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Research Article

New additions to *Sympoventuriaceae* (*Venturiales*, *Dothideomycetes*): three new species from China

Ming-Yi Zhang[1], Heng Pan[1], Yu-Lian Ren[2], Yun-Jie Wu[1], Zhi-Qing Fang[1], Bing-Da Sun[3], Gang Tao[1], Zhi-Yuan Zhang[1]

1 *College of Eco-Environmental Engineering, Guizhou Minzu University, Guiyang 550025, China*
2 *College of Ecology and Environment (College of Wetland), Southwest Forestry University, Kunming 650224, China*
3 *China General Microbiological Culture Collection Center, Institute of Microbiology, Chinese Academy of Sciences, Beijing 100101, China*
Corresponding authors: Gang Tao (ttg729@sina.com); Zhi-Yuan Zhang (zzymetac16@163.com)

Abstract

Fungi in urban soils are an indispensable component of urban ecosystems, playing a central role in maintaining soil health, promoting nutrient cycling, facilitating plant growth, and safeguarding ecosystem functions. However, taxonomic studies of fungi in urban soils remain extremely limited. During an investigation of culturable fungi from urban soils in China, eight isolates belonging to *Sympoventuriaceae* were isolated. Although recent taxonomic refinements at the generic level within *Sympoventuriaceae* have progressed, the taxonomic status of some monotypic genera remains to be stabilized. Based on integrated morphological characterization and multigene phylogenetic analyses of five loci (ITS, LSU, *tef1*, *tub2*, and *rpb2*), three novel species are described and illustrated: *Scolecobasidium campestre*, *Verruconis obovatus*, and *Veronaeopsis sinensis*. This study provides comprehensive morphological descriptions, illustrations, phylogenetic data, and comparisons with closely related species for these novel taxa. This research contributes to fungal data from urban soils and enhances the understanding of the species diversity, taxonomy, and distribution of *Sympoventuriaceae*.

Key words: Molecular systematics, soil fungi, taxonomy, three new species

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Introduction

The family *Sympoventuriaceae* belongs to the order *Venturiales* in the class *Dothideomycetes* and was established by Zhang et al. (2011) based on a multigene phylogenetic analysis, morphological characteristics, and ecological habits. The type genus of the family is *Sympoventuria*, which was established by Crous et al. (2007) based on the type species *S. capensis*. Since the family was erected, the number of genera incorporated into it has continuously increased through ongoing morphological and molecular phylogenetic studies. Based on a comprehensive analysis of seven gene fragments (SSU, ITS, LSU, *act1*, *tub2*, *tef1*, and *rpb2*), Wei et al. (2022) confirmed that 22 genera belong to *Sympoventuriaceae*. Subsequently, Crous et al. (2024) established

another new genus, *Zenophaeosphaeria*. To date, the family *Sympoventuriaceae* comprises 23 genera. Although the systematics of *Sympoventuriaceae* have become relatively stable, the delimitation of some genera and species still requires clarification through more newly collected specimens, multigene phylogenetic analyses, and phenotypic studies. For instance, the systematic positions of genera such as *Acroconidiellina* and *Matsushimaea* require further verification due to the lack of reliable molecular data or type strains. Members of *Sympoventuriaceae* exhibit high diversity in ecological habits, encompassing various lifestyles, such as saprobic, endophytic, plant pathogenic, and animal or human opportunistic pathogenic lifestyles (Satow et al. 2008; Seyedmousavi et al. 2013; Kidd et al. 2016; Zhang et al. 2018; Samerpitak et al. 2019; Benavent 2021; Murata et al. 2022). Ancestral trait reconstruction analysis suggested that the ancestral lifestyle of *Sympoventuriaceae* was saprobic and that parasitic lifestyles, such as plant pathogens and animal pathogens, evolved independently multiple times from saprobic ancestors (Wei et al. 2022).

The genus *Scolecobasidium* was erected by Abbott (1927) based on *S. terreum* (generic type) and *S. constrictum*. To date, *Scolecobasidium* is the largest genus in *Sympoventuriaceae*, comprising 56 species (Wei et al. 2022; Song et al. 2023; Zhang et al. 2024; Crous et al. 2026). This genus is characterized by brownish to black colonies, reduced, hyaline or pigmented conidiophores, and septate, smooth- or rough-walled, brown, single, dry, and rhexolytic conidia (Abbott 1927; Barron and Busch 1962; Seifert and Gams 2011). Members of *Scolecobasidium* are slow-growing and saprotrophic (Yasanthika et al. 2025), and they exhibit a worldwide distribution across diverse habitats, including soil, water, plants, humans, and fish or other cold-blooded vertebrates (Doty and Slater 1946; Ross and Yasutake 1973; Hamayun et al. 2009; Giraldo et al. 2014; Shen et al. 2020; Wei et al. 2022; Song et al. 2023; Zhang et al. 2024).

Samerpitak et al. (2014) transferred *Ochroconis gallopava* from *Ochroconis* to the newly established genus *Verruconis*, designating it as the type species. Subsequently, several new species have been introduced to the genus. Currently, 17 species are accepted in the genus, and all of them have sequence data available in GenBank (Wei et al. 2022; Shao et al. 2022; Bao et al. 2025). To date, the sexual morph has been reported only for *Verruconis mangrovei*, while all other species in this genus are described based on their asexual morphs (Bao et al. 2025). Members of *Verruconis* inhabit roots, leaves, tree latex, decaying wood, and soil (Zhang et al. 2018; Huanraluek et al. 2019; Qiao et al. 2019; Hernández-Restrepo et al. 2020; Shen et al. 2020; Shao et al. 2022; Wei et al. 2022; Yasanthika et al. 2025; Bao et al. 2025).

Arzanlou et al. (2007) removed *Veronaea simplex* from *Veronaea* and established *Veronaeopsis* with it as the type species. To date, this genus contains only a single species, *Veronaeopsis simplex*, with very few reliable strains and available molecular sequences (Wei et al. 2022). During an investigation of culturable fungi from urban soils in China, eight isolates representing *Sympoventuriaceae* were obtained. Morphological characteristics and multilocus (SSU, ITS, LSU, *tef1*, *tub2*, and *rpb2*) phylogeny were combined to determine their taxonomy. As a result, three novel species are proposed herein.

Materials and methods

Fungal isolation and morphology

Soil samples were collected from green belts in three Chinese cities: (1) Guizhou Minzu University, Guiyang, Guizhou Province; (2) Guandu District, Kunming, Yunnan Province; and (3) Fuzhou Zoo, Fuzhou, Fujian Province. Samples were collected and stored in sterile Ziploc bags at 4 °C, transported to the laboratory, and processed immediately for experimentation. Fungi were isolated using the dilution method described by Tong et al. (2023, 2025).

Pure colonies on potato dextrose agar (PDA) medium were transferred to fresh PDA, oatmeal agar (OA), and synthetic nutrient-poor agar (SNA) plates and incubated at 25 °C in darkness for 14 days to assess colony morphology and macroscopic characteristics. The color of the colony was described using the color-coding system of the German Institute for Quality Assurance and Certification (Reichs-Ausschuss für Lieferbedingungen und Gütesicherung, RAL; https://www.ral-guetezeichen.de/), abbreviated as RAL in the text. The isolates were allowed to grow onto an adjacent, sterile coverslip that had been partially inserted into the agar surface at a 60° angle to observe fungal structures (Li et al. 2011), and 25% lactic acid was used as a mounting medium for microscopy. Morphological features were observed and recorded using a Zeiss Axio Imager A2 microscope and a Zeiss AxioCam MRc color digital camera (Carl Zeiss Ltd., München, Germany).

The ex-type living cultures of the novel taxa were preserved in the China General Microbiological Culture Collection Center (CGMCC). All living cultures were preserved in sterile 30% glycerol at −80 °C and deposited at the College of Eco-Environmental Engineering, Guizhou Minzu University. Dried culture specimens, dried at 50 °C, were deposited at the same institution. The taxonomic descriptions of the new taxa were registered in MycoBank.

DNA extraction, PCR amplification, and sequencing

Genomic DNA was extracted from fungal mycelium growing on PDA plates for 14 days, according to the manufacturer's protocol of the BioTeke Fungal Genomic DNA Extraction Kit (DP2032, BioTeke, Beijing, China). Six gene markers (SSU, ITS, LSU, *tef1*, *tub2*, and *rpb2*) were amplified and sequenced using the primer pairs listed in Table 1. The 25 µL PCR reactions contained 2.0 µL DNA template, 1.0 µL each of forward and reverse primers, 8.5 µL ddH_2O, and 12.5 µL 2× MasterMix (Sangon Biotech, China). All newly generated sequences were submitted to GenBank (www.ncbi.nlm.nih.gov) (Table 2).

Phylogenetic analyses

Lasergene software (version 6.0, DNASTAR) was used to edit ambiguous bases at both ends of the raw forward and reverse reads and to assemble them. Sequences were aligned with MAFFT v7.037 (Katoh and Standley 2013), and alignments were trimmed with MEGA v6.06 (Tamura et al. 2013). The most appropriate models of sequence evolution for Bayesian inference and maximum likelihood analyses were selected using ModelFinder (Kalyaanamoorthy et al. 2017) in PhyloSuite v1.2.3 (Xiang et al. 2023).

Table 1. Gene regions and respective primers used in the study.

Gene region	Primer pairs (forward/ reverse)	Annealing temperature (°C)	Reference
ITS	ITS5	51	White et al. 1990
	ITS4		White et al. 1990
LSU	LR0R	51	Vilgalys and Hester 1990
	LR5		Vilgalys and Hester 1990
SSU	NS1	51	White et al. 1990
	NS4		White et al. 1990
tef1	983F	58	Rehner and Buckley 2005
	2218R		Rehner and Buckley 2005
	728	58	Carbone and Kohn 1999
	986		Carbone and Kohn 1999
tub2	Bt2a	55	Glass and Donaldson 1995
	Bt2b		Glass and Donaldson 1995
rpb2	5F	54	Liu et al. 1999
	7CR		Liu et al. 1999

Table 2. Strains and sequences of *Sympoventuriaceae* included in this study.

Species	Strain	GenBank and CNCB accession numbers					
		SSU	ITS	LSU	*tef1*	*tub2*	*rpb2*
Acroconidiellina arecae	NFCCI 3696		KX306747	KX306776			
Bellamyces quercus	CBS 46217 T		MK810901	MK810788	MK888726		MK887796
Clavatispora thailandiaca	MFLUCC 100107	KF770457	MH065721	KF770458			
Echinocatena sinensis	CGMCC 3.20775 T		OL897006	OL897048	ON568898	ON569026	ON568948
Echinocatena sinensis	GZUIFR 21.901		OL897007	OL897049	ON568899	ON569027	ON568949
Fuscohilum rhodensis	CBS 121641 T		MK810909	MK810796	MK888733	MK926471	MK887802
Fuscohilum siciliana	CBS 105.85 T	KP798640	MK810910	MK810797	MK888734	MK926472	MN091924
Guizhoumyces aciculaea	GUCC 18195 T	MZ503650	MZ503724	MZ503757	MZ546870	MZ546903	MZ546866
Guizhoumyces aciculaea	GUCC 18152	MZ503649	MZ503723	MZ503756	MZ546869	MZ546902	MZ546865
Helicopsis olivaceum	CBS 728.83	AY856925	MH861681	MH873393			
Matsushimaea fasciculata	GUCC 18239	MZ503651	MZ503725	MZ503758	MZ546871	MZ546904	MZ546867
Matsushimaea monilioides	CBS 143867 T		LT883468	LT883469			
Melnikomyces longisporum	HUGP 18226 T	MT731289	MT731290	MT731291	MT739516	MT739515	
Melnikomyces thailandicus	CBS 145767 T		MN794374	MN794351			
Mycosisymbrium cirrhosum	MTCC 12435	KR259885	KR259883	KR259884			KR349124
Mycosisymbrium cirrhosum	GUCC 1837	MZ503648	MZ503722	MZ503755	MZ546868	MZ546901	MZ546864
Neocoleroa cameroonensis	CBS 129041 T		MK810902	MK810789	MK888727	MN078219	MK887797
Neocoleroa metrosideri	ICMP 21139 T		KU131678	KU131677			
Neofusicladium eucalypti	CBS 128216 T		MK810903	MK810790	MK888728	MK926468	MK887798
Neofusicladium eucalypticola	CBS 141301 T		MK810904	MK810791	MK888729		MK887799
Parafusicladium amoenum	CBS 254.95 T		MK810906	MK810793	MK888730	MK926469	
Parafusicladium paraamoenum	CBS 141322 T		MK810908	MK810795	MK888732		MK887801

Species	Strain	GenBank and CNCB accession numbers					
		SSU	ITS	LSU	*tef1*	*tub2*	*rpb2*
Pinaceicola cordae	CBS 126959 T		MK810911	MK810798	MK888735	MK926473	
Pinaceicola pini	CBS 463.82 T		MK810915	MK810802	MK888739	MK926477	MK887804
Pseudosigmoidea excentrica	CBS 469.95 T	NG_065605	HQ667543	KF282669	KF155975	MK926478	
Pseudosigmoidea ibarakiensis	NBRC 107891 T	NG_078726	LC146758	LC146759			
Scolecobasidium acanthi	CGMCC 3.24352 T		OQ448957	OQ448949	OQ442215	OQ442218	OQ442212
Scolecobasidium aegiceratis	CGMCC 3.24353 T		OQ448958	OQ448950	OQ442216	OQ442219	OQ442213
Scolecobasidium ailanthi	MFLUCC 17-0923 T	MK347838	MK347730	MK347947		MK412883	
Scolecobasidium anellii	CBS 284.64 T	KF156070	FR832477	KF156138	KF155995	KF156184	KF282684
Scolecobasidium anomalum	CBS 131816 T	KF156065	HE575201	KF156137	KF155986	KF156194	HE575205
Scolecobasidium aquaticum	CBS 140316 T	KX668260	KX668258	KX668259			
Scolecobasidium bacilliforme	CBS 100442 T	KP798638	KP798632	KP798635	KT272070	KT272059	
Scolecobasidium blechni	CBS 146055 T		MN562134	MN567641	MN556826	MN556843	
Scolecobasidium burgersense	CBS 151408 T		PP565150	PP532844			
Scolecobasidium camellicola	GUCC 18242 T	MZ503654	MZ503728	MZ503761	MZ546874	MZ546907	
Scolecobasidium campestre	**CGMCC 3. 29458 = ZY 24.010 T**	**PX522227**	**PX522232**	**PX522237**	**PX586637**	**PX586642**	**PX586632**
Scolecobasidium campestre	**ZY 24.011 T**	**PX522228**	**PX522233**	**PX522238**	**PX586638**	**PX586643**	**PX586633**
Scolecobasidium capsici	CBS 142096 T		KY173427	KY173518			
Scolecobasidium coiledmyces	GUCC 18245 T	MZ503657	MZ503731	MZ503764	MZ546877	MZ546910	
Scolecobasidium constrictum	CBS 202.27 T	KF156072	MH854929	MH866423	KF156003	KF156161	
Scolecobasidium cordanae	CBS 475.80 T	KF156058	KF156022	KF156122	KF155981	KF156197	
Scolecobasidium crassihumicola	CBS 120700	KJ867431	KJ867429	KJ867430	KJ867428	KJ867433	
Scolecobasidium dracaenae	CBS 141323 T		KX228283	KX228334	KX228377		KX228370
Scolecobasidium echinulatum	GUCC 18247 T	MZ503659	MZ503733	MZ503766	MZ546879	MZ546912	
Scolecobasidium ellipsoideum	GUCC 18264	MZ503676	MZ503750	MZ503783	MZ546896	MZ546929	
Scolecobasidium. endophyticum	CBS 149762 T		MN365755	MN308484	PX047958		
Scolecobasidium ferulica	IRAN3232C T		MF186874	MH400207			
Scolecobasidium gamsii	CBS 239.78 T	KF156088	KF156019	KF156150	KF155982	KF156190	
Scolecobasidium globale	CBS 119644 T	KF961108	KF961086	KF961097	KF961075	KF961065	
Scolecobasidium guangxiense	SS23 T	MK929277	MK934570	MK956169			
Scolecobasidium guizhouense	CGMCC 3.25502 T	OR680870	OR680501	OR680568	OR858900	OR843206	OR842918
Scolecobasidium helicteris	NFCCI 4310 T		MK014833			MK321318	
Scolecobasidium humicola	CBS 116655 T	KF156068	HQ667521	KF156124	KF155984	KF156195	
Scolecobasidium icarus	CBS 536.69 T	KF156084	HQ667524	KF156132	KF156009	KF156174	KF282700
Scolecobasidium inverellipsoidisporum	CGMCC 3.25504 T	OR680875	OR680506	OR680573	OR858905	OR843211	OR842923
Scolecobasidium lascauxense	CBS 131815 T	KF156069	FR832474	KF156136	KF155994	KF156183	FR832481
Scolecobasidium laurentii	NFCCI 5982 T		PV029878	PV029879	PV023971	PV023970	
Scolecobasidium leishanicola	GUCC 18259	MZ503671	MZ503745	MZ503778	MZ546891	MZ546924	
Scolecobasidium longiphorum	CGMCC 3.25505	OR680880	OR680511	OR680578	OR858910	OR843216	OR842928
Scolecobasidium macrozamiae	CBS 102491	KF156092	KF156021	KF156152	KF155983	KF156191	
Scolecobasidium millerae	BRIP75007a T		OP903485	OP903501			

Species	Strain	GenBank and CNCB accession numbers					
		SSU	ITS	LSU	*tef1*	*tub2*	*rpb2*
Scolecobasidium minimum	CBS 510.71 T	KF156087	HQ667522	KF156134	KF156007	KF156172	
Scolecobasidium mirabilis	CBS 413.51 T	KF156076	HQ667536	KF156140	KF156001	KF156164	
Scolecobasidium musae	CBS 729.95 T	KF156082	KF156029	KF156144	KF155999	KF156171	
Scolecobasidium musicola	CBS 144441 T		MH327824	MH327860	MH327887	MH327898	MH327876
Scolecobasidium nancywakeae	BRIP72739c T		OQ917081	OQ892171			
Scolecobasidium obovoideum	GUCC 18246 T	MZ503658	MZ503732	MZ503765	MZ546878	MZ546911	
Scolecobasidium olivaceum	CBS 137170 T	LM644548	LM644521	LM644564	KT272067	LM644605	
Scolecobasidium pandanicola	CBS 140660 T		KT950850	KT950864			
Scolecobasidium parahumicola	CGMCC 3.25503 T	OR680873	OR680504	OR680571	OR858903	OR843209	OR842921
Scolecobasidium patriciamatherae	BRIP 75792a T		OR608746	OR602940			
Scolecobasidium phaeophorum	CBS 206.96 T	KP798637	KP798631	KP798634	KT272098	KT272062	KF282692
Scolecobasidium podocarpi	CBS 143174 T		MG386032	MG386085		MG386162	
Scolecobasidium podocarpicola	CBS 146057 T		MN562138	MN567645			MN556811
Scolecobasidium ramosum	CBS 137173 T	LM644551	LM644524	LM644567	KT272069	MZ546928	
Scolecobasidium robustum	CBS 112.97 T	KP798639	KP798633	KP798636	KT272071	KT272060	
Scolecobasidium sexuale	CBS 135765 T	KF156089	KF156018	KF156118	KF155976	KF156189	
Scolecobasidium terrestre	CBS 211.53 T	NG_062994	NR_145365	NG_058014	KF156005	KF156187	KF282686
Scolecobasidium terreum	CBS 203.27 T		HQ667544			HQ877665	KF282698
Scolecobasidium tshawytschae	CBS 228.66	KF156064	KF156016	KF156128	KF155992	KF156179	
Scolecobasidium tshawytschae	GUCC 18251	MZ503663	MZ503737	MZ503770	MZ546883	MZ546916	
Scolecobasidium tshawytschae	GUCC 18252	MZ503664	MZ503738	MZ503771	MZ546884	MZ546917	
Scolecobasidium tshawytschae	GUCC 18253	MZ503665	MZ503739	MZ503772	MZ546885	MZ546918	
Scolecobasidium tshawytschae	GUCC 18254	MZ503666	MZ503740	MZ503773	MZ546886	MZ546919	
Scolecobasidium tshawytschae	CBS 100438 T	KF156062	HQ667562	KF156126	KF155990	KF156180	KF282697
Scolecobasidium tshawytschae	CBS 130.65	KF156061	MH858517	MH870151	KF155989	KF156178	
Scolecobasidium tshawytschae	ZY 22.031	OR680879	OR680510	OR680577	OR858909	OR843215	OR842927
Scolecobasidium tshawytschae	CBS 454.77	KT272094		KT272089	KF155991	KF156181	
Scolecobasidium tshawytschae	CBS 850.73	KF156063	KT272079	KT272090	KF155988	KF156177	
Scolecobasidium tshawytschae	NBRC 32268	EU107353	DQ307334	EU107310	DQ307356		DQ415439
Scolecobasidium verrucarium	GUCC 18240 T	MZ503652	MZ503726	MZ503759	MZ546872	MZ546905	
Scolecobasidium verrucosum	CBS 383.81 T	KF156067	KF156015	KF156129	KT272099	KF156185	
Scolecobasidium zunyiense	GUCC 18241 T	MZ503653	MZ503727	MZ503760	MZ546873	MZ546906	
Sterila eucalypti	CBS 144019 T		MK810918	MK810805	MK888742		MK887807

Species	Strain	GenBank and CNCB accession numbers					
		SSU	ITS	LSU	*tef1*	*tub2*	*rpb2*
Sterila eucalypti	CPC 14942		MK810916	MK810803	MK888740		MK887805
Sympoventuria capensis	CBS 120136 T	KF156094	MK810921	MK810808	MK888745	MK926481	MK887810
Sympoventuria capensis	CPC 12839		MK810922	MK810809	MK888746	MK926482	MK887811
Troposporella fumosa	CBS 351.94		MK810924	MH874121			
Troposporella monilipes	MUCL 19867	AY856920	DQ351723	AY856871			
Veronaeopsis simplex	CBS 588.66 T	KF156095	EU041820	EU041877			MN091925
Veronaeopsis sinensis	**CGMCC 3.29838 = ZY 25.010 T**	**PZ315057**	**PZ315066**	**PZ315075**	**PZ341956**	**PZ341947**	**PZ341941**
Veronaeopsis sinensis	**ZY 25.011**	**PZ315058**	**PZ315067**	**PZ315076**	**PZ341957**	**PZ341948**	**PZ341942**
Veronaeopsis sinensis	**ZY 25.012**	**PZ315059**	**PZ315068**	**PZ315077**	**PZ341958**	**PZ341949**	**PZ341943**
Verruconis calidifluminalis	CBS 125818 T	KF156046	AB385698	KF156108	KF155959	KF156202	
Verruconis calidifluminalis	CBS 125817	KF156045	AB385699	KF156107	KF155958	KF156201	
Verruconis cylindricalis	GUCC 18299 T	MZ503680	MZ503754	MZ503787	MZ546900	MZ546933	
Verruconis gallopava	CBS 437.64 T	KF156053	HQ667553	KF156112	KF155968	KF156203	KF282689
Verruconis guizhouensis	CGMCC 3.20874 T	ON764294	ON184018	ON764283			
Verruconis hainanensis	YMF 1.04165 T	MK248267	MK244397	MK248269			
Verruconis heveae	MFLUCC 17-0372 T	OL780530	MH602349	MH602348			
Verruconis hyalina	KUNCC 23–14194 T		PV138744	PV138599			
Verruconis mangrovei	NFCCI-4390 T	MN241147	MN782361	MN241144		MN848140	MN231836
Verruconis pakchongensis	TBRC-BCC 51642 T	OQ121937	OQ121928	OQ121946		OQ116768	OQ116751
Verruconis panacis	CBS 142802 T	MF536879	MF536882	MF536880		MF536883	
Verruconis phayaoensis	MFLUCC 17-0347 T	OL780531	OL780498	OL782077			
Verruconis pseudotricladiata	YMF 1.04915 T	MK248268	MK244396	MK248270		MK253013	
Verruconis soli	MFLUCC 22-0082 T	OP581426	OP581411	OP581410			
Verruconis terricola	CBS 131795 T		MK810925	MK810811			KC337072
Verruconis thailandica	CBS 145768 T		MN794375	MN794352			
Verruconis thailandica	GUCC 18267	MZ503679	MZ503753	MZ503786		MZ546932	
Verruconis tricladiata	NBRC 30208	EU107354		EU107286			DQ415436
Verruconis verruculosa	CBS 119775 T	KF156055	KF156014	KF156106	KF155974	KF156193	
Verruconis obovatus	**CGMCC 3.29459 = ZY25.007 T**	**PX522224**	**PX522229**	**PX522234**	**PX586634**	**PX586639**	**PX586629**
Verruconis obovatus	**ZY 25.008**	**PX522225**	**PX522230**	**PX522235**	**PX586635**	**PX586640**	**PX586630**
Verruconis obovatus	**ZY 25.009**	**PX522226**	**PX522231**	**PX522236**	**PX586636**	**PX586641**	**PX586631**
Yunnanomyces pandanicola	MFLUCC 17-2260 T	MH388333	MH388369	MH376743			MH412736
Yunnanomyces sexualis	CGMCC 3.25507 T		OR680512	OR680579	OR858911	OR843217	OR842929
Zenophaeosphaeria calamagrostidis	CBS 150822 T		PP791434	PP791462	PP780621		PP780614
Tyrannosorus lichenicola	CBS 144018 T		MK810953	MK810838	MK888775	MK926509	MK887840
Tyrannosorus pinicola	CBS 124.88 T	DQ471025	MK810951	MK810836		MK926507	DQ470928

Notes: T: Ex-type; DNA sequences for the new isolates are shown in bold. CBS: Westerdijk Fungal Biodiversity Institute, Utrecht, the Netherlands; CGMCC: China General Microbiological Culture Collection Center, Beijing, China; GUCC: Culture Collection of the Department of Plant Pathology, Agriculture College, Guizhou University, China; ICMP: International Collection of Micro-organisms from Plants, Landcare Research, Private Bag 92170, Auckland, New Zealand; IRAN: Fungal Culture Collections of the Iranian Research Institute of Plant Protection; MFLU (CC): Mae Fah Luang University Culture Collection, Chiang Rai, Thailand; MUCL: Université catholique de Louvain, Louvain-la-Neuve, Belgium; MTCC: Institute of Microbial Technology, Chandigarh, India; NBRC: Biological Resource Center; NFCCI: National Fungal Culture Collection of India, Pune, India.

The following three analyses were employed in this study: (1) an analysis based on the ITS + LSU + *tef1* + *tub2* + *rpb2* dataset to confirm the placement of the three novel taxa within the family *Sympoventuriaceae*, as well as single-gene phylogenetic analyses for each of these loci to evaluate species placement; (2) an analysis based on the SSU + ITS + LSU + *tub2* + *tef1* dataset to confirm the placement of *Scolecobasidium campestre* in the genus *Scolecobasidium*; and (3) an analysis based on the SSU + ITS + LSU + *tub2* dataset to confirm the placement of *Verruconis obovatus* in the genus *Verruconis*.

The maximum likelihood (ML) analysis was run in IQ-TREE v1.6.11 (Nguyen et al. 2015) with 10,000 bootstrap tests, using the ultrafast algorithm (Minh et al. 2013). The Bayesian inference (BI) analysis was conducted in MrBayes v3.2 (Ronquist et al. 2012) and in PhyloSuite v1.2.3 (Xiang et al. 2023). The Markov chain Monte Carlo (MCMC) method was used to perform 5×10^6 simulations with a sampling frequency of 10^3 generations and a 25% burn-in. After the analysis was finished, Tracer v1.5 (Drummond and Rambaut 2007) was used to determine burn-in and confirm that both runs had converged. Multilocus phylogenetic trees were opened and checked using FigTree v1.4.2 (Rambaut 2012), and the final trees were edited in Microsoft PowerPoint by inserting statistical supports from ML and BI.

Results

Phylogenetic analyses

Analysis 1

The generic placements of the new isolates are confirmed in this analysis (Fig. 1). The sequence data comprised 131 taxa from *Sympoventuriaceae*, with *Tyrannosorus lichenicola* (CBS 144018) and *T. pinicola* (CBS 124.88) as the outgroup taxa. The dataset consisted of 2,959 characters (ITS, 482 bp; LSU, 822 bp; *tef1*, 378 bp; *tub2*, 478 bp; and *rpb2*, 799 bp). The best-fit model for the ML analysis was GTR+F+I+G4 for ITS, *tub2*, and *rpb2*; TN+F+I+G4 for LSU; and TIM2+F+I+G4 for *tef1*. The best-fit model for the BI analysis was GTR+F+I+G4 for ITS, LSU, *tef1*, *tub2*, and *rpb2*. In the phylogenetic tree, nearly all genera within *Sympoventuriaceae* formed monophyletic clades with high support, except for the genus *Acroconidiellina*, which was nested in the genus *Scolecobasidium* (Fig. 1). Additionally, isolates CGMCC 3.29458 and ZY 24.011 formed a stable clade in the genus *Scolecobasidium* and clustered sister to *S. patriciamatherae* and *S. tshawytschae* (Fig. 1). Isolates CGMCC 3.29459 and ZY 25.008–009 formed a stable clade in the genus *Verruconis* and clustered sister to *V. terricola*, *V. thailandica*, and *V. verruculosa* (Fig. 1). Isolates CGMCC 3.29838 and ZY 25.011–012 formed a stable clade in the genus *Veronaeopsis* and clustered sister to *V. simplex* (Fig. 1). Additionally, due to differences in dataset composition, although there were some discrepancies among the single-gene trees, as well as between the single-gene trees and the concatenated tree, the three proposed new species consistently formed independent lineages (Suppl. materials 1–5).

Analysis 2

Phylogenetic trees were generated in analysis 2 to establish the new species in the genus *Scolecobasidium* (Suppl. material 6). The sequence data comprised

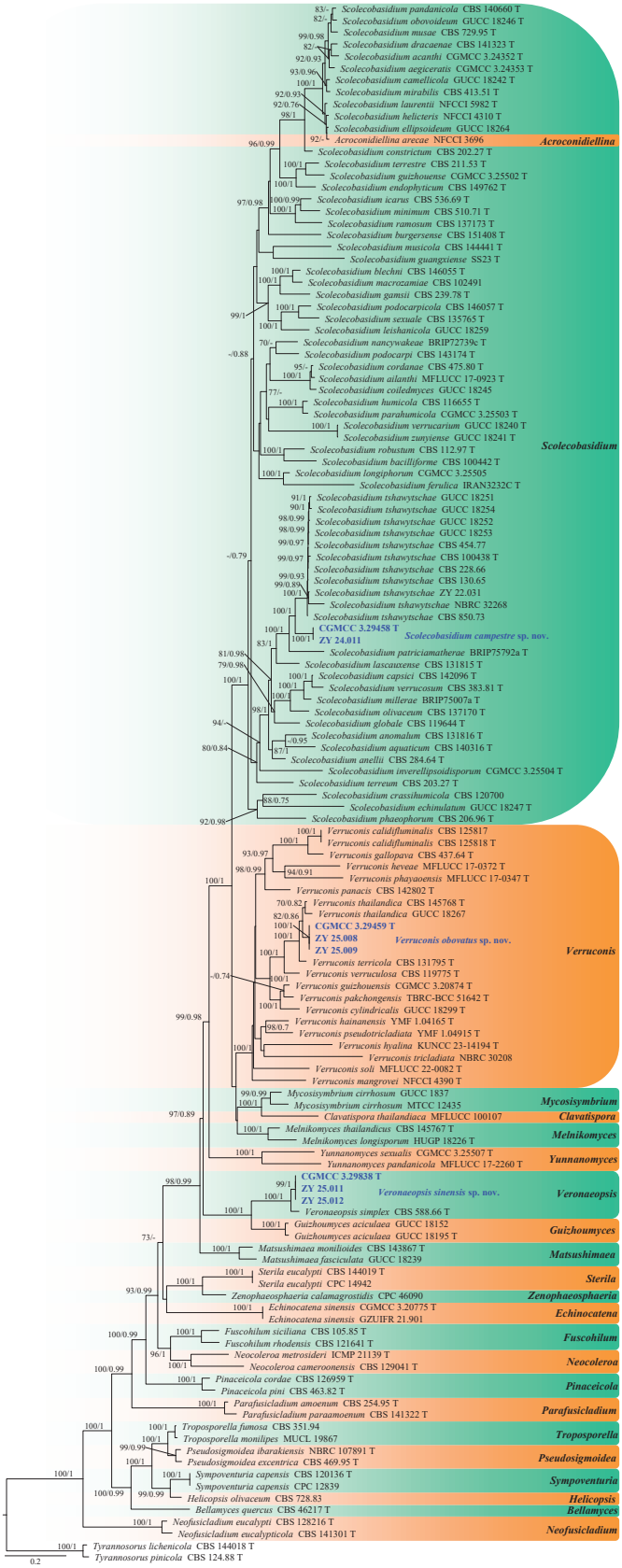


Figure 1. Phylogenetic tree inferred from a maximum likelihood analysis based on a concatenated alignment of ITS, LSU, *tef1*, *tub2*, and *rpb2* sequences from 131 isolates representing *Sympoventuriaceae* and outgroup taxa. Numbers at branches indicate support values (IQ-TREE-BS/BI-PP) above 70%/0.70. The new species are printed in blue. Strains with type status are indicated with "T." The tree is rooted with *Tyrannosorus lichenicola* (CBS 144018) and *T. pinicola* (CBS 124.88).

70 taxa from *Scolecobasidium*, with *Fuscohilum siciliana* (CBS 105.85) and *Matsushimaea fasciculata* (GUCC 18239) as the outgroup taxa. The dataset consisted of 3,361 characters (SSU, 967 bp; ITS, 705 bp; LSU, 795 bp; *tub2*, 485 bp; and *tef1*, 409 bp). The best-fit model for the ML analysis was TIM2+F+I+G4 for SSU, ITS, LSU, and *tef1*; and TIM+I+G4 for *tub2*. The best-fit model for the BI analysis was GTR+F+I+G4 for SSU, ITS, LSU, and *tef1*; and GTR+I+G4 for *tub2*. In the phylogenetic tree, isolates CGMCC 3.29458 and ZY 24.011 formed a stable clade in the genus *Scolecobasidium* and clustered sister to *S. patriciamatherae* and *S. tshawytschae* (Suppl. material 6).

Analysis 3

Phylogenetic trees were generated in analysis 3 to establish the new species in the genus *Verruconis* (Suppl. material 7). The sequence data comprised 24 taxa from *Verruconis*, with *Scolecobasidium guizhouense* (CGMCC 3.25502) and *S. parahumicola* (CGMCC 3.25503) as the outgroup taxa. The dataset consisted of 2,735 characters (SSU, 962 bp; ITS, 541 bp; LSU, 778 bp; and *tub2*, 454 bp). The best-fit model for the ML analysis was HKY+I+G4 for SSU; GTR+F+I+G4 for ITS; TIM+F+I+G4 for LSU; and TPM3u+I+G4 for *tub2*. The best-fit model for the BI analysis was K2P+I+G4 for SSU; GTR+F+G4 for ITS; GTR+F+I+G4 for LSU; and K2P+I+G4 for *tub2*. In the phylogenetic tree, isolates CGMCC 3.29459 and ZY 25.008–009 formed a stable clade in the genus *Verruconis* and clustered sister to *V. terricola*, *V. thailandica*, and *V. verruculosa* (Suppl. material 7).

Taxonomy

***Scolecobasidium campestre* H. Pan, Zhi Y. Zhang & G. Tao, sp. nov.**
MycoBank No: MB861297
Fig. 2

Etymology. The epithet "*campestre*" (Latin) refers to the location where the type was collected, Guizhou Minzu University.

Holotype. China, Guizhou Province, Guiyang City, South Campus of Guizhou Minzu University, 26.37°N, 106.62°E, altitude: 1,174 m, soil, 23 July 2024, Heng Pan (holotype ZY H-24.010, dried culture; ex-type CGMCC 3.29458, *ibid*., ZY 24.010).

Description. ***Culture characteristics*** (14 d at 25 °C): Colony on PDA 18–19 mm diam., flat, felty, circular, aerial hyphae dense, slightly raised in the center, margin entire, green beige (RAL 1000); reverse olive yellow (RAL 1020). Colony on OA 19–20 mm diam., flat, felty, circular, aerial hyphae sparse at margin, margin entire, green beige (RAL 1000); reverse brown grey (RAL 7013) to green brown (RAL 8000). Colony on SNA, 20–22 mm diam., flat, hairy, slightly raised in the center, subcircular, margin entire, green beige (RAL 1000) to olive grey (RAL 7002); reverse brown grey (RAL 7013) to olive grey (RAL 7002).

Hyphae septate, branched, hyaline to pale brown, smooth, and thin-walled, 1.5–3 µm wide, forming hyphal coils. Asexual morph: ***Conidiophores*** subcylindrical to cylindrical, arising from the aerial hyphae or hyphal coils, straight, aseptate, usually reduced to conidiogenous cells, (4.5–)6.5–22(–35) × 2–3.5 µm (av. ± SD = 12 ± 4.8 × 2.9 ± 0.2, *n* = 30). ***Conidiogenous cells*** solitary, occasionally branched, subhyaline to pale brown, clavate to subcylindrical, smooth, with

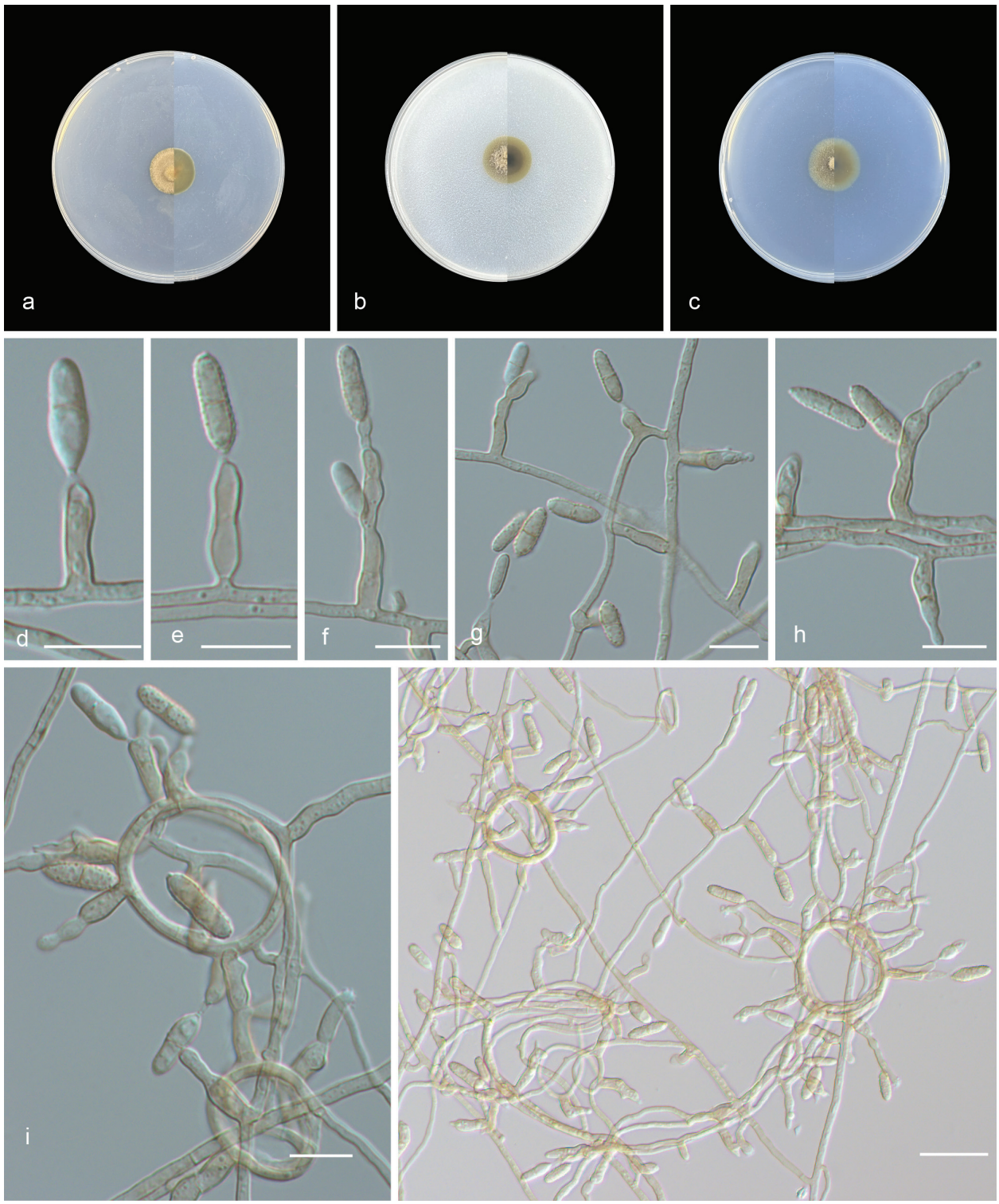


Figure 2. *Scolecobasidium campestre*. **a–c.** Upper and reverse views of cultures on PDA, OA, and SNA after 14 days at 25 °C; **d–h.** Conidiophores and conidiogenous cells bearing conidia; **i, j.** Conidiophores arising from hyphal coils and conidia. Scale bars: 10 µm (**d–i**), 20 µm (**j**).

single apical loci with rhexolytic conidiogenesis (2.5–)5.5–9 × 2–3.5 µm (av. ± SD = 6.6 ± 0.8 × 2.8 ± 0.2, *n* = 30). ***Conidia*** solitary, medianly 1-septate, subcylindrical, clavate or fusiform, smooth or rough with verruca, subhyaline to medium brown, 8.5–14.5 × 2.5–4 µm (av. ± SD = 11.6 ± 0.8 × 3.4 ± 0.2, *n* = 30). Sexual morph and chlamydospores were not observed.

Table 3. Nucleotide comparisons of *Scolecobasidium campestre* (ex-type CGMCC 3.29458) with *S. patriciamatherae* (ex-type BRIP 75792a) and *S. tshawytschae* (ex-type CBS 100438).

Taxa	ITS	LSU	*tef1*	*tub2*	*rpb2*
S. patriciamatherae (BRIP 75792a)	216/723 bp (29.8%, 114 gaps)	29/869 bp (3.3%, 3 gaps)			
S. tshawytschae (CBS 100438)	221/760 bp (29%, 103 gaps)	20/801 bp (2.5%, 6 gaps)	71/433 bp (16.3%, 21 gaps)	67/485 bp (13.8%, no gap)	64/874 bp (7.3%, 3 gaps)

Geographical distribution. Guizhou Province, China.

Additional material examined. China, Guizhou Province, Guiyang City, South Campus of Guizhou Minzu University, 26.37°N, 106.62°E, altitude: 1,174 m, soil, 23 July 2024, Heng Pan ZY 24.011.

Notes. Phylogenetically, *Scolecobasidium campestre* is strongly supported (100/1) and clusters with *S. patriciamatherae* and *S. tshawytschae* (Fig. 1, Suppl. material 6). Morphologically, *S. campestre* differs from *S. tshawytschae* by having conidiophores that may arise from hyphal coils and are slightly larger (6.5–22 × 2–3.5 µm vs. 6.5–18.5 × 3–3.5 µm) (Samerpitak et al. 2014; Wei et al. 2022). The conidia of *S. campestre* are 1-septate and smaller (8.5–14.5 × 2.5–4 µm vs. 12.5–22 × 5–6 µm) (Samerpitak et al. 2014; Wei et al. 2022). *Scolecobasidium tshawytschae* produces acrogenous, ellipsoidal to fusoid, 0(–1)-septate chlamydospores, whereas chlamydospores are absent in *S. campestre* (Wei et al. 2022). Furthermore, due to the lack of morphological descriptive data for *S. patriciamatherae*, comparison with *S. campestre* was not possible (Tan and Shivas 2023a, 2023b, 2023c). However, *S. campestre* can also be distinguished from *S. patriciamatherae* and *S. tshawytschae* by their low sequence similarities (Table 3).

Verruconis obovatus **M.Y. Zhang, Zhi Y. Zhang & G. Tao, sp. nov.**

MycoBank No: MB861298

Fig. 3

Etymology. The epithet "*obovatus*" (Latin) refers to the shape of conidia.

Holotype. China: Yunnan Province, Guandu District, 24.94°N, 102.77°E, altitude: 1,888 m, soil, 4 June 2024, Ming-Yi Zhang (holotype ZY H-25.007, dried culture; culture ex-type CGMCC 3.29459, *ibid*., ZY 25.007).

Description. ***Culture characteristics*** (14 d at 25 °C): Colony on PDA 18–19 mm diam., flat, cottony to velvety, aerial mycelium dense, margin entire, light ivory (RAL 1015); reverse ochre yellow (RAL 1024). Colony on OA 19–20 mm diam., flat to slightly raised, cottony to felty, subcircular, margin entire, beige (RAL 1001); reverse red brown (RAL 8012) to beige red (RAL 3012). Colony on SNA, 19–31 mm diam., flat to slightly raised at the center, aerial mycelium radial and sparse, brown pigment diffusing into the agar, margin fimbriate, light ivory (RAL 1015); reverse ochre yellow (RAL 1024).

Hyphae septate, branched, hyaline to pale brown, smooth, and thin-walled, 1–2.5 µm wide. Asexual morph: ***Conidiophores*** erect, straight or slightly flexuous, aseptate, subcylindrical to cylindrical, usually reduced to conidiogenous cells, 3.5–24.5 (–38) × 2–3.5 µm (av. ± SD = 12.7 ± 4.5 × 2.7 ± 0.3, *n* = 30). ***Conidiogenous cells*** clavate or subcylindrical with apex slightly swollen, lateral, subhyaline, becoming pale brown toward apex, solitary, occasional-

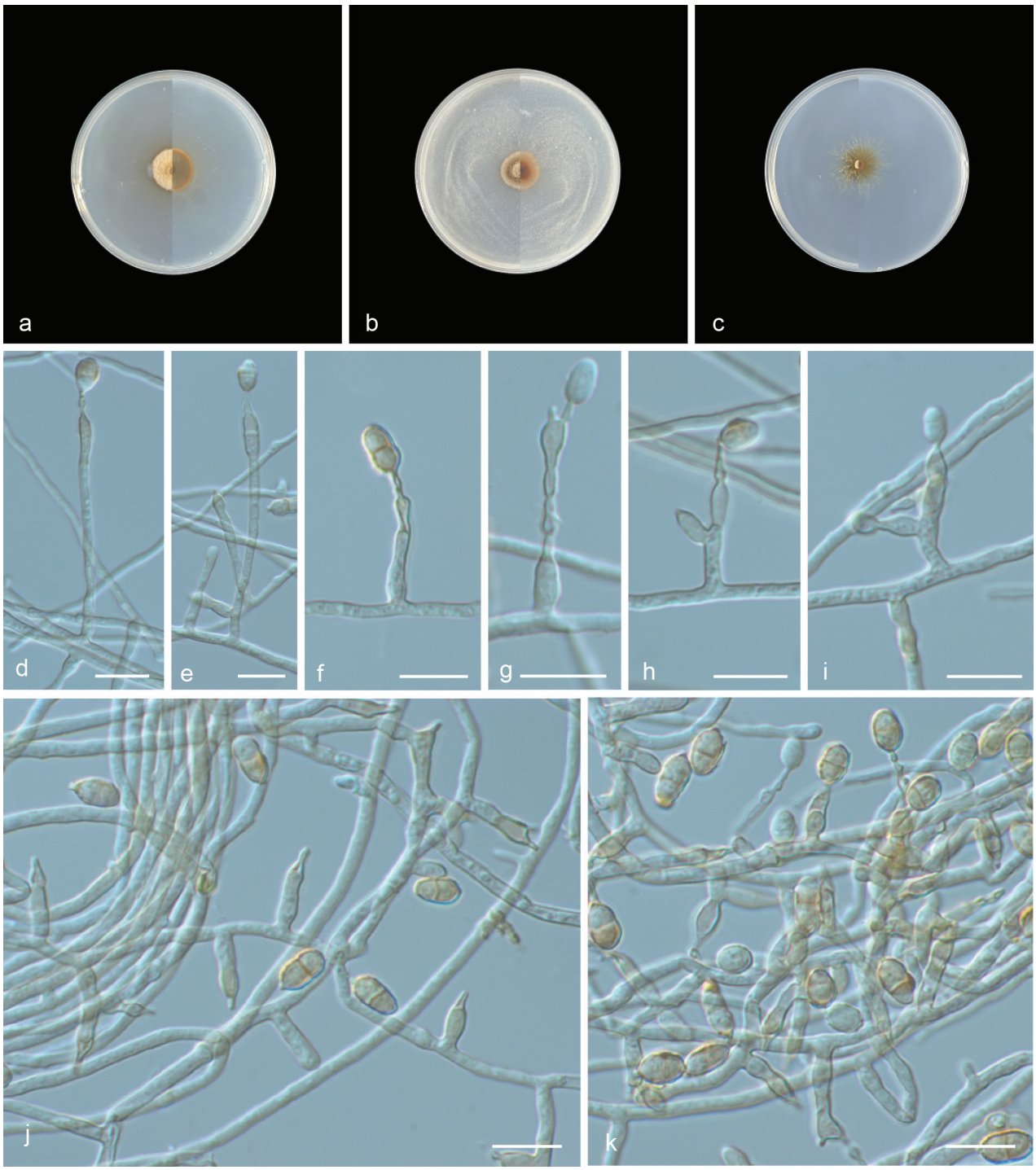


Figure 3. *Verruconis obovatus*. **a–c.** Upper and reverse views of cultures on PDA, OA, and SNA after 14 days at 25 °C; **d–k.** Conidiophores and conidiogenous cells bearing conidia. Scale bars: 10 µm (**d–k**).

ly branched, smooth, thread-like apical loci with rhexolytic conidiogenesis 4–7.5(–13) × 2–3.5 µm (av. ± SD = 7 ± 1.8 × 2.7 ± 0.2, *n* = 30). ***Conidia*** medianly 1-septate, subhyaline to pale brown, smooth, ellipsoidal to subglobose or subcylindrical, both ends rounded, base occasionally papillate, 4–10 × 3.5–4.5 µm (av. ± SD = 7.1 ± 1.9 × 3.9 ± 0.4, *n* = 30). Sexual morph and chlamydospores were not observed.

Geographical distribution. Yunnan Province, China.

Table 4. Nucleotide comparisons of *Verruconis obovatus* (ex-type CGMCC 3.29459) with *V. terricola* (ex-type CBS 131795), *V. thailandica* (ex-type CBS 145768), and *V. verruculosa* (ex-type CBS 119775).

Taxa	ITS	LSU	*tef1*	*tub2*	*rpb2*
V. terricola (CBS 131795)	62/550 bp (11.3%, 27 gaps)	17/789 bp (2.2%, 4 gaps)			51/1,022 bp (4.9%, no gap)
V. thailandica (CBS 145768)	45/636 bp (7.1%, 20 gaps)	15/775 bp (1.9%, 1 gap)			
V. verruculosa (CBS 119775)	119/606 bp (19.6%, 40 gaps)	38/791 bp (4.8%, no gap)	176/469 bp (37.5%, 74 gaps)	55/471 bp (11.7%, 4 gaps)	

Notes. Multilocus phylogenetic analyses indicate that *Verruconis obovatus* is strongly supported (100/1) and clusters with *V. terricola*, *V. thailandica*, and *V. verruculosa* (Fig. 1, Suppl. material 7). Morphologically, the conidia of *V. obovatus* are ovoidal and do not constrict at the septum, whereas those of *V. thailandica* and *V. terricola* are broadly ellipsoidal and constrict at the septum; the conidia of *V. verruculosa* are oblong and constrict at the septum (Roy et al. 1962; Ren et al. 2013; Hernández-Restrepo et al. 2020). Additionally, *V. obovatus* can also be distinguished from *V. terricola*, *V. thailandica*, and *V. verruculosa* by their low sequence similarities (Table 4).

Veronaeopsis sinensis **M.Y. Zhang, Zhi Y. Zhang & G. Tao, sp. nov.**

MycoBank No: MB863845

Fig. 4

Etymology. The epithet "*sinensis*" (Latin) refers to the location where the type was collected, China.

Holotype. China: Fujian Province, Fuzhou Zoo, 26.13°N, 119.28°E, altitude: 73 m, soil, 7 October 2025, Ming-Yi Zhang (holotype ZY H-25.010, dried culture; culture ex-type CGMCC 3.29838, *ibid*., ZY 25.010).

Description. ***Culture characteristics*** (14 d at 25 °C): Colony on PDA 20–21 mm diam., flat, dense, velvety, floccose, margin crenate, light ivory (RAL 1015); reverse curry (RAL 1027). Colony on OA 24–25 mm diam., flat, felty, circular, margin entire, beige (RAL 1001); reverse beige (RAL 1001). Colony on SNA, 19–20 mm diam., flat, hairy, slightly raised in the center, subcircular, aerial hyphae sparse at margin, green beige (RAL 1000); reverse moss grey (RAL 7003) to green beige (RAL 1000).

Hyphae septate, branched, smooth, hyaline to subhyaline, 1.5–3 µm wide. Asexual morph: ***Conidiophores*** arising vertically or at an acute angle from aerial hyphae, lateral or intercalary, simple, occasionally branched, 0–1-septate, often reduced to conidiogenous cells, hyaline to subhyaline, 12–31.5 × 1–2.5 µm (av. ± SD = 18.1 ± 3 × 1.9 ± 0.2, *n* = 30). ***Conidiogenous cells*** arising from aerial hyphae, lateral, intercalary, or terminal, occasionally terminally integrated in the conidiophores, sometimes with a single apical denticle, smooth, hyaline to subhyaline, 1.5–29 × 0.5–2.5 µm (av. ± SD = 12.2 ± 2.3 × 1.5 ± 0.2, *n* = 30), rachis generally straight or irregularly geniculate, with crowded, prominent denticles. ***Conidia*** solitary, hyaline to subhyaline, smooth, ellipsoid, obovoid, oblong-ellipsoidal to subcylindrical, (0–)1-septate, slightly constricted at the septum, 3.5–11.5 × 2.5–3.5 µm (av. ± SD = 7.8 ± 0.8 × 2.9 ± 0.2, *n* = 30). Sexual morph: not observed.

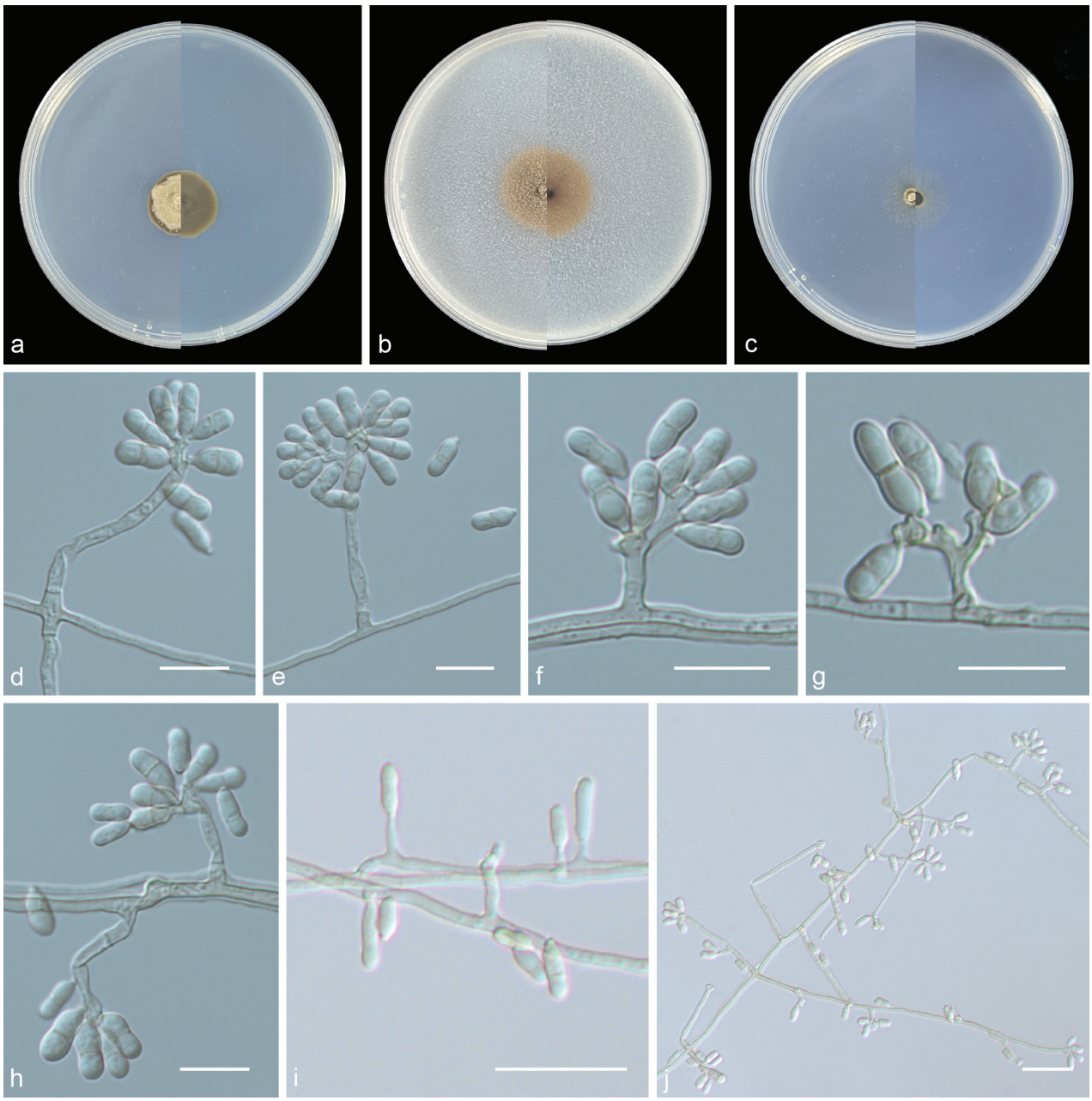


Figure 4. *Veronaeopsis sinensis*. **a–c.** Upper and reverse views of cultures on PDA, OA, and SNA after 14 days at 25 °C; **d.** Conidiogenous cells and conidia; **e–h.** Sympodially proliferating conidiogenous cells, rachis with crowded, prominent denticles, and conidia; **i.** Intercalary conidiogenous cells; **j.** Conidiophores, conidiogenous cells, and conidia. Scale bars: 10 µm (**d–h**); 20 µm (**i–j**).

Geographical distribution. Fujian Province, China.

Additional material examined. China, Fujian Province, Fuzhou City, Fuzhou Zoo, 26.14°N, 119.28°E, altitude: 107 m, soil, 7 October 2025, Ming-Yi Zhang ZY 25.011, *ibid.* ZY 25.012.

Notes. Multilocus phylogenetic analyses indicate that *Veronaeopsis sinensis* is strongly supported (99/1) and clusters with *V. simplex* (Fig. 1). Morphologically, *V. sinensis* is similar to *V. simplex*, but the conidiophores of *V. sinensis* are simple, rarely branched, 0–1-septate, and its conidia are 3.5–11.5 × 2.5–3.5 µm (av. 7.8 × 2.9 µm); whereas in *V. simplex*, the conidiophores are simple or branched, and the conidia measure (6–)10–12(–15) × (2–)2.5–3(–4) µm

(Arzanlou et al. 2007). Additionally, they can be distinguished by their low sequence similarities. Based on a pairwise comparison of ITS, LSU, and *rpb2*, *V. sinensis* (ex-type CGMCC 3.29838) differs from *V. simplex* (ex-type CBS 588.66) by 4.7% (22/461 bp, six gaps) in ITS, 2% (17/825 bp, nine gaps) in LSU, and 3.4% (28/804 bp, no gaps) in *rpb2*.

Discussion

As primary decomposers, fungi drive the mineralization and humification of organic matter, thereby sustaining soil fertility in urban green spaces, such as parks, gardens, and roadside trees (Newbound et al. 2010; Zhang et al. 2019). Research on urban soil fungi has mainly focused on the following aspects: exploring the impact of urbanization gradients on the diversity and composition of fungal communities (Abrego et al. 2020; Rusterholz and Baur 2023); analyzing differences in fungal communities across various types of urban green spaces (e.g., parks, lawns, roadside tree pits, and agricultural fields) (McGuire et al. 2013; Gómez-Brandón et al. 2022); and investigating how urban environmental factors, such as soil physicochemical properties, pollutants, and management practices, shape specific functional groups, such as mycorrhizal and pathogenic fungi (Salomon et al. 2020; Scholier et al. 2023). However, the taxonomic study of urban soil fungi has not received sufficient attention. Recently, during a project on the diversity of keratinophilic fungi in urban soils of China, the isolated taxa were taxonomically characterized (Zhang et al. 2021, 2023, 2024; Pan et al. 2025; Wang et al. 2025). Similarly, Crous et al. (2021) surveyed the culturable fungi in garden soils of the Netherlands through a citizen science project. These few studies have revealed a substantial number of undescribed fungal taxa residing in urban environments. In this study, combining morphological characteristics with multigene phylogenetic analyses, three new species of *Sympoventuriaceae* (*Scolecobasidium campestre*, *Verruconis obovatus*, and *Veronaeopsis sinensis*) are reported. This contributes to fungal data from urban soils and enhances the understanding of the species diversity, taxonomy, and distribution of *Sympoventuriaceae*.

Urbanization has swept across the globe over the last several decades, inevitably resulting in increased anthropogenic changes to the environment (Berry 2008). These human activities, construction projects, and distinct land management practices profoundly impact urban soil fungi. However, although urban soils are heavily disturbed and managed environments, their topography and complex human-induced alterations shape exceptionally high heterogeneity. Such urban soils may provide highly, heterogeneous niches that support active microbial communities, potentially fostering unique and undescribed fungi that diverge significantly from those in natural habitats. Therefore, urban environments act as overlooked reservoirs of fungal diversity. Nevertheless, whether these newly discovered taxa are uniquely adapted to urban environments or are simply ubiquitous soil generalists remains an open question. Fungi play essential roles in ecosystem processes and functions, yet research on soil fungi, particularly concerning urban environments, remains in its infancy (Hyde et al. 2024). Because the current literature regarding comprehensive investigations of fungal taxa in urban soil is still limited, the successful isolation of these specific new taxa at this stage carries a degree of sampling serendipity. It is

currently difficult to definitively conclude their exact ecological adaptations due to the limited sampling scale. Future systematic and in-depth investigations across broader urban soil habitats are required to verify whether these novel taxa exhibit specialized urban adaptation or represent incidental isolates from broadly distributed soil communities.

To date, most of the 23 genera in the family *Sympoventuriaceae* are relatively small, consisting of only a few species or even a single species, such as *Bellamyces*, *Clavatispora*, *Guizhoumyces*, *Mycosisymbrium*, *Sterila*, *Veronaeopsis*, and *Zenophaeosphaeria* (Wei et al. 2022). Furthermore, reliable strains and credible molecular data are scarce for some genera, so the current classification system may not accurately reflect reality. For example, in the phylogenetic tree (Fig. 1), *Acroconidiellina* is nested within *Scolecobasidium*. Currently, *Acroconidiellina* comprises four species (i.e., *A. arecae*, *A. chloridis*, *A. loudetiae*, and *A. urtiagae*), but DNA molecular data are available only for *A. arecae*. Therefore, the primary reason for this phenomenon may be that *A. arecae* is currently represented solely by ITS and LSU sequences, and these two genes exhibit low resolution at the generic level. Among them, only ITS provides some nucleotide differences, which do not reflect the true intergeneric relationships. In the future, collecting more specimens, isolating more species and strains, and obtaining more molecular sequences will help establish a modern taxonomic system for this family that is closer to nature. The genus *Veronaeopsis* previously comprised only one species, *V. simplex*. This study reports another species of the genus, *V. sinensis*, further solidifying the taxonomic status of the genus.

Currently, fungal taxonomy stands at a crossroads regarding whether detailed morphological descriptions are mandatory or whether reliance on molecular sequences alone suffices. Some studies have established new taxa based solely on molecular sequence differences and phylogenetic analyses, such as *Scolecobasidium millerae*, *S. nancywakeae*, and *S. patriciamatherae* (Tan and Shivas 2022, 2023a, b). Until consensus is reached, the establishment of new species within groups that produce spores in natural environments—or even under cultivation conditions—should include morphological descriptions to avoid confusion arising from differing interpretations, such as *Bisifusarium sinense* (Tan and Shivas 2023c; Zhang et al. 2024, 2025). According to the new species delineation criteria proposed by Jeewon and Hyde (2016), phylogenetic analyses should include the ITS region and at least one protein-coding gene. Unfortunately, the establishment of *S. millerae*, *S. nancywakeae*, and *S. patriciamatherae* does not meet these criteria. Furthermore, if new species-level taxa are to be established based on molecular sequence differences and phylogenetic analyses, the phylogenetic analysis should at least be conducted at a higher taxonomic level (genus level), meaning that molecular data from as many genera within the family as possible should be included to avoid erroneous results. For example, Tan and Shivas (2024) established *Chlamydocillium margaretcollinsiae* based on sequence differences and phylogenetic analyses with limited molecular data sampling. Recently, Zhao et al. (2026), using large-scale molecular data sampling within *Hypocreales*, demonstrated that *C. margaretcollinsiae* belongs to *Polyphialocladium* rather than *Chlamydocillium*. The molecular data used in this study cover 23 genera of *Sympoventuriaceae*, supporting the robustness of the results.

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Supplementary material 1

Phylogenetic tree inferred from a maximum likelihood analysis based on ITS sequences from 129 isolates representing *Sympoventuriaceae* and outgroup taxa

Authors: Ming-Yi Zhang, Heng Pan, Yu-Lian Ren, Yun-Jie Wu, Zhi-Qing Fang, Bing-Da Sun, Gang Tao, Zhi-Yuan Zhang

Data type: pdf

Explanation note: Numbers at branches indicate support values (IQ-TREE-BS/BI-PP) above 70%/0.70. The new species are printed in blue. Strains with type status are indicated with "T." The tree is rooted with *Tyrannosorus lichenicola* (CBS 144018) and *T. pinicola* (CBS 124.88).

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Link: https://doi.org/10.3897/mycokeys.133.197363.suppl1

Supplementary material 2

Phylogenetic tree inferred from a maximum likelihood analysis based on LSU sequences from 129 isolates representing *Sympoventuriaceae* and outgroup taxa

Authors: Ming-Yi Zhang, Heng Pan, Yu-Lian Ren, Yun-Jie Wu, Zhi-Qing Fang, Bing-Da Sun, Gang Tao, Zhi-Yuan Zhang

Data type: pdf

Explanation note: Numbers at branches indicate support values (IQ-TREE-BS/BI-PP) above 70%/0.70. The new species are printed in blue. Strains with type status are indicated with "T." The tree is rooted with *Tyrannosorus lichenicola* (CBS 144018) and *T. pinicola* (CBS 124.88).

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Supplementary material 3

Phylogenetic tree inferred from a maximum likelihood analysis based on *tef1* sequences from 87 isolates representing *Sympoventuriaceae* and outgroup taxa

Authors: Ming-Yi Zhang, Heng Pan, Yu-Lian Ren, Yun-Jie Wu, Zhi-Qing Fang, Bing-Da Sun, Gang Tao, Zhi-Yuan Zhang

Data type: pdf

Explanation note: Numbers at branches indicate support values (IQ-TREE-BS/BI-PP) above 70%/0.70. The new species are printed in blue. Strains with type status are indicated with "T." The tree is rooted with *Tyrannosorus lichenicola* (CBS 144018).

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Link: https://doi.org/10.3897/mycokeys.133.197363.suppl3

Supplementary material 4

Phylogenetic tree inferred from a maximum likelihood analysis based on *tub2* sequences from 91 isolates representing *Sympoventuriaceae* and outgroup taxa

Authors: Ming-Yi Zhang, Heng Pan, Yu-Lian Ren, Yun-Jie Wu, Zhi-Qing Fang, Bing-Da Sun, Gang Tao, Zhi-Yuan Zhang

Data type: pdf

Explanation note: Numbers at branches indicate support values (IQ-TREE-BS/BI-PP) above 70%/0.70. The new species are printed in blue. Strains with type status are indicated with "T." The tree is rooted with *Tyrannosorus lichenicola* (CBS 144018) and *T. pinicola* (CBS 124.88).

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Link: https://doi.org/10.3897/mycokeys.133.197363.suppl4

Supplementary material 5

Phylogenetic tree inferred from a maximum likelihood analysis based on *rpb2* sequences from 57 isolates representing *Sympoventuriaceae* and outgroup taxa

Authors: Ming-Yi Zhang, Heng Pan, Yu-Lian Ren, Yun-Jie Wu, Zhi-Qing Fang, Bing-Da Sun, Gang Tao, Zhi-Yuan Zhang

Data type: pdf

Explanation note: Numbers at branches indicate support values (IQ-TREE-BS/BI-PP) above 70%/0.70. The new species are printed in blue. Strains with type status are indicated with "T." The tree is rooted with *Tyrannosorus lichenicola* (CBS 144018) and *T. pinicola* (CBS 124.88).

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Link: https://doi.org/10.3897/mycokeys.133.197363.suppl5

Supplementary material 6

Phylogenetic tree inferred from a maximum likelihood analysis based on a concatenated alignment of SSU, ITS, LSU, *tub2*, and *tef1* sequences from 70 isolates representing the genus *Scolecobasidium* and outgroup taxa

Authors: Ming-Yi Zhang, Heng Pan, Yu-Lian Ren, Yun-Jie Wu, Zhi-Qing Fang, Bing-Da Sun, Gang Tao, Zhi-Yuan Zhang

Data type: pdf

Explanation note: Numbers at branches indicate support values (IQ-TREE-BS/BI-PP) above 70%/0.70. The new species are printed in blue. Strains with type status are indicated with "T." The tree is rooted with *Fuscohilum siciliana* (CBS 105.85) and *Matsushimaea fasciculata* (GUCC 18239).

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Link: https://doi.org/10.3897/mycokeys.133.197363.suppl6

Supplementary material 7

Phylogenetic tree inferred from a maximum likelihood analysis based on a concatenated alignment of SSU, ITS, LSU, and *tub2* sequences from 24 isolates representing the genus *Verruconis* and outgroup taxa

Authors: Ming-Yi Zhang, Heng Pan, Yu-Lian Ren, Yun-Jie Wu, Zhi-Qing Fang, Bing-Da Sun, Gang Tao, Zhi-Yuan Zhang

Data type: pdf

Explanation note: Numbers at branches indicate support values (IQ-TREE-BS/BI-PP) above 70%/0.70. The new species are printed in blue. Strains with type status are indicated with "T." The tree is rooted with *Scolecobasidium parahumicola* (CGMCC 3.25503) and *S. guizhouense* (CGMCC 3.25502).

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Additional information

Conflict of interest

The authors have declared that no competing interests exist.

Ethical statement

No ethical statement was reported.

Artificial Intelligence (AI) use

The authors accept full responsibility for the content of the manuscript, including the disclosure of any use of AI.
No AI tools were used in the preparation of this manuscript.

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Author contributions

The individual contributions are as follows: Zhi-Yuan Zhang conceptualized the study and edited and reviewed the manuscript. Ming-Yi Zhang, Heng Pan, and Yu-Lian Ren performed microscopic examinations of fungal specimens and wrote, edited, and reviewed the manuscript. Bing-Da Sun, Zhi-Qing Fang, Yun-Jie Wu, and Gang Tao conducted phylogenetic studies and reviewed and edited the manuscript. All authors have read and agreed to the published version of the manuscript.

Author ORCIDs

M.-Y. Zhang https://orcid.org/0009-0000-0691-3941
H. Pan https://orcid.org/0009-0003-7472-3199
Y.-L. Ren https://orcid.org/0000-0003-2424-1266
Y.-J. Wu https://orcid.org/0009-0005-1316-5546
Z.-Q. Fang https://orcid.org/0009-0001-0963-1760
B.-D. Sun https://orcid.org/0000-0003-0272-6422
G.Tao https://orcid.org/0000-0002-0882-3752
Z.-Y. Zhang https://orcid.org/0000-0003-2031-7518

Data availability

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