

Shedding light on the darkness: cryptic diversity of cordyceps-like fungi in karst regions of Guizhou Province, China

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Abstract

Cordyceps-like fungi are abundant in karst regions in Guizhou Province, China, but systematic investigations are still lacking. In this study, species diversity of cordyceps-like fungi in karst habitats, forests, Tiankeng regions and valleys in Guizhou Province, was conducted from 2021 to 2024. Over 700 specimens were collected. Six new genera (*Dimorphspora*, *Neolecanicillium*, *Nuciformispora*, *Paracorniculantispora*, *Rubrumomyces*, *Zongqiomycetes*), 51 new species (*Arachnidicola sinensis*, *A. zunyiensis*, *Beauveria tiankengensis*, *B. valliensis*, *Cordyceps miaolingensis*, *C. pupicola*, *C. suiyangensis*, *C. vallis*, *Dimorphspora sinensis*, *Gamszarella araneicola*, *G. formicae*, *G. pupicola*, *Lecanicillium araneae*, *L. pantatomidae*, *L. sinense*, *Metarhizium formicae*, *M. pupicola*, *M. sinense*, *Neolecanicillium sinensis*, *Nuciformispora araneicola*, *N. sinense*, *N. vallise*, *N. zunyiense*, *Papiliomyces sinensis*, *Paracorniculantispora sinensis*, *Rubrumomyces guizhouensis*, *R. sinensis*, *Samsoniella araneicola*, *S. fanjingensis*, *S. guiyangensis*, *S. houerensis*, *S. jiangkouensis*, *S. kaiyangensis*, *S. miaolingensis*, *S. simplicicola*, *S. suiyangensis*, *S. tongrenensis*, *S. wudangensis*, *S. zongqii*, *Simplicillium araneicola*, *S. bursae*, *S. cantharise*, *S. neoaraneae*, *S. wudangense*, *S. zunyiense*, *Zarea sinensis*, *Zongqiomycetes araneicola*, *Z. sinensis*) and 4 new combinations (*Chlorocillium neolepidopterorum*, *C. rongjiangense*, *Nuciformispora araneorum*, *Paracorniculantispora psalliotae*) were introduced. Our findings demonstrated significant cryptic diversity of cordyceps-like fungi across sampled karst ecosystems (forests, Tiankeng and valleys) in Guizhou Province, suggesting similar unexplored diversity may exist in other karst formations. Notably, all newly described genera in this study show evolutionary affinities with *Lecanicillium* species, underscoring the need for comprehensive molecular phylogenies to clarify taxonomic relationships within this group.

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INTRODUCTION

Cordyceps-like fungi, referred to *Cordyceps* sensu lato, represent a significant group within the Phylum *Ascomycota*, which includes members from the families viz. *Cordycipitaceae*, *Ophiocordycipitaceae*, and *Polycephalomycetaceae*, as well as some species from *Clavicipitaceae* (Chen et al. 2021a, Li et al. 2023, Xiao et al. 2023). China has an abundant diversity of cordyceps-like fungi and is one of the species-rich localities of these fungi (Song et al. 2004, 2006). Currently, there are reports of over 2,000 cordyceps-like species worldwide, and more than 400 of these species have been found in different collecting sites of China (Chen et al. 2020a, <http://indexfungorum.org/Names/Names.asp>, 20 January 2025). Recent studies on the species diversity of cordyceps-like taxa in various protected areas and forest parks across different regions of China have revealed that these areas possess rich resources and a high diversity of species in certain locations (Chen et al. 2019a, 2020b, Fan et al. 2020, Zhao et al. 2020, 2021, Zhang et al. 2021a).

The karst area, particularly in southwestern China, contains unique, expansive, and continuously spread ancient forests with a high level of biodiversity. The area's intricate ecological environment and unique geographical features offer habitats for numerous organisms, such as fungi (Özkan et al. 2010, Su et al. 2017). Previous research indicated that cordyceps-like fungi in karst regions are highly diverse and plentiful (Zhu et al. 2004, Song et al. 2011). However, research on the cordyceps-like fungi in Guizhou Province was relatively scattered and thus needs systematic evaluation (Chen et al. 2022a, b, c, 2023, 2024a, b, c, Li et al. 2024, Peng et al. 2023, 2024, Zhang et al. 2023, Zhou et al. 2022).

A survey on the species diversity of cordyceps-like fungi in karst areas of Guizhou Province was conducted from 2021 to 2024. Specimens and strains were collected and isolated. This research introduces six new genera, fifty-one new species, and four new combinations, grounded on a multi-locus phylogeny along with their morphological and ecological traits.

MATERIALS AND METHODS

Specimen collection and identification

The specimens (i.e., dead insects and spiders) were collected from the karst habitats (forests, valleys and Tiankeng regions) of Guizhou Province from 2021 to 2024. The samples were placed in sterile bags, kept separately on an ice box, and transported to the laboratory. The specimens were kept in the refrigerator at 4°C until they were processed further. The exterior of each arthropod was initially rinsed with sterile water, sterilized with 75% ethanol for 3–5 seconds, and then rinsed three times with sterilized water for surface sterilization. Once dried on sterilized filter paper, a section of the synnema, mycelium, or sclerotium was excised from the specimen and positioned on plates containing potato dextrose agar (PDA) or modified PDA by the addition of 1% w/v peptone containing 0.1 g/l streptomycin and 0.05 g/l tetracycline (Chen et al. 2019b). Once fungal colonies appeared on the plated samples, a section of mycelium from the colony's edge was moved to fresh agar plates and incubated at 25°C for 14 days with a 12-hour light and 12-hour dark cycle (Zou et al. 2010). The holotypes and ex-types were stored at the Institute of Fungus Resources, Guizhou University, previously known as the Herbarium of Guizhou Agricultural College (code: GZAC), Guiyang City, Guizhou, China. Facesoffungi and Index Fungorum numbers are given as described in Jayasiri et al. (2015) and Index Fungorum (2025), respectively.

The features of the colonies were assessed on PDA cultures kept at 25°C for 14 days, noting the growth rate, presence of octahedral crystals, and the colors of the colonies on both the surface and reverse sides. A few mycelia were taken from the colony and placed in lactophenol cotton blue or 20% lactic acid solution to examine microscopic features, and the asexual morphological traits [e.g., conidiophores, phialides or conidiogenous cells, conidia, mean values for length, width, and

length to width ratio (Q^m) are indicated by L^m , W^m , and Q^m] were observed and measured using a Leica DM4 B microscope.

DNA extraction, polymerase chain reaction (PCR) amplification and nucleotide sequencing

A fungal genomic DNA extraction kit (DP2033, BioTeke Corporation) was employed for DNA extraction, following the protocol described by Liang et al. (2011). The extracted DNA was stored at -20°C for subsequent use. PCR amplification of the target genetic loci was carried out using the following primer pairs: B5.1F/B3.1R (targeting the intergenic region of the B locus, Bloc) (Rehner et al. 2006); ITS4/ITS5 (amplifying the internal transcribed spacer region, ITS) (White et al. 1990); LR0R/LR5 (targeting the 28S large subunit ribosomal gene, LSU) (Vilgalys & Hester 1990); CRPB1/RPB1Cr (targeting the RNA polymerase II largest subunit gene, *rpb1*) (Castlebury et al. 2004); fRPB2-5F/fRPB2-7cR (targeting the RNA polymerase II second largest subunit gene, *rpb2*) (Liu et al. 1999); and 983F/2218R (amplifying the translation elongation factor 1 alpha gene, *tef-1 α*) (Castlebury et al. 2004). The thermal cycling conditions for PCR amplification were based on the methodology outlined by Chen et al. (2021b) (Table 1). The resulting PCR products were purified and sequenced by Sangon Biotech (Shanghai) Co., Ltd. All newly generated sequences were deposited into GenBank, and the corresponding accession numbers were obtained (Table 2).

Sequence alignments and phylogenetic analyses

In this study, DNA sequences were edited using DNASTAR™ Lasergene version 6.0.

Analyses 1: For strains belonging to *Clavicipitaceae* and *Ophiocordycipitaceae*, ITS, LSU, *rpb1*, *rpb2* and *tef-1 α* sequences were retrieved from GenBank following the datasets of Mongkolsamrit et al. (2020), Custódio & Pereira (2024) and Xiao et al. (2023). Additional sequences were selected through BLASTn searches.

Analyses 2: Sequences including ITS, LSU, *rpb1*, *rpb2* and *tef-1 α* , for the strains in *Cordycipitaceae* were acquired from GenBank based on Khonsanit et al. (2024). Additional sequences were chosen using BLASTn searches.

Analyses 3: Sequences of Bloc, ITS, *rpb1*, *rpb2* and *tef-1 α* for *Beauveria* strains were obtained from GenBank according to Chuang et al. (2024), with additional sequences chosen through BLASTn searches. MAFFT v.7.037b (Katoh et al. 2019) and MEGA6 (Tamura et al. 2013) were used to align and edit all the sequences. SequenceMatrix v.1.7.8 was used to obtain combined sequences for analysis 1 (dataset 1: ITS, LSU, *rpb1*, *rpb2*, *tef-1 α*), analysis 2 (dataset 2: ITS, LSU, *rpb1*, *rpb2*, *tef-1 α*) and analysis 3 (dataset 2: Bloc, ITS, *rpb1*, *rpb2*, *tef-1 α*) (Vaidya et al. 2011). ModelFinder (Kalyaanamoorthy et al. 2017) in PhyloSuite (v1.2.2) software (Zhang et al. 2020) was used to choose the model for Bayesian analyses.

Bayesian inference (BI) and maximum likelihood (ML) methods were used to analyze datasets 1, 2, and 3 for analyses 1, 2, and 3, respectively. To generate phylogenetic trees with Bayesian probabilities for the combined sequence datasets, a Markov chain Monte Carlo (MCMC) algorithm was employed using MrBayes v.3.2 for BI (Ronquist et al. 2012). Ten million generations were executed using four concurrent Markov chains. Samples of trees were taken every 1,000 generations, or until the process automatically stopped when the average standard deviation of split frequencies dropped below 0.01. The initial 25% of the trees were removed as the burn-in period for each analysis, and the leftover trees were utilized to determine the posterior probabilities (PP). After completing the analysis, Tracer v.1.5 (Drummond & Rambaut 2007) was used to verify if each run was above 200, to establish burn-in and confirm that both runs had reached convergence. Maximum likelihood analyses were performed using IQ-TREE (version 2.0) as described by Trifinopoulos et al. (2016), with the model automatically selected based on the Bayesian Information Criterion.

Table 1 List of primers information in this study

Name		Length	Direction	Sequence (5'-3') ^a	Optimized PCR protocols	References
Bloc	B5.1F	21	forward	CGACCCGGC CAACTACTTT GA	94 °C for 2min; 40 cycles at 94 °C for 30 s, 56 °C	Rehner et al. (2006)
	B3.1R	21	reverse	GTCTTCCAGT ACCACTACGC C	annealing for 30 s, 72 °C for 2min; 72 °C extension for 15min.	
ITS	ITS5	22	forward	GGAAGTAAA AGTCGTAAC AAGG	95 °C for 2min; 33 cycles at 95°C for 30 s, 51°C annealing for 50 s, 72°C for 45 s; 72 °C extension for 15min.	White et al. (1990)
	ITS4	20	reverse	TCCTCCGCTT ATTGATATGC		
LSU	LR0R	17	forward	ACCCGCTGA ACTTAAGC	94 °C for 2min; 33 cycles at 94°C for 30 s, 51°C annealing for 1 min, 72°C for 2 min; 72 °C extension for 15min.	Vilgalys & Hester (1990)
	LR5	17	reverse	TCCTGAGGG AAACTTCG		
<i>rpb1</i>	CRPB1	20	forward	CAYCCWGGY TTYATCAAGA A	94 °C for 2min; 33 cycles at 94°C for 30s, 55°C annealing for 30s, 72°C for 1min; 72 °C extension for 15min.	Castlebury et al. (2004)
	RPB1C r	23	reverse	CCNGCDATNT CRTTRTCCAT RTA		
<i>rpb2</i>	RPB2- 5F3	20	forward	GACGACCGT GATCACTTTG G	94 °C for 2min; 33 cycles at 94°C for 30 s, 54°C annealing for 40 s, 72°C for 1 min 20 s; 72 °C extension for 15min.	Liu et al. (1999)
	RPB2- 7Cr2	20	reverse	CCCATGGCCT GTTTGCCCAT		
<i>tef-1α</i>	983F	23	forward	GCYCCYGGH CAYCGTGAYT TYAT	94 °C for 2min; 33 cycles at 94°C for 30 s, 58°C annealing for 1 min 20 s, 72°C for 1 min; 72 °C extension for 15min.	Castlebury et al. (2004)
	2218R	23	reverse	ATGACACCR ACRGCRACR GTYTG		

Note – Bloc: intergenic region of the B locus, ITS: the rRNA internal transcribed spacer region, LSU: the nuclear rRNA large subunit gene, *rpb1*: the RNA polymerase II largest subunit gene, *rpb2*: the RNA polymerase II second largest subunit gene, *tef-1α*: the translation elongation factor 1-α gene region.

Table 2 Sequence accession numbers of new taxa and strains in this study.

Species	Strain	GenBank Accession No.					
		ITS	LSU	<i>rpb1</i>	<i>rpb2</i>	<i>tef-1α</i>	Bloc
<i>Arachnidicola sinensis</i>	ZY06511 ^T	PV082711	PV082832		PV171173	PV171231	
<i>Arachnidicola sinensis</i>	ZY06512	PV082712	PV082833		PV171174	PV171232	
<i>Arachnidicola zunyiensis</i>	ZY06061 ^T	PV082713	PV082834		PV171175	PV171233	
<i>Arachnidicola zunyiensis</i>	ZY06062	PV082714	PV082835		PV171176	PV171234	
<i>Beauveria tiankengensis</i>	KY07241 ^T	PV082715				PV171235	PV171339
<i>Beauveria tiankengensis</i>	KY07242	PV082716				PV171236	PV171340
<i>Beauveria valliensis</i>	SY09861 ^T	PV082717		PV171125	PV171177	PV171237	PV171341
<i>Beauveria valliensis</i>	SY09862	PV082718		PV171126	PV171178	PV171238	PV171342
<i>Cordyceps miaolingensis</i>	DY05101 ^T	PV082719	PV082836			PV171239	
<i>Cordyceps miaolingensis</i>	DY05102	PV082720	PV082837			PV171240	
<i>Cordyceps pupicola</i>	SY09561 ^T	PV082721	PV082838	PV171127	PV171179	PV171241	
<i>Cordyceps pupicola</i>	SY09562	PV082722	PV082839	PV171128	PV171180	PV171242	
<i>Cordyceps pupicola</i>	SY09591	PV082723	PV082840			PV171243	
<i>Cordyceps pupicola</i>	SY09592	PV082724	PV082841			PV171244	
<i>Cordyceps suiyangensis</i>	SY09851 ^T	PV082725	PV082842	PV171129	PV171181	PV171245	
<i>Cordyceps suiyangensis</i>	SY09852	PV082726	PV082843	PV171130	PV171182	PV171246	
<i>Cordyceps vallis</i>	SY09171 ^T	PV082727	PV082844		PV171183	PV171247	
<i>Cordyceps vallis</i>	SY09172	PV082728	PV082845		PV171184	PV171248	
<i>Dimorphospora sinensis</i>	ZY06451 ^T	PV082729	PV082846		PV171185	PV171249	
<i>Dimorphospora sinensis</i>	ZY06452	PV082730	PV082847		PV171186	PV171250	
<i>Gamszarella araneicola</i>	DY05611 ^T	PV082731	PV082848	PV171131	PV171187	PV171251	
<i>Gamszarella araneicola</i>	DY05612	PV082732	PV082849	PV171132	PV171188	PV171252	
<i>Gamszarella formicae</i>	DY09591 ^T	PV082733	PV082850			PV171253	
<i>Gamszarella formicae</i>	DY09592	PV082734	PV082851			PV171254	
<i>Gamszarella pupicola</i>	WD04111 ^T	PV082735	PV082852			PV171255	
<i>Gamszarella pupicola</i>	WD04112	PV082736	PV082853			PV171256	
<i>Keithomyces neogunnii</i>	DY05181	PV082807	PV082924	PV171165	PV171221	PV171325	
<i>Keithomyces neogunnii</i>	DY05182	PV082808	PV082925	PV171166	PV171222	PV171326	
<i>Keithomyces neogunnii</i>	DY05841	PV082809	PV082926			PV171327	
<i>Keithomyces neogunnii</i>	DY05842	PV082810	PV082927			PV171328	

Table 2 Continued

Species	Strain	GenBank Accession No.					
		ITS	LSU	<i>rpb1</i>	<i>rpb2</i>	<i>tef-1α</i>	Bloc
<i>Lecanicillium araneae</i>	KY04081 ^T	PV082737	PV082854	PV171133		PV171257	
<i>Lecanicillium araneae</i>	KY04082	PV082738	PV082855	PV171134		PV171258	
<i>Lecanicillium pantatomidae</i>	DY45191 ^T	PV082739	PV082856	PV171135	PV171189	PV171259	
<i>Lecanicillium pantatomidae</i>	DY45192	PV082740	PV082857	PV171136	PV171190	PV171260	
<i>Lecanicillium sinense</i>	DY45361 ^T	PV082741	PV082858	PV171137	PV171191	PV171261	
<i>Lecanicillium sinense</i>	DY45362	PV082742	PV082859	PV171138	PV171192	PV171262	
<i>Metarhizium formicae</i>	SY09321 ^T	PV082703	PV082824		PV171167	PV171223	
<i>Metarhizium formicae</i>	SY09322	PV082704	PV082825		PV171168	PV171224	
<i>Metarhizium pupicola</i>	DY05341 ^T	PV082705	PV082826			PV171225	
<i>Metarhizium pupicola</i>	DY05342	PV082706	PV082827			PV171226	
<i>Metarhizium sinense</i>	SY09731 ^T	PV082707	PV082828	PV171121	PV171169	PV171227	
<i>Metarhizium sinense</i>	SY09732	PV082708	PV082829	PV171122	PV171170	PV171228	
<i>Neolecanicillium sinensis</i>	DY091351 ^T	PV082743	PV082860			PV171263	
<i>Neolecanicillium sinensis</i>	DY091352	PV082744	PV082861			PV171264	
<i>Nuciformispora araneicola</i>	XY07011 ^T	PV082745	PV082862			PV171265	
<i>Nuciformispora araneicola</i>	XY07012	PV082746	PV082863			PV171266	
<i>Nuciformispora sinense</i>	DY05281 ^T	PV082747	PV082864	PV171139		PV171267	
<i>Nuciformispora sinense</i>	DY05282	PV082748	PV082865	PV171140		PV171268	
<i>Nuciformispora vallise</i>	DY09691 ^T	PV082749	PV082866	PV171141		PV171269	
<i>Nuciformispora vallise</i>	DY09692	PV082750	PV082867	PV171142		PV171270	
<i>Nuciformispora zunyiense</i>	SY09221 ^T	PV082751	PV082868	PV171143	PV171193	PV171271	
<i>Nuciformispora zunyiense</i>	SY09222	PV082752	PV082869	PV171144	PV171194	PV171272	
<i>Papiliomyces sinensis</i>	DY05831 ^T	PV082709	PV082830	PV171123	PV171171	PV171229	
<i>Papiliomyces sinensis</i>	DY05832	PV082710	PV082831	PV171124	PV171172	PV171230	
<i>Paracorniculantispora sinensis</i>	ZY06251 ^T	PV082753	PV082870	PV171145	PV171195	PV171273	
<i>Paracorniculantispora sinensis</i>	ZY06252	PV082754	PV082871	PV171146	PV171196	PV171274	
<i>Purpureocillium aranea</i>	KY07231 ^T	PV082801	PV082918			PV171319	
<i>Purpureocillium aranea</i>	KY07232	PV082802	PV082919			PV171320	
<i>Purpureocillium lavendulum</i>	KY07091	PV082811	PV082928			PV171329	
<i>Purpureocillium lavendulum</i>	KY07092	PV082812	PV082929			PV171330	

Table 2 Continued

Species	Strain	GenBank Accession No.					
		ITS	LSU	<i>rpb1</i>	<i>rpb2</i>	<i>tef-1α</i>	Bloc
<i>Purpureocillium lavendulum</i>	KY07391	PV082813	PV082930			PV171331	
<i>Purpureocillium lavendulum</i>	KY07392	PV082814	PV082931			PV171332	
<i>Purpureocillium lavendulum</i>	KY07411	PV082815	PV082932			PV171333	
<i>Purpureocillium lavendulum</i>	KY07412	PV082816	PV082933			PV171334	
<i>Purpureocillium lavendulum</i>	KY072911	PV082817	PV082934			PV171335	
<i>Purpureocillium lavendulum</i>	KY072912	PV082818	PV082935			PV171336	
<i>Purpureocillium lavendulum</i>	KY074121	PV082819	PV082936			PV171337	
<i>Purpureocillium lavendulum</i>	KY074122	PV082820	PV082937			PV171338	
<i>Purpureocillium sinense</i>	TR05091 ^T	PV082803	PV082920			PV171321	
<i>Purpureocillium sinense</i>	TR05092	PV082804	PV082921			PV171322	
<i>Purpureocillium tiankengense</i>	KY07471 ^T	PV082805	PV082922			PV171323	
<i>Purpureocillium tiankengense</i>	KY07472	PV082806	PV082923			PV171324	
<i>Rubrumomyces guizhouensis</i>	TR05311 ^T	PV082755	PV082872				
<i>Rubrumomyces guizhouensis</i>	TR05312	PV082756	PV082873				
<i>Rubrumomyces sinensis</i>	ZY06111 ^T	PV082757	PV082874	PV171147		PV171275	
<i>Rubrumomyces sinensis</i>	ZY06112	PV082758	PV082875	PV171148		PV171276	
<i>Samsoniella araneicola</i>	DY05471 ^T	PV082759	PV082876		PV171197	PV171277	
<i>Samsoniella araneicola</i>	DY05472	PV082760	PV082877		PV171198	PV171278	
<i>Samsoniella fanjingensis</i>	TR05241 ^T	PV082761	PV082878		PV171199	PV171279	
<i>Samsoniella fanjingensis</i>	TR05242	PV082762	PV082879		PV171200	PV171280	
<i>Samsoniella guiyangensis</i>	KY45341 ^T	PV082763	PV082880		PV171201	PV171281	
<i>Samsoniella guiyangensis</i>	KY45342	PV082764	PV082881		PV171202	PV171282	
<i>Samsoniella houerensis</i>	KY45141 ^T	PV082765	PV082882		PV171203	PV171283	
<i>Samsoniella houerensis</i>	KY45142	PV082766	PV082883		PV171204	PV171284	
<i>Samsoniella jiangkouensis</i>	TR05031 ^T	PV082767	PV082884	PV171149	PV171205	PV171285	
<i>Samsoniella jiangkouensis</i>	TR05032	PV082768	PV082885	PV171150	PV171206	PV171286	
<i>Samsoniella kaiyangensis</i>	KY45381 ^T	PV082769	PV082886	PV171151	PV171207	PV171287	
<i>Samsoniella kaiyangensis</i>	KY45382	PV082770	PV082887	PV171152	PV171208	PV171288	
<i>Samsoniella miaolingensis</i>	DY05811 ^T	PV082771	PV082888	PV171153	PV171209	PV171289	
<i>Samsoniella miaolingensis</i>	DY05812	PV082772	PV082889	PV171154	PV171210	PV171290	

Table 2 Continued

Species	Strain	GenBank Accession No.					
		ITS	LSU	<i>rpb1</i>	<i>rpb2</i>	<i>tef-1α</i>	Bloc
<i>Samsoniella simplicola</i>	DY45121 ^T	PV082773	PV082890	PV171155		PV171291	
<i>Samsoniella simplicola</i>	DY45122	PV082774	PV082891	PV171156		PV171292	
<i>Samsoniella suiyangensis</i>	SY09821 ^T	PV082775	PV082892	PV171157	PV171211	PV171293	
<i>Samsoniella suiyangensis</i>	SY09822	PV082776	PV082893	PV171158	PV171212	PV171294	
<i>Samsoniella tongrenensis</i>	TR05131 ^T	PV082777	PV082894	PV171159	PV171213	PV171295	
<i>Samsoniella tongrenensis</i>	TR05132	PV082778	PV082895	PV171160	PV171214	PV171296	
<i>Samsoniella wudangensis</i>	WD04121 ^T	PV082779	PV082896			PV171297	
<i>Samsoniella wudangensis</i>	WD04122	PV082780	PV082897			PV171298	
<i>Samsoniella zongqii</i>	DY45251 ^T	PV082781	PV082898	PV171161	PV171215	PV171299	
<i>Samsoniella zongqii</i>	DY45252	PV082782	PV082899	PV171162	PV171216	PV171300	
<i>Simplicillium araneicola</i>	DY11251 ^T	PV082783	PV082900			PV171301	
<i>Simplicillium araneicola</i>	DY11252	PV082784	PV082901			PV171302	
<i>Simplicillium bursae</i>	ZY06121 ^T	PV082785	PV082902			PV171303	
<i>Simplicillium bursae</i>	ZY06122	PV082786	PV082903			PV171304	
<i>Simplicillium cantharise</i>	ZY06421 ^T	PV082787	PV082904			PV171305	
<i>Simplicillium cantharise</i>	ZY06422	PV082788	PV082905			PV171306	
<i>Simplicillium neoaraneae</i>	ZY06261 ^T	PV082789	PV082906			PV171307	
<i>Simplicillium neoaraneae</i>	ZY06262	PV082790	PV082907			PV171308	
<i>Simplicillium wudangense</i>	WD04131 ^T	PV082791	PV082908	PV171163		PV171309	
<i>Simplicillium wudangense</i>	WD04132	PV082792	PV082909	PV171164		PV171310	
<i>Simplicillium zunyiense</i>	ZY06581 ^T	PV082793	PV082910			PV171311	
<i>Simplicillium zunyiense</i>	ZY06582	PV082794	PV082911			PV171312	
<i>Zarea sinensis</i>	ZY06611 ^T	PV082795	PV082912		PV171217	PV171313	
<i>Zarea sinensis</i>	ZY06612	PV082796	PV082913		PV171218	PV171314	
<i>Zongqiomycetes araneicola</i>	ZY09191 ^T	PV082797	PV082914			PV171315	
<i>Zongqiomycetes araneicola</i>	ZY09192	PV082798	PV082915			PV171316	
<i>Zongqiomycetes sinensis</i>	SY09201 ^T	PV082799	PV082916		PV171219	PV171317	
<i>Zongqiomycetes sinensis</i>	SY09202	PV082800	PV082917		PV171220	PV171318	

Notes: Ex-type strains are indicated with ^T.

RESULTS

Phylogenetic analyses

Analysis 1: The creation of phylogenetic trees in analysis 1 aimed to determine the establishment of the new species in *Clavicipitaceae* and *Ophiocordycipitaceae* (Fig. 1). *Pleurocordyceps aurantiaca* (Y.P. Xiao et al.) Y.H. Wang et al. (MFLUCC 17-2113) and *P. marginaliradians* (Y.P. Xiao et al.) Y.H. Wang et al. (MFLU 17-1582) served as the outgroup taxa in the study. The dataset included 56 taxa and consisted of 3,508 (ITS, 639, LSU, 782, *rpb1*, 535, *rpb2*, 742 and *tef-1 α* , 810) characters with gaps.

The selected model for ML analysis was TIM2+F+I+G4. The final value of the highest scoring tree was -29,632.694, which was obtained from the ML analysis of the dataset. The GTR model was applied to the dataset with the following parameter estimates: nucleotide frequencies A = 0.235, C = 0.278, G = 0.276, T = 0.211; relative substitution rates AC = 1.33493, AG = 3.44865, AT = 1.33493, CG = 1.00000, CT = 7.67654, GT = 1.00000; and a gamma distribution shape parameter (α) of 0.686. For Bayesian Inference (BI) analysis, the best-fit model identified for the dataset was GTR+F+I+G4. The maximum likelihood (ML) and Bayesian inference (BI) methods produced highly concordant phylogenetic trees (Fig. 1), with strong statistical support for most clades. The majority of genera formed distinct monophyletic groups. The new strains were grouped into the families, *Clavicipitaceae* and *Ophiocordycipitaceae*. In the family *Clavicipitaceae*, the new strains mainly grouped into the genera *Keithomyces* Samson et al. *Metarhizium* Sorokin and *Papiliomyces* Luangsa-ard et al. In the family *Ophiocordycipitaceae*, the new strains mainly grouped into the genus *Purpureocillium* Luangsa-ard et al.

Analysis 2: Phylogenetic relationships established through analysis 2 supported the recognition of the new *Cordycipitaceae* species (Fig. 2). *Purpureocillium lilacinum* (Thom) Luangsa-ard et al. (CBS 431.87 and CBS 284.36) was used as the outgroup taxon in the analysis. The dataset included 119 taxa and consisted of 3,607 (ITS, 646, LSU, 779, *rpb1*, 529, *rpb2*, 761 and *tef-1 α* , 892) characters with gaps.

Maximum likelihood analysis employed the TIM3+F+I+G4 substitution model, yielding an optimal tree with a final log-likelihood score of -64,005.964. The GTR model parameters for dataset analysis were estimated as follows: nucleotide frequencies (A = 0.237, C = 0.281, G = 0.271, T = 0.212), substitution rate matrix (AC = 1.12913, AG = 2.88655, AT = 1.00000, CG = 1.12913, CT = 6.28813, GT = 1.00000), and gamma distribution shape parameter (α = 0.524). For Bayesian inference, we applied partitioned models: GTR+F+I+G4 for ITS, *rpb1* and *tef-1 α* loci, and SYM+G4 for LSU and *rpb2*. Both ML and BI approaches produced highly concordant tree topologies (Fig. 2), with strong nodal support observed across most branches. The majority of genera formed distinct monophyletic groups in the phylogenetic reconstruction. The new strains were grouped into the genera *Arachnidicola* Khons. et al., *Beauveria* Vuill., *Cordyceps* Fr., *Gamszarella* Crous, *Lecanicillium* W. Gams & Zare, *Samsoniella* Mongkols. et al. *Zarea* Khons. et al. and *Simplicillium* W. Gams & Zare.

Analysis 3: The phylogenetic reconstruction in analysis 3 was performed to evaluate the taxonomic position of the novel species within *Beauveria* (Fig. 3). The analysis utilized *Cordyceps cicadae* (ARSEF 7260) and *C. tenuipes* (ARSEF 4096) as outgroup taxa. The dataset included 40 taxa and consisted of 4,527 (Bloc, 1337, ITS, 639, *rpb1*, 657, *rpb2*, 984 and *tef-1 α* , 919) characters with gaps. For maximum likelihood analysis, the TIM2+F+G4 substitution model was identified as optimal, yielding a best-scoring tree with a log-likelihood value of -29,321.489. Parameter estimates for the GTR model analysis included nucleotide frequencies (A: 0.243, C: 0.287, G: 0.255, T: 0.215), relative substitution rates (AC: 0.84454, AG: 2.86287, AT: 0.84454, CG: 1.00000, CT: 3.69070, GT: 1.00000), and a gamma distribution parameter (α = 0.797). Bayesian inference employed partitioned models with HKY+F+G4 for Bloc, and SYM+G4 for ITS, *rpb1*, *rpb2*, and *tef-1 α* loci. Both maximum likelihood and Bayesian inference approaches yielded highly concordant tree topologies (Fig. 3), with most nodes showing strong statistical support. The majority of genera formed distinct monophyletic groups in the phylogenetic analysis. Strains

KY07241, KY07242, SY09861 and SY09862 clustered into two independent clades with high statistical support (100% ML/1 PP) and clustered in a clade with high statistical support in ML analysis (100% ML/1 PP).

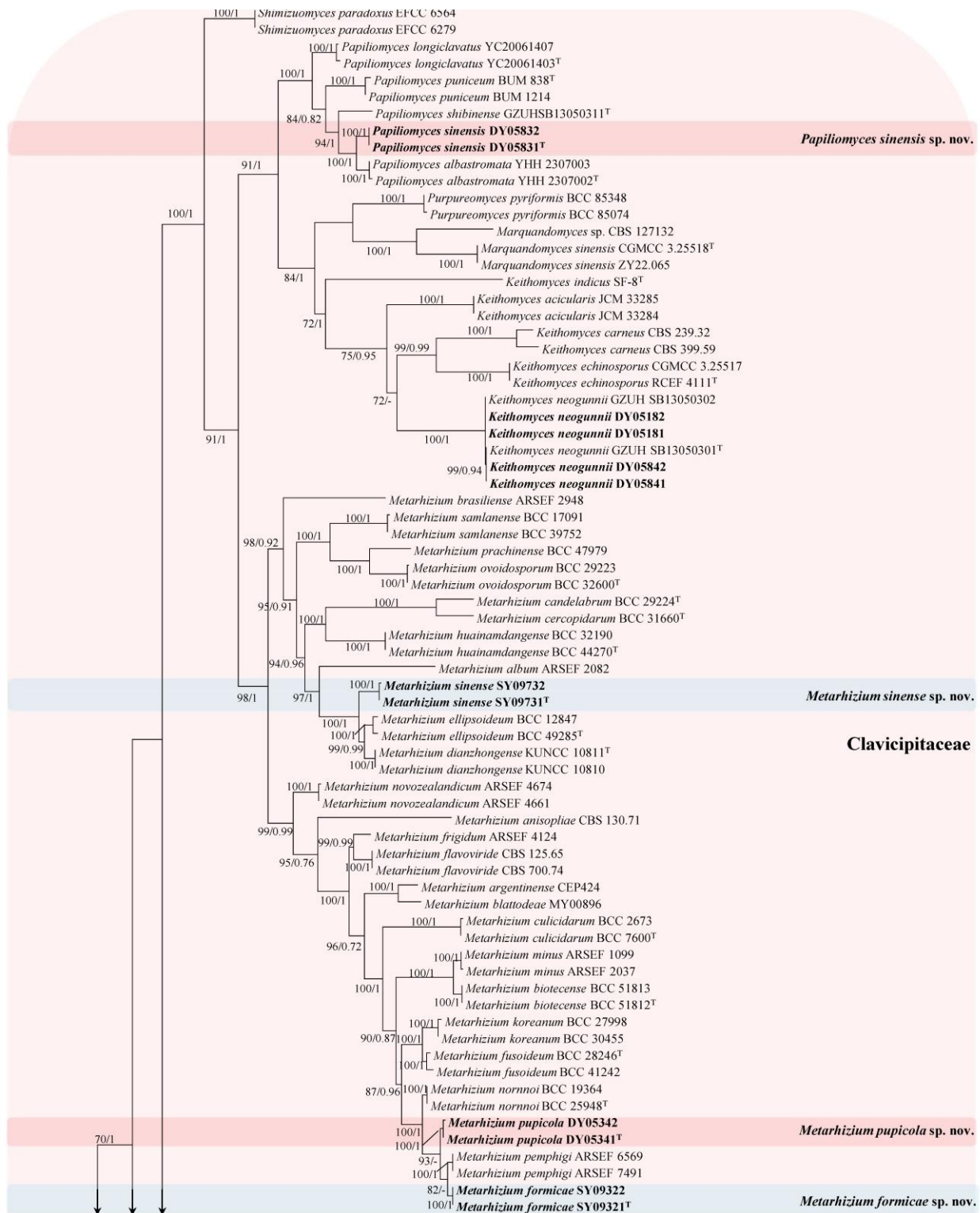


Figure 1 – Phylogram retrieved from IQTREE of the new species and related species in Clavicipitaceae and Ophiocordycipitaceae using the combined dataset of ITS, LSU, *rpb1*, *rpb2* and *tef-1a* gene regions. The statistical values are provided at nodes as ML/PP (ML value above 70% and BI value above 0.70). The tree is rooted with *Pleurocordyceps aurantiaca* (MFLUCC 17-2113) and *P. marginaliradians* (MFLU 17-1582). Ex-types, new strains and new species are indicated by the superscript "T" and in bold, respectively.

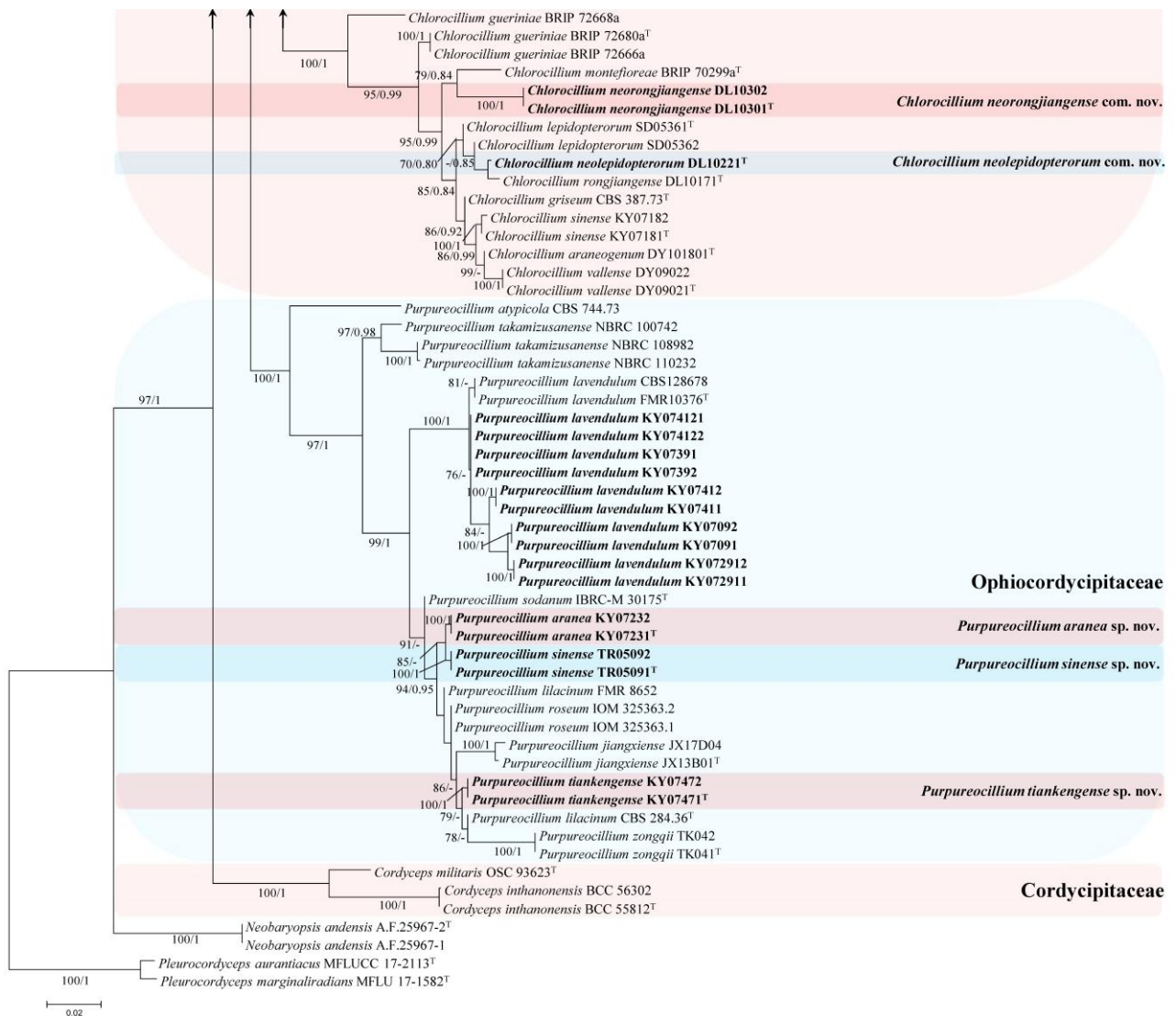


Figure 1 – Continued.

Taxonomy

Clavicipitaceae Rogerson, Mycologia 62(5): 900 (1970)

Chlorocillium Zare & W. Gams, Mycol. Progr. 15: 1005 (2016)

New combinations

Chlorocillium neolepidopterorum (W.H. Chen, Y.F. Han, J.D. Liang & Z.Q. Liang) W.H. Chen, Y.F. Han & J.D. Liang comb. nov.

Index Fungorum number: 903356; Facesoffungi number: FoF 17462

≡ *Metarhizium lepidopterorum* W.H. Chen, Y.F. Han, J.D. Liang & Z.Q. Liang, Phytotaxa 419(2): 192 (2019)

MycoBank No. MB 831960

Type – China, Guizhou Province, Qiandongnan Miao and Dong Autonomous Prefecture, Rongjiang County (26°01'58.70"N, 108°24'48.06"E), on a *Lepidopteran* pupa, 1 October 2018, W.H. Chen, holotype GZAC DL1022, ex-type GZAC DL10221.

Description – See Chen et al. (2019c).

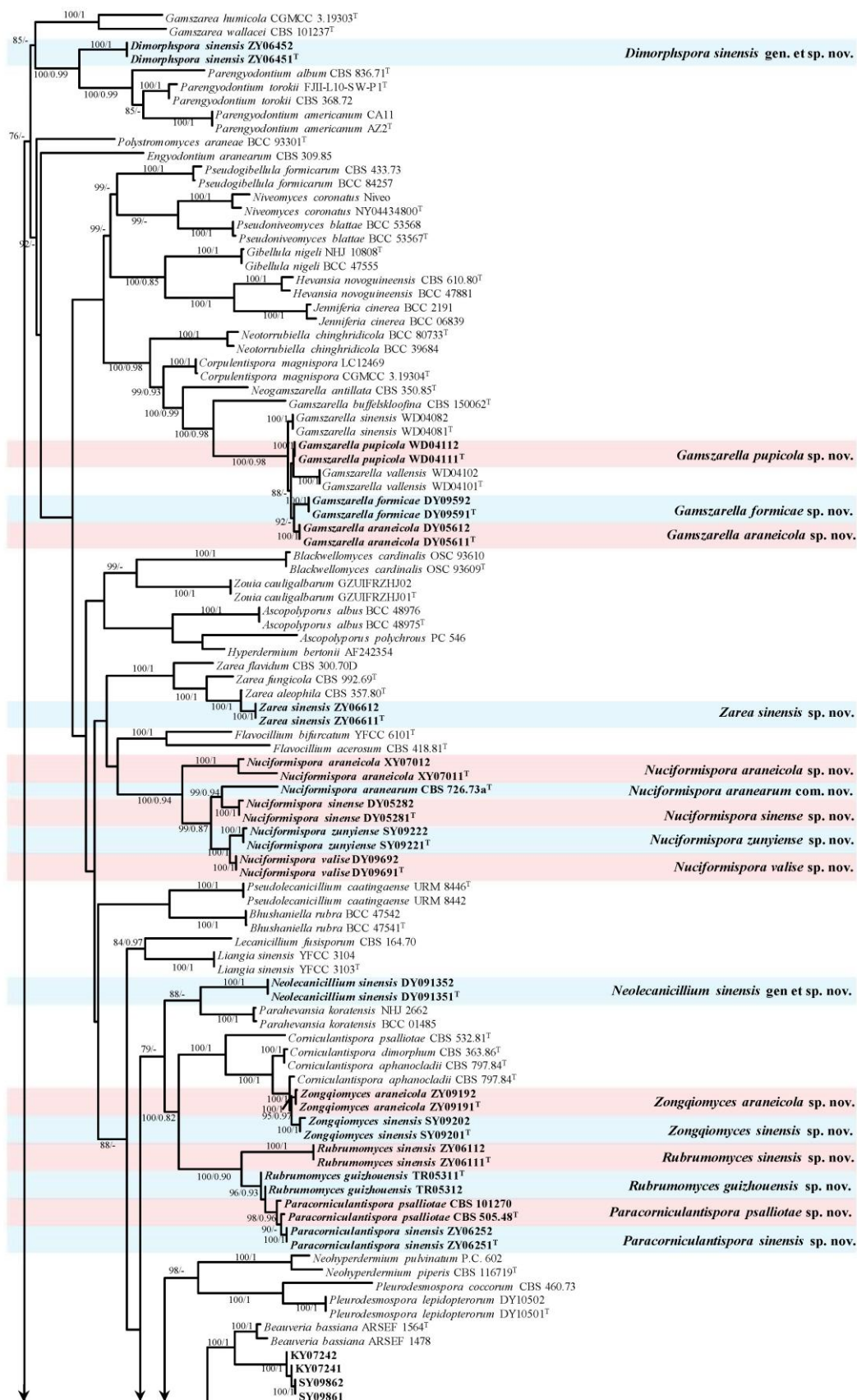


Figure 2 – Phylogram retrieved from IQTREE of the new species and related species in *Cordycipitaceae* using the combined dataset of ITS, LSU, *rpb1*, *rpb2* and *tef-1α* gene regions. The statistical values are provided at nodes as ML/PP (ML value above 70% and BI value above 0.70). The tree is rooted with *Purpureocillium lilacinum* (CBS 284.36 and CBS 431.87). Ex-types, new strains and new species are indicated by the superscript “T” and in bold, respectively.

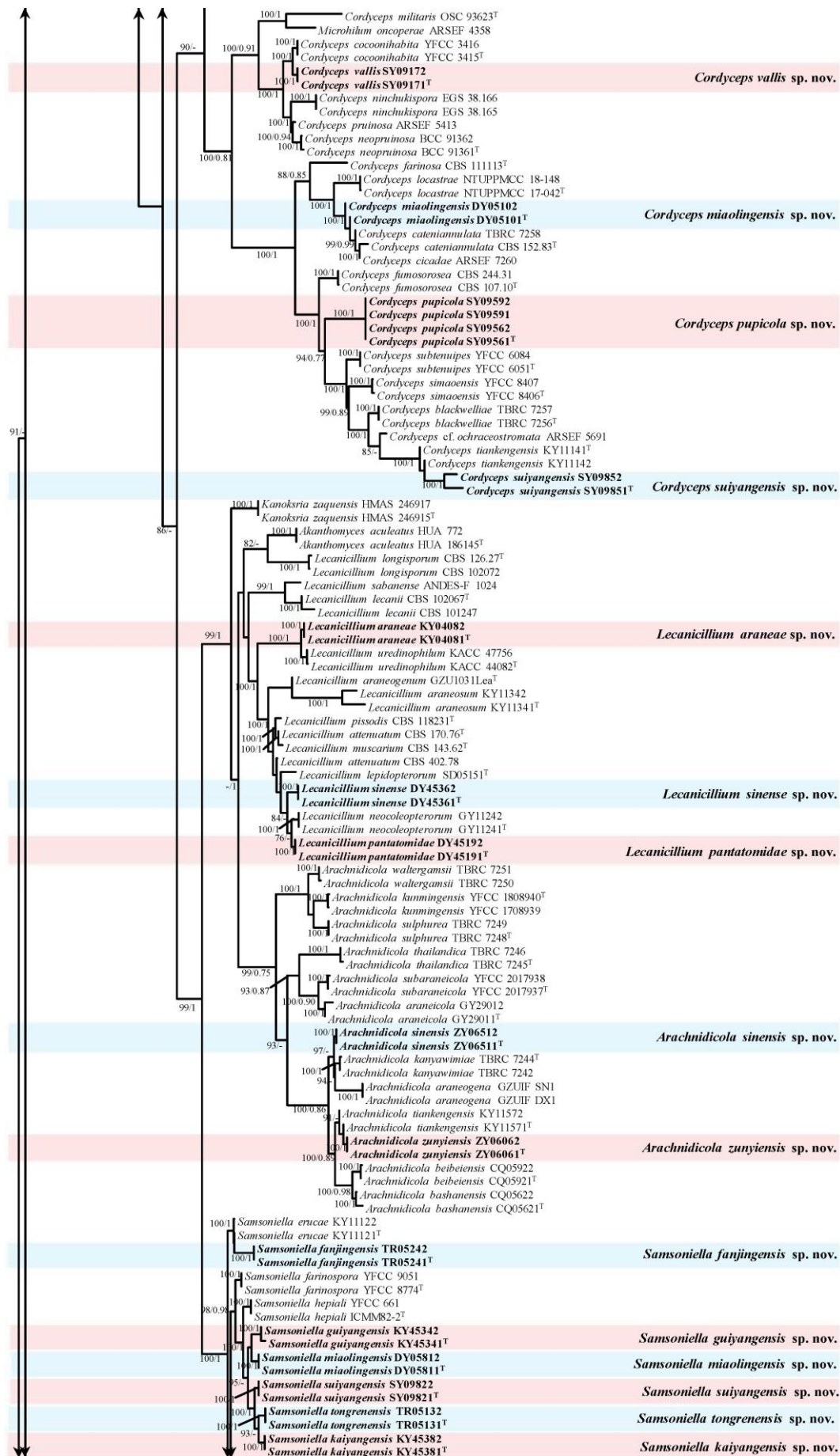


Figure 2 – Continued.

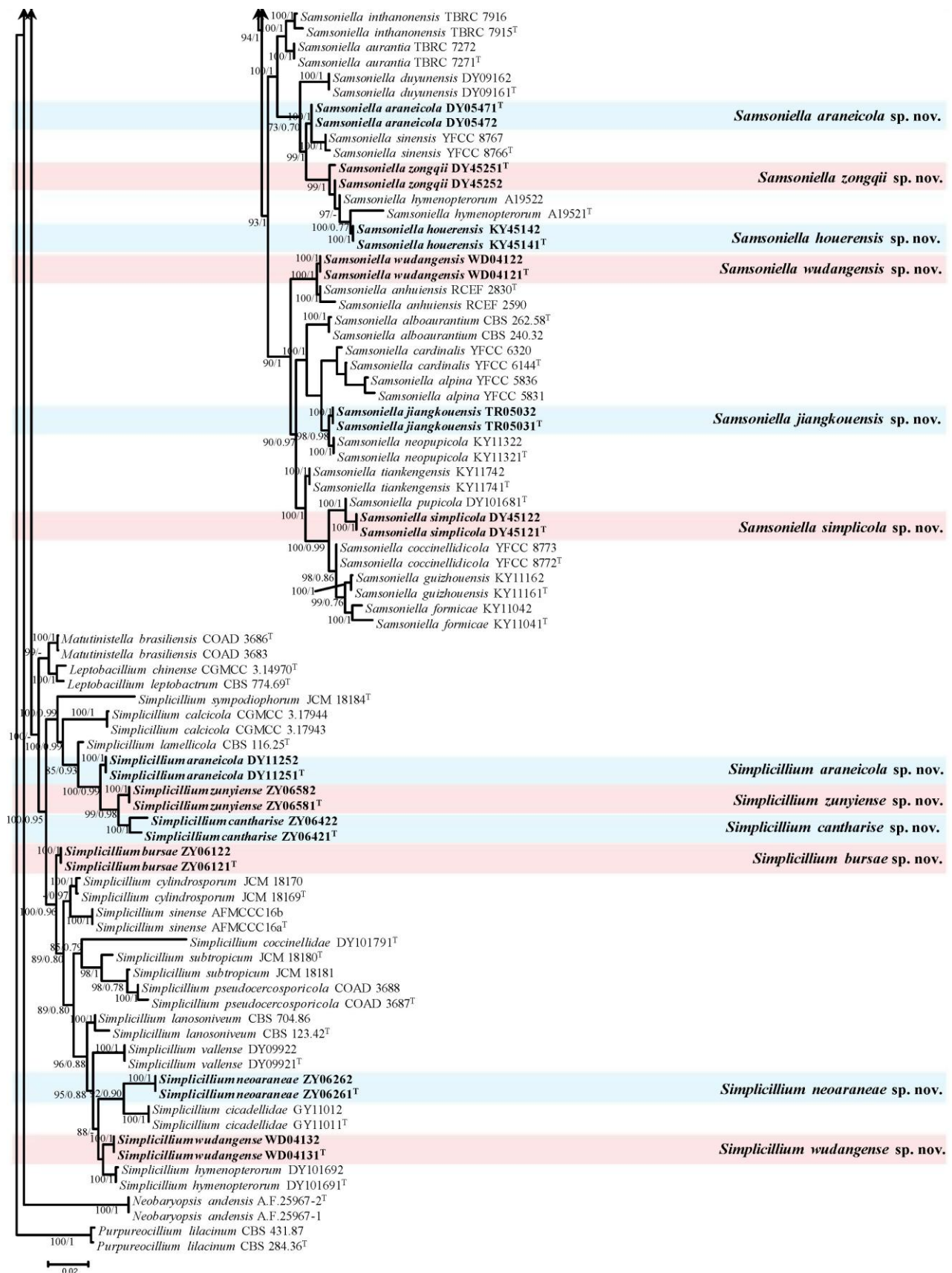


Figure 2 – Continued.

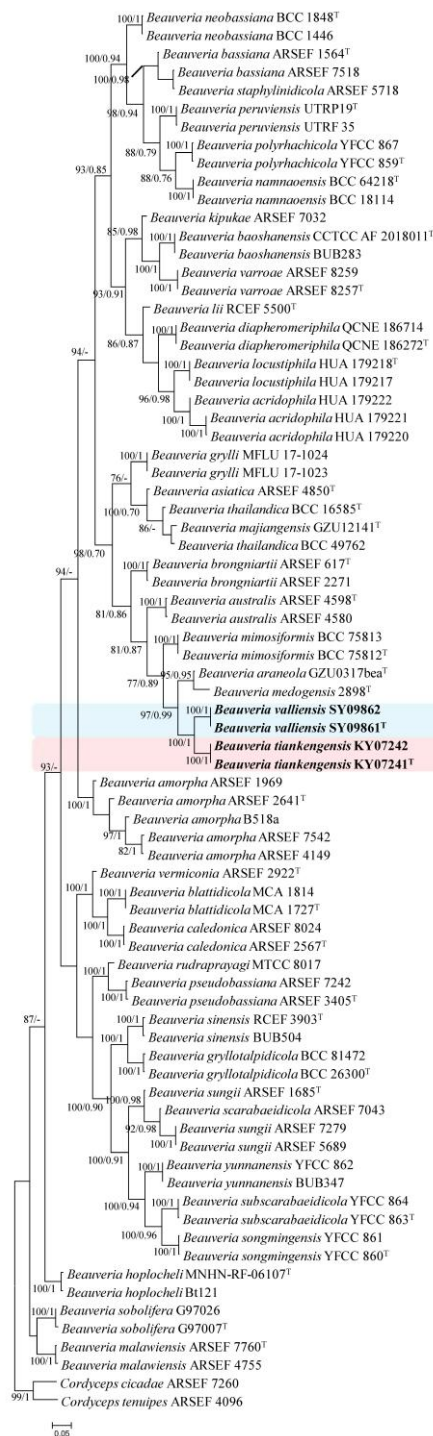


Figure 3 – Phylogram retrieved from IQTREE of the new species and related species in *Beauveria* using the combined dataset of Bloc, ITS, *rpb1*, *rpb2* and *tef-1α* gene regions. The statistical values are provided at nodes as ML/PP (ML value above 70% and BI value above 0.70). The tree is rooted with *Cordyceps cicadae* (ARSEF 7260) and *Cordyceps tenuipes* (ARSEF 4096). Ex-types, new strains and new species are indicated by the superscript “T” and in bold, respectively.

Chlorocillium neorongjiangense (W.H. Chen, Y.F. Han, J.D. Liang & Z.Q. Liang) W.H. Chen, Y.F. Han & J.D. Liang comb. nov.

Index Fungorum number: 903357; Facesoffungi number: FoF 17463

≡ *Metarhizium rongjiangense* W.H. Chen, Y.F. Han, J.D. Liang & Z.Q. Liang, Phytotaxa 419(2): 193 (2019)

Mycobank No. MB 831961

Type – China, Guizhou Province, Qiandongnan Miao and Dong Autonomous Prefecture, Rongjiang County (26°01'58.70"N, 108°24'48.06"E), on a *Lepidopteran* pupa, 1 October 2018, W.H. Chen, holotype GZAC DL1030, ex-type GZAC DL10301.

Description – See Chen et al. (2019c).

Metarhizium Sorokīn, Veg. Parasitenk. Mensch Tieren 2: 268 (1879)

Type species – *Metarhizium anisopliae* (Metschn.) Sorokīn 1883

Notes – The genus *Metarhizium* was originally described by Metschnikoff as *Entomophthora anisopliae* Metschn. and was later reclassified into its current genus by Sorokīn (1883). Tulloch (1976) delimited *Metarhizium* into two species, *M. anisopliae* (Metschn.) Sorokīn (with its variety *majus*) and *M. flavoviride* W. Gams & Rozsypal. Currently, the genus *Metarhizium* comprises 74 species. Among these, 23 belong to the *M. anisopliae* species complex and 13 to the *M. flavoviride* species complex (Wei et al. 2024). *Metarhizium* (Metschn.) Sorokīn represents a globally distributed and morphologically diverse genus of asexual entomopathogenic fungi that parasitize various insect hosts. In the present study, three new species were introduced based on the morphological characteristics and phylogenetic analysis. Interestingly, these newly species were collected from valley habitats, marking the first reported occurrence in such environments. Thus, the species diversity of *Metarhizium* in valley habitats and other special habitats needs more attention.

Metarhizium formicae W.H. Chen, Y.F. Han & J.D. Liang, sp. nov.

Fig. 4

Index Fungorum number: 903358; Facesoffungi number: FoF 17464

Etymology – referring to an ant host in family *Formicidae*.

Description – Colonies on PDA reaching 31–33 mm diam. in 14 d at 25°C, white, consisting of a basal felt and cottony, floccose overgrowth, reverse brown to light brown. Prostrate hyphae smooth, septate, hyaline, 1.3–1.7 µm diam. Conidial structures consisting of erect conidiophores usually arising from the aerial hyphae, solitary or paecilomyces-like with phialides in whorls of two to three. Phialides 16.7–28.4 × 1.3–1.9 µm ($\bar{x}$ = 23.3 × 1.5 µm, n=30), with a cylindrical basal portion, tapering into a distinct neck. Conidia in chains, hyaline, cylindrical, 1-celled, 5.4–7.3 × 1.4–1.8 µm ($\bar{x}$ = 6.6 × 1.6 µm, n=30). Octahedral crystals not observed.

Habitat – Near the road, located on or under the rock.

Material examined – China, Guizhou Province, Zunyi City, Suiyang County, Shuangmen Valley (28°1'39.05"N, 107°7'58.65"E). On a dead ant (*Formicidae*), 30 September 2023, Wanhao Chen, GZAC SY0932 (holotype), SY09321 (ex-type), SY09322 (living culture).

Notes – Based on NCBI BLASTn and phylogenetic analysis of the combined dataset 1 (Fig. 1), *Metarhizium formicae* (SY09321 and SY09322) was grouped within *Metarhizium* species. It formed a distinct clade closely related to *Metarhizium nornnoi*, *M. pemphigi* and *M. pupicola* supported by strong bootstrap values (100% ML /1 PP), which was also supported by the phylogenetic analyses among *Metarhizium* species (Suppl. Fig. 2). Compared with the typical characteristics, *M. formicae* was distinguished from *M. nornnoi* by its longer phialides [16.7–28.4 × 1.3–1.9 µm vs (5–)6.5–9(–10.0) × 2.0–3.0 µm] and smaller conidia [2.6–3.3 × 2.2–2.6 µm vs (4.0–)4.5–6.0 × 1.5–2.0 µm] (Mongkolsamrit et al. 2020). *Metarhizium formicae* was distinguished from *M. pemphigi* by its larger conidia (cylindrical, 5.4–7.3 × 1.4–1.8 µm vs ovoid to elongate, 5.4 × 2.4 µm) (Driver et al. 2000). *Metarhizium formicae* was distinguished from *M. pupicola* by its longer phialides (16.7–28.4 × 1.3–1.9 µm vs 8.5–14.4 × 1.8–2.4 µm) and larger conidia (cylindrical, 5.4–7.3 × 1.4–1.8 µm vs ellipsoidal, 2.6–3.7 × 1.6–2.3 µm). The combined morphological and molecular phylogenetic data provide conclusive evidence for recognizing *M. formicae* as a new species.

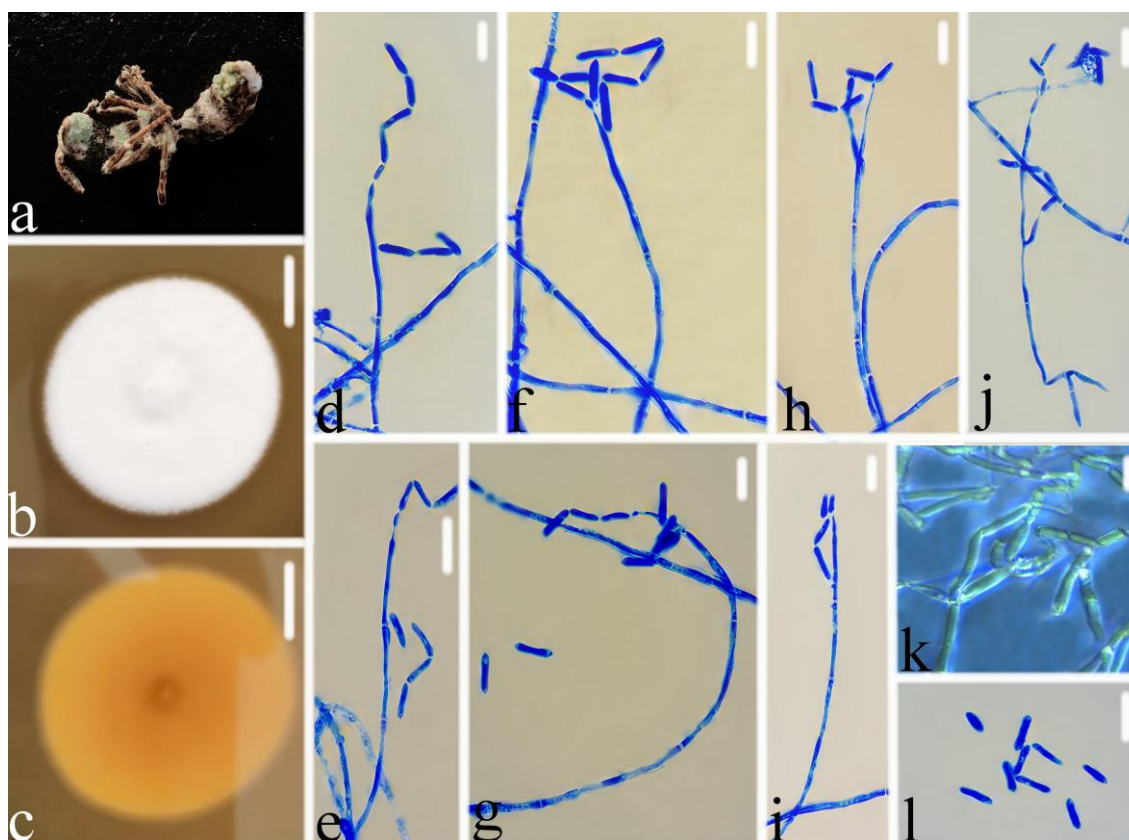


Figure 4 – *Metarhizium formicae* (SY09321, ex-type) a Infected ant. b–c Colonies on PDA culture media with upper (b) and reverse (c) views. d–i, l Phialides and conidia were stained with cotton blue. k Phialides and conidia. Scale bars: b–c = 10 mm, d–l = 10 μ m.

Metarhizium pupicola W.H. Chen, Y.F. Han & J.D. Liang, sp. nov.

Fig. 5

Index Fungorum number: 903359; Facesoffungi number: FoF 17465

Etymology – referring to a pupa host in order *Lepidoptera*.

Description – Colonies on PDA reaching 42–43 mm diam. in 14 d at 25°C, white, consisting of a basal felt and cottony, floccose overgrowth, reverse yellowish. Prostrate hyphae smooth, septate, hyaline, 1.8–2.5 μ m diam. Conidial structures consisting of erect conidiophores usually arising from the aerial hyphae, solitary or paecilomyces-like with phialides in whorls of two to three. Phialides 8.5–14.4 $\times$ 1.8–2.4 μ m ($\bar{x}$ = 11.4 $\times$ 1.9 μ m, n=30), with a cylindrical basal portion, tapering into a distinct neck. Conidia in chains, hyaline, ellipsoidal, 1-celled, 2.6–3.7 $\times$ 1.6–2.3 μ m ($\bar{x}$ = 3.0 $\times$ 2.0 μ m, n=30). Octahedral crystals not observed.

Material examined – China, Guizhou Province, Qiannan Buyei and Miao Autonomous Prefecture, Duyun City, Mayao River Valley (26°22'8.3748"N, 107°23'16.96"E). On a pupa (*Lepidoptera*), 1 May 2022, Wanhao Chen, GZAC DY0534 (holotype), DY05341 (ex-type), DY05342 (living culture).

Habitat – Near the road, buried in soil.

Notes – Phylogenetic analysis using combined dataset 1 (Fig. 1) and NCBI BLASTn analysis revealed that *Metarhizium pupicola* (DY05341 and DY05342) is grouped within *Metarhizium* species. It formed into an independent clade with a close relationship with *M. formicae*, *M. noronoi* and *M. pemphigi* with high bootstrap value (100% ML/ 1 PP), which was also supported by the phylogenetic analyses among *Metarhizium* species (Suppl. Fig. 2). Compared with the typical characteristics, *M. pupicola* was distinguished from *M. formicae* by its shorter phialides (8.5–14.4 $\times$ 1.8–2.4 μ m vs 16.7–28.4 $\times$ 1.3–1.9 μ m) and smaller conidia (ellipsoidal, 2.6–3.7 $\times$ 1.6–2.3 μ m vs cylindrical, 5.4–7.3 $\times$ 1.4–1.8 μ m). *Metarhizium pupicola* was distinguished from *M. noronoi* by its longer phialides [8.5–14.4 $\times$ 1.8–2.4 μ m vs (5–)6.5–9(–10.0) $\times$ 2.0–3.0 μ m] and smaller conidia [ellipsoidal, 2.6–3.3 $\times$ 2.2–2.6 μ m vs cylindrical, (4.0–)4.5–6.0 $\times$ 1.5–2.0 μ m] (Mongkolsamrit

et al. 2020). *Metarhizium pupicola* was distinguished from *M. pemphigi* by its smaller conidia (ellipsoidal, $2.6\text{--}3.3 \times 2.2\text{--}2.6 \mu\text{m}$ vs ovoid to elongate, $5.4 \times 2.4 \mu\text{m}$) (Driver et al. 2000). Thus, the combined morphological and molecular phylogenetic evidence substantiates the recognition of *M. pupicola* as a novel species.

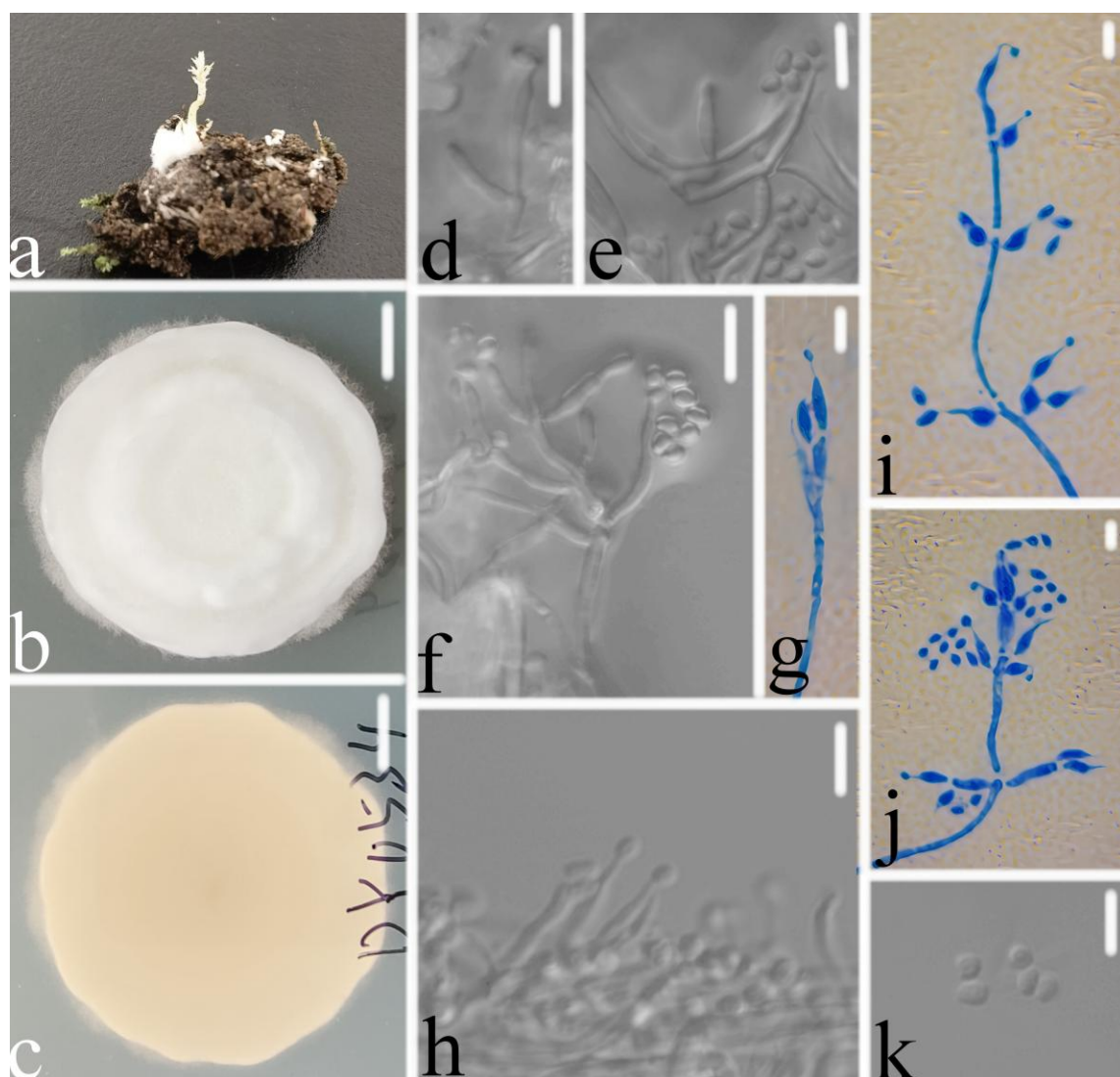


Figure 5 – *Metarhizium pupicola* (DY05341, ex-type) a Infected pupa. b–c Colonies on PDA culture media with upper (b) and reverse (c) views. d–f, h, k Phialides and conidia. g, i, j Phialides and conidia were stained with cotton blue. Scale bars: b–c = 10 mm, d–k = 10 μm .

Metarhizium sinense W.H. Chen, Y.F. Han & J.D. Liang, sp. nov.

Fig. 6

Index Fungorum number: 903360; Facesoffungi number: FoF 17466

Etymology – referring to the country, China, where the fungus was first discovered.

Description – Colonies on PDA reaching 24–25 mm diam. in 14 d at 25°C, white, consisting of a basal felt and cottony, floccose overgrowth, reverse brown to light brown. Prostrate hyphae smooth, septate, hyaline, 2.7–3.5 μm diam. Conidial structures consisting of erect conidiophores usually arising from the aerial hyphae, solitary or paecilomyces-like with phialides in whorls of two to three. Phialides 6.5–12.0 $\times$ 1.9–2.7 μm ($\bar{x} = 9.8 \times 2.3 \mu\text{m}$, $n=30$), with a cylindrical basal portion, tapering into a distinct neck. Conidia in chains, hyaline, fusiform to subglobose, 1-celled, 2.6–3.3 $\times$ 2.2–2.6 μm ($\bar{x} = 3.0 \times 2.3 \mu\text{m}$, $n=30$). Octahedral crystals not observed.

Material examined – China, Guizhou Province, Zunyi City, Suiyang County, Shuangmen Valley (28°1'39.05"N, 107°7'58.65"E). On a dead leafhopper (*Cicadellidae*), 30 September 2023, Wanhao Chen, GZAC SY0973 (holotype), SY09731 (ex-type), SY09732 (living culture).

Habitat – On the underside of leaves of broad-leaved plant species.

Notes – Phylogenetic analysis of concatenated dataset 1 (Fig. 1) and NCBI BLASTn results revealed that *Metarhizium sinense* (SY09731 and SY09732) was grouped with *Metarhizium* species. This species grouped in a well-supported clade (97% ML/1 PP) together with *M. album*, *M. dianzhongense* and *M. ellipsoideum*, which was also supported by the phylogenetic analyses among *Metarhizium* species (Suppl. Fig. 2). Compared with the typical characteristics, *M. sinense* was distinguished from *M. album* by its smaller conidia (fusiform to subglobose, $2.6\text{--}3.3 \times 2.2\text{--}2.6 \mu\text{m}$ vs elongated ellipsoidal to cylindrical, $5.0\text{--}7.5 \times 1.5\text{--}2.0 \mu\text{m}$) (Rombach et al. 1987). *Metarhizium sinense* was distinguished from *M. dianzhongense* by its longer phialides ($6.5\text{--}12.0 \times 1.9\text{--}2.7 \mu\text{m}$ vs $4.0\text{--}7.5 \times 1.0\text{--}3.0 \mu\text{m}$) and smaller conidia (fusiform to subglobose, $2.6\text{--}3.3 \times 2.2\text{--}2.6 \mu\text{m}$ vs ellipsoidal or cylindrical, $7.0\text{--}9.0 \times 2.0\text{--}3.0 \mu\text{m}$) (Wei et al. 2024). *Metarhizium sinense* was distinguished from *M. ellipsoideum* by its longer phialides [$6.5\text{--}12.0 \times 1.9\text{--}2.7 \mu\text{m}$ vs $4.0\text{--}5.5(6.0) \times 2.0\text{--}3.0 \mu\text{m}$] and smaller conidia [fusiform to subglobose, $2.6\text{--}3.3 \times 2.2\text{--}2.6 \mu\text{m}$ vs cylindrical or ellipsoidal, $5.0\text{--}6.5(7.0) \times 1.5\text{--}2.0 \mu\text{m}$] (Mongkolsamrit et al. 2020). The combined morphological diagnostic features and phylogenetic analyses provide conclusive support for establishing *M. sinense* as a new species.

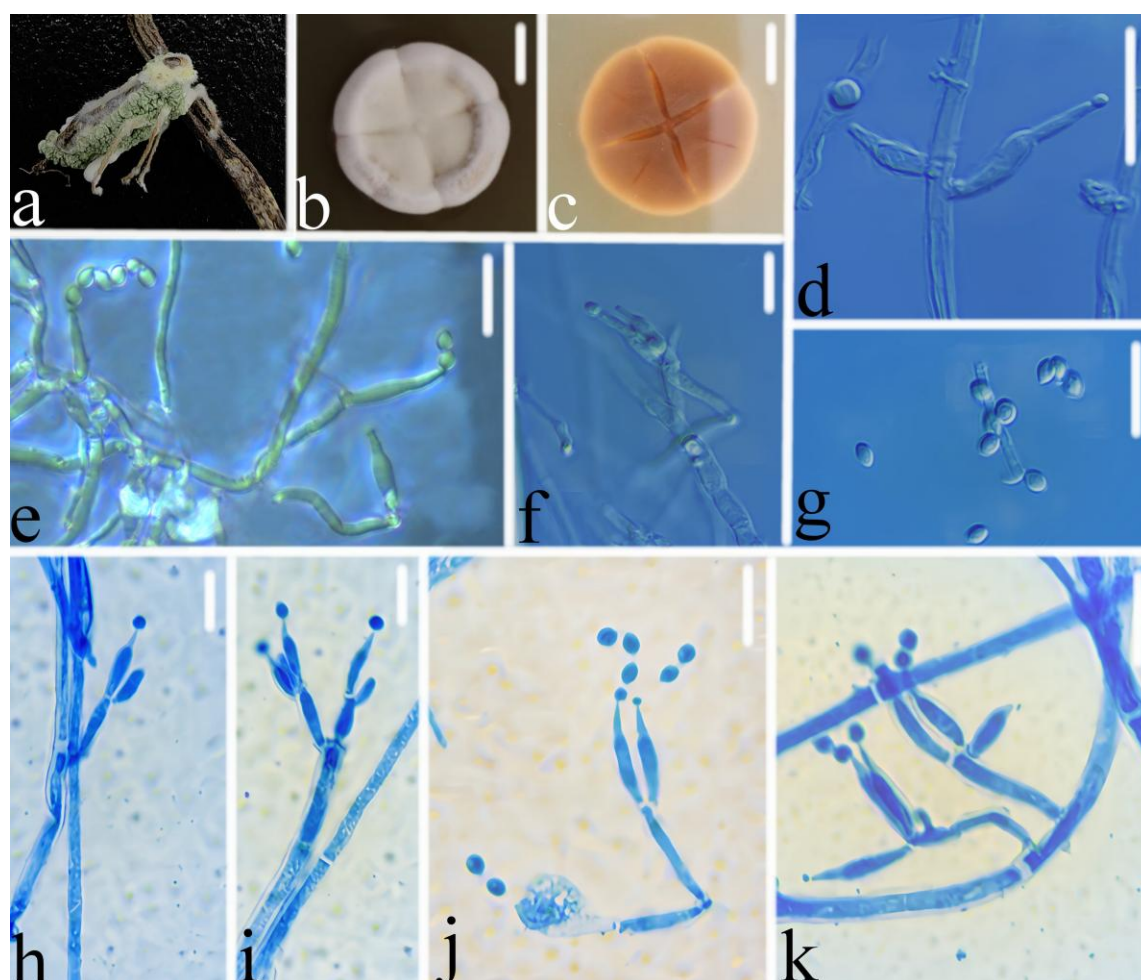


Figure 6 – *Metarhizium sinense* (SY09731, ex-type) a Infected leafhopper. b–c Colonies on PDA culture media with upper (b) and reverse (c) views. d–g Phialides and conidia. h–k Phialides and conidia were stained with cotton blue. Scale bars: b–c = 10 mm, d–k = 10 μm .

Papiliomyces Luangsa-ard, Samson & Thanakitp., Stud. Mycol. 95: 240 (2020)

Type species – *Papiliomyces liangshanensis* (M. Zang, D. Liu & R. Hu) Luangsa-ard, Samson & Thanakitp. 2020

Notes – The genus *Papiliomyces* was originally established to encompass two species, *P. liangshanensis* (M. Zang et al.) Luangsa-ard et al. and *P. shibinensis* (T.C. Wen et al.) Luangsa-ard et al. (Mongkolsamrit et al. 2020). However, following the reclassification of its type species *P. liangshanensis* into *Ophiocordyceps* Petch (Wang et al. 2021), the taxonomic validity of this genus requires critical reassessment. In the present, the name *Papiliomyces* was still used and a new species *P. sinensis* was introduced.

Papiliomyces sinensis W.H. Chen, Y.F. Han & J.D. Liang, sp. nov.

Fig. 7

Index Fungorum number: 903361; Facesoffungi number: FoF 17467

Etymology – referring to the country, China, where the fungus was first discovered.

Description – Colonies on PDA reaching 45–47 mm diam. in 14 d at 25°C, white, consisting of a basal felt and cottony, floccose overgrowth, reverse yellowish. Prostrate hyphae smooth, septate, hyaline, 2.1–2.6 µm diam. Conidial structures consisting of erect conidiophores usually arising from the aerial hyphae, solitary or lecanicillium-like with phialides in whorls of two to three. Conidiophores 7.0–10.8 × 2.7–3.3 µm. Phialides 14.1–16.2 × 2.1–2.9 µm ($\bar{x}$ = 14.9 × 2.3 µm, n=30), with a cylindrical basal portion, tapering into a distinct neck. Conidia in chains, hyaline, fusiform to subglobose, 1-celled, 2.7–4.0 × 2.6–2.9 µm ($\bar{x}$ = 3.5 × 2.7 µm, n=30). Octahedral crystals not observed.

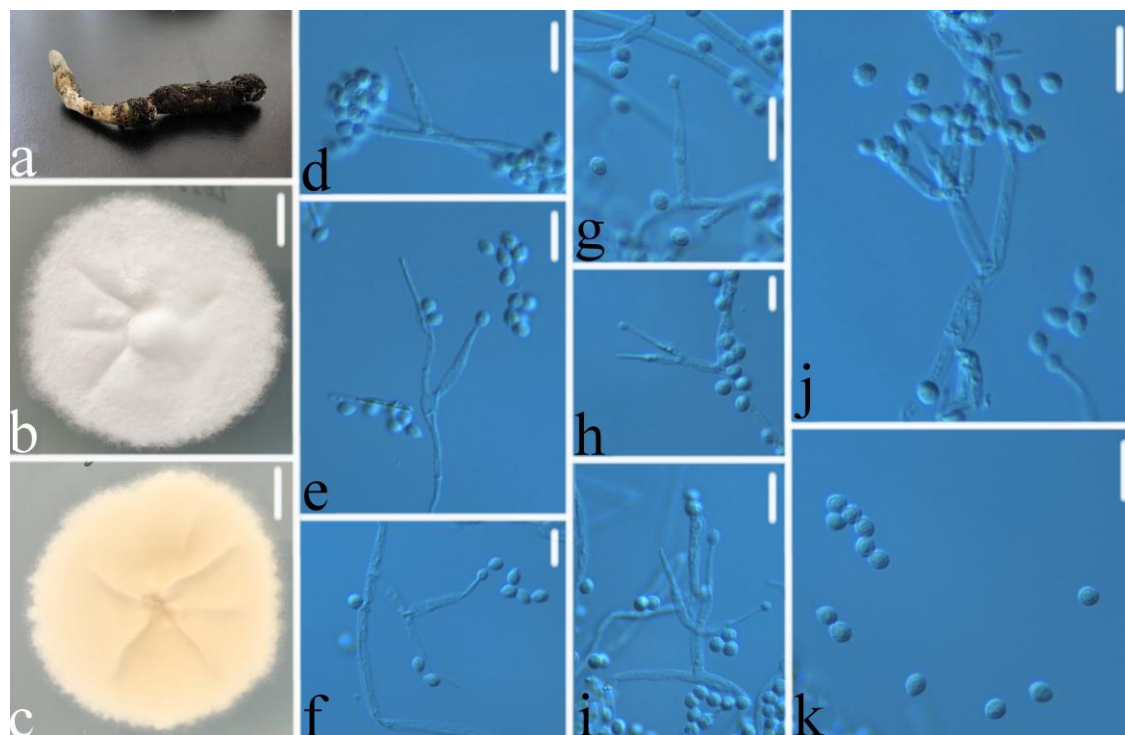


Figure 7 – *Papiliomyces sinensis* (DY05831, ex-type) a Infected larva. b–c Colonies on PDA culture media with upper (b) and reverse (c) views. d–k Phialides and conidia. Scale bars: b–c = 10 mm, d–k = 10 µm.

Material examined – China, Guizhou Province, Qiannan Buyei and Miao Autonomous Prefecture, Duyun City, Mayao River Valley (26°22'8.3748"N, 107°23'16.96"E). On a dead larva (*Lepidoptera*), 1 May 2022, Wanhao Chen, GZAC DY0583 (holotype), DY05831 (ex-type), DY05832 (living culture).

Habitat – Near the road, buried in soil.

Notes – Phylogenetic analysis of concatenated dataset 1 (Fig. 1) and NCBI BLASTn comparisons revealed that *Papiliomyces sinensis* (DY05831 and DY0582) was grouped with *Papiliomyces* species. Phylogenetic reconstruction placed the species within a distinct clade sister

to *P. shibinensis* and *P. albobromaticus*, with strong nodal support (100% ML/1 PP). Compared with the typical characteristics, *P. sinensis* was distinguished from *P. shibinensis* by its shorter conidiophores ($7.0\text{--}10.8 \times 2.7\text{--}3.3 \mu\text{m}$ vs up to $60 \mu\text{m}$), shorter phialides ($14.1\text{--}16.2 \times 2.1\text{--}2.9 \mu\text{m}$ vs $7.6\text{--}37.5 \times 1.3\text{--}3.2 \mu\text{m}$) and the shape of conidia (fusiform to subglobose vs ellipsoidal, ovoid or fusiform) (Wen et al. 2015, Zhang et al. 2023). *Papiliomyces sinensis* was distinguished from *P. albobromaticus* by its shorter phialides ($14.1\text{--}16.2 \times 2.1\text{--}2.9 \mu\text{m}$ vs $9.8\text{--}24.3 \times 1.5\text{--}3.1 \mu\text{m}$) and fusiform to subglobose conidia (Chen et al. 2024d). The combined morphological characteristics and phylogenetic analyses provide robust support for recognizing *P. sinensis* as a new species.

Cordycipitaceae Kreisel ex G.H. Sung, J.M. Sung, Hywel-Jones & Spatafora, in Sung, Hywel-Jones, Sung, Luangsa-ard, Shrestha & Spatafora, Stud. Mycol. 57: 48 (2007)

Arachnidicola Khons., Thanakitp. & Luangsa-ard, Fungal Systematics and Evolution 14: 294 (2024)

Type species – *Arachnidicola sulphurea* (Mongkols., Noisrip., Thanakitp., Spatafora & Luangsa-ard) Khons., Thanakitp. & Luangsa-ard 2024

Notes – Khonsanit et al. (2024) established the genus *Arachnidicola*, designating *A. sulphurea* (Mongkols. et al.) Khons. et al. as its type species and consists of 11 species. The hosts in this genus were spider. Interestingly, all *Arachnidicola* species produce mononematous conidiophores. The present study documented differential conidiophore development, with synnematus formations under natural conditions and mononematous structures in culture. Such phenotypic variation likely reflects evolutionary convergence in response to environmental adaptation (Chen et al. 2020d).

Arachnidicola sinensis W.H. Chen, Y.F. Han & J.D. Liang, sp. nov.

Fig. 8

Index Fungorum number: 903362; Facesoffungi number: FoF 17468

Etymology – referring to the country, China, where the fungus was first discovered.

Description – Colonies on PDA reaching 21–23 mm diam. in 14 d at 25°C , white, consisting of a basal felt and cottony, floccose overgrowth, reverse yellowish. Prostrate hyphae smooth, septate, hyaline, $1.2\text{--}2.0 \mu\text{m}$ diam. Conidial structures consisting of erect conidiophores usually arising from the aerial hyphae, solitary or verticillium-like with phialides in whorls of two to three. Conidiophores $25.7\text{--}39.5 \times 1.1\text{--}1.7 \mu\text{m}$. Phialides $11.3\text{--}18.6 \times 1.0\text{--}1.7 \mu\text{m}$ ($\bar{x} = 17.4 \times 1.9 \mu\text{m}$, $n=30$), with a cylindrical basal portion, tapering into a distinct neck. Conidia in chains, hyaline, subglobose to ellipsoidal, 1-celled, $2.4\text{--}3.3 \times 1.7\text{--}2.9 \mu\text{m}$ ($\bar{x} = 2.7 \times 2.2 \mu\text{m}$, $n=30$). Octahedral crystals not observed.

Material examined – China, Guizhou Province, Zunyi City, Honghuagang District, Dabanshui National Forest Park ($27^{\circ}46'35.904''\text{N}$, $106^{\circ}48'30.89''\text{E}$). On a dead spider (*Araneae*), 3 June 2022, Wanhao Chen, GZAC ZY0651 (holotype), ZY06511 (ex-type), ZY06512 (living culture).

Habitat – Near the road, located on or under the rock.

Notes – Molecular phylogenetic analysis of concatenated dataset 2 (Fig. 2) and NCBI BLASTn comparisons revealed that *Arachnidicola sinensis* (ZY06511 and ZY06512) was grouped with *Arachnidicola* species. Phylogenetic analysis placed the species within a distinct clade sister to *A. araneogena* and *A. kanyawimiae*, with strong nodal support (97% ML), which was also supported by the phylogenetic analyses among *Arachnidicola* species (Suppl. Fig. 3). Compared with the typical characteristics, *A. sinensis* was distinguished from *A. araneogena* by its shorter conidiophores ($25.7\text{--}39.5 \times 1.1\text{--}1.7 \mu\text{m}$ vs $78.0\text{--}121.0 \times 2.2 \mu\text{m}$) (Chen et al. 2018). *Arachnidicola sinensis* was distinguished from *A. kanyawimiae* by its longer phialides [$11.3\text{--}18.6 \times 1.0\text{--}1.7 \mu\text{m}$ vs $(8.0\text{--})9.0\text{--}12(15.0) \times 2.0\text{--}3.0 \mu\text{m}$] and subglobose to ellipsoidal conidia (Mongkolsamrit et al. 2018). The combined morphological characteristics and phylogenetic analyses provide conclusive support for establishing *A. sinensis* as a new species.

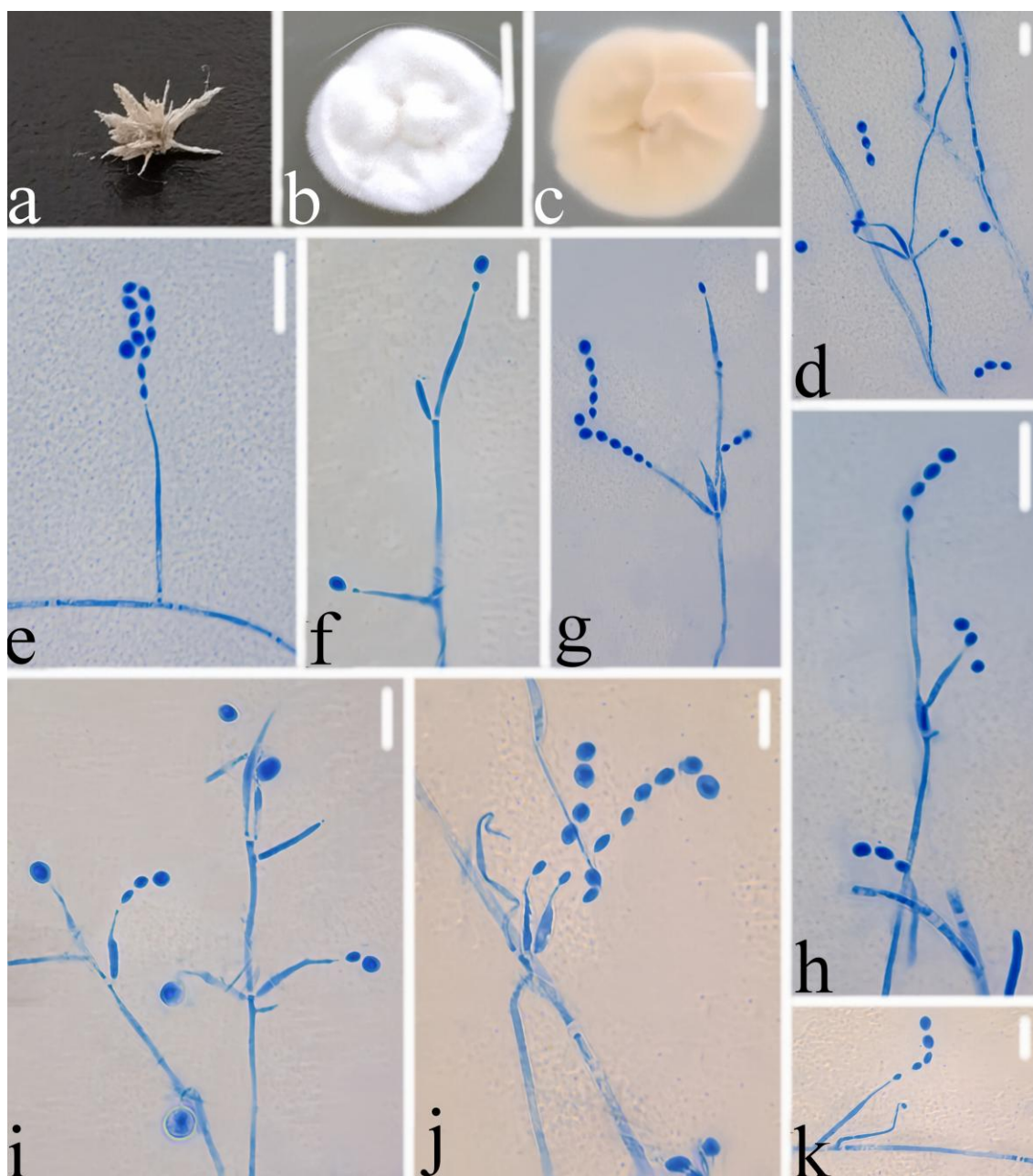


Figure 8 – *Arachnidicola sinensis* (ZY06511, ex-type) a Infected spider. b–c Colonies on PDA culture media with upper (b) and reverse (c) views. d–k Phialides and conidia were stained with cotton blue. Scale bars: b–c = 10 mm, d–k = 10 μ m.

Arachnidicola zunyiensis W.H. Chen, Y.F. Han & J.D. Liang, sp. nov.

Fig. 9

Index Fungorum number: 903363; Facesoffungi number: FoF 17469

Etymology – referring to the location, Zunyi City, where the fungus was first discovered.

Description – Colonies on PDA reaching 48–49 mm diam. in 14 d at 25°C, white, consisting of a basal felt and cottony, floccose overgrowth, reverse yellowish. Prostrate hyphae smooth, septate, hyaline, 1.4–1.9 μ m diam. Conidial structures consisting of erect conidiophores usually arising from the aerial hyphae, solitary or verticillium-like with phialides in whorls of two to three. Phialides 9.5–14.9 $\times$ 2.3–2.8 μ m ($\bar{x}$ = 11.5 $\times$ 2.4 μ m, n=30), with a cylindrical basal portion, tapering into a distinct neck. Conidia in chains, hyaline, subglobose to ellipsoidal, 1-celled, 2.6–3.4 $\times$ 2.3–3.1 μ m ($\bar{x}$ = 2.8 $\times$ 2.5 μ m, n=30). Octahedral crystals not observed.

Material examined – China, Guizhou Province, Zunyi City, Honghuagang District, Dabanshui National Forest Park (27°46'35.904"N, 106°48'30.89"E). On a dead spider (*Araneae*), 3

June 2022, Wanhao Chen, GZAC ZY0606 (holotype), ZY06061 (ex-type), ZY06062 (living culture).

Habitat – Near the road, located on or under the rock.

Notes – Molecular characterization through NCBI BLASTn alignment and phylogenetic reconstruction of dataset 2 (Fig. 2) revealed that *Arachnidicola zunyiensis* (ZY06061 and ZY06062) was grouped with *Arachnidicola* species. Phylogenetic analysis revealed a distinct clade comprising *A. zunyiensis* and *A. tiankengensis*, supported by strong bootstrap values (91% ML), which was also supported by the phylogenetic analyses among *Arachnidicola* species (Suppl. Fig. 3). Compared with the typical characteristics, *A. zunyiensis* was distinguished from *A. tiankengensis* by its shorter phialides ($11.5 \times 2.4 \mu\text{m}$ vs $13.9\text{--}17.1 \times 1.1\text{--}1.6 \mu\text{m}$) and subglobose to ellipsoidal conidia (Chen et al. 2022b). The combined morphological and molecular phylogenetic evidence substantiates the recognition of *A. zunyiensis* as a novel species.

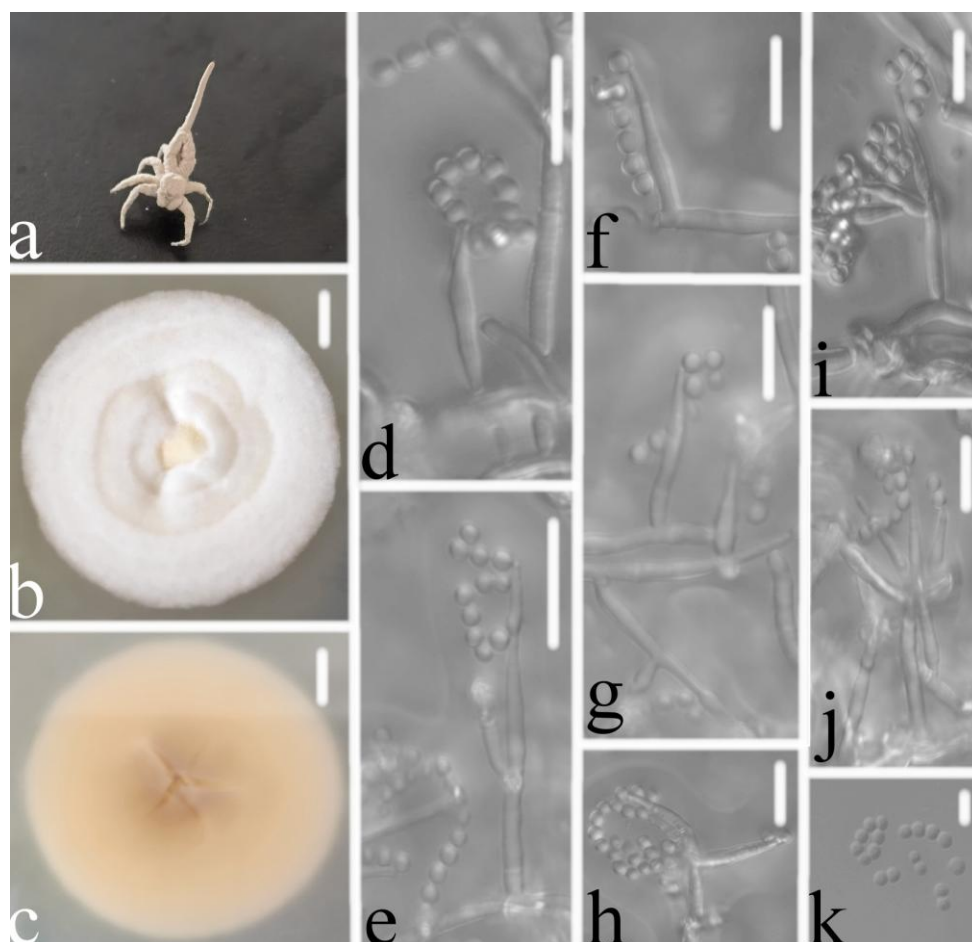


Figure 9 – *Arachnidicola zunyiensis* (ZY06061, ex-type) a Infected spider. b–c Colonies on PDA culture media with upper (b) and reverse (c) views. d–k Phialides and conidia. Scale bars: b–c = 10 mm, d–k = 10 μm .

Beauveria Vuill., Bull. Soc. bot. Fr. 59: 40 (1912)

Type species – *Beauveria bassiana* (Bals.-Criv.) Vuill. 1912

Notes – The genus *Beauveria* was established with the type species *B. bassiana* (Bals.-Criv.) Vuill. Rehner et al. (2011) delimited the genus *Beauveria* into 12 species based on the phylogenetic analysis. Kepler et al. (2017) re-evaluated the *Cordycipitaceae* by phylogenetic analysis and transferred five *Cordyceps* species to the genus *Beauveria*. Currently, *Beauveria* consists of 36 species (Chen & Han 2024). *Beauveria* species display broad host specificity, pathogenic to insects belonging to thirteen distinct orders including *Hemiptera*, *Neuroptera* and *Siphonaptera* (Zimmermann 2007). In the present study, two new species with ant hosts were introduced.

Beauveria tiankengensis W.H. Chen, Y.F. Han & J.D. Liang, sp. nov.

Fig. 10

Index Fungorum number: 903364; Facesoffungi number: FoF 17470

Etymology – referring to its location, Monkey-Ear Tiankeng, where the fungus was first discovered.

Description – Colonies on PDA reaching 21–24 mm diam. in 14 d at 25°C, non-odorous, aerial mycelium white, dense, velutinous, powdery while sporulating, white to yellowish white, reverse yellowish to pale brown. Prostrate hyphae smooth, septate, hyaline, 1.7–2.1 μm diam. Conidiogenous cells solitary or occurring in lateral clusters, base cylindrical to subspherical, 3.8–8.4 $\times$ 0.8–2.0 μm ($\bar{x}$ = 6.2 $\times$ 1.2 μm , n=30), apex with an indeterminate, denticulate rachis less than 1 μm wide. Conidia hyaline, 1-celled, 2.3–3.2 $\times$ 1.6–2.3 μm ($\bar{x}$ = 2.7 $\times$ 2.1 μm , n=30), Q = 1.0–1.5 (L^m = 2.7, W^m = 2.1, Q^m = 1.3), globose to ellipsoidal, aseptate.

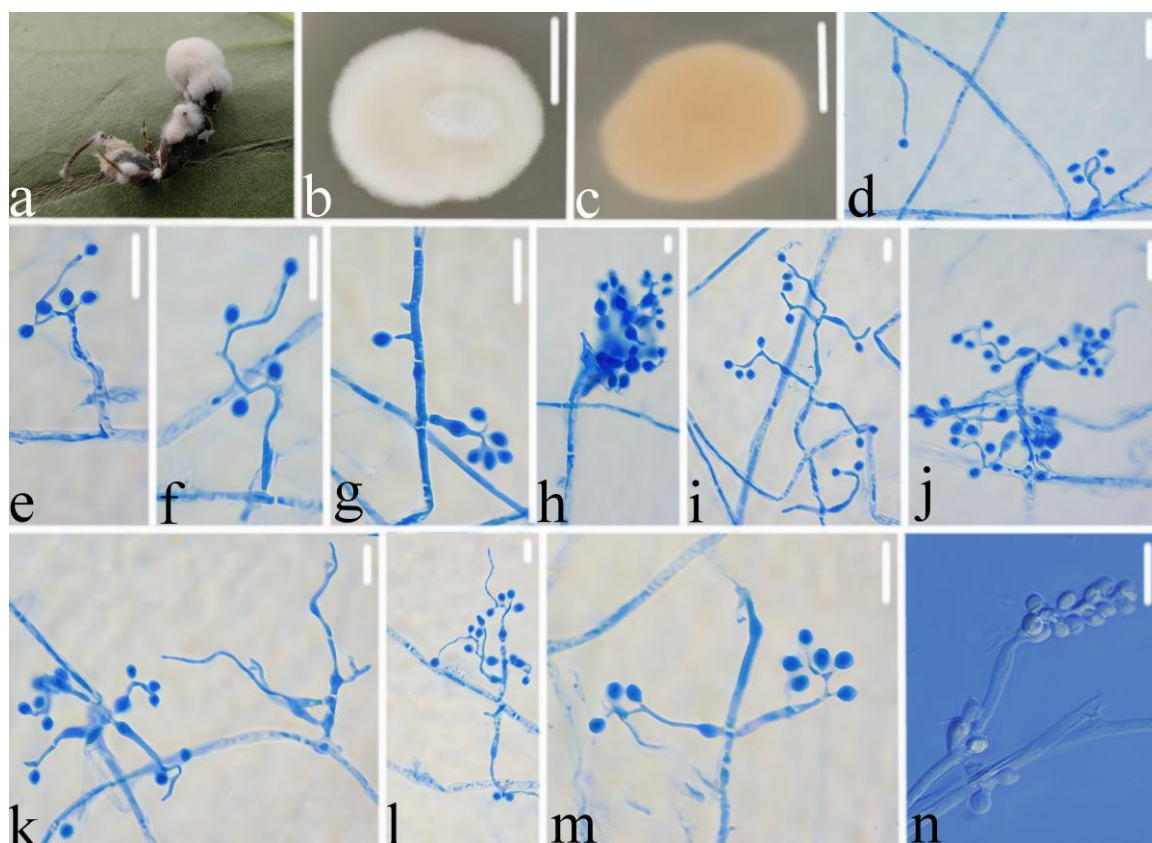


Figure 10 – *Beauveria tiankengensis* (KY07241, ex-type) a Infected ant. b–c Colonies on PDA culture media with upper (b) and reverse (c) views. d–m Phialides and conidia were stained with cotton blue. n Phialides and conidia. Scale bars: b–c = 10 mm, d–n = 10 μm .

Material examined – China, Guizhou Province, Guiyang City, Kaiyang County, Monkey-Ear Tiankeng (27°5'12.138"N, 107°40'48.42"E). On an ant (*Formicidae*), 6 April 2024, Wanhao Chen, GZAC KY0724 (holotype), KY07241 (ex-type), KY07242 (living culture).

Habitat – On the underside of leaves of broad-leaved plant species.

Notes – Phylogenetic analysis of combined dataset 3 (Fig. 3) and NCBI BLASTn comparisons revealed that *Beauveria tiankengensis* (KY07241 and KY07242) was grouped within the genus *Beauveria*. Maximum likelihood and Bayesian inference analyses placed within a well-supported clade (100% ML/1 PP) sister to *B. valliensis*. Compared with the typical characteristics, *B. tiankengensis* was distinguished from *B. valliensis* by its shorter conidiogenous cells (3.8–8.4 $\times$ 0.8–2.0 μm vs 7.7–12.3 $\times$ 1.9–2.7 μm) and the PHI test (Suppl. Fig. 1). The combined evidence

from morphological characteristics and robust molecular phylogenetic analyses substantiates the recognition of *B. tiankengensis* as a novel species.

Beauveria valliensis W.H. Chen, Y.F. Han & J.D. Liang, sp. nov.

Fig. 11

Index Fungorum number: 903365; Facesoffungi number: FoF 17471

Etymology – referring to its location, Shuangmen Valley, where the fungus was first discovered.

Description – Colonies on PDA reaching 38–41 mm diam. in 14 d at 25°C, non-odorous, aerial mycelium white, dense, velutinous, powdery while sporulating, white to yellowish white, reverse yellowish to pale brown. Prostrate hyphae smooth, septate, hyaline, 1.5–2.1 µm diam. Conidiogenous cells solitary or occurring in lateral clusters, base cylindrical to subspherical, 7.7–12.3 × 1.9–2.7 µm ($\bar{x}$ = 10.5 × 2.4 µm, n=30), apex with an indeterminate, denticulate rachis less than 1 µm wide. Conidia hyaline, 1-celled, 2.1–3.9 × 1.8–3.2 µm ($\bar{x}$ = 2.9 × 2.2 µm, n=30), Q = 1.1–1.3 (L^m = 2.7, W^m = 2.2, Q^m = 1.1), globose to ellipsoidal, aseptate.

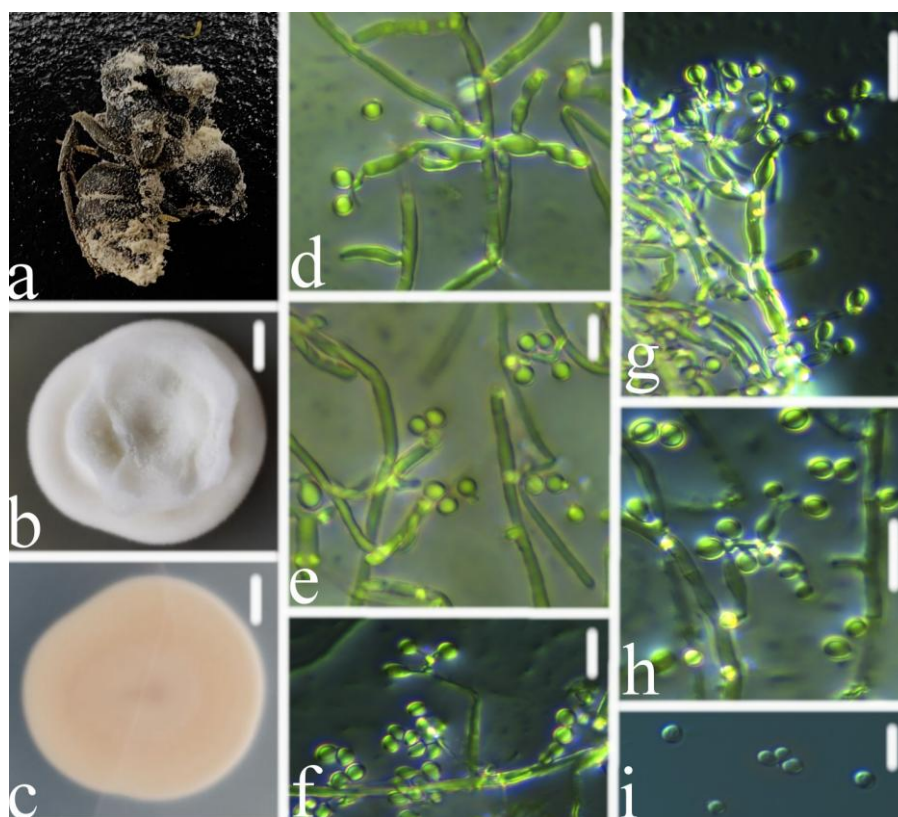


Figure 11 – *Beauveria valliensis* (SY09861, ex-type) a Infected ant. b–c Colonies on PDA culture media with upper (b) and reverse (c) views. d–i Phialides and conidia. Scale bars: b–c = 10 mm, d–i = 10 µm.

Material examined – China, Guizhou Province, Zunyi City, Suiyang County, Shuangmen Valley (28°1'39.05"N, 107°7'58.65"E). On an ant (*Formicidae*), 30 September 2023, Wanhao Chen, GZAC SY0986 (holotype), SY09861 (ex-type), SY09862 (living culture).

Habitat – On the underside of leaves of broad-leaved plant species.

Notes – Integrative molecular evidence (BLASTn and multi-gene phylogeny) classified *B. valliensis* within *Beauveria*, forming a maximally supported monophyletic group (100% ML/1 PP) with *B. tiankengensis*. Compared with the typical characteristics, *Beauveria valliensis* was distinguished from *B. tiankengensis* by its longer conidiogenous cells (7.7–12.3 × 1.9–2.7 µm vs 3.8–8.4 × 0.8–2.0 µm) and the PHI test (Suppl. Fig. 1). The distinct morphological characteristics coupled with robust phylogenetic support confirm *B. valliensis* as a new species.

Cordyceps Fr., *Observ. mycol.*, Cancellans Edn (Havniae) 2: 316 (1818)

Type species – *Cordyceps militaris* (L.) Fr. 1818

Notes – The family *Cordycipitaceae* was formally erected with *Cordyceps* designated as its type genus in the taxonomic revision by Sung et al. (2007). The taxonomic revisions proposed by Kepler et al. (2017) led to the rejection of several genera, including *Isaria*, *Microhilum* H.Y. Yip & A.C. Rath, *Phytocordyceps* C.H. Su & H.H. Wang, and *Evlachovaea* B.A. Borisov & Tarasov. Subsequent studies have continued to expand the genus *Cordyceps*, with numerous new species described in recent years, bringing the total number of recognized species to over 100. The *Cordyceps* resource in Guizhou Province demonstrates significant species richness. Initial surveys recorded 38 species (Song et al. 2004), with subsequent studies adding new taxa, though sampling remained largely forest-focused (Li et al. 2020, Peng et al. 2023). We describe four new valley-dwelling *Cordyceps* species, suggesting valley ecosystems merit targeted biodiversity exploration and protection.

Cordyceps miaolingensis W.H. Chen, Y.F. Han & J.D. Liang, sp. nov.

Fig. 12

Index Fungorum number: 903366; Facesoffungi number: FoF 17472

Etymology – referring to the location, Miaoling Mountains, where the fungus was first discovered.

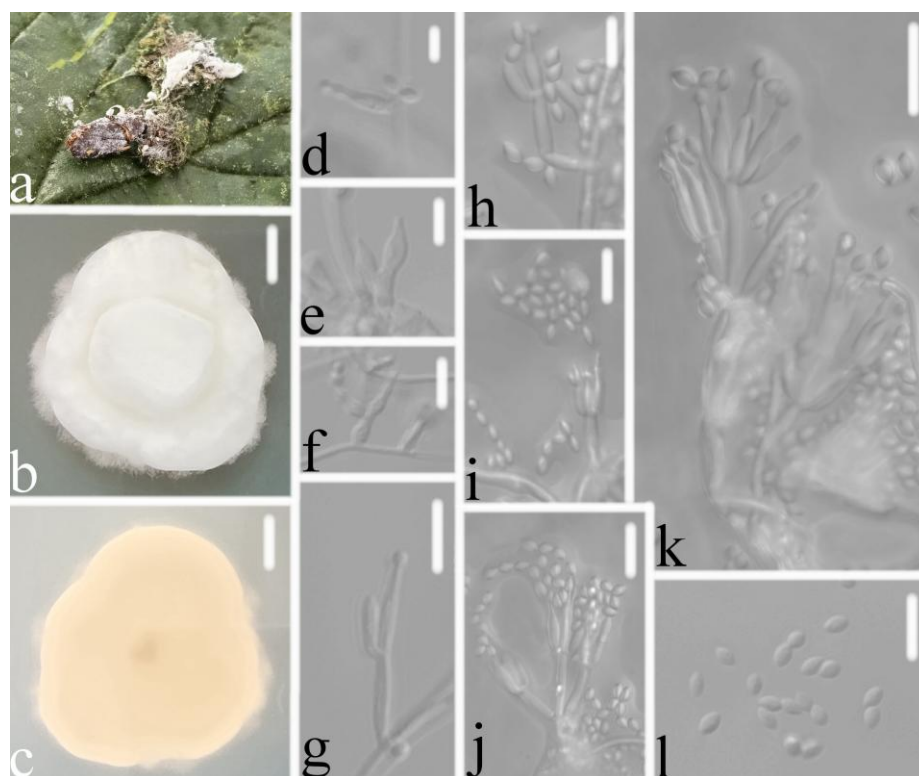


Figure 12 – *Cordyceps miaolingensis* (DY05101, ex-type) a Infected larva. b–c Colonies on PDA culture media with upper (b) and reverse (c) views. d–k Phialides and conidia. Scale bars: b–c = 10 mm, d–k = 10 μ m.

Description – Colonies on PDA reaching 31–33 mm diam. in 14 d at 25°C, yellowish to pale orange, consisting of a basal felt and cottony, floccose overgrowth, reverse yellowish to pale orange. Prostrate hyphae smooth, septate, hyaline, 2.2–2.3 μ m diam. Conidial structures consisting of erect conidiophores usually arising from the aerial hyphae, solitary or phialides in whorls of two. Phialides 7.6–10.4 $\times$ 1.9–2.8 μ m ($\bar{x}$ = 9.5 $\times$ 2.4 μ m, n=30), with a cylindrical basal portion, tapering

into a distinct neck. Conidia in chains, hyaline, 1-celled, ellipsoidal to fusiform, $2.8\text{--}3.4 \times 1.9\text{--}2.0\ \mu\text{m}$ ($\bar{x} = 3.1 \times 2.0\ \mu\text{m}$, $n=30$).

Material examined – China, Guizhou Province, Qiannan Buyei and Miao Autonomous Prefecture, Duyun City, Mayao River Valley ($26^{\circ}22'8.3748''\text{N}$, $107^{\circ}23'16.96''\text{E}$). On a larva (*Lepidoptera*), 1 May 2022, Wanhao Chen, GZAC DY0510 (holotype), DY05101 (ex-type), DY05102 (living culture).

Habitat – Near the road, buried in soil.

Notes – Phylogenetic analyses of concatenated dataset 2 (Fig. 2) and NCBI BLASTn comparisons revealed that *Cordyceps miaolingensis* (DY05101 and DY05102) was grouped with *Cordyceps* species. Maximum likelihood and Bayesian inference analyses placed it within a well-supported clade (100% ML/1 PP) sister to *C. cateniannulata* and *C. cicadae*, which was also supported by the phylogenetic analyses among *Cordyceps* species (Suppl. Fig. 4). Compared with the typical characteristics, *C. miaolingensis* was distinguished from *C. cateniannulata* by its longer phialides ($7.6\text{--}10.4 \times 1.9\text{--}2.8\ \mu\text{m}$ vs $3.0\text{--}8.0 \times 1.5\text{--}3.0\ \mu\text{m}$) and conidia in chains (Liang 1981). *Cordyceps miaolingensis* was distinguished from *C. cicadae* by its longer phialides ($7.6\text{--}10.4 \times 1.9\text{--}2.8\ \mu\text{m}$ vs $4.2\text{--}6.5 \times 2.5\text{--}3.5\ \mu\text{m}$) and smaller conidia (ellipsoidal to fusiform, $2.8\text{--}3.4 \times 1.9\text{--}2.0\ \mu\text{m}$ vs cylindrical, $3.5\text{--}8.0 \times 1.5\text{--}3.5\ \mu\text{m}$) (Mycobank, <https://mycobank.org/details/26/8110>). The combined evidence from morphological characteristics and robust molecular phylogenetic analyses substantiates the recognition of *C. miaolingensis* as a novel species.

Cordyceps pupicola W.H. Chen, Y.F. Han & J.D. Liang, sp. nov.

Fig. 13

Index Fungorum number: 903367; Facesoffungi number: FoF 17473

Etymology – referring to its pupa host in *Lepidoptera*.

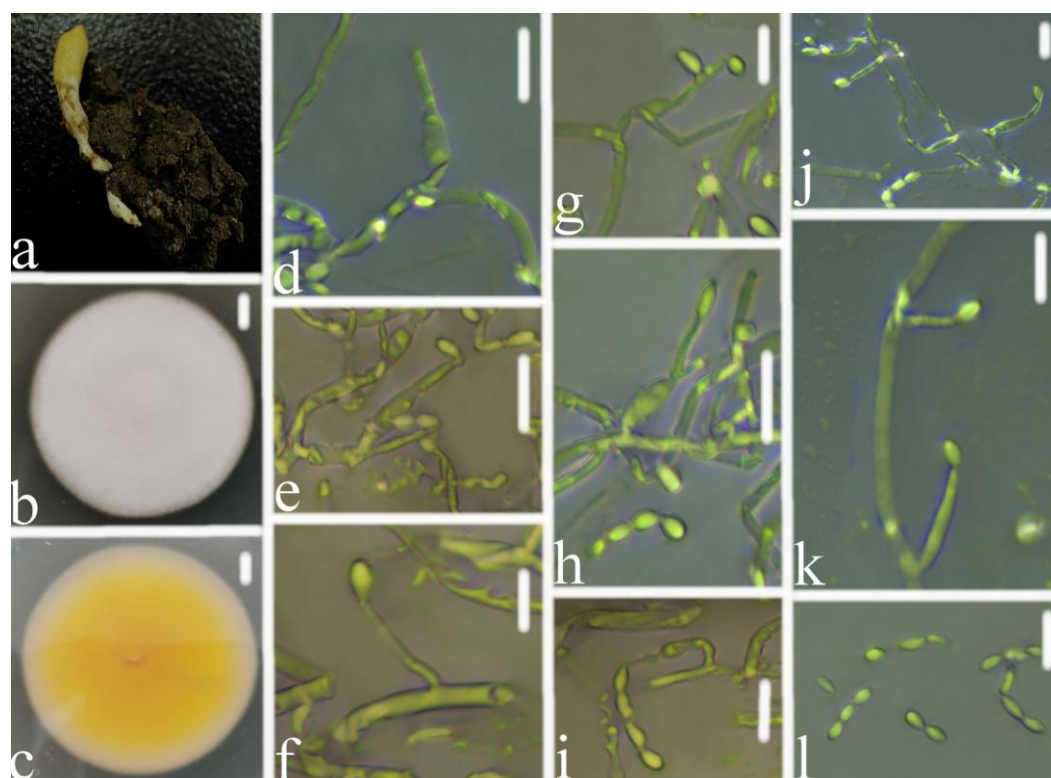


Figure 13 – *Cordyceps pupicola* (SY09561, ex-type) a Infected pupa. b–c Colonies on PDA culture media with upper (b) and reverse (c) views. d–l Phialides and conidia. Scale bars: b–c = 10 mm, d–l = 10 μm .

Description – Colonies on PDA reaching 31–33 mm diam. in 14 d at 25°C , yellowish to pale orange, consisting of a basal felt and cottony, floccose overgrowth, reverse yellowish to pale orange.

Prostrate hyphae smooth, septate, hyaline, 2.2–2.3 μm diam. Conidial structures consisting of erect conidiophores usually arising from the aerial hyphae, solitary or phialides in whorls of two. Conidiophores 9.6–20.2 $\times$ 1.2–2.3 μm . Phialides 7.6–10.4 $\times$ 1.9–2.8 μm ($\bar{x}$ = 9.2 $\times$ 2.1 μm , n=30), with a cylindrical basal portion, tapering into a distinct neck. Conidia in chains, hyaline, 1-celled, ellipsoidal to fusiform, 2.8–3.4 $\times$ 1.9–2.0 μm ($\bar{x}$ = 3.6 $\times$ 2.1 μm , n=30).

Material examined – China, Guizhou Province, Zunyi City, Suiyang County, Shuangmen Valley (28°1'39.05"N, 107°7'58.65"E). On a pupa (*Lepidoptera*), 30 September 2023, Wanhao Chen, GZAC SY0956 (holotype), SY09561 (ex-type), SY09562 (living culture); On a pupa (*Lepidoptera*), 30 September 2023, Wanhao Chen, SY0959 (specimen), SY09591, SY09592 (living culture).

Habitat – Near the road, buried in soil.

Notes – Molecular characterization through NCBI BLASTn analysis and multi-locus phylogenetic reconstruction (dataset 2, Fig. 2) revealed that *Cordyceps pupicola* (SY09591 and SY09592) was grouped with *Cordyceps* species and have close relationship with *C. fumosorosea* (Wize) Kepler et al. which was also supported by the phylogenetic analyses among *Cordyceps* species (Suppl. Fig. 4). Compared with the typical characteristics, *C. pupicola* was distinguished from *C. fumosorosea* by its shorter conidiophores (9.6–20.2 $\times$ 1.2–2.3 μm vs up to 100 μm) and the shape of conidia (ellipsoidal to fusiform vs cylindrical to fusiform) (<https://mycobank.org/details/26/8118>). The combined evidence from morphological characteristics and robust molecular phylogenetic analyses substantiates the recognition of *C. pupicola* as a novel species.

Cordyceps suiyangensis W.H. Chen, Y.F. Han & J.D. Liang, sp. nov.

Fig. 14

Index Fungorum number: 903368; Facesoffungi number: FoF 17474

Etymology – referring to the location, Suiyang County, where the fungus was first discovered.

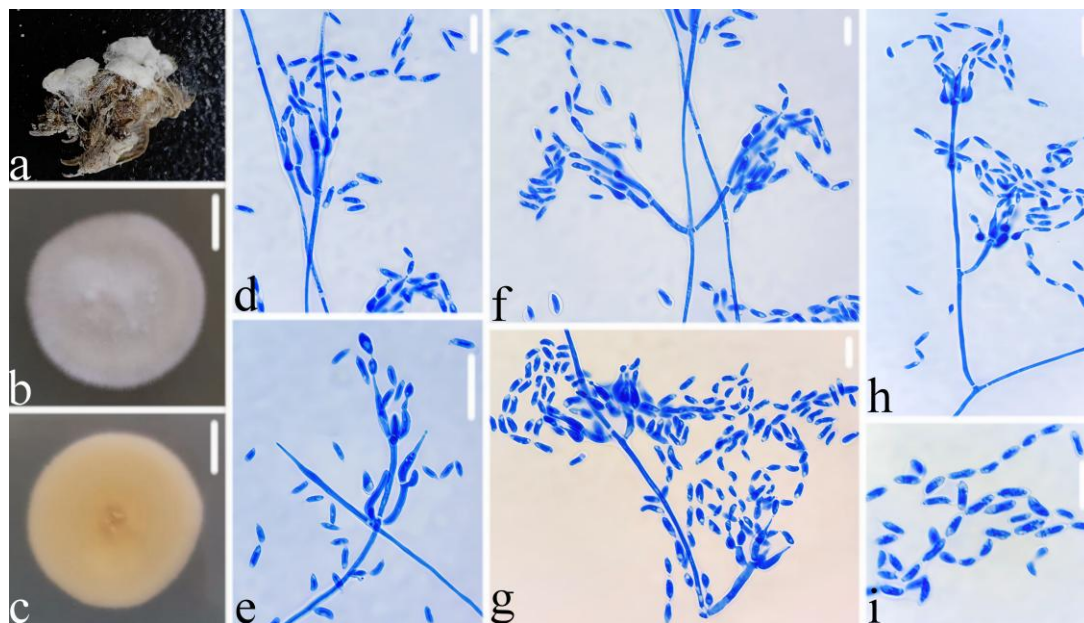


Figure 14 – *Cordyceps suiyangensis* (SY09851, ex-type) a Infected larva. b–c Colonies on PDA culture media with upper (b) and reverse (c) views. d–i Phialides and conidia were stained with cotton blue. Scale bars: b–c = 10 mm, d–i = 10 μm .

Description – Colonies on PDA reaching 27–29 mm diam. in 14 d at 25°C, yellowish to pale orange, consisting of a basal felt and cottony, floccose overgrowth, reverse yellowish to pale orange. Prostrate hyphae smooth, septate, hyaline, 1.5–2.1 μm diam. Conidial structures consisting of erect

conidiophores usually arising from the aerial hyphae, solitary or phialides in whorls of two. Phialides $4.8\text{--}9.4 \times 2.0\text{--}2.6 \mu\text{m}$ ($\bar{x} = 7.0 \times 2.3 \mu\text{m}$, $n=30$), with a cylindrical basal portion, tapering into a distinct neck. Conidia in chains, hyaline, 1-celled, cylindrical, $3.6\text{--}6.9 \times 1.3\text{--}2.0 \mu\text{m}$ ($\bar{x} = 5.2 \times 1.6 \mu\text{m}$, $n=30$).

Material examined – China, Guizhou Province, Zunyi City, Suiyang County, Shuangmen Valley ($28^{\circ}1'39.05''\text{N}$, $107^{\circ}7'58.65''\text{E}$). On a larva (*Lepidoptera*), 30 September 2023, Wanhao Chen, GZAC SY0985 (holotype), SY09851 (ex-type), SY09852 (living culture).

Habitat – On the underside of leaves of broad-leaved plant species.

Notes – Phylogenetic analyses of concatenated dataset 2 (Fig. 2) and NCBI BLASTn comparisons revealed that *Cordyceps suiyangensis* (SY09851 and SY09852) was grouped within the genus *Cordyceps*. Maximum likelihood and Bayesian inference analyses revealed a strongly supported clade (100% ML/1 PP) comprising *C. suiyangensis* and its closest relative *C. tiangkengensis*, which was also supported by the phylogenetic analyses among *Cordyceps* species (Suppl. Fig. 4). Compared with the typical characteristics, *C. suiyangensis* was distinguished from *C. tiangkengensis* by its shorter phialides ($4.8\text{--}9.4 \times 2.0\text{--}2.6 \mu\text{m}$ vs $7.1\text{--}12.2 \times 1.9\text{--}2.5 \mu\text{m}$) and larger conidia (cylindrical, $3.6\text{--}6.9 \times 1.3\text{--}2.0 \mu\text{m}$ vs fusiform, $4.1\text{--}5.1 \times 1.8\text{--}2.7 \mu\text{m}$) (Chen et al. 2022b). The distinct morphological characteristics coupled with robust phylogenetic support confirm *C. suiyangensis* as a new species.

Cordyceps vallis W.H. Chen, Y.F. Han & J.D. Liang, sp. nov.

Fig. 15

Index Fungorum number: 903369; Facesoffungi number: FoF 17475

Etymology – referring to its location, Shuangmen Valley, where the fungus was first discovered.

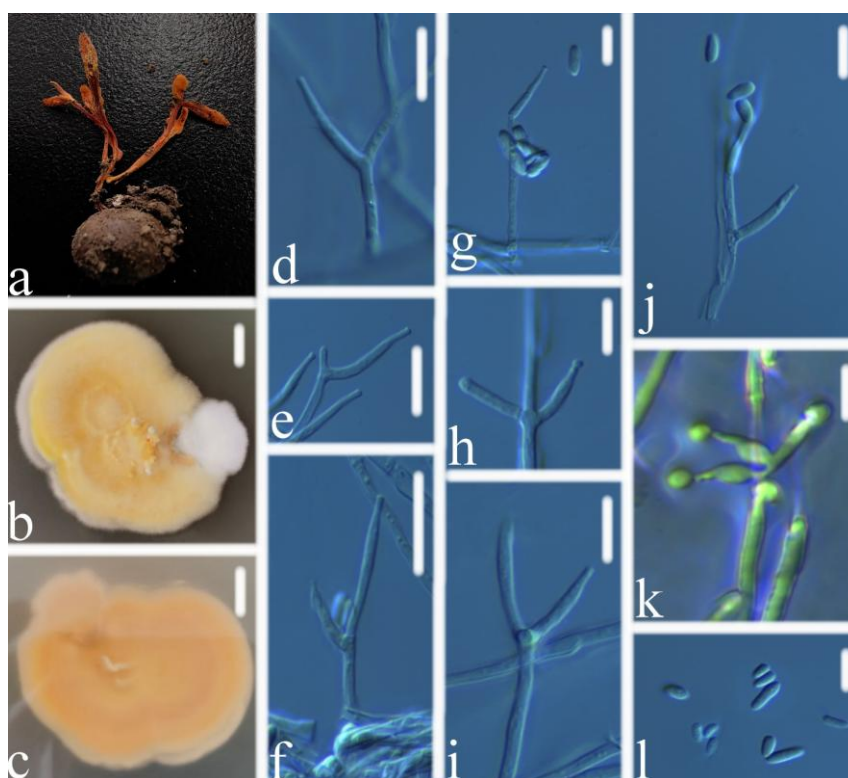


Figure 15 – *Cordyceps vallis* (SY09171, ex-type) a Infected pupa. b–c Colonies on PDA culture media with upper (b) and reverse (c) views. d–l Phialides and conidia. Scale bars: b–c = 10 mm, d–l = 10 μm .

Description – Colonies on PDA reaching 35–44 mm diam. in 14 d at 25°C , yellowish to pale orange, consisting of a basal felt and cottony, floccose overgrowth, reverse yellowish to pale orange.

Prostrate hyphae smooth, septate, hyaline, 1.2–1.9 μm diam. Conidial structures consisting of erect conidiophores usually arising from the aerial hyphae, solitary or phialides in whorls of two. Phialides 8.9–12.6 $\times$ 1.4–2.0 μm ($\bar{x}$ = 12.5 $\times$ 1.7 μm , n=30), with a cylindrical basal portion, tapering into a distinct neck. Conidia in chains, hyaline, 1-celled, cylindrical, 5.1–8.5 $\times$ 2.1–2.5 μm ($\bar{x}$ = 6.3 $\times$ 2.3 μm , n=30).

Material examined – China, Guizhou Province, Zunyi City, Suiyang County, Shuangmen Valley (28°1'39.05"N, 107°7'58.65"E). On a cocoon (*Lepidoptera*), 30 September 2023, Wanhao Chen, GZAC SY0917 (holotype), SY09171 (ex-type), SY09172 (living culture).

Habitat – Near the road, buried in soil.

Notes – Phylogenetic analyses of concatenated dataset 2 (Fig. 2) and NCBI BLASTn comparisons revealed that *Cordyceps vallis* (SY09171 and SY09172) was grouped within the genus *Cordyceps*. Maximum likelihood and Bayesian inference revealed a strongly supported clade (100% ML/1 PP) comprising *C. vallis* and its closest relative *C. cocoonihabita*, which was also supported by the phylogenetic analyses among *Cordyceps* species (Suppl. Fig. 4). Compared with the typical characteristics, *C. vallis* was distinguished from *C. cocoonihabita* by its larger conidia (cylindrical, 5.1–8.5 $\times$ 2.1–2.5 μm vs oval to fusiform, 1.6–3.0 $\times$ 0.7–1.5 μm) (Wang et al. 2020). The integrative assessment of both morphological characteristics and genomic data provides conclusive support for establishing *C. vallis* as a new species.

Dimorphspora W.H. Chen, Y.F. Han & J.D. Liang gen. nov.

Index Fungorum number: 903415; Facesoffungi number: FoF 17456

Type species – *Dimorphspora sinensis* W.H. Chen, Y.F. Han & J.D. Liang

Etymology – referring to its two types of conidia in this genus.

Description – Colonies on PDA, white, reverse yellowish, pale gray to brownish. Conidiophores mononematous, usually arising from aerial hyphae, phialides solitary or in groups of two. Phialides emerging laterally from hyphae, forming a compact hymenium, abruptly narrowing into a neck. Conidia one-celled, hyaline, macroconidia nuciformis, microconidia fusiform. Octahedral crystals absent.

Notes – Molecular phylogenetic reconstruction placed *Dimorphspora* in a well-supported monophyletic group (Fig. 2), showing closest affinity to *Parengyodontium* while maintaining distinct separation. However, *Dimorphspora* species show significant different from *Parengyodontium* species by its two types of conidia and absent of zigzag rachides in the phialides (conidiogenous cells). Among the family *Cordycipitaceae*, *Dimorphspora* is closely related to the genera *Akanthomyces*, *Arachnidicola*, *Corniculantispora*, *Corpulentispora*, *Flavocillium*, *Gamszarea*, *Neogamszarella*, *Zarea* and *Zouia* based on the lecanicillium-like conidiogenous structures. Compared with the typical characteristics, *Dimorphspora* species was significant different from *Akanthomyces*, *Arachnidicola* and *Zouia* species by its two types of conidia. *Dimorphspora* species was significant different from *Corniculantispora* and *Zarea* species by its nuciformis or fusiform conidia and absent of octahedral crystals. *Dimorphspora* species was significant different from *Corpulentispora* and *Flavocillium* species by its spider hosts and nuciformis or fusiform conidia. *Dimorphspora* species was significant different from *Gamszarea* and *Neogamszarella* species by its absent of a cluster of denticles on the conidiogenous cells. The combined evidence from distinctive morphological characteristics and robust molecular phylogenetic analyses substantiates the establishment of *Dimorphspora* as a novel genus.

Dimorphspora sinensis W.H. Chen, Y.F. Han & J.D. Liang, sp. nov.

Fig. 16

Index Fungorum number: 903370; Facesoffungi number: FoF 17476

Etymology – referring to its location, China, where the fungus was first discovered.

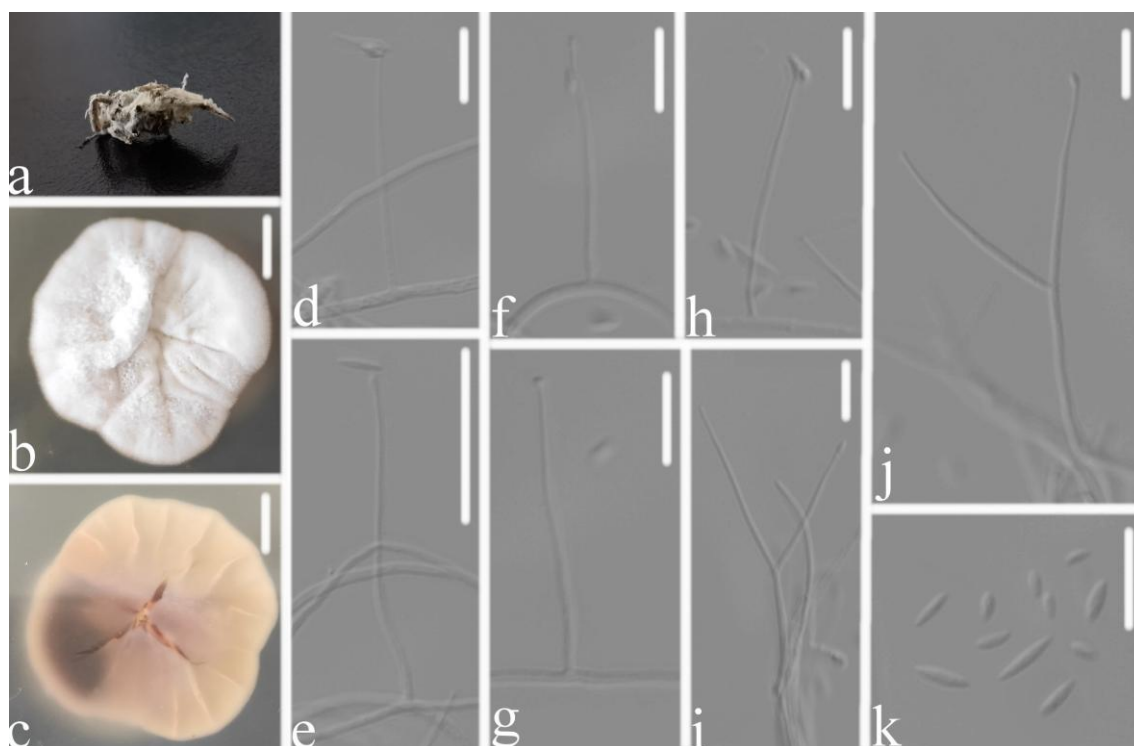


Figure 16 – *Dimorphospora sinensis* (ZY06451, ex-type) a Infected spider. b–c Colonies on PDA culture media with upper (b) and reverse (c) views. d–k Phialides and conidia. Scale bars: b–c = 10 mm, d–k = 10 μ m.

Description – Colonies on PDA reaching 35–36 mm diam. in 14 d at 25°C, white, consisting of a basal felt and cottony, floccose overgrowth, reverse yellowish, pale gray to brownish. Prostrate hyphae smooth, septate, hyaline, 1.3–2.0 μ m diam. Conidial structures consisting of erect conidiophores usually arising from the aerial hyphae, solitary or phialides in whorls of two. Phialides 18.3–27.6 $\times$ 1.1–1.8 μ m ($\bar{x}$ = 23.6 $\times$ 1.4 μ m, n=30), with a cylindrical basal portion, tapering into a distinct neck. Conidia hyaline, 1-celled, macroconidia nuciformis, 5.0–7.0 $\times$ 1.3–1.6 μ m ($\bar{x}$ = 5.7 $\times$ 1.4 μ m, n=30); microconidia fusiform, 2.6–3.1 $\times$ 1.4–1.7 μ m ($\bar{x}$ = 3.0 $\times$ 1.5 μ m, n=30).

Material examined – China, Guizhou Province, Zunyi City, Honghuagang District, Dabanshui National Forest Park (27°46'35.904"N, 106°48'30.89"E). On a dead spider (*Araneae*), 3 June 2022, Wanhao Chen, GZAC ZY0645 (holotype), ZY06451 (ex-type), ZY06452 (living culture).

Habitat – Near the road, located on or under the rock.

Notes – Phylogenetic analysis of concatenated dataset 2 (Fig. 2) confirmed the taxonomic placement of *Dimorphospora sinensis* within the newly established genus *Dimorphospora*. Phylogenetic analysis placed the taxon in a distinct clade sister to *Parengyodontium* species, with maximum statistical support (100% ML/0.99 PP). Compared with the typical characteristics, *Dimorphospora sinensis* was distinguished from *Parengyodontium* species by its two types of conidia and absent of zigzag rachides in the phialides (conidiogenous cells) (Tsang et al. 2016). The combined evidence from morphological characteristics and robust molecular phylogenetic analyses substantiates the recognition of *Dimorphospora sinensis* as a novel species, necessitating the establishment of the new genus *Dimorphospora*.

Gamszarella Crous, Persoonia 51: 391 (2023)

Type species – *Gamszarella buffelskloofina* Crous 2023

Notes – Crous et al. (2023) established the genus *Gamszarella*, with *G. buffelskloofina* designated as the type species, along with two additional taxa: *G. antillana* (R.F. Castañeda &

G.R.W. Arnold) Crous and *G. magnispora* (Z.F. Zhang & L. Cai) Crous. Khonsanit et al. (2024) erected the new genus *Corpulentispora* Khons. et al. to accommodate *Gamszarella magnispora*. Subsequently, Chen et al. (2025) proposed *Neogamszarella* W.H. Chen et al. for *Gamszarella antillana*, while describing two additional species within *Gamszarella*, *Gamszarella sinensis* W.H. Chen et al. and *G. vallensis* W.H. Chen et al. Thus, *Gamszarella* consists of 3 species. Our study expands this taxonomic framework by introducing three new *Gamszarella* species.

Gamszarella araneicola W.H. Chen, Y.F. Han & J.D. Liang, sp. nov.

Fig. 17

Index Fungorum number: 903371; Facesoffungi number: FoF 17477

Etymology – referring to its host spider.

Description – Colonies on PDA reaching 45–47 mm diam. in 14 d at 25°C, white, consisting of a basal felt and cottony, floccose overgrowth, reverse yellowish. Prostrate hyphae smooth, septate, hyaline, 1.3–1.7 µm diam. Conidial structures consisting of erect conidiophores usually arising from the aerial hyphae, solitary or conidiogenous cells in whorls of two to three. Conidiogenous cells 27.7–36.9 × 1.5–1.9 µm ($\bar{x}$ = 33.5 × 1.7 µm, n=30), with a cylindrical basal portion, bearing numerous denticles, tapering into a distinct neck. Conidia hyaline, 1-celled, fusiform to ellipsoidal, 3.5–6.0 × 2.1–2.3 µm ($\bar{x}$ = 4.8 × 2.2 µm, n=30).

Material examined – China, Guizhou Province, Qiannan Buyei and Miao Autonomous Prefecture, Duyun City, Mayao River Valley (26°22'8.3748"N, 107°23'16.96"E). On a spider (*Araneae*), 1 May 2022, Wanhao Chen, GZAC DY0561 (holotype), DY05611 (ex-type), DY05612 (living culture).

Habitat – On the underside of leaves of broad-leaved plant species.

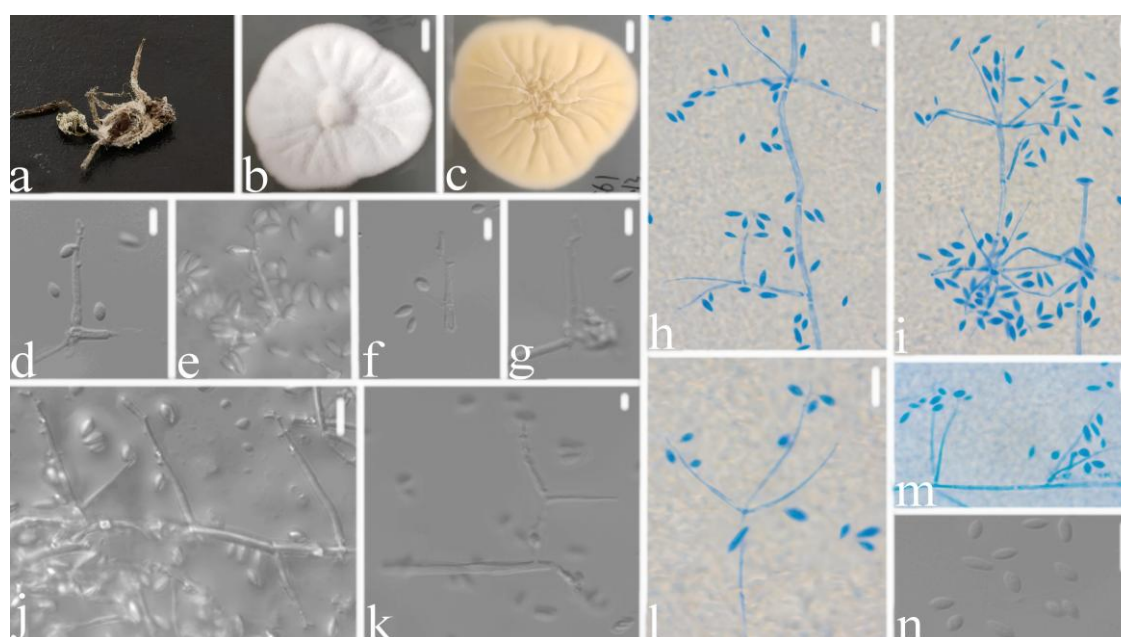


Figure 17 – *Gamszarella araneicola* (DY05611, ex-type) a Infected spider. b–c Colonies on PDA culture media with upper (b) and reverse (c) views. d–g, j, k, n Conidiogenous cells and conidia. h, i, l, m Conidiogenous cells and conidia were stained with cotton blue. Scale bars: b–c = 10 mm, d–n = 10 µm.

Notes – Phylogenetic analyses of concatenated dataset 2 (Fig. 2) and NCBI BLASTn comparisons revealed that *Gamszarella araneicola* (DY05611 and DY05612) was grouped within the genus *Gamszarella*. Maximum likelihood analysis revealed a strongly supported clade (92% ML) comprising *G. araneicola* and its closest relative *G. formicae*. Compared with the typical characteristics, *G. araneicola* was distinguished from *G. formicae* by its larger conidia (3.5–6.0 × 2.1–2.3 µm vs 2.2–3.8 × 1.7–2.5 µm) and spider host. The combined evidence from morphological

characteristics and robust molecular phylogenetic analyses substantiates the recognition of *G. araneicola* as a novel species.

Gamszarella formicae W.H. Chen, Y.F. Han & J.D. Liang, sp. nov.

Fig. 18

Index Fungorum number: 903372; Facesoffungi number: FoF 17478

Etymology – referring to its host ant.

Description – Colonies on PDA reaching 43–44 mm diam. in 14 d at 25°C, white, consisting of a basal felt and cottony, floccose overgrowth, reverse yellowish. Prostrate hyphae smooth, septate, hyaline, 0.9–1.2 µm diam. Conidial structures consisting of erect conidiophores usually arising from the aerial hyphae, solitary or conidiogenous cells in whorls of two to three. Conidiogenous cells 13.7–21.3 × 1.3–2.3 µm ($\bar{x}$ = 18.5 × 1.7 µm, n=30), with a cylindrical basal portion, bearing numerous denticles, tapering into a distinct neck. Conidia hyaline, 1-celled, fusiform to ellipsoidal, 2.2–3.8 × 1.7–2.5 µm ($\bar{x}$ = 3.2 × 2.0 µm, n=30).

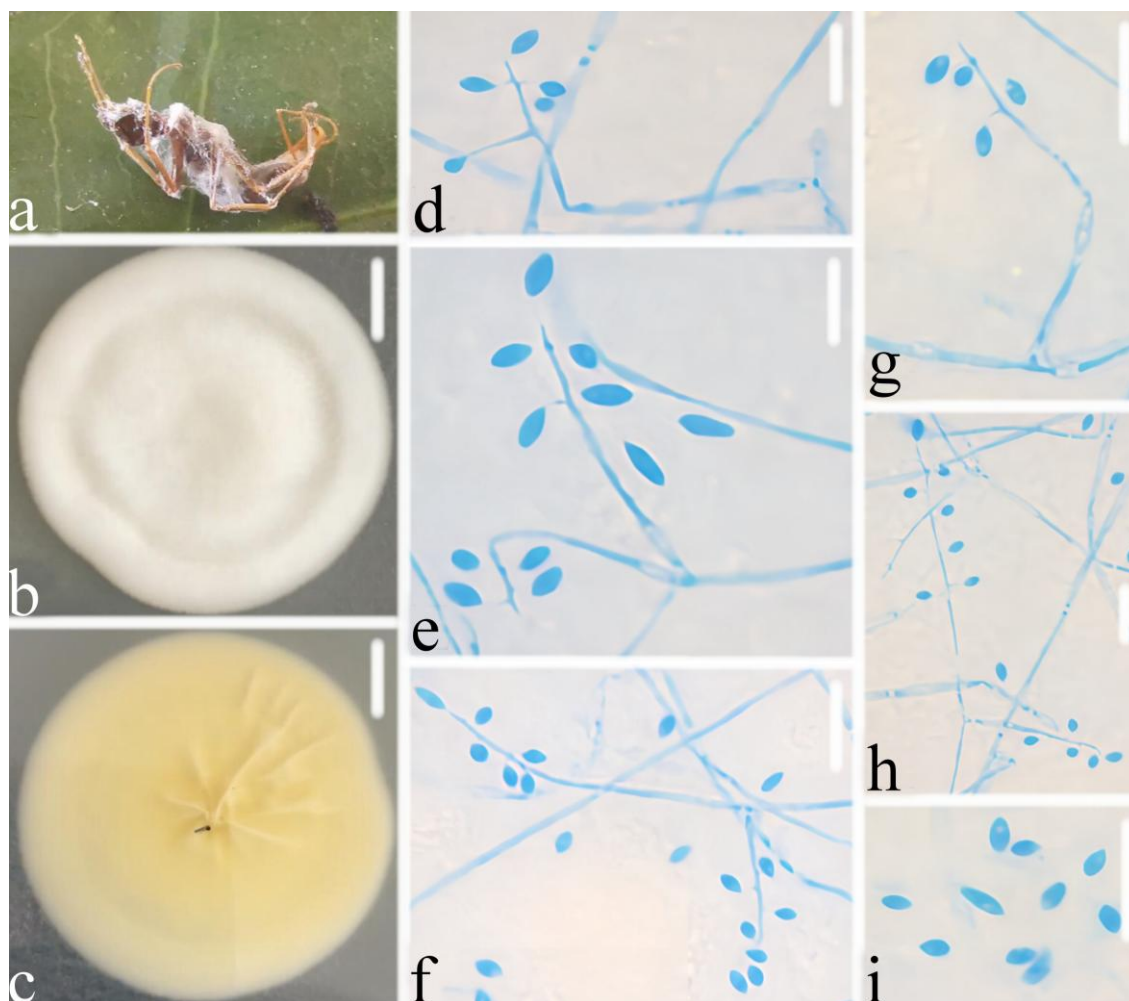


Figure 18 – *Gamszarella formicae* (DY09591, ex-type) a Infected ant. b–c Colonies on PDA culture media with upper (b) and reverse (c) views. d–i Conidiogenous cells and conidia were stained with cotton blue. Scale bars: b–c = 10 mm, d–i = 10 µm.

Material examined – China, Guizhou Province, Qiannan Buyei and Miao Autonomous Prefecture, Duyun City, Mayao River Valley (26°22'8.3748"N, 107°23'16.96"E). On an ant (*Formicidae*), 4 September 2021, Wanhao Chen, GZAC DY0959 (holotype), DY09591 (ex-type), DY09592 (living culture).

Habitat – On the underside of leaves of broad-leaved plant species.

Notes – Phylogenetic analyses of concatenated dataset 2 (Fig. 2) and NCBI BLASTn comparisons revealed that *Gamszarella formicae* (DY09591 and DY09592) was grouped with *Gamszarella* species. Maximum likelihood analysis revealed a strongly supported clade (92% ML) comprising *G. formicae* and its closest relative *G. araneicola*. Compared with the typical characteristics, *G. formicae* was distinguished from *G. araneicola* by its smaller conidia ($2.2\text{--}3.8 \times 1.7\text{--}2.5 \mu\text{m}$ vs $3.5\text{--}6.0 \times 2.1\text{--}2.3 \mu\text{m}$) and ant host. The combined evidence from distinctive morphological characteristics and robust molecular phylogenetic analyses substantiates the recognition of *G. formicae* as a novel species.

Gamszarella pupicola W.H. Chen, Y.F. Han & J.D. Liang, sp. nov.

Fig. 19

Index Fungorum number: 903373; Facesoffungi number: FoF 17479

Etymology – referring to its pupa host.

Description – Colonies on PDA reaching 47–49 mm diam. in 14 d at 25°C, white, consisting of a basal felt and cottony, floccose overgrowth, reverse yellowish. Prostrate hyphae smooth, septate, hyaline, $1.8\text{--}2.5 \mu\text{m}$ diam. Conidial structures consisting of erect conidiophores usually arising from the aerial hyphae, solitary or conidiogenous cells in whorls of two to three. Conidiogenous cells $10.0\text{--}23.4 \times 0.7\text{--}1.0 \mu\text{m}$ ($\bar{x} = 18.1 \times 0.9 \mu\text{m}$, $n=30$), with a cylindrical basal portion, bearing numerous denticles, tapering into a distinct neck. Conidia hyaline, 1-celled, fusiform to ellipsoidal, $2.5\text{--}4.2 \times 1.0\text{--}2.1 \mu\text{m}$ ($\bar{x} = 3.2 \times 1.7 \mu\text{m}$, $n=30$).

Material examined – China, Guizhou Province, Guiyang City, Wudang District, Bala Valley ($26^{\circ}45'7.0344''\text{N}$, $106^{\circ}58'57.09''\text{E}$). On a pupa (*Lepidoptera*), 5 April 2024, Wanhao Chen, GZAC WD0411 (holotype), WD04111 (ex-type), WD04112 (living culture).

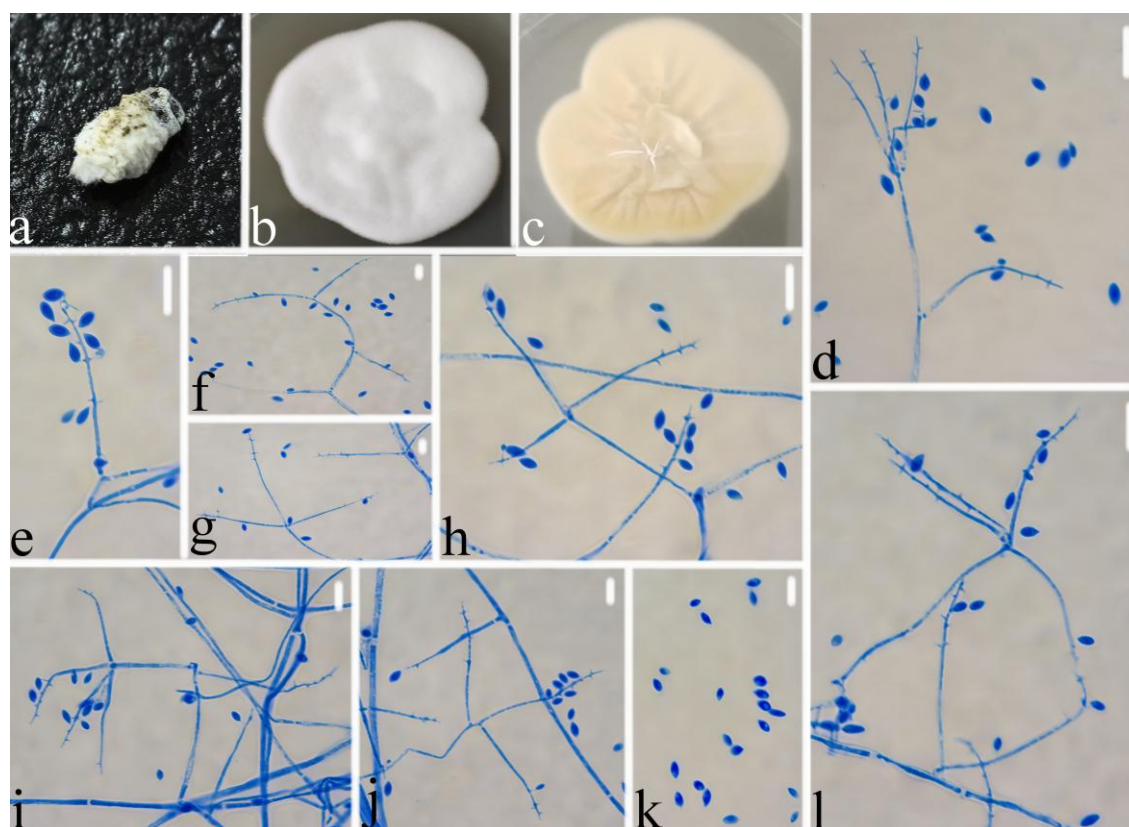


Figure 19 – *Gamszarella pupicola* (WD04111, ex-type) a Infected pupa. b–c Colonies on PDA culture media with upper (b) and reverse (c) views. d–l Conidiogenous cells and conidia were stained with cotton blue. Scale bars: b–c = 10 mm, d–l = 10 μm .

Habitat – On the underside of leaves of broad-leaved plant species.

Notes – Molecular analyses including NCBI BLASTn comparisons and multi-locus phylogenetic reconstruction (dataset 2, Fig. 2) revealed that *Gamszarella pupicola* (WD04111 and WD04112) was grouped within the genus *Gamszarella*, forming a distinct clade with *G. vallensis*. Compared with the typical characteristics, *G. pupicola* was distinguished from *G. vallensis* by its longer conidiogenous cells ($10.0\text{--}23.4 \times 0.7\text{--}1.0\ \mu\text{m}$ vs $3.8\text{--}5.4 \times 1.3\text{--}1.9\ \mu\text{m}$) and pupa host (Chen et al. 2025). Distinct morphological characteristics coupled with robust phylogenetic support confirm *G. pupicola* as a new species.

Lecanicillium W. Gams & Zare, Nova Hedwigia 72: 50 (2001)

Type species – *Lecanicillium lecanii* (Zimm.) Zare & W. Gams 2001

Notes – Zare & Gams (2001) introduced the genus *Lecanicillium* for the entomogenous and fungicolous species in *Verticillium* section *Prostrata*, and later rejected by Kepler et al. (2017) based on phylogenetic analyses of *Cordycipitaceae*. Khonsanit et al. (2024) subsequently reinstated the genus *Lecanicillium*, recognizing 17 valid species. Our study expands this taxonomic framework by describing three additional novel species.

Lecanicillium araneae W.H. Chen, Y.F. Han & J.D. Liang, sp. nov.

Fig. 20

Index Fungorum number: 903374; Facesoffungi number: FoF 17480

Etymology – referring to its spider host.

Description – Colonies on PDA reaching 23–24 mm diam. in 14 d at 25°C, white to purple, consisting of a basal felt and cottony, floccose overgrowth, reverse yellowish. Prostrate hyphae smooth, septate, hyaline, 1.3–1.5 μm diam. Conidial structures consisting of erect conidiophores usually arising from the aerial hyphae, solitary or verticillium-like with phialides in whorls of two to three. Phialides $13.2\text{--}22.2 \times 1.2\text{--}1.8\ \mu\text{m}$ ($\bar{x} = 18.2 \times 1.8\ \mu\text{m}$, $n=30$), with a cylindrical basal portion, tapering into a distinct neck. Conidia in chains, hyaline, cylindrical to fusiform, 1-celled, $2.8\text{--}6.2 \times 1.3\text{--}2.2\ \mu\text{m}$ ($\bar{x} = 3.9 \times 1.6\ \mu\text{m}$, $n=30$).

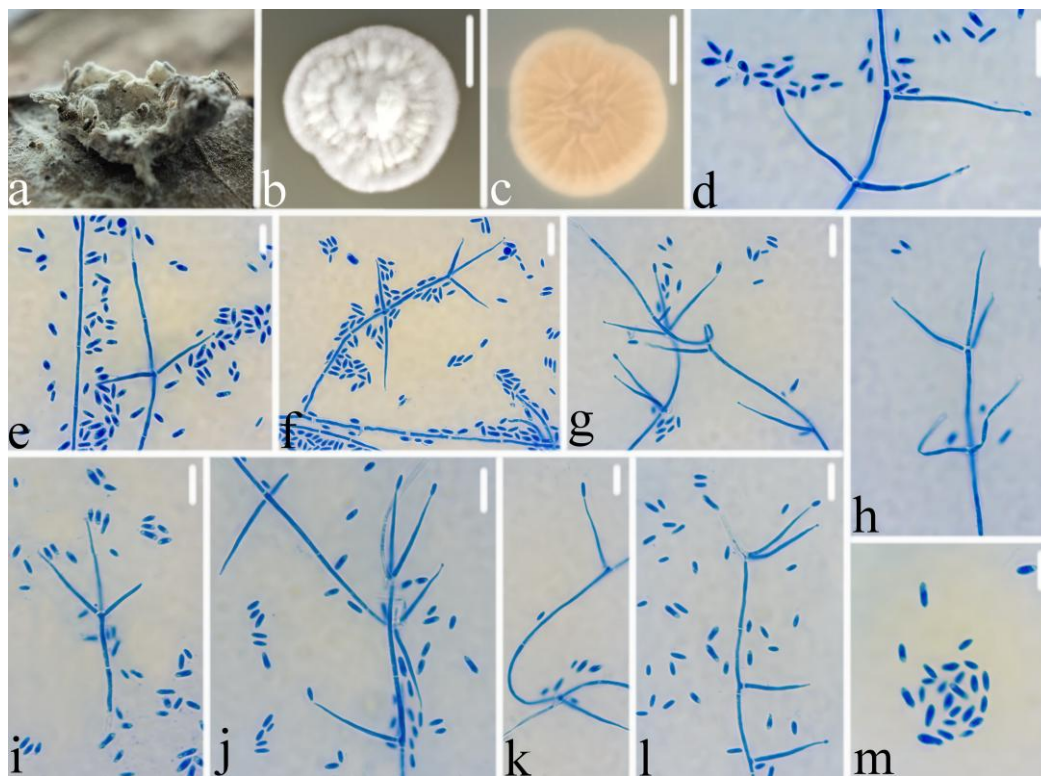


Figure 20 – *Lecanicillium araneae* (KY04081, ex-type) a Infected spider. b–c Colonies on PDA culture media with upper (b) and reverse (c) views. d–m Phialides and conidia were stained with cotton blue. Scale bars: b–c = 10 mm, d–m = 10 μm .

Material examined – China, Guizhou Province, Guiyang City, Kaiyang County, Monkey-Ear Tiankeng (27°5'12.138"N, 107°40'48.42"E). On a spider (*Araneae*), 6 April 2024, Wanhao Chen, GZAC KY0408 (holotype), KY04081 (ex-type), KY04082 (living culture).

Habitat – On the underside of leaves of broad-leaved plant species.

Notes – Phylogenetic analyses of concatenated dataset 2 (Fig. 2) and NCBI BLASTn comparisons revealed that *Lecanicillium araneae* (KY04081 and KY04082) was grouped within the genus *Lecanicillium*, forming a maximally supported clade (100% ML/1 PP) with *L. uredinophilum*, which was also supported by the phylogenetic analyses among *Lecanicillium* species (Suppl. Fig. 3). Compared with the typical characteristics, *L. araneae* was distinguished from *L. uredinophilum* by its shorter phialides [$13.2\text{--}22.2 \times 1.2\text{--}1.8 \mu\text{m}$ vs $20.0\text{--}60.0 \times 1.0\text{--}2.5 (-3.0) \mu\text{m}$] (Park et al. 2015). The combined morphological and molecular phylogenetic evidence substantiates the recognition of *L. araneae* as a novel species.

Lecanicillium pantatomidae W.H. Chen, Y.F. Han & J.D. Liang, sp. nov.

Fig. 21

Index Fungorum number: 903375; Facesoffungi number: FoF 17481

Etymology – referring to its host stink bug in the family *Pantatomidae*.

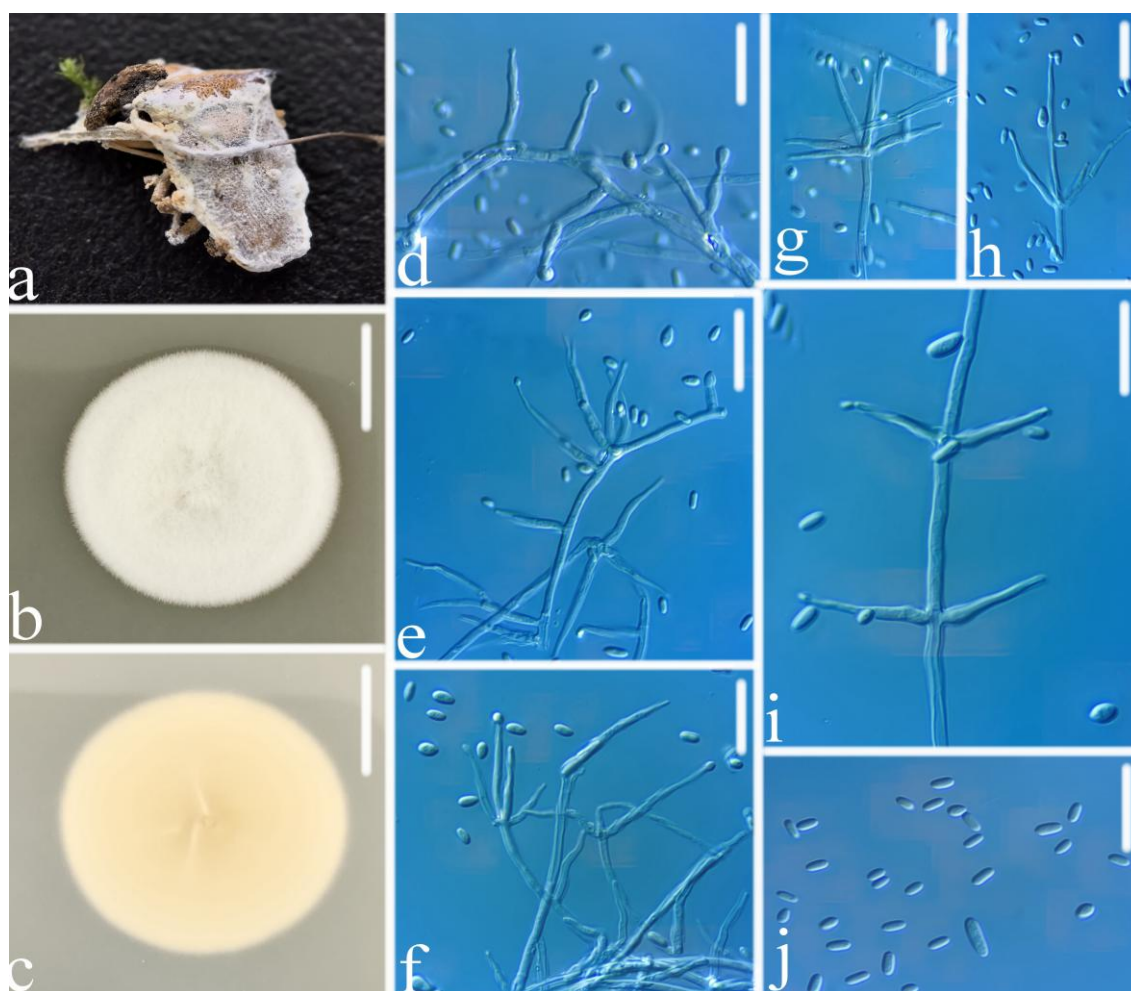


Figure 21 – *Lecanicillium pantatomidae* (DY45191, ex-type) a Infected stink bug. b–c Colonies on PDA culture media with upper (b) and reverse (c) views. d–j Phialides and conidia. Scale bars: b–c = 10 mm, d–j = 10 μm .

Description – Colonies on PDA reaching 22–23 mm diam. in 14 d at 25°C, white to purple, consisting of a basal felt and cottony, floccose overgrowth, reverse yellowish. Prostrate hyphae smooth, septate, hyaline, 0.9–1.7 μm diam. Conidial structures consisting of erect conidiophores

usually arising from the aerial hyphae, solitary or verticillium-like with phialides in whorls of two to three. Phialides $8.2\text{--}11.8 \times 1.3\text{--}1.8 \mu\text{m}$ ($\bar{x} = 9.8 \times 1.4 \mu\text{m}$, $n=30$), with a cylindrical basal portion, tapering into a distinct neck. Conidia in chains, hyaline, cylindrical to fusiform, 1-celled, $2.1\text{--}4.3 \times 1.3\text{--}1.9 \mu\text{m}$ ($\bar{x} = 3.7 \times 1.5 \mu\text{m}$, $n=30$).

Material examined – China, Guizhou Province, Qiannan Buyei and Miao Autonomous Prefecture, Duyun City, Mayao River Valley ($26^{\circ}22'8.3748''\text{N}$, $107^{\circ}23'16.96''\text{E}$). On a dead stink bug (*Pantatomidae*), 3 May 2024, Wanhao Chen, GZAC DY4519 (holotype), DY45191 (ex-type), DY45192 (living culture).

Habitat – On the underside of leaves of broad-leaved plant species.

Notes – Phylogenetic analyses of concatenated dataset 2 (Fig. 2) and NCBI BLASTn comparisons revealed that *Lecanicillium pantatomidae* (DY45191 and DY45192) was grouped with *Lecanicillium* species, forming a distinct clade with *L. sinense* and *L. neocoleopterorum*, which was also supported by the phylogenetic analyses among *Lecanicillium* species (Suppl. Fig. 3). Compared with the typical characteristics, *L. pantatomidae* was distinguished from *L. sinense* by its shorter phialides ($8.2\text{--}11.8 \times 1.3\text{--}1.8 \mu\text{m}$ vs $7.6\text{--}14.0 \times 1.2\text{--}1.5 \mu\text{m}$) and stink bug host. *Lecanicillium pantatomidae* was distinguished from *L. neocoleopterorum* by its shorter phialides ($8.2\text{--}11.8 \times 1.3\text{--}1.8 \mu\text{m}$ vs $19.9\text{--}29.6 \times 1.6\text{--}2.0 \mu\text{m}$) and smaller conidia (cylindrical to fusiform, $2.1\text{--}4.3 \times 1.3\text{--}1.9 \mu\text{m}$ vs cylindrical, $3.3\text{--}6.6 \times 1.5\text{--}1.8 \mu\text{m}$) (Chen et al. 2020c). The combined evidence from morphological characteristics and robust molecular phylogenetic analyses substantiates the recognition of *L. pantatomidae* as a novel species.

Lecanicillium sinense W.H. Chen, Y.F. Han & J.D. Liang, sp. nov.

Fig. 22

Index Fungorum number: 903376; Facesoffungi number: FoF 17482

Etymology – referring to the country, China, where the fungus was first discovered.

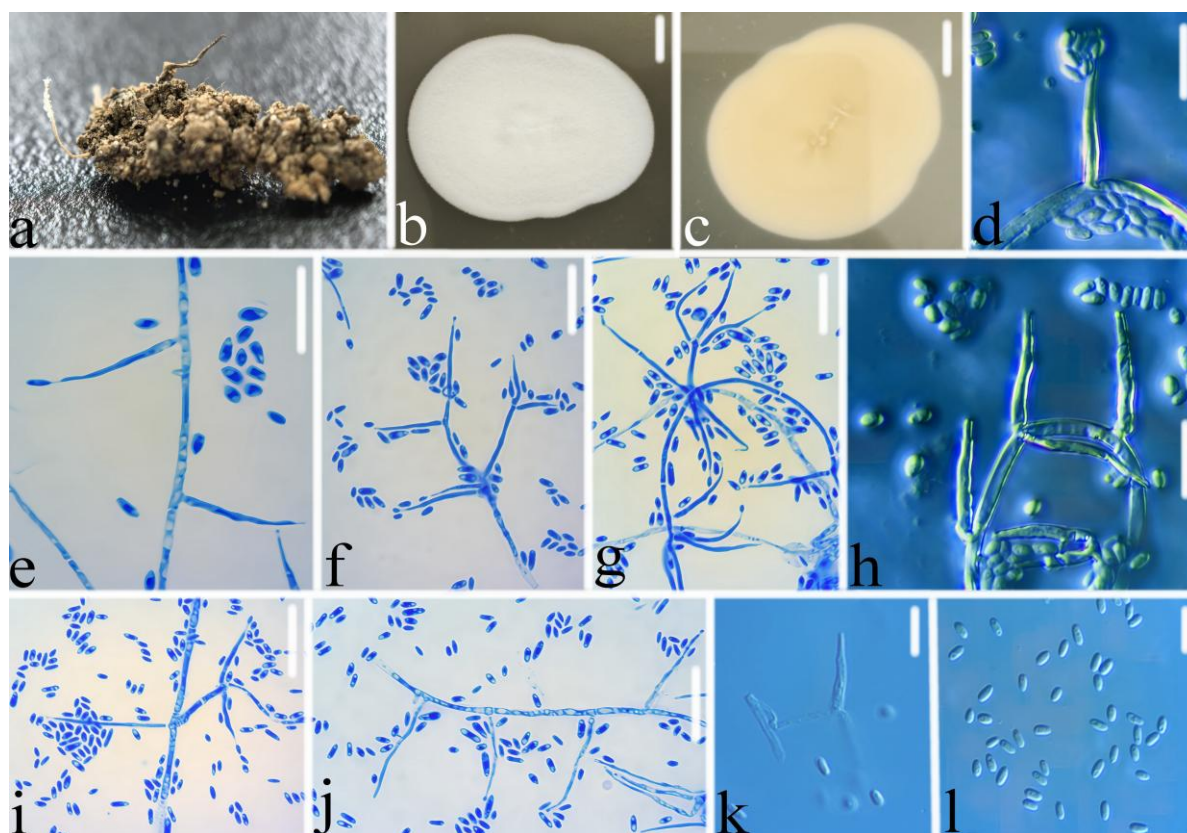


Figure 22 – *Lecanicillium sinense* (DY45361, ex-type) a Infected pupa. b–c Colonies on PDA culture media with upper (b) and reverse (c) views. d, h, k, l Phialides and conidia. e–g, i, j Phialides and conidia were stained with cotton blue. Scale bars: b–c = 10 mm, d–l = 10 μm .

Description – Colonies on PDA reaching 37–43 mm diam. in 14 d at 25°C, white to purple, consisting of a basal felt and cottony, floccose overgrowth, reverse yellowish. Prostrate hyphae smooth, septate, hyaline, 1.0–2.0 µm diam. Conidial structures consisting of erect conidiophores usually arising from the aerial hyphae, solitary or verticillium-like with phialides in whorls of two to three. Phialides 7.6–14.0 × 1.2–1.5 µm ($\bar{x}$ = 11.9 × 1.3 µm, n=30), with a cylindrical basal portion, tapering into a distinct neck. Conidia in chains, hyaline, cylindrical to fusiform, 1-celled, 2.5–4.2 × 1.2–1.5 µm ($\bar{x}$ = 3.3 × 1.4 µm, n=30).

Material examined – China, Guizhou Province, Qiannan Buyei and Miao Autonomous Prefecture, Duyun City, Mayao River Valley (26°22'8.3748"N, 107°23'16.96"E). On a dead pupa (*Lepidoptera*), 3 May 2024, Wanhao Chen, GZAC DY4536 (holotype), DY45361 (ex-type), DY45362 (living culture).

Habitat – Near the road, buried in soil.

Notes – Maximum likelihood and Bayesian analyses of dataset 2 (Fig. 2) placed *L. sinense* (DY45361 and DY45362) in a well-supported clade together with *L. Pantatomidae* and *L. neocoleopterorum*, which was also supported by the phylogenetic analyses among *Lecanicillium* species (Suppl. Fig. 3), while BLASTn results confirmed its placement within *Lecanicillium*. Compared with the typical characteristics, *L. sinense* was distinguished from *L. pantatomidae* by its longer phialides (7.6–14.0 × 1.2–1.5 µm vs 8.2–11.8 × 1.3–1.8 µm) and pupa host. *Lecanicillium sinense* was distinguished from *L. neocoleopterorum* by its shorter phialides (7.6–14.0 × 1.2–1.5 µm vs 19.9–29.6 × 1.6–2.0 µm) and smaller conidia (cylindrical to fusiform, 2.5–4.2 × 1.2–1.5 µm vs cylindrical, 3.3–6.6 × 1.5–1.8 µm). The combined evidence from morphological characteristics and robust molecular phylogenetic analyses substantiates the recognition of *L. sinense* as a novel species.

Neolecanicillium W.H. Chen, Y.F. Han & J.D. Liang gen. nov.

Index Fungorum number: 903416; Facesoffungi number: FoF 17457

Type species – *Neolecanicillium sinensis* W.H. Chen, Y.F. Han & J.D. Liang

Etymology – referring to a new genus with morphological characteristics similar to the genus *Lecanicillium*.

Description – Colonies on PDA, white, reverse yellowish. Conidiophores mononematous, usually arising from aerial hyphae, phialides solitary or in groups of two to three. Phialides emerging laterally from hyphae, forming a compact hymenium, abruptly narrowing into a neck. Conidia in chains, one-celled, hyaline, cylindrical or fusiform. Octahedral crystals absent.

Notes – The newly proposed genus *Neolecanicillium* forms a distinct evolutionary lineage sister to *Parahevensia* in our phylogenetic reconstruction (Fig. 2). However, *Neolecanicillium* species was significant different from *Parahevensia* species by its conidiophores mononematous, cylindrical phialides and cylindrical or fusiform conidia. Among the family *Cordycipitaceae*, *Neolecanicillium* is closely related to the genera *Akanthomyces*, *Arachnidicola*, *Corniculantispora*, *Corpulentispora*, *Dimorphospora*, *Flavocillium*, *Gamszarea*, *Neogamszarella*, *Zarea* and *Zouia* based on the lecanicillium-like conidiogenous structures. Compared with the typical characteristics, *Neolecanicillium* species was significant different from *Akanthomyces*, *Arachnidicola* and *Zouia* species by its two types of conidia. *Neolecanicillium* species was significant different from *Corniculantispora* and *Zarea* species by its cylindrical or fusiform conidia and absent of octahedral crystals. *Neolecanicillium* species was significant different from *Corpulentispora*, *Dimorphospora* and *Flavocillium* species by its cylindrical or fusiform conidia. *Neolecanicillium* species was significant different from *Gamszarea* and *Neogamszarella* species by its absent of a cluster of denticles on the conidiogenous cells. This combined evidence substantiates the establishment of *Neolecanicillium* as a new genus.

Neolecanicillium sinensis W.H. Chen, Y.F. Han & J.D. Liang, sp. nov.

Fig. 23

Index Fungorum number: 903377; Facesoffungi number: FoF 17483

Etymology – referring to its location, China, where the fungus was first discovered.

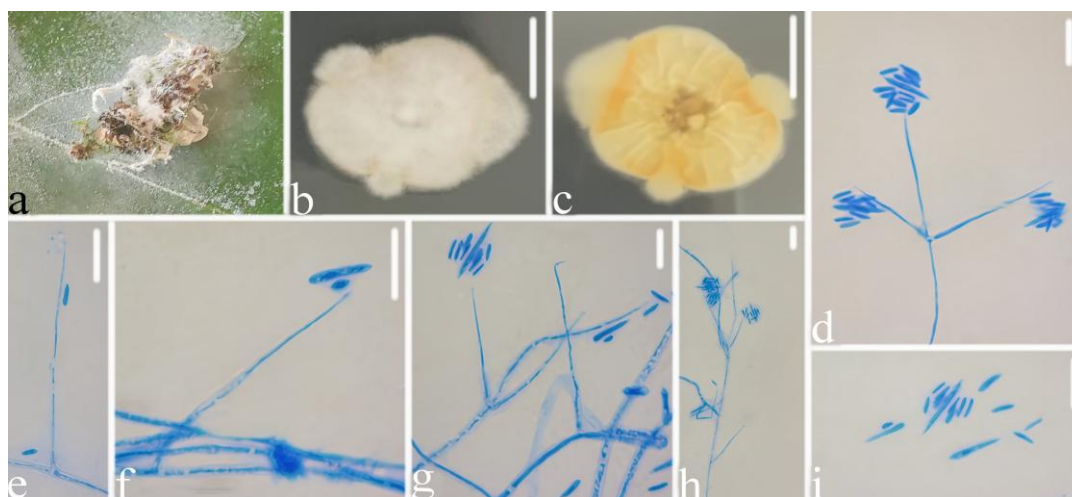


Figure 23 – *Neolecanicillium sinensis* (DY091351, ex-type) a Infected spider. b–c Colonies on PDA culture media with upper (b) and reverse (c) views. d–i Phialides and conidia were stained with cotton blue. Scale bars: b–c = 10 mm, d–i = 10 μ m.

Description – Colonies on PDA reaching 20–25 mm diam. in 14 d at 25°C, yellowish to pale orange, consisting of a basal felt and cottony, floccose overgrowth, reverse yellowish to pale orange. Prostrate hyphae smooth, septate, hyaline, 0.7–1.8 μ m diam. Conidial structures consisting of erect conidiophores usually arising from the aerial hyphae, solitary or phialides in whorls of two. Phialides 13.9–24.8 $\times$ 0.4–1.3 μ m ($\bar{x}$ = 19.5 $\times$ 1.0 μ m, n=30), with a cylindrical basal portion, tapering into a distinct neck. Conidia in subglobose head, hyaline, 1-celled, cylindrical, macrospore, 7.4–11.7 $\times$ 0.4–0.9 μ m ($\bar{x}$ = 9.1 $\times$ 0.7 μ m, n=30); microspore, 3.0–3.9 $\times$ 0.4–0.9 μ m ($\bar{x}$ = 3.3 $\times$ 0.6 μ m, n=30). Octahedral crystals absent.

Material examined – China, Guizhou Province, Qiannan Buyei and Miao Autonomous Prefecture, Duyun City, Mayao River Valley (26°22'8.3748"N, 107°23'16.96"E). On a spider (*Araneae*), 4 September 2021, Wanhao Chen, GZAC DY09135 (holotype), DY091351 (ex-type), DY091352 (living culture).

Habitat – Near the road, buried in soil.

Notes – Phylogenetic analysis revealed that *Neolecanicillium sinensis* forms a distinct lineage sister to *Parahevansia koratensis*. Compared with the typical characteristics, *Neolecanicillium sinensis* was distinguished from *Parahevansia koratensis* by its conidiophores mononematous, cylindrical phialides and cylindrical or fusiform conidia (Mongkolsamrit et al. 2022). The combined morphological and molecular phylogenetic evidence substantiates *Neolecanicillium sinensis* as a new species. Therefore, we introduced *Neolecanicillium* as a new genus that accommodates the species, *N. sinensis*.

Nuciformispora W.H. Chen, Y.F. Han & J.D. Liang gen. nov.

Index Fungorum number: 903417; Facesoffungi number: FoF 17458

Type species – *Nuciformispora sinense* W.H. Chen, Y.F. Han & J.D. Liang

Etymology – referring to its nuciformis-like conidia.

Description – Colonies on PDA, white, reverse yellowish. Conidiophores mononematous, usually arising from aerial hyphae, phialides solitary or in groups of two to four. Phialides emerging laterally from hyphae, forming a compact hymenium, abruptly narrowing into a neck. Conidia one-celled, hyaline, nuciformis. Octahedral crystals present or absent.

Notes – In our phylogenetic reconstruction (Fig. 2), *Nuciformispora* was resolved as a distinct clade with closest affinity to *Flavocillium*. However, *Nuciformispora* species was significant different from *Flavocillium* species by its nuciformis-like macroconidia, cylindrical and ellipsoidal microconidia and spider or insect host. Among the family *Cordycipitaceae*, *Nuciformispora* is

closely related to the genera *Akanthomyces*, *Arachnidicola*, *Corniculantispora*, *Corpulentispora*, *Dimorphospora*, *Gamszarea*, *Neogamszarella*, *Neolecanicillium*, *Zarea* and *Zouia* based on the lecanicillium-like conidiogenous structures. Compared with the typical characteristics, *Nuciformispora* species was significant different from *Akanthomyces*, *Arachnidicola* and *Zouia* species by its two types of conidia and present or absent of octahedral crystals. *Nuciformispora* species was significant different from *Corniculantispora* and *Zarea* species by its nuciformis-like macroconidia. *Nuciformispora* species was significant different from *Corpulentispora*, *Flavocillium* and *Neolecanicillium* species by its nuciformis-like macroconidia and present or absent of octahedral crystals. *Nuciformispora* species was significant different from *Dimorphospora* species by its present or absent of octahedral crystals. *Nuciformispora* species was significant different from *Gamszarea* and *Neogamszarella* species by its absent of a cluster of denticles on the conidiogenous cells. The combined evidence from morphological characteristics and robust molecular phylogenetic analyses substantiates the establishment of *Nuciformispora* as a novel genus.

Nuciformispora araneorum (Petch) W.H. Chen, Y.F. Han & J.D. Liang, comb. nov.

Index Fungorum number: 903378; Facesoffungi number: FoF 17484

≡ *Cephalosporium araneorum* Petch, Trans. Br. mycol. Soc. 16(4): 226 (1932)

≡ *Engyodontium arachnophilum* H.C. Evans & Samson, Persoonia 12(2): 143 (1984)

≡ *Verticillium araneorum* (Petch) W. Gams, Cephalosporium-artige Schimmelpilze (Stuttgart): 186 (1971)

≡ *Lecanicillium araneorum* (Petch) Zare & W. Gams, Nova Hedwigia 73(1-2): 30 (2001)

≡ *Torrubiella alba* Petch, Trans. Br. mycol. Soc. 16(4): 224 (1932)

Mycobank No. MB 197082

Type – Ghana, on a spider (*Araneida*), 1973, H.C. Evans, ex-type, CBS 726.73a.

Description – See Zare & Gams (2001).

Notes – Kepler et al. (2017) proposed the synonymization of *Torrubiella* with *Akanthomyces*. However, the placement of *Torrubiella abla* was still unresolved. *Lecanicillium araneorum* was treated as the anamorph of *Torrubiella abla* (Zare & Games 2001). In the present study (Fig. 2), *Lecanicillium araneorum* grouped with the new strains into a monophyletic clade in the family Cordycipitaceae. Thus, *Nuciformispora araneorum* is proposed as a new combination.

Nuciformispora araneicola W.H. Chen, Y.F. Han & J.D. Liang, sp. nov.

Fig. 24

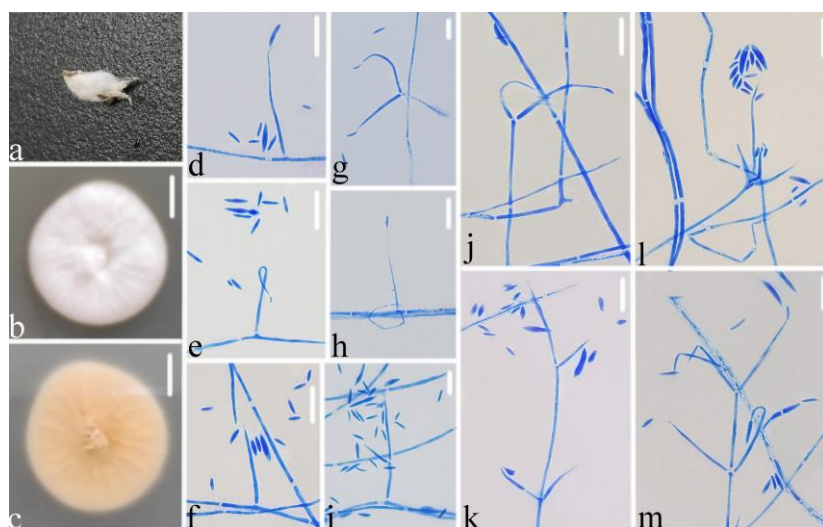


Figure 24 – *Nuciformispora araneicola* (XY07011, ex-type) a Infected spider. b–c Colonies on PDA culture media with upper (b) and reverse (c) views. d–m Phialides and conidia were stained with cotton blue. Scale bars: b–c = 10 mm, d–m = 10 μ m.

Index Fungorum number: 903379; Facesoffungi number: FoF 17485

Etymology – referring to its host spider.

Description – Colonies on PDA reaching 29–31 mm diam. in 14 d at 25 °C, white, consisting of a basal felt and cottony, floccose overgrowth, reverse yellowish. Prostrate hyphae smooth, septate, hyaline, 0.9–1.5 µm diam. Conidial structures consisting of erect conidiophores usually arising from the aerial hyphae, solitary or phialides in whorls of two to three. Phialides 10.5–24.1 × 1.0–1.7 µm ($\bar{x}$ = 16.7 × 1.3 µm, n=30), with a cylindrical basal portion, tapering into a distinct neck. Conidia hyaline, 1-celled, macroconidia date-pit shape, 8.0–12.9 × 1.4–2.1 µm ($\bar{x}$ = 10.6 × 1.6 µm, n=30); microconidia, cylindrical, 2.8–4.6 × 0.9–1.4 µm ($\bar{x}$ = 3.9 × 1.2 µm, n=30). Octahedral crystals not observed.

Material examined – China, Guizhou Province, Qianxinan Buyei-Miao Autonomous Prefecture, Xiyang City, Maling River Valley (25°8'19.66"N, 104°57'43.17"E). On a dead spider (*Araneae*), 17 July 2022, Wanhao Chen, GZAC XY0701 (holotype), XY07011 (ex-type), XY07012 (living culture).

Habitat – Near the road, located on or under the rock.

Notes – Molecular analyses of concatenated dataset 1 (Fig. 2) confirmed *Nuciformispora araneicola* as a distinct species within *Nuciformispora*, forming an independent lineage with significant genetic divergence from other species. Compared with the typical characteristics, *N. araneicola* was distinguished from *N. araneorum* by its shorter phialides (10.5–24.1 × 1.0–1.7 µm vs 20.0–30.0 × 1.2–1.5 µm), two type of conidia and absent of octahedral crystals (Zare & Gams 2001). *Nuciformispora araneicola* was distinguished from *N. sinense* by its shorter phialides (16.7 × 1.3 µm vs 19.7 × 1.1 µm) and larger macroconidia (10.6 × 1.6 µm vs 8.9 × 1.6 µm). *Nuciformispora araneicola* was distinguished from *N. vallise* by its shorter phialides (16.7 × 1.3 µm vs 20.2 × 0.7 µm) and larger macroconidia (10.6 × 1.6 µm vs 12.0 × 1.0 µm). *Nuciformispora araneicola* was distinguished from *N. vallise* by its shorter phialides (16.7 × 1.3 µm vs 31.0 × 1.7 µm) and larger macroconidia (10.6 × 1.6 µm vs 8.1 × 1.7 µm). Thus, the molecular phylogenetic results and morphological characteristics support *N. araneicola* as a new species.

Nuciformispora sinense W.H. Chen, Y.F. Han & J.D. Liang, sp. nov.

Fig. 25

Index Fungorum number: 903381; Facesoffungi number: FoF 17486

Etymology – referring to its location, China, where the fungus was first discovered.

Description – Colonies on PDA reaching 36–40 mm diam. in 14 d at 25°C, white, consisting of a basal felt and cottony, floccose overgrowth, reverse yellowish. Prostrate hyphae smooth, septate, hyaline, 1.5–2.1 µm diam. Conidial structures consisting of erect conidiophores usually arising from the aerial hyphae, solitary or phialides in whorls of two to three. Phialides 18.4–23.2 × 1.0–1.1 µm ($\bar{x}$ = 19.7 × 1.1 µm, n=30), with a cylindrical basal portion, tapering into a distinct neck. Conidia hyaline, 1-celled, macroconidia date-pit shape, 8.2–9.4 × 1.2–1.8 µm ($\bar{x}$ = 8.9 × 1.6 µm, n=30); microconidia, cylindrical to fusiform, 3.2–3.8 × 1.2–1.8 µm ($\bar{x}$ = 3.6 × 1.4 µm, n=30). Octahedral crystals not observed.

Material examined – China, Guizhou Province, Qiannan Buyei and Miao Autonomous Prefecture, Duyun City, Mayao River Valley (26°22'8.3748"N, 107°23'16.96"E). On a spider (*Araneae*), 1 May 2022, Wanhao Chen, GZAC DY0528 (holotype), DY05281 (ex-type), DY05282 (living culture).

Habitat – Near the road, located on or under the rock.

Notes – Molecular analyses of concatenated dataset 2 (Fig. 2) confirmed *Nuciformispora sinense* within the genus *Nuciformispora*, forming a strongly supported clade (99% ML/0.94 PP) with its closest relative *N. araneorum*. Compared with the typical characteristics, *Nuciformispora sinense* was distinguished from *N. araneorum* by its shorter phialides (19.7 × 1.1 µm vs 20.0–30.0 × 1.2–1.5 µm), two type of conidia and absent of octahedral crystals (Zare & Gams 2001). Based on distinctive morphological characteristics and well-supported phylogenetic results, we formally propose *N. sinense* as a newly described species.

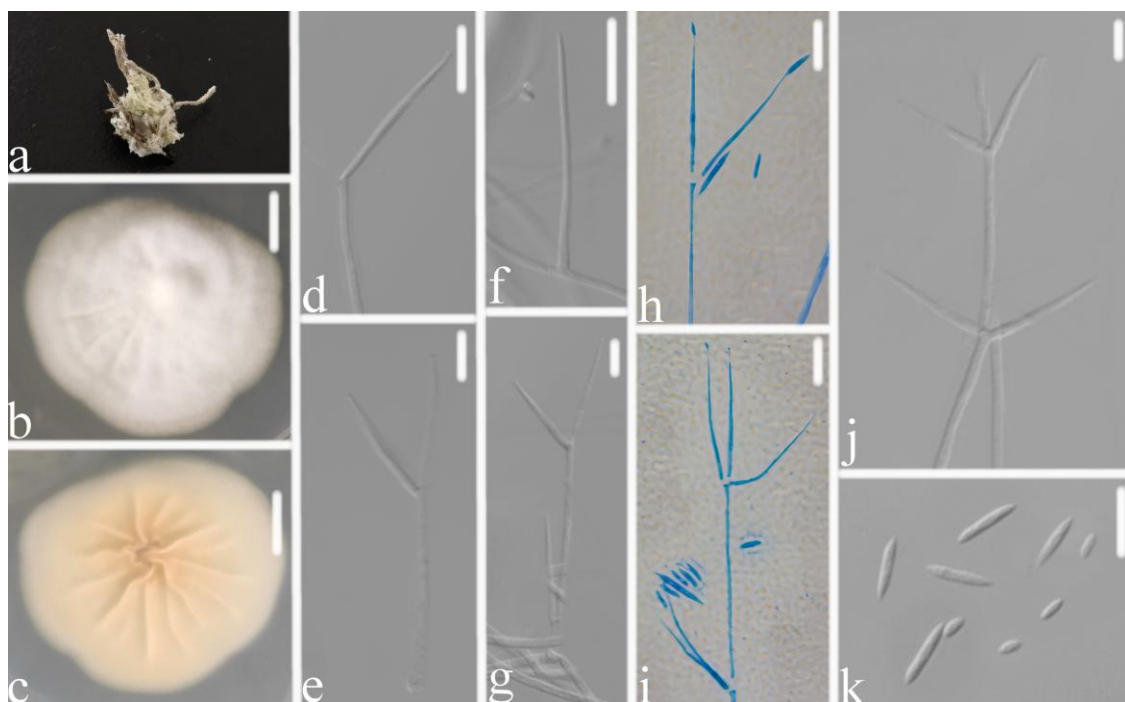


Figure 25 – *Nuciformispora sinense* (DY05281, ex-type) a Infected spider. b–c Colonies on PDA culture media with upper (b) and reverse (c) views. d–g, j, k Phialides and conidia; h, i Phialides and conidia were stained with cotton blue. Scale bars: b–c = 10 mm, d–k = 10 μ m.

Nuciformispora vallise W.H. Chen, Y.F. Han & J.D. Liang, sp. nov.

Fig. 26

Index Fungorum number: 903382; Facesoffungi number: FoF 17487

Etymology – referring to its location, Mayao River Valley, where the fungus was first discovered.

Description – Colonies on PDA reaching 35–36 mm diam. in 14 d at 25°C, white, consisting of a basal felt and cottony, floccose overgrowth, reverse yellowish. Prostrate hyphae smooth, septate, hyaline, 1.4–1.7 μ m diam. Conidial structures consisting of erect conidiophores usually arising from the aerial hyphae, solitary or phialides in whorls of two to three. Phialides 16.7–23.7 $\times$ 0.6–0.9 μ m ($\bar{x}$ = 20.2 $\times$ 0.7 μ m, n=30), with a cylindrical basal portion, tapering into a distinct neck. Conidia hyaline, 1-celled, macroconidia date-pit shape, 11.0–12.8 $\times$ 0.7–1.1 μ m ($\bar{x}$ = 12.0 $\times$ 1.0 μ m, n=30); microconidia, cylindrical, 2.1–4.2 $\times$ 0.7–1.1 μ m ($\bar{x}$ = 3.2 $\times$ 0.8 μ m, n=30). Octahedral crystals not observed.

Material examined – China, Guizhou Province, Qiannan Buyei and Miao Autonomous Prefecture, Duyun City, Mayao River Valley (26°22'8.3748"N, 107°23'16.96"E). On a spider (*Araneae*), 4 September 2021, Wanhao Chen, GZAC DY0969 (holotype), DY09691 (ex-type), DY09692 (living culture).

Habitat – Near the road, located on or under the rock.

Notes – Molecular analyses of concatenated dataset 2 (Fig. 2) confirmed *Nuciformispora vallise* within the genus *Nuciformispora*, forming a maximally supported clade (100% ML/1 PP) with its closest relative *N. zunyiense*. Compared with the typical characteristics, *Nuciformispora vallise* was distinguished from *N. zunyiense* by its shorter phialides (16.7–23.7 $\times$ 0.6–0.9 μ m vs 27.7–36.9 $\times$ 1.5–1.9 μ m) and larger macroconidia (11.0–12.8 $\times$ 0.7–1.1 μ m vs 6.4–9.3 $\times$ 1.4–1.8 μ m). The combined evidence from morphological characteristics and robust molecular phylogenetic analyses substantiates the recognition of *N. vallise* as a novel species.

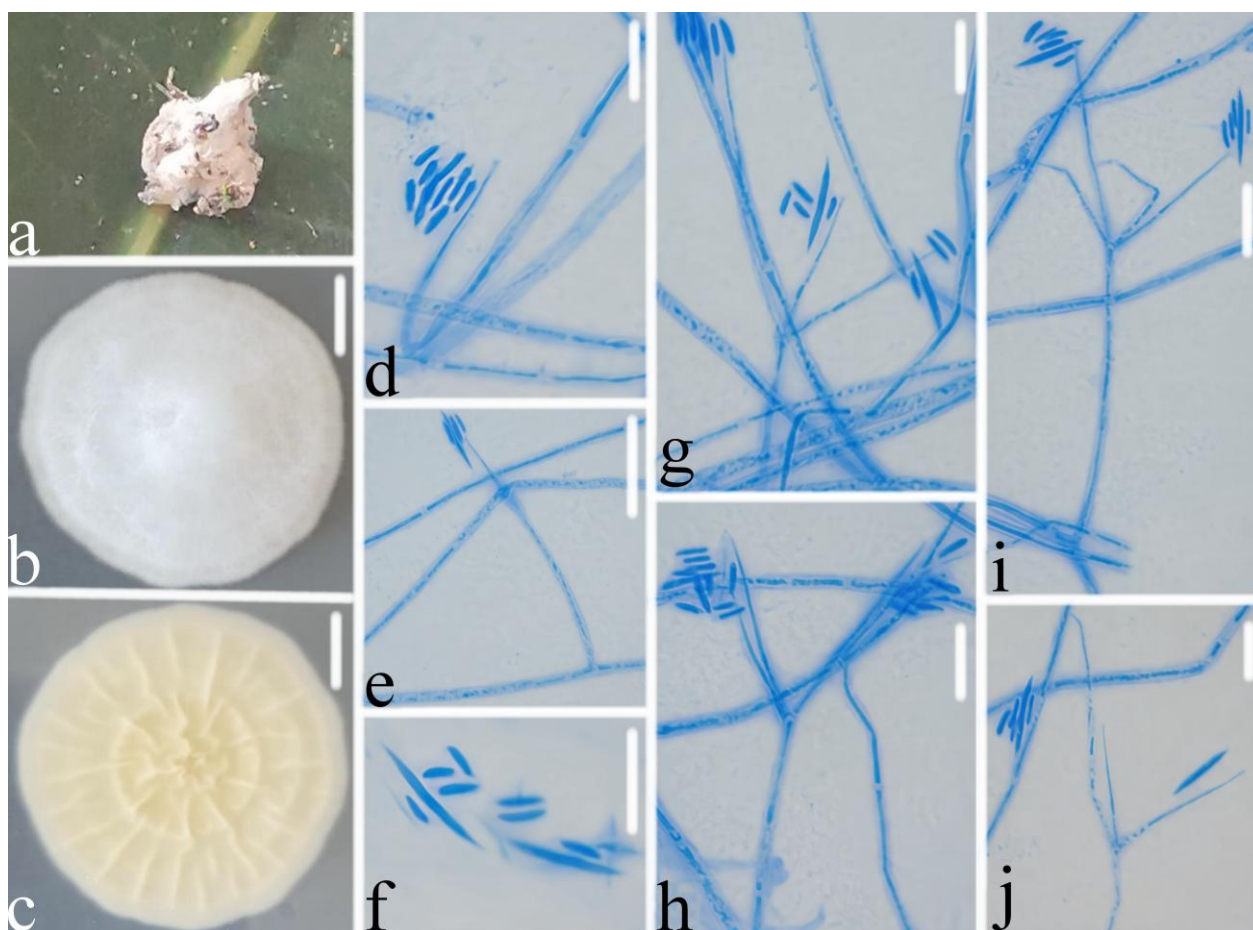


Figure 26 – *Nuciformispora vallise* (DY09691, ex-type) a Infected spider. b–c Colonies on PDA culture media with upper (b) and reverse (c) views. d–j Phialides and conidia were stained with cotton blue. Scale bars: b–c = 10 mm, d–j = 10 μ m.

Nuciformispora zunyiense W.H. Chen, Y.F. Han & J.D. Liang, sp. nov.

Fig. 27

Index Fungorum number: 903383; Facesoffungi number: FoF 17488

Etymology – referring to its location, Zunyi City, where the fungus was first discovered.

Description – Colonies on PDA reaching 26–29 mm diam. in 14 d at 25°C, white, consisting of a basal felt and cottony, floccose overgrowth, reverse yellowish. Prostrate hyphae smooth, septate, hyaline, 1.8–2.1 μ m diam. Conidial structures consisting of erect conidiophores usually arising from the aerial hyphae, solitary or phialides in whorls of two to three. Phialides 27.7–36.9 $\times$ 1.5–1.9 μ m ($\bar{x}$ = 31.0 $\times$ 1.7 μ m, n=30), with a cylindrical basal portion, tapering into a distinct neck. Conidia hyaline, 1-celled, macroconidia date-pit shape, 6.4–9.3 $\times$ 1.4–1.8 μ m ($\bar{x}$ = 8.1 $\times$ 1.7 μ m, n=30); microconidia, cylindrical, 3.2–3.7 $\times$ 1.9–2.0 μ m ($\bar{x}$ = 3.4 $\times$ 2.0 μ m, n=30). Octahedral crystals not observed.

Material examined – China, Guizhou Province, Zunyi City, Suiyang County, Shuangmen Valley (28°1'39.05"N, 107°7'58.65"E). On a pupa (*Lepidoptera*), 30 September 2023, Wanhao Chen, GZAC SY0922 (holotype), SY09221 (ex-type), SY09222 (living culture).

Habitat – Near the road, buried in soil.

Notes – Molecular analyses of concatenated dataset 2 (Fig. 2) confirmed *Nuciformispora zunyiense* within the genus *Nuciformispora*, forming a maximally supported clade (100% ML/1 PP) with its closest relative *N. vallise*. Compared with the typical characteristics, *Nuciformispora zunyiense* was distinguished from *N. vallise* by its longer phialides (27.7–36.9 $\times$ 1.5–1.9 μ m vs 16.7–23.7 $\times$ 0.6–0.9 μ m) and smaller macroconidia (6.4–9.3 $\times$ 1.4–1.8 μ m vs 11.0–12.8 $\times$ 0.7–1.1 μ m). Our polyphasic approach, incorporating detailed morphological examination and multi-locus phylogenetic reconstruction, validates *N. zunyiense* as a previously unrecognized species.

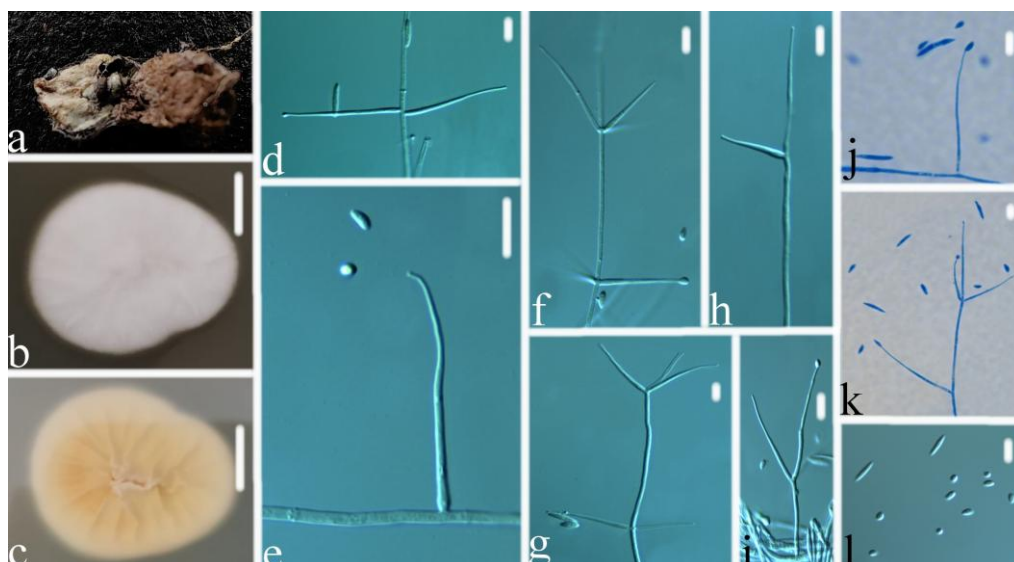


Figure 27 – *Nuciformispora zunyiense* (SY09221, ex-type) a Infected pupa. b–c Colonies on PDA culture media with upper (b) and reverse (c) views. d–i, l Phialides and conidia; j, k Phialides and conidia were stained with cotton blue. Scale bars: b–c = 10 mm, d–l = 10 μ m.

Paracorniculantispora W.H. Chen, Y.F. Han & J.D. Liang gen. nov.

Index Fungorum number: 903418; Facesoffungi number: FoF 17459

Type species – *Paracorniculantispora psalliotae* (Treschew) W.H. Chen, Y.F. Han & J.D. Liang

Etymology – referring to a new genus with similar morphological characteristics with the genus *Corniculantispora*.

Description – Colonies on PDA, white, reverse reddish. Red or reddish pigment usually diffusing into the agar. Phialides arising from undifferentiated prostrate conidiophores, solitary or more often 3–4 (–6) in whorls on each node. Conidia typically solitary or few fasciculate at right angles to the phialide tip, one-celled, hyaline, commonly falcate. Octahedral crystals present or absent.

Notes – Khonsanit et al. (2024) introduced the genus *Corniculantispora* with the type species *Corniculantispora psalliotae* (Treschew) Khons. et al. Zare & Gams (2001) designated the strain CBS 505.48 as the neotype for *Lecanicillium psalliotae* (Treschew) Zare & W. Gams. The strain CBS 532.81 was the ex-type of *Lecanicillium saksenae* (Kushwaha) Kurihara & Sukarno. However, the strain CBS 505.48 was not included in the phylogenetic analysis provided by Khonsanit et al. (2024). Strains CBS 505.48 and CBS 532.81 can be clearly distinguished through phylogenetic analysis in the present study (Fig. 2). Among the family *Cordycipitaceae*, *Lecanicillium psalliotae* is closely related to the genera *Akanthomyces*, *Arachnidicola*, *Corniculantispora*, *Corpulentispora*, *Dimorphospora*, *Gamszarea*, *Neogamszarella*, *Neolecanicillium*, *Nuciformispora*, *Zarea* and *Zouia* based on the lecanicillium-like conidiogenous structures. Compared with the typical characteristics, *Lecanicillium psalliotae* was significant different from *Akanthomyces*, *Arachnidicola* and *Zouia* species by its two types of conidia and present or absent of octahedral crystals. *Lecanicillium psalliotae* was significant different from *Corniculantispora* and *Zarea* species by its present of red or reddish pigment in the agar. *Lecanicillium psalliotae* was significant different from *Corpulentispora*, *Dimorphospora*, *Flavocillium* and *Neolecanicillium* species by its red or reddish pigment in the agar and present or absent of octahedral crystals. *Lecanicillium psalliotae* was significant different from *Gamszarea* and *Neogamszarella* species by its absent of a cluster of denticles on the conidiogenous cells. Thus, a new genus *Paracorniculantispora* was proposed for *Lecanicillium psalliotae*.

Paracorniculantispora psalliotae (Treschew) W.H. Chen, Y.F. Han & J.D. Liang, comb. nov.

Index Fungorum number: 903384; Facesoffungi number: FoF 17489

≡ *Verticillium psalliotae* Treschew, Dan. Bot. Arkiv. 11(1): 7 (1941)

≡ *Lecanicillium psalliotae* (Treschew) Zare & W. Gams, Nova Hedwig. 73: 21 (2001)

MycoBank No. MB 291975

Type – England, from casing soil in mushroom culture, 1947, J.C. La Touche, ex-type, CBS 505.48.

Description – See Zare & Gams (2001).

Paracorniculantispora sinensis W.H. Chen, Y.F. Han & J.D. Liang, sp. nov.

Fig. 28

Index Fungorum number: 903385; Facesoffungi number: FoF 17490

Etymology – referring to its location, China, where the fungus was first discovered.

Description – Colonies on PDA reaching 25–30 mm diam. in 14 d at 25°C, white, consisting of a basal felt and cottony, floccose overgrowth, reverse reddish, red or reddish pigment usually diffusing into the agar. Prostrate hyphae smooth, septate, hyaline, 0.8–1.3 µm diam. Conidial structures consisting of erect conidiophores usually arising from the aerial hyphae, solitary or phialides in whorls of two to three. Phialides 21.3–23.1 × 0.8–1.3 µm ($\bar{x}$ = 22.5 × 1.0 µm, n=30), with a cylindrical basal portion, tapering into a distinct neck. Conidia hyaline, 1-celled, macroconidia, falcate, 5.4–6.6 × 0.8–1.7 µm ($\bar{x}$ = 6.1 × 1.3 µm, n=30); microconidia, cylindrical to ellipsoidal, 2.1–3.1 × 1.0–1.4 µm ($\bar{x}$ = 2.7 × 1.3 µm, n=30). Octahedral crystals not observed.

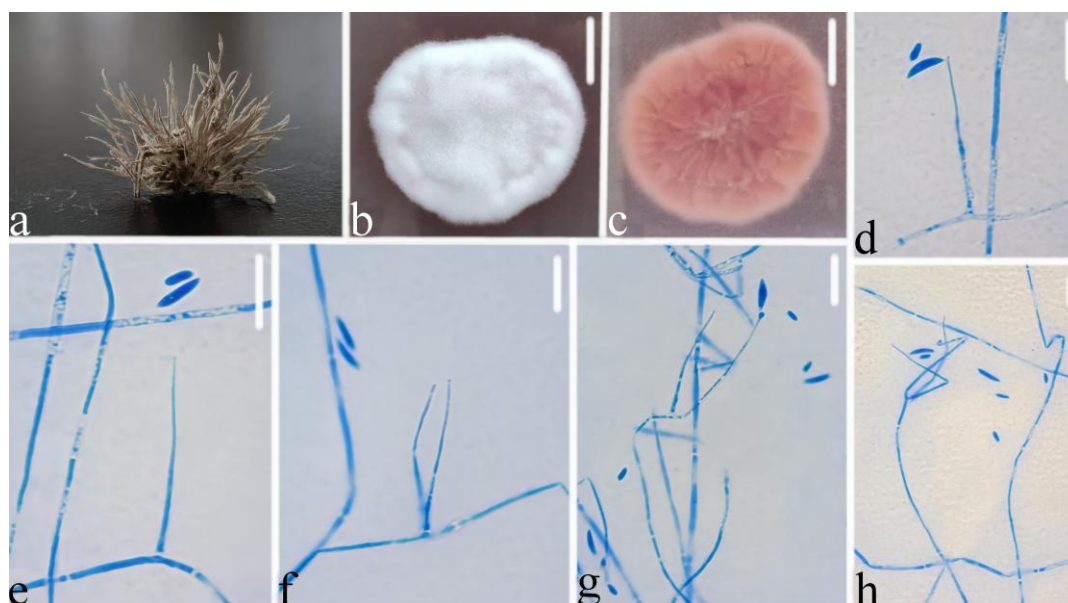


Figure 28 – *Paracorniculantispora sinensis* (ZY06251, ex-type) a Infected spider. b–c Colonies on PDA culture media with upper (b) and reverse (c) views. (c) sides of the colony. d–h Phialides and conidia were stained with cotton blue. Scale bars: b–c = 10 mm, d–h = 10 µm.

Material examined – China, Guizhou Province, Zunyi City, Honghuagang District, Dabanshui National Forest Park (27°46'35.904"N, 106°48'30.89"E). On a dead spider (*Araneae*), 3 June 2022, Wanhao Chen, GZAC ZY0625 (holotype), ZY06251 (ex-type), ZY06252 (living culture).

Habitat – Near the road, located on or under the rock.

Notes – Molecular analyses of concatenated dataset 2 (Fig. 2) confirmed *Paracorniculantispora sinensis* within the genus *Paracorniculantispora*, forming a strongly supported clade (98% ML/0.96 PP) with its closest relative *P. psalliotae*. Compared with the typical characteristics, *Paracorniculantispora sinensis* was distinguished from *P. psalliotae* by its

longer phialides ($21.3\text{--}23.1 \times 0.8\text{--}1.3 \mu\text{m}$ vs $5.0\text{--}10.0 \times 1.2\text{--}1.7 \mu\text{m}$), cylindrical to ellipsoidal conidia and absent of octahedral crystals (Zare & Gams 2001). The combined evidence from morphological characteristics and robust molecular phylogenetic analyses substantiates the recognition of *P. sinensis* as a novel species.

Rubrumomyces W.H. Chen, Y.F. Han & J.D. Liang gen. nov.

Index Fungorum number: 903419; Facesoffungi number: FoF 17460

Type species – *Rubrumomyces sinensis* W.H. Chen, Y.F. Han & J.D. Liang

Etymology – From the Latin “*rubrem*” means the characteristics of red, refers to the red or reddish pigment usually produces in the genus.

Description – Colonies on PDA, white, reverse reddish, red or reddish pigment usually produces in the agar. Conidiophores mononematous, usually arising from aerial hyphae, phialides solitary or in groups of two to four. Phialides emerging laterally from hyphae, forming a compact hymenium, abruptly narrowing into a neck. Conidia in chains, one-celled, hyaline, fusiform or ellipsoidal.

Notes – Among the family *Cordycipitaceae*, *Rubrumomyces* species is closely related to the genus *Paracorniculantispora* based on the present of red or reddish pigment in agar. In our phylogenetic reconstruction (Fig. 2), *Rubrumomyces* was resolved as a distinct clade with closest affinity to *Paracorniculantispora*. However, *Rubrumomyces* species was significant different from *Paracorniculantispora* species by its paecilomyces-like conidiogenous structure, fusiform or ellipsoidal conidia and only one type of conidia. Among the family *Cordycipitaceae*, the genera *Akanthomyces*, *Arachnidicola*, *Corniculantispora*, *Corpulentispora*, *Dimorphospora*, *Gamszarea*, *Neogamszarella*, *Neolecanicillium*, *Nuciformispora*, *Zarea* and *Zouia* were associated with *Lecanicillium* species. Compared with the typical characteristics, *Rubrumomyces* species was significant different from *Akanthomyces*, *Arachnidicola*, *Corniculantispora*, *Corpulentispora*, *Dimorphospora*, *Neolecanicillium*, *Nuciformispora*, *Zarea* and *Zouia* species by its present of red or reddish pigment in agar. *Rubrumomyces* species was significant different from *Gamszarea* and *Neogamszarella* species by its present of red or reddish pigment in agar, and absent of a cluster of denticles on the conidiogenous cells. The combined evidence from morphological characteristics and robust molecular phylogenetic analyses substantiates the establishment of *Rubrumomyces* as a novel genus.

Rubrumomyces guizhouensis W.H. Chen, Y.F. Han & J.D. Liang, sp. nov.

Fig. 29

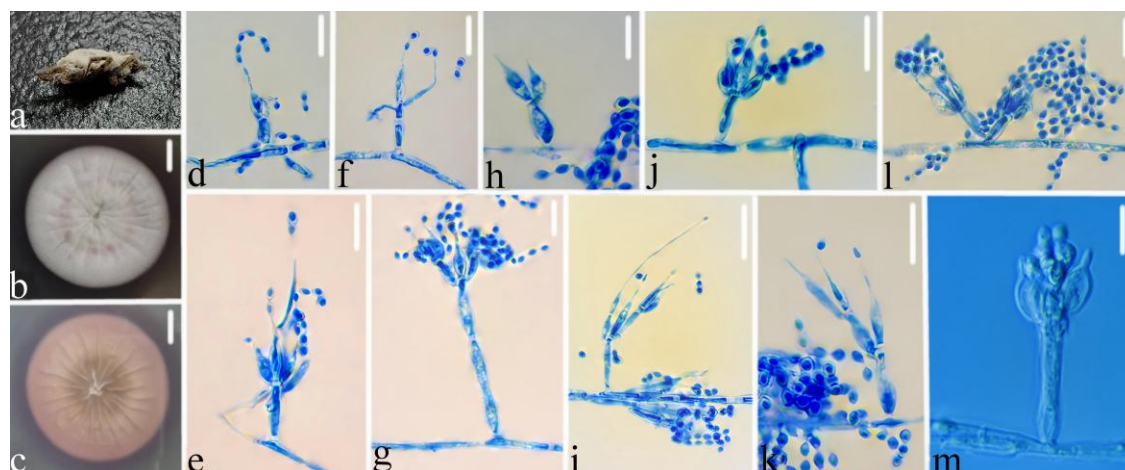


Figure 29 – *Rubrumomyces guizhouensis* (TR05311, ex-type) a Infected larva. b–c Colonies on PDA culture media with upper (b) and reverse (c) views. d–l Phialides and conidia were stained with cotton blue. m Phialides and conidia. Scale bars: b–c = 10 mm, d–m = 10 μm .

Index Fungorum number: 903386; Facesoffungi number: FoF 17491

Etymology – referring to its location, Guizhou Province, where the fungus was first discovered.

Description – Colonies on PDA reaching 44–45 mm diam. in 14 d at 25°C, white, consisting of a basal felt and cottony, floccose overgrowth, reverse reddish, red or reddish pigment usually diffusing into the agar. Prostrate hyphae smooth, septate, hyaline, 1.3–1.7 µm diam. Conidial structures consisting of erect conidiophores usually arising from the aerial hyphae, solitary or phialides in whorls of two to three. Phialides 7.3–12.7 × 1.9–2.9 µm ($\bar{x}$ = 10.9 × 2.2 µm, n=30), with a cylindrical basal portion, tapering into a distinct neck. Conidia hyaline, 1-celled, fusiform to ellipsoidal, 1.8–2.6 × 1.3–1.8 µm ($\bar{x}$ = 2.1 × 1.5 µm, n=30). Octahedral crystals not observed.

Material examined – China, Guizhou Province, Tongren City, Jiangkou County, Fanjing Mountain (27°50'56.98"N, 108°46'52.28"E). On a larva (*Lepidoptera*), 1 May 2023, Wanhao Chen, GZAC TR0531 (holotype), TR05311 (ex-type), TR05312 (living culture).

Habitat – Near the road, located on or under the rock.

Notes – Molecular analyses of concatenated dataset 2 (Fig. 2) confirmed *Rubrumomyces guizhouensis* within the newly established genus *Rubrumomyces*, forming a distinct evolutionary lineage sister to *R. sinensis*. Compared with the typical characteristics, *Rubrumomyces guizhouensis* was distinguished from *R. sinensis* by its longer phialides (7.3–12.7 × 1.9–2.9 µm vs 5.8–10.4 × 2.1–3.2 µm) and smaller conidia (1.8–2.6 × 1.3–1.8 µm vs 3.1–4.2 × 1.9–2.2 µm). The combined evidence from morphological characteristics and robust molecular phylogenetic analyses substantiates the recognition of *R. guizhouensis* as a novel species.

Rubrumomyces sinensis W.H. Chen, Y.F. Han & J.D. Liang, sp. nov.

Fig. 30

Index Fungorum number: 903387; Facesoffungi number: FoF 17492

Etymology – referring to its location, China, where the fungus was first discovered.

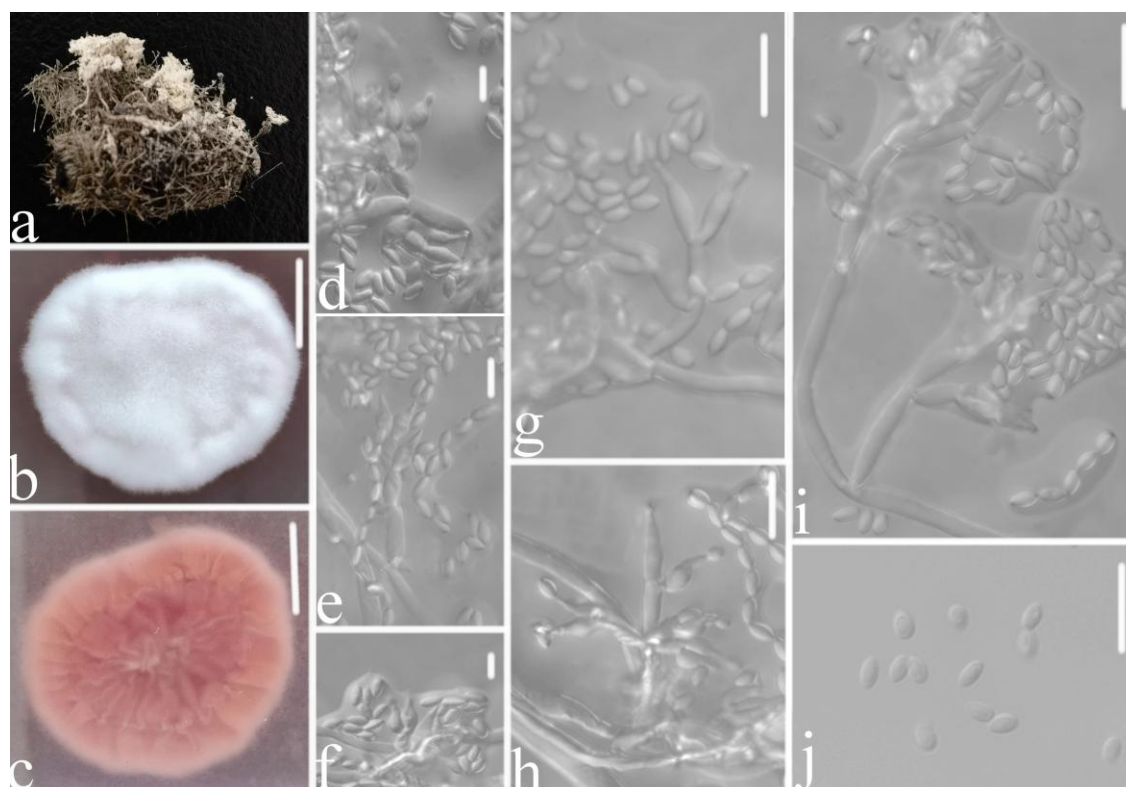


Figure 30 – *Rubrumomyces sinensis* (ZY06111, ex-type) a Infected pupa. b–c Colonies on PDA culture media with upper (b) and reverse (c) views. d–j Phialides and conidia. Scale bars: b–c = 10 mm, d–j = 10 µm.

Description – Colonies on PDA reaching 25–30 mm diam. in 14 d at 25°C, white, consisting of a basal felt and cottony, floccose overgrowth, reverse reddish, red or reddish pigment usually diffusing into the agar. Prostrate hyphae smooth, septate, hyaline, 2.2–3.0 µm diam. Conidial structures consisting of erect conidiophores usually arising from the aerial hyphae, solitary or phialides in whorls of two to three. Phialides 5.8–10.4 × 2.1–3.2 µm ($\bar{x}$ = 8.0 × 2.6 µm, n=30), with a cylindrical basal portion, tapering into a distinct neck. Conidia hyaline, 1-celled, fusiform to ellipsoidal, 3.1–4.2 × 1.9–2.2 µm ($\bar{x}$ = 3.8 × 2.0 µm, n=30). Octahedral crystals not observed.

Material examined – China, Guizhou Province, Zunyi City, Honghuagang District, Dabanshui National Forest Park (27°46'35.904"N, 106°48'30.89"E). On a pupa (*Lepidoptera*), 3 June 2022, Wanhao Chen, GZAC ZY0611 (holotype), ZY06111 (ex-type), ZY06112 (living culture).

Habitat – On the underside of leaves of broad-leaved plant species.

Notes – Molecular analyses of concatenated dataset 2 (Fig. 2) confirmed *Rubrumomyces sinensis* within the genus *Rubrumomyces*, forming a distinct evolutionary lineage with its closest relative *R. guizhouensis*. Compared with the typical characteristics, *Rubrumomyces sinensis* was distinguished from *R. guizhouensis* by its shorter phialides (8.0 × 2.6 µm vs 10.9 × 2.2 µm) and larger conidia (3.8 × 2.0 µm vs 2.1 × 1.5 µm). The combined morphological and molecular phylogenetic evidence substantiates the recognition of *R. sinensis* as a novel species.

Samsoniella Mongkols., Noisrip., Thanakitp., Spatafora & Luangsa-ard, *Mycologia* 110(1): 248 (2018)

Type species – *Samsoniella inthanonensis* Mongkols., Noisrip., Thanakitp., Spatafora & Luangsa-ard 2018

Notes – Mongkolsamrit et al. (2018) circumscribed the genus *Samsoniella* with the type species *S. inthanonensis* Mongkols. et al. along with two additional taxa, *S. alboaurantia* (G. Sm.) Mongkols. et al. and *S. aurantia* Mongkols. et al. (Mongkolsamrit et al. 2018). Chen et al. (2023) summarized that *Samsoniella* consists of twenty-nine species and introduced two new species. Six new *Samsoniella* species were reported by Wang et al. (2024a), Pu et al. (2025), Evans et al. (2025) and Zeng et al. (2025). In the present study, eleven new species were introduced.

Samsoniella araneicola W.H. Chen, Y.F. Han & J.D. Liang, sp. nov.

Fig. 31

Index Fungorum number: 903388; Facesoffungi number: FoF 17493

Etymology – referring to its host spider.

Description – Colonies on PDA reaching 30–33 mm diam. in 14 d at 25°C, white, consisting of a basal felt and cottony, floccose overgrowth, reverse yellowish. Prostrate hyphae smooth, septate, hyaline, 1.1–2.2 µm diam. Conidial structures consisting of erect conidiophores usually arising from the aerial hyphae, solitary or verticillium-like with phialides in whorls of two to three. Phialides 6.4–10.8 × 2.0–2.5 µm ($\bar{x}$ = 9.5 × 2.2 µm, n=30), with a cylindrical basal portion, tapering into a distinct neck. Conidia in chains, hyaline, 1-celled, fusiform, 2.5–3.1 × 2.0–2.4 µm ($\bar{x}$ = 2.9 × 2.3 µm, n=30).

Material examined – China, Guizhou Province, Qiannan Buyei and Miao Autonomous Prefecture, Duyun City, Mayao River Valley (26°22'8.3748"N, 107°23'16.96"E). On a spider (*Araneae*), 1 May 2022, Wanhao Chen, GZAC DY0547 (holotype), DY05471 (ex-type), DY05472 (living culture).

Habitat – On the underside of leaves of broad-leaved plant species.

Notes – Molecular characterization through NCBI BLASTn comparisons and multi-locus phylogenetic analysis (dataset 2, Fig. 2) revealed that *Samsoniella araneicola* (DY05471 and DY05472) was grouped within the genus *Samsoniella*, forming a maximally supported clade (100% ML/1 PP) with *S. sinensis*, which was also supported by the phylogenetic analyses among *Samsoniella* species (Suppl. Fig. 3). Compared with the typical characteristics, *S. araneicola* was distinguished from *S. sinensis* by its longer phialides (9.5 × 2.2 µm vs 5.6–9.3 × 1.5–2.1 µm), fusiform conidia, conidiophores mononematous and spider host (Wang et al. 2023). The combined

evidence from morphological characteristics and robust molecular phylogenetic analyses substantiates the recognition of *S. araneicola* as a novel species.

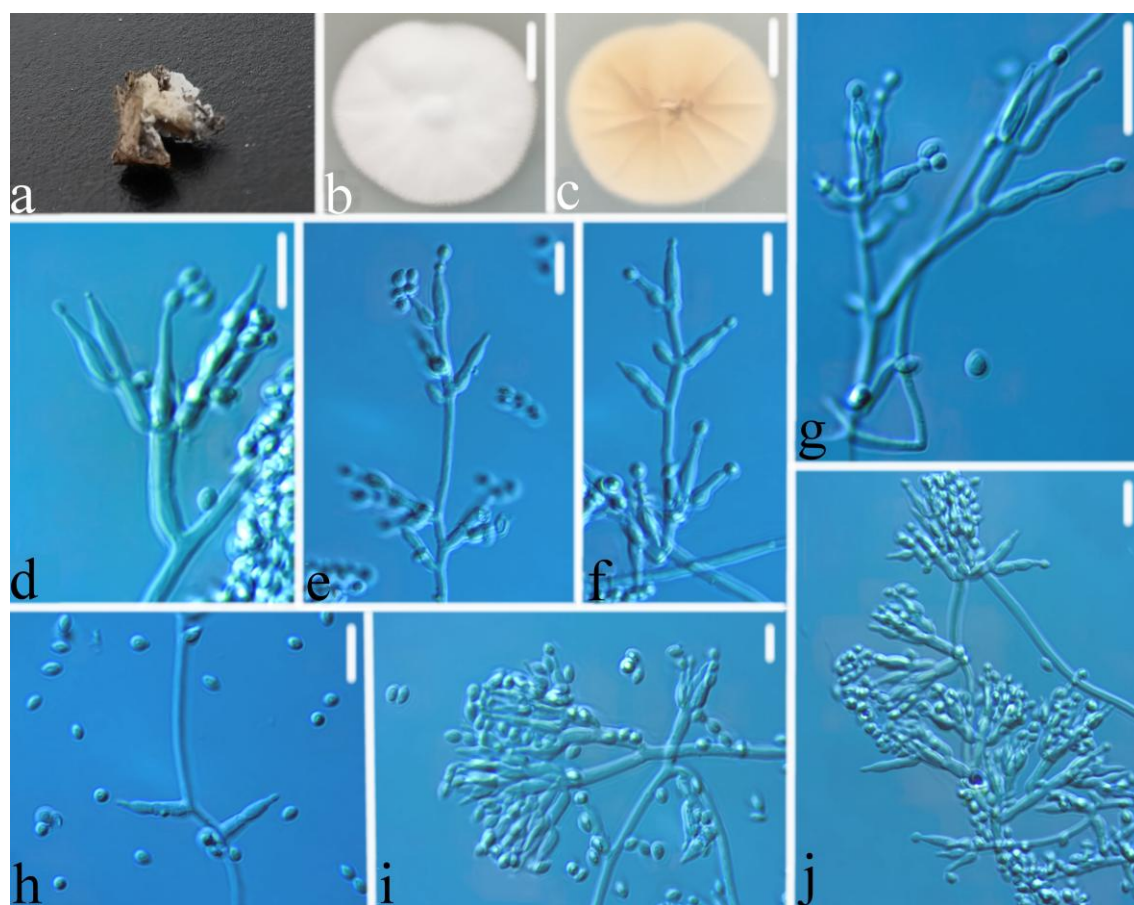


Figure 31 – *Samsoniella araneicola* (DY05471, ex-type) a Infected spider. b–c Colonies on PDA culture media with upper (b) and reverse (c) views. d–j Phialides and conidia. Scale bars: b–c = 10 mm, d–j = 10 μ m.

Samsoniella fanjingensis W.H. Chen, Y.F. Han & J.D. Liang, sp. nov.

Fig. 32

Index Fungorum number: 903389; Facesoffungi number: FoF 17494

Etymology – referring to the location, Fanjing Mountain, where the fungus was first discovered.

Description – Colonies on PDA reaching 30–31 mm diam. in 14 d at 25°C, white, consisting of a basal felt and cottony, floccose overgrowth, reverse yellowish. Prostrate hyphae smooth, septate, hyaline, 1.6–2.5 μ m diam. Conidial structures consisting of erect conidiophores usually arising from the aerial hyphae, solitary or verticillium-like with phialides in whorls of two to three. Phialides 6.8–10.0 $\times$ 1.8–3.0 μ m ($\bar{x}$ = 8.9 $\times$ 2.3 μ m, n=30), with a cylindrical basal portion, tapering into a distinct neck. Conidia in chains, hyaline, 1-celled, ellipsoidal, 1.7–2.2 $\times$ 1.2–1.6 μ m ($\bar{x}$ = 2.0 $\times$ 1.5 μ m, n=30), or globose, 1.9–2.4 μ m ($\bar{x}$ = 2.1 μ m, n=30).

Material examined – China, Guizhou Province, Tongren City, Jiangkou County, Fanjing Mountain (27°50'56.98"N, 108°46'52.28"E). On a pupa (*Lepidoptera*), 1 May 2023, Wanhao Chen, GZAC TR0524 (holotype), TR05241 (ex-type), TR05242 (living culture).

Habitat – On the underside of leaves of broad-leaved plant species.

Notes – Molecular analyses including NCBI BLASTn comparisons and multi-locus phylogenetic reconstruction (dataset 2, Fig. 2) revealed that *Samsoniella fanjingensis* (TR05241 and TR05242) was group with *Samsoniella* species, forming a maximally supported clade (100% ML/1 PP) with *S. erucaae*, which was also supported by the phylogenetic analyses among

Samsoniella species (Suppl. Fig. 3). Compared with the typical characteristics, *S. fanjingensis* was distinguished from *S. erucaae* by its smaller conidia (ellipsoid, $2.0 \times 1.5 \mu\text{m}$, globose, $2.1 \mu\text{m}$ vs fusiform to ellipsoidal, $2.3\text{--}2.9 \times 1.1\text{--}1.5 \mu\text{m}$) (Chen et al. 2022c). The combined evidence from morphological characteristics and robust molecular phylogenetic analyses substantiates the recognition of *S. fanjingensis* as a novel species.

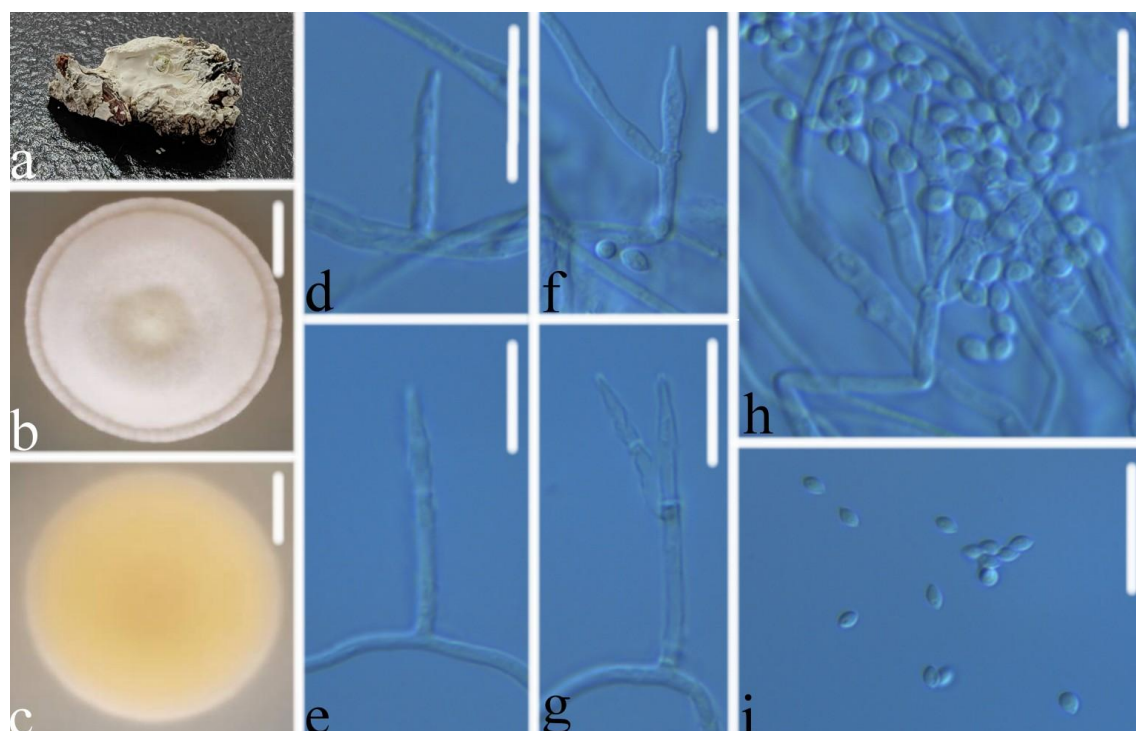


Figure 32 – *Samsoniella fanjingensis* (TR05241, ex-type) a Infected pupa. b–c Colonies on PDA culture media with upper (b) and reverse (c) views. d–i Phialides and conidia. Scale bars: b–c = 10 mm, d–i = 10 μm .

Samsoniella guiyangensis W.H. Chen, Y.F. Han & J.D. Liang, sp. nov.

Fig. 33

Index Fungorum number: 903390; Facesoffungi number: FoF 17495

Etymology – referring to the location, Guiyang City, where the fungus was first discovered.

Description – Colonies on PDA reaching 20–21 mm diam. in 14 d at 25°C, white, consisting of a basal felt and cottony, floccose overgrowth, reverse yellowish. Prostrate hyphae smooth, septate, hyaline, $2.0\text{--}3.0 \mu\text{m}$ diam. Conidial structures consisting of erect conidiophores usually arising from the aerial hyphae, solitary or verticillium-like with phialides in whorls of two to three. Phialides $7.0\text{--}10.6 \times 1.6\text{--}2.1 \mu\text{m}$ ($\bar{x} = 8.8 \times 1.8 \mu\text{m}$, $n=30$), with a cylindrical basal portion, tapering into a distinct neck. Conidia in chains, hyaline, 1-celled, fusiform to ellipsoidal, $1.9\text{--}2.8 \times 1.4\text{--}2.1 \mu\text{m}$ ($\bar{x} = 2.4 \times 1.6 \mu\text{m}$, $n=30$).

Material examined – China, Guizhou Province, Guiyang City, Kaiyang County, Monkey-Ear Tiankeng ($27^{\circ}5'12.138''\text{N}$, $107^{\circ}40'48.42''\text{E}$). On a pupa (*Lepidoptera*), 1 May 2024, Wanhao Chen, GZAC KY4534 (holotype), KY45341 (ex-type), KY45342 (living culture).

Habitat – Near the road, buried in soil.

Notes – Molecular characterization through NCBI BLASTn comparisons and multi-locus phylogenetic analysis (dataset 2, Fig. 2) revealed that *Samsoniella guiyangensis* (KY45341 and KY45342) was grouped within the genus *Samsoniella*, forming a distinct clade with *S. miaolingensis*, which was also supported by the phylogenetic analyses among *Samsoniella* species (Suppl. Fig. 3). Compared with the typical characteristics, *S. guiyangensis* was distinguished from *S. miaolingensis* by its longer phialides ($8.8 \times 1.8 \mu\text{m}$ vs $7.0 \times 2.3 \mu\text{m}$) and smaller conidia (fusiform to ellipsoidal, $2.4 \times 1.6 \mu\text{m}$ vs ellipsoidal, $3.0\text{--}3.8 \times 1.6\text{--}2.2 \mu\text{m}$). The

combined morphological and molecular phylogenetic evidence substantiates the recognition of *S. guiyangensis* as a novel species.

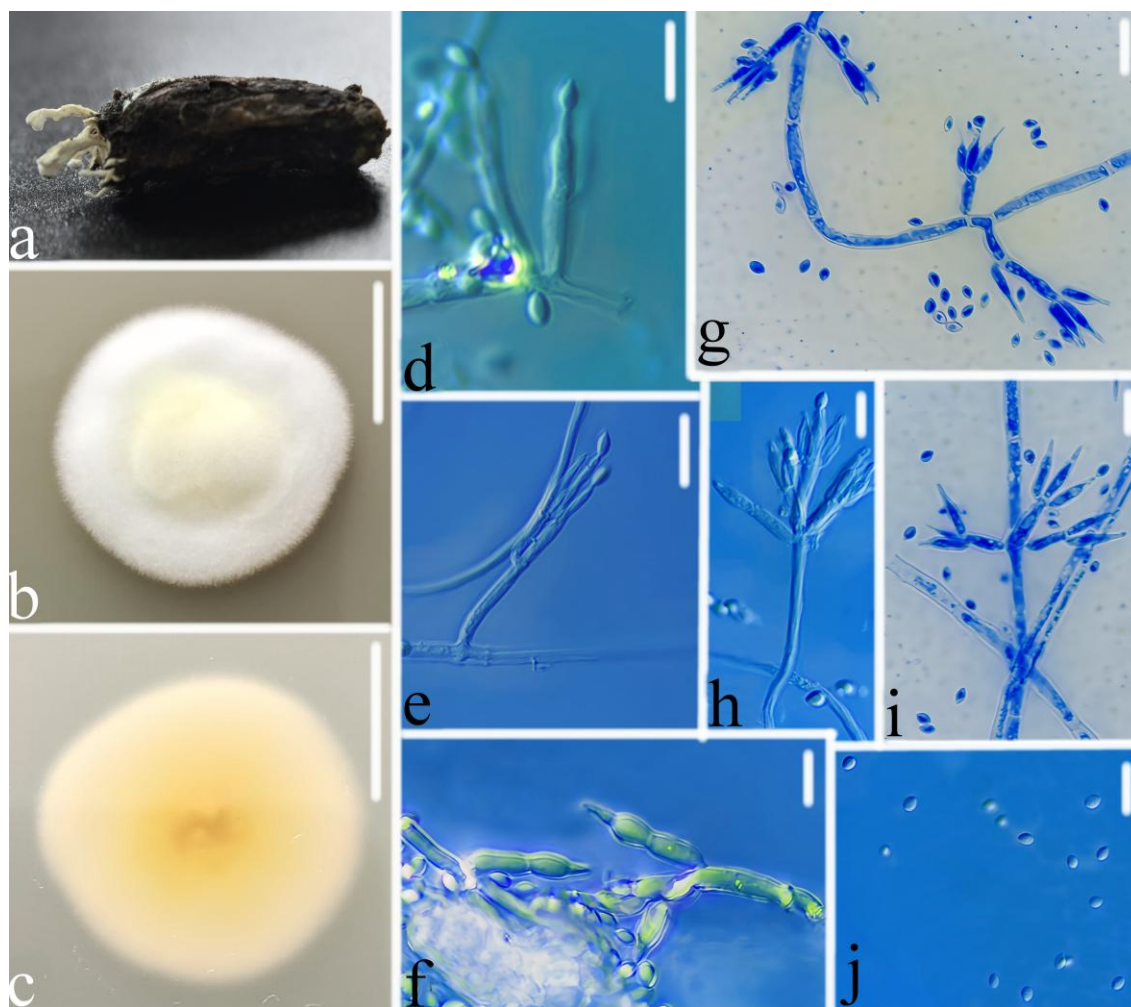


Figure 33 – *Samsoniella guiyangensis* (KY45341, ex-type) a Infected pupa. b–c Colonies on PDA culture media with upper (b) and reverse (c) views. d–f, h, j Phialides and conidia. g, i Phialides and conidia were stained with cotton blue. Scale bars: b–c = 10 mm, d–j = 10 μ m.

Samsoniella houerensis W.H. Chen, Y.F. Han & J.D. Liang, sp. nov.

Fig. 34

Index Fungorum number: 903391; Facesoffungi number: FoF 17496

Etymology – referring to the location, Monkey-Ear Tiankeng, where the fungus was first discovered.

Description – Colonies on PDA reaching 28–32 mm diam. in 14 d at 25°C, white, consisting of a basal felt and cottony, floccose overgrowth, reverse yellowish. Prostrate hyphae smooth, septate, hyaline, 0.7–1.3 μ m diam. Conidial structures consisting of erect conidiophores usually arising from the aerial hyphae, solitary or verticillium-like with phialides in whorls of two to three. Phialides 8.1–11.8 $\times$ 1.0–1.4 μ m ($\bar{x}$ = 9.7 $\times$ 1.2 μ m, n=30), with a cylindrical basal portion, tapering into a distinct neck. Conidia in chains, hyaline, 1-celled, fusiform, 1.1–2.3 $\times$ 0.8–1.4 μ m ($\bar{x}$ = 1.8 $\times$ 1.1 μ m, n=30).

Material examined – China, Guizhou Province, Guiyang City, Kaiyang County, Monkey-Ear Tiankeng (27°5'12.138"N, 107°40'48.42"E). On a pupa (*Lepidoptera*), 1 May 2024, Wanhao Chen, GZAC KY4514 (holotype), KY45141 (ex-type), KY45142 (living culture).

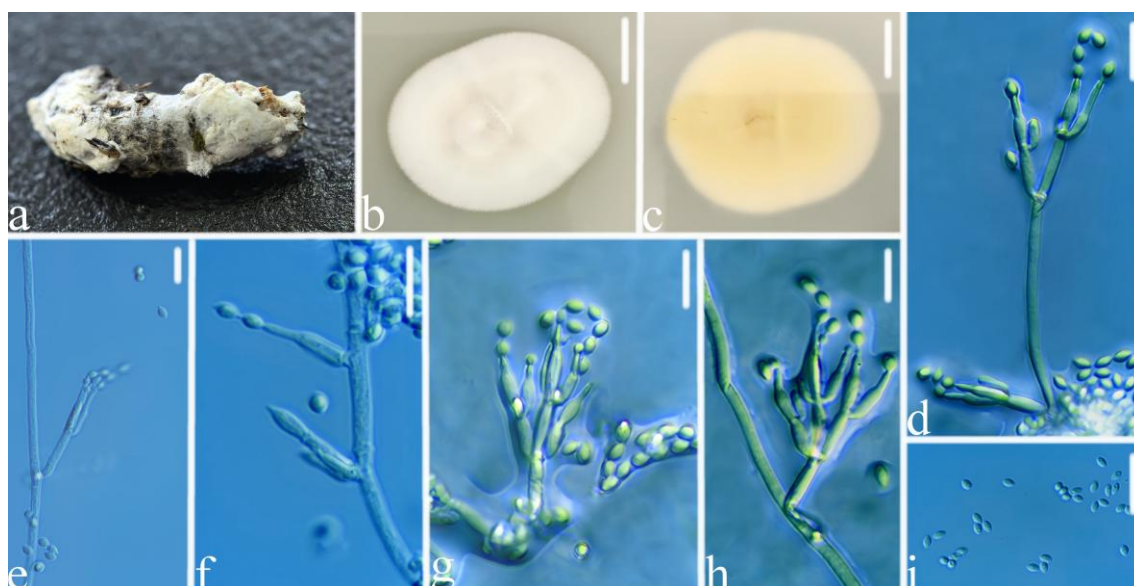


Figure 34 – *Samsoniella houerensis* (KY45141, ex-type) a Infected pupa. b–c Colonies on PDA culture media with upper (b) and reverse (c) views. d–i Phialides and conidia. Scale bars: b–c = 10 mm, d–i = 10 µm.

Habitat – On the underside of leaves of broad-leaved plant species.

Notes – Molecular analyses of concatenated dataset 2 (Fig. 2) and NCBI BLASTn comparisons revealed that *Samsoniella houerensis* (KY45141 and KY45142) was grouped within the genus *Samsoniella*, forming a strongly supported clade (99% ML/1 PP) with its closest relatives *S. hymenopterorum* and *S. zongqii*, which was also supported by the phylogenetic analyses among *Samsoniella* species (Suppl. Fig. 3). Compared with the typical characteristics, *S. houerensis* was distinguished from *S. hymenopterorum* by its longer phialides ($8.1\text{--}11.8 \times 1.0\text{--}1.4 \mu\text{m}$ vs $6.5\text{--}10.6 \times 1.2\text{--}2.0 \mu\text{m}$), smaller fusiform conidia ($1.8 \times 1.1 \mu\text{m}$ vs $1.9\text{--}2.5 \times 1.5\text{--}2.1 \mu\text{m}$) and pupa host (Chen et al. 2020d). *Samsoniella houerensis* was distinguished from *S. zongqii* by its smaller conidia ($1.8 \times 1.1 \mu\text{m}$ vs $2.5\text{--}2.8 \times 1.6\text{--}1.9 \mu\text{m}$) and pupa host. The combined morphological and molecular phylogenetic evidence substantiates the recognition of *S. houerensis* as a novel species.

Samsoniella jiangkouensis W.H. Chen, Y.F. Han & J.D. Liang, sp. nov.

Fig. 35

Index Fungorum number: 903394; Facesoffungi number: FoF 17497

Etymology – referring to the location, Jiangkou County, where the fungus was first discovered.

Description – Colonies on PDA reaching 18–19 mm diam. in 14 d at 25°C, white, consisting of a basal felt and cottony, floccose overgrowth, reverse yellowish. Prostrate hyphae smooth, septate, hyaline, $1.2\text{--}1.3 \mu\text{m}$ diam. Conidial structures consisting of erect conidiophores usually arising from the aerial hyphae, solitary or verticillium-like with phialides in whorls of two to three. Phialides $7.1\text{--}8.8 \times 1.9\text{--}2.4 \mu\text{m}$ ($\bar{x} = 8.1 \times 2.1 \mu\text{m}$, $n=30$), with a cylindrical basal portion, tapering into a distinct neck. Conidia in chains, hyaline, 1-celled, ellipsoidal to subglobose, $2.7\text{--}3.4 \times 2.0\text{--}2.1 \mu\text{m}$ ($\bar{x} = 3.0 \times 2.0 \mu\text{m}$, $n=30$).

Material examined – China, Guizhou Province, Tongren City, Jiangkou County, Fanjing Mountain ($27^{\circ}50'56.98''\text{N}$, $108^{\circ}46'52.28''\text{E}$). On a pupa (*Lepidoptera*), 1 May 2023, Wanhao Chen, GZAC TR0503 (holotype), TR05031 (ex-type), TR05032 (living culture).

Habitat – On the underside of leaves of broad-leaved plant species.

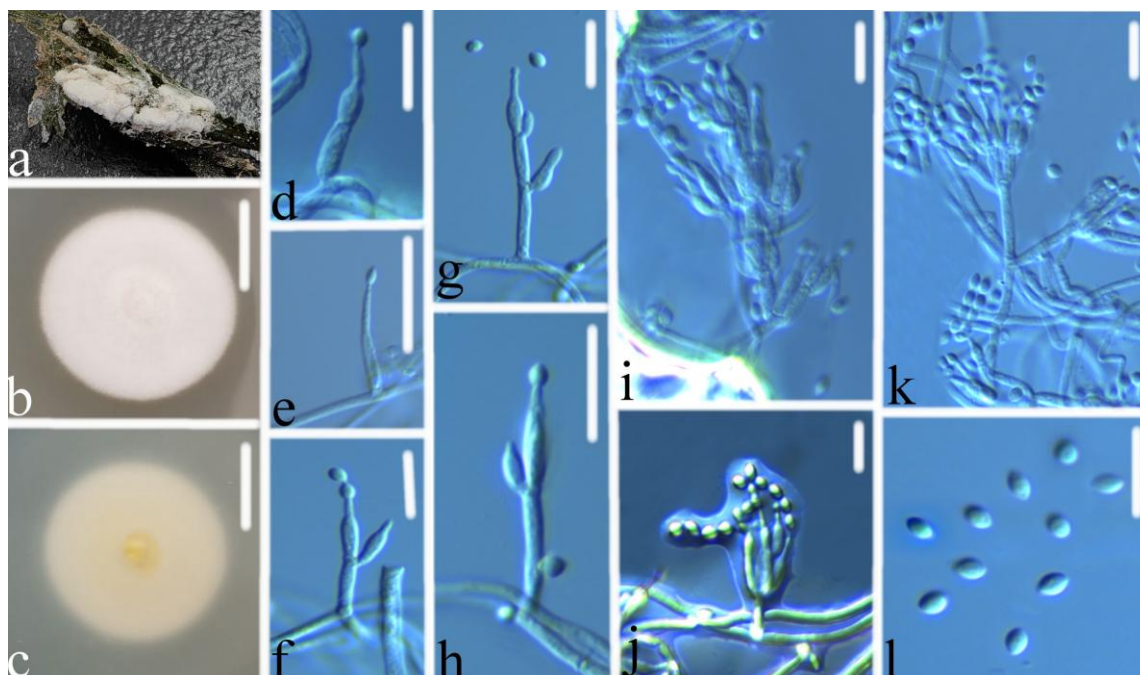


Figure 35 – *Samsoniella jiangkouensis* (TR05031, ex-type) a Infected pupa. b–c Colonies on PDA culture media with upper (b) and reverse (c) views. d–l Phialides and conidia. Scale bars: b–c = 10 mm, d–l = 10 μ m.

Notes – Molecular characterization through NCBI BLASTn comparisons and multi-locus phylogenetic analysis (dataset 2, Fig. 2) revealed that *Samsoniella jiangkouensis* (TR05031 and TR05032) was grouped with *Samsoniella* species, forming a strongly supported clade (98% ML/0.98 PP) with *S. neopupicola*, which was also supported by the phylogenetic analyses among *Samsoniella* species (Suppl. Fig. 3). Compared with the typical characteristics, *S. jiangkouensis* was distinguished from *S. neopupicola* by its shorter phialides ($8.1 \times 2.1 \mu\text{m}$ vs $8.2\text{--}11.7 \times 1.5\text{--}2.3 \mu\text{m}$) and slowly growth on PDA (Chen et al. 2022c). The combined evidence from morphological characteristics and robust molecular phylogenetic analyses substantiates the recognition of *S. jiangkouensis* as a novel species.

Samsoniella kaiyangensis W.H. Chen, Y.F. Han & J.D. Liang, sp. nov.

Fig. 36

Index Fungorum number: 903395; Facesoffungi number: FoF 17498

Etymology – referring to the location, Kaiyang County, where the fungus was first discovered.

Description – Colonies on PDA reaching 36–39 mm diam. in 14 d at 25°C, white, consisting of a basal felt and cottony, floccose overgrowth, reverse yellowish. Prostrate hyphae smooth, septate, hyaline, 1.5–2.0 μm diam. Conidial structures consisting of erect conidiophores usually arising from the aerial hyphae, solitary or verticillium-like with phialides in whorls of two to three. Phialides $7.9\text{--}14.8 \times 1.8\text{--}2.8 \mu\text{m}$ ($\bar{x} = 10.5 \times 2.3 \mu\text{m}$, $n=30$), with a cylindrical basal portion, tapering into a distinct neck. Conidia in chains, hyaline, 1-celled, ellipsoidal to globose, $2.2\text{--}3.2 \times 1.7\text{--}2.2 \mu\text{m}$ ($\bar{x} = 2.9 \times 1.9 \mu\text{m}$, $n=30$).

Material examined – China, Guizhou Province, Guiyang City, Kaiyang County, Monkey-Ear Tiankeng ($27^{\circ}5'12.138''\text{N}$, $107^{\circ}0'48.42''\text{E}$). On a pupa (*Lepidoptera*), 1 May 2024, Wanhao Chen, GZAC KY4538 (holotype), KY45381 (ex-type), KY45382 (living culture).

Habitat – On the underside of leaves of broad-leaved plant species.

Notes – Molecular analyses of concatenated dataset 2 (Fig. 2) and NCBI BLASTn comparisons revealed that *Samsoniella kaiyangensis* (KY45381 and KY45382) was grouped within the genus *Samsoniella*, forming a maximally supported clade (100% ML/1 PP) with its closest relatives *S. tongrenensis* and *S. suiyangensis*, which was also supported by the phylogenetic

analyses among *Samsoniella* species (Suppl. Fig. 3). Compared with the typical characteristics, *S. kaiyangensis* was distinguished from *S. tongrenensis* by its longer phialides ($10.5 \times 2.3 \mu\text{m}$ vs $9.2 \times 1.8 \mu\text{m}$). *Samsoniella kaiyangensis* was distinguished from *S. suiyangensis* by its longer phialides ($10.5 \times 2.3 \mu\text{m}$ vs $8.0 \times 1.8 \mu\text{m}$). The combined morphological and molecular phylogenetic evidence substantiates the recognition of *S. kaiyangensis* as a new species.

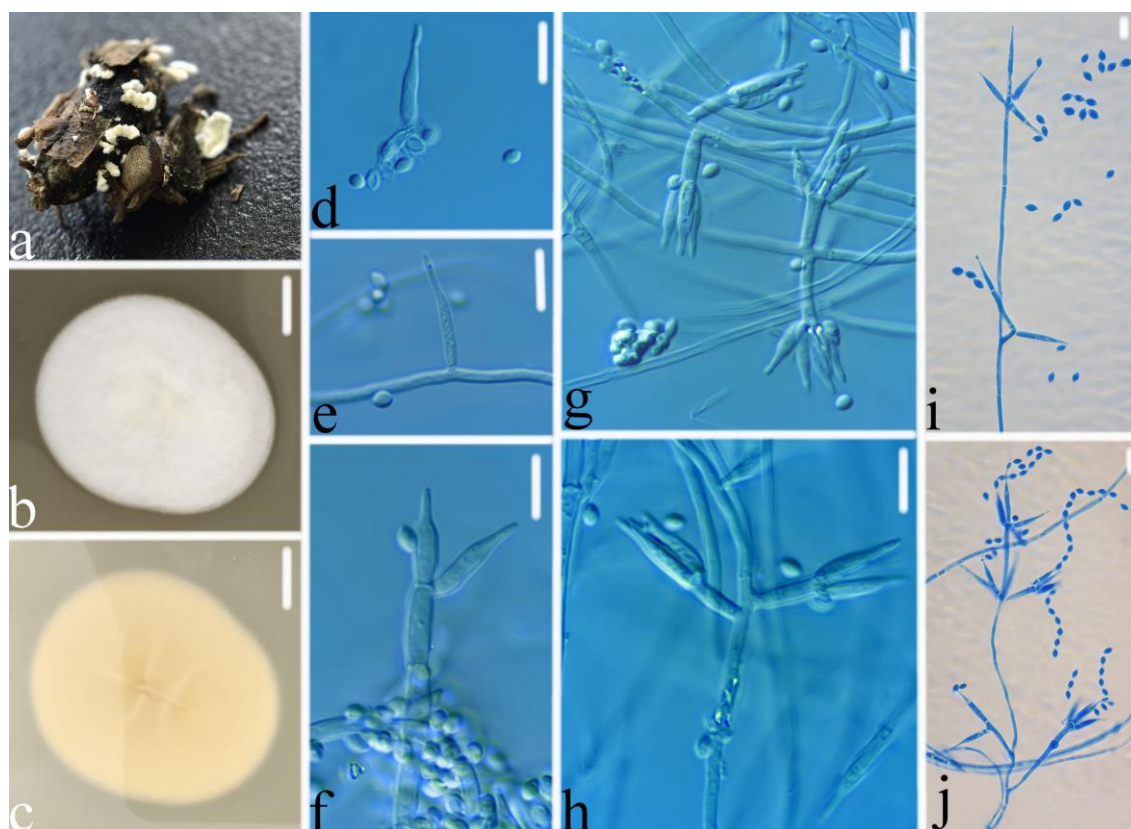


Figure 36 – *Samsoniella kaiyangensis* (KY45381, ex-type) a Infected pupa. b–c Colonies on PDA culture media with upper (b) and reverse (c) views. d–h Phialides and conidia. i, j Phialides and conidia were stained with cotton blue. Scale bars: b–c = 10 mm, d–j = 10 μm .

Samsoniella miaolingensis W.H. Chen, Y.F. Han & J.D. Liang, sp. nov.

Fig. 37

Index Fungorum number: 903396; Facesoffungi number: FoF 17499

Etymology – referring to the location, Miaoling Mountains, where the fungus was first discovered.

Description – Colonies on PDA reaching 64–66 mm diam. in 14 d at 25°C, white, consisting of a basal felt and cottony, floccose overgrowth, reverse yellowish. Prostrate hyphae smooth, septate, hyaline, 1.7–2.2 μm diam. Conidial structures consisting of erect conidiophores usually arising from the aerial hyphae, solitary or verticillium-like with phialides in whorls of two to three. Phialides $6.2\text{--}8.2 \times 1.9\text{--}2.6 \mu\text{m}$ ($\bar{x} = 7.0 \times 2.3 \mu\text{m}$, $n=30$), with a cylindrical basal portion, tapering into a distinct neck. Conidia in chains, hyaline, 1-celled, ellipsoidal, $3.0\text{--}3.8 \times 1.6\text{--}2.2 \mu\text{m}$ ($\bar{x} = 3.3 \times 1.7 \mu\text{m}$, $n=30$).

Material examined – China, Guizhou Province, Qiannan Buyei and Miao Autonomous Prefecture, Duyun City, Mayao River Valley ($26^{\circ}22'8.3748''\text{N}$, $107^{\circ}23'16.96''\text{E}$). On a pupa (*Lepidoptera*), 1 May 2022, Wanhao Chen, GZAC DY0581 (holotype), DY05811 (ex-type), DY05812 (living culture).

Habitat – On the underside of leaves of broad-leaved plant species.

Notes – Molecular characterization through NCBI BLASTn comparisons and multi-locus phylogenetic analysis (dataset 2, Fig. 2) revealed that *Samsoniella miaolingensis* (DY05811 and DY05812) was grouped with *Samsoniella* species, forming a distinct clade with *S. guiyangensis*,

which was also supported by the phylogenetic analyses among *Samsoniella* species (Suppl. Fig. 3). Compared with the typical characteristics, *S. miaolingensis* was distinguished from *S. guiyangensis* by its shorter phialides ($7.0 \times 2.3 \mu\text{m}$ vs $8.8 \times 1.8 \mu\text{m}$) and larger conidia (ellipsoidal, $3.3 \times 1.7 \mu\text{m}$ vs fusiform to ellipsoidal, $2.4 \times 1.6 \mu\text{m}$). The combined morphological and molecular phylogenetic evidence substantiates the recognition of *S. miaolingensis* as a new species.

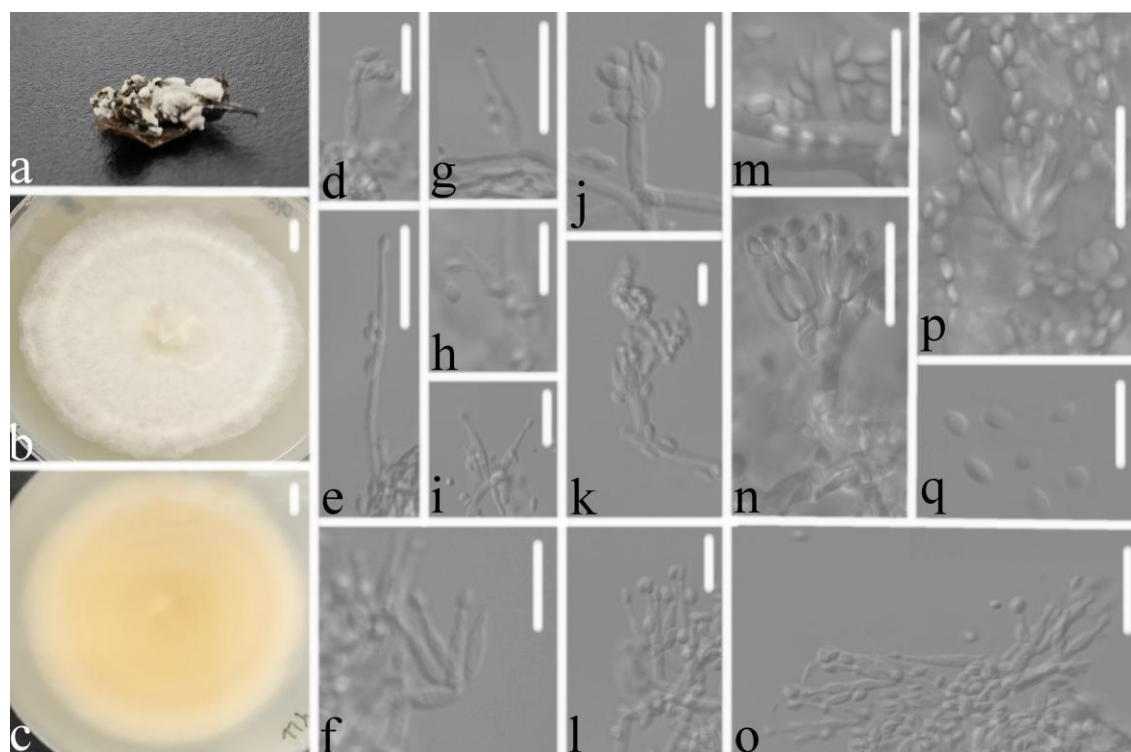


Figure 37 – *Samsoniella miaolingensis* (DY05811, ex-type) a Infected pupa. b–c Colonies on PDA culture media with upper (b) and reverse (c) views. d–q Phialides and conidia. Scale bars: b–c = 10 mm, d–q = 10 μm .

Samsoniella simplicola W.H. Chen, Y.F. Han & J.D. Liang, sp. nov.

Fig. 38

Index Fungorum number: 903397; Facesoffungi number: FoF 17500

Etymology – referring to its simply arrangement of phialides.

Description – Colonies on PDA reaching 26–28 mm diam. in 14 d at 25°C, white, consisting of a basal felt and cottony, floccose overgrowth, reverse yellowish. Prostrate hyphae smooth, septate, hyaline, 1.5–2.8 μm diam. Conidial structures consisting of erect conidiophores usually arising from the aerial hyphae, solitary or phialides in whorls of two. Phialides 8.9–16.3 $\times$ 2.3–3.1 μm ($\bar{x}$ = 11.8 $\times$ 2.7 μm , n=30), with a cylindrical basal portion, tapering into a distinct neck. Conidia in chains, hyaline, 1-celled, fusiform to ellipsoidal, 2.3–3.2 $\times$ 1.8–2.2 μm ($\bar{x}$ = 2.8 $\times$ 2.0 μm , n=30).

Material examined – China, Guizhou Province, Qiannan Buyei and Miao Autonomous Prefecture, Duyun City, Mayao River Valley (26°22'8.3748"N, 107°23'16.96"E). On a pupa (*Lepidoptera*), 1 May 2024, Wanhao Chen, GZAC DY4512 (holotype), DY45121 (ex-type), DY45122 (living culture).

Habitat – On the underside of leaves of broad-leaved plant species.

Notes – Molecular analyses of concatenated dataset 2 (Fig. 2) and NCBI BLASTn comparisons revealed that *Samsoniella simplicola* (DY45121 and DY45122) was grouped within the genus *Samsoniella*, forming a maximally supported clade (100% ML/1 PP) with its closest relative *S. pupicola*, which was also supported by the phylogenetic analyses among *Samsoniella* species (Suppl. Fig. 3). Compared with the typical characteristics, *S. simplicola* was distinguished from *S. pupicola* by its longer phialides (11.8 $\times$ 2.7 μm vs 7.0–9.2 $\times$ 2.5–3.3 μm) (Chen et al.

2021b). The combined morphological and molecular phylogenetic evidence substantiates the recognition of *S. simplicola* as a novel species.

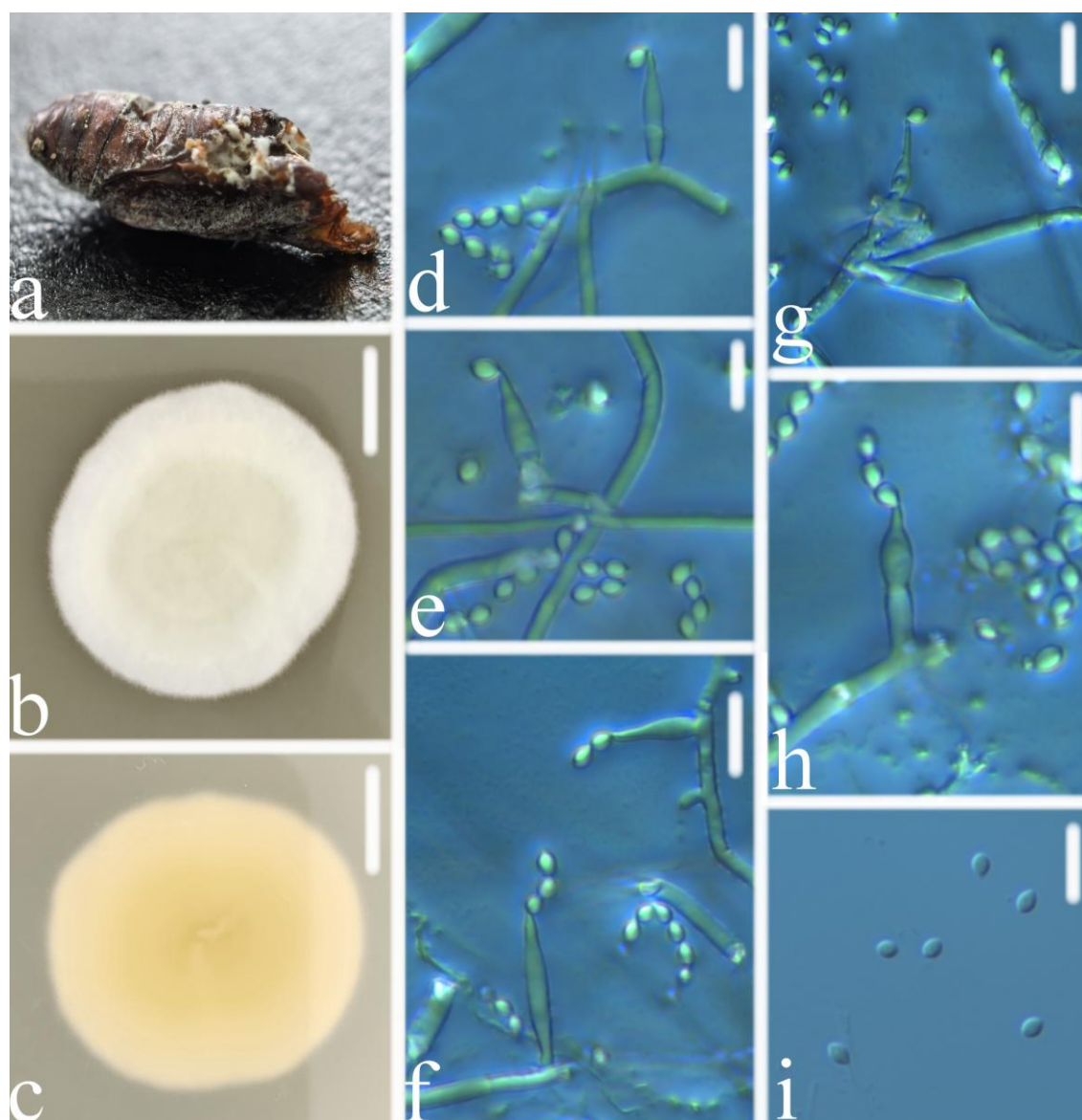


Figure 38 – *Samsoniella simplicola* (DY45121, ex-type) a Infected pupa. b–c Colonies on PDA culture media with upper (b) and reverse (c) views. d–i Phialides and conidia. Scale bars: b–c = 10 mm, d–i = 10 μ m.

Samsoniella suiyangensis W.H. Chen, Y.F. Han & J.D. Liang, sp. nov.

Fig. 39

Index Fungorum number: 903398; Facesoffungi number: FoF 17501

Etymology – referring to the location, Suiyang County, where the fungus was first discovered.

Description – Colonies on PDA reaching 25–29 mm diam. in 14 d at 25°C, white, consisting of a basal felt and cottony, floccose overgrowth, reverse yellowish. Prostrate hyphae smooth, septate, hyaline, 1.7–1.9 μ m diam. Conidial structures consisting of erect conidiophores usually arising from the aerial hyphae, solitary or verticillium-like with phialides in whorls of two to three. Phialides 6.6–9.3 $\times$ 1.6–2.2 μ m ($\bar{x}$ = 8.0 $\times$ 1.8 μ m, n=30), with a cylindrical basal portion, tapering into a distinct neck. Conidia in chains, hyaline, 1-celled, ellipsoidal, 2.5–2.9 $\times$ 1.6–2.1 μ m ($\bar{x}$ = 2.7 $\times$ 1.9 μ m, n=30).

Material examined – China, Guizhou Province, Zunyi City, Suiyang County, Shuangmen Valley (28°1'39.05"N, 107°7'58.65"E). On a dead leafhopper (*Cicadellidae*), 30 September 2023, Wanhao Chen, GZAC SY0982 (holotype), SY09821 (ex-type), SY09822 (living culture).

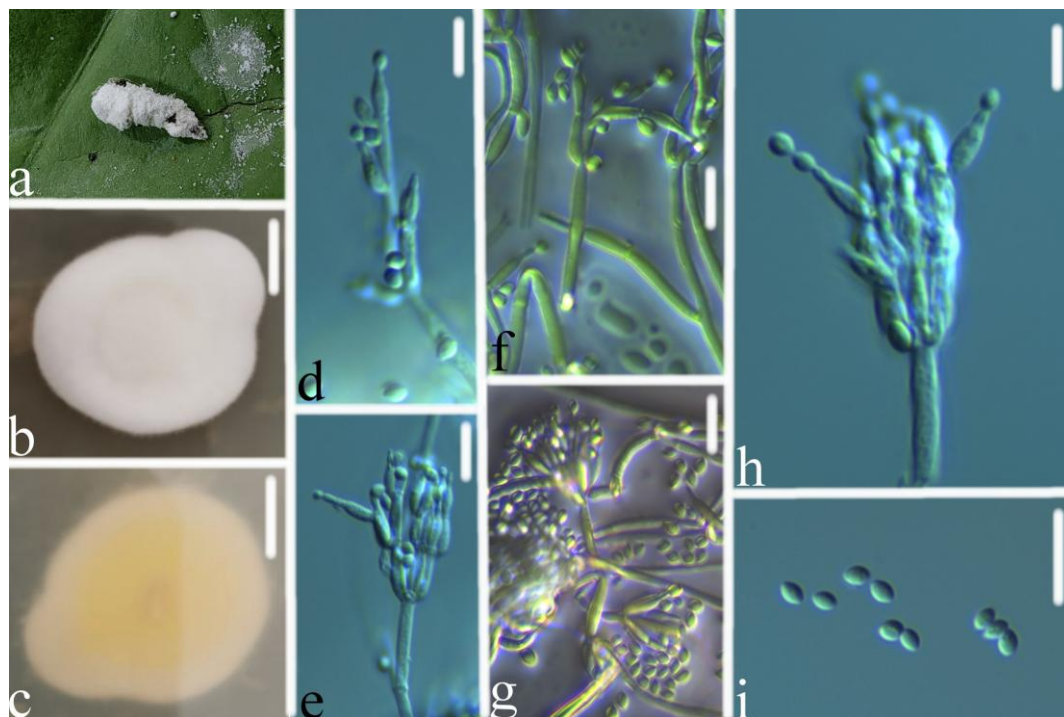


Figure 39 – *Samsoniella suiyangensis* (SY09821, ex-type) a Infected pupa. b–c Colonies on PDA culture media with upper (b) and reverse (c) views. d–i Phialides and conidia. Scale bars: b–c = 10 mm, d–i = 10 µm.

Habitat – On the underside of leaves of broad-leaved plant species.

Notes – Molecular characterization through NCBI BLASTn comparisons and multi-locus phylogenetic analysis (dataset 2, Fig. 2) revealed that *Samsoniella suiyangensis* (SY09821 and SY09822) was grouped with *Samsoniella* species, forming a maximally supported clade (100% ML/1 PP) with its closest relatives *S. kaiyangensis* and *S. tongrenensis*, which was also supported by the phylogenetic analyses among *Samsoniella* species (Suppl. Fig. 3). Compared with the typical characteristics, *S. suiyangensis* was distinguished from *S. kaiyangensis* by its shorter phialides ($8.0 \times 1.8 \mu\text{m}$ vs $10.5 \times 2.3 \mu\text{m}$). *Samsoniella suiyangensis* was distinguished from *S. tongrenensis* by its shorter phialides ($8.0 \times 1.8 \mu\text{m}$ vs $9.2 \times 1.8 \mu\text{m}$). The combined morphological and molecular phylogenetic evidence substantiates the recognition of *S. suiyangensis* as a novel species.

Samsoniella tongrenensis W.H. Chen, Y.F. Han & J.D. Liang, sp. nov.

Fig. 40

Index Fungorum number: 903399; Facesoffungi number: FoF 17502

Etymology – referring to the location, Tongren City, where the fungus was first discovered.

Description – Colonies on PDA reaching 24–25 mm diam. in 14 d at 25°C, white, consisting of a basal felt and cottony, floccose overgrowth, reverse yellowish. Prostrate hyphae smooth, septate, hyaline, 1.5–2.1 µm diam. Conidial structures consisting of erect conidiophores usually arising from the aerial hyphae, solitary or verticillium-like with phialides in whorls of two to three. Phialides 8.0–11.0 × 1.7–1.9 µm ($\bar{x} = 9.2 \times 1.8 \mu\text{m}$, n=30), with a cylindrical basal portion, tapering into a distinct neck. Conidia in chains, hyaline, 1-celled, ellipsoidal to globose, 2.5–3.2 × 1.9–2.5 µm ($\bar{x} = 2.9 \times 2.1 \mu\text{m}$, n=30).

Material examined – China, Guizhou Province, Tongren City, Jiangkou County, Fanjing Mountain (27°50'56.98"N, 108°46'52.28"E). On a pupa (*Lepidoptera*), 1 May 2023, Wanhao Chen, GZAC TR0513 (holotype), TR05131 (ex-type), TR05132 (living culture).

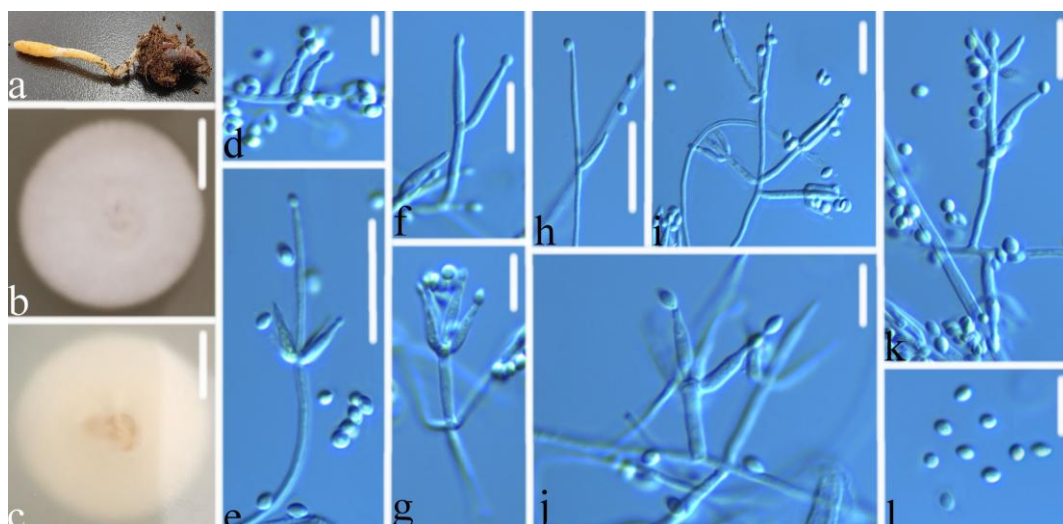


Figure 40 – *Samsoniella tongrenensis* (TR05131, ex-type) a Infected pupa. b–c Colonies on PDA culture media with upper (b) and reverse (c) views. d–l Phialides and conidia. Scale bars: b–c = 10 mm, d–l = 10 μ m.

Habitat – Near the road, buried in soil.

Notes – Molecular analyses of concatenated dataset 2 (Fig. 2) and NCBI BLASTn comparisons revealed that *Samsoniella tongrenensis* (TR05131 and TR05132) was grouped within the genus *Samsoniella*, forming a maximally supported clade (100% ML/1 PP) with its closest relatives *S. kaiyangensis* and *S. suiyangensis*, which was also supported by the phylogenetic analyses among *Samsoniella* species (Suppl. Fig. 3). Compared with the typical characteristics, *S. tongrenensis* was distinguished from *S. kaiyangensis* by its shorter phialides ($9.2 \times 1.8 \mu\text{m}$ vs $10.5 \times 2.3 \mu\text{m}$). *Samsoniella tongrenensis* was distinguished from *S. suiyangensis* by its longer phialides ($9.2 \times 1.8 \mu\text{m}$ vs $8.0 \times 1.8 \mu\text{m}$). The distinct morphological features and molecular phylogenetic data collectively validate *S. tongrenensis* as a novel species.

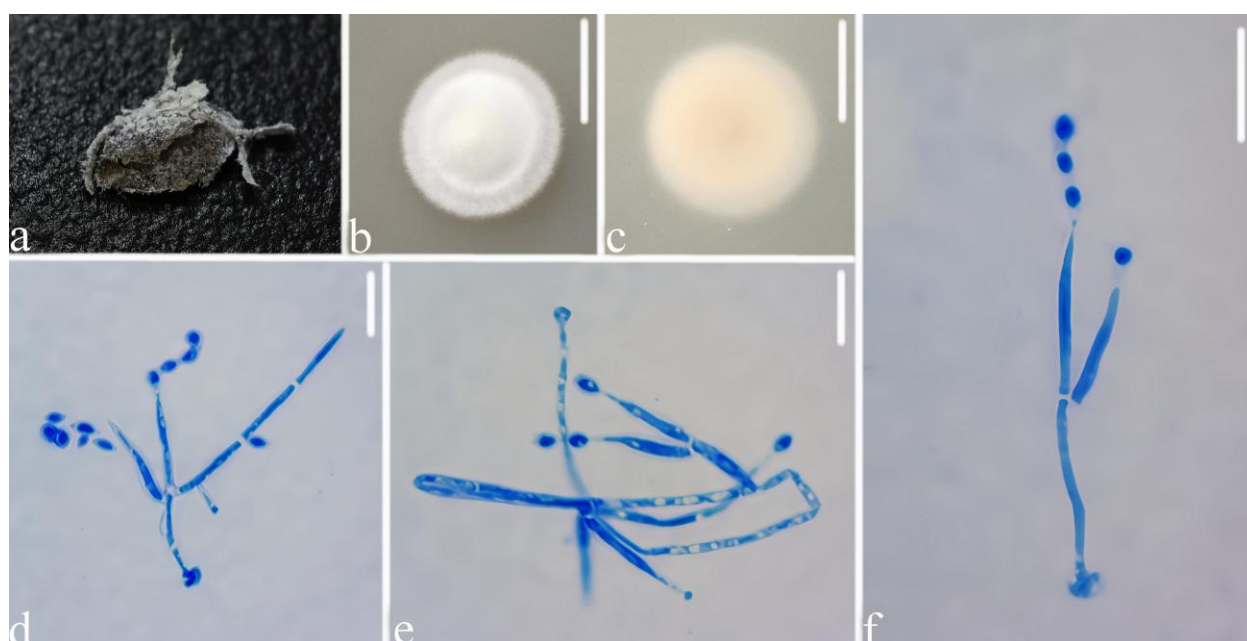


Figure 41 – *Samsoniella wudangensis* (WD04121, ex-type) a Infected pupa. b–c Colonies on PDA culture media with upper (b) and reverse (c) views. d–f Phialides and conidia were stained with cotton blue. Scale bars: b–c = 10 mm, d–f = 10 μ m.

Samsoniella wudangensis W.H. Chen, Y.F. Han & J.D. Liang, sp. nov.

Fig. 41

Index Fungorum number: 903400; Facesoffungi number: FoF 17503

Etymology – referring to the location, Wudang District, where the fungus was first discovered.

Description – Colonies on PDA reaching 15–16 mm diam. in 14 d at 25°C, white, consisting of a basal felt and cottony, floccose overgrowth, reverse yellowish. Prostrate hyphae smooth, septate, hyaline, 1.3–1.6 µm diam. Conidial structures consisting of erect conidiophores usually arising from the aerial hyphae, solitary or verticillium-like with phialides in whorls of two to three. Phialides 10.6–15.0 × 1.5–2.2 µm ($\bar{x}$ = 12.5 × 1.6 µm, n=30), with a cylindrical basal portion, tapering into a distinct neck. Conidia in chains, hyaline, 1-celled, ellipsoidal, 2.7–3.2 × 1.7–2.2 µm ($\bar{x}$ = 2.9 × 1.9 µm, n=30).

Material examined – China, Guizhou Province, Guiyang City, Wudang District, Bala Valley (26°45'7.0344"N, 106°58'57.09"E). On a larva (*Lepidoptera*), 5 April 2024, Wanhao Chen, GZAC WD0412 (holotype), WD04121 (ex-type), WD04122 (living culture).

Habitat – On the underside of leaves of broad-leaved plant species.

Notes – Molecular characterization through NCBI BLASTn comparisons and multi-locus phylogenetic analysis (dataset 2, Fig. 2) revealed that *Samsoniella wudangensis* (WD04121 and WD04122) was grouped within the genus *Samsoniella*, forming a maximally supported clade (100% ML/1 PP) with *S. anhuiensis*, which was also supported by the phylogenetic analyses among *Samsoniella* species (Suppl. Fig. 3). Compared with the typical characteristics, *S. wudangensis* was distinguished from *S. anhuiensis* by its longer phialides [10.6–15.0 × 1.5–2.2 µm vs (7.0–)8.0–11.5(–13.0) × 1.3–2.2 µm] and larva host (Wang et al. 2024a). Based on the morphological characteristics and robust phylogenetic support, we formally describe *S. wudangensis* as a novel taxon.

Samsoniella zongqii W.H. Chen, Y.F. Han & J.D. Liang, sp. nov.

Fig. 42

Index Fungorum number: 903401; Facesoffungi number: FoF 17504

Etymology – In honor of Prof. Zongqi Liang, for his support and guidance in arthropod pathogenic fungi research.

Description – Colonies on PDA reaching 27–28 mm diam. in 14 d at 25°C, white, consisting of a basal felt and cottony, floccose overgrowth, reverse yellowish. Prostrate hyphae smooth, septate, hyaline, 1.5–2.9 µm diam. Conidial structures consisting of erect conidiophores usually arising from the aerial hyphae, solitary or verticillium-like with phialides in whorls of two to three. Phialides 6.8–11.3 × 1.8–2.2 µm ($\bar{x}$ = 8.8 × 2.1 µm, n=30), with a cylindrical basal portion, tapering into a distinct neck. Conidia in chains, hyaline, 1-celled, fusiform, 2.5–2.8 × 1.6–1.9 µm ($\bar{x}$ = 2.6 × 1.8 µm, n=30).

Material examined – China, Guizhou Province, Qiannan Buyei and Miao Autonomous Prefecture, Duyun City, Mayao River Valley (26°22'8.3748"N, 107°23'16.96"E). On a larva (*Lepidoptera*), 1 May 2024, Wanhao Chen, GZAC DY4525 (holotype), DY45251 (ex-type), DY45252 (living culture).

Habitat – Near the road, living in soil.

Notes – Molecular analyses of concatenated dataset 2 (Fig. 2) and NCBI BLASTn comparisons revealed that *Samsoniella zongqii* (DY45251 and DY45252) was grouped within the genus *Samsoniella*, forming a strongly supported clade (99% ML/1 PP) with *S. houerensis* and *S. hymenopterorum*, which was also supported by the phylogenetic analyses among *Samsoniella* species (Suppl. Fig. 3). Compared with the typical characteristics, *S. zongqii* was distinguished from *S. houerensis* by its larger conidia (2.6 × 1.8 µm vs 1.8 × 1.1 µm) and pupa host. *Samsoniella zongqii* was distinguished from *S. hymenopterorum* by its larger conidia (2.6 × 1.8 µm vs 1.9–2.5 × 1.5–2.1 µm) and larva host (Chen et al. 2020d). The congruent morphological and molecular phylogenetic evidence conclusively establishes *S. zongqii* as a new species.

Simplicillium W. Gams & Zare, Nova Hedwigia 73(1-2): 38 (2001)

Type species – *Simplicillium lanosoniveum* (J.F.H. Beyma) Zare & W. Gams 2001

Notes – The genus *Simplicillium* was circumscribed by Zare & Gams with *S. lanosoniveum* designated as the type species, along with other three species, *S. lamellicola* (F.E.V. Sm.) Zare & W. Gams, *S. obclavatum* (W. Gams) Zare & W. Gams and *S. wallacei* H.C. Evans. Chen et al. (2024c) summarized that *Simplicillium* consists of 29 species and introduced 2 new species. Custódio & Pereira (2024) introduced a new species, *Simplicillium pseudocercosporicola* F.A. Custódio & O.L. Pereira. In the present study, 6 new species were introduced.

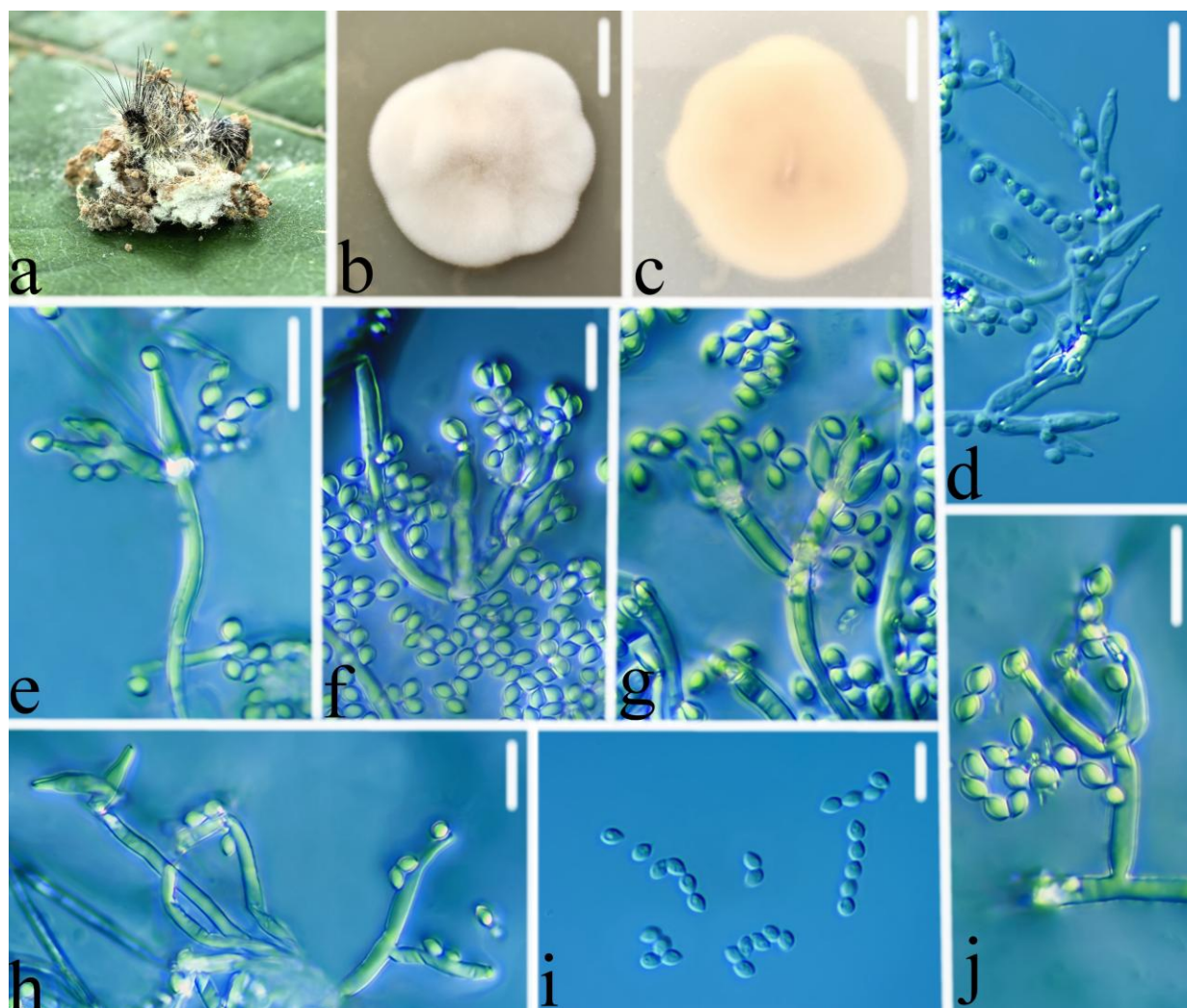


Figure 42 – *Samsoniella zongqii* (DY45251, ex-type) a Infected larva. b–c Colonies on PDA culture media with upper (b) and reverse (c) views. d–j Phialides and conidia. Scale bars: b–c = 10 mm, d–j = 10 μ m.

Simplicillium araneicola W.H. Chen, Y.F. Han & J.D. Liang, sp. nov.

Fig. 43

Index Fungorum number: 903402; Facesoffungi number: FoF 17505

Etymology – referring to its spider host.

Description – Colonies on PDA reaching 19–20 mm diam. in 14 d at 25°C, white, consisting of a basal felt and cottony, floccose overgrowth, reverse yellowish. Prostrate hyphae smooth, septate, hyaline, 1.1–1.8 μ m diam. Conidial structures consisting of erect conidiophores usually arising from the aerial hyphae, solitary or phialides in whorls of two. Phialides 10.6–14.4 $\times$ 0.8–1.1 μ m ($\bar{x}$ = 12.3 $\times$ 0.9 μ m, n=30), with a cylindrical basal portion, tapering into a distinct neck. Conidia hyaline, 1-celled, macroconidia nuciformis, 4.0–5.1 $\times$ 0.9–1.1 μ m ($\bar{x}$ = 4.6 $\times$ 1.0 μ m, n=30); microconidia fusiform, 1.7–2.5 $\times$ 0.9–1.1 μ m ($\bar{x}$ = 2.2 $\times$ 1.0 μ m, n=30).

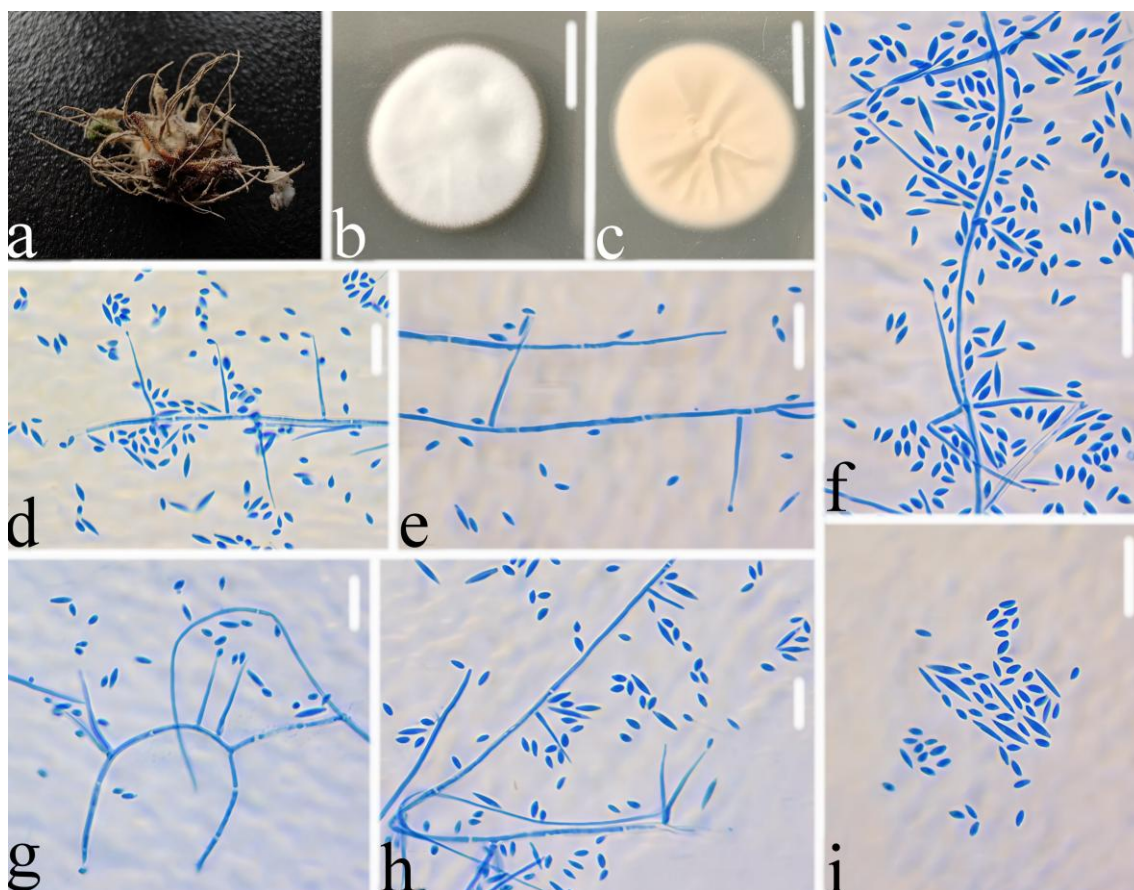


Figure 43 – *Simplicillium araneicola* (DY11251, ex-type) a Infected spider. b–c Colonies on PDA culture media with upper (b) and reverse (c) views. d–i Phialides and conidia were stained with cotton blue. Scale bars: b–c = 10 mm, d–i = 10 µm.

Material examined – China, Guizhou Province, Qiannan Buyei and Miao Autonomous Prefecture, Duyun City, Mayao River Valley (26°22'8.3748"N, 107°23'16.96"E). On a spider (*Araneae*), 25 November 2023, Wanhao Chen, GZAC DY1125 (holotype), DY11251 (ex-type), DY11252 (living culture).

Habitat – Near the road, located on or under the rock.

Notes – Molecular analyses of concatenated dataset 2 (Fig. 2) and NCBI BLASTn comparisons revealed that *Simplicillium araneicola* (DY11251 and DY11252) was grouped within the genus *Simplicillium*, forming a maximally supported clade (100% ML/0.99 PP) with its closest relatives *S. cantharise* and *S. zunyiense*, which was also supported by the phylogenetic analyses among *Simplicillium* species (Suppl. Fig. 5). Compared with the typical characteristics, *S. araneicola* was distinguished from *S. cantharise* by its two types of conidia, shorter phialides ($10.6\text{--}14.4 \times 0.8\text{--}1.1 \mu\text{m}$ vs $47.1\text{--}74.9 \times 1.8\text{--}2.8 \mu\text{m}$) and spider host. *Simplicillium araneicola* was distinguished from *S. zunyiense* by its shorter phialides ($12.3 \times 0.9 \mu\text{m}$ vs $16.1 \times 1.2 \mu\text{m}$) and smaller conidia (macroconidia, $4.0\text{--}5.1 \times 0.9\text{--}1.1 \mu\text{m}$, microconidia, $1.7\text{--}2.5 \times 0.9\text{--}1.1 \mu\text{m}$ vs macroconidia, $4.1\text{--}6.7 \times 1.2\text{--}1.7 \mu\text{m}$, microconidia, $2.1\text{--}3.0 \times 1.3\text{--}1.5 \mu\text{m}$). The combined morphological and molecular phylogenetic evidence substantiates the recognition of *S. araneicola* as a novel species.

Simplicillium bursae W.H. Chen, Y.F. Han & J.D. Liang, sp. nov.

Index Fungorum number: 903403; Facesoffungi number: FoF 17506

Etymology – from the Latin “bursae” means the cocoon, refers to its cocoon host.

Fig. 44

Description – Colonies on PDA reaching 19–21 mm diam. in 14 d at 25°C, white, consisting of a basal felt and cottony, floccose overgrowth, reverse yellowish. Prostrate hyphae smooth, septate, hyaline, 0.9–1.4 μm diam. Conidial structures consisting of erect conidiophores usually arising from the aerial hyphae, solitary or phialides in whorls of two. Phialides 13.1–26.2 $\times$ 0.7–1.1 μm ($\bar{x}$ = 21.0 $\times$ 0.8 μm , n=30), with a cylindrical basal portion, tapering into a distinct neck. Conidia hyaline, 1-celled, ellipsoidal to subglobose, 1.6–2.5 $\times$ 1.2–1.6 μm ($\bar{x}$ = 1.9 $\times$ 1.3 μm , n=30).

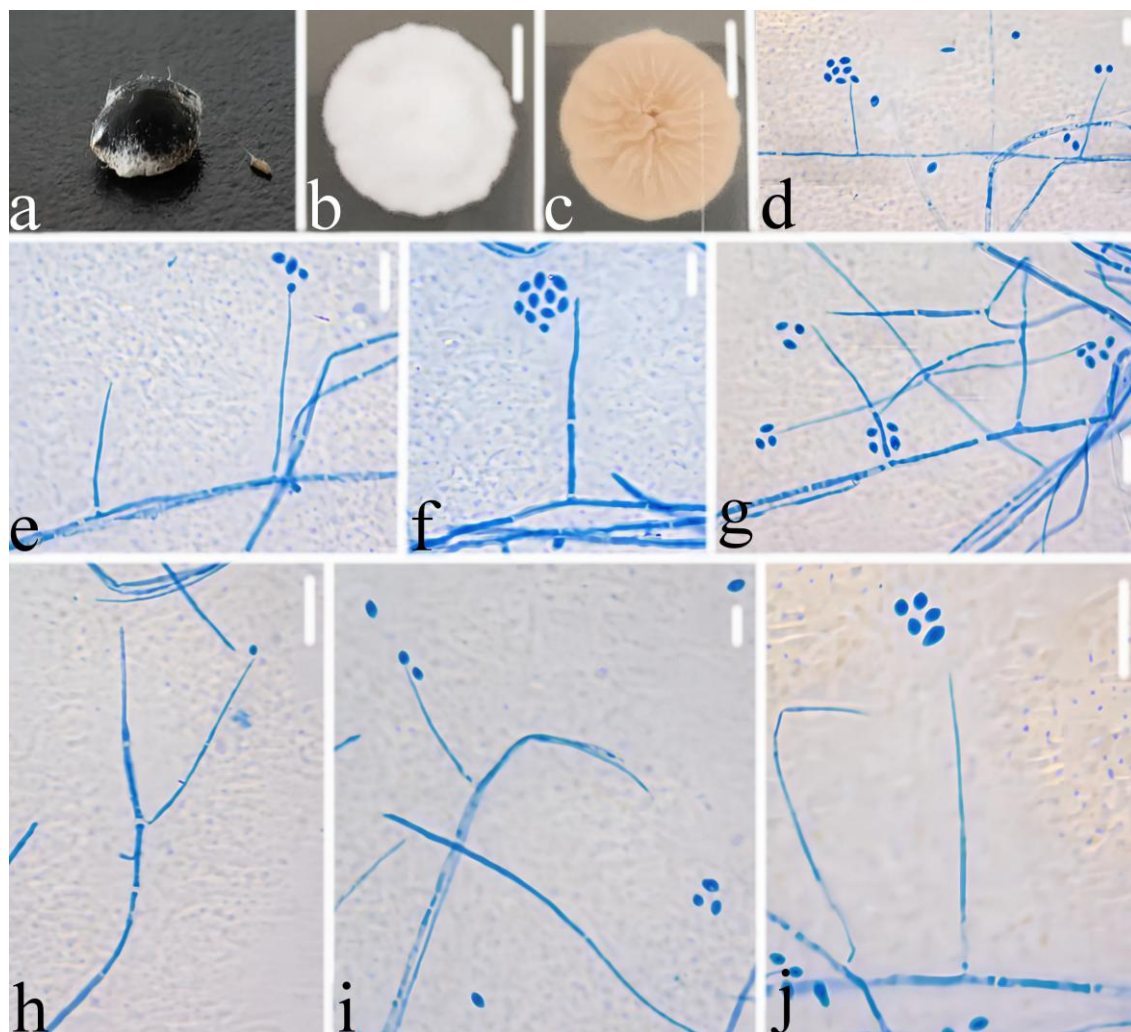


Figure 44 – *Simplicillium bursae* (ZY06121, ex-type) a Infected cocoon. b–c Colonies on PDA culture media with upper (b) and reverse (c) views. d–j Phialides and conidia were stained with cotton blue. Scale bars: b–c = 10 mm, d–j = 10 μm .

Material examined – China, Guizhou Province, Zunyi City, Honghuagang District, Dabanshui National Forest Park (27°46'35.904"N, 106°48'30.89"E). On a cocoon (*Lepidoptera*), 3 June 2022, Wanhao Chen, GZAC ZY0612 (holotype), ZY06121 (ex-type), ZY06122 (living culture).

Habitat – On the underside of leaves of broad-leaved plant species.

Notes – Molecular characterization through NCBI BLASTn comparisons and multi-locus phylogenetic analysis (dataset 2, Fig. 2) revealed that *Simplicillium bursae* (ZY06121 and ZY06122) as a distinct species within the genus *Simplicillium*, and have close relationship with *S. cylindrosporum* Nonaka et al. and *S. sinense* X.Y. Yuan et al., which was also supported by the phylogenetic analyses among *Simplicillium* species (Suppl. Fig. 5). Compared with the typical characteristics, *S. bursae* were distinguished from *S. cylindrosporum* by its smaller conidia [ellipsoidal to subglobose, 1.9 $\times$ 1.3 μm vs cylindrical, 3.0–4.5(–5.0) $\times$ 1.0–2.0 μm]. *S. bursae* were

distinguished from *S. cylindrosporum* by its shorter phialides ($21.0 \times 0.8 \mu\text{m}$ vs $26.0 \times 1.0 \mu\text{m}$). The morphological characteristics and phylogenetic analysis supported *S. bursae* as a new species.

Simplicillium cantharise W.H. Chen, Y.F. Han & J.D. Liang, sp. nov.

Fig. 45

Index Fungorum number: 903404; Facesoffungi number: FoF 17507

Etymology – from the Latin “cantharise” means the beetle, refers to its beetle host.

Description – Colonies on PDA reaching 49–52 mm diam. in 14 d at 25°C, white, consisting of a basal felt and cottony, floccose overgrowth, reverse yellowish. Prostrate hyphae smooth, septate, hyaline, 2.2–3.3 μm diam. Conidial structures consisting of erect conidiophores usually arising from the aerial hyphae, solitary or phialides in whorls of two. Phialides $47.1\text{--}74.9 \times 1.8\text{--}2.8 \mu\text{m}$ ($\bar{x} = 56.3 \times 2.3 \mu\text{m}$, $n=30$), with a cylindrical basal portion, tapering into a distinct neck. Conidia hyaline, 1-celled, cylindrical to ellipsoidal, $3.5\text{--}6.7 \times 1.9\text{--}2.4 \mu\text{m}$ ($\bar{x} = 4.7 \times 2.2 \mu\text{m}$, $n=30$).

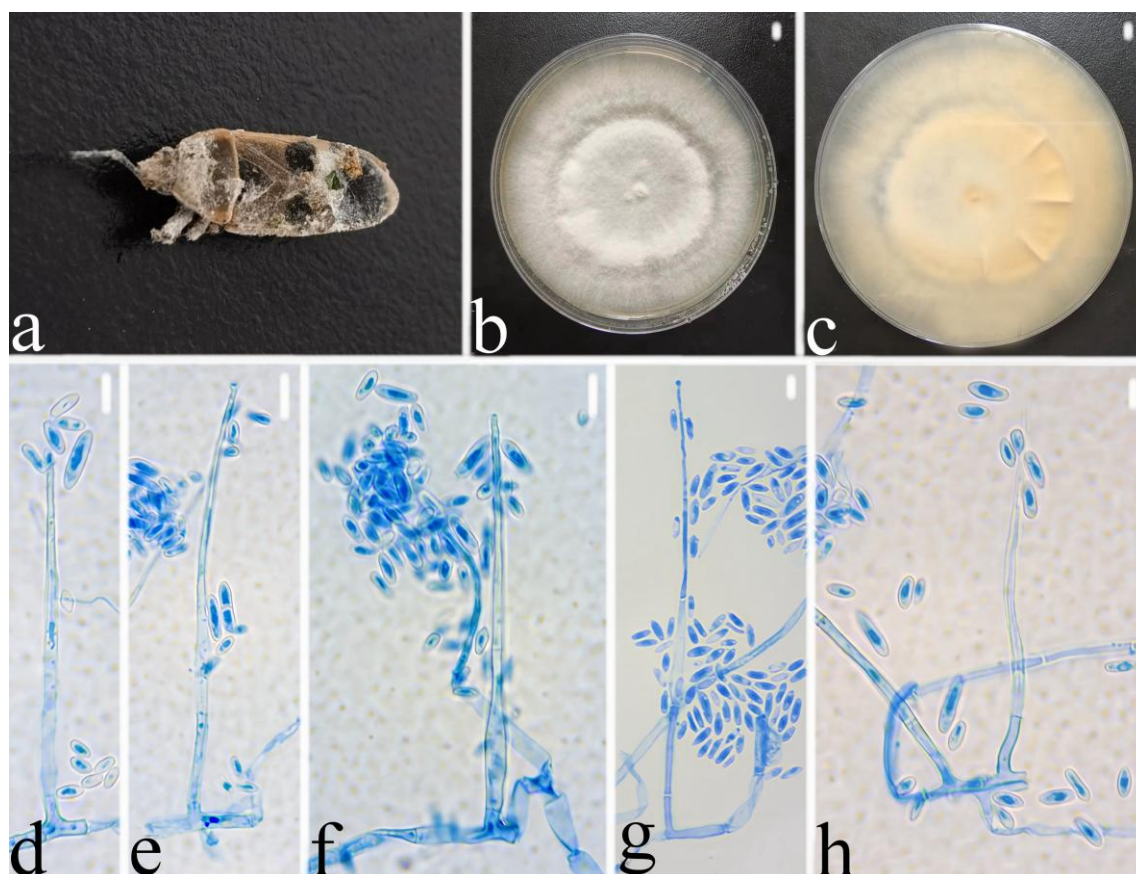


Figure 45 – *Simplicillium cantharise* (ZY06421, ex-type) a Infected beetle. b–c Colonies on PDA culture media with upper (b) and reverse (c) views. d–h Phialides and conidia were stained with cotton blue. Scale bars: b–c = 10 mm, d–h = 10 μm .

Material examined – China, Guizhou Province, Zunyi City, Honghuagang District, Dabanshui National Forest Park (27°46'35.904"N, 106°48'30.89"E). On a beetle (*Coleoptera*), 3 June 2022, Wanhao Chen, GZAC ZY0642 (holotype), ZY06421 (ex-type), ZY06422 (living culture).

Habitat – On the underside of leaves of broad-leaved plant species.

Notes – Molecular analyses of concatenated dataset 2 (Fig. 2) and NCBI BLASTn comparisons revealed that *Simplicillium cantharise* (ZY06421 and ZY06422) was grouped within the genus *Simplicillium*, forming a maximally supported clade (100% ML/0.99 PP) with its closest relatives *S. araneicola* and *S. zunyiense*, which was also supported by the phylogenetic analyses among *Simplicillium* species (Suppl. Fig. 5). Compared with the typical characteristics, *S. cantharise* was distinguished from *S. araneicola* by its one types of conidia, longer phialides

($47.1\text{--}74.9 \times 1.8\text{--}2.8 \mu\text{m}$ vs $10.6\text{--}14.4 \times 0.8\text{--}1.1 \mu\text{m}$) and beetle host. *Simplicillium cantharise* was distinguished from *S. zunyiense* by its longer phialides ($47.1\text{--}74.9 \times 1.8\text{--}2.8 \mu\text{m}$ vs $11.8\text{--}22.3 \times 1.1\text{--}1.5 \mu\text{m}$), one type of conidia and beetle host. The combined morphological and molecular phylogenetic evidence substantiates the recognition of *S. cantharise* as a novel species.

Simplicillium neoaraneae W.H. Chen, Y.F. Han & J.D. Liang, sp. nov.

Index Fungorum number: 903405; Facesoffungi number: FoF 17508

Etymology – referring to a new species with spider host.

Fig. 46

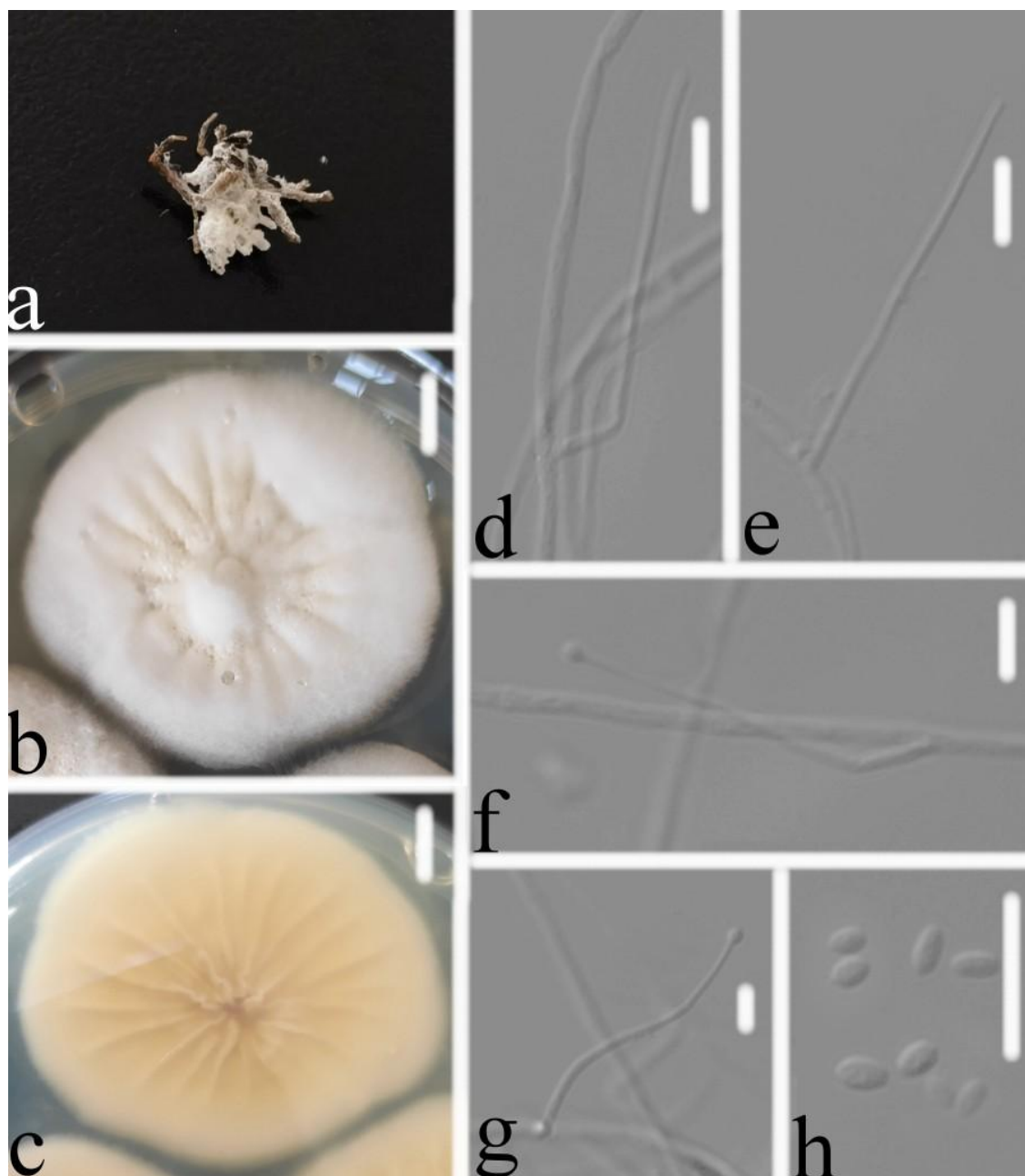


Figure 46 – *Simplicillium neoaraneae* (ZY06261, ex-type) a Infected spider. b–c Colonies on PDA culture media with upper (b) and reverse (c) views. d–h Phialides and conidia. Scale bars: b–c = 10 mm, d–h = 10 μm .

Description – Colonies on PDA reaching 45–50 mm diam. in 14 d at 25°C, white, consisting of a basal felt and cottony, floccose overgrowth, reverse yellowish. Prostrate hyphae smooth, septate, hyaline, 1.0–1.6 μm diam. Conidial structures consisting of erect conidiophores usually

arising from the aerial hyphae, solitary or phialides in whorls of two. Phialides $21.5\text{--}41.1 \times 1.1\text{--}1.5 \mu\text{m}$ ($\bar{x} = 30.3 \times 1.4 \mu\text{m}$, $n=30$), with a cylindrical basal portion, tapering into a distinct neck. Conidia hyaline, 1-celled, cylindrical to ellipsoidal, $2.6\text{--}3.2 \times 1.1\text{--}1.6 \mu\text{m}$ ($\bar{x} = 2.9 \times 2.0 \mu\text{m}$, $n=30$).

Material examined – China, Guizhou Province, Zunyi City, Honghuagang District, Dabanshui National Forest Park ($27^{\circ}46'35.904''\text{N}$, $106^{\circ}48'30.89''\text{E}$). On a dead spider (*Araneae*), 3 June 2022, Wanhao Chen, GZAC ZY0626 (holotype), ZY06261 (ex-type), ZY06262 (living culture).

Habitat – Near the road, located on or under the rock.

Notes – Molecular analyses of concatenated dataset 2 (Fig. 2) and NCBI BLASTn comparisons revealed that *Simplicillium neoaraneae* (ZY06261 and ZY06262) was grouped within the genus *Simplicillium*, forming a strongly supported clade (92% ML/0.90 PP) with its closest relative *S. cicadellidae*, which was also supported by the phylogenetic analyses among *Simplicillium* species (Suppl. Fig. 5). Compared with the typical characteristics, *S. neoaraneae* was distinguished from *S. cicadellidae* by its longer phialides ($21.5\text{--}41.1 \times 1.1\text{--}1.5 \mu\text{m}$ vs $12.9\text{--}18.3 \times 0.8\text{--}1.1 \mu\text{m}$) and larger conidia ($2.9 \times 2.0 \mu\text{m}$ vs $1.8\text{--}2.8 \times 1.4\text{--}1.8 \mu\text{m}$) (Chen et al. 2019c). The congruent morphological and molecular phylogenetic evidence conclusively establishes *S. neoaraneae* as a new species.

Simplicillium wudangense W.H. Chen, Y.F. Han & J.D. Liang, sp. nov.

Fig. 47

Index Fungorum number: 903406; Facesoffungi number: FoF 17509

Etymology – referring to its location, Wudang District, where the fungus was first discovered.

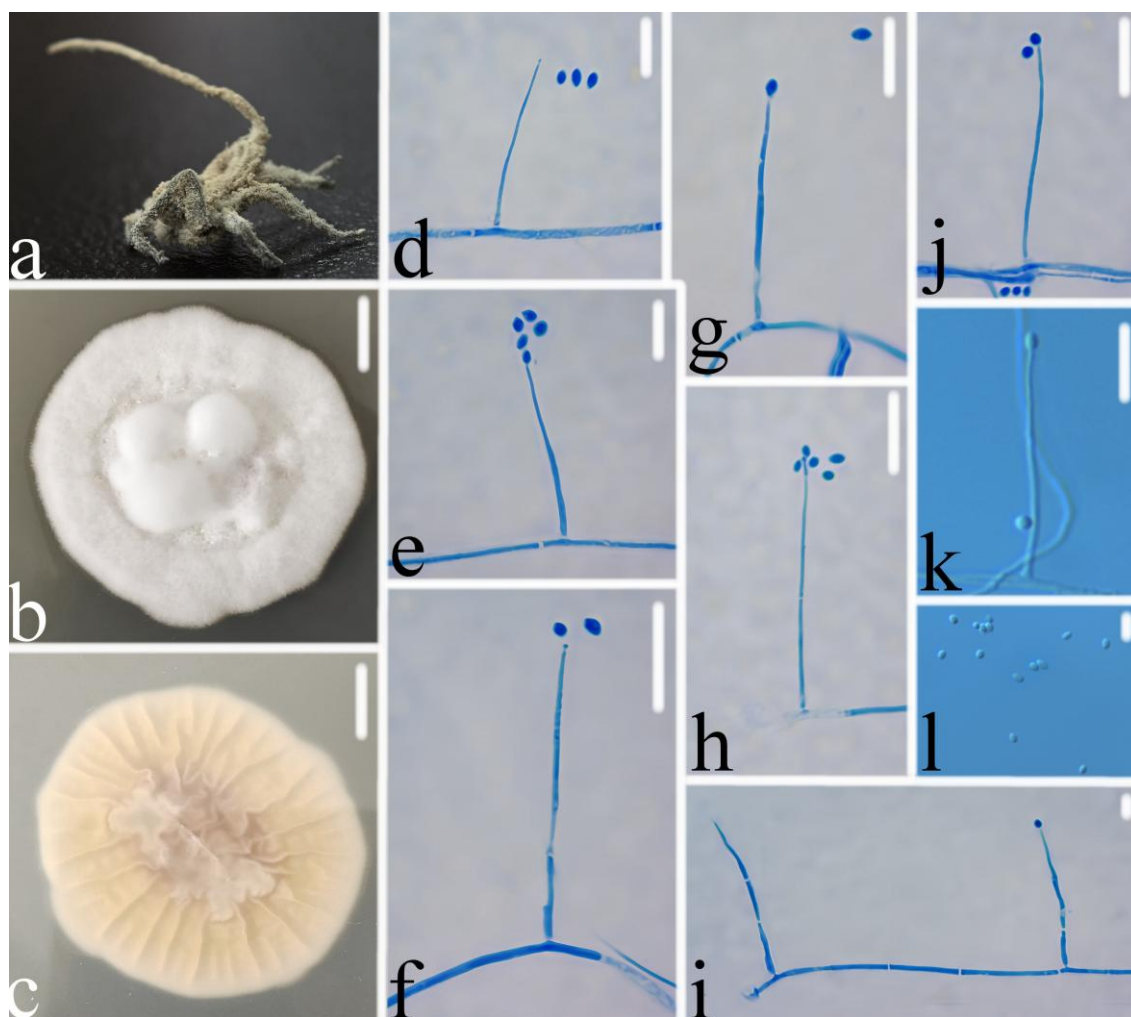


Figure 47 – *Simplicillium wudangense* (WD04131, ex-type) a Infected spider. b–c Colonies on PDA culture media with upper (b) and reverse (c) views. d–i, l Phialides and

conidia were stained with cotton blue. j, k Phialides and conidia. Scale bars: b–c = 10 mm, d–l = 10 μ m.

Description – Colonies on PDA reaching 39–42 mm diam. in 14 d at 25°C, white, consisting of a basal felt and cottony, floccose overgrowth, reverse yellowish. Prostrate hyphae smooth, septate, hyaline, 1.5–1.6 μ m diam. Conidial structures consisting of erect conidiophores usually arising from the aerial hyphae, solitary or phialides in whorls of two. Phialides 18.9–27.6 $\times$ 1.1–1.3 μ m ($\bar{x}$ = 25.0 $\times$ 1.1 μ m, n=30), with a cylindrical basal portion, tapering into a distinct neck. Conidia hyaline, 1-celled, ellipsoidal to subglobose, 1.7–2.7 $\times$ 1.3–1.6 μ m ($\bar{x}$ = 2.3 $\times$ 1.5 μ m, n=30).

Material examined – China, Guizhou Province, Guiyang City, Wudang District, Bala Valley (26°45'7.0344"N, 106°58'57.09"E). On a spider (*Araneae*), 5 April 2024, Wanhao Chen, GZAC WD0413 (holotype), WD04131 (ex-type), WD04132 (living culture).

Habitat – Near the road, located on or under the rock.

Notes – Molecular analyses of concatenated dataset 2 (Fig. 2) and NCBI BLASTn comparisons revealed that *Simplicillium wudangense* (WD04131 and WD04132) was grouped within the genus *Simplicillium*, forming a distinct clade with its closest relative *S. hymenopterorum*, which was also supported by the phylogenetic analyses among *Simplicillium* species (Suppl. Fig. 5). Compared with the typical characteristics, *S. wudangense* was distinguished from *S. cicadellidae* by its ellipsoidal to subglobose conidia and spider host (Chen et al. 2021b). The combined morphological and molecular phylogenetic evidence substantiates the recognition of *S. wudangense* as a novel species.

Simplicillium zunyiense W.H. Chen, Y.F. Han & J.D. Liang, sp. nov.

Fig. 48

Index Fungorum number: 903407; Facesoffungi number: FoF 17510

Etymology – referring to its location, Zunyi City, where the fungus was first discovered.

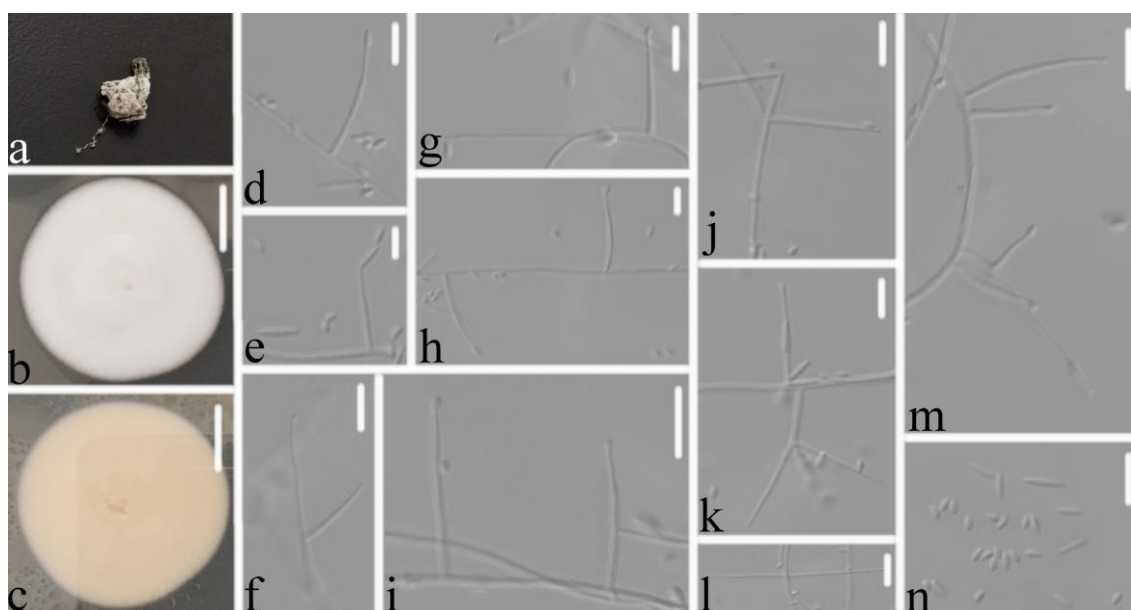


Figure 48– *Simplicillium zunyiense* (ZY06581, ex-type) a Infected spider. b–c Colonies on PDA culture media with upper (b) and reverse (c) views. d–n Phialides and conidia. Scale bars: b–c = 10 mm, d–n = 10 μ m.

Description – Colonies on PDA reaching 29–30 mm diam. in 14 d at 25°C, white, consisting of a basal felt and cottony, floccose overgrowth, reverse yellowish. Prostrate hyphae smooth, septate, hyaline, 1.0–1.3 μ m diam. Conidial structures consisting of erect conidiophores usually arising from the aerial hyphae, solitary or phialides in whorls of two. Phialides 11.8–22.3 $\times$ 1.1–1.5 μ m ($\bar{x}$ = 16.1 $\times$ 1.2 μ m, n=30), with a cylindrical basal portion, tapering into a distinct neck.

Conidia hyaline, 1-celled, macroconidia nuciformis, $4.1\text{--}6.7 \times 1.2\text{--}1.7 \mu\text{m}$ ($\bar{x} = 5.1 \times 1.4 \mu\text{m}$, $n=30$); microconidia fusiform, $2.1\text{--}3.0 \times 1.3\text{--}1.5 \mu\text{m}$ ($\bar{x} = 2.4 \times 1.4 \mu\text{m}$, $n=30$).

Material examined – China, Guizhou Province, Zunyi City, Honghuagang District, Dabanshui National Forest Park ($27^{\circ}46'35.904''\text{N}$, $106^{\circ}48'30.89''\text{E}$). On a spider (*Araneae*), 3 June 2022, Wanhao Chen, GZAC ZY0658 (holotype), ZY06581 (ex-type), ZY06582 (living culture).

Habitat – Near the road, located on or under the rock.

Notes – Molecular characterization through NCBI BLASTn comparisons and multi-locus phylogenetic analysis (dataset 2, Fig. 2) revealed that *Simplicillium zunyiense* (ZY06581 and ZY06582) was grouped with *Simplicillium* species, forming a maximally supported clade (100% ML/0.99 PP) with its closest relatives *S. araneicola* and *S. cantharise*, which was also supported by the phylogenetic analyses among *Simplicillium* species (Suppl. Fig. 5). Compared with the typical characteristics, *S. zunyiense* was distinguished from *S. araneicola* by its longer phialides ($16.1 \times 1.2 \mu\text{m}$ vs $12.3 \times 0.9 \mu\text{m}$) and spider host. *Simplicillium zunyiense* was distinguished from *S. cantharise* by its shorter phialides ($16.1 \times 1.2 \mu\text{m}$ vs $56.3 \times 2.3 \mu\text{m}$), two type of conidia and spider host. The combined morphological and phylogenetic evidence substantiates *S. zunyiense* as a novel species.

Zarea Khons., Thanakitp. & Luangsa-ard, Fungal Systematics and Evolution 14: 300 (2024)

Type species – *Zarea fungicola* (Preuss) Khons., Thanakitp. & Luangsa-ard 2024

Notes – Khonsanit et al. (2024) introduced the genus *Zarea* with the type species *Zarea fungicola* (Preuss) Khons. et al. and two species, *Z. aleophila* (W. Gams & Zaayen) Khons. and *Z. flavida* (W. Gams & Zaayen) Khons. et al. In the present study, a new species was introduced.

Zarea sinensis W.H. Chen, Y.F. Han & J.D. Liang, sp. nov.

Fig. 49

Index Fungorum number: 903408; Facesoffungi number: FoF 17511

Etymology – referring to its location, China, where the fungus was first discovered.

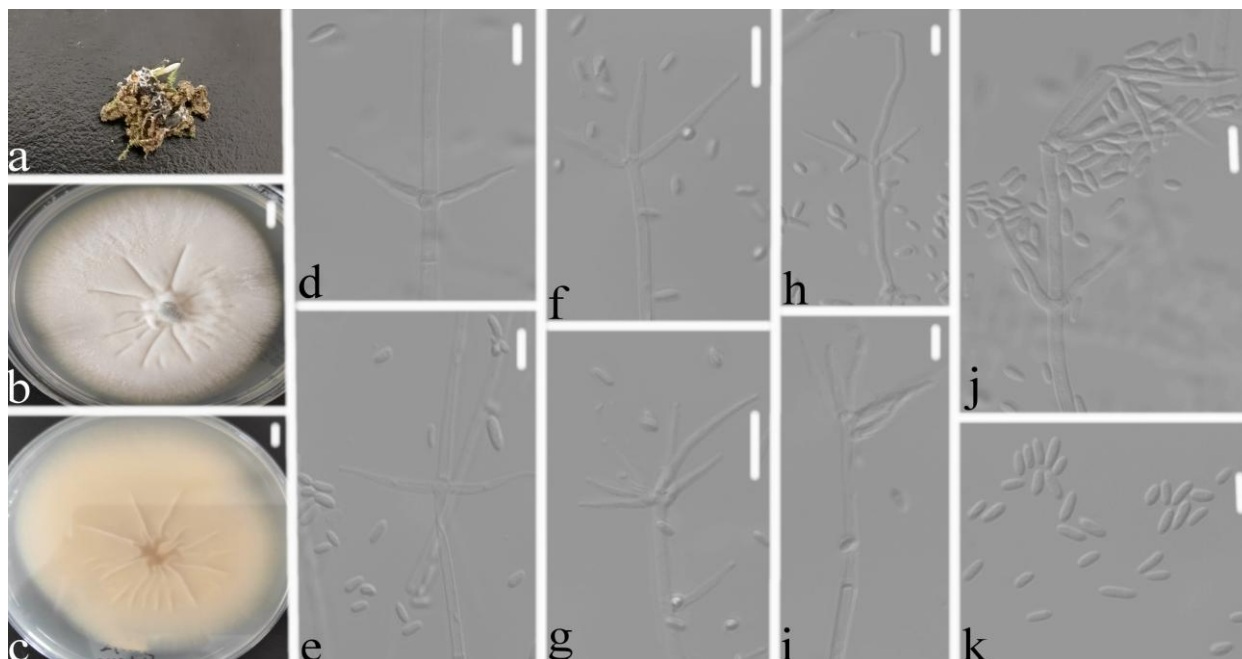


Figure 49 – *Zarea sinensis* (ZY06611, ex-type) a Infected ant. b–c Colonies on PDA culture media with upper (b) and reverse (c) views. d–k Phialides and conidia. Scale bars: b–c = 10 mm, d–k = 10 μm .

Description – Colonies on PDA reaching 75–77 mm diam. in 14 d at 25°C , white, consisting of a basal felt and cottony, floccose overgrowth, reverse yellowish. Prostrate hyphae smooth,

septate, hyaline, 2.7–2.8 µm diam. Conidial structures consisting of erect conidiophores usually arising from the aerial hyphae, solitary or phialides in whorls of two to three. Conidiophores 22.5–36.1 × 2.2–2.3 µm. Phialides 12.9–19.9 × 1.6–2.8 µm ($\bar{x}$ = 17.1 × 2.3 µm, n=30), with a cylindrical basal portion, tapering into a distinct neck. Conidia hyaline, 1-celled, cylindrical, 3.6–7.0 × 2.1–2.2 µm ($\bar{x}$ = 5.6 × 2.1 µm, n=30). Octahedral crystals not observed.

Material examined – China, Guizhou Province, Zunyi City, Honghuagang District, Dabanshui National Forest Park (27°46'35.904"N, 106°48'30.89"E). On a dead ant (*Formicidae*), 3 June 2023, Wanhao Chen, GZAC ZY0661 (holotype), ZY06611 (ex-type), ZY06612 (living culture).

Habitat – Near the road, buried in soil.

Notes – Molecular analyses of concatenated dataset 2 (Fig. 2) revealed that *Zarea sinensis* (ZY06611 and ZY06612) was grouped within the genus *Zarea*, forming a maximally supported clade (100% ML/1 PP) with its closest relatives *Z. aleophila*, *Z. flavida*, and *Z. fungicola*. Compared with the typical characteristics, *Z. sinensis* was distinguished from *Z. aleophila* by its shorter conidiophores (22.5–36.1 × 2.2–2.3 µm vs over 400 µm) and ant host (Zare & Gams 2001). *Zarea sinensis* was distinguished from *Z. flavida* by its absent of octahedral crystals and ant host (Zare & Gams 2008). *Zarea sinensis* was distinguished from *Z. flavida* by its absent of octahedral crystals and slimy head, and ant host (Zare & Gams 2008). The congruent morphological and molecular phylogenetic evidence conclusively establishes *Zarea sinensis* as a new species.

Zongqiomycetes W.H. Chen, Y.F. Han & J.D. Liang gen. nov.

Index Fungorum number: 903420; Facesoffungi number: FoF 17461

Type species – *Zongqiomycetes araneicola* W.H. Chen, Y.F. Han & J.D. Liang

Etymology – *Zongqiomycetes* is named in honour of professor Zongqi Liang, who is working on invertebrate pathogenic fungi for more than 40 years.

Description – Colonies on PDA, white, reverse yellowish. Conidiophores mononematous, usually arising from aerial hyphae, phialides solitary or in groups of two to four. Phialides emerging laterally from hyphae, forming a compact hymenium, abruptly narrowing into a neck. Conidia in chains, one-celled, hyaline, cylindrical or ellipsoidal.

Notes – Phylogenetic analyses (Fig. 2) revealed a close relationship between the newly proposed genus *Zongqiomycetes* and *Corniculantispora*. However, *Zongqiomycetes* is morphologically distinct, characterized by producing only one type of conidia that are cylindrical to ellipsoidal in shape, contrasting with *Corniculantispora* species (Khonsanit et al. 2024). Among the family *Cordycipitaceae*, the genera *Akanthomyces*, *Arachnidicola*, *Corniculantispora*, *Corpulentispora*, *Dimorphospora*, *Gamszarea*, *Neogamszarella*, *Neolecanicillium*, *Nuciformispora*, *Paracorniculantispora*, *Rubrumomyces*, *Zarea* and *Zouia* were associated with *Lecanicillium* species. Compared with the typical characteristics, *Zongqiomycetes* species was significant different from *Corniculantispora*, *Corpulentispora*, *Dimorphospora*, *Neolecanicillium*, *Nuciformispora* and *Zarea* species by its only one type of conidia. *Zongqiomycetes* species was significant different from *Rubrumomyces* species by its absent of red or reddish pigment in agar. *Zongqiomycetes* species was significant different from *Gamszarea* and *Neogamszarella* species by its absent of a cluster of denticles on the conidiogenous cells. However, species of *Zongqiomycetes* cannot be distinguished from those of *Akanthomyces*, *Arachnidicola*, and *Zouia* based on morphological characteristics alone. These diagnostic differences, combined with molecular evidence, justify the establishment of *Zongqiomycetes* as a novel genus.

Zongqiomycetes araneicola W.H. Chen, Y.F. Han & J.D. Liang, sp. nov.

Fig. 50

Index Fungorum number: 903409; Facesoffungi number: FoF 17512

Etymology – referring to its host spider, where the fungus was first discovered.

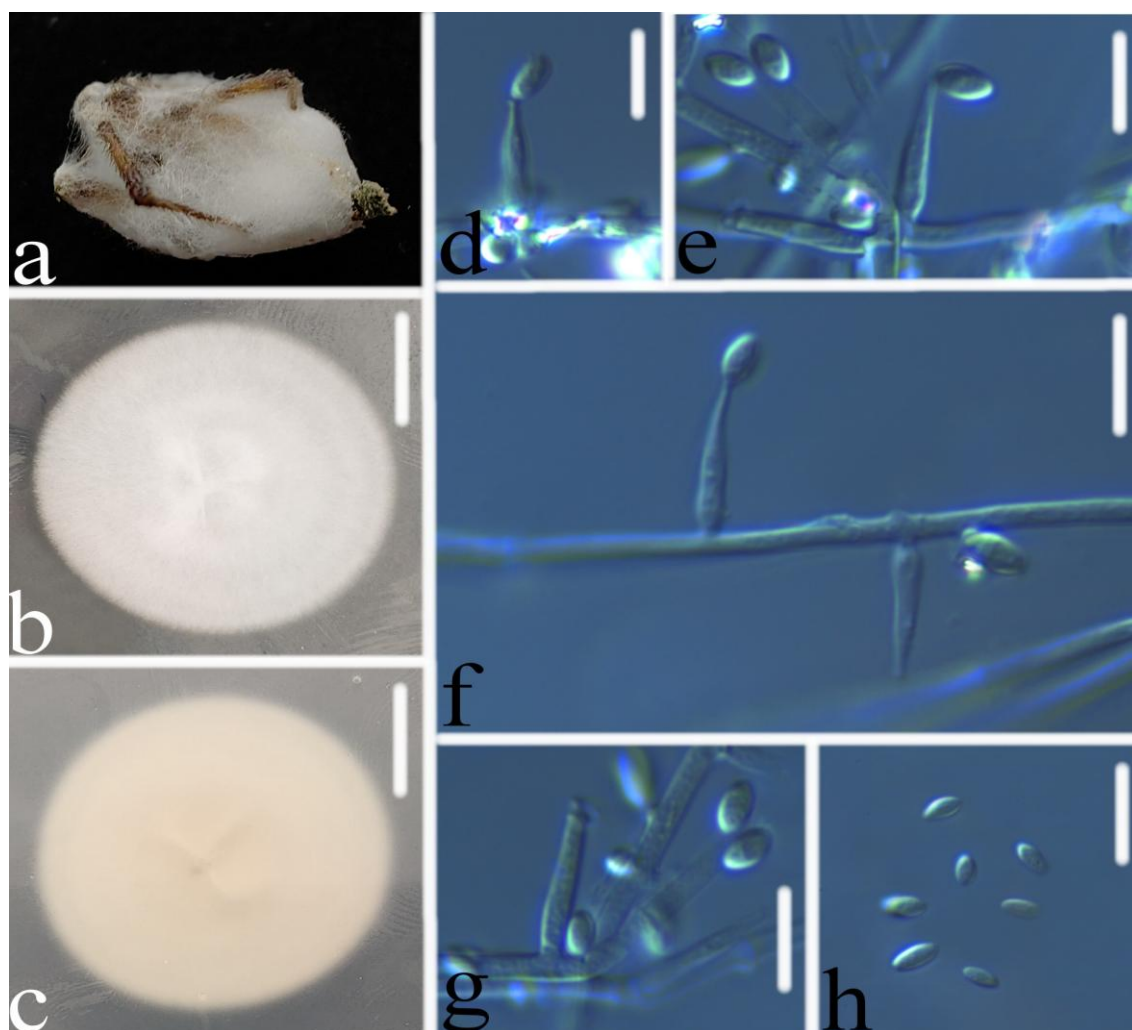


Figure 50 – *Zongqiomycetes araneicola* (ZY09191, ex-type) a Infected spider. b–c Colonies on PDA culture media with upper (b) and reverse (c) views. d–h Phialides and conidia. Scale bars: b–c = 10 mm, d–h = 10 µm.

Description – Colonies on PDA reaching 26–27 mm diam. in 14 d at 25°C, yellowish, consisting of a basal felt and cottony, floccose overgrowth, reverse yellowish. Prostrate hyphae smooth, septate, hyaline, 1.8–2.2 µm diam. Conidial structures consisting of erect conidiophores usually arising from the aerial hyphae, solitary. Phialides 9.4–11.4 × 1.7–2.3 µm ($\bar{x}$ = 10.7 × 1.8 µm, n=30), with a cylindrical basal portion, tapering into a distinct neck. Conidia, hyaline, 1-celled, cylindrical to ellipsoidal, 3.1–4.4 × 1.5–2.5 µm ($\bar{x}$ = 3.7 × 2.1 µm, n=30).

Material examined – China, Guizhou Province, Zunyi City, Honghuagang District, Dabanshui National Forest Park (27°46'35.904"N, 106°48'30.89"E). On a dead spider (*Araneae*), 2 September 2023, Wanhao Chen, GZAC ZY0919 (holotype), ZY09191 (ex-type), ZY09192 (living culture).

Habitat – Near the road, located on or under the rock.

Notes – Molecular analyses placed *Zongqiomycetes araneicola* in a well-supported clade (100% ML/1 PP) with *Corniculantispora* species and *Zongqiomycetes sinensis*. Compared with the typical characteristics, *Zongqiomycetes araneicola* was distinguished from *Corniculantispora* species by its cylindrical or ellipsoidal conidia and only one type of conidia. *Zongqiomycetes araneicola* was distinguished from *Z. sinensis* by its longer phialide (9.4–11.4 × 1.7–2.3 µm vs 5.3–7.5 × 1.6–2.2 µm). The combined morphological and molecular phylogenetic evidence substantiates the recognition of *Z. araneicola* as a novel species.

Zongqiomycetes sinensis W.H. Chen, Y.F. Han & J.D. Liang, sp. nov.

Fig. 51

Index Fungorum number: 903411; Facesoffungi number: FoF 17513

Etymology – referring to its location, China, where the fungus was first discovered.

Description – Colonies on PDA reaching 11–12 mm diam. in 14 d at 25 °C, yellowish, consisting of a basal felt and cottony, floccose overgrowth, reverse yellowish. Prostrate hyphae smooth, septate, hyaline, 1.5–1.8 µm diam. Conidial structures consisting of erect conidiophores usually arising from the aerial hyphae, solitary. Phialides $5.3\text{--}7.5 \times 1.6\text{--}2.2$ µm ($\bar{x} = 6.3 \times 2.0$ µm, $n=30$), with a cylindrical basal portion, tapering into a distinct neck. Conidia, hyaline, 1-celled, cylindrical to ellipsoidal, $2.9\text{--}4.0 \times 2.0\text{--}2.4$ µm ($\bar{x} = 3.9 \times 2.1$ µm, $n=30$).

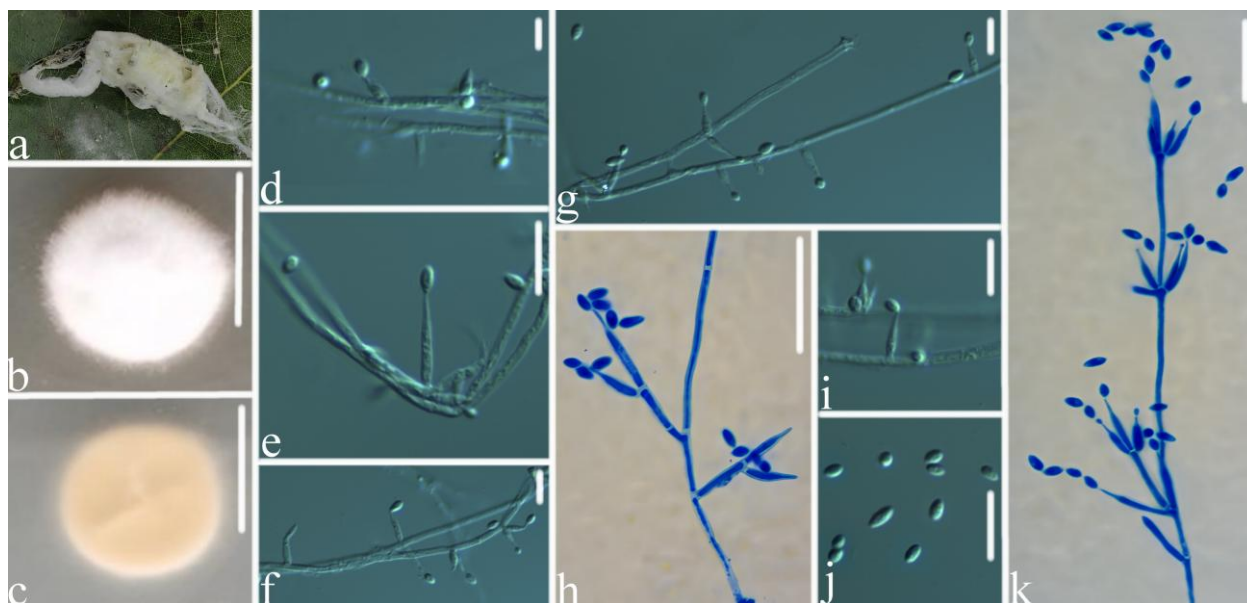


Figure 51 – *Zongqiomycetes sinensis* (SY09201, ex-type) a Infected spider. b–c Colonies on PDA culture media with upper (b) and reverse (c) views. d–g, i, j Phialides and conidia. h, k Phialides and conidia were stained with cotton blue. Scale bars: b–c = 10 mm, d–k = 10 µm.

Material examined – China, Guizhou Province, Zunyi City, Suiyang County, Shuangmen Valley (28°1'39.05"N, 107°7'58.65"E). On a spider (*Araneae*), 30 September 2023, Wanhao Chen, GZAC SY0920 (holotype), SY09201 (ex-type), SY09202 (living culture).

Habitat – Near the road, located on or under the rock.

Notes – Molecular analyses placed *Zongqiomycetes sinensis* in a well-supported clade (100% ML/1 PP) with *Corniculantispora* species and *Zongqiomycetes araneicola* with high bootstrap value (100% ML/ 1 PP). Compared with the typical characteristics, *Zongqiomycetes sinensis* was distinguished from *Corniculantispora* species by its cylindrical or ellipsoidal conidia and only one type of conidia. *Zongqiomycetes sinensis* was distinguished from *Z. araneicola* by its shorter phialide ($5.3\text{--}7.5 \times 1.6\text{--}2.2$ µm vs $9.4\text{--}11.4 \times 1.7\text{--}2.3$ µm). The combined morphological and molecular phylogenetic evidence substantiates the recognition of *Z. sinensis* as a novel species.

Ophiocordycipitaceae G.H. Sung, J.M. Sung, Hywel-Jones & Spatafora, Stud. Mycol. 57: 35 (2007)

Purpureocillium Luangsa-ard, Hywel-Jones, Houbraken & Samson, FEMS Microbiol. Lett. 321(2): 144 (2011)

Type species – *Purpureocillium lilacinum* (Thom) Luangsa-ard, Houbraken, Hywel-Jones & Samson 2011.

Notes – Luangsa-ard et al. (2011) established the genus *Purpureocillium* to accommodate the reclassified species *Paecilomyces lilacinus* Thom. Perdomo et al. (2013) introduced a new species

P. lavendulum Perdomo et al., based on morphological characteristics and phylogenetic analyses. Subsequently, two species, *Nomuraea atypicola* (Yasuda) Samson and *Isaria takamizusanensis* Kobayasi was transferred to the genus *Purpureocillium* by Quandt et al. (2014) and Ban et al. (2015). Additionally, two new species, *P. sodanum* Papizadeh et al. and *P. roseum* Calvillo & Raymundo were established by Hyde et al. (2016) and Calvillo-Medina et al. (2021). Chen et al. (2024d) summarized that *Purpureocillium* consists of 7 species. In the present study, 3 new species were introduced.

Purpureocillium aranea W.H. Chen, Y.F. Han & J.D. Liang, sp. nov.

Fig. 52

Index Fungorum number: 903412; Facesoffungi number: FoF 17514

Etymology – referring to its spider host.

Description – Colonies on PDA reaching 30–34 mm diam. in 14 d at 25 °C, white to purple, consisting of a basal felt and cottony, floccose overgrowth, reverse yellowish. Prostrate hyphae smooth, septate, hyaline, 0.9–1.9 µm diam. Conidial structures consisting of erect conidiophores usually arising from the aerial hyphae, solitary or paecilomyces-like with phialides in whorls of two to three. Phialides 5.7–10.8 × 1.6–3.2 µm ($\bar{x}$ = 7.8 × 2.3 µm, n=30), with a cylindrical basal portion, tapering into a distinct neck. Conidia in chains, hyaline, fusiform to subglobose, 1-celled, 1.4–2.8 × 1.3–2.4 µm ($\bar{x}$ = 2.2 × 1.9 µm, n=30).

Material examined – China, Guizhou Province, Guiyang City, Kaiyang County, Monkey-Ear Tiankeng (27°5'12.138"N, 107°40'48.42"E). On a spider (*Araneae*), 19 July 2023, Wanhao Chen, GZAC KY0723 (holotype), KY07231 (ex-type), KY07232 (living culture).

Habitat – Near the road, located on or under the rock.

Notes – Molecular analyses of concatenated dataset 1 (Fig. 1) and NCBI BLASTn comparisons revealed that *Purpureocillium aranea* (KY07231 and KY07232) was grouped within the genus *Purpureocillium*, forming a strongly supported clade (85% ML) with its closest relative *P. sinense*, which was also supported by the phylogenetic analyses among *Purpureocillium* species (Suppl. Fig. 6). Compared with the typical characteristics, *P. aranea* was distinguished from *P. sinense* by its shorter phialides (7.8 × 2.3 µm vs 11.6 × 2.6 µm). The combined morphological and molecular phylogenetic evidence substantiates the recognition of *P. aranea* as a novel species.

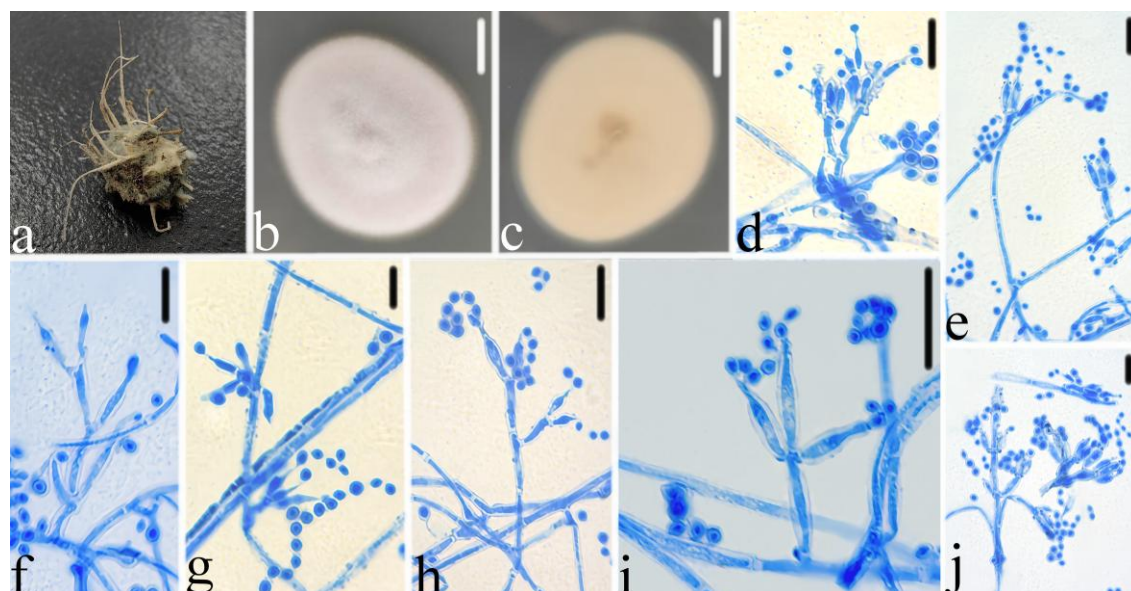


Figure 52 – *Purpureocillium aranea* (KY07231, ex-type) a Infected spider. b–c Colonies on PDA culture media with upper (b) and reverse (c) views. d–j Phialides and conidia were stained with cotton blue. Scale bars: b–c = 10 mm, d–j = 10 µm.

Purpureocillium sinense W.H. Chen, Y.F. Han & J.D. Liang, sp. nov.

Fig. 53

Index Fungorum number: 903413; Facesoffungi number: FoF 17515
 Etymology – referring to the country, China, where the fungus was first discovered.

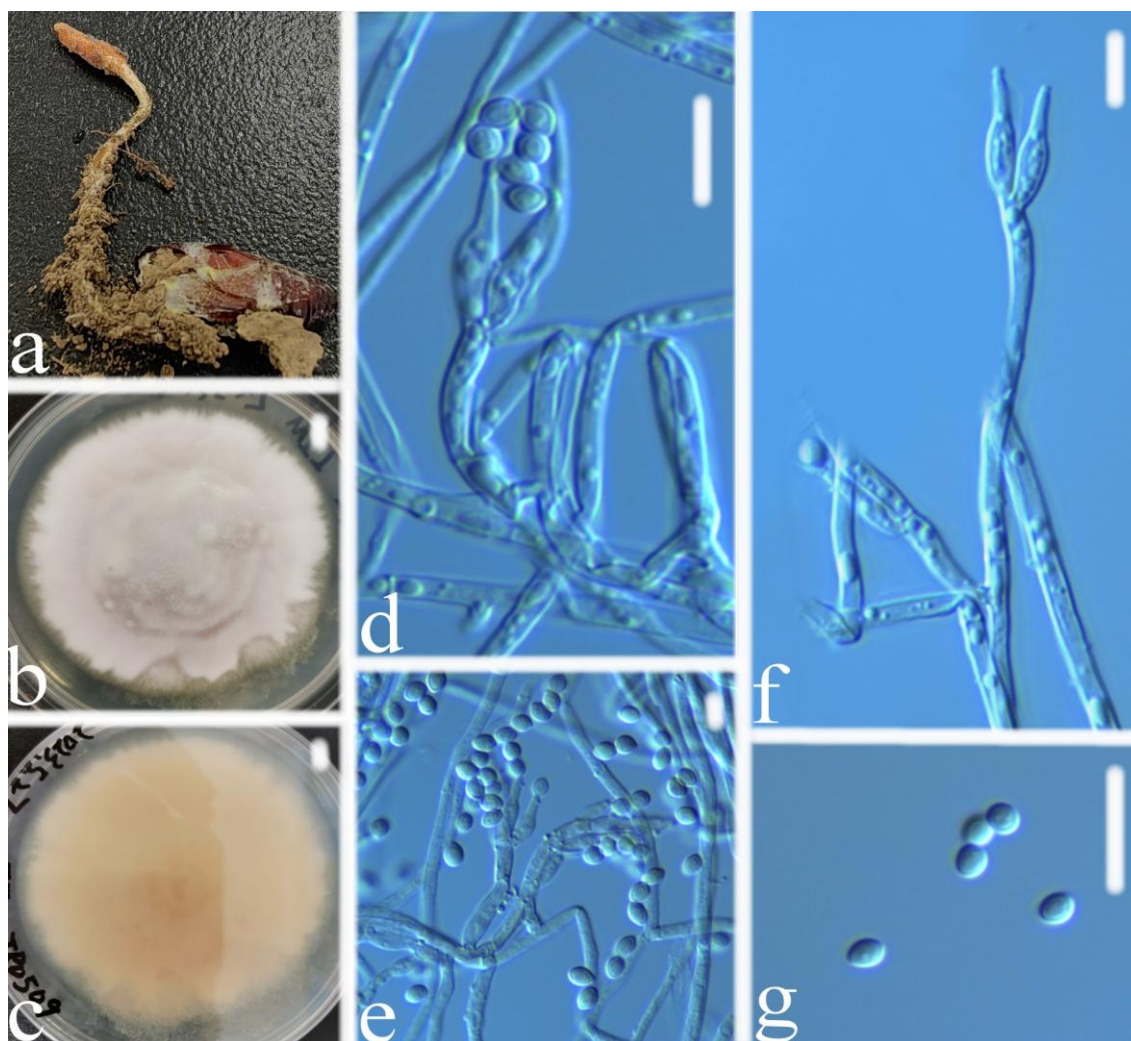


Figure 53 – *Purpureocillium sinense* (TR05091, ex-type) a Infected pupa. b–c Colonies on PDA culture media with upper (b) and reverse (c) views. d–g. Phialides and conidia. Scale bars: b–c = 10 mm, d–g = 10 μ m.

Description – Colonies on PDA reaching 73–74 mm diam. in 14 d at 25°C, white to purple, consisting of a basal felt and cottony, floccose overgrowth, reverse yellowish to light brown. Prostrate hyphae smooth, septate, hyaline, 1.7–2.1 μ m diam. Conidial structures consisting of erect conidiophores usually arising from the aerial hyphae, solitary or paecilomyces-like with phialides in whorls of two to three. Phialides 9.1–13.9 $\times$ 2.2–3.4 μ m ($\bar{x}$ = 11.6 $\times$ 2.6 μ m, n=30), with a cylindrical basal portion, tapering into a distinct neck. Conidia in chains, hyaline, fusiform to subglobose, 1-celled, 2.7–3.0 $\times$ 2.0–2.4 μ m ($\bar{x}$ = 2.8 $\times$ 2.2 μ m, n=30).

Material examined – China, Guizhou Province, Tongren City, Jiangkou County, Fanjing Mountain (27°50'56.98"N, 108°46'52.28"E). On a pupa (*Lepidoptera*), 1 May 2023, Wanhao Chen, GZAC TR0509 (holotype), TR05091 (ex-type), TR05092 (living culture).

Habitat – Near the road, buried in soil.

Notes – Molecular analyses of concatenated dataset 1 (Fig. 1) and NCBI BLASTn comparisons revealed that *Purpureocillium sinense* (TR05091 and TR05092) was grouped with *Purpureocillium* species, forming a strongly supported clade (85% ML) with its closest relative *P. aranea*, which was also supported by the phylogenetic analyses among *Purpureocillium* species (Suppl. Fig. 6). Compared with the typical characteristics, *P. sinense* was distinguished from

P. aranea by its longer phialides ($11.6 \times 2.6 \mu\text{m}$ vs $7.8 \times 2.3 \mu\text{m}$). The combined morphological and molecular phylogenetic evidence substantiates the recognition of *P. sinense* as a novel species.

Purpureocillium tiankengense W.H. Chen, Y.F. Han & J.D. Liang, sp. nov.

Fig. 54

Index Fungorum number: 903414; Facesoffungi number: FoF 17516

Etymology – referring to its location in Tiankeng, where the fungus was first discovered.

Description – Colonies on PDA reaching 31–32 mm diam. in 14 d at 25°C, white to purple, consisting of a basal felt and cottony, floccose overgrowth, reverse yellowish. Prostrate hyphae smooth, septate, hyaline, $1.9\text{--}2.3 \mu\text{m}$ diam. Conidial structures consisting of erect conidiophores usually arising from the aerial hyphae, solitary or paecilomyces-like with phialides in whorls of two to three. Conidiophores $15.1\text{--}17.5 \times 2.0\text{--}3.0 \mu\text{m}$. Phialides $6.5\text{--}9.8 \times 2.3\text{--}2.8 \mu\text{m}$ ($\bar{x} = 7.7 \times 2.5 \mu\text{m}$, $n=30$), with a cylindrical basal portion, tapering into a distinct neck. Conidia in chains, hyaline, fusiform to subglobose, 1-celled, $1.7\text{--}4.7 \times 1.5\text{--}2.6 \mu\text{m}$ ($\bar{x} = 2.9 \times 1.9 \mu\text{m}$, $n=30$).

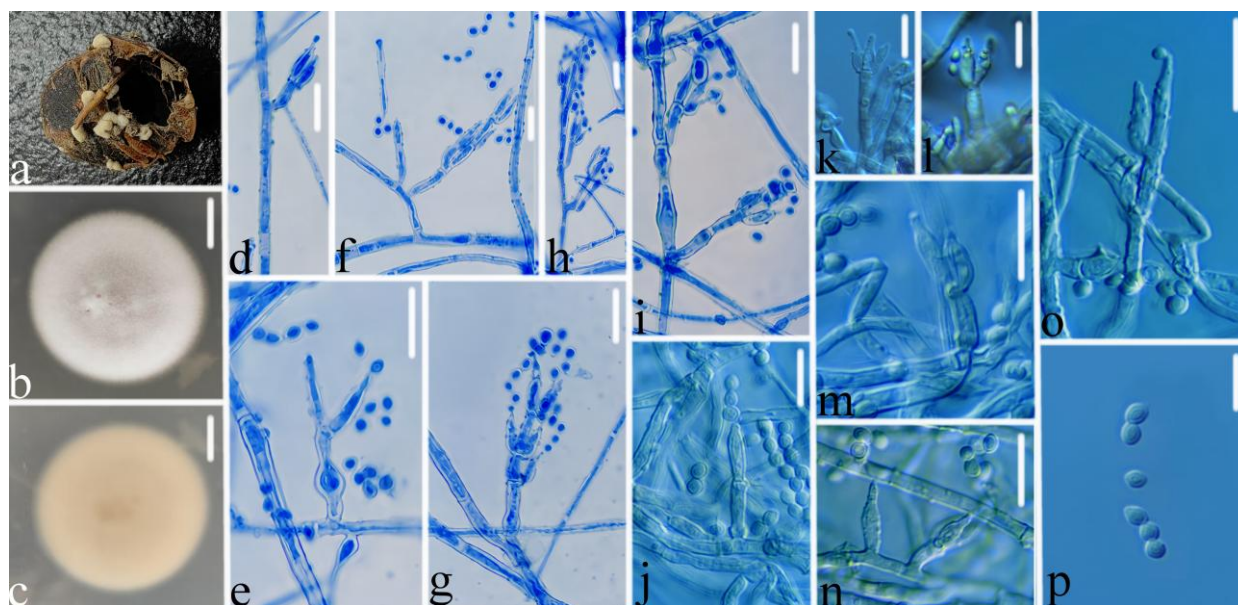


Figure 54 – *Purpureocillium tiankengense* (KY07471, ex-type) a Infected pupa. b–c Colonies on PDA culture media with upper (b) and reverse (c) views. d–i Phialides and conidia were stained with cotton blue. j–p Phialides and conidia. Scale bars: b–c = 10 mm, d–p = 10 μm .

Material examined – China, Guizhou Province, Guiyang City, Kaiyang County, Monkey-Ear Tiankeng ($27^{\circ}5'12.138''\text{N}$, $107^{\circ}40'48.42''\text{E}$). On a stinkbug (*Pentatomidae*), 19 July 2023, Wanhao Chen, GZAC KY0747 (holotype), KY07471 (ex-type), KY07472 (living culture).

Habitat – On the underside of leaves of broad-leaved plant species.

Notes – Molecular characterization through NCBI BLASTn comparisons and multi-locus phylogenetic analysis (dataset 1, Fig. 1) revealed that *Purpureocillium tiankengense* (KY07471 and KY07472) was grouped with *Purpureocillium* species, forming a distinct evolutionary lineage with *P. jiangxiense*, *P. lilacinum*, and *P. zongqii*, which was also supported by the phylogenetic analyses among *Purpureocillium* species (Suppl. Fig. 6). Compared with the typical characteristics, *P. tiankengense* was distinguished from *P. jiangxiense* by its shorter phialides ($6.5\text{--}9.8 \times 2.3\text{--}2.8 \mu\text{m}$ vs $12.41\text{--}15.07 \times 0.88\text{--}3.01 \mu\text{m}$) and insect host (Chen et al. 2024e). *Purpureocillium tiankengense* was distinguished from *P. lilacinum* by its absent of Acremonium-like structures (Luangsa-ard et al. 2011). *Purpureocillium tiankengense* was distinguished from *P. zongqii* by its longer conidiophores ($15.1\text{--}17.5 \times 2.0\text{--}3.0 \mu\text{m}$ vs $9.3\text{--}12.7 \times 2.1\text{--}2.4 \mu\text{m}$) and spider host (Chen et al. 2024b). The congruent morphological and molecular phylogenetic evidence conclusively establishes *P. tiankengense* as a new species.

DISCUSSION

Guizhou Province is known as biodiversity hotspots in China (Xu et al. 2017). As a typical karst landform area in China, Guizhou has numerous mountain ranges that stretch vertically and horizontally. The large altitude difference has created a variety of environmental features, formed a complex ecosystem, and provided different habitats for the survival of various organisms (Liu et al. 2018). Research investigations have documented a remarkable diversity of cordyceps-like fungal taxa throughout Guizhou Province's varied ecosystems, but compared to other research disciplines, it is understudied (Zhu et al. 2004, Song et al. 2011, Chen et al. 2024c). The landforms in Guizhou are composed of an average of 61.92% karst, with broadleaf and mixed forests being the dominant vegetation types (Liu et al. 2018). Despite the presence of unique geological formations like Tiankeng and valleys in Guizhou's karst landscapes, their cordyceps-like fungal communities remain largely unstudied.

Our systematic surveys across Guizhou's karst landscapes (2021-2024) yielded more than 700 cordyceps-like fungal specimens, representing diverse microhabitats including forests, Tiankeng regions and valleys. Six new genera, 51 new species and four new combinations were established in this study. Among those species, 28, 16 and 7 new species were collected from valleys, forest habitats and Tiankeng regions, respectively. Valley is a deep-seated valley with unique structural morphology in karst areas (Xiao 1996). Its main characteristics are that the valley is far-reaching and larger than the valley width, the three-dimensional climate is obvious, the niche is complex and diverse, the characteristics of biodiversity are extremely prominent, and the natural ecosystem is fragile (Mei & Ying 2005). At present, the research on microorganisms in Karst valley mainly focuses on the study of stony microorganisms (Tang & Lian 2012, Tang et al. 2016) and soil microbial community (Wei et al. 2009, 2010, Cui et al. 2011, Tan et al. 2014, Fan et al. 2014). Research on cordyceps-like fungi in the valley remains scarce (Chen et al. 2023, 2024c). Interestingly, the sampling sites in this study are less studied. Furthermore, Wijayawardene et al. (2021) suggested that species diversity in karst habitats should be considered, especially for the less-studied habitats. Future studies should prioritize surveying cordyceps-like fungi in these distinctive yet poorly explored karst forests.

In recent years, studies on the diversity of cordyceps-like fungi in various nature reserves and forest parks across different regions of China have revealed rich resources of these fungi, with notably high species diversity in certain areas (Chen et al. 2020a, 2025, Zhang et al. 2021b, 2024a, b, Zhao et al. 2020, 2021, Fan et al. 2020). Over the past decade, Yunnan and Guizhou provinces have emerged as prominent hotspots for research on cordyceps-like fungi. A total of 158 new species, 8 new records, and 6 new combinations have been reported from these regions, accounting for 92.3% of all newly described cordyceps-like fungi in China during this period (Li et al. 2023, Chen et al. 2023, Dai et al. 2024, Peng et al. 2024, Tang et al. 2023a, b, Wang et al. 2024b, Xiao et al. 2023). However, the majority of sampling sites were located in forest habitats. In the present study, valleys, forest habitats and Tiankeng regions in Guizhou Province were selected for the species diversity of cordyceps-like fungi and 51 new species were established. Notably, valley environments in Guizhou exhibited outstanding fungal diversity and high abundance of undescribed taxa. The unique ecological conditions of karst valleys—such as pronounced microclimatic gradients, high humidity retention, nutrient accumulation, and relative isolation from anthropogenic disturbance—likely contribute to the emergence and preservation of specialized cordyceps-like fungal lineages (Cui et al. 2011, Tan et al. 2014). These findings emphasize the importance of valley habitats as underexplored reservoirs of fungal diversity and underscore the need for further systematic surveys in other poorly studied karst microhabitats.

Phylogenetic analysis revealed that all newly proposed genera in this study share evolutionary affinities with *Lecanicillium* species. Khonsanit et al. (2024) analysed *Akanthomyces* sensu lato in *Cordycipitaceae*, and resurrected *Lecanicillium*. Meanwhile, four new genera, *Corniculantispora* Khons. et al., *Corpulentispora* Khons. et al., *Zarea* and *Zouia* Khons. et al. were introduced to accommodate species previously identified as *Lecanicillium*. The newly erected genus *Neogamszarella* was created to reclassify the taxon previously known as *Gamszarella antillana*

(Chen et al. 2025). Consequently, numerous *Lecanicillium* species have undergone taxonomic reclassification, now placed within *Arachnidicola*, *Corniculantispora*, *Corpulentispora*, *Engyodontium*, *Flavocillium*, and the recently proposed genera *Gamszarea* Zhang & Cai, *Gamszarella*, *Neogamszarella*, *Zarea* and *Zouia* (Chen et al. 2025, Khonsanit et al. 2024). However, the ex-type strain of *Corniculantispora psalliotae* was CBS 505.48, and the strain CBS 532.81 was the ex-type of *Lecanicillium saksenae* (Zare & Gams 2001). In the present study, the strain CBS 505.48 was added in the phylogenetics analysis and two strains can be significantly distinguished (Fig. 2). Thus, the new genus *Paracorniculantispora* was proposed for the strain CBS 505.48. However, there are still some *Lecanicillium* species has not been resolved in the phylogenetics trees (Fig. 2), such as the species, *Lecanicillium fusisporum* and *L. longisporum*. Consequently, comprehensive molecular phylogenies remain essential for resolving taxonomic uncertainties within *Lecanicillium* species.

Shrestha et al. (2016) summarized that Coleoptera and *Lepidoptera* are the two major orders of hosts in cordyceps-like fungi. In our study, the hosts of the new species were mainly *Lepidoptera* insects and spiders. Studies indicate spiders show selective habitat utilization across various microenvironments, ranging from vegetative structures (foliage, stems, bark) to decomposing organic matter and cultivated fields (Shrestha et al. 2016). In fact, the species diversity of spider in Guizhou Province is abundant, especially in caves (Liu et al. 2023, Zhao et al. 2024). Moreover, Man et al. (2015) reported that the of species diversity of fungi in Heshang Hole, Qingjiang, Hubei Province, is abundant, and including some unique fungal genera that have not been reported before, such as *Metacordyceps* and *Stibella*. The results of species diversity of fungi from two unnamed caves in Guizhou revealed that the cordyceps-like fungi were also abundant (Zhang et al. 2017, 2021b). The present research was limited to particular karst microenvironments, and future studies should explore the hidden fungal diversity in other specialized niches of this ecosystem.

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DECLARATION ON CONFLICT OF INTEREST

The authors have declared that no competing interests exist.

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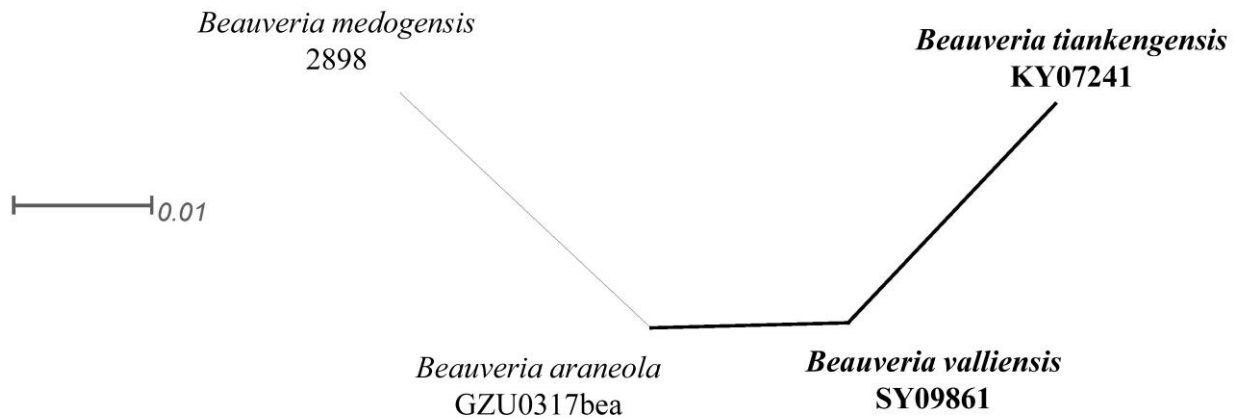
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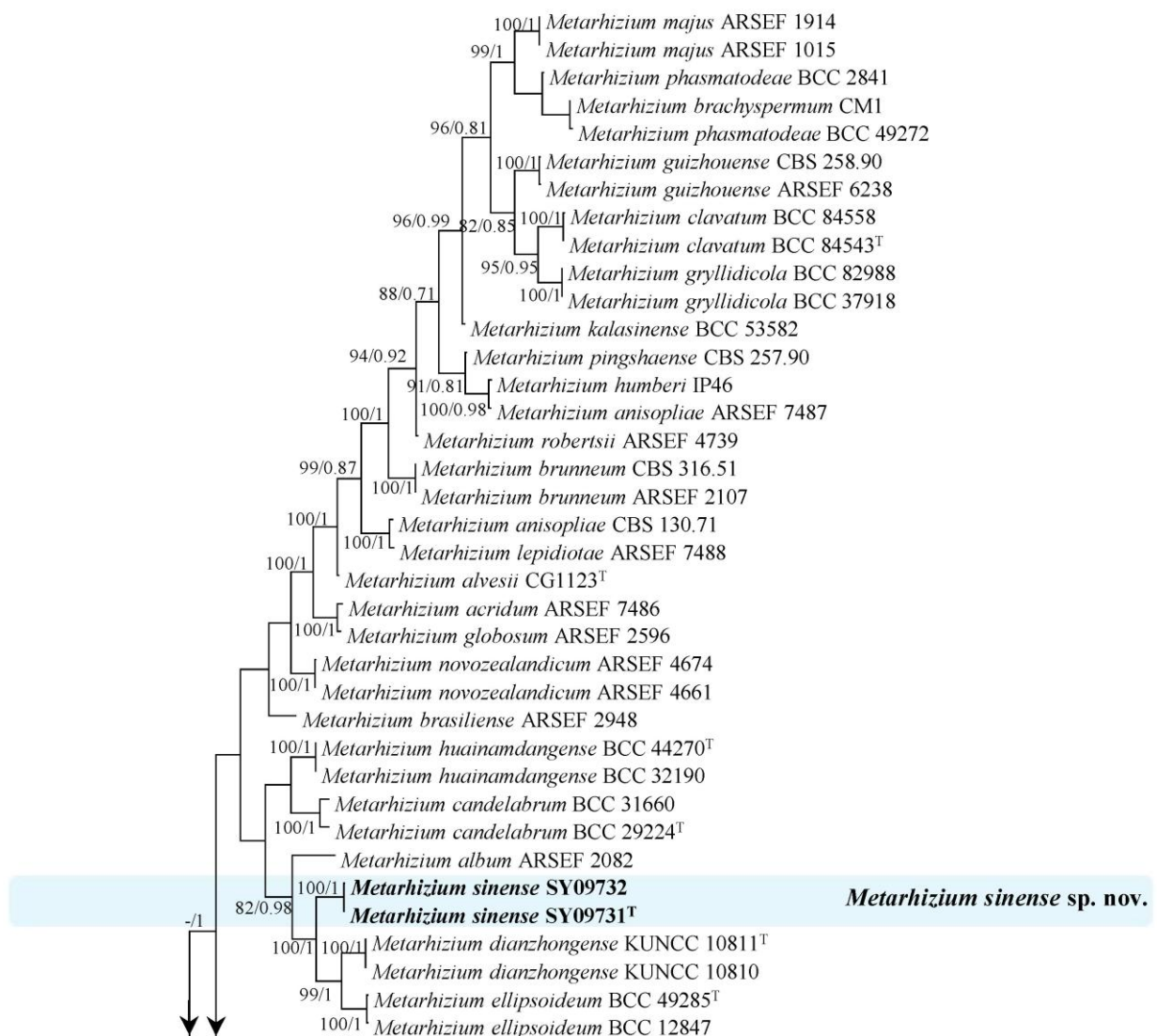
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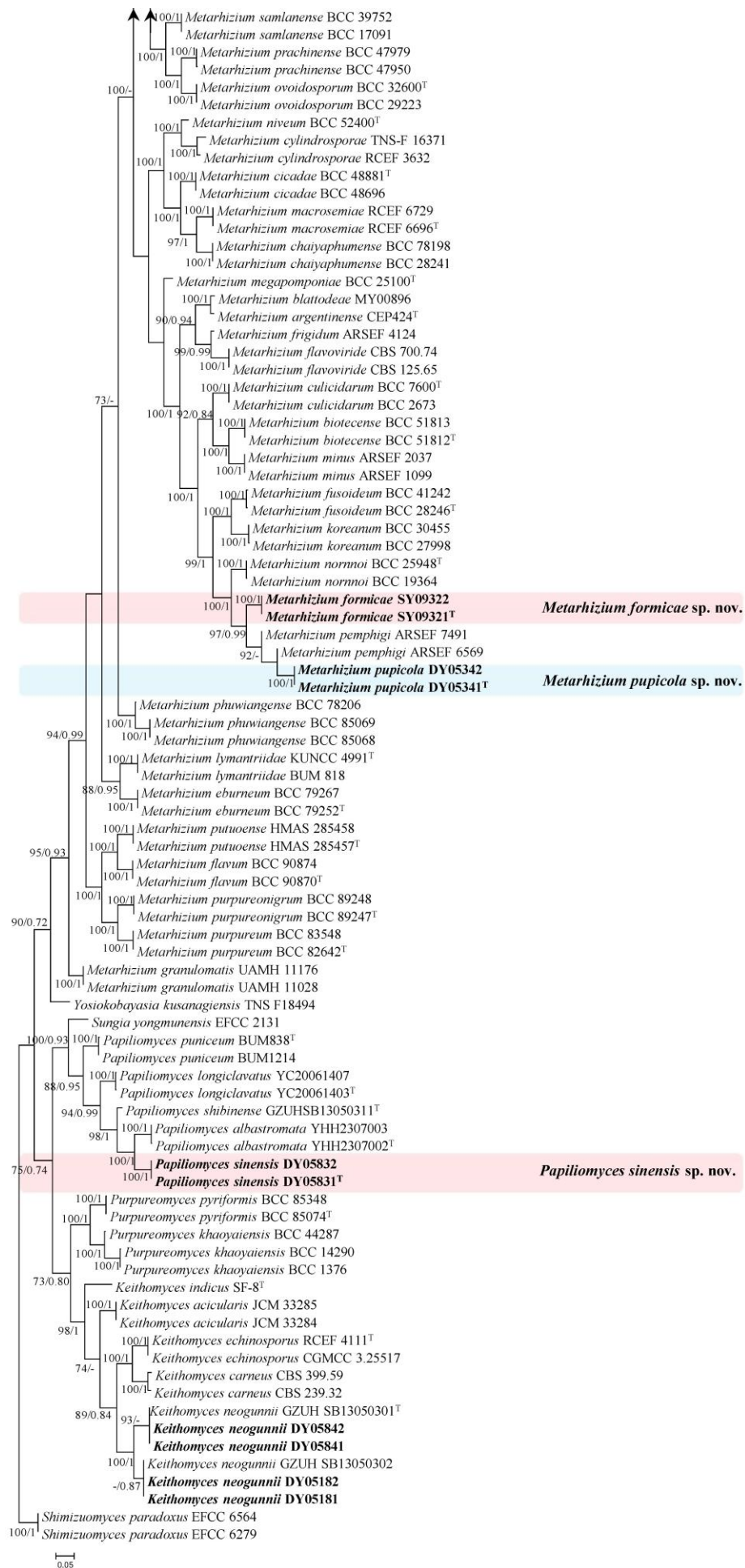
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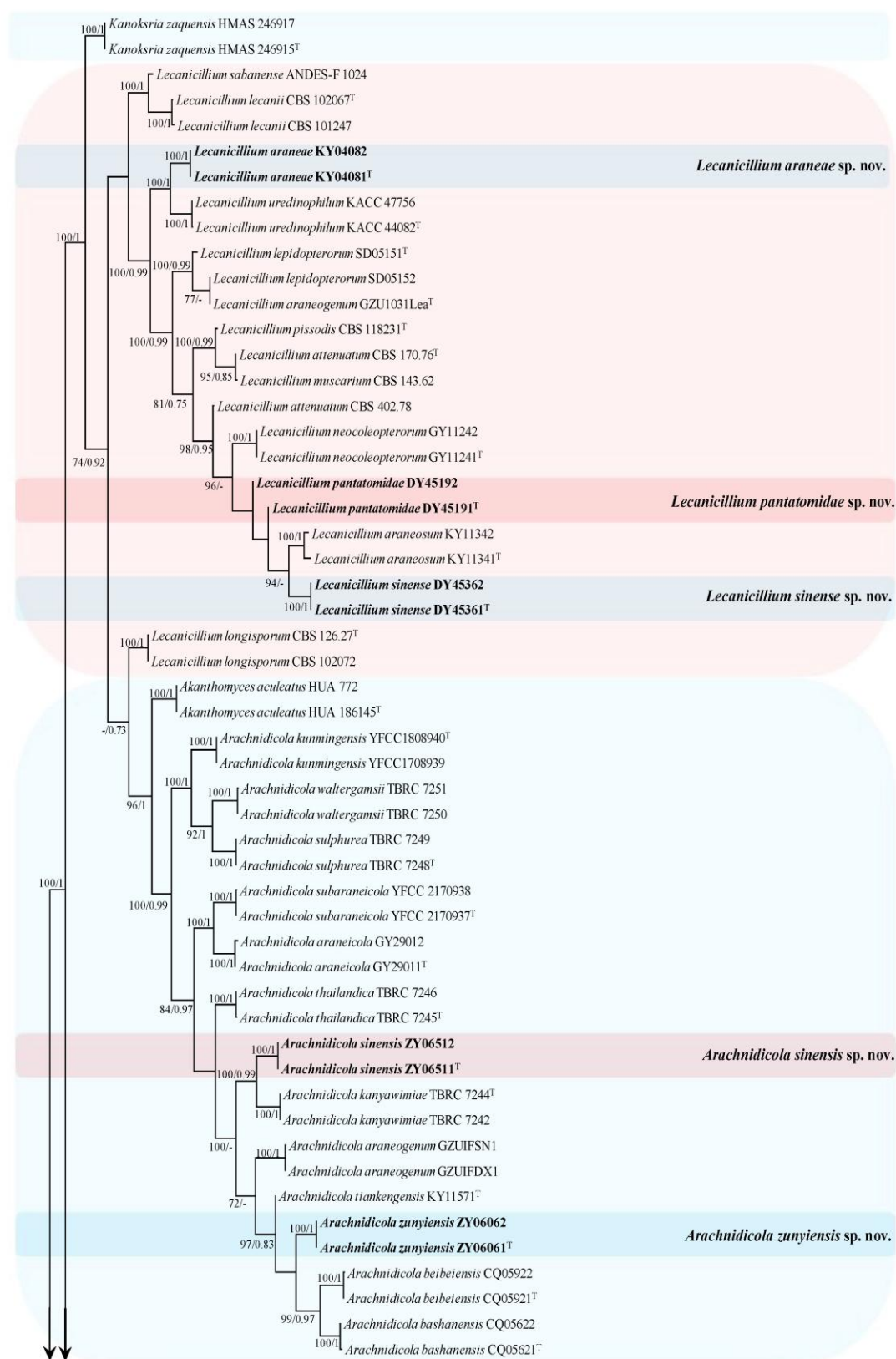


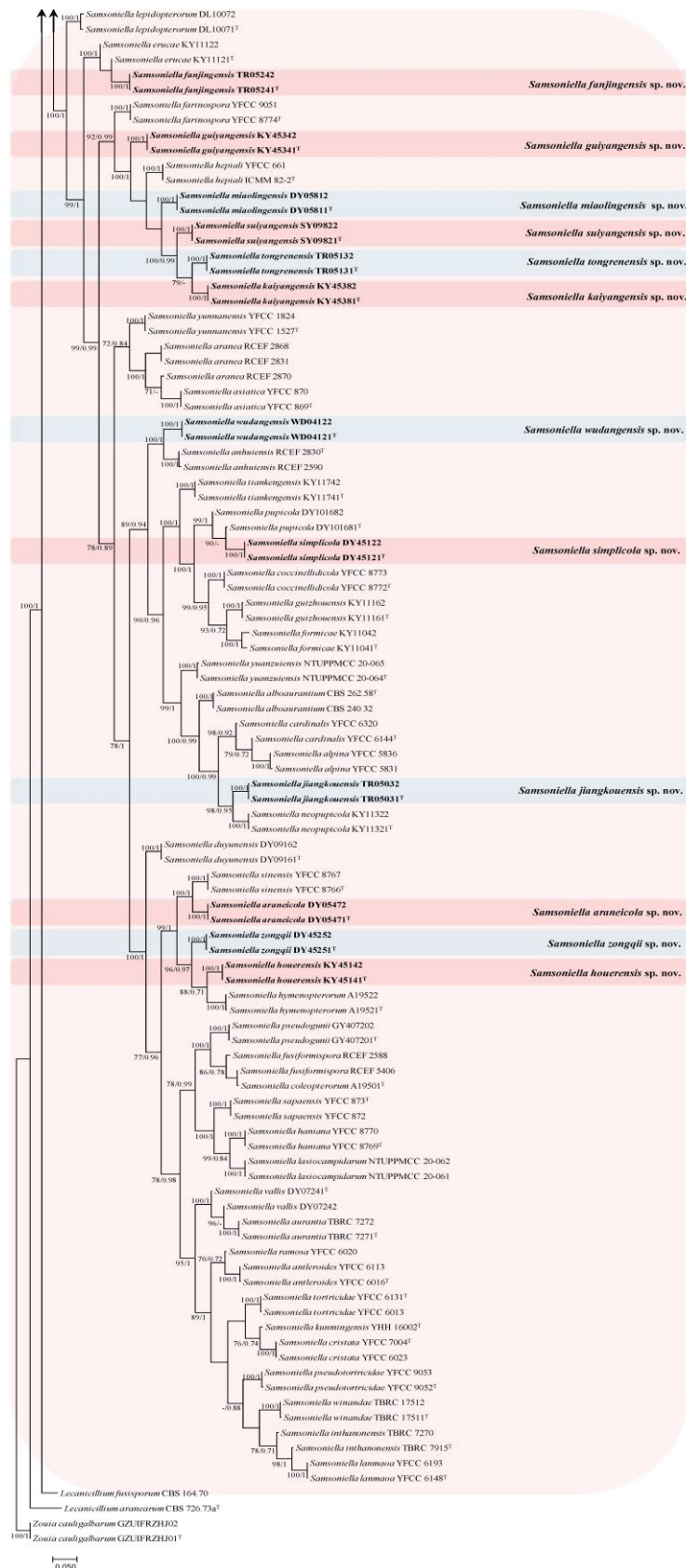
Supplementary Figure 1 – Results of the pairwise homoplasy index (PHI) test of closely-related species using both LogDet transformation and splits decomposition. PHI test results (Φ_w) < 0.05 indicate significant recombination within the dataset. The new strains or species are in bold type.



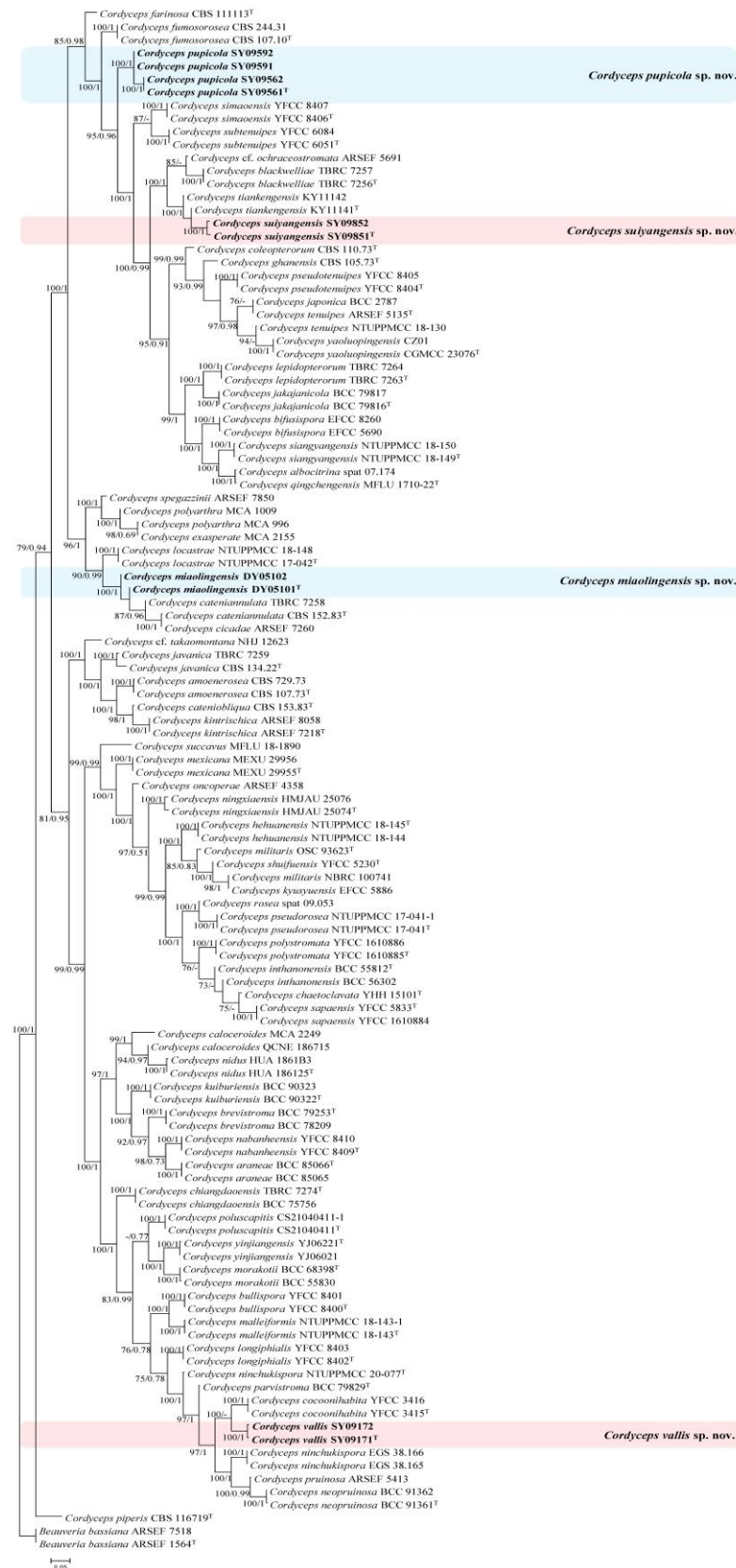


Supplementary Figure 2 – Phylogram retrieved from IQTREE of the new species and related species in *Clavicipitaceae* using the combined dataset of ITS, LSU, *rpb1*, *rpb2* and *tef-1a* gene regions. The statistical values are provided at nodes as ML/PP (ML value above 70% and BI value above 0.70). The tree is rooted with *Shimizuomyces paradoxus* (EFCC 6279 and EFCC 6564). Ex-types, new strains and new species are indicated by the superscript “T” and in bold, respectively.

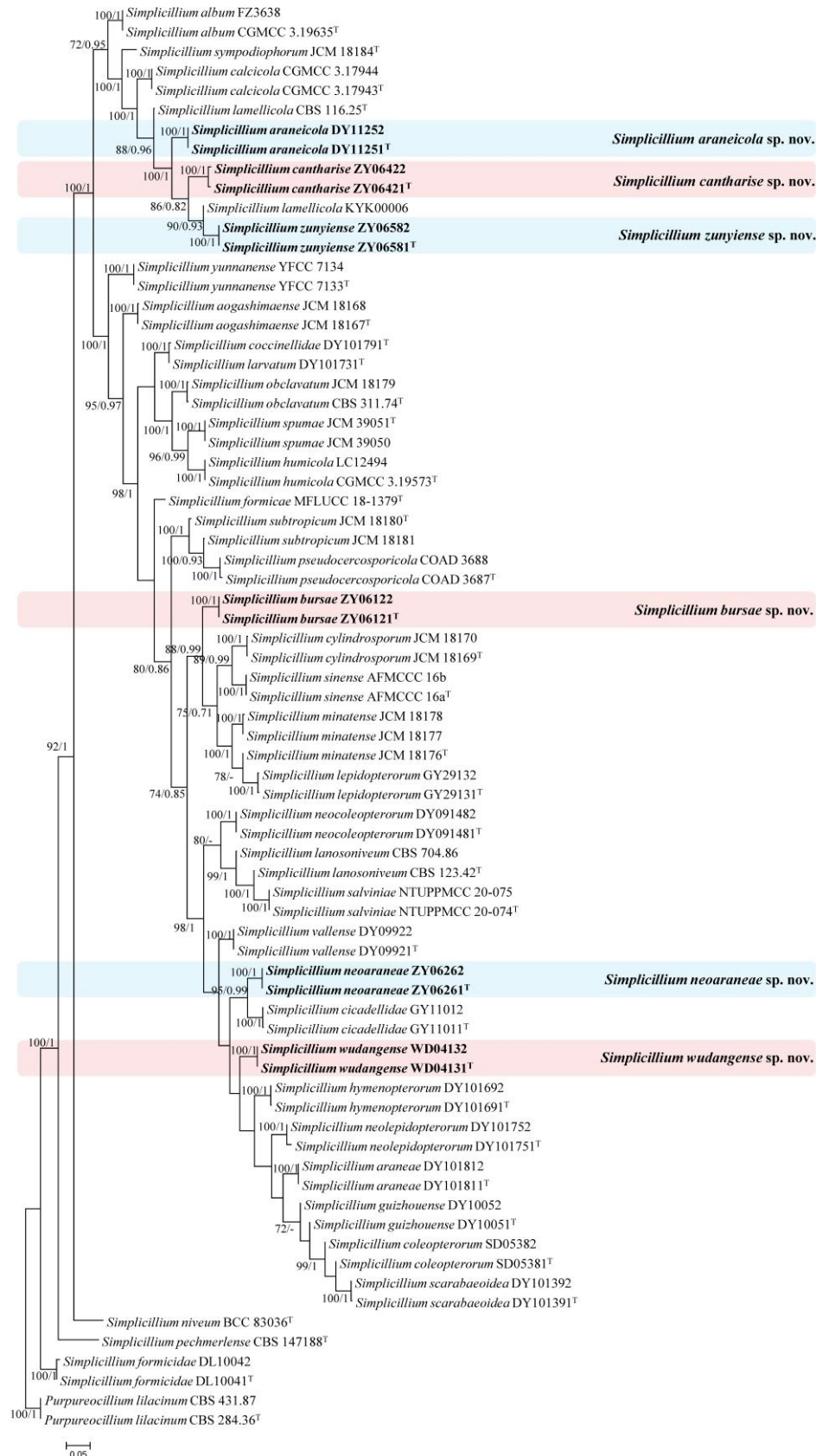




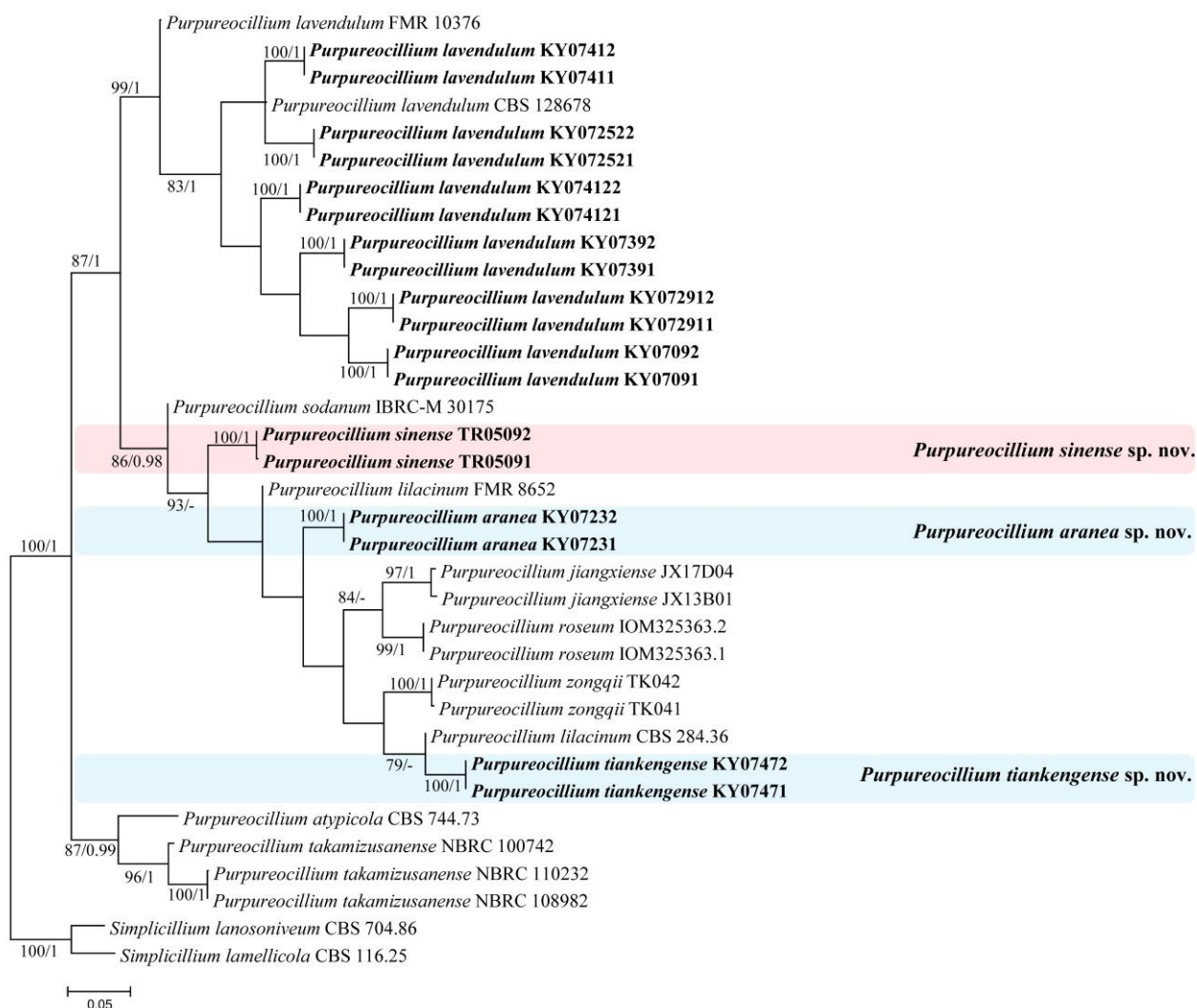
Supplementary Figure 3 – Phylogram retrieved from IQTREE of the new species and related species in *Cordycipitaceae* using the combined dataset of ITS, LSU, *rpb1*, *rpb2* and *tef-1a* gene regions. The statistical values are provided at nodes as ML/PP (ML value above 70% and BI value above 0.70). The tree is rooted with *Zouia cauligalbarum* (GZUIFRZHI01 and GZUIFRZHI02). Ex-types, new strains and new species are indicated by the superscript “T” and in bold, respectively.



Supplementary Figure 4 – Phylogram retrieved from IQTREE of the new species and related species in the genus *Cordyceps* using the combined dataset of ITS, LSU, *rpb1*, *rpb2* and *tef1-α* gene regions. The statistical values are provided at nodes as ML/PP (ML value above 70% and BI value above 0.70). The tree is rooted with *Beauveria bassiana* (ARSEF 1564 and ARSEF 7518). Ex-types, new strains and new species are indicated by the superscript “T” and in bold, respectively.



Supplementary Figure 5 – Phylogram retrieved from IQTREE of the new species and related species in the genus *Simplicillium* using the combined dataset of ITS, LSU, *rpb1* and *tef-1a* gene regions. The statistical values are provided at nodes as ML/PP (ML value above 70% and BI value above 0.70). The tree is rooted with *Purpureocillium lilacinum* (CBS 284.36 and CBS 431.87). Ex-types, new strains and new species are indicated by the superscript “T” and in bold, respectively.



Supplementary Figure 5 – Phylogram retrieved from IQTREE of the new species and related species in the genus *Purpureocillium* using the combined dataset of ITS, LSU and *tef-1α* gene regions. The statistical values are provided at nodes as ML/PP (ML value above 70% and BI value above 0.70). The tree is rooted with *Simplicillium lamellicola* (CBS 116.25) and *S. lanosoniveum* (CBS 704.86). Ex-types, new strains and new species are indicated by the superscript “T” and in bold, respectively.