbers				
		ITS	LSU	MCM7	RPB2	EF1A
<i>Pseudogymnoascus zhejiangensis</i>	GZUIFR 21.811	MZ444076	MZ444103	MZ490758	MZ488541	MZ488518
<i>Pseudogymnoascus zongqii</i>	CGMCC 3.20878 T	ON365919	ON366346	ON568926	ON568976	ON568911
<i>Pseudogymnoascus zongqii</i>	GZUIFR 22.042	ON365920	ON366347	ON568927	ON568977	ON568912
<i>Solomyces guizhouensis</i>	CGMCC 3.20477 T	MZ444069	MZ444096	MZ490751	MZ488534	MZ488511
<i>Solomyces guizhouensis</i>	GZUIFR 21.805	MZ444070	MZ444097	MZ490752	MZ488535	MZ488512
<i>Solomyces sinensis</i>	CGMCC 3.18498 T	MT509373	MT509387	MT534213		MT534238
<i>Solomyces sinensis</i>	CGMCC 3.18499	MT509374	MT509388	MT534214		MT534239
Undetermined	12NJ10	JX270456	KF017837	KF017666	KF017721	KF017777
<i>Zongqia sinensis</i>	CGMCC 3.20471 T	MZ444088	MZ444115	MZ490770	MZ488553	
<i>Zongqia sinensis</i>	GZUIFR 21.824	MZ444089	MZ444116	MZ490771	MZ488554	

Fig. 29

Species	Strains	GenBank accession numbers			
		ITS	LSU	EF1A	TUB
<i>Apiospora acutiapica</i>	KUMCC 20-0210 T	MT946343	MT946339	MT947360	MT947366
<i>Apiospora adinandrae</i>	SAUCC 1282B-1 T	OR739431	OR739572	OR753448	OR757128
<i>Apiospora agari</i>	KUC 21333 T	MH498520	MH498440	MH544663	MH498478
<i>Apiospora aquatica</i>	S-642	MK828608	MK835806		
<i>Apiospora arctoscopi</i>	KUC 21331 T	MH498529	MH498449	MN868918	MH498487
<i>Apiospora arundinis</i>	CBS 133509	KF144886	KF144930	KF145018	KF144976
<i>Apiospora aurea</i>	CBS 244.83 T	AB220251	KF144935	KF145023	KF144981
<i>Apiospora balearica</i>	CBS 145129 T	MK014869	MK014836		MK017975
<i>Apiospora bambusae</i>	ALV 17304	MK014874	MK014841	MK017951	MK017980
<i>Apiospora bambusicola</i>	MFLUCC 20-0144 T	MW173030	MW173087	MW183262	
<i>Apiospora bawanglingensis</i>	SAUCC BW0444 T	OR739429	OR739570	OR753446	OR757126
<i>Apiospora biserialis</i>	CGMCC 3.20135 T	MW481708	MW478885	MW522938	MW522955
<i>Apiospora camelliae-sinensis</i>	LC 5007 T	KY494704	KY494780	KY705103	KY705173
<i>Apiospora cannae</i>	ZHKUCC 22-0127	OR164901	OR164948	OR166285	OR166321
<i>Apiospora chiangraiense</i>	MFLUCC 21-0053 T	MZ542520	MZ542524		MZ546409
<i>Apiospora chromolaenae</i>	MFLUCC 17-1505 T	NR_168859			
<i>Apiospora cordylines</i>	GUCC 10027 T	MT040106		MT040127	MT040148
<i>Apiospora coryli</i>	CFCC 58978 T	OR125564	OR133586	OR139974	OR139978
<i>Apiospora cyclobalanopsidis</i>	CGMCC 3.20136 T	MW481713	MW478892	MW522945	MW522962
<i>Apiospora dematiacea</i>	KUNCC 23-14202 T	OR590346	OR590339	OR634953	OR634948

Supplementary Table 2 Continued.

Species	Strains	GenBank accession numbers			
		ITS	LSU	<i>EF1A</i>	<i>TUB</i>
<i>Apiospora dendrobii</i>	MFLUCC 14-0152 T	MZ463151	MZ463192		
<i>Apiospora descalsii</i>	CBS 145130 T	MK014870	MK014837		MK017976
<i>Apiospora dichotomanthi</i>	LC 4950 T	KY494697	KY494773	KY705096	KY705167
<i>Apiospora dicranopteridis</i>	KUNCC 23-14171 T	OR590342	OR590336	OR634950	OR634944
<i>Apiospora dongyingensis</i>	SAUCC 0302 T	OP563375	OP572424	OP573264	OP573270
<i>Apiospora elliptica</i>	ZHKUCC 22-0132	OR164905	OR164952	OR166284	OR166323
<i>Apiospora endophytica</i>	ZHKUCC 23-0006 T	OQ587996	OQ587984	OQ586062	OQ586075
<i>Apiospora esporlensis</i>	CBS 145136 T	MK014878	MK014845		MK017983
<i>Apiospora euphorbiae</i>	IMI 285638b	AB220241	AB220335		AB220288
<i>Apiospora fermenti</i>	KUC 21289 T	MF615226	MF615213	MH544667	MF615231
<i>Apiospora gaoyouensis</i>	CFCC 52301 T	MH197124		MH236793	MH236789
<i>Apiospora garethjonesii</i>	KUMCC 16-0202 T	KY356086	KY356091		
<i>Apiospora gelatinosa</i>	KHAS 11962 T	MW481706	MW478888	MW522941	MW522958
<i>Apiospora globosa</i>	KUNCC 23-14210 T	OR590347	OR590340	OR634954	
<i>Apiospora guangdongensis</i>	ZHKUCC 23-0004 T	OQ587994	OQ587982	OQ586060	OQ586073
<i>Apiospora guiyangensis</i>	MFLU 19-2113 T	NR_175678	MW240577		MW775604
<i>Apiospora guizhouensis</i>	LC 5322 T	KY494709	KY494785	KY705108	KY705178
<i>Apiospora hainanensis</i>	SAUCC 1681 T	OP563373	OP572422	OP573262	OP573268
<i>Apiospora hispanica</i>	IMI 326877 T	AB220242	AB220336		AB220289
<i>Apiospora hydei</i>	CBS 114990 T	KF144890	KF144936	KF145024	KF144982
<i>Apiospora hyphopodii</i>	MFLUCC 15-0003 T	KR069110			
<i>Apiospora iberica</i>	CBS 145137 T	MK014879	MK014846		MK017984
<i>Apiospora intestini</i>	CBS 135835 T	KR011352	MH877577	KR011351	KR011350
<i>Apiospora italica</i>	CBS 145138 T	MK014880	MK014847	MK017956	MK017985
<i>Apiospora jatrophae</i>	AMH-9557 T	JQ246355			
<i>Apiospora jiangxiensis</i>	LC 4577 T	KY494693	KY494769	KY705092	KY705163
<i>Apiospora kogelbergensis</i>	CBS 113333 T	KF144892	KF144938	KF145026	KF144984
<i>Apiospora koreana</i>	KUC 21332	MH498524		MH544664	MH498482
<i>Apiospora lageniformis</i>	KUC 21686 T	ON764022	ON787761	ON806626	ON806636
<i>Apiospora locuta-pollinis</i>	LC 11683 T	MF939595		MF939616	MF939622
<i>Apiospora longistroma</i>	MFLUCC 11-0479 T	KU940142	KU863130		
<i>Apiospora lophatheri</i>	CFCC 58975 T	OR125566	OR133588	OR139970	OR139980
<i>Apiospora machili</i>	SAUCC 1175A-4 T	OR739433	OR739574	OR753450	OR757130

Supplementary Table 2 Continued.

Species	Strains	GenBank accession numbers			
		ITS	LSU	<i>EF1A</i>	<i>TUB</i>
<i>Apiospora machili</i>	SAUCC 1175	OQ592560	OQ615289	OQ613333	OQ613307
<i>Apiospora magnispora</i>	ZHKUCC 22-0001 T	OM728647	OM486971	OM543543	OM543544
<i>Apiospora malaysiana</i>	CBS 102053 T	KF144896	KF144942	KF145030	KF144988
<i>Apiospora marianiae</i>	AP18219 T	ON692406	ON692422		ON677186
<i>Apiospora marii</i>	CBS 497.90 T	AB220252	KF144947	KF145035	KF144993
<i>Apiospora marina</i>	KUC 21328 T	MH498538		MH544669	MH498496
<i>Apiospora mediterranea</i>	IMI 326875 T	AB220243	AB220337		AB220290
<i>Apiospora minutispora</i>	17E-042 T	LC517882		LC518889	LC518888
<i>Apiospora montagnei</i>	AP 301120 T	ON692408	ON692424	ON677182	ON677188
<i>Apiospora mori</i>	MFLUCC 20-0181 T	MW114313	MW114393		
<i>Apiospora mukdahanensis</i>	MFLUCC 22-0056	OP377735	OP377742		
<i>Apiospora multiloculata</i>	MFLU 20-0024 T	OL873137	OL873138		OL874718
<i>Apiospora mytilomorpha</i>	DAOM 214595 T	KY494685			
<i>Apiospora neobambusae</i>	LC 7106 T	KY494718	KY494794	KY806204	KY705186
<i>Apiospora neochinensis</i>	CFCC 53036 T	MK819291		MK818545	MK818547
<i>Apiospora neogarethjonesii</i>	DQD 2019a T	MK070897	MK070898		
<i>Apiospora neosubglobosa</i>	KUMCC 16-0203 T	KY356090	KY356095		
<i>Apiospora obovata</i>	LC 4940 T	KY494696	KY494772	KY705095	KY705166
<i>Apiospora oenotherae</i>	CFCC 58972 T	OR125568	OR133590	OR139972	OR139982
<i>Apiospora ovata</i>	CBS 115042 T	KF144903	KF144950	KF145037	KF144995
<i>Apiospora pallidesporae</i>	ZHKUCC 22-0129	OR164903	OR164950		
<i>Apiospora paraphaeosperma</i>	MFLUCC 13-0644 T	KX822128	KX822124		
<i>Apiospora phragmitis</i>	CPC 18900 T	KF144909	KF144956	KF145043	KF145001
<i>Apiospora phyllostachydis</i>	MFLUCC 18-1101 T	MK351842		MK340918	MK291949
<i>Apiospora piptatheri</i>	CBS 145149 T	MK014893	MK014860	MK017969	
<i>Apiospora pseudohyphopodii</i>	KUC 21680 T	ON764026	ON787765	ON806630	ON806640
<i>Apiospora pseudomarii</i>	GUCC 10228 T	MT040124		MT040145	MT040166
<i>Apiospora pseudoparenchymatica</i>	LC 7234 T	KY494743	KY494819	KY705139	KY705211
<i>Apiospora pseudorasikravindrae</i>	KUMCC 20-0208 T	MT946344		MT947361	MT947367
<i>Apiospora pseudosinensis</i>	CPC 21546 T	KF144910	KF144957	KF145044	
<i>Apiospora pseudospegazzinii</i>	CBS 102052 T	KF144911	KF144958	KF145045	KF145002
<i>Apiospora pterosperma</i>	CPC 20193 T	KF144913	KF144960	KF145046	KF145004
<i>Apiospora pusillisperma</i>	KUC 21321 T	MH498533		MN868930	MH498491

Supplementary Table 2 Continued.

Species	Strains	GenBank accession numbers			
		ITS	LSU	<i>EF1A</i>	<i>TUB</i>
<i>Apiospora qinlingensis</i>	CFCC 52303 T	MH197120		MH236795	MH236791
<i>Apiospora rasikravindrae</i>	NFCCI 2144 T	JF326454			
<i>Apiospora sacchari</i>	CBS 372.67	KF144918	KF144964	KF145049	KF145007
<i>Apiospora saccharicola</i>	CBS 191.73	KF144920	KF144966	KF145051	KF145009
<i>Apiospora sargassi</i>	KUC 21228 T	KT207746		MH544677	KT207644
<i>Apiospora sasae</i>	CPC 38165 T	MW883402	MW883797		MW890120
<i>Apiospora septata</i>	CGMCC 3.20134 T	MW481711	MW478890	MW522943	MW522960
<i>Apiospora serenensis</i>	IMI 326869 T	AB220250	AB220344		AB220297
<i>Apiospora setariae</i>	CFCC 54041 T	MT492004			
<i>Apiospora setostroma</i>	KUMCC 19-0217 T	MN528012	MN528011	MN527357	
<i>Apiospora sichuanensis</i>	HKAS 107008 T	MW240648	MW240578		MW775605
<i>Apiospora sorghi</i>	RVO-2019a T	MK371706			MK348526
<i>Apiospora sphaerosperma</i>	CBS 114314	KF144904	KF144951	KF145038	KF144996
<i>Apiospora stipae</i>	CBS 146804 T	MW883403	MW883798	MW890082	MW890121
<i>Apiospora subglobosa</i>	MFLUCC 11-0397 T	KR069112	KR069113		
<i>Apiospora subrosea</i>	LC 7292 T	KY494752	KY494828	KY705148	KY705220
<i>Apiospora taeianensis</i>	KUC 21322 T	MH498515		MH544662	MH498473
<i>Apiospora thailandica</i>	MFLUCC 15-0202 T	KU940145	KU863133		
<i>Apiospora tropica</i>	MFLU 21-0084 T	OK491657	OK491653		OK560922
<i>Apiospora vietnamensis</i>	IMI 99670 T	KX986096	KX986111		KY019466
<i>Apiospora wurfbainiae</i>	ZHKUCC 23-0008 T	OQ587998	OQ587986	OQ586064	OQ586077
<i>Apiospora xenocordella</i>	CBS 478.86 T	KF144925	KF144970	KF145055	KF145013
<i>Apiospora xishuangbannaensis</i>	KUMCC 21-0695 T	ON426832	OP363248	OR025969	OR025930
<i>Apiospora yunnana</i>	MFLUCC 15-0002 T	KU940147	KU863135		
<i>Apiospora yunnanensis</i>	ZHKUCC 23-0014 T	OQ588004	OQ587992	OQ586070	OQ586083
<i>Nigrospora osmanthi</i>	CGMCC 3.18126 T	NR_153474	NG_069400	KY019421	KY019461
<i>Nigrospora vesicularis</i>	CGMCC3.18128 T	KX986088	KX986099	KY019294	KY019463

Fig. 31

Species	Strain	GenBank accession numbers		
		ITS	LSU	<i>EF1A</i>
<i>Achrochaeta talbotii</i>	ICMP 15161	MT454480	MT454495	OL653988
<i>Adautomilanezia caesalpiniae</i>	CC-LAMIC 102/12 T	KX821777	KU170671	
<i>Anacacumisporium appendiculatum</i>	HMAS 245593 T	KP347129	KT001553	

Supplementary Table 2 Continued.

Species	Strain	GenBank accession numbers		
		ITS	LSU	EF1A
<i>Arcuatosporea novae-zelandiae</i>	CBS 109474	MW984569	MW984552	OL653989
<i>Arcuatosporea seorsa</i>	CBS 147510 T	MW984572	MW984555	OL653990
<i>Aunstrupia nodipes</i>	NN043149	OL627566	OL655011	
<i>Brunneodinemasporium brasiliense</i>	CBS 112007 T	JQ889272	JQ889288	
<i>Brunneodinemasporium jonesii</i>	GZCC 16-0050 T	KY026058	KY026055	
<i>Cacumisporium acutatum</i>	CBS 101315 T	OR134682	OR134626	OR130762
<i>Cacumisporium capitulatum</i>	CBS 131690	OR134684	OR134628	OR130764
<i>Caliciastrum bicolor</i>	ICMP 15136	OR134689	OR134633	OR130769
<i>Caliciastrum bicolor</i>	PRA-21507 T		OR134634	
<i>Caligospora dilabens</i>	CBS 735.83 T	MH861684		
<i>Caligospora dilabens</i>	CBS 734.83 ET	OR134691	OR134636	OR130771
<i>Caligospora pannosa</i>	CBS 551.89 T	OR134692	OR134637	OR130772
<i>Calvolachnella guaviyunis</i>	CBS 134695 T	KJ834524	KJ834525	
<i>Capillisphaeria crustacea</i>	CBS 144664	OR134694	OR134639	OR130774
<i>Capillisphaeria crustacea</i>	CBS 144665	OR134695	OR134640	OR130775
<i>Catenularia angulospora</i>	MFLUCC 18-1331	MK828638	MK835840	MN194089
<i>Catenularia minor</i>	PRM 900544 T	MW987827	MW987822	OL653993
<i>Chaetosphaeria abietis</i>	CBS 427.83	OR134697	OR134642	OR130777
<i>Chaetosphaeria conirostris</i>	S.M.H. 2183 T		AF466066	
<i>Chaetosphaeria cylindrospora</i>	S.M.H. 3568 T		AY017373	
<i>Chaetosphaeria guttulata</i>	MFLUCC 17-1703 T	MK828636	MK835837	MN194087
<i>Chaetosphaeria innumera</i>	CBS 145639	OP455358	OP455464	OP465036
<i>Chaetosphaeria innumera</i>	CBS 131270	OR134698	OR134643	OR130778
<i>Chaetosphaeria mangrovei</i>	MCD 069 T	MG813821	MG813820	
<i>Chaetosphaeria metallicans</i>	PDD 92557	EU037894		
<i>Chaetosphaeria metallicans</i>	PDD 92539 T	EU037893	EU037899	
<i>Chaetosphaeria polygonalis</i>	GZCC 20-0438 T	OP377861	OP377946	OP473040
<i>Chalarodes obpyramidata</i>	PDD 119364	MW987828	MW987823	OL653995
<i>Chloridiopsiella preussii</i>	CBS 263.75	OR134700	OR134645	OR130780
<i>Chloridiopsiella preussii</i>	CBS 262.76	OR134701	OR134646	OR130781
<i>Chloridium bellum</i>	CBS 709.73A T	OP455360	OP455466	OP464934
<i>Chloridium virescens</i>	CBS 145481	OP455439	OP455547	OP465014
<i>Codinaea assamica</i>	CBS 139907 T	OL654077	OL654134	OL653997

Supplementary Table 2 Continued.

Species	Strain	GenBank accession numbers		
		ITS	LSU	<i>EF1A</i>
<i>Codinaea fertilis</i>	IMI 233824	OL654080	OL654137	OL654000
<i>Codinaeella lambertiae</i>	CBS 143419 T	OL654084	OL654141	OL654009
<i>Codinaeella parvilobata</i>	CBS 144536 T	OL654100	OL654157	OL654027
<i>Conicomycetes pseudotransvaalensis</i>	HHUF 29956 T	LC001710	LC001708	
<i>Craspedodidymum elatum</i>	NN042874	OL627547	OL655004	
<i>Cryptophiale udagawae</i>	GZCC 18-0047	MN104608	MN104619	
<i>Cryptophialoidea fasciculata</i>	MFLU 18-1499	MH758195	MH758208	
<i>Curvichaeta curvispora</i>	ICMP 15115 T	OR134705	OR134650	OR130785
<i>Curvichaeta curvispora</i>	ICMP 15118	OR134706	OR134651	OR130786
<i>Dendrophoma cytisporoides</i>	CBS 144107	MT118234	MT118205	OL654032
<i>Dictyochaeta callimorpha</i>	ICMP 15130	MT454483	MT454498	MT454673
<i>Dictyochaeta fuegiana</i>	ICMP 15153 T	MT454487	EF063574	MT454677
<i>Dinemasporium cruciferum</i>	HHUF 30001	AB900895	AB934039	AB934089
<i>Dinemasporium pseudoindicum</i>	CBS 127402 T	JQ889277	JQ889293	
<i>Ellisembia aurea</i>	CBS 144403 T	MH836375	MH836376	
<i>Ellisembia folliculata</i>	CBS 147152	OL654105	OL654162	OL654033
<i>Ericiosphaeria spinosa</i>	S.M.H. 2754 T	MW984575	AF466079	
<i>Eucalyptostroma eucalypti</i>	CBS 142074 T	KY173408	KY173500	
<i>Eucalyptostroma hongluosiense</i>	NN076613	OL628127	OL655185	
<i>Eucalyptostromiella beijingensis</i>	NN078016	OL628501	OL655251	
<i>Flectospora laminata</i>	CBS 112964 T	MW984576	MW984558	OL654034
<i>Fuscocatenua submersa</i>	MFLUCC 18-1342 T	MK828634	MK835835	MN194085
<i>Fuscocatenua variegata</i>	NN055332	OL627817	OL655124	
<i>Fusichloridium cylindrosporum</i>	CBS 101429 ET	OR134709	OR134653	OR130789
<i>Fusichloridium cylindrosporum</i>	CBS 101430	OR134710	OR134654	OR130790
<i>Gongromeriza myriocarpa</i>	CBS 141.53 T	OP455456	OP455564	OP465029
<i>Gongromeriza myriocarpa</i>	CBS 264.76 NT	OP455457	OP455565	OP465028
<i>Gongromeriza pygmaea</i>	CBS 144786	OP455458	OP455566	OP465030
<i>Gongromeriza pygmaea</i>	CBS 699.74 T	OP455459	OP455567	OP465031
<i>Gongromerizella lignicola</i>	CBS 143.54 IT	OP455460	OP455568	OP465032
<i>Gongromerizella pini</i>	CBS 146011 T	MT223787	MT223882	
<i>Infundibulomyces cupulatus</i>	BCC 11929 T	EF113976	EF113979	
<i>Infundibulomyces oblongisporus</i>	BCC 13400 T	EF113977	EF113980	

Supplementary Table 2 Continued.

Species	Strain	GenBank accession numbers		
		ITS	LSU	EF1A
<i>Kionochaeta microspora</i>	GZCC 18-0036 T	MN104607	MN104618	
<i>Kionochaeta ramifera</i>	MUCL 39164	MW144421	MW144404	OL654036
<i>Kionochaetiella ivoriensis</i>	CBS 374.76 T	MH860988	MH872758	
<i>Kylindrochaeta lignomollis</i>	S.M.H. 3015 T	EU037896	AF466073	
<i>Linkosia multiseptum</i>	NN042961	OL627557	OL655008	
<i>Linkosia rostrata</i>	NN047479	OL627662	OL655059	
<i>Menispora caesia</i>	CBS 145022	OL654107	OL654164	OL654039
<i>Menispora ciliata</i>	CBS 122131 T	EU488736	OL654165	OL654040
<i>Menisporopsis pirozynskii</i>	MUCL 47217	MW984579	MW984561	OL654047
<i>Menisporopsis theobromae</i>	MUCL 41079	MW984580	MW984562	OL654048
<i>Morrisiella indica</i>	NN042908	OL627551	OL655005	
<i>Multiguttulispora dimorpha</i>	CBS 140002	MW984582	MW984564	OL654049
<i>Multiguttulispora triseptata</i>	IMI 353690	MW984584	MW984566	OL654050
<i>Nawawia filiformis</i>	MFLUCC 17-2394	MH758196	MH758209	OP473069
<i>Neopseudolachnella acutispora</i>	MAFF 244358 T	AB934065	AB934041	AB934091
<i>Neopseudolachnella magnispora</i>	MAFF 244359 T	AB934066	AB934042	AB934092
<i>Nimesporella capillacea</i>	IMI 358908 T	OL654114	OL654171	OL654051
<i>Paliphora intermedia</i>	CBS 896.97 IT	MH862682	EF204501	
<i>Papillospora hebetiseta</i>	CBS 102340 T	AF178549	AF178549	OL653994
<i>Papillospora hebetiseta</i>	S.M.H. 2729	AY906955	AF466069	
<i>Paraceratocladia polysetosa</i>	NN044119	OL627605	OL655027	
<i>Paraceratocladium silvestre</i>	NN055375	OL627830	OL655132	
<i>Paracryptophiale pirozynskii</i>	NN044888	OL627641	OL655047	
<i>Paragaеumannomyces panamensis</i>	S.M.H. 3596 T	AY906948	MT118218	
<i>Paragaеumannomyces rubicundus</i>	S.M.H. 3221 T	MT118242	MT118224	
<i>Phaeodischloridium aquaticum</i>	MFLUCC 18-1341 T	MK828639	MK835841	MN194090
<i>Phaeostalagmus cyclosporus</i>	CBS 663.70	MH859892	MH871680	
<i>Phialocephala fusca</i>	CBS 301.85	AF486122	MH873571	
<i>Phialogeniculata guadalcanalensis</i>	MFLUCC 18-0260 T	MK828625	MK835825	MN194078
<i>Phialosporostilbe scutiformis</i>	MFLUCC 17-0227 T	MH758194	MH758207	
<i>Phialoturbella calva</i>	ICMP 23826 T	MW984585	MW984567	OL654052
<i>Phialoturbella lunata</i>	MFLUCC 18-0642 T	MK828624	MK835824	MN194077
<i>Polynema podocarpi</i>	CBS 144415 T	MH327797	MH327833	

Supplementary Table 2 Continued.

Species	Strain	GenBank accession numbers		
		ITS	LSU	<i>EF1A</i>
<i>Pseudodinemasporium fabiforme</i>	CBS 140010	KR611889	KR611906	
<i>Pseudolachnea fraxini</i>	CBS 113701 T	JQ889287	JQ889301	AB934096
<i>Pseudolachnea hispidula</i>	MAFF 244365	AB934072	AB934048	AB934098
<i>Pseudolachnella asymmetrica</i>	MAFF 244366 T	AB934073	AB934049	AB934099
<i>Pseudolachnella scolecospora</i>	MAFF 244379	AB934086	AB934062	AB934112
<i>Pseudothozetella lunata</i>	CGMCC 3.20661 T	OL628034	OL655157	
<i>Psilobotrys minutus</i>	CBS 223.74	OP455462	OP455570	OP465034
<i>Psilobotrys minutus</i>	CBS 247.75	OP455463	OP455571	OP465035
<i>Pyrigemmula aurantiaca</i>	CBS 126743 T	HM241692	HM241692	
<i>Rattania setulifera</i>	GUFCC 15501 T	GU191794	HM171322	
<i>Riisgaardia longispora</i>	CGMCC 3.20794 T	OL627701	OL655085	
<i>Riisgaardia obclavata</i>	CGMCC 3.20787 T	OL627568	OL655013	
<i>Spicatispora fennica</i>	CBS 101641	AF178562		
<i>Sporendocladia beijingensis</i>	CGMCC 3.20738 T	OL628290	OL655217	
<i>Sporendocladia fumosa</i>	NN047731	OL627669	OL655065	
<i>Sporoschisma hemipsilum</i>	MUCL 56487	MW987829	MW987824	
<i>Sporoschisma mirabile</i>	CBS 144794	MW987830	MW987825	
<i>Stilbochaeta malaysiana</i>	IMI 312436 T	OL654121	OL654178	OL654059
<i>Stilbochaeta ramulosestula</i>	IMI 313452 ET	OL654124	OL654181	OL654062
<i>Striatosphaeria castanea</i>	CBS 145352 T	MT118244	MT118229	
<i>Striatosphaeria codinaeophora</i>	M.R. 1230	AF178546	AF178546	
<i>Tainosphaeria cecropiae</i>	CBS 101687 T	MW984586	MW984568	OL654064
<i>Tainosphaeria crassiparies</i>	S.M.H. 1934 T	MW984587	AF466089	
<i>Tainosphaeriella aquatica</i>	MFLUCC 17-2370 T	MZ161197	MZ161195	MZ170694
<i>Tainosphaeriella thailandense</i>	MFLUCC 18-1282 T	MZ161198	MZ161196	MZ170695
<i>Thozetella cristata</i>	CBS 101112	OL654126	OL654183	OL654065
<i>Thozetella tocklaiensis</i>	CBS 378.58 T	OL654128	OL654185	OL654067
<i>Verhulstia biformis</i>	NN077655	OL628434	OL655237	
<i>Verhulstia trisororum</i>	CBS 143234 T	MG022181	MG022160	
<i>Zanclospora novae-zelandiae</i>	ICMP 15781 ET	MW144429	MW144411	MW147330
<i>Zanclospora ramifera</i>	ICMP 22738 T	MW144433	MW144415	MW147334
<i>Tracylla aristata</i>	CBS 141404 ET	OL654129	OL654186	OL654068
<i>Tracylla eucalypti</i>	CBS 144429 T	OL654130	OL654187	OL654069

Supplementary Table 2 Continued.

Fig. 34						
Species	Strains	GenBank accession numbers				
		SSU	ITS	LSU	RPB2	EF1A
<i>Keithomyces carneus</i>	CBS 239.32	EF468988	NR_131993	NG_057769	EF468938	EF468789
<i>Keithomyces indica</i>	NFCCI 5105	OL584173	OL584170	OL584176	OM032808	OM032805
<i>Keithomyces indica</i>	NFCCI 5106 T	OL584174	OL584171	OL584177	OM032809	OM032806
<i>Keithomyces aciculare</i>	JCM 33284	LC435738	NR_164567	LC435741		LC462188
<i>Keithomyces aciculare</i>	JCM 33285	LC435739	LC463198	LC435742		LC462189
<i>Keithomyces carneus</i>	CBS 399.59	EF468989	MT078887	EF468842	EF468939	EF468788
<i>Keithomyces carneus</i>	CBS 128252		MH864863	MH876307		
<i>Keithomyces carneus</i>	SGSF001	MN590228	MN589738	MN589966		MN917163
<i>Keithomyces neogunnii</i>	BUM415	MH143845	MH143811	MH143828	MH143891	MH143861
<i>Keithomyces neogunnii</i>	GZUH SB13050305	KU729724	KY423507			KU729729
<i>Keithomyces</i> sp.	CBS 127407	MT078873		MT078858	MT078923	MT078850
<i>Marquandomyces marquandii</i>	CBS 182.27 T	EF468990	MH854923	MH866418	EF468942	EF468793
<i>Marquandomyces</i> sp.	CBS 127132	MT078872	MT078882	MT078857	MT078922	MT078849
<i>Marquandomyces</i> sp.	CBS 129413	MT078874	MT561567	MT078859		MT078851
<i>Paecilomyces echinosporus</i>	RCEF4111 T		GU108582			
<i>Metapochonia bulbillosa</i>	JCM 18596	AB758252	AB709836	AB709809	AB758690	AB758460
<i>Metapochonia bulbillosa</i>	CBS 145.70 T	AF339591	MH859529	AF339542	EF468943	EF468796
<i>Metapochonia cordycipiticonsociata</i>	CGMCC 3.17365	KM263572	KM263569	KM263573	KM263579	KM263584
<i>Metapochonia cordycipiticonsociata</i>	CGMCC 3.17366 T	KM263570	KM263567	KM263574	KM263580	KM263582
<i>Metarhizium anisopliae</i>	ARSEF 7487		HQ331446		DQ468370	DQ463996
<i>Metarhizium anisopliae</i>	CBS 130.71 NT	MT078868	MT078884	MT078853	MT078918	MT078845
<i>Metarhizium flavoviride</i>	CBS 125.65	MT078869	MT078885	MT078854	MT078919	MT078846
<i>Metarhizium flavoviride</i>	CBS 700.74	MT078870		MT078855	MT078920	MT078847
<i>Neobarya parasitica</i>	Marsons/n		KP899626	KP899626		
<i>Nigelia aurantiaca</i>	BCC 13019	GU979939		GU979948	GU979971	GU979957
<i>Nigelia martialis</i>	EFCC 6863			JF415974		JF416016
<i>Papiliomyces liangshanensis</i>	EFCC 1452	EF468962		EF468815		EF468756
<i>Papiliomyces liangshanensis</i>	EFCC 1523	EF468961		EF468814	EF468918	EF468755
<i>Papiliomyces shibinensis</i>	GZUH SB13050311 T	KR153588	KR153585			KR153589
<i>Parametarhizium changbaiense</i>	CGMCC 19143 T	MN590231	MN589741	MN589994	MT921829	MN908589
<i>Parametarhizium hingganense</i>	CGMCC 19144 T	MN055706	MN055703	MN061635	MT939494	MN065770
<i>Pochonia boninensis</i>	JCM 18597	AB758255	AB709858	AB709831	AB758693	AB758463

Supplementary Table 2 Continued.

Species	Strains	GenBank accession numbers				
		SSU	ITS	LSU	<i>RPB2</i>	<i>EF1A</i>
<i>Pochonia chlamydosporia</i>	CBS 101244	DQ522544	JN049821	DQ518758	DQ522424	DQ522327
<i>Pochonia sinensis</i>	ZY 22.009 T	OQ709251	OQ709257	OQ709263	OQ719624	OQ719629
<i>Pochonia sinensis</i>	ZY 22.010	OQ709252	OQ709258	OQ709264	OQ719625	OQ719630
<i>Purpureomyces khaoyaiensis</i>	BCC 1376 T	KX983468		KX983462	KX983465	KX983457
<i>Purpureomyces maesotensis</i>	BCC 88441		MN781916	MN781877	MN781824	MN781734
<i>Purpureomyces pyriformis</i>	BCC 85074 T		MN781929	MN781873	MN781821	MN781730
<i>Rotiferophthora angustispora</i>	CBS 101437	AF339584	AJ292412	AF339535	DQ522460	AF543776
<i>Sungia yongmunensis</i>	EFCC 2131 T	EF468977	JN049856	EF468833		EF468770
<i>Sungia yongmunensis</i>	EFCC 2135	EF468979		EF468834		EF468769
<i>Yosikobayasia kusanagiensis</i>	TNS-F18494	JF415954	JN049873	JF415972		JF416014
<i>Pleurocordyceps aurantiaca</i>	MFLUCC 17-2113 T	MG136904	MG136916	MG136910	MG136870	MG136875
<i>Pleurocordyceps marginaliradians</i>	MFLU 17-1582 T	MG136908	MG136920	MG136914	MG271931	MG136878

Fig. 36

Species	Strains	GenBank accession numbers			
		ITS	LSU	<i>EF1A</i>	<i>TUB</i>
<i>Bisifusarium allantoides</i>	UBOCC-A-120035	MW654536	MW654511	MW811075	MW811090
<i>Bisifusarium allantoides</i>	UBOCC-A-120036 T	MW654548	MW654523	MW811087	MW811102
<i>Bisifusarium allantoides</i>	UBOCC-A-120037	MW654549	MW654524	MW811088	MW811103
<i>Bisifusarium aseptatum</i>	CGMCC 3.20816 T	MW016389		MW580429	MW533716
<i>Bisifusarium aseptatum</i>	LC13607	MW016390		MW580430	MW533717
<i>Bisifusarium aseptatum</i>	LC13608	MW016391		MW580431	MW533718
<i>Bisifusarium biseptatum</i>	CBS 110311 T	MW654547	MW654522	MW811086	MW811101
<i>Bisifusarium biseptatum</i>	CBS 110144	EU926253	EU926253	EU926320	EU926386
<i>Bisifusarium delphinoides</i>	CBS 120718 T	EU926229	EU926229	EU926296	EU926362
<i>Bisifusarium delphinoides</i>	CBS 110140	EU926235	EU926235	EU926302	EU926368
<i>Bisifusarium delphinoides</i>	CBS 110310	EU926240	EU926240	EU926307	EU926373
<i>Bisifusarium dimerum</i>	MNHN RF-05625 T	MW654546	MW654521	MW811085	MW811100
<i>Bisifusarium dimerum</i>	NRRL 37398	EU926260	EU926260	EU926327	EU926393
<i>Bisifusarium dimerum</i>	CBS 489.81	EU926282	EU926282	EU926349	EU926415
<i>Bisifusarium dimerum</i>	CBS 175.31	EU926285	EU926285	EU926352	EU926418
<i>Bisifusarium domesticum</i>	CBS 102407	EU926221	EU926221	EU926288	EU926355
<i>Bisifusarium domesticum</i>	CBS 244.82	EU926220	EU926220	EU926287	EU926354
<i>Bisifusarium domesticum</i>	CBS 434.34 T	MH855596	MH867106		JQ434532

Supplementary Table 2 Continued.

Species	Strains	GenBank accession numbers			
		ITS	LSU	<i>EF1A</i>	<i>TUB</i>
<i>Bisifusarium lunatum</i>	CBS 632.76 T	EU926224	EU926224	EU926291	EU926357
<i>Bisifusarium lunatum</i>	CBS 110312	EU926223	EU926223	EU926290	EU926356
<i>Bisifusarium keratinophilum</i>	CGMCC 3.23621 T	OP693473	OP693469	OR168082	OR168085
<i>Bisifusarium keratinophilum</i>	GZUIFR 22.371	OP693474	OP693470	OR168083	OR168086
<i>Bisifusarium keratinophilum</i>	GZUIFR 22.372	OP693475	OP693471	OR168084	OR168087
<i>Bisifusarium nectrioides</i>	CBS 176.31	EU926245	EU926245	EU926312	EU926378
<i>Bisifusarium penicilloides</i>	UBOCC-A-120021 T	MW654542	MW654517	MW811081	MW811096
<i>Bisifusarium penicilloides</i>	UBOCC-A-120034	MW654541	MW654516	MW811080	MW811095
<i>Bisifusarium penicilloides</i>	VTT-D-041022	MW654535	MW654510	MW811074	MW811089
<i>Bisifusarium penzigii</i>	CBS 317.34 T	EU926257	EU926257	EU926324	EU926390
<i>Bisifusarium penzigii</i>	CBS 116508	EU926256	EU926256	EU926323	EU926389
<i>Bisifusarium</i> sp.	CBS 119875	EU926222	EU926222	EU926289	EU926419
<i>Bisifusarium</i> sp.	CBS 110307	EU926248	EU926248	EU926315	EU926381
<i>Bisifusarium</i> sp.	NRRL 37393	EU926250	EU926250	EU926317	EU926383
<i>Bisifusarium</i> sp.	CBS 110318	EU926246	EU926246	EU926313	EU926379
<i>Bisifusarium tonghuanum</i>	CGMCC 3.17369 T	KX790413	KX790414	KX790418	KX790417
<i>Bisifusarium tonghuanum</i>	CGMCC 3.17370	KX790415	KX790416	KX790420	KX790419
<i>Longinectria lagenoides</i>	UBOCC-A-120039 T	MW654539	MW654514	MW811078	MW811093
<i>Longinectria verticilliforme</i>	UBOCC-A-120043 T	MW654540	MW654515	MW811079	MW811094

Fig. 38

Species	Strains	GenBank accession numbers		
		ITS	LSU	<i>EF1A</i>
<i>Volutella aeria</i>	CGMCC3.17945 T	KU746708	KU746754	KX855253
<i>Volutella aeria</i>	CGMCC3.17946	KU746707	KU746753	KX855254
<i>Volutella ciliata</i>	CBS 127312	MH864520	MH875955	
<i>Volutella ciliata</i>	CBS 483.61	MH892587	MH869686	
<i>Volutella citrinella</i>	DAOM 226720	HQ897821	HQ843771	
<i>Volutella citrinella</i>	DAOM 165520		HQ843772	
<i>Volutella consors</i>	CBS 328.77	MH892584	JF937570	
<i>Volutella consors</i>	CBS 122767	KM231767	KM231632	KM231898
<i>Volutella delonicis</i>	MFLU 19-1384 T	NR_171101	NG_073864	
<i>Volutella krabiense</i>	MFLUCC 16-0268 T	MH388367	MH376741	MH388401
<i>Volutella leucaenae</i>	MFLU 19-0977 T	ON787631	ON787622	ON892551

Supplementary Table 2 Continued.

Species	Strains	GenBank accession numbers		
		ITS	LSU	EF1A
<i>Volutella minutissima</i>	BRFM 3396 T	ON152387	ON181653	
<i>Volutella ramkumarii</i>	CABI IMI136704	JQ647453		
<i>Volutella rosea</i>	CBS 128258	KM231769	KM231634	KM231900
<i>Volutella roseola</i>	CBS 377.55	MH857521	MH869058	
<i>Volutella salvadorae</i>	CBS 147070 T	MZ064450	MZ064507	MZ078234
<i>Volutella saulensis</i>	BRFM 3418 T	ON453969	ON453967	
<i>Volutella thailandensis</i>	MFLUCC 16-0366 T	MH388368	MH376742	MH388402
<i>Volutella thonnelliana</i>	BRFM 3397 T	ON181663	ON181657	
<i>Atractium crassum</i>	CBS 180.31	KM231790	MH866623	KM231919
<i>Atractium stilbaster</i>	CBS 410.67	MH859011	MH870712	KM231920
<i>Chaetopsina acutispora</i>	CBS 667.92	MH862382	MH874045	KM231901
<i>Chaetopsina chaetopsinae-penicillatae</i>	CBS 608.92	MH862377	MH874041	HM054064
<i>Chaetopsina fulva</i>	CBS 142.56	MH857549	MH869087	KM231902
<i>Pseudonectria buxi</i>	CBS 324.53	MH857225	MH868763	KM231909
<i>Pseudonectria folicola</i>	CBS 123190	KM231776	KM231642	KM231907

Fig. 40

Species	Strains	GenBank accession numbers			
		ITS	LSU	EF1A	RPB2
<i>Parasarocladium aestuarinum</i>	CMG 31	MK986714			
<i>Parasarocladium aestuarinum</i>	CMG 30 T	MK986713			
<i>Parasarocladium alavariense</i>	CMG 32 T	MK986715			
<i>Parasarocladium breve</i>	CBS 150.62 T	OQ429781	OQ055677	OQ471107	OQ454192
<i>Parasarocladium breve</i>	CBS 102443	OQ429780	OQ055676	OQ471106	OQ454191
<i>Parasarocladium breve</i>	CBS 303.96	OQ429783	OQ055679	OQ471109	OQ454194
<i>Parasarocladium breve</i>	CBS 387.96	OQ429782	OQ055678	OQ471108	OQ454193
<i>Parasarocladium breve</i>	CBS 427.96	OQ429784	OQ055680	OQ471110	OQ454195
<i>Parasarocladium chondroidum</i>	CBS 652.93 T	OQ429785	OQ055681	OQ471111	OQ454196
<i>Parasarocladium debruynii</i>	CBS 144942 T	MK069420	MK069416		OQ454197
<i>Parasarocladium funiculosum</i>	CBS 141.62 T	OQ429786	OQ055682	OQ471307	OQ454198
<i>Parasarocladium fusiforme</i>	CMG 36 T	MK986719			
<i>Parasarocladium gamsii</i>	CBS 726.71 T	OQ429787	OQ055683	OQ471112	OQ454199
<i>Parasarocladium radiatum</i>	CBS 142.62 T	OQ429788	OQ055684	OQ471308	OQ454200
<i>Parasarocladium tasmaniae</i>	CBS 146807 T	MW175340	MW175380		

Supplementary Table 2 Continued.

Species	Strains	GenBank accession numbers			
		ITS	LSU	EF1A	RPB2
<i>Parasarocladium wereldwiansianum</i>	CBS 147226 T	MW883440	MW883831	MW890113	MW890072
<i>Parasarocladium wereldwiansianum</i>	CBS 147224 T	MW883439	MW883830	MW890112	MW890071
<i>Sarocladium implicatum</i>	CBS 959.72 T	OQ429842	HG965072	OQ471305	OQ454239
<i>Sarocladium ochraceum</i>	CBS 428.67 T	OQ429846	HQ232070	OQ471176	OQ454245
Fig. 42					
Species	Strains	GenBank accession numbers			
		ITS	LSU	TUB	RPB2
<i>Idriella chlamydospora</i>	CGMCC 3.20778 T	OL897016	OL897058	ON569069	
<i>Idriella chlamydospora</i>	GZUIFR 21.922	OL897017	OL897059	ON569070	
<i>Idriella lunata</i>	CBS 204.56 T	KP859044	KP858981		
<i>Idriella lunata</i>	CBS 177.57	KP859043	KP858980		
<i>Idriella multiformispora</i>	CGMCC 3.20779 T	OL897018	OL897060	ON569071	ON568988
<i>Idriella multiformispora</i>	GZUIFR 21.924	OL897019	OL897061	ON569072	ON568989
<i>Idriella multiformispora</i>	GZUIFR 21.925	OL897020	OL897062	ON569073	ON568990
<i>Microdochium albescens</i>	CBS 290.79	KP859014	KP858950	KP859077	KP859123
<i>Microdochium albescens</i>	CBS 291.79	KP858996	KP858932	KP859059	KP859105
<i>Microdochium neoqueenslandicum</i>	CBS 445.95	KP858997	KP858933	KP859060	KP859106
<i>Microdochium neoqueenslandicum</i>	CBS 108926 T	KP859002	KP858938	KP859065	KP859111
<i>Microdochium tainanense</i>	CBS 269.76 T	KP859009	KP858945	KP859072	KP859118
<i>Microdochium tainanense</i>	CBS 270.76	KP858995	KP858931	KP859058	KP859104
<i>Selenodriella cubensis</i>	CBS 683.96 T	KP859053	KP858990		
<i>Selenodriella fertilis</i>	CBS 772.83	KP859055	KP858992		
<i>Selenodriella brasiliiana</i>	CBS 140227 T	ON400769	ON400821		ON399356
<i>Xenoidriella cinnamomi</i>	CBS 149458 T	OQ628471	OQ629053		OQ627937
<i>Guayaquilina cubensis</i>	MUCL 39017	KC775733	KC775708		
<i>Ciliosporella italica</i>	MFLUCC 16-1146 T	NR_169717	NG_073833		
<i>Neoidriella desertorum</i>	CBS 985.72 T	MH860635	NG_058150		
<i>Xenoidriella cinnamomi</i>	CBS 149458 T	OQ628471	OQ629053		OQ627937
<i>Cryptostroma corticale</i>	CBS 218.52	HG934112	MH868531	HG934104	HG934118
<i>Cryptostroma corticale</i>	CBS 217.52	HG934111	MH868530	HG934103	HG934117

Supplementary Table 2 Continued.

Fig. 44					
Species	Strains	GenBank accession numbers			
		ITS	LSU	RPB2	TUB
<i>Nemania abortiva</i>	BISH 467 T	GU292816		GQ844768	GQ470219
<i>Nemania aquilariae</i>	KUMCC 20-0268 T	MW729422	MW729420	MW717891	MW881142
<i>Nemania beaumontii</i>	HAST 405	GU292819		GQ844772	GQ470222
<i>Nemania bipapillata</i>	HAST 90080610	GU292818		GQ844771	GQ470221
<i>Nemania camelliae</i>	GMB0068 T	MW851889	MW851872	MW836055	MW836029
<i>Nemania caries</i>	GMB0070	MW851874	MW851857	MW836071	MW836036
<i>Nemania changningensis</i>	GMB0056 T	MW851875	MW851858	MW836061	MW836027
<i>Nemania chestersii</i>	JF 04024		DQ840072	DQ631949	DQ840089
<i>Nemania cyclobalanopsina</i>	GMB0062 T	MW851883	MW851866	MW836057	MW836025
<i>Nemania delonicis</i>	MFLU 19-2124 T	MW240613	MW240542	MW342617	MW775574
<i>Nemania diffusa</i>	HAST 91020401	GU292817		GQ844769	GQ470220
<i>Nemania ethancrensonii</i>	CBS 148337 T	ON869311	ON869311	ON808489	ON808533
<i>Nemania feicuiensis</i>	GMB0059 T	MW851880	MW851863	MW836063	MW836023
<i>Nemania fusoidispora</i>	GZUH0098	MW851881	MW851864	MW836070	MW836037
<i>Nemania hyrcana</i>	MUCL 57704 T	OP359332	OP359329	OP359598	OP359603
<i>Nemania hyrcana</i>	MUCL 57703	OP359333	OP359330	OP359599	OP359604
<i>Nemania illita</i>	YMJ 236	EF026122		GQ844770	EF025608
<i>Nemania lishuicola</i>	GMB0065 T	MW851886	MW851869	MW836065	MW836033
<i>Nemania longipedicellata</i>	MFLU 18-0819 T	MW240612	MW240541	MW342616	MW775573
<i>Nemania macrocarpa</i>	WSP 265 T	GU292823		GQ844776	GQ470226
<i>Nemania maritima</i>	HAST 89120401 ET	GU292822		GQ844775	GQ470225
<i>Nemania paraphysata</i>	MFLU 19-2121 T	MW240609	MW240538	MW342613	
<i>Nemania phetchaburiensis</i>	MFLUCC 15-0953 T	MN047124	MF615402		
<i>Nemania plumbea</i>	JF TH-04-01 T	DQ641634	DQ840071	DQ631952	DQ840084
<i>Nemania prava</i>	CBS 679.86	KU683765	KU683765	KU684284	KU684188
<i>Nemania prava</i>	TROM 104 T	OP289674			
<i>Nemania primolutea</i>	HAST 91102001 T	EF026121		GQ844767	EF025607
<i>Nemania rubi</i>	GMB0064 T	MW851885	MW851868	MW836059	MW836021
<i>Nemania serpens</i>	TROM 174 NT	OP289675			
<i>Nemania serpens</i>	MUCL 57702	OP359334	OP359331	OP359600	OP359605
<i>Nemania serpens</i>	HAST 235	GU292820		GQ844773	GQ470223
<i>Nemania sphaeriosstoma</i>	JDR 261	GU292821		GQ844774	GQ470224

Supplementary Table 2 Continued.

Species	Strains	GenBank accession numbers			
		ITS	LSU	<i>RPB2</i>	<i>TUB</i>
<i>Nemania thailandensis</i>	MFLU 19-2117 T	MW240611	MW240540	MW342615	MW775572
<i>Nemania uda</i>	CBS 148422 T	ON869312	ON869312	ON808488	ON808532
<i>Nemania viridis</i>	MFLUCC 17-2470 T	MN047123	MN017887		
<i>Nemania yunnanensis</i>	KUMCC 20-0267 T	MW729423	MW729421	MW717892	MW881141
<i>Kretzschmaria deusta</i>	MUCL 57705	MH084755	OP359327	OP359596	OP359601
<i>Kretzschmaria hedjaroudei</i>	MUCL 57706	MH084757	OP359328	OP359597	OP359602

T, ET, IT, and NT denote ex-type, ex-epitype, ex-isotype and ex-neotype strains, respectively.