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Culturable mycobiota from Karst caves in China II, with descriptions of 33 new species

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Abstract

Karst caves are characterized by darkness, low temperature, high humidity, and oligotrophic organisms due to its relatively closed and strongly zonal environments. Up to now, 1626 species in 644 genera of fungi have been reported from caves and mines worldwide. In this study, we investigated the culturable mycobiota in karst caves in southwest China. In total, 251 samples from thirteen caves were collected and 2344 fungal strains were isolated using dilution plate method. Preliminary ITS analyses showed that these strains belonged to 610 species in 253 genera. Among these species, 88.0% belonged to Ascomycota, 8.0% Basidiomycota, 1.9% Mortierellomycota, 1.9% Mucoromycota, and 0.2% Glomeromycota. The majority of these species have been previously known from other environments, and some of them are known as mycorrhizal or pathogenic fungi. About 52.8% of these species were discovered for the first time in karst caves. Based on morphological and phylogenetic distinctions, 33 new species were identified and described in this paper. Meanwhile, one new genus of *Cordycipitaceae*, *Gamszarea*, and five new combinations are established. This work further demonstrated that Karst caves encompass a high fungal diversity, including a number of previously unknown species. Taxonomic novelties: New genus: *Gamszarea* Z.F. Zhang & L. Cai; Novel species: *Amphichorda cavernicola*, *Aspergillus limoniformis*, *Aspergillus phialiformis*, *Aspergillus phialosimplex*, *Auxarthron chinense*, *Auxarthron guangxiense*, *Auxarthronopsis globiasca*, *Auxarthronopsis pedicellaris*, *Auxarthronopsis pulverea*, *Auxarthronopsis stercicola*, *Chrysosporium pallidum*, *Gamszarea humicola*, *Gamszarea lunata*, *Gamszarea microspora*, *Gymnoascus flavus*, *Jattaea reniformis*, *Lecanicillium magnisporum*, *Microascus collaris*, *Microascus levis*, *Microascus sparsimycelialis*, *Microascus superficialis*, *Microascus trigonus*, *Nigrospora globosa*, *Paracremonium apiculatum*, *Paracremonium ellipsoideum*, *Paraphaeosphaeria hydei*, *Pseudoscopulariopsis asperispora*, *Setophaeosphaeria microspora*, *Simplicillium album*, *Simplicillium humicola*, *Wardomycopsis dolichi*, *Wardomycopsis ellipsoconidiophora*, *Wardomycopsis fusca*; New combinations: *Gamszarea indonesiaca* (Kurihara & Sukarno) Z.F. Zhang & L. Cai, *Gamszarea kalimantanensis* (Kurihara & Sukarno) Z.F. Zhang & L. Cai, *Gamszarea restricta* (Hubka, Kubátová, Nonaka, Čmoková & Řehulka) Z.F. Zhang & L. Cai, *Gamszarea testudinea* (Hubka, Kubátová, Nonaka, Čmoková & Řehulka) Z.F. Zhang & L. Cai, *Gamszarea wallacei* (H.C. Evans) Z.F. Zhang & L. Cai.

Keywords Fungal diversity · Karst cave · Morphology · Phylogeny · Troglobitic fungi · 39 new taxa

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Introduction

Caves are strongly zonal environment with unique characteristics determined by the karst morphology, subterranean water and surrounding rocks (Kuzmina et al. 2012; Gabriel and Northup 2013). Caves thus have distinctly characteristics, such as darkness, constantly low temperature, high humidity, and oligotrophy (Gabriel and Northup 2013; Zhang et al. 2017, 2018). As a relatively closed space, caves usually have one or several entrances and the environments may be affected by various factors, such as the air currents, chemolithoautotrophy, visitors, and water movements (streams or water seeps; Hose et al. 2000; Barton and Jurado 2007; Gabriel and Northup 2013; Ortiz et al. 2014). Meanwhile, caves are totally dark and lack photosynthesis thus believed to be generally oligotrophic in nature (Hose et al. 2000; Barton and Jurado 2007; Gabriel and Northup 2013; Ortiz et al. 2014; Jiang et al. 2017a). The microbial flora in caves might be shaped by these above affecting factors and oligotrophic environment (Ogórek et al. 2013; Ortiz et al. 2014).

Fungi play important roles in cave ecosystem, such as biomineralization or serving as food of cave fauna (Northup and Lavoie 2001; Barton and Northup 2007; Nováková 2009; Li et al. 2015). While, most of the previous studies were focused on cave fauna and fungal diversity has rarely been documented (Zhang et al. 2017). The studies on culturable fungi in caves can be divided into three periods, namely, early stage, developing stage, and explosive stage.

Early stage: before 1980s. The earliest description of fungi in caves was published as early as 1794 by Humboldt, as described in Dobat (1967), and the first ecological literature of caves was that by Megušar (1914). In 1913, Lagarde investigated the fungal diversity in several caves in Europe and described a new species, *Ombrophila speluncarum* Lagarde. During 1950s–1980s, studies on cave fungi were mostly about animal pathogens, e.g., *Histoplasma capsulatum* Darling (Ajello et al. 1960a, b; Al-Doory and Rhoades 1968; Di Salvo et al. 1969; Zamora 1977), *Trichophyton mentagrophytes* (C.P. Robin) Sabour and other dermatophytes (Lurie and Borok 1955; Lurie and Way 1957; Kajihiro 1965).

Developing stage: During 1980s to early 2010s, a number of studies on fungal diversity in caves were reported. Cunningham et al. (1995) investigated the microorganisms in Lechuguilla Cave in New Mexico and obtained nine fungal genera, of which, *Aspergillus* P. Micheli ex Haller and *Penicillium* Link were most common. Koilraj et al. (1999) isolated 35 sporulating fungi, belonging to 18 genera and seven sterile fungi from six different caves in India. In the investigation on mycobiota in caves in Slovakia, 195 species belonging to 73 genera, including 92 species were obtained from bat droppings and guano (Nováková 2009).

Explosive stage: since bat White Nose Syndrome (WNS) outbreak in America in 2006. WNS was caused by pathogenic fungus *Pseudogymnoascus destructans* (Blehert & Gargas) Minnis & D.L. Lindner (Syn: *Geomyces destructans* Blehert & Gargas), a species isolated from many caves in Europe and North America (Blehert et al. 2009; Martínková et al. 2010; Kubátová et al. 2011; Minnis and Lindner 2013), and resulted in 6 million deaths of bat and ca. 3.7 billion dollars loss in America in 2011 (Boyles et al. 2011). Studies on *P. destructans* signigicantly improved our knowledge on mycobiota in caves. According to our statistics, about 110 research papers on fungi in caves have been published since 2006 worldwide, indicating a high fungal diversity in caves. In total, about 1000 species of fungi in 550 genera have been documented from caves and mines worldwide by 2012 (Vanderwolf et al. 2013). Common genera are mostly cosmopolitans, i.e. *Aspergillus*, *Penicillium*, *Mucor* Fresen, *Fusarium* Link, *Trichoderma* Pers., etc. The most common species are also widespread, i.e. *Aspergillus versicolor* (Vuill.) Tirab., *A. niger* Tiegh., *Penicillium chrysogenum* Thom, *Cladosporium cladosporioides* (Fresen.) G.A. de Vries, *A. fumigatus* Fresen., etc. (Vanderwolf et al. 2013).

The Karst landform covers more than 1/3 of the total land area of China and there are more than half million karst caves scattered in China (Ran and Chen 1998; Chen 2006; Zhang and Zhu 2012). However, most studies on cave microorganisms in China were focus on bacteria, and the investigation on fungal diversity was rare, with only several documentations (Hsu and Agoramoorthy 2001; Man et al. 2015; Jiang et al. 2017a; Zhang et al. 2017). In Zhang et al. (2017), 563 fungal strains belonging to 246 species in 116 genera were reported from two unnamed karst cave in Guizhou, China, including 20 new species. Using oligotrophic carbon free silica gel medium, Jiang et al. (2017a, b) studied the oligotrophic fungi from a carbonate cave in China. 169 oligotrophic strains belonging to at least 84 taxa were isolated and four new species were described. With the development of tourism, more and more caves have been heavily affected by human activities. The fungal diversity and resources in caves are thus urgent to be investigated. The objective of this study was to systematically investigate the culturable fungal resources from karst caves in China. In response to this, 13 caves in five provinces were visited and sample of organic litter, rock, soil and water were collected for isolation. Novel species were identified and described based on morphological characters and phylogenetic affinities.

Material and methods

Sampling collection

Southwest China, including Yunnan-Guizhou Plateau, the center of East Asia developing Karst area, is the largest and most complex developing karst area in the world (Zhou et al. 2007). Thirteen accessible caves in Southwest China were selected for this study (Figs. 1 and 2, Table 1).

Samples of rock, soil and water were collected along these thirteen caves and preserved at 4 °C before isolation. From the entrance of the caves, the distance of each two adjacent sampling sites was same and depend on the length of caves (Table 1).

Seeping, stream and pool water was collected for 10 mL, respectively, and kept in 15 mL sterile centrifuge tubes. Ten grams of soil samples were collected at shallow depth (0.5–5.0 cm) after removing surface layer (ca. 0.5 cm) from three sites of each location. Rock samples were collected and packed in zip-locked plastic bags following Ruibal et al. (2005). At each sample site, 5 pieces of rock in different orientations were collected. Rocks that were apparently being colonized by fungi were also chipped off and collected along the caves. Organic litter, when discovered, were collected, including bat droppings, guano, animal dung, animal carcass, and plant debris (Zhang et al. 2017).

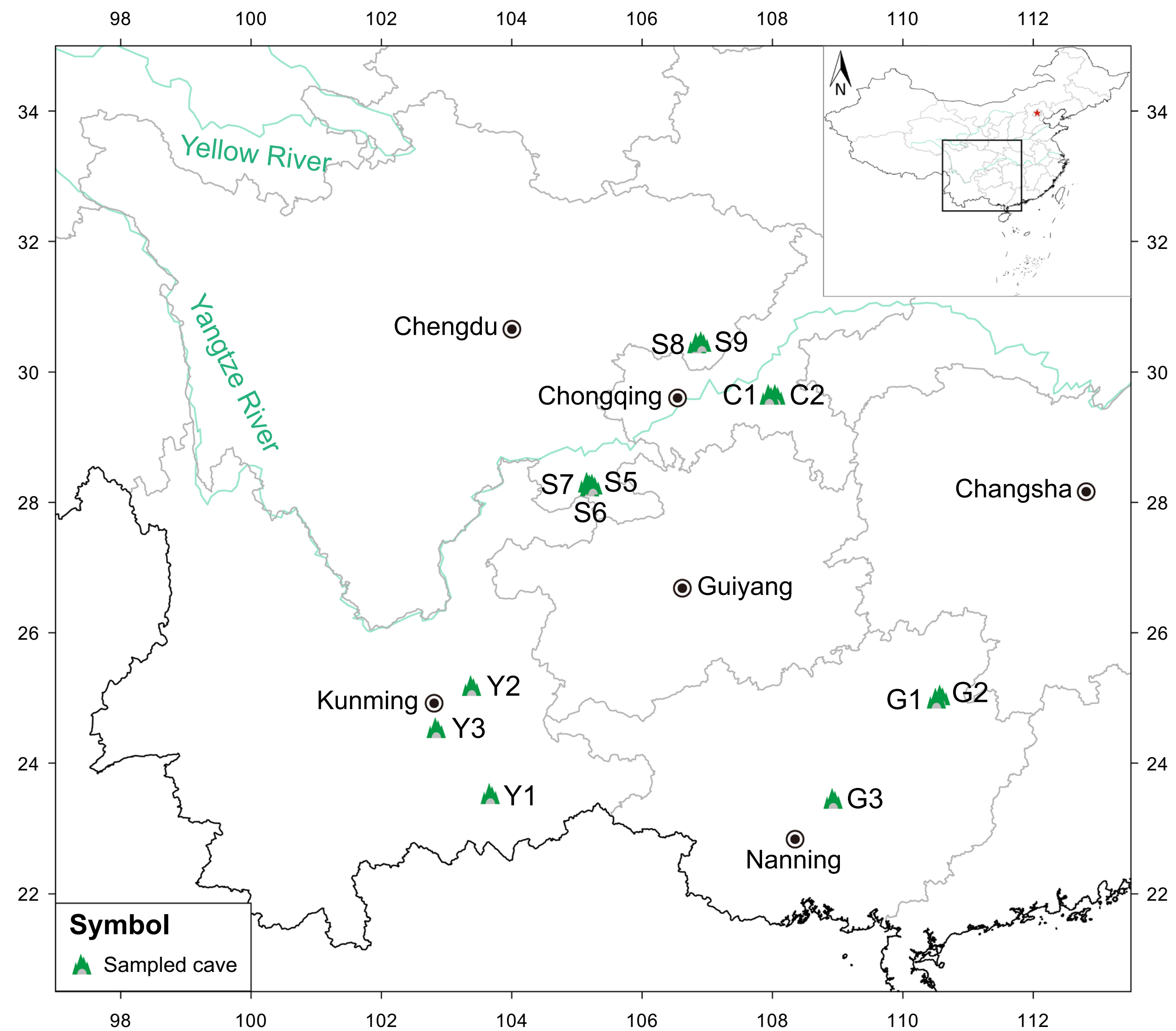
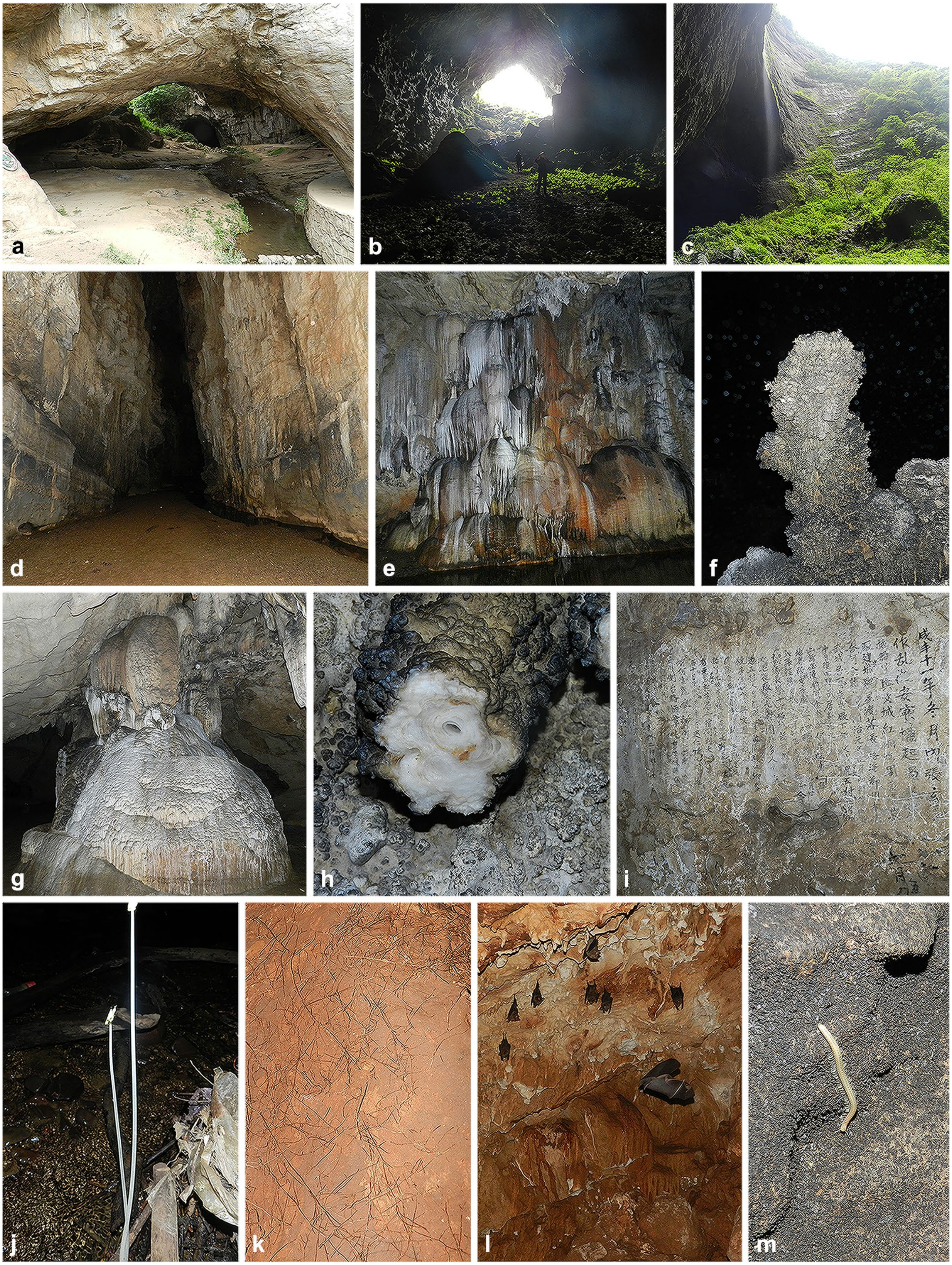


Fig. 1 Locations of the 13 visited caves in southwest China. Cave names are abbreviated and full names are in Table 1


a
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◂**Fig. 2** Scenes of visited caves. **a**, **b** Entrances to Sanjiao Cave and E'gu Cave; **c** tiankeng at the end of Er'wang Cave; **d** tunnel of Sanjiao Cave; **e**–**g** beautiful stalactite and stalagmite; **h** broken stalactite; **i** poetry of Qing dynasty (1861 AD) on the wall at 500 m in Tianliang cave; **j** colorless plant; **k** roots; **l** bats; **m** myriapod

Isolation

Fungi were isolated following the dilution plate method (Zhang et al. 2015). One gram of each collected sample was suspended in 9 mL sterile water in a 15 mL sterile centrifuge tube. The tubes were shaken with Vortex vibration meter thoroughly. The suspension was then diluted to a series of concentrations, i.e. 10^{-1}, 10^{-2}, 10^{-3}, 10^{-4}, 10^{-5} and 10^{-6}. Diluted concentration of 10^{-3} and 10^{-4} appeared to be most convenient for colony pickup in the isolating process from organic litters, while that for water and soil samples were 10^{-1} and 10^{-2} respectively. Two hundred microliters suspensions from each concentration were spread onto 1/4 PDA containing ampicillin (50 µg/mL) and streptomycin (50 µg/mL) with three replicates.

Rock samples were processed following the protocol of Ruibal et al. (2005) with some modifications. Firstly, the rock surface was washed with 95% ethanol to eliminate the contamination from dust and airborne spores, and washed once with sterile water containing 0.1% of Tween 20. The small pieces of rocks were then ground into powder using a sterilized mortar and pestle. Suspensions were made by adding sterilized water to the concentration of 10^{-1}. Three different volumes of the rock powder suspension, i.e. 300, 500, and 1000 µL, were respectively placed onto three 1/4 PDA plates supplemented with ampicillin (50 µg/mL) and streptomycin (50 µg/mL) (Ruibal et al. 2005; Selbmann et al. 2005; Collado et al. 2007; Zhang et al. 2017).

All the plates were incubated at room temperature (25 ± 2 °C) for 3–4 weeks, and from which the single colonies were picked up and inoculated onto new PDA plates every two days. All fungal strains were stored at 4 °C for further studies.

Molecular analyses

Total fungal genomic DNAs were extracted following a modified CTAB method of Doyle (1987). The internal transcribed spacer regions and intervening 5.8S nrRNA gene (ITS), the large subunit (LSU) rDNA, the small subunit (SSU) rDNA, the translation elongation factor 1-alpha (EF-1α), RNA polymerase II subunit (RPB2), Twenty S rRNA accumulation (Tsr1), and β-tubulin (TUB) regions were amplified using primer pairs ITS1/ITS4 (White et al. 1990), LR0R/LR5 (Vilgalys and Hester 1990), NS1/NS4 (White et al. 1990), 983F/2218R (Rehner and Buckley 2005), RPB2-5F2/fRPB2-7cR (Liu et al. 1999; Sung et al. 2007b) F1526Pc/R2434 (Houbraken and Samson 2011) and Bt2a/Bt2b (Glass and Donaldson 1995), respectively. Amplification reactions were performed in a 25 µL reaction volume including 2.5 µL 10 × PCR Buffer (Dingguo, Beijing, China), 2 mM $MgCl_2$, 50 µM dNTPs, 0.1 µM of each forward and reverse primer, 0.5 U Taq DNA polymerase and 1–10 ng genomic DNA in amplifier (Dongsheng, EDC-810, China). PCR parameters were as follows: 94 °C for 10 min, followed by 35 cycles of 94 °C for 30 s, 54 °C for 30 s, 72 °C for 30 s and a final elongation step at 72 °C for 10 min. Annealing temperature for each gene were 50 °C for LSU and Tsr1, 54 °C for ITS, RPB2 and SSU, and 57 °C for EF-1α and TUB. Sequencing reactions were performed by OmegaGenetcis Company Limited, Beijing, China.

All obtained strains were BLASTn searched in NCBI and assigned to potential genera and species. The strains whose ITS sequences had closest similarities below 97% were recognized as potential new species and further identified through morphological characterization and phylogenetic analyses.

To reveal the order placements of new species described in this paper, a LSU tree was constructed. To reveal the phylogenetic relationships and taxonomic distinctions of novel species, analyses were performed based on ITS, LSU and genetic markers recommended in recent publications, such as EF1-α, Tsr1 and TUB. All sequences of different loci were aligned using MAFFT (http://www.ebi.ac.uk/Tools/msa/mafft/) (Katoh and Toh 2010) and edited manually using MEGA v. 7 (Kumar et al. 2016) separately. Individual alignments were then concatenated and used for phylogenetic analysis next step. Ambiguously aligned regions were excluded from all analyses.

Maximum Likelihood (ML) and Bayesian inference (BI) methods were used to construct the phylogenetic trees. The ML analyses were implemented using RAxML-HPC v. 8.2.7 (Stamatakis 2014) with 1000 replicates under the GTR-GAMMA model. The robustness of branches was assessed by bootstrap analysis with 1000 replicates. For Bayesian analysis, the best model of evolution was estimated using jModelTest v. 2.1.7 (Guindon and Gascuel 2003; Darriba et al. 2012). Posterior probabilities (PP) (Rannala and Yang 1996; Zhaxybayeva and Gogarten 2002) were calculated by Markov Chain Monte Carlo sampling (MCMC) in MrBayes v. 3.2.1 (Huelsenbeck and Ronquist 2001), using the estimated evolutionary models. Six simultaneous Markov chains were run for 1,000,000 generations, and trees were sampled every 1000th generations (resulting 10,000 trees totally). The first 2000 trees, representing the burn-in phase of the analyses, were discarded and the remaining 8000 trees were used to calculate posterior probabilities (PP) in the majority rule consensus tree. The final trees were visualized in TreeView (Page 1996). All the sequences generated were deposited in GenBank (Table 2), typifications in Index

Table 1 Information of sampled caves

Cave name	Abbreviation	Location	Longitude	Latitude	Altitude (m)	Length (m)	Temperature	Humidity	Sample sites	Samples
Erwang cave	C1	Chongqing Wulong	108.001	29.585	890	1300	11–13 °C	88–93%	6	20
Sanwang cave	C2	Chongqing Wulong	108.001	29.591	1020	950	11–11.5°C	88–94%	5	18
E'gu cave	G1	Guangxi Guilin	110.511	24.942	269	320	24–27 °C	80–90%	5	28
Luotian cave	G2	Guangxi Guilin	110.524	24.948	330	450	23–26 °C	80–90%	4	20
Sanshan cave	G3	Guangxi Laibin	108.931	23.41	129	300	25 °C	80%	4	24
Feng cave	S5	Sichuan Xingwen	105.148	28.186	780	300	15–18 °C	75–90%	4	16
Yuguan cave	S6	Sichuan Xingwen	105.143	28.179	720	100	15 °C	85%	2	9
Tianliang cave	S7	Sichuan Xingwen	105.139	18.19	750	600	11–13 5°C	88–91%	5	20
Liujia cave	S8	Sichuan Huaying	106.878	30.41	850	300	14–15 °C	90–93%	4	19
Bijia Cave	S9	Sichuan Huaying	106.898	30.43	850	210	11–12 °C	91–93%	4	18
Mingjiu cave	Y1	Yunnan Mengzi	103.619	23.487	1838	400	15.5–19.5 °C	85–90%	3	14
Sanjiao cave	Y2	Yunnan Yiliang	103.383	25.134	1870	750	15–18 °C	85–91%	5	33
Niumo cave	Y3	Yunnan Yuxi	102.842	24.476	1840	200	15.5–18 °C	85–87%	3	12

Fungorum (http://www.indexfungorum.org), novel taxonomic descriptions in Faces of Fungi (Jayasiri et al. 2015), and the multi-locus alignments and trees in TreeBASE (submission number: 26362).

Morphological studies

Strains of potentially new species were transferred to new plates of PDA, OA and synthetic nutrient-poor agar (SNA; Nirenberg 1976) and were incubated at room temperature (25 ± 2 °C). Growth rates were measured after 7 days, while slow growing strains were measured after 10 days or even 8 weeks. Colony morphologies were determined after 10 days and colony colors on the surface and reverse of inoculated petri dishes were assessed according to the Methuen handbook of colour (Kornerup and Wanscher 1978). Cultures were examined periodically for the development of reproductive structures. Photomicrographs were taken using a Nikon 80i microscope with differential interference contrast. Measurements for each structure were made according to methods described by Liu et al. (2012). The dry cultures were deposited in the Herbarium of Microbiology, Academia Sinica (HMAS), while living cultures were deposited in the China General Microbiological Culture Collection Center (CGMCC) and LC Culture Collection (personal culture collection held in the lab of Dr Lei Cai).

Results

In this study, 251 samples from these thirteen caves were collected and 2344 fungal strains were isolated. These strains belong to 253 genera, 610 species by employing a BLASTn search in GenBank using the ITS sequences (Table S1). Among these species, 88.0 % (i.e., 536 species, 2115 strains) belong to 213 genera of Ascomycota; 8.0 % (i.e., 49 species, 133 strains) belong to 33 genera of Basidiomycota; 1.9 % (i.e., 12 species, 22 strains) belong to five genera of Mucoromycota, 1.9 % (i.e., 12 species, 73 strains) belong to one genera of Mortierellomycota; 0.2 % (i.e., 1 species, 1 strains) belong to one genera of Glomeromycota (Fig. 3a, Table S1). The most common genera included: *Penicillium* (12.0 %), *Aspergillus* (5.7 %), *Trichoderma* (3.4 %), *Arthrinium* Kunze (2.3 %), *Fusarium* (2.1 %), *Microascus* Zukal (2.1 %), *Mortierella* Coem. (2.0 %), *Cephalotrichum* Link (1.3 %), *Clonostachys* Corda (1.1 %), and *Simplicillium* Zare & W. Gams (1 %) (Fig. 3c, Table 3). The most common species included *Purpureocillium lilacinum* (Thom) Luangsa-ard (59 strains), *Mortierella alpine* Peyronel (56 strains), *Penicillium* (*Pe.*) *citrinum* Thom (55 strains), *Pe. simplicissimum* (Oudem.) Thom (53 strains), *Acremonium* sp. 6 (51 strains), *Cladosporium cladosporioides* (Fresen.) G.A. de Vries (45 strains), *Amphichorda cavernicola* Z.F.

Table 2 Strain and sequence accession numbers of new species

Species name	Strain No[a]	Cave	Substrate	Genbank accession number						
				ITS	LSU	TUB	TEF	SSU	RPB2	Tsr
Amphichorda cavernicola	CGMCC3.19571[T]	Feng cave	Bird faeces	MK329056	MK328961	MK336083	MK335997	–	–	–
	LC12481	Sanwang cave	Soil	MK329057	MK328962	MK336084	MK335998	–	–	–
	LC12485	Yuguan cave	Soil	MK329058	MK328963	MK336085	MK335999	–	–	–
	LC12553	Tianliang cave	Animal faeces	MK329059	MK328964	MK336086	MK336000	–	–	–
	LC12554	Feng cave	Bird faeces	MK329060	MK328965	MK336087	MK336001	–	–	–
	LC12560	Bijia cave	Animal faeces	MK329061	MK328966	MK336088	MK336002	–	–	–
	LC12577	Feng cave	Bird faeces	MK329062	MK328967	MK336089	MK336003	–	–	–
	LC12593	Liujia cave	Bird faeces	MK329063	MK328968	MK336090	MK336004	–	–	–
	LC12638	Liujia cave	Bat guano	MK329064	MK328969	MK336091	MK336005	–	–	–
	LC12674	E'gu cave	Plant debris	MK329065	MK328970	MK336092	MK336006	–	–	–
Aspergillus limoniformis	CGMCC3.19323[T]	Mingjiu cave	Bat guano	MK329066	MK328971	MK336093	MK336007	–	MK335972	MK335990
	LC12610	Mingjiu cave	Bat guano	MK329067	MK328972	MK336094	MK336008	–	MK335973	MK335991
Aspergillus phialiformis	CGMCC3.19314[T]	Sanjiao cave	Rock	MK329068	MK328973	MK336095	MK336009	–	MK335974	MK335992
	LC12537	Sanjiao cave	Rock	MK329069	MK328974	MK336096	MK336010	–	MK335975	MK335993
Aspergillus phialosimplex	CGMCC3.19637[T]	Liujia cave	Plant debris	MK329070	MK328975	MK336097	MK336011	–	MK335976	MK335994
	LC12625	Niumo cave	Plant root	MK329071	MK328976	MK336098	MK336012	–	MK335977	MK335995
	LC12658	E'gu cave	Animal faeces	MK329072	MK328977	MK336099	MK336013	–	MK335978	MK335996
Auxarthron chinense	CGMCC3.19572[T]	Luotian cave	Soil	MK329076	MK328981	MK336102	MK336017	–	–	–
	LC12463	Mingjiu cave	Soil	MK329073	MK328978	–	MK336014	–	–	–
	LC12473	E'gu cave	Soil	MK329074	MK328979	MK336100	MK336015	–	–	–
	LC12474	E'gu cave	Soil	MK329075	MK328980	MK336101	MK336016	–	–	–
	LC12477	Luotian cave	Soil	MK329077	MK328982	MK336103	MK336018	–	–	–
	LC12550	luotian cave	Soil	MK329078	MK328983	MK336104	MK336019	–	–	–
	LC12580	Luotian cave	Animal faeces	MK329079	MK328984	MK336105	MK336020	–	–	–
Auxarthron guangxiense	CGMCC3.19634[T]	E'gu cave	Soil	MK329080	MK328985	MK336106	MK336021	–	–	–
	LC12465	E'gu cave	Soil	MK329081	MK328986	MK336107	MK336022	–	–	–
Auxarthronopsis globiasca	CGMCC3.19305[T]	Luotian cave	Soil	MK329082	MK328987	MK336108	–	–	–	–
	LC12667	E'gu cave	Soil	MK329083	MK328988	MK336109	–	–	–	–
Auxarthronopsis pedicellaris	CGMCC3.19318[T]	Erwang cave	Rock	MK329084	MK328989	MK336110	–	–	–	
	LC12576	Erwang cave	Rock	MK329085	MK328990	MK336111	–	–	–	
Auxarthronopsis pulverea	CGMCC3.19312[T]	Liujia cave	Plant debris	MK329086	MK328991	MK336112	–	–	–	
	LC12522	Liujia cave	Plant debris	MK329087	MK328992	MK336113	–	–	–	
Auxarthronopsis stercicola	CGMCC3.19639[T]	Mingjiu cave	Animal faeces	MK329088	MK328993	MK336114	MK336023	–	–	
	LC12611	Mingjiu cave	Animal faeces	MK329089	MK328994	MK336115	MK336024	–	–	
Chrysosporium pallidum	CGMCC3.19575[T]	E'gu cave	Animal faeces	MK329090	MK328995	–	MK336025	–	–	–
	LC12670	E'gu cave	Animal faeces	MK329091	MK328996	–	MK336026	–	–	–

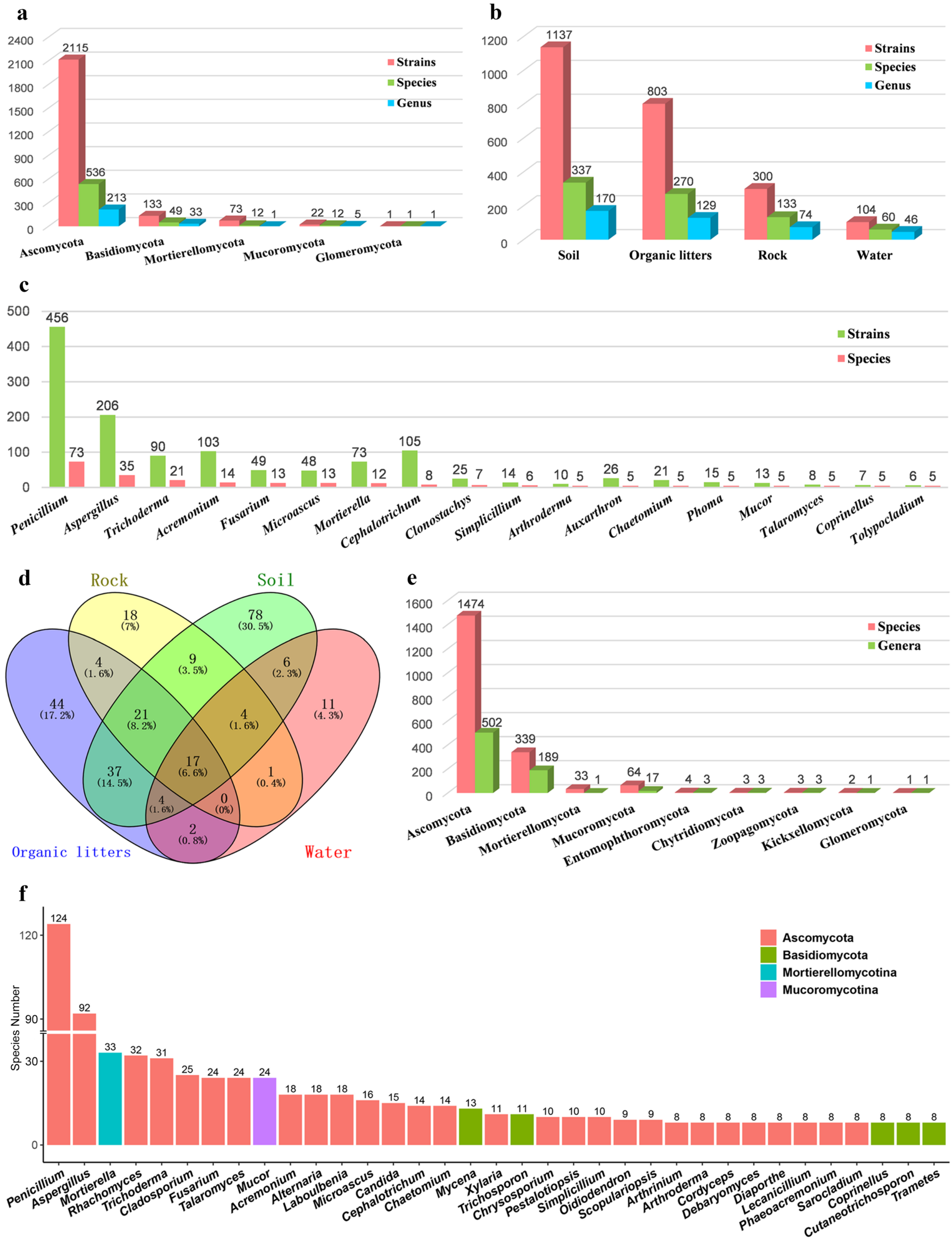
Table 2 (continued)

Species name	Strain No[a]	Cave	Substrate	Genbank accession number						
				ITS	LSU	TUB	TEF	SSU	RPB2	Tsr
Gamszarea humicola	CGMCC3.19303[T]	E'gu cave	Soil	MK329092	MK328997	–	MK336027	MK311230	MK335979	–
	LC12462	E'gu cave	Soil	MK329093	MK328998	–	MK336028	MK311231	MK335980	–
Gamszarea lunata	CGMCC3.19315[T]	E'gu cave	Rock	MK329094	MK328999	–	MK336029	MK311232	MK335981	–
	LC12546	E'gu cave	Rock	MK329095	MK329000	–	MK336030	MK311233	MK335982	–
Gamszarea microspora	CGMCC3.19313[T]	Tianliang cave	Rock	MK329096	MK329001	–	MK336031	MK311234	MK335983	–
	LC12531	Tianliang cave	Rock	MK329097	MK329002	–	MK336032	MK311235	MK335984	–
Gymnoascus flavus	CGMCC3.19574[T]	Feng cave	Soil	MK329098	MK329003	MK336116	MK336033			–
	LC12511	Tianliang cave	Soil	MK329099	MK329004	MK336117	MK336034			–
Jattaea reniformis	CGMCC3.19311[T]	Luotian cave	Water	MK329100	MK329005	MK336118	MK336035	–	–	–
	LC12510	Luotian cave	Water	MK329101	MK329006	MK336119	MK336036	–	–	–
Lecanicillium magnisporum	CGMCC3.19304[T]	Erwang cave	Soil	MK329102	MK329007	–	MK336037	MK311236	MK335985	–
	LC12469	Erwang cave	Soil	MK329103	MK329008	–	MK336038	MK311237	MK335986	–
	LC12470	Erwang cave	Soil	MK329104	MK329009	–	MK336039	MK311238	MK335987	–
	LC12647	Sanwang cave	Soil	MK329105	MK329010	–	MK336040	MK311239	MK335988	–
	LC12663	Sanwang cave	Soil	MK329106	MK329011	–	MK336041	MK311240	MK335989	–
Microascus collaris	CGMCC3.19321[T]	Sanshan cave	Plant debris	MK329109	MK329012	MK336120	MK336042	–	–	–
	LC12599	Sanshan cave	Plant debris	MK329110	MK329013	MK336121	MK336043	–	–	–
Microascus levis	CGMCC3.19308[T]	Luotian cave	Soil	MK329108	MK329015	MK336123	MK336045	–	–	–
	LC12447	Luotian cave	Soil	MK329107	MK329014	MK336122	MK336044	–	–	–
Microascus sparsimycelialis	CGMCC3.19307[T]	Sanshan cave	Soil	MK329111	MK329016	MK336124	MK336046	–	–	–
	LC12480	Sanshan cave	Soil	MK329112	MK329017	MK336125	MK336047	–	–	–
Microascus superficialis	CGMCC3.19638[T]	Sanshan cave	Animal faeces	MK329113	MK329018	MK336126	MK336048	–	–	–
	LC12600	Sanshan cave	Animal faeces	MK329114	MK329019	MK336127	MK336049	–	–	–
	LC12601	Sanshan cave	Animal faeces	MK329115	MK329020	MK336128	MK336050	–	–	–
Microascus trigonus	CGMCC3.19636[T]	Luotian cave	Soil	MK329117	MK329022	MK336130	MK336052	–	–	–
	LC12513	Luotian cave	Soil	MK329116	MK329021	MK336129	MK336051	–	–	–
	LC12559	E'gu cave	Animal faeces	MK329118	MK329023	MK336131	MK336053	–	–	–
	LC12586	E'gu cave	Animal faeces	MK329119	MK329024	MK336132	MK336054	–	–	–
	LC12631	E'gu cave	Animal faeces	MK329120	MK329025	MK336133	MK336055	–	–	–
Nigrospora globosa	CGMCC3.19633[T]	Luotian cave	Soil	MK329121	MK329026	MK336134	MK336056	–	–	–
	LC12441	Luotian cave	Soil	MK329122	MK329027	MK336135	MK336057	–	–	–
Paracremonium apiculatum	CGMCC3.19309[T]	Sanjiao cave	Soil	MK329123	MK329028	MK336136	MK336058	–	–	–
	LC12502	Sanjiao cave	Soil	MK329124	MK329029	MK336137	MK336059	–	–	–

Table 2 (continued)

Species name	Strain No[a]	Cave	Substrate	Genbank accession number						
				ITS	LSU	TUB	TEF	SSU	RPB2	Tsr
Paracremonium ellipsoideum	CGMCC3.19316^T	Sanjiao cave	Sewage	MK329125	MK329030	MK336138	MK336060	–	–	–
	LC12552	Sanjiao cave	Sewage	MK329126	MK329031	MK336139	MK336061	–	–	–
Paraphaeosphaeria hydei	CGMCC3.19317^T	Sanjiao cave	Plant debris	MK329127	MK329032	MK336140	MK336062	–	–	–
	LC12565	Sanjiao cave	Plant debris	MK329128	MK329033	MK336141	MK336063	–	–	–
Pseudoscopulariopsis asperispora	CGMCC3.19302^T	Luotian cave	Soil	MK329129	MK329034	MK336142	MK336064	–	–	–
	LC12446	Luotian cave	Soil	MK329130	MK329035	MK336143	MK336065	–	–	–
Setophaeosphaeria microspora	CGMCC3.19301^T	Sanshan cave	Soil	MK329131	MK329036	MK336144	MK336066	–	–	–
	LC10444	Sanshan cave	Soil	MK329132	MK329037	MK336145	MK336067	–	–	–
Simplicillium album	CGMCC3.19635^T	Sanshan cave	Soil	MK329133	MK329038	–	MK336068	–	–	–
	LC12543	E'gu cave	Animal faeces	MK329134	MK329039	–	MK336069	–	–	–
	LC12557	E'gu cave	Animal faeces	MK329135	MK329040	–	MK336070	–	–	–
Simplicillium humicola	CGMCC3.19573^T	E'gu cave	Soil	MK329136	MK329041	–	MK336071	–	–	–
	LC12494	E'gu cave	Soil	MK329137	MK329042	–	MK336072	–	–	–
Wardomycopsis dolichi	CGMCC3.19310^T	E'gu cave	Soil	MK329138	MK329043	–	MK336073	–	–	–
	LC12504	E'gu cave	Soil	MK329139	MK329044	–	MK336074	–	–	–
Wardomycopsis ellipsoconidiophora	CGMCC3.19322^T	Sanshan cave	Animal faeces	MK329141	MK329046	MK336147	MK336076	–	–	–
	LC12588	Sanshan cave	Animal faeces	MK329140	MK329045	MK336146	MK336075	–	–	–
Wardomycopsis fusca	CGMCC3.19306^T	Luotian cave	Soil	MK329142	MK329047	MK336148	MK336077	–	–	–
	LC12526	Luotian cave	Soil	MK329143	MK329048	MK336149	MK336078	–	–	–
	LC12607	Mingjiu cave	Animal faeces	MK329144	MK329049	MK336150	MK336079	–	–	–
	LC12636	E'gu cave	Animal faeces	MK329145	MK329050	MK336151	MK336080	–	–	–
	LC12643	Sanjiao cave	Soil	MK329146	MK329051	MK336152	MK336081	–	–	–
	LC12661	Mingjiu cave	Animal faeces	MK329147	MK329052	MK336153	MK336082	–	–	–

[a]Ex-type strains are indicated with T


a
Strains
Species
Genus
Ascomycota
Basidiomycota
Mortierellomycota
Mucoromycota
Glomeromycota
2115 536 213
133 49 33
73 12 1
22 12 5
1 1 1
b
Strains
Species
Genus
Soil
Organic litters
Rock
Water
1137 337 170
803 270 129
300 133 74
104 60 46
c
Strains
Species
Penicillium 456 73
Aspergillus 206 35
Trichoderma 90 21
Acremonium 103 14
Fusarium 49 13
Microascus 48 13
Mortierella 73 12
Cephalotrichum 105 8
Clonostachys 25 7
Simplicillium 14 6
Arthroderma 10 5
Auxarthron 26 5
Chaetomium 21 5
Phoma 15 5
Mucor 13 5
Talaromyces 8 5
Coprinellus 7 5
Tolypocladium 6 5
d
Rock
Soil
Organic litters
Water
18 (7%)
78 (30.5%)
4 (1.6%)
9 (3.5%)
6 (2.3%)
44 (17.2%)
21 (8.2%)
4 (1.6%)
11 (4.3%)
37 (14.5%)
17 (6.6%)
1 (0.4%)
4 (1.6%)
0 (0%)
2 (0.8%)
e
Species
Genera
Ascomycota 1474 502
Basidiomycota 339 189
Mortierellomycota 33 1
Mucoromycota 64 17
Entomophthoromycota 4 3
Chytridiomycota 3 3
Zoopagomycota 3 3
Kickxellomycota 2 1
Glomeromycota 1 1
f
Species Number
Ascomycota
Basidiomycota
Mortierellomycotina
Mucoromycotina
Penicillium 124
Aspergillus 92
Mortierella 33
Rhachomyces 32
Trichoderma 31
Cladosporium 25
Fusarium 24
Talaromyces 24
Mucor 24
Acremonium 18
Alternaria 18
Laboulbenia 18
Microascus 16
Candida 15
Cephalotrichum 14
Chaetomium 14
Mycena 13
Xylaria 11
Trichosporon 11
Chrysosporium 10
Pestalotiopsis 10
Simplicillium 10
Oidiodendron 9
Scopulariopsis 9
Arthrinium 8
Arthroderma 8
Cordyceps 8
Debaryomyces 8
Diaporthe 8
Lecanicillium 8
Phaeoacremonium 8
Sarocladium 8
Coprinellus 8
Cutaneotrichosporon 8
Trametes 8

◂**Fig. 3** Statistics of fungi in caves in this study (**a**–**d**) and worldwide (**e**–**f**). **a** The number of fungal genera, species and strains in different phyla obtained in this study; **b** the number of fungal genera, species and strains isolated from different substrates in this study; **c** most abundant fungal genera observed in this study; **d** venn diagram of fungal genera obtained from different substrates in this study. **e** the number of fungal genera and species reported in caves worldwide; **f** fungal genera with highest diversity reported in caves worldwide

Table 3 Most common genera (≥ 5 species) obtained from Karst caves in this study

Genus	Species	Strains	Genus	Species	Strains
Penicillium	73	456	*Simplicillium*	6	14
Aspergillus	35	206	*Arthroderma*	5	10
Trichoderma	21	90	*Auxarthron*	5	26
Acremonium	14	103	*Chaetomium*	5	21
Fusarium	13	49	*Phoma*	5	15
Microascus	13	48	*Talaromyces*	5	8
Mortierella	12	73	*Tolypocladium*	5	6
Cephalotrichum	8	105	*Coprinellus*	5	7
Clonostachys	7	25	*Mucor*	5	13

Zhang & L. Cai (42 strains), *Trichoderma harzianum* Rifai (40 strains), *Cephalotrichum asperulum* (J.E. Wright & S. Marchand) Sand.-Den., Guarro & Gené (36 strains), *Aspergillus versicolor* (Vuill.) Tirab. (32 strains), *Parengyodontium album* (Limber) C.C. Tsang, et al. (30 strains), and *Plectosphaerella cucumerina* (Lindf.) W. Gams (30 strains).

For the isolations of substrate, 1137 strains from soil samples belong to 377 species in 170 genera; 803 strains from organic litters belong to 270 species in 129 genera; 300 strains from rock samples belong to 133 species in 74 genera; 104 strains from water samples belong to 60 species in 46 genera (Fig. 3b). Seventeen genera were found in these four types of substrate, i.e. *Acremonium* Link, *Arthrinium* Kunze, *Aspergillus*, *Beauveria* Vuill, *Cephalotrichum*, *Chaetomium* Kunze, *Cladosporium* Link, *Cutaneotrichosporon* Xin Zhan Liu, F.Y. Bai, M. Groenew. & Boekhout, *Didymella* Sacc, *Fusarium*, *Leptosphaeria* Ces. & De Not., *Mortierella*, *Mucor*, *Penicillium*, *Plectosphaerella* Kleb, *Purpureocillium* Luangsa-ard, Hywel-Jones, Houbraken & Samson, *Trichoderma* (Fig. 3d).

Meanwhile, we summarized data on the fungi of caves from 56 papers published in the peer-reviewed literatures (Table 4) since 2013 in English based on Vanderwolf et al. (2013). Following the newest records in Index Fungorum (http://www.indexfungorum.org/Names/Names.asp), we revised the fungal names documented in caves. By February 2020, 1626 species in 644 genera of fungi have been reported from caves and mines worldwide. In our study, 76 of the 253 genera and 247 of the 468 identified species (52.8 %) were reported for the first time from caves. With our data, totally, 1923 fungal species in 720 genera were documented from caves and mines (Table 4). Of the fungal taxa reported from caves and mines, nine phyla were observed (Fig. 3e), Ascomycota (1474 species in 502 genera), Basidiomycota (339 species in 189 genera), Mucoromycota (64 species in 17 genera), Mortierellomycota (33 species in 1 genus), Entomophthoromycota (4 species in 3 genera), Chytridiomycota (3 species in 3 genera), Zoopagomycota (3 species in 3 genera), Kickxellomycota (2 species in 1 genera) and Glomeromycota (1 species in 1 genus). Twenty-two genera have more than 10 species reported in caves worldwide, most of which belong to Ascomycota (Fig. 3f).

Thirty-three new species were described and illustrated in this paper, based on the morphological characteristics and phylogenetic analyses. The LSU phylogenetic tree (Fig. 4) showed that these 33 new species (marked with bold font) scattered in seven different orders, i.e., *Calosphaeriales*, *Eurotiales*, *Hypocreales*, *Microascales*, *Onygenales*, *Pleosporales*, and *Xylariales*. Significant ML bootstrap values (≥ 70 %) and Bayesian posterior probabilities (≥ 90 %) are shown in the phylogenetic tree.

Taxonomy

Phylum Ascomycota Caval.-Sm.

We follow the latest treatment of Ascomycota (Wijayawardene et al. 2018, 2020), with classes, subclasses, orders, families, genera and species listed below in alphabetical order.

Class Dothideomycetes O.E. Erikss. & Winka

Based on molecular dating evidence, Liu et al. (2017) updated the multi-locus phylogeny of Dothideomycetes and unraveled the evolutionary relationships. In this paper, the classification of families in Dothideomycetes follow Liu et al. (2017) and Wijayawardene et al. (2018, 2020).

Subclass Pleosporomycetidae C.L. Schoch, Spatafora, Crous & Shoemaker

Pleosporales Luttr. ex M.E. Barr

The order *Pleosporales* was introduced by Luttrell (1955) to accommodate a highly diverse fungal group of Dothideomycetes having perithecioid ascomata and asci with pseudoparaphyses (Zhang et al. 2009). More details see Zhang et al. (2012) and Hyde et al. (2013).

Didymosphaeriaceae Munk

We follow the treatment of Ariyawansa et al. (2014), Hyde et al. (2017) and Wijayawardene et al. (2020) in the study.

Table 4 Fungi documented from caves and mines worldwide with references. New species described in this study are in bold

Genus	Species	China[a]	This study[b]	References
Ascomycota				
Acidea	*Acidea extrema*			Burow et al. (2019)
Acaulium	*Acaulium caviariforme*			Vanderwolf et al. (2013, 2015, 2019)
Acidomyces	*Acidomyces acidothermus*			Brad et al. (2018)
Acremoniella	*Acremoniella atra*			Pusz et al. (2018a)
Acremonium	*Acremonium alternatum*	Y	Y	Vanderwolf et al. (2013)
	A. antarcticum	Y	Y	
	A. atrogriseum			Vanderwolf et al. (2013)
	A. biseptum			Vanderwolf et al. (2013)
	A. cereale			Vanderwolf et al. (2013)
	A. charticola	Y		Vanderwolf et al. (2013), Popkova and Mazina (2019), Zhang (2019)
	A. furcatum	Y	Y	Vanderwolf et al. (2013), Jiang et al. (2017a, b)
	A. hennebertii	Y		Zhang (2019)
	A. longisporum	Y	Y	
	A. murorum	Y	Y	Vanderwolf et al. (2013), Martin-Sanchez et al. (2014), Zhang et al. (2017), Pusz et al. (2018a)
	A. nepalense	Y	Y	Saiz-Jimenez et al. (2012), Vanderwolf et al. (2013), Martin-Sanchez et al. (2014), Zhang et al. (2017)
	A. persicinum	Y	Y	Vanderwolf et al. (2013), Zhang et al. (2017)
	A. polychromum			Vanderwolf et al. (2013)
	A. roseolum			Vanderwolf et al. (2013)
	A. rutilum			Vanderwolf et al. (2013, 2019)
	A. verruculosum			Vanderwolf et al. (2013)
	A. vitis			Vanderwolf et al. (2013)
	Acremonium sp.	Y	Y	Connell and Staudigel (2013), Vanderwolf et al. (2013, 2015, 2019), Man et al. (2015), Jiang et al. (2017a, b), Zhang et al. (2017), Leplat et al. (2018), Popkova and Mazina (2019)
Acrocalymma	*Acrocalymma vagum*	Y	Y	
Acrocylindrium	*Acrocylindrium* sp.			Vanderwolf et al. (2013)
Acrodontium	*Acrodontium crateriforme*	Y		Vanderwolf et al. (2013), Zhang et al. (2017)
	Acrodontium sp.			Vanderwolf et al. (2013, 2019)
Acrophialophora	*Acrophialophora fusispora*			Vanderwolf et al. (2013)
Acrostalagmus	*Acrostalagmus luteoalbus*	Y	Y	Vanderwolf et al. (2013), Man et al. (2015), Zhang et al. (2017)
Adelphella	*Adelphella babingtonii*			Vanderwolf et al. (2013)
Ajellomyces	*Ajellomyces capsulatus*			Vanderwolf et al. (2013)
	Ajellomyces sp.	Y	Y	
Akanthomyces	*Akanthomyces lecanii*	Y	Y	Vanderwolf et al. (2013)
Albifimbria	*Albifimbria verrucaria*	Y	Y	Connell and Staudigel (2013), Vanderwolf et al. (2013), Nováková et al. (2018)
	Albifimbria sp.			Leplat et al. (2018)
Allantophomopsiella	*Allantophomopsiella pseudotsugae*			Pusz et al. (2017)
Allophoma	*Allophoma* sp.	Y		Jiang et al. (2017a, b)
Alternaria	*Alternaria abundans*			Pusz et al. (2015), Ogórek et al. (2017, 2018), Ogórek (2018a)
	Al. alternata	Y	Y	Connell and Staudigel (2013), Vanderwolf et al. (2013), Ogórek et al. (2014a, b, c, 2016b, c, d), Man et al. (2015), Pusz et al. (2015, 2017, 2018a, b), Kokurewicz et al. (2016), Jiang et al. (2017a, b), Zhang et al. (2017), Nováková et al. (2018), Pusz et al. (2018a), Popkova and Mazina (2019)
	Al. alternariae			Ogórek et al. (2013)
	Al. atra			Vanderwolf et al. (2013)
	Al. botrytis			Vanderwolf et al. (2013), Kokurewicz et al. (2016), Pusz et al. (2018a, b)
	Al. brevicolla			Vanderwolf et al. (2013)
	Al. chartarum			Vanderwolf et al. (2013)
	Al. humicola			Vanderwolf et al. (2013)
	Al. infectoria			Connell and Staudigel (2013)
	Al. longipes			Nováková et al. (2018)
	Al. mali	Y		Zhang (2019)
	Al. mouchaccae			Vanderwolf et al. (2013)
	Al. oudemansii			Vanderwolf et al. (2013)

Table 4 (continued)

Genus	Species	China[a]	This study[b]	References
	Al. radicina			Vanderwolf et al. (2013)
	Al. solani	Y	Y	
	Al. tamaricis	Y		Zhang et al. (2017)
	Al. tenuissima	Y	Y	Vanderwolf et al. (2013), Popović et al. (2015), Pusz et al. (2015), Zhang et al. (2017), Nováková et al. (2018)
	Alternaria sp.	Y		Vanderwolf et al. (2013), Martin-Sanchez et al. (2014), Popović et al. (2015), Belyagoubi et al. (2018), Bercea et al. (2018), Nováková et al. (2018), Leplat et al. (2018), Zhang (2019)
Amauroascus	*Amauroascus albicans*			Vanderwolf et al. (2013)
	Am. kuehnii			Vanderwolf et al. (2013)
	Amauroascus sp.	Y		Vanderwolf et al. (2013), Zhang (2019)
Amblyosporium	*Amblyosporium botrytis*			Vanderwolf et al. (2013)
Amesia	*Amesia nigricolor*	Y	Y	Zhang et al. (2017)
Amorphotheca	*Amorphotheca resinae*			Vanderwolf et al. (2013)
Ampelomyces	*Ampelomyces humuli*	Y	Y	
Amphichorda	***Amp. cavernicola***	Y	Y	
	Amphichorda felina	Y	Y	Vanderwolf et al. (2013), Zhang et al. (2017), Belyagoubi et al. (2018)
	Amp. guana	Y		Zhang et al. (2017)
Annulohypoxylon	*Annulohypoxylon* sp.	Y	Y	
	An. stygium	Y	Y	
Aphanoascus	*Aphanoascus fulvescens*			Vanderwolf et al. (2013)
	Ap. keratinophilus			Vanderwolf et al. (2013)
	Aphanoascus sp.			Vanderwolf et al. (2013)
Aphanocladium	*Aphanocladium album*			Vanderwolf et al. (2013, 2019), Nováková et al. (2018)
	Aphanocladium sp.			Zhang et al. (2014), Vanderwolf et al. (2019)
Arachniotus	*Arachniotus dankaliensis*			Vanderwolf et al. (2013)
	Ar. ruber			Vanderwolf et al. (2013)
	Ar. verruculosus	Y	Y	
	Arachniotus sp.			Vanderwolf et al. (2013)
Arachnomyces	*Arachnomyces glareosus*			Vanderwolf et al. (2013)
	Arachnomyces sp.	Y		Vanderwolf et al. (2013), Zhang (2019)
Arachnotheca	*Arachnotheca albicans*			Vanderwolf et al. (2013)
Arcopilus	*Arcopilus aureus*			Vanderwolf et al. (2013)
Arthopyrenia	*Arthopyrenia salicis*	Y	Y	
Arthrinium	*Arthrinium arundinis*	Y	Y	Vanderwolf et al. (2013), Man et al. (2015), Jiang et al. (2017a, b), Mitova et al. (2017), Zhang et al. (2017)
	Art. kogelbergense			Ogórek et al. (2017), Ogórek et al. (2018)
	Art. malaysianum	Y		Zhang et al. (2017)
	Art. marii	Y		Zhang et al. (2017)
	Art. phaeospermum	Y	Y	Vanderwolf et al. (2013), Popović et al. (2015), Zhang et al. (2017)
	Art. sacchari	Y		Zhang et al. (2017)
	Art. sphaerospermum			Vanderwolf et al. (2013)
	Arthrinium sp.	Y		Vanderwolf et al. (2013), Zhang et al. (2017), Leplat et al. (2018)
Arthrobotrys	*Arthrobotrys oligospora*			Vanderwolf et al. (2013)
	Arth. arthrobotryoides			Vanderwolf et al. (2013)
Arthroderma	*Arthroderma ciferrii*	Y	Y	
	Arthr. curreyi	Y		Vanderwolf et al. (2013), Zhang et al. (2017)
	Arthr. melis			Vanderwolf et al. (2013)
	Arthr. quadrifidum	Y	Y	Vanderwolf et al. (2013), Zhang et al. (2017)
	Arthr. silverae			Vanderwolf et al. (2013, 2015, 2019)
	Arthr. tuberculatum	Y	Y	Vanderwolf et al. (2013)
	Arthr. uncinatum			Vanderwolf et al. (2013)
	Arthroderma sp.	Y	Y	Vanderwolf et al. (2013, 2015), Zhang et al. (2014)
Arthrographis	*Arthrographis kalrae*	Y	Y	
	Arthrographis sp.	Y	Y	Vanderwolf et al. (2013, 2015, 2019)
Arthropsis	*Arthropsis hispanica*	Y		Zhang et al. (2017)
Arthrorhynchus	*Arthrorhynchus nycteribiae*			Vanderwolf et al. (2013)
Arxiella	*Arxiella* sp.	Y	Y	
Asaphomyces	*Asaphomyces tubanticus*			Vanderwolf et al. (2013)

Table 4 (continued)

Genus	Species	China[a]	This study[b]	References
Ascobolus	*Ascobolus* sp.			Vanderwolf et al. (2013)
Aspergillus	*Aspergillus aculeatus*	Y	Y	
	As. affinis			Nováková et al. (2018)
	As. alliaceus			Nováková et al. (2018)
	As. amstelodami			Taylor et al. (2013), Vanderwolf et al. (2013)
	As. amylovorus			Vanderwolf et al. (2013)
	As. asperescens			Vanderwolf et al. (2013)
	As. aureolatus	Y	Y	Vanderwolf et al. (2013), Ogórek et al. (2017), Tavares et al. (2018)
	As. aureolus	Y	Y	
	As. awamori			Vanderwolf et al. (2013)
	As. baeticus			Vanderwolf et al. (2013), Nováková et al. (2018)
	As. brunneoviolaceus	Y	Y	
	As. caespitosus			Taylor et al. (2013), Vanderwolf et al. (2013)
	As. calidoustus	Y		Jiang et al. (2017a, b), Nováková et al. (2018)
	As. cavernicola	Y	Y	Zhang et al. (2017)
	As. candidus	Y	Y	Taylor et al. (2013), Vanderwolf et al. (2013), Zhang et al. (2017)
	As. carbonarius			Vanderwolf et al. (2013)
	As. carneus	Y		Vanderwolf et al. (2013), Zhang (2019)
	As. chevalieri			Vanderwolf et al. (2013)
	As. clavatus			Taylor et al. (2013), Vanderwolf et al. (2013), Popović et al. (2015)
	As. conjunctus			Vanderwolf et al. (2013)
	As. creber	Y		Zhang et al. (2017), Nováková et al. (2018)
	As. cremeus			Vanderwolf et al. (2013)
	As. crustosus			Vanderwolf et al. (2013)
	As. deflectus	Y	Y	Vanderwolf et al. (2013)
	As. elegans			Ogórek (2018a, b)
	As. europaeus			Nováková et al. (2018)
	As. fijiensis	Y	Y	
	As. fischeri			Vanderwolf et al. (2013)
	As. flavipes			Vanderwolf et al. (2013), Popkova and Mazina (2019)
	As. flavofurcatus			Vanderwolf et al. (2013)
	As. flavus	Y	Y	Taylor et al. (2013), Vanderwolf et al. (2013), Pusz et al. (2014), Man et al. (2015), Yoder et al. (2015), Jiang et al. (2017a, b), Zhang et al. (2017), Nováková et al. (2018), Ogórek (2018a)
	As. foetidus			Vanderwolf et al. (2013), Ogórek et al. (2016b)
	As. fumigatus	Y	Y	Vanderwolf et al. (2013), Pusz et al. (2015), Yoder et al. (2015), Ogórek et al. (2016b, c, d), Zhang et al. (2017), Dyląg et al. (2019), Popkova and Mazina (2019)
	As. giganteus			Vanderwolf et al. (2013)
	As. glaucus			Vanderwolf et al. (2013)
	As. granulosus			Vanderwolf et al. (2013)
	As. hongkongensis	Y	Y	
	As. humicola			Vanderwolf et al. (2013)
	As. iizukae			Nováková et al. (2018)
	As. inflatus	Y	Y	
	As. insuetus			Vanderwolf et al. (2013)
	As. janus			Vanderwolf et al. (2013)
	As. japonicus	Y	Y	Taylor et al. (2013), Vanderwolf et al. (2013)
	As. jensenii			Nováková et al. (2018)
	As. kanagawaensis			Vanderwolf et al. (2013)
	As. keveii			Tavares et al. (2018)
	As. limoniformis	Y	Y	
	As. movilensis			Nováková et al. (2018)
	As. neoniveus			Taylor et al. (2013), Vanderwolf et al. (2013)
	As. nidulans			Vanderwolf et al. (2013)
	As. niger	Y	Y	Ogórek et al. (2013, 2014a, b, c, 2016c, d, 2017, 2018), Taylor et al. (2013), Vanderwolf et al. (2013), Pusz et al. (2014, 2015, 2017), Popović et al. (2015), Yoder et al. (2015), Jiang et al. (2017a, b), Zhang et al. (2017), Ogórek (2018a, b), Pusz et al. (2018a), Popkova and Mazina (2019)

Table 4 (continued)

Genus	Species	China[a]	This study[b]	References
	As. niveoglaucus	Y		Zhang et al. (2017)
	As. nomius	Y	Y	
	As. ochraceus			Taylor et al. (2013), Vanderwolf et al. (2013), Popović et al. (2015), Jacobs et al. (2017), Popkova and Mazina (2019)
	As. parasiticus			Vanderwolf et al. (2013)
	As. penicillioides			Connell and Staudigel (2013), Vanderwolf et al. (2013)
	As. persii	Y	Y	
	As. phialiformis	Y	Y	
	As. phialosimplex	Y	Y	
	As. phoenicis			Vanderwolf et al. (2013)
	As. polyporicola	Y	Y	
	As. pragensis	Y	Y	Zhang et al. (2017)
	As. proliferans			Vanderwolf et al. (2013)
	As. protuberus			Nováková et al. (2018)
	As. pseudodeflectus			Nováková et al. (2018)
	As. pseudoglaucus			Nováková et al. (2018)
	As. puniceus			Vanderwolf et al. (2013)
	As. puulaauensis			Nováková et al. (2018)
	As. reptans	Y		Vanderwolf et al. (2013), Zhang (2019)
	As. repens	Y		Jiang et al. (2017a, b), Zhang et al. (2017)
	As. restrictus	Y		Taylor et al. (2013), Vanderwolf et al. (2013), Zhang (2019), Popkova and Mazina (2019)
	As. ruber	Y		Zhang et al. (2017)
	As. rugulosus			Taylor et al. (2013), Vanderwolf et al. (2013)
	As. sclerotiorum	Y	Y	Taylor et al. (2013), Vanderwolf et al. (2013)
	As. silvaticus			Vanderwolf et al. (2013)
	As. spelunceus	Y	Y	Vanderwolf et al. (2013), Zhang et al. (2017)
	As. stellatus	Y	Y	
	As. sulphureus			Vanderwolf et al. (2013)
	As. sydowii	Y	Y	Taylor et al. (2013), Vanderwolf et al. (2013), Jiang et al. (2017a, b), Nováková et al. (2018), Tavares et al. (2018)
	As. tabacinus	Y	Y	Nováková et al. (2018)
	As. tamarii			Vanderwolf et al. (2013)
	As. templicola			Nováková et al. (2018)
	As. tennesseensis	Y	Y	Zhang et al. (2017), Nováková et al. (2018)
	As. terreus	Y	Y	Vanderwolf et al. (2013), Popkova and Mazina (2019)
	As. thesauricus	Y	Y	Vanderwolf et al. (2013), Zhang et al. (2017), Nováková et al. (2018)
	As. tubingensis	Y	Y	Zhang et al. (2017)
	As. unguis			Vanderwolf et al. (2013)
	As. ustus	Y	Y	Taylor et al. (2013), Vanderwolf et al. (2013), Zhang et al. (2017), Nováková et al. (2018), Paula et al. (2019), Popkova and Mazina (2019)
	As. versicolor	Y	Y	Taylor et al. (2013), Vanderwolf et al. (2013), Martin-Sanchez et al. (2014), Man et al. (2015), Jacobs et al. (2017), Jiang et al. (2017a, b), Mitova et al. (2017), Zhang et al. (2017), Popkova and Mazina (2019)
	As. wentii	Y		Taylor et al. (2013), Vanderwolf et al. (2013), Zhang et al. (2017), Belyagoubi et al. (2018)
	As. westerdijkiae			Jacobs et al. (2017), Nováková et al. (2018)
	Aspergillus sp.	Y	Y	Connell and Staudigel (2013), Taylor et al. (2013), Vanderwolf et al. (2013), Busquets et al. (2014), Popović et al. (2015), Yoder et al. (2015), Kokurewicz et al. (2016), Jiang et al. (2017a, b), Zhang et al. (2017), Belyagoubi et al. (2018), Bercea et al. (2018), Nováková et al. (2018), Leplat et al. (2018), Paula et al. (2019)
Asperisporium	*Asperisporium* sp.			Vanderwolf et al. (2013)
Athelia	*Athelia rolfsii*			Pusz et al. (2018b)
Aureobasidium	*Aureobasidium pullulans*			Connell and Staudigel (2013), Vanderwolf et al. (2013), Popović et al. (2015), Brad et al. (2018), Pusz et al. (2018a), Popkova and Mazina (2019)
	Aureobasidium sp.			Connell and Staudigel (2013), Vanderwolf et al. (2013), Leplat et al. (2018)
Auxarthron	*Auxarthron alboluteum*	Y	Y	Man et al. (2015)
	Au. californiense			Vanderwolf et al. (2015), Nováková et al. (2018)

Table 4 (continued)

Genus	Species	China[a]	This study[b]	References
	Au. chinense	Y	Y	
	Au. guangxiense	Y	Y	
	Au. thaxteri			Vanderwolf et al. (2013)
	Au. umbrinum	Y		Zhang et al. (2017)
	Auxarthron sp.	Y	Y	Vanderwolf et al. (2013), Zhang et al. (2014)
Auxarthronopsis	***Auxarthronopsis globiasca***	Y	Y	
	Aux. guizhouensis	Y		Zhang et al. (2017)
	Aux. pedicellaris	Y	Y	
	Aux. pulverea	Y	Y	
	Aux. stercicola	Y	Y	
Barnettozyma	*Barnettozyma californica*	Y	Y	Vanderwolf et al. (2013)
Bartalinia	*Bartalinia robillardoides*	Y	Y	
Basipetospora	*Basipetospora* sp.			Vanderwolf et al. (2013)
Beauveria	*Beauveria bassiana*	Y	Y	Ogórek et al. (2013, 2014a), Vanderwolf et al. (2013), Zhang et al. (2014), Yoder et al. (2015), Pusz et al. (2018a)
	B. brongniartii	Y	Y	Vanderwolf et al. (2013)
	B. caledonica	Y	Y	Yoder et al. (2015)
	Beauveria sp.			Vanderwolf et al. (2013, 2019), Leplat et al. (2018)
Beltrania	*Beltrania* sp.			Vanderwolf et al. (2013)
Bionectria	*Bionectria ochroleuca*	Y	Y	Vanderwolf et al. (2013), Zhang et al. (2014), Jacobs et al. (2017), Zhang et al. (2017)
	Bi. rossmaniae	Y	Y	Mitova et al. (2017)
	Bi. solani			Nováková et al. (2018)
	Bionectria sp.	Y		Zhang (2019)
Bipolaris	*Bipolaris sorokiniana*			Pusz et al. (2018b)
	Bipolaris sp.			Vanderwolf et al. (2013)
Biscogniauxia	*Biscogniauxia petrensis*	Y	Y	Zhang et al. (2017)
	Biscogniauxia sp.	Y	Y	Zhang et al. (2017)
Bisifusarium	*Bisifusarium delphinoides*	Y	Y	
Bispora	*Bispora antennata*			Vanderwolf et al. (2013)
	Bis. betulina			Vanderwolf et al. (2013)
	Bis. effusa			Vanderwolf et al. (2013)
	Bispora sp.			Vanderwolf et al. (2013)
Bisporella	*Bisporella citrina*			Vanderwolf et al. (2013)
Blastobotrys	*Blastobotrys chiropterorum*			Vanderwolf et al. (2013)
	Bl. malaysiensis	Y	Y	
	Bl. persicus			Nouri et al. (2017)
	Blastobotrys sp.	Y	Y	
Blastotrichum	*Blastotrichum* sp.			Vanderwolf et al. (2013)
Boeremia	*Boeremia exigua*	Y		Vanderwolf et al. (2013), Zhang (2019)
	Boeremia sp.	Y		Jiang et al. (2017a, b)
Botryosporium	*Botryosporium longibrachiatum*			Vanderwolf et al. (2013)
Botryotinia	*Botryotinia fuckeliana*	Y		Vanderwolf et al. (2013), Zhang et al. (2014), Zhang (2019)
Botryotrichum	*Botryotrichum murorum*	Y	Y	Vanderwolf et al. (2013)
Botrytis	*Botrytis cinerea*	Y		Vanderwolf et al. (2013), Ogórek et al. (2014a, b, c, 2016b, d, 2017), Man et al. (2015), Pusz et al. (2017, 2018a, b), Nováková et al. (2018), Ogórek (2018a, b), Ogórek et al. (2018), Pusz et al. (2018a), Popkova and Mazina (2019)
	Botrytis sp.			Vanderwolf et al. (2013), Leplat et al. (2018)
Boudiera	*Boudiera* sp.			Vanderwolf et al. (2013)
Brachiosphaera	*Brachiosphaera jamaicensis*			Vanderwolf et al. (2013)
Brachyconidiella	*Brachyconidiella monilispora*			Brad et al. (2018)
Brachysporium	*Brachysporium echinoides*			Vanderwolf et al. (2013)
Brunneomyces	*Brunneomyces brunnescens*	Y		Zhang (2019)
Bulgaria	*Bulgaria inquinans*			Vanderwolf et al. (2013)
Byssochlamys	*Byssochlamys fulva*			Vanderwolf et al. (2013)
	Byssochlamys sp.			Vanderwolf et al. (2013)
Cadophora	*Cadophora fastigiata*	Y		Out et al. (2016), Zhang (2019)
	C. malorum			Nováková et al. (2018)

Table 4 (continued)

Genus	Species	China[a]	This study[b]	References
	C. melinii			Vanderwolf et al. (2013)
	Cadophora sp.			Zhang et al. (2014), Vanderwolf et al. (2019)
Calcarisporiella	*Calcarisporiella* sp.			Vanderwolf et al. (2013)
Calcarisporium	*Calcarisporium sp.*	Y		Taylor et al. (2013), Zhang et al. (2017)
Camarosporium	*Camarosporium aequivocum*			Vanderwolf et al. (2013)
Candida	*Candida albicans*			Ogórek et al. (2013, 2016c, d), Vanderwolf et al. (2013), Kokurewicz et al. (2016)
	Ca. deformans			Vanderwolf et al. (2013)
	Ca. fimetaria var. fimetaria			Vanderwolf et al. (2013)
	Ca. glabrata			Vanderwolf et al. (2013)
	Ca. guilliermondii			Vanderwolf et al. (2013)
	Ca. lusitaniae			Vanderwolf et al. (2013)
	Ca. norvegica			Vanderwolf et al. (2013)
	Ca. palmioleophila			Vanderwolf et al. (2013)
	Ca. parapsilosis			Vanderwolf et al. (2013)
	Ca. pseudoglaebosa			Zhang et al. (2014)
	Ca. saitoana			Vanderwolf et al. (2013)
	Ca. tropicalis			Vanderwolf et al. (2013)
	Ca. viswanathii			Vanderwolf et al. (2013)
	Ca. zeylanoides			Connell and Staudigel (2013), Vanderwolf et al. (2013)
	Candida sp.	Y		Vanderwolf et al. (2013), Jiang et al. (2017a, b), Burow et al. (2019)
Capnodium	*Capnodium* sp.	Y		Zhang et al. (2017)
Cenococcum	*Cenococcum* sp.			Vanderwolf et al. (2013)
Cephalosporium	*Cephalosporium atrum*			Vanderwolf et al. (2013)
	Ce. lanosoniveum	Y		Zhang (2019)
	Cephalosporium sp.			Vanderwolf et al. (2013)
Cephalotheca	*Cephalotheca* sp.	Y	Y	
Cephalotrichiella	*Cephalotrichiella penicillata*	Y	Y	
Cephalotrichum	*Cephalotrichum asperulum*	Y	Y	
	Cep. castaneum	Y	Y	Vanderwolf et al. (2013)
	Cep. columnare	Y	Y	
	Cep. dendrocephalum	Y		Zhang (2019)
	Cep. guizhouense	Y		Jiang et al. (2017a, b)
	Cep. leave	Y		Jiang et al. (2017a, b)
	Cep. medium			Vanderwolf et al. (2013)
	Cep. microsporum	Y	Y	Vanderwolf et al. (2013)
	Cep. nanum	Y	Y	Vanderwolf et al. (2013), Zhang et al. (2017)
	Cep. oligotriphicum	Y		Jiang et al. (2017a, b)
	Cep. purpureofuscum	Y	Y	Vanderwolf et al. (2013)
	Cep. stemonitis	Y	Y	Vanderwolf et al. (2013, 2015, 2019), Nováková et al. (2018)
	Cep. verrucisporum	Y	Y	Zhang et al. (2017)
	Cephalotrichum sp.			Vanderwolf et al. (2019)
Ceratocystis	*Ceratocystis autographa*			Vanderwolf et al. (2013)
	Ceratocystis sp.			Vanderwolf et al. (2013)
Cercophora	*Cercophora solaris*	Y	Y	
	Cer. sparsa	Y	Y	
	Cercophora sp.	Y	Y	
Cercospora	*Cercospora* sp.			Vanderwolf et al. (2013)
Chaetomidium	*Chaetomidium arxii*	Y	Y	Zhang et al. (2017)
	Ch. fimeti			Vanderwolf et al. (2013)
	Chaetomidium sp.	Y		Vanderwolf et al. (2019), Zhang (2019)
Chaetomium	*Chaetomium ancistrocladum*	Y		Zhang (2019)
	Cha. crispatum	Y		Vanderwolf et al. (2013), Zhang et al. (2014), Ogórek et al. (2017), Zhang et al. (2017)
	Cha. elatum	Y	Y	Vanderwolf et al. (2013)
	Cha. fimeti			Vanderwolf et al. (2013)
	Cha. globosum	Y	Y	Vanderwolf et al. (2013), Kokurewicz et al. (2016), Zhang et al. (2017), Nováková et al. (2018), Pusz et al. (2018a), Popkova and Mazina (2019)
	Cha. heterothallicum	Y	Y	

Table 4 (continued)

Genus	Species	China[a]	This study[b]	References
	Cha. murorum	Y		Zhang et al. (2017)
	Cha. piluliferum	Y	Y	Vanderwolf et al. (2013), Mitova et al. (2017)
	Cha. spinosum			Vanderwolf et al. (2013)
	Cha. succineum			Vanderwolf et al. (2013)
	Cha. thermophilum			Vanderwolf et al. (2013)
	Cha. trigonosporum	Y		Zhang et al. (2017)
	Cha. udagawae	Y		Zhang et al. (2017)
	Chaetomium sp.	Y	Y	Taylor et al. (2013), Vanderwolf et al. (2013), Mitova et al. (2017), Zhang et al. (2017), Leplat et al. (2018), Popkova and Mazina (2019)
Chaetosphaeria	*Chaetosphaeria inaequalis*			Vanderwolf et al. (2013)
	Chae. vermicularioides	Y	Y	Vanderwolf et al. (2013)
Chalara	*Chalara holubovae*	Y		Zhang et al. (2017)
	Chal. microspora			Vanderwolf et al. (2013)
	Chalara sp.	Y	Y	Vanderwolf et al. (2013, 2019)
Chloridium	*Chloridium minus*			Vanderwolf et al. (2013)
	Chloridium sp.	Y	Y	Zhang et al. (2017)
	Chl. virescens			Vanderwolf et al. (2013)
Chrysosporium	*Chrysosporium carmichaelii*	Y	Y	
	Chr. chiropterorum			Vanderwolf et al. (2013)
	Chr. lobatum			Vanderwolf et al. (2013)
	Chr. merdarium			Vanderwolf et al. (2013), Dyląg et al. (2019)
	Chr. pallidum	Y	Y	
	Chr. pannicola			Vanderwolf et al. (2013)
	Chr. pseudomerdarium	Y		Vanderwolf et al. (2013), Zhang et al. (2017)
	Chr. speluncarum			Vanderwolf et al. (2013)
	Chr. tropicum			Vanderwolf et al. (2013)
	Chrysosporium sp.	Y	Y	Vanderwolf et al. (2013, 2015, 2019), Zhang et al. (2014, 2017)
Ciliciopodium	*Ciliciopodium hyalinum*	Y	Y	Burow et al. (2019)
Circinotrichum	*Circinotrichum* sp.			Vanderwolf et al. (2013)
Cladobotryum	*Cladobotryum* sp.			Nováková et al. (2018)
Cladophialophora	*Cladophialophora minutissima*			Burow et al. (2019)
	Cladophialophora sp.			Vanderwolf et al. (2013), Burow et al. (2019)
Cladorrhinum	*Cladorrhinum globisporum*	Y	Y	Zhang et al. (2017)
	Cladorrhinum sp.	Y		Zhang et al. (2017)
Cladosporium	*Cladosporium allicinum*			Nováková et al. (2018)
	Cl. angustisporum			Nováková et al. (2018)
	Cl. anthropophilum	Y		Jiang et al. (2017a, b)
	Cl. asperulatum	Y		Zhang (2019)
	Cl. cladosporioides	Y	Y	Taylor et al. (2013), Vanderwolf et al. (2013), Ogórek et al. (2014b, c, 2016c, d, 2017, 2018), Zhang et al. (2014), Pusz et al. (2015, 2018a, b), Yoder et al. (2015), Kokurewicz et al. (2016), Jiang et al. (2017a, b), Zhang et al. (2017), Nováková et al. (2018), Ogórek (2018a, b), Popkova and Mazina (2019)
	Cl. colombiae	Y		Zhang (2019)
	Cl. cucumerinum			Vanderwolf et al. (2013)
	Cl. grevilleae			Connell and Staudigel (2013)
	Cl. halotolerans	Y	Y	
	Cl. herbarum	Y		Ogórek et al. (2013, 2014a, b, c, 2016b, c), Taylor et al. (2013), Vanderwolf et al. (2013), Kokurewicz et al. (2016), Jiang et al. (2017a, b), Ogórek et al. (2017, 2018), Nováková et al. (2018), Ogórek (2018a), Pusz et al. (2018a), Popkova and Mazina (2019)
	Cl. linicola			Vanderwolf et al. (2013)
	Cl. macrocarpum			Vanderwolf et al. (2013), Ogórek et al. (2017, 2018), Nováková et al. (2018), Ogórek (2018b)
	Cl. oxysporum	Y		Vanderwolf et al. (2013), Popović et al. (2015), Nováková et al. (2018), Zhang (2019)
	Cl. paracladosporioides			Nováková et al. (2018)
	Cl. perangustum	Y		Jiang et al. (2017a, b)
	Cl. pseudocladosporioides			Belyagoubi et al. (2018)
	Cl. rectoides	Y		Jiang et al. (2017a, b)

Table 4 (continued)

Genus	Species	China[a]	This study[b]	References
	Cl. scabrellum	Y		Jiang et al. (2017a, b)
	Cl. sphaerospermum	Y	Y	Connell and Staudigel (2013), Vanderwolf et al. (2013), Popović et al. (2015), Zhang et al. (2017), Nováková et al. (2018), Popkova and Mazina (2019)
	Cl. spongiosum			Vanderwolf et al. (2013)
	Cl. subuliforme	Y		Zhang (2019)
	Cl. tenuissimum	Y	Y	Vanderwolf et al. (2013), Jiang et al. (2017a, b)
	Cl. uredinicola	Y		Man et al. (2015), Pusz et al. (2015)
	Cl. variabile			Mitova et al. (2017), Nováková et al. (2018)
	Cladosporium sp.	Y		Connell and Staudigel (2013), Vanderwolf et al. (2013, 2015, 2019), Martin-Sanchez et al. (2014), Popović et al. (2015), Out et al. (2016), Jiang et al. (2017a, b), Bercea et al. (2018), Leplat et al. (2018)
Clavariopsis	*Clavariopsis azlanii*			Vanderwolf et al. (2013)
Claviceps	*Claviceps purpurea*			Vanderwolf et al. (2013)
	Claviceps sp.	Y	Y	
Clavispora	*Clavispora lusitaniae*			Connell and Staudigel (2013)
Clonostachys	*Clonostachys candelabrum*			Vanderwolf et al. (2013)
	Clo. intermedia	Y	Y	
	Clo. phyllophila	Y	Y	
	Clo. rhizophaga	Y	Y	
	Clo. rogersoniana	Y	Y	
	Clo. rosea	Y	Y	Taylor et al. (2013), Vanderwolf et al. (2013), Kokurewicz et al. (2016), Ogórek et al. (2016b, d), Jiang et al. (2017a, b), Zhang et al. (2017), Nováková et al. (2018), Pusz et al. (2018a)
	Clonostachys sp.	Y	Y	Vanderwolf et al. (2013, 2015), Jiang et al. (2017a, b), Zhang et al. (2017)
Coccidioides	*Coccidioides immitis*			Vanderwolf et al. (2013)
Cochliomyces	*Cochliomyces trinitatis*			Vanderwolf et al. (2013)
Collariella	*Collariella bostrychodes*	Y		Vanderwolf et al. (2013), Man et al. (2015), Zhang et al. (2017)
	Co. quadrum	Y		Zhang et al. (2017)
Colletotrichum	*Colletotrichum acutatum*			Vanderwolf et al. (2013)
	Col. fioriniae	Y	Y	
	Col. gloeosporioides	Y	Y	Zhang et al. (2017)
	Col. karstii	Y		Zhang et al. (2017)
	Col. pisi	Y	Y	
	Colletotrichum sp.	Y		Vanderwolf et al. (2013), Jiang et al. (2017a, b), Zhang et al. (2017), Leplat et al. (2018)
Compsomyces	*Compsomyces lestevi*			Vanderwolf et al. (2013)
Coniochaeta	*Coniochaeta hoffmannii*	Y	Y	
	Con. mutabilis	Y	Y	
	Coniochaeta sp.	Y	Y	
Coniothyrium	*Coniothyrium* sp.			Martin-Sanchez et al. (2014)
Conoideocrella	*Conoideocrella luteorostrata*			Vanderwolf et al. (2013)
Corallinopsis	*Corallinopsis pilulifera*			Vanderwolf et al. (2013)
Cordyceps	*Cordyceps cicadae*	Y	Y	
	Cor. militaris	Y	Y	
	Cor. odyneri			Vanderwolf et al. (2013)
	Cor. polyarthra	Y		Zhang et al. (2017)
	Cor. riverae			Vanderwolf et al. (2013)
	Cor. sphingum			Vanderwolf et al. (2013)
	Cor. tenuipes	Y	Y	
	Cordyceps sp.			Vanderwolf et al. (2013, 2015)
Corynespora	*Corynespora* sp.	Y		Zhang et al. (2017)
Cosmospora	*Cosmospora berkeleyana*			Vanderwolf et al. (2013)
	Cos. butyri			Vanderwolf et al. (2013)
	Cos. diminuta	Y	Y	
	Cos. viridescens			Burow et al. (2019)
	Cosmospora sp.	Y	Y	Vanderwolf et al. (2013), Jiang et al. (2017a, b)
Creosphaeria	*Creosphaeria sassafras*	Y		Zhang (2019)
Cryomyces	*Cryomyces* sp.			Vanderwolf et al. (2015)
Ctenomyces	*Ctenomyces serratus*			Vanderwolf et al. (2013)

Table 4 (continued)

Genus	Species	China[a]	This study[b]	References
	Ct. vellereus			Vanderwolf et al. (2013)
Culicinomyces	*Culicinomyces* sp.			Vanderwolf et al. (2019)
Cumuliphoma	*Cumuliphoma omnivirens*	Y	Y	
Curreya	*Curreya* sp.	Y	Y	
Curvularia	*Curvularia brachyspora*			Vanderwolf et al. (2013)
	Cu. eragrostidis			Vanderwolf et al. (2013)
	Cu. hawaiiensis			Vanderwolf et al. (2013)
	Cu. lunata	Y	Y	Connell and Staudigel (2013), Vanderwolf et al. (2013)
	Cu. senegalensis			Vanderwolf et al. (2013)
	Cu. trifolii	Y	Y	
	Curvularia sp.			Taylor et al. (2013), Vanderwolf et al. (2013)
Cylindrocarpon	*Cylindrocarpon didymum*			Vanderwolf et al. (2013), Nováková et al. (2018)
	Cy. obtusiusculum			Nováková et al. (2018)
	Cy. olidum	Y		Jiang et al. (2017a, b), Zhang et al. (2017)
	Cylindrocarpon sp.	Y	Y	Vanderwolf et al. (2013, 2019), Zhang et al. (2017)
Cylindrocephalum	*Cylindrocephalum stellatum*			Vanderwolf et al. (2013)
Cylindrocladiella	*Cylindrocladiella lanceolata*	Y	Y	
	Cyl. stellenboschensis	Y	Y	
Cylindrocladium	*Cylindrocladium scoparium*			Vanderwolf et al. (2013)
	Cylindrocladium sp.			Vanderwolf et al. (2013)
Cylindrodendrum	*Cylindrodendrum album*			Vanderwolf et al. (2013)
	Cyli. alicantinum	Y	Y	
Cyphellophora	*Cyphellophora laciniata*			Connell and Staudigel (2013)
	Cyp. olivacea			Vanderwolf et al. (2013)
Dactylaria	*Dactylaria lanosa*			Vanderwolf et al. (2013)
	Dactylaria sp.	Y	Y	
Dactylella	*Dactylella* sp.			Vanderwolf et al. (2013)
Dactylonectria	*Dactylonectria macrodidyma*			Vanderwolf et al. (2013)
Dactylosporium	*Dactylosporium* sp.			Vanderwolf et al. (2013)
Daldinia	*Daldinia concentrica*			Vanderwolf et al. (2013)
Dasyscyphella	*Dasyscyphella* sp.			Vanderwolf et al. (2013)
Debaryomyces	*Debaryomyces hansenii*			Vanderwolf et al. (2013)
	D. maramus			Zhang et al. (2014)
	D. nepalensis			Vanderwolf et al. (2013)
	D. prosopidis			Vanderwolf et al. (2013)
	D. psychrosporus			Vanderwolf et al. (2013)
	D. singareniensis			Vanderwolf et al. (2013)
	Debaryomyces sp.			Vanderwolf et al. (2013), Martin-Sanchez et al. (2014), Mitova et al. (2017)
	D. subglobosus			Vanderwolf et al. (2013)
Delitschia	*Delitschia* sp.			Vanderwolf et al. (2013)
Dematioscypha	*Dematioscypha catenata*			Vanderwolf et al. (2013)
Dendrosporium	*Dendrosporium lobatum*			Vanderwolf et al. (2013)
Dendryphion	*Dendryphion* sp.			Vanderwolf et al. (2013)
Dialonectria	*Dialonectria* sp.	Y	Y	
Diaporthe	*Diaporthe eres*	Y		Zhang (2019)
	Di. fukushii	Y		Zhang (2019)
	Di. melonis	Y		Jiang et al. (2017a, b)
	Diaporthe nobilis	Y		Zhang (2019)
	Di. phaseolorum	Y	Y	
	Di. phoenicicola	Y		Zhang et al. (2017)
	Di. vaccinii	Y		Zhang (2019)
	Diaporthe sp.	Y	Y	
Diatrype	*Diatrype palmicola*	Y		Zhang (2019)
	Dia. stigma	Y		Zhang (2019)
Diatrypella	*Diatrypella major*	Y	Y	
	Dia. pulvinata	Y	Y	
Dichotomopilus	*Dichotomopilus funicola*	Y	Y	Vanderwolf et al. (2013)
	Dic. indicus			Vanderwolf et al. (2013)

Table 4 (continued)

Genus	Species	China[a]	This study[b]	References
Dictyosporium	*Dictyosporium elegans*			Vanderwolf et al. (2013)
	Dictyosporium sp.			Vanderwolf et al. (2013)
	Dictyosporium toruloides			Vanderwolf et al. (2013)
Didymella	*Didymella bellidis*	Y	Y	
	Did. glomerata			Vanderwolf et al. (2013)
	Did. macrostoma	Y		Vanderwolf et al. (2013), Zhang et al. (2017)
	Did. pinodella	Y	Y	
	Did. rhei	Y	Y	
	Didymella sp.	Y	Y	Vanderwolf et al. (2013), Jiang et al. (2017a, b)
Didymosphaeria	*Didymosphaeria variabile*	Y		Zhang (2019)
	Didymosphaeria sp.	Y	Y	
Diplococcium	*Diplococcium* sp.			Vanderwolf et al. (2015)
Diplodina	*Diplodina* sp.			Vanderwolf et al. (2013)
Diplopodomyces	*Diplopodomyces callipodos*			Vanderwolf et al. (2013)
Dipodascus	*Dipodascus fermentans*			Vanderwolf et al. (2013)
	Dip. geotrichum	Y	Y	Vanderwolf et al. (2013), Yoder et al. (2015), Zhang et al. (2017), Nováková et al. (2018)
Discosia	*Discosia pseudoartocreas*	Y	Y	
	Discosia sp.			Ogórek et al. (2017, 2018a), Ogórek (2018a, b)
Discostroma	*Discostroma corticola*	Y	Y	
Diutina	*Diutina catenulata*			Vanderwolf et al. (2013)
	Diu. rugosa			Vanderwolf et al. (2013)
Doratomyces	*Doratomyces microsporus*			Mitova et al. 2017
	Doratomyces sp.	Y		Vanderwolf et al. (2013), Martin-Sanchez et al. (2014), Zhang et al. (2014, 2017), Leplat et al. (2018)
Dothidella	*Dothidella ulmi*	Y	Y	
Drechslera	*Drechslera avenacea*			Vanderwolf et al. (2013)
	Drechslera sp.			Vanderwolf et al. (2013), Leplat et al. (2018)
Echinobotryum	*Echinobotryum parasitans*			Vanderwolf et al. (2013)
	E. subterraneum			Vanderwolf et al. (2013)
	Echinobotryum sp.			Vanderwolf et al. (2013)
Emericella	*Emericella* sp.			Vanderwolf et al. (2013)
Emericellopsis	*Emericellopsis minima*	Y	Y	
	Em. terricola			Vanderwolf et al. (2013)
	Emericellopsis sp.	Y		Man et al. (2015)
Emmonsia	*Emmonsia* sp.	Y	Y	
Endophoma	*Endophoma elongata*			Vanderwolf et al. (2013)
Endophragmiella	*Endophragmiella* sp.			Vanderwolf et al. (2013)
Engyodontium	*Engyodontium aranearum*			Vanderwolf et al. (2013)
	En. parvisporum			Vanderwolf et al. (2013)
	En. rectidentatum			Vanderwolf et al. (2013)
	Engyodontium sp.			Vanderwolf et al. (2013), Leplat et al. (2018)
Epicoccum	*Epicoccum draconis*	Y	Y	
	Ep. nigrum	Y	Y	Connell and Staudigel (2013), Vanderwolf et al. (2013), Martin-Sanchez et al. (2014), Ogórek et al. (2014a, b, c, 2016b, c, d, 2017, 2018), Pusz et al. (2015), Zhang et al. (2017), Nováková et al. (2018), Pusz et al. (2018a), Tavares et al. (2018)
	Ep. plurivorum	Y	Y	
	Epicoccum sp.			Vanderwolf et al. (2013), Leplat et al. (2018)
Eremomyces	*Eremomyces* sp.			Vanderwolf et al. (2013, 2015)
Erysiphe	*Erysiphe polygoni*			Connell and Staudigel (2013)
Eupenicillium	*Eupenicillium* sp.			Vanderwolf et al. (2013)
Eutypella	*Eutypella citricola*	Y	Y	
	Eu. scoparia	Y		Jiang et al. (2017a, b)
	Eurotium sp.	Y		Vanderwolf et al. (2013), Zhang (2019)
Eurotium	*Eurotium* sp.			Vanderwolf et al. (2013)
Exophiala	*Exophiala castellanii*			Vanderwolf et al. (2013)
	Ex. moniliae			Vanderwolf et al. (2013)
	Ex. pisciphila	Y	Y	

Table 4 (continued)

Genus	Species	China[a]	This study[b]	References
	Ex. salmonis			Mitova et al. (2017)
	Ex. xenobiotica			Ogórek (2018a, b)
	Exophiala sp.	Y	Y	Vanderwolf et al. (2013)
Farrowia	*Farrowia seminuda*			Vanderwolf et al. (2013)
Forliomyces	*Forliomyces* sp.			Leplat et al. (2018)
Fusariella	*Fusariella* sp.			Vanderwolf et al. (2013)
Fusarium	*Fusarium asiaticum*	Y		Jiang et al. (2017a, b)
	F. avenaceum			Vanderwolf et al. (2013), Ogórek et al. (2014b)
	F. chlamydosporum	Y	Y	Vanderwolf et al. (2013), Nováková et al. (2018)
	F. coeruleum			Vanderwolf et al. (2013)
	F. culmorum			Vanderwolf et al. (2013), Ogórek et al. (2014b, c), Pusz et al. (2018b)
	F. dimerum			Vanderwolf et al. (2013)
	F. equiseti	Y	Y	Vanderwolf et al. (2013), Ogórek et al. (2014c, 2016c), Pusz et al. (2018a)
	F. fujikuroi	Y	Y	Vanderwolf et al. (2013), Zhang et al. (2017)
	F. graminearum	Y	Y	Ogórek et al. (2013), Jiang et al. (2017a, b), Zhang et al. (2017)
	F. incarnatum	Y	Y	Vanderwolf et al. (2013)
	F. lateritium	Y	Y	Vanderwolf et al. (2013), Ogórek (2018b)
	F. merismoides	Y		Zhang et al. (2017)
	F. nematophilum	Y		Jiang et al. (2017a, b)
	F. oxysporum	Y	Y	Ogórek et al. (2013, 2014b, c), Taylor et al. (2013), Vanderwolf et al. (2013), Kokurewicz et al. (2016), Jiang et al. (2017a, b), Nováková et al. (2018), Pusz et al. (2018b), Popkova and Mazina (2019)
	F. poae			Ogórek et al. (2014c)
	F. proliferatum	Y	Y	Vanderwolf et al. (2013)
	F. roseum	Y	Y	Vanderwolf et al. (2013), Zhang et al. (2017)
	F. sacchari	Y	Y	
	F. solani	Y	Y	Taylor et al. (2013), Vanderwolf et al. (2013), Man et al. (2015), Jiang et al. (2017a, b), Zhang et al. (2017), Nováková et al. (2018), Popkova and Mazina (2019)
	F. sporotrichioides			Vanderwolf et al. (2013), Ogórek et al. (2014c), Popkova and Mazina (2019)
	F. subglutinans			Vanderwolf et al. (2013)
	F. thapsinum	Y		Jiang et al. (2017a, b)
	F. tricinctum	Y	Y	
	Fusarium sp.	Y	Y	Vanderwolf et al. (2013, 2015, 2019), Yoder et al. (2015), Zhang et al. (2017), Nováková et al. (2018), Leplat et al. (2018), Pusz et al. (2018a), Popkova and Mazina (2019)
Fusicolla	*Fusicolla matuoi*	Y	Y	
	Fu. merismoides			Vanderwolf et al. (2013), Zhang et al. (2014)
Gabarnaudia	*Gabarnaudia* sp.			Leplat et al. (2018)
Gamsia	*Gamsia aggregata*	Y	Y	
	G. columbina	Y	Y	
	G. simplex	Y	Y	Jiang et al. (2017a, b)
Gamszarea	***Gamszarea humicola***	Y	Y	
	Ga. kalimantanensis	Y	Y	Vanderwolf et al. (2013)
	Ga. lunata	Y	Y	
	Ga. microspora	Y	Y	
Geomyces	*Geomyces auratus*	Y	Y	
	Ge. vinaceus			Vanderwolf et al. (2013)
	Geomyces sp.	Y	Y	Vanderwolf et al. (2013), Zhang et al. (2014), Man et al. (2015), Leplat et al. (2018), Burow et al. (2019), Pfendler et al. (2019)
Geosmithia	*Geosmithia namyslowskii*			Vanderwolf et al. (2013)
	Geo. putterillii			Vanderwolf et al. (2013)
	Geosmithia sp.			Leplat et al. (2018)
Geotrichum	*Geotrichum* sp.			Taylor et al. (2013), Vanderwolf et al. (2013)
Gibellula	*Gibellula* sp.			Vanderwolf et al. (2013)
Gibellulopsis	*Gibellulopsis nigrescens*	Y		Connell and Staudigel (2013), Vanderwolf et al. (2013), Zhang (2019)
	Gibellulopsis sp.	Y		Jiang et al. (2017a, b)
Gilmaniella	*Gilmaniella* sp.			Vanderwolf et al. (2013)
Gliocephalotrichum	*Gliocephalotrichum simplex*			Vanderwolf et al. (2013)
Gliocladiopsis	*Gliocladiopsis* sp.	Y		Zhang (2019)

Table 4 (continued)

Genus	Species	China[a]	This study[b]	References
Gliocladium	*Gliocladium atrum*			Vanderwolf et al. (2013)
	Gl. cibotii			Vanderwolf et al. (2013)
	Gl. roseum	Y		Jiang et al. (2017a, b)
	Gliocladium sp.			Vanderwolf et al. (2013)
Gliomastix	*Gliomastix luzulae*	Y	Y	
	Gliomastix sp.	Y	Y	Vanderwolf et al. (2013), Leplat et al. (2018)
	Gli. murorum	Y		Jiang et al. (2017a, b), Mitova et al. (2017)
Gnomoniopsis	*Gnomoniopsis* sp.	Y		Zhang (2019)
Graphiothecium	*Graphiothecium* sp.			Vanderwolf et al. (2013)
Graphium	*Graphium penicillioides*	Y	Y	Vanderwolf et al. (2013)
Guanomyces	*Guanomyces polythrix*			Vanderwolf et al. (2013)
Gymnascella	*Gymnascella citrina*			Vanderwolf et al. (2013)
	Gy. hyalinospora			Vanderwolf et al. (2013)
	Gymnascella sp.			Vanderwolf et al. (2013), Zhang (2019)
Gymnoascoideus	*Gymnoascoideus* sp.			Vanderwolf et al. (2013)
Gymnoascus	*Gymnoascus exasperatus*	Y	Y	Zhang et al. (2017)
	Gym. flavus	Y	Y	
	Gym. intermedius			Vanderwolf et al. (2013)
	Gym. reessii	Y	Y	Vanderwolf et al. (2013, 2019), Mitova et al. (2017), Zhang et al. (2017)
	Gym. udagawae	Y	Y	
	Gymnoascus sp.			Vanderwolf et al. (2013)
Gymnostellatospora	*Gymnostellatospora* sp.			Vanderwolf et al. (2013)
Gyrothrix	*Gyrothrix sp.*	Y		Zhang et al. (2017)
Halenospora	*Halenospora varia*			Zhang et al. (2014)
Hamigera	*Hamigera ingelheimensis*			Vanderwolf et al. (2013)
Hanseniaspora	*Hanseniaspora osmophila*			Vanderwolf et al. (2013)
	Hanseniaspora sp.			Vanderwolf et al. (2013)
Hansfordia	*Hansfordia* sp.			Connell and Staudigel (2013)
Harzia	*Harzia acremonioides*			Vanderwolf et al. (2013)
Helicogermslita	*Helicogermslita* sp.			Vanderwolf et al. (2013)
Helicoma	*Helicoma* sp.			Vanderwolf et al. (2013)
Helicomyces	*Helicomyces* sp.			Vanderwolf et al. (2013)
Helminthosporium	*Helminthosporium* sp.			Vanderwolf et al. (2013)
	H. trichellum			Vanderwolf et al. (2013)
Helotium	*Helotium* sp.			Vanderwolf et al. (2013)
Herpomyces	*Herpomyces arietinus*			Vanderwolf et al. (2013)
Herpotrichia	*Herpotrichia* sp.			Vanderwolf et al. (2013)
Hirsutella	*Hirsutella dipterigena*			Vanderwolf et al. (2013)
	Hi. guignardii			Vanderwolf et al. (2013)
	Hirsutella sp.			Vanderwolf et al. (2013), Martin-Sanchez et al. (2014)
Hormiactis	*Hormiactis candida*			Vanderwolf et al. (2013)
	Hormiactis sp.			Vanderwolf et al. (2013), Nováková et al. (2018)
Hormiscium	*Hormiscium* sp.			Vanderwolf et al. (2013)
Hormodendrum	*Hormodendrum* sp.			Vanderwolf et al. (2013)
Hormographiella	*Hormographiella* sp.			Vanderwolf et al. (2015)
Humaria	*Humaria jeannelii*			Vanderwolf et al. (2013)
Humicola	*Humicola brunnea*			Vanderwolf et al. (2013)
	Hu. fuscoatra	Y	Y	Vanderwolf et al. (2013), Nováková et al. (2018), Pusz et al. (2018a)
	Hu. grisea			Vanderwolf et al. (2013), Pusz et al. (2015), Mitova et al. (2017)
	Hu. limonisporum	Y		Zhang et al. (2017)
	Hu. nigrescens			Vanderwolf et al. (2013)
	Humicola sp.	Y	Y	Vanderwolf et al. (2013, 2015, 2019), Popkova and Mazina (2019)
Hyalopus	*Hyalopus curtipes*			Vanderwolf et al. (2013)
Hyaloseta	*Hyaloseta sp.*	Y	Y	
Hydropisphaera	*Hydropisphaera* sp.			Vanderwolf et al. (2013)
Hyphopichia	*Hyphopichia burtonii*			Vanderwolf et al. (2013)
Hyphozyma	*Hyphozyma* sp.			Vanderwolf et al. (2015, 2019)
Hypocrea	*Hypocrea lactea*	Y		Zhang (2019)

Table 4 (continued)

Genus	Species	China[a]	This study[b]	References
	Hy. pachybasioides	Y		Zhang et al. (2014), Pusz et al. (2015), Zhang (2019)
	Hypocrea sp.			Vanderwolf et al. (2013)
Hypomyces	*Hypomyces rosellus*			Vanderwolf et al. (2013)
	Hypomyces sp.			Vanderwolf et al. (2013)
Hypoxylon	*Hypoxylon fragiforme*			Vanderwolf et al. (2013)
	Hy. monticulosum	Y	Y	
	Hy. perforatum	Y		Zhang et al. (2017)
	Hypoxylon sp.			Vanderwolf et al. (2013)
Idriella	*Idriella lunata*	Y	Y	
	Idriella sp.	Y	Y	
Ilyonectria	*Ilyonectria destructans*	Y	Y	Vanderwolf et al. (2013)
	I. radicicola	Y	Y	
	I. robusta	Y		Zhang et al. (2017)
	Ilyonectria sp.	Y		Zhang et al. (2017)
Inaequalispora	*Inaequalispora prestonii*	Y		Zhang (2019)
	Inaequalispora sp.	Y		Zhang (2019)
Infundichalara	*Infundichalara microchona*			Vanderwolf et al. (2013)
Isaria	*Isaria amoene-rosea*			Vanderwolf et al. (2013)
	Is. cateniannulata	Y		Zhang (2019)
	Is. farinosa	Y		Vanderwolf et al. (2013, 2015), Zhang et al. (2017), Pusz et al. (2018a)
	Is. fumosorosea	Y	Y	Vanderwolf et al. (2013), Jiang et al. (2017a, b), Zhang et al. (2017)
	Isaria sp.			Vanderwolf et al. (2013, 2019), Leplat et al. (2018)
Isthmolongispora	*Isthmolongispora quadricellularis*			Vanderwolf et al. (2013)
Jackrogersella	*Jackrogersella sp.*	Y	Y	
Jattaea	***Jattaea reniformis***	Y	Y	
Juxtiphoma	*Juxtiphoma eupyrena*	Y	Y	Vanderwolf et al. (2013)
Keissleriella	*Keissleriella* sp.			Vanderwolf et al. (2013)
Kernia	*Kernia columnaris*	Y		Zhang (2019)
	Kernia sp.	Y		Vanderwolf et al. (2013), Zhang et al. (2014, 2019)
)Kretzschmaria	*Kretzschmaria deusta*			Vanderwolf et al. (2013)
Lambertella	*Laboulbenia arawaka*	Y		Zhang (2019)
Laboulbenia	*Laboulbenia arawaka*			Vanderwolf et al. (2013)
	L. bolivarii			Vanderwolf et al. (2013)
	L. bordonii			Vanderwolf et al. (2013)
	L. cantabrica			Vanderwolf et al. (2013)
	L. coiffaitii			Vanderwolf et al. (2013)
	L. flagellata			Vanderwolf et al. (2013)
	L. lecoareri			Vanderwolf et al. (2013)
	L. nebriae			Vanderwolf et al. (2013)
	L. orghidanii			Vanderwolf et al. (2013)
	L. picardii			Vanderwolf et al. (2013)
	L. polyphaga			Vanderwolf et al. (2013)
	L. sbordonii			Vanderwolf et al. (2013)
	L. shanorii			Vanderwolf et al. (2013)
	L. stilicicola			Vanderwolf et al. (2013)
	L. subterranea			Vanderwolf et al. (2013)
	L. vignae			Vanderwolf et al. (2013)
	L. vulgaris			Vanderwolf et al. (2013)
	Laboulbenia sp.			Vanderwolf et al. (2013)
Lachancea	*Lachancea kluyveri*			Vanderwolf et al. (2013)
	La. thermotolerans			Vanderwolf et al. (2013)
Lachnea	*Lachnea spelaea*			Vanderwolf et al. (2013)
Lachnellula	*Lachnellula resinaria*			Vanderwolf et al. (2013)
Lachnum	*Lachnum brevipilosum*			Vanderwolf et al. (2013)
Latorua	*Latorua caligans*	Y	Y	Zhang et al. (2017)
Lecanicillium	*Le. antillanum*			Vanderwolf et al. (2013)
	Le. aphanocladii	Y		Tavares et al. (2018), Cardoso et al. (2019), Zhang (2019)
	Le. dimorphum			Nováková et al. (2018)

Table 4 (continued)

Genus	Species	China[a]	This study[b]	References
	Le. fusisporum	Y		Vanderwolf et al. (2013), Zhang et al. (2017)
	Le. magnisporum	Y	Y	
	Le. muscarium			Vanderwolf et al. (2013)
	Le. psalliotae			Vanderwolf et al. (2013), Nováková et al. (2018)
	Lecanicillium sp.	Y	Y	Vanderwolf et al. (2013), Man et al. (2015), Leplat et al. (2018)
Lectera	*Lectera colletotrichoides*			Connell and Staudigel (2013)
Lecythophora	*Lecythophora* sp.			Vanderwolf et al. (2019)
Lepidosphaeria	*Lepidosphaeria* sp.	Y	Y	
Leptobacillium	*Leptobacillium leptobactrum*			Vanderwolf et al. (2013), Martin-Sanchez et al. (2014), Zhang et al. (2014), Leplat et al. (2018), Burow et al. (2019)
Leptodontidium	*Leptodontidium trabinellum*			Vanderwolf et al. (2013)
Leptosphaeria	*Leptosphaeria fuscella*	Y		Zhang (2019)
	Le. maculans			Vanderwolf et al. (2013)
	Leptosphaeria sp.	Y	Y	Vanderwolf et al. (2013), Jiang et al. (2017a, b), Zhang et al. (2017)
Leptosphaerulina	*Leptosphaerulina chartarum*	Y		Jiang et al. (2017a, b)
	Leptosphaerulina sp.			Vanderwolf et al. (2013)
Letendraea	*Letendraea helminthicola*	Y		Zhang (2019)
Leuconeurospora	*Leuconeurospora capsici*			Vanderwolf et al. (2013, 2015, 2019), Malloch et al. (2016)
	Leu. polypaeciloides			Vanderwolf et al. (2013, 2015, 2019), Malloch et al. (2016)
	Leu. pulcherrima			Zhang et al. (2014)
	Leuconeurospora sp.			Vanderwolf et al. (2013)
Leucothecium	*Leucothecium emdenii*	Y	Y	
Linderina	*Linderina pennispora*			Vanderwolf et al. (2013)
Lophiostoma	*Lophiostoma corticola*	Y	Y	Zhang et al. (2017)
	Lophiostoma sp.	Y	Y	Jiang et al. (2017a, b), Zhang et al. (2017)
Lophiotrema	*Lophiotrema* sp.	Y	Y	
Malbranchea	*Malbranchea aurantiaca*			Vanderwolf et al. (2013)
	M. gypsea			Vanderwolf et al. (2013)
	Malbranchea sp.	Y	Y	Vanderwolf et al. (2013)
Mammaria	*Mammaria echinobotryoides*			Vanderwolf et al. (2013, 2019)
	Mammaria sp.			Vanderwolf et al. (2015)
Mariannaea	*Mariannaea camptospora*			Vanderwolf et al. (2013)
	Ma. elegans	Y	Y	Vanderwolf et al. (2013)
	Ma. nipponica			Vanderwolf et al. (2013)
Massarina	*Massarina igniaria*	Y	Y	
	Massarina sp.	Y	Y	Vanderwolf et al. (2013), Zhang et al. (2017)
Melanconium	*Melanconium* sp.	Y	Y	
Melanocarpus	*Melanocarpus albomyces*			Vanderwolf et al. (2013)
Melanospora	*Melanospora* sp.			Vanderwolf et al. (2013)
	Me. zamiae			Vanderwolf et al. (2013)
Memnoniella	*Memnoniella* sp.	Y	Y	
Menispora	*Menispora cobaltina*			Vanderwolf et al. (2013)
Metacordyceps	*Metacordyceps chlamydosporia*	Y	Y	Vanderwolf et al. (2013), Man et al. (2015), Nováková et al. (2018)
Metapochonia	*Metapochonia bulbillosa*	Y	Y	Zhang et al. (2017)
	Met. rubescens	Y		Zhang et al. (2017)
	Met. suchlasporia	Y	Y	Vanderwolf et al. (2013), Martin-Sanchez et al. (2014)
	Met. variabilis	Y	Y	Zhang et al. (2017)
	Metapochonia sp.			Mitova et al. (2017)
Metarhizium	*Metarhizium anisopliae*	Y	Y	Vanderwolf et al. (2013), Zhang et al. (2017), Nováková et al. (2018)
	Meta. marquandii	Y	Y	Vanderwolf et al. (2013), Man et al. (2015), Jiang et al. (2017a, b), Nováková et al. (2018)
	Meta. rileyi	Y		Vanderwolf et al. (2013), Zhang (2019)
	Meta. robertsii	Y		Zhang (2019)
	Metarhizium sp.	Y	Y	Vanderwolf et al. (2013), Jiang et al. (2017a, b), Leplat et al. (2018), Bercea et al. (2018)
Metschnikowia	*Metschnikowia pulcherrima*			Vanderwolf et al. (2013)
Meyerozyma	*Meyerozyma caribbica*			Jacobs et al. (2017)
Microascus	*Microascus anfractus*	Y	Y	Zhang et al. (2017)
	Mi. boulangeri			Vanderwolf et al. (2013)

Table 4 (continued)

Genus	Species	China[a]	This study[b]	References
	Mi. brevicaulis	Y	Y	Vanderwolf et al. (2013), Yoder et al. (2015), Pusz et al. (2018a)
	Mi. chartarum	Y	Y	Vanderwolf et al. (2013), Zhang et al. (2017)
	Mi. cirrosus	Y	Y	Vanderwolf et al. (2013)
	Mi. collaris	Y	Y	
	Mi. croci	Y	Y	Vanderwolf et al. (2013)
	Mi. globulosus	Y	Y	Zhang et al. (2017)
	Mi. levis	Y	Y	
	Mi. longirostris			Vanderwolf et al. (2013)
	Mi. murinus	Y	Y	
	Mi. paisii	Y	Y	
	Mi. sparsimycelialis	Y	Y	
	Mi. superficialis	Y	Y	
	Mi. trigonus	Y	Y	
	Microascus sp.			Vanderwolf et al. (2013, 2019)
Microdiplodia	*Microdiplodia miyakei*	Y		Man et al. (2015), Zhang (2019)
	Microdiplodia sp.	Y		Zhang (2019)
Microdochium	*Microdochium bolleyi*	Y	Y	Pusz et al. (2018a)
	Mic. chrysanthemoides	Y		Zhang et al. (2017)
	Mic. fisheri	Y		Zhang (2019)
	Mic. lycopodinum	Y		Jiang et al. (2017a, b)
	Mic. nivale			Vanderwolf et al. (2013)
	Mic. seminicola			Ogórek et al. (2017, 2018), Ogórek (2018b)
Microsphaeropsis	*Microsphaeropsis arundinis*	Y	Y	Zhang et al. (2017)
Microsporum	*Microsporum canis*			Vanderwolf et al. (2013)
	Micr. gypseum			Vanderwolf et al. (2013), Nováková et al. (2018)
	Microsporum sp.			Vanderwolf et al. (2013)
Monascus	*Monascus ruber*			Vanderwolf et al. (2013)
	Mo. purpureus	Y		Man et al. (2015)
Monocillium	*Monocillium granulatum*			Vanderwolf et al. (2013)
	Monocillium sp.	Y	Y	Vanderwolf et al. (2013)
Monographella	*Monographella* sp.	Y		Zhang (2019)
Monosporium	*Monosporium* sp.			Vanderwolf et al. (2013)
Montagnula	*Montagnula* sp.	Y	Y	
Myceliophthora	*Myceliophthora* sp.			Vanderwolf et al. (2013, 2015), Nováková et al. (2018)
Mycoarthris	*Mycoarthris* sp.			Vanderwolf et al. (2013)
Mycogone	*Mycogone nigra*			Vanderwolf et al. (2013)
	Mycogone sp.			Vanderwolf et al. (2013)
Mycosphaerella	*Mycosphaerella polygoni-cuspidati*	Y		Zhang (2019)
	Mycosphaerella sp.	Y		Zhang (2019)
Myriodontium	*Myriodontium keratinophilum*	Y	Y	Man et al. (2015), Zhang et al. (2017), Nováková et al. (2018)
	Myriodontium sp.	Y	Y	Leplat et al. (2018)
Myrmecridium	*Myrmecridium schulzeri*	Y	Y	
Myrothecium	*Myrothecium* sp.	Y	Y	Vanderwolf et al. (2013), Zhang et al. (2017)
Myxotrichum	*Myxotrichum chartarum*			Vanderwolf et al. (2013)
	My. deflexum	Y	Y	Vanderwolf et al. (2013)
	My. setosum			Vanderwolf et al. (2013)
	Myxotrichum sp.			Vanderwolf et al. (2013, 2015), Zhang et al. (2014)
Nannizzia	*Nannizzia fulva*			Vanderwolf et al. (2013)
Nectria	*Nectria ellisii*			Vanderwolf et al. (2013)
	N. ramulariae			Zhang et al. (2014)
	Nectria sp.	Y	Y	Vanderwolf et al. (2013)
	N. pseudotrichia	Y		Jiang et al. (2017a, b)
Nemania	*Nemania bipapillata*	Y		Zhang et al. (2017)
	Ne. diffusa	Y	Y	Zhang et al. (2017)
	Ne. serpens	Y		Zhang (2019)
	Nemania sp.	Y	Y	
Neoascochyta	*Neoascochyta paspali*	Y		Zhang (2019)
	Neoascochyta sp.	Y		Jiang et al. (2017a, b)

Table 4 (continued)

Genus	Species	China[a]	This study[b]	References
Neoconiothyrium	*Neoconiothyrium sp.*	Y	Y	
Neocosmospora	*Neocosmospora ipomoeae*	Y	Y	
Neobulgaria	*Neobulgaria* sp.			Zhang et al. (2014)
Neofusicoccum	*Neofusicoccum ribis*			Zhang et al. (2014)
Neogymnomyces	*Neogymnomyces* sp.	Y	Y	Vanderwolf et al. (2013)
	Neo. virgineus			Vanderwolf et al. (2013)
Neomassarina	*Neomassarina thailandica*	Y	Y	
Neonectria	*Neonectria obtusispora*			Out et al. (2016)
	Neonectria sp.			Vanderwolf et al. (2013)
Neopyrenochaeta	*Neopyrenochaeta inflorescentiae*	Y	Y	
Neurospora	*Neurospora crassa*			Vanderwolf et al. (2013)
	Neu. intermedia	Y		Zhang et al. (2017)
	Neu. tetrasperma			Pusz et al. (2015)
	Neurospora sp.			Vanderwolf et al. (2013)
Nigrograna	*Nigrograna cangshanensis*	Y		Zhang (2019)
	Nigrograna mackinnonii	Y	Y	
	Nigrograna sp.	Y	Y	
Nigrospora	***Nigrospora globosa***	Y	Y	
	Ni. oryzae	Y	Y	Vanderwolf et al. (2013)
	Ni. sphaerica			Vanderwolf et al. (2013)
	Nigrospora sp.			Vanderwolf et al. (2013), Bercea et al. (2018)
Nomuraea	*Nomuraea rileyi*			Vanderwolf et al. (2013)
Ochroconis	*Ochroconis* sp.	Y	Y	Vanderwolf et al. (2013)
	O. tshawytschae			Vanderwolf et al. (2013)
Oedocephalum	*Oedocephalum* sp.			Vanderwolf et al. (2013)
Oidiodendron	*Oidiodendron cereale*			Vanderwolf et al. (2013)
	Oi. flavum			Vanderwolf et al. (2013)
	Oi. griseum			Vanderwolf et al. (2013), Nováková et al. (2018)
	Oi. maius			Vanderwolf et al. (2013)
	Oi. myxotrichoides			Vanderwolf et al. (2013)
	Oi. rhodogenum			Vanderwolf et al. (2013)
	Oi. tenuissimum	Y		Vanderwolf et al. (2013), Zhang (2019)
	Oi. truncatum			Vanderwolf et al. (2013, 2015, 2019), Zhang et al. (2014)
	Oidiodendron sp.	Y		Vanderwolf et al. (2013, 2019), Zhang et al. (2014), Man et al. (2015), Leplat et al. (2018)
Ombrophila	*Ombrophila alba*			Vanderwolf et al. (2013)
	Om. janthina			Vanderwolf et al. (2013)
	Om. speluncarum			Vanderwolf et al. (2013)
Ophiocordyceps	*Ophiocordyceps entomorrhiza*			Vanderwolf et al. (2013)
	Op. sinensis	Y		Zhang (2019)
	Op. sobolifera	Y	Y	
Ophiognomonia	*Ophiognomonia ischnostyla*	Y		Zhang (2019)
Ophiostoma	*Ophiostoma polyporicola*			Vanderwolf et al. (2013)
	Oph. stenoceras			Vanderwolf et al. (2013)
Ovadendron	*Ovadendron sulphureoochraceum*			Vanderwolf et al. (2013)
Paecilomyces	*Paecilomyces divaricatus*			Vanderwolf et al. (2013)
	P. fumosoroseus			Pusz et al. (2015), Kokurewicz et al. (2016)
	P. hepiali	Y	Y	
	P. lilacinus			Vanderwolf et al. (2013)
	P. tenuis	Y	Y	
	P. variotii			Taylor et al. (2013), Vanderwolf et al. (2013), Kokurewicz et al. (2016)
	Paecilomyces sp.	Y		Vanderwolf et al. (2013, 2015, 2019), Man et al. (2015), Popović et al. (2015), Yoder et al. (2015), Zhang et al. (2017), Leplat et al. (2018)
Pallidocercospora	*Pallidocercospora heimioides*	Y	Y	
Papulaspora	*Papulaspora rubida*			Vanderwolf et al. (2013)
	Papulaspora sp.			Vanderwolf et al. (2013)
Paraboeremia	*Paraboeremia oligotrophica*	Y		Jiang et al. (2017a, b)
	Pa. selaginellae	Y	Y	
Paracamarosporium	*Paracamarosporium hawaiiense*	Y	Y	

Table 4 (continued)

Genus	Species	China[a]	This study[b]	References
Paracoccidioides	*Paracoccidioides brasiliensis*			Vanderwolf et al. (2013)
Paraconiothyrium	*Paraconiothyrium brasiliense*	Y	Y	
	Pa. estuarinum	Y	Y	
	Paraconiothyrium sp.	Y		Zhang (2019)
Paracremonium	***Paracremonium apiculatum***	Y	Y	
	Par. ellipsoideum	Y	Y	
	Par. variiforme	Y		Zhang et al. (2017)
	Paracremonium sp.	Y	Y	
Paramicrothyrium	*Paramicrothyrium sp.*	Y	Y	
Paramyrothecium	*Paramyrothecium roridum*	Y	Y	Vanderwolf et al. (2013)
Paranomuraea	*Paranomuraea carnea*			Vanderwolf et al. (2013)
Paraphaeosphaeria	***Paraphaeosphaeria hydei***	Y	Y	
	Para. michotii	Y	Y	
	Para. neglecta	Y		Zhang (2019)
	Para. sporulosa	Y	Y	Vanderwolf et al. (2013), Man et al. (2015), Pusz et al. (2015)
	Paraphaeosphaeria sp.	Y		Zhang (2019)
Paraphoma	*Paraphoma chrysanthemicola*	Y	Y	Vanderwolf et al. (2013)
	Parap. fimeti			Ogórek et al. (2016b, c)
	Parap. radicina	Y		Vanderwolf et al. (2013), Zhang et al. (2017)
Paraphyton	*Paraphyton Cookei*			Ogórek et al. (2019)
Parastagonospora	*Parastagonospora nodorum*	Y	Y	
Parengyodontium	*Parengyodontium album*	Y	Y	Vanderwolf et al. (2013), Nováková et al. (2018)
	Parengyodontium sp.	Y		Zhang (2019)
Pectinotrichum	*Pectinotrichum chinense*	Y		Zhang et al. (2017)
Penicillifer	*Penicillifer diparietisporus*	Y	Y	
Penicillium	*Penicillium adametzioides*	Y	Y	
	Pe. adametzii			Vanderwolf et al. (2013)
	Pe. aeneum	Y	Y	
	Pe. albidum			Vanderwolf et al. (2013)
	Pe. astrolabium	Y	Y	
	Pe. atramentosum	Y	Y	Vanderwolf et al. (2013), Jacobs et al. (2017), Nováková et al. (2018)
	Pe. atrosanguineum	Y	Y	Nováková et al. (2018)
	Pe. aurantiogriseum			Vanderwolf et al. (2013), Mitova et al. (2017), Nováková et al. (2018), Ogórek (2018b), Popkova and Mazina (2019)
	Pe. bialowiezense			Visagie et al. (2019)
	Pe. bilaiae	Y	Y	
	Pe. biourgeianum	Y		Ogórek et al. (2017), Pusz et al. (2017), Zhang (2019)
	Pe. brasilianum	Y		Nováková et al. (2018), Zhang (2019)
	Pe. brevicompactum	Y	Y	Taylor et al. (2013), Vanderwolf et al. (2013), Zhang et al. (2014), Pusz et al. (2015), Out et al. (2016), Jiang et al. (2017a, b), Ogórek et al. (2017, 2018), Belyagoubi et al. (2018), Nováková et al. (2018), Ogórek (2018a, b)
	Pe. brevistpitatum			Visagie et al. (2019)
	Pe. buchwaldii	Y		Zhang et al. (2017)
	Pe. bussumense	Y	Y	
	Pe. cairnsense	Y		Zhang (2019)
	Pe. camemberti	Y		Vanderwolf et al. (2013), Zhang et al. (2017)
	Pe. canariense	Y	Y	
	Pe. canescens			Vanderwolf et al. (2013), Nováková et al. (2018)
	Pe. capsulatum			Vanderwolf et al. (2013)
	Pe. cavernicola			Vanderwolf et al. (2013)
	Pe. chalabudae	Y	Y	
	Pe. chermesinum			Vanderwolf et al. (2013)
	Pe. chrysogenum	Y	Y	Ogórek et al. (2013, 2014a, b, c, 2016b, c, d, 2017), Taylor et al. (2013), Vanderwolf et al. (2013, 2019), Pusz et al. (2014, 2015, 2018a, b), Jacobs et al. (2017), Jiang et al. (2017a, b), Zhang et al. (2017), Nováková et al. (2018), Pusz et al. (2018a), Dyląg et al. (2019), Popkova and Mazina (2019), Visagie et al. (2019)
	Pe. citreonigrum	Y	Y	Vanderwolf et al. (2013), Pusz et al. (2018a)
	Pe. citrinum	Y	Y	Taylor et al. (2013), Vanderwolf et al. (2013), Ogórek et al. (2014a, b, c), Pusz et al. (2014, 2018a, b)

Table 4 (continued)

Genus	Species	China[a]	This study[b]	References
	Pe. commune	Y	Y	Vanderwolf et al. (2013), Pusz et al. (2014, 2017), Out et al. (2016), Jacobs et al. (2017), Mitova et al. (2017), Ogórek et al. (2017, 2018)
	Pe. concentricum	Y	Y	Vanderwolf et al. (2013), Mitova et al. (2017), Visagie et al. (2019)
	Pe. consobrinum			Visagie et al. (2019)
	Pe. contaminatum	Y		Zhang (2019)
	Pe. coprobium	Y	Y	
	Pe. coprophilum	Y	Y	Mitova et al. (2017), Zhang et al. (2017)
	Pe. copticola	Y	Y	
	Pe. corylophilum			Vanderwolf et al. (2013), Nováková et al. (2018), Visagie et al. (2019)
	Pe. daleae	Y	Y	Vanderwolf et al. (2013)
	Pe. decumbens			Taylor et al. (2013), Vanderwolf et al. (2013)
	Pe. dierckxii	Y		Vanderwolf et al. (2013), Man et al. (2015), Zhang et al. (2017)
	Pe. digitatum	Y	Y	Vanderwolf et al. (2013)
	Pe. dipodomyicola	Y		Zhang (2019)
	Pe. dipodomyis	Y	Y	
	Pe. echinulatum	Y	Y	Vanderwolf et al. (2013), Out et al. (2016)
	Pe. expansum	Y	Y	Ogórek et al. (2013, 2014a, b, c), Taylor et al. (2013), Vanderwolf et al. (2013, 2015), Pusz et al. (2014), Zhang et al. (2017), Nováková et al. (2018), Pusz et al. (2018a), Dyląg et al. (2019), Visagie et al. (2019)
	Pe. flavigenum	Y	Y	Nováková et al. (2018), Tavares et al. (2018)
	Pe. funiculosum	Y	Y	
	Pe. glabrum	Y	Y	Taylor et al. (2013), Vanderwolf et al. (2013), Zhang et al. (2014), Pusz et al. (2015), Ogórek et al. (2017), Zhang et al. (2017), Visagie et al. (2019)
	Pe. gladioli	Y	Y	Vanderwolf et al. (2013)
	Pe. glandicola	Y	Y	Vanderwolf et al. (2013), Ogórek et al. (2016a), Nováková et al. (2018)
	Pe. glaucoalbidum			Vanderwolf et al. (2013, 2015, 2019), Pusz et al. (2017), Nováková et al. (2018), Visagie et al. (2019)
	Pe. granulatum			Ogórek et al. (2016b, c)
	Pe. griseofulvum	Y		Taylor et al. (2013), Vanderwolf et al. (2013, 2019), Pusz et al. (2014), Zhang et al. (2014), Ogórek et al. (2016b, c, d), Jacobs et al. (2017), Zhang et al. (2017), Nováková et al. (2018), Pusz et al. (2018a)
	Pe. griseolum			Vanderwolf et al. (2013)
	Pe. guanacastense	Y	Y	
	Pe. halotolerans	Y	Y	
	Pe. herquei	Y	Y	Vanderwolf et al. (2013), Zhang et al. (2017)
	Pe. hirsutum			Vanderwolf et al. (2013)
	Pe. hordei			Vanderwolf et al. (2013)
	Pe. implicatum			Vanderwolf et al. (2013), Pusz et al. (2018a)
	Pe. inflatum	Y		Zhang et al. (2017)
	Pe. italicum			Vanderwolf et al. (2013)
	Pe. jacksonii	Y	Y	
	Pe. janczewskii			Vanderwolf et al. (2013)
	Pe. javanicum			Vanderwolf et al. (2013)
	Pe. jensenii			Vanderwolf et al. (2013)
	Pe. lagerheimii			Vanderwolf et al. (2013)
	Pe. lanosocoeruleum			Vanderwolf et al. (2013), Ogórek et al. (2016b, d)
	Pe. lanosum			Vanderwolf et al. (2013)
	Pe. lividum	Y	Y	
	Pe. ludwigii	Y	Y	
	Pe. madriti	Y	Y	
	Pe. magnielliptisporum	Y	Y	
	Pe. malachiteum	Y		Mitova et al. (2017), Zhang et al. (2017)
	Pe. mallochii	Y	Y	
	Pe. meleagrinum	Y	Y	Man et al. (2015), Pusz et al. (2018a)
	Pe. melanoconidium			Vanderwolf et al. (2013)
	Pe. melinii			Vanderwolf et al. (2013)
	Pe. mexicanum	Y	Y	
	Pe. miczynskii			Vanderwolf et al. (2013), Zhang et al. (2014)
	Pe. nalgiovense	Y	Y	Vanderwolf et al. (2013)

Table 4 (continued)

Genus	Species	China[a]	This study[b]	References
	Pe. notatum	Y		Jiang et al. (2017a, b), Pusz et al. (2018a)
	Pe. ochrochloron	Y	Y	
	Pe. olsonii	Y	Y	Vanderwolf et al. (2013)
	Pe. oxalicum	Y	Y	Connell and Staudigel (2013), Taylor et al. (2013), Vanderwolf et al. (2013), Busquets et al. (2014), Popović et al. (2015), Yoder et al. (2015), Kokurewicz et al. (2016), Jiang et al. (2017a, b), Zhang et al. (2017), Belyagoubi et al. (2018), Nováková et al. (2018), Leplat et al. (2018), Pusz et al. (2018a)
	Pe. palitans			Vanderwolf et al. (2013)
	Pe. pancosmium	Y	Y	Mitova et al. (2017), Zhang et al. (2017)
	Pe. parvulum	Y		Zhang et al. (2017)
	Pe. paxilli	Y	Y	Vanderwolf et al. (2013), Jiang et al. (2017a, b), Pusz et al. (2018a)
	Pe. phoeniceum			Nováková et al. (2018)
	Pe. piceum			Vanderwolf et al. (2013)
	Pe. pimiteouiense	Y	Y	
	Pe. polonicum	Y	Y	Vanderwolf et al. (2013), Jacobs et al. (2017), Ogórek et al. (2017), Nováková et al. (2018)
	Pe. purpurascens			Vanderwolf et al. (2013), Pusz et al. (2018a)
	Pe. purpurogenum			Taylor et al. (2013), Vanderwolf et al. (2013), Nováková et al. (2018)
	Pe. raistrickii			Vanderwolf et al. (2013)
	Pe. raperi	Y	Y	
	Pe. raphiae	Y	Y	
	Pe. restrictum	Y	Y	Vanderwolf et al. (2013)
	Pe. robsamsonii	Y	Y	
	Pe. roqueforti			Vanderwolf et al. (2013)
	Pe. roseopurpureum	Y	Y	Vanderwolf et al. (2013), Ogórek et al. (2016b, d)
	Pe. rubens	Y	Y	Visagie et al. (2019)
	Pe. rubrum	Y		Jiang et al. (2017a, b)
	Pe. sacculum			Vanderwolf et al. (2013)
	Pe. sanguifluum	Y	Y	
	Pe. scabrosum	Y	Y	Vanderwolf et al. (2013)
	Pe. sclerotiorum	Y	Y	
	Pe. simplicissimum	Y	Y	Taylor et al. (2013), Vanderwolf et al. (2013), Mitova et al. (2017), Ogórek et al. (2017), Zhang et al. (2017), Nováková et al. (2018), Popkova and Mazina (2019)
	Pe. sizovae	Y	Y	
	Pe. solitum	Y	Y	Taylor et al. (2013), Vanderwolf et al. (2013, 2015), Out et al. (2016), Jacobs et al. (2017), Mitova et al. (2017), Ogórek et al. (2017, 2018), Ogórek (2018a, b)
	Pe. spathulatum			Visagie et al. (2019)
	Pe. speluncae			Visagie et al. (2019)
	Pe. spinulosum	Y		Vanderwolf et al. (2013), Pusz et al. (2015, 2017), Ogórek et al. (2017), Zhang (2019)
	Pe. sumatraense	Y	Y	
	Pe. swiecickii	Y	Y	Zhang et al. (2014), Pusz et al. (2017)
	Pe. tardochrysogenum	Y	Y	
	Pe. thomii	Y	Y	Taylor et al. (2013), Vanderwolf et al. (2013, 2019), Ogórek et al. (2017), Zhang et al. (2017)
	Pe. tularense			Zhang et al. (2014)
	Pe. ubiquetum	Y	Y	
	Pe. virgatum	Y	Y	
	Pe. viticola	Y	Y	
	Pe. vulpinum	Y		Vanderwolf et al. (2013), Zhang et al. (2014), Zhang (2019)
	Pe. waksmanii			Vanderwolf et al. (2013), Ogórek et al. (2014b), Pusz et al. (2014), Pusz et al. (2018a)
	Pe. westlingii			Visagie et al. (2019)
	Penicillium sp.	Y	Y	Vanderwolf et al. (2013, 2015, 2019), Martin-Sanchez et al. (2014), Zhang et al. (2014), Man et al. (2015), Popović et al. (2015), Yoder et al. (2015), Kokurewicz et al. (2016), Jacobs et al. (2017), Jiang et al. (2017a, b), Mitova et al. (2017), Zhang et al. (2017), Belyagoubi et al. (2018), Bercea et al. (2018), Nováková et al. (2018), Pusz et al. (2018a), Leplat et al. (2018), Burow et al. (2019), Pfendler et al. (2019), Popkova and Mazina (2019)

Table 4 (continued)

Genus	Species	China[a]	This study[b]	References
Periconia	*Periconia macrospinosa*	Y	Y	Vanderwolf et al. (2013), Brad et al. (2018)
	Periconia sp.	Y	Y	Vanderwolf et al. (2013), Zhang et al. (2017), Nováková et al. (2018)
Peroneutypa	*Peroneutypa scoparia*	Y	Y	Zhang et al. (2017)
	Peroneutypa sp.	Y	Y	
Pestalotia	*Pestalotia cocculi*	Y	Y	
	Pestalotia sp.			Vanderwolf et al. (2013)
Pestalotiopsis	*Pestalotiopsis cocculi*	Y		Zhang (2019)
	Pes. guepinii	Y		Zhang et al. (2017)
	Pes. hainanensis	Y		Zhang (2019)
	Pes. maculiformans			Vanderwolf et al. (2013)
	Pes. mangiferae	Y	Y	
	Pes. microspora	Y	Y	Zhang et al. (2017)
	Pes. palmarum			Vanderwolf et al. (2013)
	Pes. uvicola	Y		Zhang (2019)
	Pes. vismiae	Y	Y	
	Pestalotiopsis sp.			Vanderwolf et al. (2013)
Petriella	*Petriella setifera*			Vanderwolf et al. (2013)
	Petriella sp.	Y	Y	
Peziza	*Peziza micropus*			Vanderwolf et al. (2013)
	Peziza sp.			Vanderwolf et al. (2013)
Phaeoacremonium	*Phaeoacremonium argentinense*	Y		Zhang et al. (2017)
	Ph. iranianum	Y		Zhang (2019)
	Ph. minimum	Y		Zhang (2019)
	Ph. novae-zealandiae	Y	Y	
	Ph. occidentale	Y		Zhang (2019)
	Ph. rubrigenum	Y		Jiang et al. (2017a, b)
	Ph. viticola	Y		Zhang (2019)
	Phaeoacremonium sp.	Y		Jiang et al. (2017a, b), Vanderwolf et al. (2019)
Phaeococcomyces	*Phaeococcomyces nigricans*			Connell and Staudigel (2013)
Phaeocytostroma	*Phaeocytostroma ambiguum*	Y	Y	
	Pha. sacchari	Y	Y	
Phaeoisaria	*Phaeoisaria clematidis*	Y		Zhang (2019)
Phaeosphaeria	*Phaeosphaeria annulata*			Vanderwolf et al. (2013)
	Phae. fusispora	Y		Zhang et al. (2017)
	Phae. microscopica	Y		Zhang (2019)
	Phae. nodorum			Vanderwolf et al. (2013)
	Phae. oryzae	Y		Zhang (2019)
	Phaeosphaeria sp.	Y		Connell and Staudigel (2013), Zhang (2019)
Phaeosphaeriopsis	*Phaeosphaeriopsis* sp.	Y		Zhang (2019)
Phaeostilbella	*Phaeostilbella* sp.			Vanderwolf et al. (2013)
Phaeotrichum	*Phaeotrichum hystricinum*			Vanderwolf et al. (2013, 2015, 2019)
	Phaeotrichum sp.			Vanderwolf et al. (2015)
Phialemoniopsis	*Phialemoniopsis sp.*	Y	Y	Jiang et al. (2017a, b)
Phialemonium	*Phialemonium dimorphosporum*	Y	Y	
	Phi. inflatum			Vanderwolf et al. (2013)
	Phialemonium sp.	Y	Y	Zhang et al. (2017)
Phialocephala	*Phialocephala humicola*	Y	Y	
	Phialocephala sp.			Vanderwolf et al. (2013)
Phialophora	*Phialophora cinerescens*			Vanderwolf et al. (2013)
	Phia. fastigiata			Vanderwolf et al. (2013)
	Phia. foetens	Y	Y	
	Phia. hyalina			Vanderwolf et al. (2013)
	Phia. olivacea	Y	Y	
	Phia. verrucosa			Pusz et al. (2018a)
	Phialophora sp.	Y	Y	Vanderwolf et al. (2013, 2019), Leplat et al. (2018)
Phoma	*Phoma herbarum*	Y	Y	Ogórek et al. (2014c), Zhang et al. (2017)
	Pho. insulana	Y	Y	Zhang et al. (2017)
	Pho. leveillei			Ogórek et al. (2016d)

Table 4 (continued)

Genus	Species	China[a]	This study[b]	References
	Pho radicina			Vanderwolf et al. (2019)
	Pho. senecionis	Y		Zhang et al. (2017)
	Phoma sp.	Y	Y	Vanderwolf et al. (2013, 2015), Man et al. (2015), Kokurewicz et al. (2016), Zhang et al. (2017), Leplat et al. (2018)
Phomopsis	*Phomopsis vaccinii*	Y		Zhang (2019)
	Phomopsis sp.	Y	Y	Vanderwolf et al. (2013), Zhang et al. (2017)
Phylacia	*Phylacia bomba*			Vanderwolf et al. (2013)
Phyllachora	*Phyllachora sp.*	Y	Y	Zhang (2019)
Phymatotrichopsis	*Phymatotrichopsis omnivora*			Vanderwolf et al. (2013)
Pidoplitchkoviella	*Pidoplitchkoviella terricola*			Vanderwolf et al. (2013)
Pilidium	*Pilidium concavum*	Y		Zhang (2019)
Pirostoma	*Pirostoma* sp.			Vanderwolf et al. (2013)
Pithoascus	*Pithoascus ater*	Y	Y	
	Pi. platysporus	Y	Y	
Pithomyces	*Pithomyces chartarum*			Vanderwolf et al. (2013)
	Pithomyces sp.			Vanderwolf et al. (2013), Leplat et al. (2018)
Plagiostoma	*Plagiostoma pulchellum*	Y		Zhang (2019)
	Plagiostoma sp.	Y		Zhang (2019)
Plectosphaerella	*Plectosphaerella cucumerina*	Y	Y	Vanderwolf et al. (2013), Jiang et al. (2017a, b), Zhang et al. (2017)
	Pl. niemeijerarum	Y		Zhang (2019)
	Pl. oligotrophica	Y	Y	Jiang et al. (2017a, b)
	Plectosphaerella sp.	Y		Zhang et al. (2017)
Pleospora	*Pleospora* sp.			Vanderwolf et al. (2013)
Pleotrichocladium	*Pleotrichocladium opacum*			Vanderwolf et al. (2013)
Pochonia	*Pochonia* sp.	Y		Vanderwolf et al. (2013), Zhang (2019)
Podospora	*Podospora* sp.	Y	Y	Vanderwolf et al. (2013), Zhang et al. (2014)
Polycephalomyces	*Polycephalomyces agaricus*	Y	Y	
	Po. ramosus			Vanderwolf et al. (2013)
Polythrincium	*Polythrincium* sp.			Vanderwolf et al. (2013)
Preussia	*Preussia aemulans*	Y	Y	Zhang et al. (2017)
	Pr. funiculata	Y		Vanderwolf et al. (2015), Zhang (2019)
	Preussia sp.	Y	Y	Vanderwolf et al. (2013, 2015, 2019)
	Pr. terricola	Y	Y	
Prosthecium	*Prosthecium sp.*	Y	Y	
Protocrea	*Protocrea farinosa*	Y		Zhang et al. (2017)
Pseudallescheria	*Pseudallescheria boydii*	Y	Y	Vanderwolf et al. (2013)
	Ps. fimeti	Y	Y	Zhang et al. (2017)
	Pseudallescheria sp.	Y	Y	Vanderwolf et al. (2013)
Pseudeurotium	*Pseudeurotium bakeri*			Burow et al. (2019), Zhang (2019)
	Pse. hygrophilum			Brad et al. (2018)
	Pse. zonatum			Vanderwolf et al. (2013)
	Pseudeurotium sp.	Y		Vanderwolf et al. (2013), Out et al. (2016), Zhang (2019)
Pseudoarachniotus	*Pseudoarachniotus trochleosporus*			Vanderwolf et al. (2013)
Pseudocercosporella	*Pseudocercosporella fraxini*	Y		Zhang (2019)
	Pseudocercosporella sp.	Y		Vanderwolf et al. (2013), Jiang et al. (2017a, b)
Pseudocoleophoma	*Pseudocoleophoma sp.*	Y	Y	
Pseudocosmospora	*Pseudocosmospora rogersonii*	Y	Y	
Pseudogymnoascus	*Pseudogymnoascus destructans*			Zhang et al. (2014), Vanderwolf et al. (2015, 2019), Kokurewicz et al. (2016), Burow et al. (2019)
	Pseu. pannorum	Y	Y	Vanderwolf et al. (2013, 2015, 2019), Zhang et al. (2014), Out et al. (2016), Jiang et al. (2017a, b), Mitova et al. (2017), Ogórek et al. (2017), Popkova and Mazina (2019)
	Pseu. roseus			Vanderwolf et al. (2013, 2015, 2019)
	Pseudogymnoascus sp.			Out et al. (2016), Burow et al. (2019)
Pseudopestalotiopsis	*Pseudopestalotiopsis theae*	Y	Y	
Pseudopithomyces	*Pseudopithomyces chartarum*			Pusz et al. (2015)
	Pseud. maydicus	Y	Y	
Pseudoscopulariopsis	***Pseudoscopulariopsis asperispora***	Y	Y	

Table 4 (continued)

Genus	Species	China[a]	This study[b]	References
	Pseudo. hibernica	Y	Y	
Purpureocillium	*Purpureocillium lavendulum*	Y	Y	Jiang et al. (2017a, b)
	Pu. lilacinum	Y	Y	Taylor et al. (2013), Zhang et al. (2017), Nováková et al. (2018), Pusz et al. (2018a)
	Purpureocillium sp.	Y		Jiang et al. (2017a, b)
Pycnostysanus	*Pycnostysanus* sp.			Vanderwolf et al. (2013)
Pyrenochaeta	*Pyrenochaeta* sp.			Vanderwolf et al. (2013)
Pyrenochaetopsis	*Pyrenochaetopsis decipiens*	Y		Zhang (2019)
	Pyrenochaetopsis sp.	Y	Y	Jiang et al. (2017a, b)
Pyrenopeziza	*Pyrenopeziza dilutella*			Vanderwolf et al. (2013)
Pyrenophora	*Pyrenophora tritici-repentis*	Y	Y	
Radulum	*Radulum* sp.			Vanderwolf et al. (2013)
Ramichloridium	*Ramichloridium indicum*			Vanderwolf et al. (2013)
	Ramichloridium sp.	Y	Y	Vanderwolf et al. (2013)
Ramophialophora	*Ramophialophora globispora*	Y		Zhang et al. (2017)
	R. petraea	Y		Zhang et al. (2017)
	Ramophialophora sp.	Y	Y	
Readeriella	*Readeriella eucalypti*			Belyagoubi et al. (2018)
Rhachomyces	*Rhachomyces alluaudii*			Vanderwolf et al. (2013)
	Rh. anophthalmi			Vanderwolf et al. (2013)
	Rh. aphaenopsis			Vanderwolf et al. (2013)
	Rh. beronii			Vanderwolf et al. (2013)
	Rh. bolivarii			Vanderwolf et al. (2013)
	Rh. bucciarellii			Vanderwolf et al. (2013)
	Rh. canariensis			Vanderwolf et al. (2013)
	Rh. capucinus			Vanderwolf et al. (2013)
	Rh. dedyi			Vanderwolf et al. (2013)
	Rh. girardii			Vanderwolf et al. (2013)
	Rh. gratiellae			Vanderwolf et al. (2013)
	Rh. hypogaeus			Vanderwolf et al. (2013)
	Rh. ilerdensis			Vanderwolf et al. (2013)
	Rh. maublancii			Vanderwolf et al. (2013)
	Rh. middelhoekii			Vanderwolf et al. (2013)
	Rh. orotrechorum			Vanderwolf et al. (2013)
	Rh. pacei			Vanderwolf et al. (2013)
	Rh. peyerimhoffii			Vanderwolf et al. (2013)
	Rh. proliferans			Vanderwolf et al. (2013)
	Rh. pyrenaeus			Vanderwolf et al. (2013)
	Rh. quetzalcoatl			Vanderwolf et al. (2013)
	Rh. reveilletii			Vanderwolf et al. (2013)
	Rh. reymondi			Vanderwolf et al. (2013)
	Rh. richardi			Vanderwolf et al. (2013)
	Rh. spadiceus			Vanderwolf et al. (2013)
	Rh. speluncalis			Vanderwolf et al. (2013)
	Rh. stipitatus			Vanderwolf et al. (2013)
	Rh. urbaini			Vanderwolf et al. (2013)
	Rh. vayssierei			Vanderwolf et al. (2013)
	Rh. venetianus			Vanderwolf et al. (2013)
	Rh. vignae			Vanderwolf et al. (2013)
	Rhachomyces sp.			Vanderwolf et al. (2013)
Rhinocladiella	*Rhinocladiella* sp.			Vanderwolf et al. (2013)
Rhytidhysteron	*Rhytidhysteron rufulum*	Y	Y	
Rosellinia	*Rosellinia arcuata*			Vanderwolf et al. (2013)
Roussoella	*Ro. siamensis*	Y	Y	
	Roussoella sp.	Y	Y	
Saccharomyces	*Saccharomyces bayanus*			Vanderwolf et al. (2013)
	S. carlsbergensis			Vanderwolf et al. (2013)
	S. cerevisiae			Connell and Staudigel (2013), Vanderwolf et al. (2013)
	S. paradoxus			Vanderwolf et al. (2013)

Table 4 (continued)

Genus	Species	China[a]	This study[b]	References
Saccharomycopsis	*Saccharomycopsis fibuligera*	Y	Y	
Sagenomella	*Sagenomella* sp.			Vanderwolf et al. (2013)
Sarcopodium	*Sarcopodium sp.*	Y	Y	
Sarocladium	*Sarocladium bacillisporum*			Vanderwolf et al. (2013)
	Sa. bactrocephalum			Vanderwolf et al. (2013)
	Sa. glaucum			Vanderwolf et al. (2013)
	Sa. implicatum			Connell and Staudigel (2013), Vanderwolf et al. (2013)
	Sa. kiliense	Y	Y	Vanderwolf et al. (2013)
	Sarocladium sp.	Y		Jiang et al. (2017a, b)
	Sa. strictum	Y	Y	Ogórek et al. (2013, 2014a, b), Vanderwolf et al. (2013), Kokurewicz et al. (2016), Pusz et al. (2018a), Dyląg et al. (2019)
	Sa. zeae			Mitova et al. (2017)
Scedosporium	*Scedosporium sp.*	Y	Y	
Schizothecium	*Schizothecium inaequale*	Y		Jiang et al. (2017a, b)
	Schizothecium sp.	Y	Y	
Sclerotinia	*Sclerotinia sclerotiorum*			Ogórek et al. (2013, 2014a, b, c), Pusz et al. (2018a)
	Sclerotinia sp.			Vanderwolf et al. (2013)
Scolecobasidium	*Scolecobasidium anellii*			Vanderwolf et al. (2013)
	Sc. anomalum			Vanderwolf et al. (2013)
	Sc. constrictum			Vanderwolf et al. (2013)
	Sc. lascauxense			Vanderwolf et al. (2013), Martin-Sanchez et al. (2014), Pfendler et al. (2019)
	Sc. terreum			Vanderwolf et al. (2013)
Scopulariopsis	*Scopulariopsis asperula*	Y	Y	Vanderwolf et al. (2013)
	Sco. brumptii			Vanderwolf et al. (2013)
	Sco. candida			Vanderwolf et al. (2013), Dyląg et al. (2019)
	Sco. crassa	Y		Zhang et al. 2017
	Sco. flava	Y	Y	
	Sco. fusca			Vanderwolf et al. (2013)
	Sco. lanosa			Vanderwolf et al. (2013)
	Scopulariopsis sp.			Vanderwolf et al. (2013)
	Sco. sphaerospora	Y	Y	Vanderwolf et al. (2013)
Scutellinia	*Scutellinia* sp.	Y		Zhang et al. (2017)
Scytalidium	*Scytalidium cuboideum*			Vanderwolf et al. (2013)
	Scy. lignicola	Y	Y	Vanderwolf et al. (2013)
	Scytalidium sp.			Vanderwolf et al. (2015)
Seimatosporium	*Seimatosporium sp.*	Y	Y	
Selinia	*Selinia* sp.			Vanderwolf et al. (2013)
Sepedonium	*Sepedonium* sp.			Vanderwolf et al. (2013)
Septonema	*Septonema secedens*			Vanderwolf et al. (2013)
	Septonema sp.	Y		Vanderwolf et al. (2013), Jiang et al. (2017a, b)
Septoria	*Septoria arundinacea*	Y	Y	
	Septoria sp.			Vanderwolf et al. (2013)
Septoriella	*Septoriella oudemansii*	Y	Y	
Setophaeosphaeria	*Setophaeosphaeria hemerocallidis*	Y	Y	
	Se. microspora	Y	Y	
	Setophaeosphaeria sp.	Y	Y	
Setophoma	*Setophoma terrestris*	Y	Y	Zhang (2019)
	Set. vernoniae	Y		Zhang (2019)
	Setophoma sp.	Y		Jiang et al. (2017a, b)
Shanorella	*Shanorella* sp.			Vanderwolf et al. (2013)
Simplicillium	***Simplicillium album***	Y	Y	
	Si. aogashimaense	Y	Y	
	Si. calcicola	Y		Zhang et al. (2017)
	Si. cylindrosporum	Y		Zhang (2019)
	Si. humicola	Y	Y	
	Si. lamellicola	Y	Y	Vanderwolf et al. (2013), Nováková et al. (2018)
	Si. lanosoniveum			Zhang et al. (2014)

Table 4 (continued)

Genus	Species	China[a]	This study[b]	References
	Si. minatense	Y	Y	Mitova et al. (2017)
	Si. subtropicum	Y	Y	
	Simplicillium sp.	Y		Vanderwolf et al. (2013), Jiang et al. (2017a, b), Leplat et al. (2018)
Sirastachys	*Sirastachys longispora*	Y		Zhang et al. (2017)
	Sir. phaeospora	Y	Y	
Sordaria	*Sordaria fimicola*	Y		Vanderwolf et al. (2013), Ogórek et al. (2014a, b), Jiang et al. (2017a, b), Pusz et al. (2017)
	Sordaria sp.			Vanderwolf et al. (2013)
Spegazzinia	*Spegazzinia* sp.			Vanderwolf et al. (2013)
Sphaerodes	*Sphaerodes fimicola*			Vanderwolf et al. (2013)
Sphaerostilbella	*Sphaerostilbella penicillioides*			Vanderwolf et al. (2013)
Sporidesmium	*Sporidesmium atrum*			Vanderwolf et al. (2013)
Sporocybe	*Sporocybe* sp.			Vanderwolf et al. (2013)
Sporormia	*Sporormia subticinensis*	Y	Y	
Sporormiella	*Sporormiella insignis*			Nováková et al. (2018)
	Sp. minima	Y	Y	
	Sp. minimoides			Vanderwolf et al. (2013)
	Sporormiella sp.			Vanderwolf et al. (2013)
Sporothrix	*Sporothrix catenata*			Vanderwolf et al. (2013)
	Spo. inflata	Y	Y	Burow et al. (2019)
	Spo. schenckii			Vanderwolf et al. (2013)
	Sporothrix sp.			Vanderwolf et al. (2013), Leplat et al. (2018), Burow et al. (2019)
Stachybotrys	*Stachybotrys chartarum*	Y	Y	Vanderwolf et al. (2013), Zhang et al. (2017), Nováková et al. (2018)
	St. chlorohalonatus	Y	Y	Vanderwolf et al. (2013)
	St. cylindrosporus			Vanderwolf et al. (2013), Pusz et al. (2017)
	St. echinatus			Vanderwolf et al. (2013)
	St. parvisporus	Y	Y	
	Stachybotrys sp.			Vanderwolf et al. (2013), Leplat et al. (2018)
Stachylidium	*Stachylidium* sp.			Vanderwolf et al. (2013)
Stagonospora	*Stagonospora* sp.	Y		Jiang et al. (2017a, b), Leplat et al. (2018)
Stagonosporopsis	*Stagonosporopsis cucurbitacearum*	Y	Y	Jiang et al. (2017a, b)
Staphylotrichum	*Staphylotrichum boninense*	Y		Zhang et al. (2017)
	Sta. coccosporum	Y	Y	Vanderwolf et al. (2013)
	Staphylotrichum sp.	Y		Zhang et al. (2017)
Stemphylium	*Stemphylium botryosum*			Vanderwolf et al. (2013)
	Ste. vesicarium			Vanderwolf et al. (2013)
	Stemphylium sp.			Vanderwolf et al. (2013)
Stephanonectria	*Stephanonectria keithii*	Y	Y	Jiang et al. (2017a, b), Zhang et al. (2017)
Stigmatomyces	*Stigmatomyces oecotheae*			Vanderwolf et al. (2013)
Stilbella	*Stilbella* sp.	Y		Vanderwolf et al. (2013), Man et al. (2015)
Striatibotrys	*Striatibotrys eucylindrosporus*	Y	Y	
Stysanus	*Stysanus amyli*			Vanderwolf et al. (2013)
	Stysanus sp.			Vanderwolf et al. (2013)
	Sty. typhoides			Vanderwolf et al. (2013)
Sydowia	*Sydowia polyspora*			Martin-Sanchez et al. (2014), Ogórek et al. (2017), Pusz et al. (2017)
Symplectromyces	*Symplectromyces* sp.			Vanderwolf et al. (2013)
	Sy. vulgaris			Vanderwolf et al. (2013)
Synnematium	*Synnematium* sp.			Vanderwolf et al. (2013)
Talaromyces	*Talaromyces aculeatus*	Y		Vanderwolf et al. (2013), Zhang (2019)
	T. brinneus			Paula et al. (2019)
	T. cellulolyticus	Y		Zhang (2019)
	T. diversus			Vanderwolf et al. (2013)
	T. duclauxii			Vanderwolf et al. (2013)
	T. flavus	Y	Y	Vanderwolf et al. (2013), Pusz et al. (2014), Ogórek et al. (2017), Pusz et al. (2018a), Popkova and Mazina (2019)
	T. funiculosus			Vanderwolf et al. (2013)
	T. islandicus			Taylor et al. (2013)
	T. kendrickii			Nováková et al. (2018)

Table 4 (continued)

Genus	Species	China[a]	This study[b]	References
	T. loliensis			Vanderwolf et al. (2013)
	T. luteus			Vanderwolf et al. (2013), Pusz et al. (2014), Pusz et al. (2018a)
	T. minioluteus			Vanderwolf et al. (2013)
	T. pinophilus	Y	Y	Taylor et al. (2013), Vanderwolf et al. (2013), Zhang et al. (2017), Nováková et al. (2018)
	T. purpureogenus	Y	Y	Popkova and Mazina (2019)
	T. radicus	Y		Jiang et al. (2017a, b)
	T. ruber			Vanderwolf et al. (2013), Nováková et al. (2018)
	T. rugulosus	Y	Y	Vanderwolf et al. (2013), Pusz et al. (2018a)
	T. sublevisporus	Y	Y	
	T. thermophilus			Vanderwolf et al. (2013)
	T. variabilis			Taylor et al. (2013), Vanderwolf et al. (2013)
	T. varians			Vanderwolf et al. (2013)
	T. verruculosus			Vanderwolf et al. (2013)
	T. wortmannii			Vanderwolf et al. (2013)
	Talaromyces sp.	Y		Vanderwolf et al. (2013), Popović et al. (2015), Zhang et al. (2017), Nováková et al. (2018)
Tapesia	*Tapesia fusca*			Vanderwolf et al. (2013)
Tarzetta	*Tarzetta* sp.			Vanderwolf et al. (2013)
Teichospora	*Teichospora* sp.	Y	Y	
Tetracladium	*Tetracladium furcatum*			Vanderwolf et al. (2013)
	Tetracladium sp.			Connell and Staudigel (2013), Zhang et al. (2014), Out et al. (2016)
Tetracoccosporium	*Tetracoccosporium paxianum*			Vanderwolf et al. (2013)
Thelebolus	*Thelebolus crustaceus*			Vanderwolf et al. (2013, 2015)
	Th. ellipsoideus	Y	Y	Out et al. (2016)
	Th. globosus			Vanderwolf et al. (2013)
	Th. microsporus			Brad et al. (2018)
	Thelebolus sp.			Vanderwolf et al. (2013), Out et al. (2016), Brad et al. (2018)
Thelonectria	*Thelonectria discophora*	Y		Jiang et al. (2017a, b), Zhang et al. (2017)
	The. olida	Y	Y	
	Thelonectria sp.	Y	Y	
Thermoascus	*Thermoascus* sp.			Vanderwolf et al. (2013)
Thermomyces	*Thermomyces lanuginosus*			Vanderwolf et al. (2013)
Thermothelomyces	*Thermothelomyces thermophilus*			Vanderwolf et al. (2013)
Thielavia	*Thielavia hyalocarpa*	Y	Y	
	Thi. hyrcaniae			Vanderwolf et al. (2013)
	Thi. terrestris			Vanderwolf et al. (2013)
	Thi. terricola			Vanderwolf et al. 2013
	Thielavia sp.	Y		Vanderwolf et al. (2013), Zhang et al. (2017), Leplat et al. (2018)
Thysanophora	*Thysanophora* sp.			Vanderwolf et al. (2013, 2019)
Thysanorea	*Thysanorea* sp.			Vanderwolf et al. (2013)
Tilachlidium	*Tilachlidium* sp.			Vanderwolf et al. (2013)
Togninia	*Togninia* sp.	Y		Zhang (2017)
Tolypocladium	*Tolypocladium album*	Y	Y	
	Tol. cylindrosporum	Y	Y	Vanderwolf et al. (2013)
	Tol. inflatum			Vanderwolf et al. (2013, 2015)
	Tolypocladium sp.	Y	Y	Vanderwolf et al. (2013, 2019), Man et al. (2015), Zhang et al. (2017)
Torrubiella	*Torrubiella arachnophila*			Vanderwolf et al. (2013)
	Tor. minutissima			Vanderwolf et al. (2013)
	Torrubiella sp.			Vanderwolf et al. (2013)
Torula	*Torula herbarum*	Y		Vanderwolf et al. (2013), Zhang et al. (2017), Pusz et al. (2018a), Zhang (2019)
	Torula sp.			Vanderwolf et al. (2013)
Torulaspora	*Torulaspora delbrueckii*			Mitova et al. (2017)
Torulomyces	*Torulomyces* sp.			Leplat et al. (2018)
Toxicocladosporium	*Toxicocladosporium irritans*			Connell and Staudigel (2013), Vanderwolf et al. (2013)
Tremateia	*Tremateia arundicola*	Y	Y	
Tricellula	*Tricellula* cf. *aquatica*			Vanderwolf et al. (2019)
Trichobotrys	*Trichobotrys effusus*			Vanderwolf et al. (2013)

Table 4 (continued)

Genus	Species	China[a]	This study[b]	References
	Trichobotrys sp.	Y		Zhang (2019)
Trichocladium	*Trichocladium asperum*	Y		Zhang et al. (2017)
	Trichocladium sp.	Y	Y	Vanderwolf et al. (2013)
Trichoderma	*Trichoderma asperelloides*			Nováková et al. (2018)
	Tr. asperellum	Y	Y	
	Tr. atroviride	Y	Y	Vanderwolf et al. (2013), Zhang et al. (2017), Nováková et al. (2018)
	Tr. aureoviride	Y	Y	
	Tr. brevicompactum	Y		Zhang (2019)
	Tr. citrinoviride	Y		Zhang et al. (2017), Ogórek (2018a, b)
	Tr. deliquescens			Vanderwolf et al. (2013)
	Tr. gamsii	Y	Y	
	Tr. hamatum	Y	Y	Vanderwolf et al. (2013), Zhang et al. (2017), Popkova and Mazina (2019)
	Tr. harzianum	Y	Y	Ogórek et al. (2013, 2016c), Vanderwolf et al. (2013), Kokurewicz et al. (2016), Jiang et al. (2017a, b), Mitova et al. (2017), Pusz et al. (2017), Nováková et al. (2018), Popkova and Mazina (2019)
	Tr. koningii			Vanderwolf et al. (2013), Nováková et al. (2018)
	Tr. koningiopsis	Y	Y	Pusz et al. (2017), Zhang et al. (2017)
	Tr. lixii	Y	Y	Vanderwolf et al. (2013), Zhang et al. (2017)
	Tr. longibrachiatum	Y		Vanderwolf et al. (2013), Ogórek et al. (2017, 2018), Zhang et al. (2017)
	Tr. parareesei	Y	Y	
	Tr. paraviridescens	Y		Zhang et al. (2014), Zhang (2019)
	Tr. piluliferum			Vanderwolf et al. (2013)
	Tr. polysporum	Y	Y	Vanderwolf et al. (2013), Popkova and Mazina (2019)
	Tr. reesei	Y	Y	Man et al. (2015)
	Tr. rossicum	Y	Y	Zhang et al. (2017)
	Tr. samuelsii	Y	Y	
	Tr. saturnisporum	Y	Y	
	Tr. spirale	Y	Y	
	Tr. stramineum	Y	Y	
	Tr. strictipile	Y	Y	
	Tr. tomentosum	Y	Y	Jiang et al. (2017a, b)
	Tr. velutinum	Y	Y	
	Tr. virens			Vanderwolf et al. (2013), Popović et al. (2015), Nováková et al. (2018)
	Tr. viride	Y	Y	Taylor et al. (2013), Vanderwolf et al. (2013), Pusz et al. (2017, 2018a), Burow et al. (2019), Popkova and Mazina (2019)
	Tr. viridescens	Y	Y	
	Trichoderma sp.	Y		Vanderwolf et al. (2013, 2015, 2019), Martin-Sanchez et al. (2014), Yoder et al. (2015), Mitova et al. (2017), Zhang et al. (2017), Nováková et al. (2018), Leplat et al. (2018)
Trichophyton	*Trichophyton ajelloi*			Vanderwolf et al. (2013)
	Tri. mentagrophytes			Vanderwolf et al. (2013)
	Tri. rubrum	Y		Vanderwolf et al. (2013), Zhang et al. (2017)
	Tri. schoenleinii			Vanderwolf et al. (2013)
	Tri. terrestre	Y	Y	Vanderwolf et al. (2013), Zhang et al. (2014)
	Trichophyton sp.	Y	Y	Vanderwolf et al. (2013, 2019), Martin-Sanchez et al. (2014)
Trichosporiella	*Trichosporiella cerebriformis*			Vanderwolf et al. (2013)
	Tric. multisporum			Vanderwolf et al. (2013)
	Trichosporiella sp.			Vanderwolf et al. (2013, 2015, 2019)
Trichothecium	*Trichothecium roseum*			Vanderwolf et al. (2013), Pusz et al. (2018a, b)
	Trich. crotocinigenum	Y	Y	
Trichurus	*Trichurus terrophilus*	Y	Y	Vanderwolf et al. (2013)
	Trichurus sp.			Vanderwolf et al. (2013)
Tricladium	*Tricladium brunneum*			Vanderwolf et al. (2013)
Tripospermum	*Tripospermum* sp.			Vanderwolf et al. (2013)
Tritirachium	*Tritirachium cinnamomeum*			Vanderwolf et al. (2013)
	Trit. dependens			Vanderwolf et al. (2013)
	Trit. isariae			Vanderwolf et al. (2013)
	Trit. oryzae			Vanderwolf et al. (2013)
	Tritirachium sp.			Vanderwolf et al. (2013)

Table 4 (continued)

Genus	Species	China[a]	This study[b]	References
Troglomyces	*Troglomyces bilabiatus*			Enghoff and Santamaria (2015)
	Tro. manfredii			Vanderwolf et al. (2013)
	Tro. pusillus			Enghoff and Santamaria (2015)
	Tro. triandrus			Enghoff and Santamaria (2015)
Truncatella	*Truncatella angustata*			Vanderwolf et al. (2013), Burow et al. (2019)
	Truncatella sp.			Burow et al. (2019)
Tubercularia	*Tubercularia* sp.			Vanderwolf et al. (2013)
Ulocladium	*Ulocladium* sp.			Vanderwolf et al. (2013)
Uncinocarpus	*Uncinocarpus uncinatus*			Vanderwolf et al. (2013)
Varicosporium	*Varicosporium giganteum*			Vanderwolf et al. (2013)
	Varicosporium sp.			Vanderwolf et al. (2013)
Venturia	*Venturia* sp.			Vanderwolf et al. (2013)
Veronaea	*Veronaea compacta*	Y	Y	
	Veronaea sp.	Y	Y	
Verticillium	*Verticillium albo-atrum*	Y		Vanderwolf et al. (2013), Zhang (2019)
	V. dahliae			Connell and Staudigel (2013), Vanderwolf et al. (2013)
	V. insectorum	Y		Vanderwolf et al. (2013), Zhang (2019)
	V. nanum			Vanderwolf et al. (2013)
	V. terrestre			Vanderwolf et al. (2013)
	V. tricorpus	Y	Y	Jiang et al. (2017a, b)
	Verticillium sp.	Y	Y	Vanderwolf et al. (2013, 2019), Yoder et al. (2015), Zhang et al. (2017), Leplat et al. (2018)
Vibrissea	*Vibrissea truncorum*			Vanderwolf et al. (2013)
Virgaria	*Virgaria nigra*	Y		Zhang et al. (2017)
Volutella	*Volutella aeria*	Y	Y	Zhang et al. (2017)
	Vo. ciliata	Y	Y	Vanderwolf et al. (2013), Jiang et al. (2017a, b)
	Vo. citrinella	Y	Y	
	Vo. roseola			Vanderwolf et al. (2013)
	Volutella sp.			Vanderwolf et al. (2013)
Volutellonectria	*Volutellonectria consors*	Y	Y	Vanderwolf et al. (2013)
Wardomyces	*Wardomyces anomalus*			Vanderwolf et al. (2013)
	W. giganteus			Vanderwolf et al. (2019)
	W. humicola			Vanderwolf et al. (2013, 2015)
	W. inflatus	Y		Vanderwolf et al. (2013, 2015, 2019), Zhang (2019)
	W. sp.			Vanderwolf et al. (2013, 2015, 2019), Leplat et al. (2018)
Wardomycopsis	***Wardomycopsis dolichi***	Y	Y	
	Wa. ellipsoconidiophora	Y	Y	
	Wa. fusca	Y	Y	
	Wa. humicola	Y	Y	
	Wa. longicatenata	Y		Zhang et al. (2017)
Whalleya	*Whalleya microplaca*	Y	Y	
Wickerhamomyces	*Wickerhamomyces anomalus*			Vanderwolf et al. (2013)
	Wi. subpelliculosus			Vanderwolf et al. (2013)
Xenosporium	*Xenosporium berkeleyi*			Vanderwolf et al. (2013)
Xepicula	*Xepicula sp.*	Y	Y	
Xylaria	*Xylaria arbuscula*	Y		Zhang et al. (2017)
	X. anisopleura			Vanderwolf et al. (2013)
	X. corniformis			Vanderwolf et al. (2013)
	X. hypoxylon	Y		Vanderwolf et al. (2013), Zhang (2019)
	X. kegeliana			Vanderwolf et al. (2013)
	X. longipes			Vanderwolf et al. (2013)
	X. palmicola	Y	Y	
	X. polymorpha			Vanderwolf et al. (2013)
	X. schweinitzii	Y		Zhang et al. (2017)
	X. venosula	Y	Y	
	Xylaria sp.	Y	Y	Vanderwolf et al. (2013), Zhang et al. (2017)
Yarrowia	*Yarrowia bubula*			Burow et al. (2019)
Yunnania	*Yunnania carbonaria*	Y	Y	
	Yunnania penicillata	Y	Y	

Table 4 (continued)

Genus	Species	China[a]	This study[b]	References
Zakatoshia	*Zakatoshia* sp.			Vanderwolf et al. (2013)
Zalerion	*Zalerion* sp.			Vanderwolf et al. (2019)
Zasmidium	*Zasmidium cellare*			Vanderwolf et al. (2013)
	Z. syzygii	Y		Zhang (2019)
Zopfiella	*Zopfiella pleuropora*			Vanderwolf et al. (2013, 2015)
	Z. tabulata	Y	Y	
Zygosaccharomyces	*Zygosaccharomyces microellipsoides*			Vanderwolf et al. (2013)
Basidiomycota				
Abortiporus	*Abortiporus biennis*			Vanderwolf et al. (2013)
	Abortiporus sp.			Busquets et al. (2014)
Agaricus	*Agaricus* sp.			Vanderwolf et al. (2013)
Agrocybe	*Agrocybe* sp.			Vanderwolf et al. (2013)
Alysidium	*Alysidium* sp.			Vanderwolf et al. (2013)
Amyloporia	*Amyloporia sinuosa*			Vanderwolf et al. (2013)
Antrodia	*Antrodia xantha*			Vanderwolf et al. (2013)
Apiotrichum	*Apiotrichum dehoogii*	Y	Y	Burow et al. (2019)
	Api. dulcitum	Y	Y	Vanderwolf et al. (2013, 2019), Burow et al. (2019)
	Api. laibachii	Y	Y	Vanderwolf et al. (2013), Zhang et al. (2017)
	Api. lignicola			Vanderwolf et al. (2013)
	Apiotrichum sp.	Y	Y	
Armillaria	*Armillaria mellea*			Vanderwolf et al. (2013)
Asterotremella	*Asterotremella* sp.			Vanderwolf et al. (2013, 2015, 2019)
Atheniella	*Atheniella flavoalba*			Vanderwolf et al. (2013)
Auricularia	*Auricularia auricula-judae*			Vanderwolf et al. (2013)
	Aur. fuscosuccinea			Vanderwolf et al. (2013)
	Aur. polytricha			Vanderwolf et al. (2013)
Baeospora	*Baeospora myosura*			Vanderwolf et al. (2013)
	Ba. myriadophylla			Vanderwolf et al. (2013)
	Baeospora sp.			Vanderwolf et al. (2013, 2015)
Bjerkandera	*Bjerkandera adusta*	Y	Y	Vanderwolf et al. (2013), Man et al. (2015), Ogórek (2018a, b)
Boletus	*Boletus* sp.			Vanderwolf et al. (2013)
Bovista	*Bovista* sp.			Vanderwolf et al. (2013)
Bridgeoporus	*Bridgeoporus nobilissimus*			Vanderwolf et al. (2013)
Buglossoporus	*Buglossoporus pulvinus*			Vanderwolf et al. (2013)
Bulleribasidium	*Bulleribasidium variabile*			Vanderwolf et al. (2013)
Bulleromyces	*Bulleromyces albus*			Martin-Sanchez et al. (2014)
Byssomerulius	*Byssomerulius corium*			Vanderwolf et al. (2013)
Calvatia	*Calvatia* sp.			Vanderwolf et al. (2013)
Ceratobasidium	*Ceratobasidium sp.*	Y		Vanderwolf et al. (2013), Zhang et al. (2017)
Cerioporus	*Cerioporus mollis*	Y		Zhang et al. (2017)
	Ceri. varius			Vanderwolf et al. (2013)
Ceriporia	*Ceriporia lacerata*	Y		Man et al. (2015)
Ceriporiopsis	*Ceriporiopsis subvermispor*			Connell and Staudigel (2013)
Cerrena	*Cerrena unicolor*			Vanderwolf et al. (2013)
Clavaria	*Clavaria* sp.			Vanderwolf et al. (2013)
Climacocystis	*Climacocystis borealis*			Vanderwolf et al. (2013)
Clitocybe	*Clitocybe* sp.			Vanderwolf et al. (2013)
Clitopilus	*Clitopilus kamaka*	Y		Zhang et al. (2017)
	Cli. prunulus	Y	Y	
	Cli. scyphoides			Vanderwolf et al. (2013)
	Cli. sp.	Y	Y	
Collybia	*Collybia* sp.			Vanderwolf et al. (2013)
Coniophora	*Coniophora cerebella*			Vanderwolf et al. (2013)
	Coni. puteana			Vanderwolf et al. (2013)
	Coniophora sp.			Vanderwolf et al. (2013)
Coprinarius	*Coprinarius subtilis*			Vanderwolf et al. (2013)
Coprinellus	*Coprinellus disseminatus*			Vanderwolf et al. (2013), Ogórek (2018b)

Table 4 (continued)

Genus	Species	China[a]	This study[b]	References
	Coprinellus domesticus			Vanderwolf et al. (2013)
	Copr. ephemerus			Vanderwolf et al. (2013)
	Copr. micaceus	Y	Y	Vanderwolf et al. (2013)
	Copr. radians	Y	Y	Vanderwolf et al. (2013), Zhang et al. (2017)
	Copr. truncorum			Vanderwolf et al. (2013)
	Copr. xanthothrix	Y	Y	
	Coprinellus sp.	Y	Y	Vanderwolf et al. (2013), Man et al. (2015)
Coprinopsis	*Coprinopsis atramentaria*	Y		Vanderwolf et al. (2013), (Zhang 2019)
	Copri. cinerea			Vanderwolf et al. (2013)
	Copri. radiata			Vanderwolf et al. (2013)
Coprinus	*Coprinus sterquilinus*			Vanderwolf et al. (2013)
	Coprinus sp.			Vanderwolf et al. (2013)
Coriolopsis	*Coriolopsis gallica*			Vanderwolf et al. (2013)
Cortinarius	*Cortinarius* sp.			Vanderwolf et al. (2013)
Cotylidia	*Cotylidia aurantiaca*			Vanderwolf et al. (2013)
Craterellus	*Craterellus minimus*			Vanderwolf et al. (2013)
Crepidotus	*Crepidotus applanatus*			Vanderwolf et al. (2013)
	Cr. mollis			Vanderwolf et al. (2013)
Crucibulum	*Crucibulum crucibuliforme*			Vanderwolf et al. (2013)
Cryptococcus	*Cryptococcus festucosus*	Y	Y	
	Cry. macerans			Vanderwolf et al. (2013)
	Cry. neoformans			Vanderwolf et al. (2013)
	Cry. tephrensis	Y		Zhang (2019)
	Cryptococcus sp.			Burow et al. (2019)
Cutaneotrichosporon	*Cutaneotrichosporon curvatum*			Ogórek et al. (2017, 2018), Ogórek (2018a, b)
	Cut. cutaneum			Vanderwolf et al. (2013)
	Cut. dermatis	Y	Y	
	Cut. guehoae	Y	Y	
	Cut. jirovecii			Mitova et al. (2017)
	Cut. moniliiforme	Y	Y	Burow et al. (2019)
	Cut. mucoides			Vanderwolf et al. (2013)
	Cut. smithiae	Y	Y	
Cylindrobasidium	*Cylindrobasidium evolvens*	Y		Zhang (2019)
Cystobasidium	*Cystobasidium minuta*			Vanderwolf et al. (2013)
	Cys. slooffiae	Y		Zhang (2019)
Cystofilobasidium	*Cystofilobasidium macerans*			Connell and Staudigel (2013)
	Cystofilobasidium sp.			Vanderwolf et al. (2013, 2015)
Daedalea	*Daedalea quercina*			Vanderwolf et al. (2013)
Deconica	*Deconica hartii*			Vanderwolf et al. (2013)
Delicatula	*Delicatula integrella*			Vanderwolf et al. (2013)
	De. microscopica			Vanderwolf et al. (2013)
Donkioporia	*Donkioporia expansa*			Vanderwolf et al. (2013)
Duportella	*Duportella lassa*	Y	Y	
Effuseotrichosporon	*Effuseotrichosporon vanderwaltii*	Y	Y	
Elmerina	*Elmerina caryae*			Vanderwolf et al. (2013)
Entomocorticium	*Entomocorticium* sp.			Pusz et al. (2017)
Exidia	*Exidia glandulosa*			Connell and Staudigel (2013)
Exobasidium	*Exobasidium* sp.			Connell and Staudigel (2013)
Favolus	*Favolus tenuiculus*			Vanderwolf et al. (2013)
Fayodia	*Fayodia gracilipes*			Vanderwolf et al. (2013)
	Fayodia sp.			Vanderwolf et al. (2013)
Fibroporia	*Fibroporia vaillantii*			Vanderwolf et al. (2013)
Filobasidium	*Filobasidium floriforme*			Connell and Staudigel (2013)
	Fi. magnum			Vanderwolf et al. (2013)
	Fi. wieringae			Connell and Staudigel (2013)
Fistulina	*Fistulina hepatica*			Vanderwolf et al. (2013)
Flaviporus	*Flaviporus brownii*			Vanderwolf et al. (2013)
Flavodon	*Flavodon flavus*	Y	Y	

Table 4 (continued)

Genus	Species	China[a]	This study[b]	References
Fomes	*Fomes fomentarius*			Vanderwolf et al. (2013), Ogórek et al. (2017,2018)
	Fomes sp.			Vanderwolf et al. (2013)
Fomitopsis	*Fomitopsis pinicola*			Vanderwolf et al. (2013)
Galerina	*Galerina camerina*			Vanderwolf et al. (2013)
	Ga. praticola			Vanderwolf et al. (2013)
	Ga. pumila			Vanderwolf et al. (2013)
	Galerina sp.			Vanderwolf et al. (2013)
Ganoderma	*Ganoderma applanatum*			Connell and Staudigel (2013)
	Gan. carnosum	Y	Y	
	Gan. gibbosum	Y		Zhang et al. (2017)
	Gan. lipsiense			Vanderwolf et al. (2013)
	Gan. lucidum			Vanderwolf et al. (2013)
	Gan. resinaceum			Vanderwolf et al. (2013)
	Ganoderma sp.			Vanderwolf et al. (2013)
Geastrum	*Geastrum minimum*			Vanderwolf et al. (2013)
	Ge. saccatum			Vanderwolf et al. (2013)
Glaciozyma	*Glaciozyma antarctica*			Brad et al. (2018)
	Gla. watsonii			Connell and Staudigel (2013)
Gloeohypochnicium	*Gloeohypochnicium analogum*			Vanderwolf et al. (2013)
Gloeophyllum	*Gloeophyllum abietinum*			Vanderwolf et al. (2013)
	Glo. odoratum			Vanderwolf et al. (2013)
	Glo. sepiarium			Vanderwolf et al. (2013)
	Glo. trabeum			Vanderwolf et al. (2013)
	Gloeophyllum sp.			Vanderwolf et al. (2013)
Golubevia	*Golubevia pallescens*	Y	Y	
Gymnopus	*Gymnopus johnstonii*			Vanderwolf et al. (2013)
Hannaella	*Hannaella luteola*			Vanderwolf et al. (2013)
	Ha. oryzae	Y	Y	
Hemimycena	*Hemimycena cucullata*			Vanderwolf et al. (2013)
	He. lactea			Vanderwolf et al. (2013)
Heterobasidion	*Heterobasidion annosum*			Vanderwolf et al. (2013), Nováková et al. (2018)
Hexagonia	*Hexagonia hydnoides*			Vanderwolf et al. (2013)
Hohenbuehelia	*Hohenbuehelia petaloides*			Vanderwolf et al. (2013)
Holtermanniella	*Holtermanniella watticus*			Zhang et al. (2014)
Hydnopolyporus	*Hydnopolyporus palmatus*			Vanderwolf et al. (2013)
Hydnum	*Hydnum spinuliferum*			Vanderwolf et al. (2013)
Hygrophorus	*Hygrophorus* sp.			Vanderwolf et al. (2013)
Hymenochaete	*Hymenochaete corrugata*			Vanderwolf et al. (2013)
	Hymenochaete sp.			Connell and Staudigel (2013)
Hymenogaster	*Hymenogaster vulgaris*			Vanderwolf et al. (2013)
	Hymenogaster sp.			Vanderwolf et al. (2013)
Hyphodermella	*Hyphodermella corrugata*	Y		Zhang et al. (2017)
	Hyphodermella sp.	Y		Zhang et al. (2017)
Hyphodontia	*Hyphodontia arguta*			Vanderwolf et al. (2013)
	Hyp. hastata			Vanderwolf et al. (2013)
	Hyp. palmae	Y	Y	
Hypholoma	*Hypholoma dispersum*			Vanderwolf et al. (2013)
	Hyph. fasciculare			Vanderwolf et al. (2013)
	Hyph. radicosum			Vanderwolf et al. (2013)
	Hypholoma sp.			Vanderwolf et al. (2013, 2015)
Hypochnicium	*Hypochnicium punctulatum*			Vanderwolf et al. (2013)
Inocybe	*Inocybe* sp.			Vanderwolf et al. (2013)
Irpex	*Irpex lacteus*	Y	Y	Connell and Staudigel (2013)
Junghuhnia	*Junghuhnia nitida*			Vanderwolf et al. (2013)
Laccaria	*Laccaria laccata*			Vanderwolf et al. (2013)
Lentinus	*Lentinus* sp.			Vanderwolf et al. (2013)
Lenzites	*Lenzites betulina*			Vanderwolf et al. (2013)
Lepiota	*Lepiota* sp.			Vanderwolf et al. (2013)

Table 4 (continued)

Genus	Species	China[a]	This study[b]	References
Leucogyrophana	*Leucogyrophana mollusca*			Vanderwolf et al. (2013)
	Leuc. pinastri			Vanderwolf et al. (2013)
Leucosporidium	*Leucosporidium fellii*			Vanderwolf et al. (2013)
Lycoperdon	*Lycoperdon perlatum*	Y	Y	
	Lycoperdon sp.	Y	Y	
Malassezia	*Malassezia furfur*			Vanderwolf et al. (2013)
	Mal. globosa			Connell and Staudigel (2013)
	Mal. restricta			Connell and Staudigel (2013)
Marasmiellus	*Marasmiellus ramealis*			Vanderwolf et al. (2013)
Marasmius	*Marasmius atrorubens*			Vanderwolf et al. (2013)
	Mar. epiphyllus			Vanderwolf et al. (2013)
	Marasmius sp.			Vanderwolf et al. (2013)
Meira	*Meira nashicola*	Y	Y	
Merulius	*Merulius melanoceras*			Vanderwolf et al. (2013)
	Merulius sp.			Vanderwolf et al. (2013)
Moesziomyces	*Moesziomyces antarcticus*			Vanderwolf et al. (2013)
Mrakia	*Mrakia gelida*			Brad et al. (2018)
	Mra. frigida			Brad et al. (2018)
Mycena	*Mycena acicula*			Vanderwolf et al. (2013)
	Myc. amicta			Vanderwolf et al. 2013
	Myc. capillaris			Vanderwolf et al. (2013)
	Myc. galericulata			Vanderwolf et al. (2013)
	Myc. metata			Vanderwolf et al. (2013)
	Myc. mucor			Vanderwolf et al. (2013)
	Myc. polyadelpha			Vanderwolf et al. (2013)
	Myc. polygramma			Vanderwolf et al. (2013)
	Myc. strobilicola			Vanderwolf et al. (2013)
	Myc. stylobates			Vanderwolf et al. (2013)
	Myc. supina			Vanderwolf et al. (2013)
	Myc. vitilis			Vanderwolf et al. (2013)
	Mycena sp.			Connell and Staudigel (2013), Vanderwolf et al. (2013)
Naganishia	*Naganishia albida*			Vanderwolf et al. (2013)
	Na. diffluens			Vanderwolf et al. (2013)
Naucoria	*Naucoria* sp.			Vanderwolf et al. 2013
Neoantrodia	*Neoantrodia serialis*			Vanderwolf et al. (2013)
Neolentinus	*Neolentinus suffrutescens*			Vanderwolf et al. (2013)
Omphalina	*Omphalina* sp.			Vanderwolf et al. (2013)
Onnia	*Onnia tomentosa*			Vanderwolf et al. (2013)
Osteina	*Osteina obducta*			Vanderwolf et al. (2013)
Ozonium	*Ozonium aureum*			Vanderwolf et al. (2013)
	Oz. auricomum			Vanderwolf et al. (2013)
	Oz. stuposum			Vanderwolf et al. (2013)
Panellus	*Panellus stipticus*			Vanderwolf et al. (2013)
Panus	*Panus neostrigosus*			Vanderwolf et al. (2013)
	Panus sp.			Vanderwolf et al. (2013)
Papiliotrema	*Papiliotrema flavescens*	Y	Y	
	Pap. laurentii	Y	Y	Vanderwolf et al. (2013)
Parasola	*Parasola plicatilis*			Vanderwolf et al. (2013)
Paxillus	*Paxillus* sp.			Vanderwolf et al. (2013)
Peniophora	*Peniophora cinerea*	Y		Zhang et al. (2017)
	Pen. incarnata	Y		Zhang (2019)
	Pen. limitata	Y		Zhang et al. (2017)
	Pen. lycii			Connell and Staudigel (2013)
	Pen. quercina			Vanderwolf et al. (2013)
	Peniophora sp.	Y	Y	Zhang et al. (2017)
Perenniporia	*Perenniporia medulla-panis*	Y	Y	
Phaeocollybia	*Phaeocollybia sp.*	Y	Y	
Phaeomarasmius	*Phaeomarasmius* sp.			Vanderwolf et al. (2013)

Table 4 (continued)

Genus	Species	China[a]	This study[b]	References
Phanerochaete	*Phanerochaete sordida*	Y		Zhang et al. (2017)
	Phanerochaete sp.			Connell and Staudigel (2013), Vanderwolf et al. (2013)
Phanerodontia	*Phanerodontia chrysosporium*			Vanderwolf et al. (2013)
Phellinus	*Phellinus ferruginosus*			Vanderwolf et al. (2013)
	Phe. gilvus			Vanderwolf et al. (2013)
	Phe. punctatus			Vanderwolf et al. (2013)
Phlebia	*Phlebia livida*	Y	Y	
	Phl. rufa	Y	Y	
	Phl. tremellosa			Vanderwolf et al. (2013)
Phlebiopsis	*Phlebiopsis gigantea*			Ogórek (2018b)
	Phlebiopsis sp.	Y	Y	
Phloeomana	*Phloeomana alba*			Vanderwolf et al. (2013)
	Phlo. minutula			Vanderwolf et al. (2013)
Pholiota	*Pholiota multicingulata*	Y	Y	
	Pholiota sp.			Vanderwolf et al. (2013)
Physisporinus	*Physisporinus vitreus*	Y	Y	Vanderwolf et al. (2013)
Pluteus	*Pluteus* sp.			Vanderwolf et al. (2013)
Podoscypha	*Podoscypha* sp.			Vanderwolf et al. (2013)
Polyporus	*Polyporus* sp.			Connell and Staudigel (2013), Vanderwolf et al. (2013)
	Poly. venetus			Vanderwolf et al. (2013)
Poria	*Poria* sp.			Vanderwolf et al. (2013)
Postia	*Postia balsamea*			Vanderwolf et al. (2013)
	Pos. caesia			Vanderwolf et al. (2013)
	Pos. floriformis			Vanderwolf et al. (2013)
	Pos. stiptica			Vanderwolf et al. (2013)
Psathyra	*Psathyra corrugis*			Vanderwolf et al. (2013)
Psathyrella	*Psathyrella candolleana*	Y		Vanderwolf et al. (2013), Zhang et al. (2017)
	Psa. corrugis	Y		Zhang et al. (2017)
	Psathyrella sp.			Vanderwolf et al. (2013)
Pseudoinonotus	*Pseudoinonotus dryadeus*			Vanderwolf et al. (2013)
Pseudozyma	*Pseudozyma* sp.			Vanderwolf et al. (2013)
Psilocybe	*Psilocybe sp.*	Y	Y	
Puccinia	*Puccinia* sp.			Vanderwolf et al. (2013)
Ramaria	*Ramaria* sp.			Vanderwolf et al. (2013)
Resinicium	*Resinicium bicolor*			Connell and Staudigel (2013)
Resinoporia	*Resinoporia crassa*			Vanderwolf et al. (2013)
Rhizoctonia	*Rhizoctonia solani*			Pusz et al. (2018a)
Rhizomarasmius	*Rhizomarasmius setosus*			Vanderwolf et al. (2013)
Rhizomorpha	*Rhizomorpha* sp.			Vanderwolf et al. (2013)
Rhodofomes	*Rhodofomes roseus*			Vanderwolf et al. (2013)
Rhodonia	*Rhodonia placenta*			Vanderwolf et al. (2013)
Rhodotorula	*Rhodotorula dairenensis*			Vanderwolf et al. (2013)
	Rho. glutinis			Vanderwolf et al. (2013), Ogórek et al. (2013, 2016b, d)
	Rho. mucilaginosa	Y	Y	Connell and Staudigel (2013), Vanderwolf et al. (2013)
	Rho. rubra			Ogórek et al. (2013, 2016c, d), Kokurewicz et al. (2016)
	Rhodotorula sp.			Vanderwolf et al. (2013)
Rigidoporus	*Rigidoporus lineatus*			Vanderwolf et al. (2013)
	Ri. microporus			Vanderwolf et al. (2013)
	Ri. sanguinolentus			Vanderwolf et al. (2013)
	Ri. undatus			Vanderwolf et al. (2013)
	Ri. vinctus	Y		Zhang (2019)
	Rigidoporus sp.	Y		Zhang et al. (2017)
Russula	*Russula* sp.			Vanderwolf et al. (2013)
Saitozyma	*Saitozyma podzolica*	Y	Y	Vanderwolf et al. (2013)
Sampaiozyma	*Sampaiozyma ingeniosa*	Y	Y	
Schizophyllum	*Schizophyllum commune*	Y	Y	Vanderwolf et al. (2013), Zhang et al. (2017)
Schizopora	*Schizopora paradoxa*			Vanderwolf et al. (2013)
Scleroderma	*Scleroderma* sp.			Vanderwolf et al. (2013)

Table 4 (continued)

Genus	Species	China[a]	This study[b]	References
Serpula	*Serpula himantioides*			Vanderwolf et al. (2013)
	Ser. lacrymans			Vanderwolf et al. (2013)
Sistotrema	*Sistotrema brinkmannii*			Connell and Staudigel (2013)
Skeletocutis	*Skeletocutis chrysella*			Connell and Staudigel (2013)
Sporobolomyces	*Sporobolomyces coprosmae*			Vanderwolf et al. (2013)
	Spor. roseus			Vanderwolf et al. (2013), Martin-Sanchez et al. (2014)
	Spor. ruberrimus			Martin-Sanchez et al. (2014)
	Sporobolomyces sp.			Connell and Staudigel (2013), Martin-Sanchez et al. (2014)
Sporotrichum	*Sporotrichum flavissimum*			Vanderwolf et al. (2013)
	Sporotrichum sp.			Vanderwolf et al. (2013)
Steccherinum	*Steccherinum* sp.	Y		Zhang (2019)
Stereum	*Stereum hirsutum*			Vanderwolf et al. (2013)
	Ster. sanguinolentum			Connell and Staudigel (2013)
	Stereum sp.			Connell and Staudigel (2013), Vanderwolf et al. (2013)
Strobilurus	*Strobilurus esculentus*			Vanderwolf et al. (2013)
Tapinella	*Tapinella panuoides*			Vanderwolf et al. (2013)
Tausonia	*Tausonia pullulans*			Vanderwolf et al. (2013), Zhang et al. (2014)
Tetrapyrgos	*Tetrapyrgos nigripes*			Vanderwolf et al. (2013)
Thanatephorus	*Thanatephorus cucumeris*			Vanderwolf et al. (2013)
Thelephora	*Thelephora penicillata*			Vanderwolf et al. (2013)
Tilletia	*Tilletia* sp.			Vanderwolf et al. (2013)
Tinctoporellus	*Tinctoporellus epimiltinus*	Y		Zhang et al. (2017)
Tomentella	*Tomentella lapida*			Vanderwolf et al. (2013)
	Tomentella sp.			Vanderwolf et al. (2013)
Trametes	*Trametes cubensis*			Connell and Staudigel (2013)
	Tra. gibbosa			Vanderwolf et al. (2013)
	Tra. hirsuta	Y		Vanderwolf et al. (2013), Man et al. (2015), Ogórek et al. (2017, 2018a)
	Tra. ochracea			Vanderwolf et al. (2013)
	Tra. pubescens			Vanderwolf et al. (2013)
	Trametes sp.			Vanderwolf et al. (2013)
	Tra. trogii	Y	Y	Vanderwolf et al. (2013)
	Tra. versicolor	Y		Vanderwolf et al. (2013), Zhang et al. 2017
Trechispora	*Trechispora alnicola*			Vanderwolf et al. (2013)
Tremella	*Tremella mesenterica*			Vanderwolf et al. (2013)
	Tremella sp.			Vanderwolf et al. (2013)
Trichaptum	*Trichaptum* sp.			Connell and Staudigel (2013)
Tricholoma	*Tricholoma saponaceum*			Vanderwolf et al. (2013)
Tricholomopsis	*Tricholomopsis aurea*			Vanderwolf et al. (2013)
Trichosporon	*Trichosporon aggtelekiense*			Nováková et al. (2015)
	Tricho. akiyoshidainum	Y	Y	Vanderwolf et al. (2013), Zhang et al. (2017)
	Tricho. dulcitum			Zhang et al. (2014), Vanderwolf et al. (2015)
	Tricho. cavernicola	Y	Y	Vanderwolf et al. (2013)
	Tricho. chiropterorum	Y	Y	Vanderwolf et al. (2013)
	Tricho. coprophilum			Vanderwolf et al. (2013)
	Tricho. ovoides			Vanderwolf et al. (2013)
	Tricho. porosum			Vanderwolf et al. (2013), Mitova et al. (2017)
	Tricho. shinodae	Y	Y	
	Tricho. spelunceum			Nováková et al. (2015)
	Trichosporon sp.	Y		Vanderwolf et al. (2013, 2015, 2019), Man et al. (2015), Bercea et al. (2018), Burow et al. (2019)
Tubaria	*Tubaria furfuracea*			Vanderwolf et al. (2013)
Ustilago	*Ustilago tritici*			Connell and Staudigel (2013), Vanderwolf et al. (2013)
	Ustilago sp.			Connell and Staudigel (2013)
Vishniacozyma	*Vishniacozyma dimennae*			Martin-Sanchez et al. (2014)
Vanrija	*Vanrija fragicola*			Zhang et al. (2014)
Volvariella	*Volvariella* sp.			Vanderwolf et al. (2013)
Wallemia	*Wallemia mellicola*	Y	Y	
	Wal. sebi			Vanderwolf et al. (2013)

Table 4 (continued)

Genus	Species	China[a]	This study[b]	References
Xylodon	*Xylodon rimosissimus*			Connell and Staudigel (2013)
Mortierellomycotina				
Mortierella	*Mortierella alliacea*			Vanderwolf et al. (2013)
	Mo. alpina	Y	Y	Vanderwolf et al. (2013), Zhang et al. (2014), Man et al. (2015), Zhang et al. (2017), Dyląg et al. (2019), Popkova and Mazina (2019)
	Mo. amoeboidea			Zhang et al. (2014)
	Mo. bainieri			Vanderwolf et al. (2013)
	Mo. chienii			Vanderwolf et al. (2013)
	Mo. clonocystis	Y	Y	
	Mo. dichotoma	Y	Y	Vanderwolf et al. (2013), Zhang et al. (2014)
	Mo. elongata			Vanderwolf et al. (2013)
	Mo. epicladia	Y	Y	Vanderwolf et al. (2013)
	Mo. exigua			Vanderwolf et al. (2013)
	Mo. fimbricystis			Out et al. (2016)
	Mo. gamsii			Vanderwolf et al. (2013), Zhang et al. (2014)
	Mo. histoplasmatoides			Zhang et al. (2014)
	Mo. horticola	Y		Zhang et al. (2017)
	Mo. humilis			Vanderwolf et al. (2013)
	Mo. hyalina	Y	Y	Vanderwolf et al. (2013), Zhang et al. (2014), Pusz et al. (2015), Out et al. (2016), Pusz et al. (2017), Zhang et al. (2017)
	Mo. hypsicladia	Y	Y	
	Mo. indohii	Y	Y	Zhang et al. (2017)
	Mo. jenkinii			Zhang et al. (2014)
	Mo. minutissima	Y		Zhang et al. (2017)
	Mo. nantahalensis			Vanderwolf et al. (2013)
	Mo. oligospora			Vanderwolf et al. (2013)
	Mo. parvispora			Ogórek et al. (2017), Burow et al. (2019)
	Mo. polycephala			Vanderwolf et al. (2013), Zhang et al. (2014), Out et al. (2016)
	Mo. pulchella			Vanderwolf et al. (2013)
	Mo. reticulata	Y	Y	
	Mo. sarnyensis			Vanderwolf et al. (2013), Zhang et al. (2014)
	Mo. sclerotiella			Out et al. (2016)
	Mo. selenospora	Y		Man et al. (2015)
	Mo. stylospora			Zhang et al. (2014)
	Mo. verticillata	Y	Y	Vanderwolf et al. (2013)
	Mo. zonata	Y	Y	
	Mortierella sp.	Y	Y	Vanderwolf et al. (2013, 2015, 2019), Martin-Sanchez et al. (2014), Zhang et al. (2014), Yoder et al. (2015), Out et al. (2016), Mitova et al. (2017), Zhang et al. (2017), Nováková et al. (2018), Leplat et al. (2018), Burow et al. (2019)
Mucoromycotina				
Absidia	*Absidia caerulea*			Vanderwolf et al. (2013)
	Ab. cylindrospora			Vanderwolf et al. (2013), Popkova and Mazina (2019)
	Ab. glauca			Vanderwolf et al. (2013), Kokurewicz et al. (2016), Ogórek et al. (2016b)
	Ab. repens			Vanderwolf et al. (2013)
	Ab. spinosa			Vanderwolf et al. (2013), Nováková et al. (2018)
	Absidia sp.			Vanderwolf et al. (2013), Leplat et al. (2018), Dyląg et al. (2019), Popkova and Mazina (2019)
Actinomucor	*Actinomucor elegans*			Vanderwolf et al. (2013), Nováková et al. (2018)
	Actinomucor sp.	Y		Jiang et al. (2017a, b)
Choanephora	*Choanephora cucurbitarum*			Vanderwolf et al. (2013)
Circinella	*Circinella muscae*			Vanderwolf et al. (2013)
	Ci. simplex			Vanderwolf et al. (2013)
	Ci. umbellata	Y	Y	Vanderwolf et al. (2013)
	Circinella sp.	Y	Y	Vanderwolf et al. (2013)
Cunninghamella	*Cunninghamella echinulata*	Y	Y	Vanderwolf et al. (2013), Nováková et al. (2018)
	Cun. elegans			Vanderwolf et al. (2013), Nováková et al. (2018)
	Cunninghamella sp.	Y	Y	Vanderwolf et al. (2013)
Gongronella	*Gongronella sp.*	Y	Y	

Table 4 (continued)

Genus	Species	China[a]	This study[b]	References
Helicostylum	*Helicostylum elegans*			Vanderwolf et al. (2013), Zhang et al. (2014)
	Hel. pulchrum			Zhang et al. (2014)
	Helicostylum sp.			Vanderwolf et al. (2013)
Lichtheimia	*Lichtheimia blakesleeana*			Vanderwolf et al. (2013)
	Li. corymbifera			Vanderwolf et al. (2013)
Mucor	*Mucor abundans*			Burow et al. (2019)
	Mu. aligarensis			Mitova et al. (2017), Ogórek et al. (2017), Dyląg et al. (2019)
	Mu. bacilliformis			Vanderwolf et al. (2013)
	Mu. circinelloides	Y	Y	Vanderwolf et al. (2013), Jacobs et al. (2017), Mitova et al. (2017)
	Mu. corticola			Vanderwolf et al. (2013)
	Mu. flavus	Y		Vanderwolf et al. (2013), Zhang et al. (2014), Kokurewicz et al. (2016), Jacobs et al. (2017), Jiang et al. (2017a, b), Zhang et al. (2017), Burow et al. (2019)
	Mu. fragilis	Y	Y	Vanderwolf et al. (2013), Man et al. (2015)
	Mu. fuscus	Y	Y	
	Mu. hiemalis	Y	Y	Vanderwolf et al. (2013), Zhang et al. (2014), Pusz et al. (2015), Kokurewicz et al. (2016), Ogórek et al. (2016b, c, 2017, 2018), Pusz et al. (2017), Zhang et al. (2017), Popkova and Mazina (2019)
	Mu. indicus			Vanderwolf et al. (2013)
	Mu. irregularis	Y		Zhang et al. (2017)
	Mu. luteus			Kokurewicz et al. (2016), Zhang et al. (2014), Pusz et al. (2015)
	Mu. moelleri	Y		Zhang et al. (2017)
	Mu. mucedo			Ogórek et al. (2013, 2014a), Vanderwolf et al. (2013)
	Mu. piriformis			Vanderwolf et al. (2013)
	Mu. plumbeus			Vanderwolf et al. (2013), Dyląg et al. (2019)
	Mu. racemosus	Y		Vanderwolf et al. (2013), Out et al. (2016), Kokurewicz et al. (2016), Zhang et al. (2017)
	Mu. ramosissimus			Vanderwolf et al. (2013)
	Mu. rouxii	Y		Jiang et al. (2017a, b), Popkova and Mazina (2019)
	Mu. silvaticus			Vanderwolf et al. (2013)
	Mu. strictus			Out et al. (2016)
	Mu. subtilissimus			Vanderwolf et al. (2013)
	Mu. troglophilus			Vanderwolf et al. (2013)
	Mucor sp.	Y	Y	Taylor et al. (2013), Vanderwolf et al. (2013, 2015, 2019), Ogórek et al. (, 2014b, c), Zhang et al. (2014), Popović et al. (2015), Yoder et al. (2015), Jiang et al. (2017a, b), Mitova et al. (2017), Zhang et al. (2017), Leplat et al. (2018), Burow et al. (2019)
Phycomyces	*Phycomyces* sp.			Vanderwolf et al. 2013)
Pilobolus	*Pilobolus* sp.			Vanderwolf et al. (2013)
Rhizomucor	*Rhizomucor pusillus*			Vanderwolf et al. (2013)
	Rhizomucor sp.			Pfendler et al. (2019)
Rhizopus	*Rhizopus arrhizus*			Vanderwolf et al. (2013), Pusz et al. (2018a), Popkova and Mazina (2019)
	Rhi. microsporus			Vanderwolf et al. (2013)
	Rhi. oryzae	Y		Zhang et al. (2017)
	Rhi. stolonifer	Y		Ogórek et al. (2013, 2014a, 2016b, c, d), Vanderwolf et al. (2013), Kokurewicz et al. (2016), Jiang et al. (2017a, b), Nováková et al. (2018), Popkova and Mazina (2019)
	Rhizopus sp.			Taylor et al. (2013), Vanderwolf et al. (2013), Ogórek et al. (2014a, b), Yoder et al. (2015)
Syncephalastrum	*Syncephalastrum racemosum*			Vanderwolf et al. (2013)
	Syncephalastrum sp.			Vanderwolf et al. (2013)
Thamnidium	*Thamnidium elegans*			Vanderwolf et al. (2013, 2015)
	Thamnidium sp.			Popkova and Mazina (2019), Vanderwolf et al. (2019)
Thamnostylum	*Thamnostylum piriforme*			Vanderwolf et al. (2013)
Umbelopsis	*Umbelopsis angularis*			Burow et al. (2019)
	Um. dimorpha	Y	Y	
	Um. isabellina	Y	Y	Vanderwolf et al. (2013)
	Um. ramanniana			Vanderwolf et al. (2013), Zhang et al. (2014)
Entomophthoromycotina				
Conidiobolus	*Conidiobolus coronatus*			Burow et al. (2019)
	Conidiobolus sp.			Vanderwolf et al. (2013)

Table 4 (continued)

Genus	Species	China[a]	This study[b]	References
Entomophaga	*Entomophaga grylli*			Vanderwolf et al. (2013)
Entomophthora	*Entomophthora destruens*			Vanderwolf et al. (2013)
Chytridiomycota				
Batrachochytrium	*Batrachochytrium dendrobatidis*			Vanderwolf et al. (2013)
Cladochytrium	*Cladochytrium tenue*			Vanderwolf et al. (2013)
Rhizophydium	*Rhizophydium* sp.			Vanderwolf et al. (2013)
Zoopagomycotina				
Rhopalomyces	*Rhopalomyces elegans*			Vanderwolf et al. (2013)
Syncephalis	*Syncephalis* sp.			Vanderwolf et al. (2013)
Kickxella	*Kickxella alabastrina*			Vanderwolf et al. (2019)
Kickxellomycotina				
Coemansia	*Coemansia aciculifera*			Vanderwolf et al. (2013)
	Coemansia sp.			Vanderwolf et al. (2013)
Glomeromycota				
Entrophospora	*Entrophospora* sp.	Y	Y	

[a]"Y" means this fungus was documented in caves in China

[b]"Y" means this fungus was isolated from caves in this study

Paraphaeosphaeria O.E. Erikss.

Paraphaeosphaeria was introduced by Eriksson (1967) to accommodate four species with oblong-cylindric ascospores, and placed in *Didymosphaeriaceae* (= Montagnulaceae) by Ariyawansa et al. (2014) based on multi-locus phylogeny. Currently there are 33 species in *Paraphaeosphaeria* (Wijayawardene et al. 2020). Here, we introduce a new species of *Paraphaeosphaeria* named as *P. hydei* isolated from plant debris (Fig. 5).

Paraphaeosphaeria hydei Z.F. Zhang & L. Cai, ***sp. nov.***

Index Fungorum number: 556392, *Facesoffungi number*: FoF 08425, Fig. 6

Etymology: "*hydei"* named for in honour of Prof. Kevin D. Hyde for his contribution to ascomycetes taxonomy.

Holotype: HMAS 247988.

Hyphae hyaline to brown, septate, branched, sometimes swollen to chlamydospore-like cell, brown, thick-walled, up to 12µm diam. **Asexual morph** *Conidiomata* pycnidial, erumpent, single, or eustromatic and more complex, mostly superficial, globose, glabrous, dark brown, up to 200 µm diam, with central ostiole. *Pycnidial wall* composed of an outer layer of yellow-brown, thick-walled textura angularis, and an inner layer with hyaline, thin-walled cells. *Conidiogenous cells* lining the inner cavity, ampulliform or flask-shaped, smooth, hyaline, 4.0–7.5 × 5.0–8.0 µm. *Conidia* abundant, solitary, unicellular, ovoid or ellipsoidal with obtuse ends, smooth, thick-walled, brown, 6.0–8.0 × 4.0–6.0 µm ($\bar{x} \pm$ SD = 7.1 ± 0.55 × 5.2 ± 0.45 µm, n = 60), average L/W ratio 1.36 ± 0.15. **Sexual morph** not observed.

Culture characteristics—Colonies on PDA attaining 45 mm diam. after 21 days, flat, felty, margin entire, dark olive (27F4) at margin, pale gray (28B1) at middle, olive (27D3) in center with pale gray (28B1) patches, aerial mycelia sparse. Reverse dark olive (27F2). Colonies on OA attaining 45 mm diam. after 21 days, flat, black to dark olive (26F5), aerial mycelia sparse, with abundant black conidiomata scattered. Reverse black. Colonies on SNA attaining 45 mm diam. after 21 days, aerial mycelia sparse, colorless. Reverse colorless. Sporulation within 20 days on PDA and OA.

Material examined: CHINA, Yunnan, Yiliang, Sanjiao Cave, N 25.134°, E 103.383°, on plant debris, May 2016, Z.F. Zhang, HMAS 247988 (holotype designated here), ex-type living culture CGMCC3.19317 = LC12564; ibid., LC12565.

Notes: In the multi-locus phylogenetic analysis, this new species clustered with *Paraphaeosphaeria arecacearum* Verkley, Göker & Stielow in a distinct clade (Fig. 5). However, conidia of *P. arecacearum* are longer than that of *P. dispersa* (3.5–6.0 µm vs. 3.0–4.0 µm, 2.0 ± 0.04 vs. 1.36 ± 0.15 for average L/W ratio). In addition, *P. dispersa* growing on OA (45 mm/14 days) is much slower than *P. arecacearum* (70–75 mm/10 days).

Setophaeosphaeria Crous & Y. Zhang ter

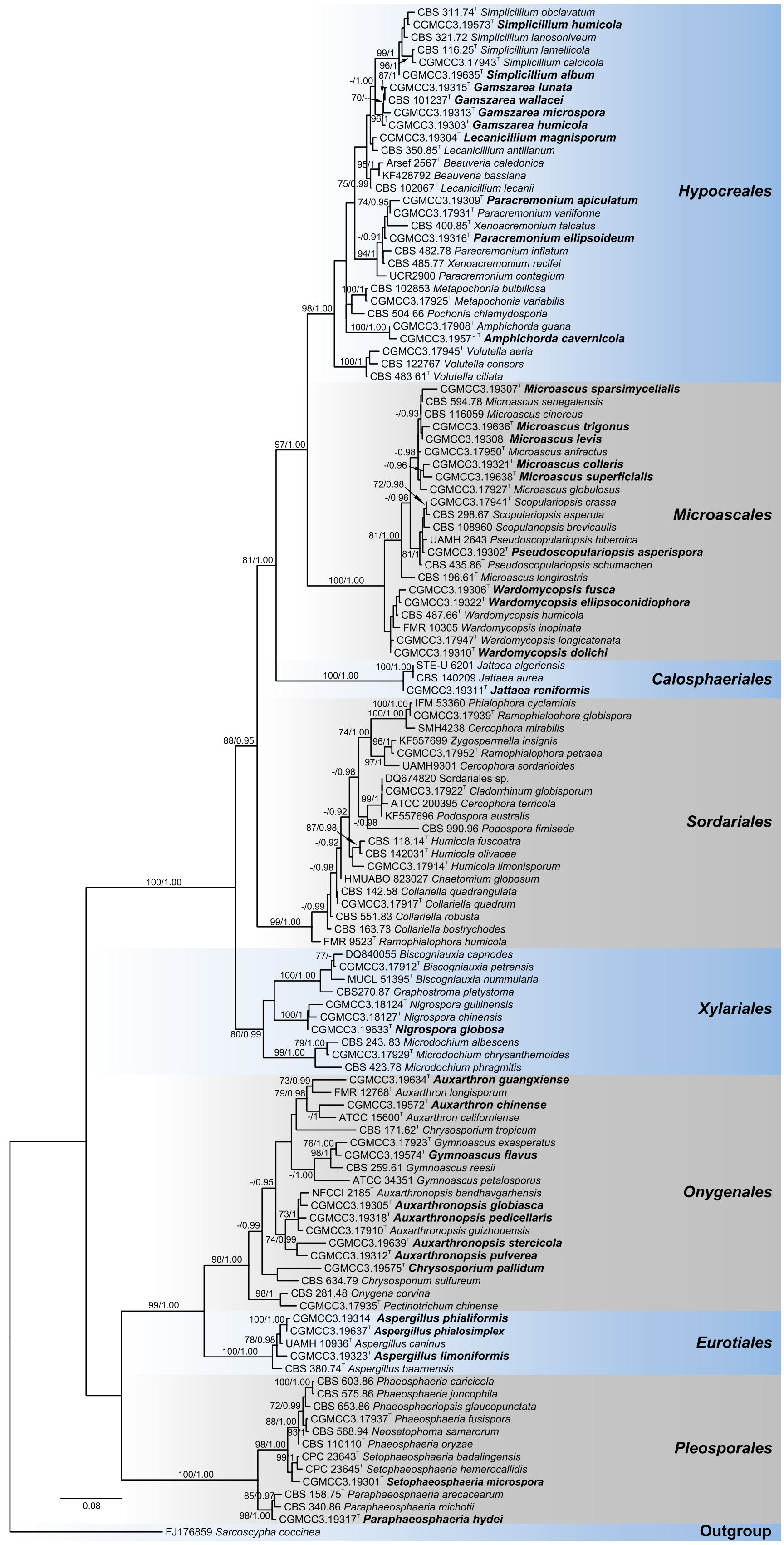
Setophaeosphaeria was established by Crous et al. (2014) to accommodate ascomycetes that are dissimilar to *Phaeosphaeria* in the absence of ascomatal setae, and with phoma-like anamorphs. *Setophaeosphaeria* currently comprises six species, with *S. hemerocallidis* Crous & Y. Zhang ter as type, and one new species described herein as *S. microsporai* (Fig. 7).

Setophaeosphaeria microspora Z.F. Zhang & L. Cai, ***sp. nov.***

Index Fungorum number: 556393, *Facesoffungi number:* FoF 08426; Fig. 8

Etymology: Referring to its smaller conidia than other species in this genus.

Fig. 4 Maximum likelihood (ML) tree based on LSU sequences showing the order placements of new species described in this study. 122 strains belong to eight orders are used. The tree is rooted with *Sarcoscypha coccinea* (FF176859). Tree topology of the ML analysis was similar to the BI. The Best scoring RAxML tree with a final likelihood value of − 9721.274792. The matrix had 422 distinct alignment patterns, with 7.98 % of undetermined characters or gaps. Base frequencies estimated by jModelTest were as follows, A = 0.1940, C = 0.2411, G = 0.3481, T = 0.2168; substitution rates AC = 0.9460, AG = 3.5105, AT = 1.8719, CG = 0.5969, CT = 8.3876, GT = 1.0000; gamma shape = 0.5390. ML bootstrap values (≥ 70 %) and Bayesian posterior probability (≥ 90 %) are indicated along branches (ML/PP). Novel species are indicated in bold font and the orders are shown on the right side of the figure



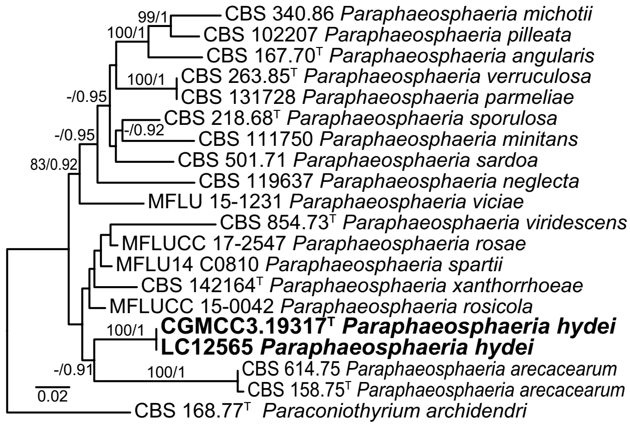


Fig. 5 Maximum likelihood (ML) tree of *Paraphaeosphaeria* and allied genera based on ITS, LSU, Actin and TUB sequences. Twenty strains are used. The tree is rooted with *Paraconiothyrium archidendri* (CBS 168.77). Tree topology of the ML analysis was similar to the BI. The Best scoring RAxML tree with a final likelihood value of – 7370.589451. The matrix had 487 distinct alignment patterns, with 12.14 % of undetermined characters or gaps. Base frequencies estimated by jModelTest were as follows, A = 0.2240, C = 0.2745, G = 0.2723, T = 0.2292; substitution rates AC = 1.7609, AG = 4.2567, AT = 1.7609, CG = 1.0000, CT = 7.3594, GT = 1.0000; gamma shape = 0.2610. ML bootstrap values (≥ 70 %) and Bayesian posterior probability (≥ 90 %) are indicated along branches (ML/PP). Novel species are in bold font and "T" indicates type derived sequences

Holotype: HMAS 247990.

Hyphae hyaline to brown, septate, branched. **Asexual morph** *Conidiomata* pycnidial, single or eustromatic, superficial or immersed, globose, brown, up to 260 µm diam, with central ostiole. *Pycnidial wall* of 2–3 layers of the brown textura angularis. *Setae* slightly flexuous, septate, unbranched, smooth, thick-walled, brown to pale brown from base to apex, more abundant surrounding ostiole, with obtuse ends, 45–130 µm long, 2.0–4.0 µm wide. *Conidiogenous cells* lining the inner cavity, ampulliform, proliferating several times percurrently at apex, smooth, hyaline, 7.0–10.0 × 2.5–4.0 µm. *Conidia* abundant, unicellular, cylindrical, guttulate, with obtuse ends, smooth, hyaline, 3.0–4.5 × 1.5–2.0 µm ($\bar{x} \pm SD = 4.0 \pm 0.25 \times 1.7 \pm 0.13$ µm, n = 60). **Sexual morph** not observed.

Culture characteristics—Colonies on PDA attaining 30–34 mm diam. after 10 days, flat, margin entire, beige (2B4) to olive (2E3) from margin to center. Reverse beige (2B4) to olive (2E3). Colonies on OA attaining 34–37 mm diam. after 10 days, flat, ulotrichy, white to pale gray (3B1) from margin to center. Reverse white to olive (28E5). Colonies on SNA attaining 39–40 mm diam. after 10 days, flat, cottony, margin entire, beige (3B3). Reverse beige (3B3). Sporulation within 15 d on OA and SNA.

Material examined: CHINA, Guangxi, Laibin, Sanshan Cave, N 23.41°, E 108.931°, on soil, May 2016, Z.F. Zhang, HMAS 247990 (holotype designated here), ex-type living culture CGMCC3.19301 = LC9240; ibid., LC10444.

Notes: Our strains form a distinct clade with *Setophaeosphaeria* species based on ITS, LSU and TUB sequences (Fig. 7), but can be distinguished from known species by its smaller conidia (> 6.0 µm long and 2.0–3.0 µm wide in other species) and larger conidiogenous cells (< 7.0 µm long in other species).

Class Eurotiomycetes O.E. Erikss. & Winka

Eurotiomycetes is one of the most diverse classes in the subphylum Pezizomycotina. We follow the latest classification of Gueidan et al. (2014) and Geiser et al. (2015).

Subclass Eurotiomycetidae

Eurotiales G.W. Martin ex Benny & Kimbr.

Eurotiales comprises some of the most commonly encountered microfungi, including the well known genera *Aspergillus* and *Penicillium*, some species of which can survive at extreme environments, such as deep water and high temperature (Geiser et al. 2015).

Aspergillaceae Link

Aspergillaceae was established by Link (1826), and re-instated by Houbraken and Samson (2011) based on multi-locus phylogeny. Species belonging to this family have diverse physiological properties; some could tolerant extreme conditions, such as high sugar or salt concentrations, low or high temperatures, low acidity or low oxygen levels (Houbraken et al. 2014). *Aspergillaceae* species are predominantly saprobic, while a few species are pathogenic (Houbraken et al. 2014).

Aspergillus P. Micheli ex Haller

Aspergillus is one of the most economically important genera of fungi. The aspergillum-like sporebearing structure is the defining characteristic of *Aspergillus*. Currently, 4 subgenera and 19 sections are accepted in *Aspergillus* (Houbraken et al. 2014). In this study, three new species are described as *A. limoniformis*, *A. phialiformis* and *A. phialosimplex* (Fig. 9).

Aspergillus limoniformis Z.F. Zhang & L. Cai, ***sp. nov.***

Index Fungorum number: 556394, *Facesoffungi number:* FoF 08427; Fig. 10

Etymology: Referring to the shape of its limoniform conidia.

Holotype: HMAS 248014.

Hyphae hyaline, septate, smooth, branched, 1.0–2.5 µm wide. **Asexual morph** *Conidiogenous cells* simple phialides arising laterally on vegetative hyphae. *Phialides* cylindrical, ampulliform, or tapering with enlarged base, smooth, hyaline,

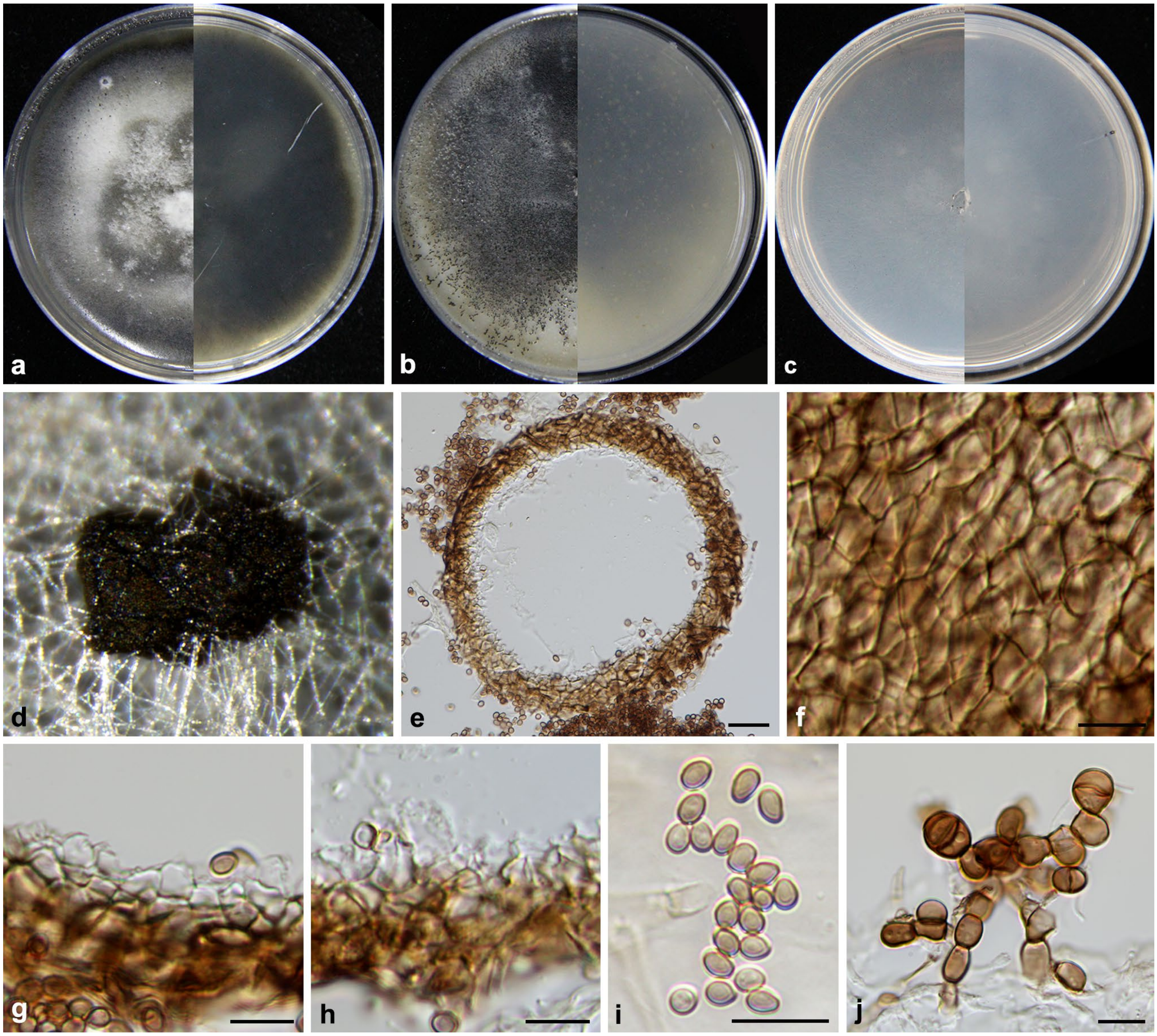


Fig. 6 *Paraphaeosphaeria hydei* (from ex-holotype CGMCC3.19317). **a–c** Upper and reverse views of cultures on PDA, OA and SNA 14 d after inoculation; **d** pycnidia on OA; **e** section of pycnidia; **f** pycnidial wall; **g**, **h** conidiogenous cells; **i** conidia; **j** chlamydospore-like hyphae. Scale bars: **e** 20 µm; **f–j** 10 µm

variable in length, 4.0–10.0 µm long, 1.5–5.0 µm diam. at base, tapering to 1.0–2.0 µm diam. at apex. *Conidia* formed in long chains, limoniform or subglobose, obviously apiculate, thick-walled, rough initially, then becoming smooth with age, hyaline, 3.0–4.5 × 2.5–4.0 µm ($\bar{x} \pm SD = 3.7 \pm 0.33 \times 3.3 \pm 0.25$ µm, n = 60). **Sexual morph** not observed.

Culture characteristics—Colonies on PDA attaining 25–31 mm diam. after 4 weeks, flat, felty to pulverulent, margin entire, beige (5B3) at fruiting region, white to dark brown (5F8) from middle to aging region. Reverse cream yellow (3A2) to dark brown (5F8). Colonies on OA attaining 24–35 mm diam. after 4 weeks, flat, margin entire, white to pale brown (5A2), aerial mycelia extremely sparse. Reverse pale brown (5A2) to brown (6D8). Colonies on SNA attaining 29–39 mm diam. after 4 weeks, flat, pulverulent, whitesmoke. Reverse whitesmoke. Sporulation within 3 weeks.

Material examined: CHINA, Yunnan, Mengzi, Mingjiu old Cave, N 23.487°, E 103.619°, on bat guano, May 2016, Z.F. Zhang, HMAS 248014 (holotype designated here), ex-type living culture CGMCC3.19323 = LC126098; ibid., LC12610.

Notes: Phylogenetic analyses based on ITS, RPB2, Tsr and TUB sequences showed that our new species should be classified in *Aspergillus* subgenus *Polypaecilum* (Fig. 9), which were also supported by the phialosimplex-like morphologies. *Aspergillus limoniformis* is phylogenetically closely related

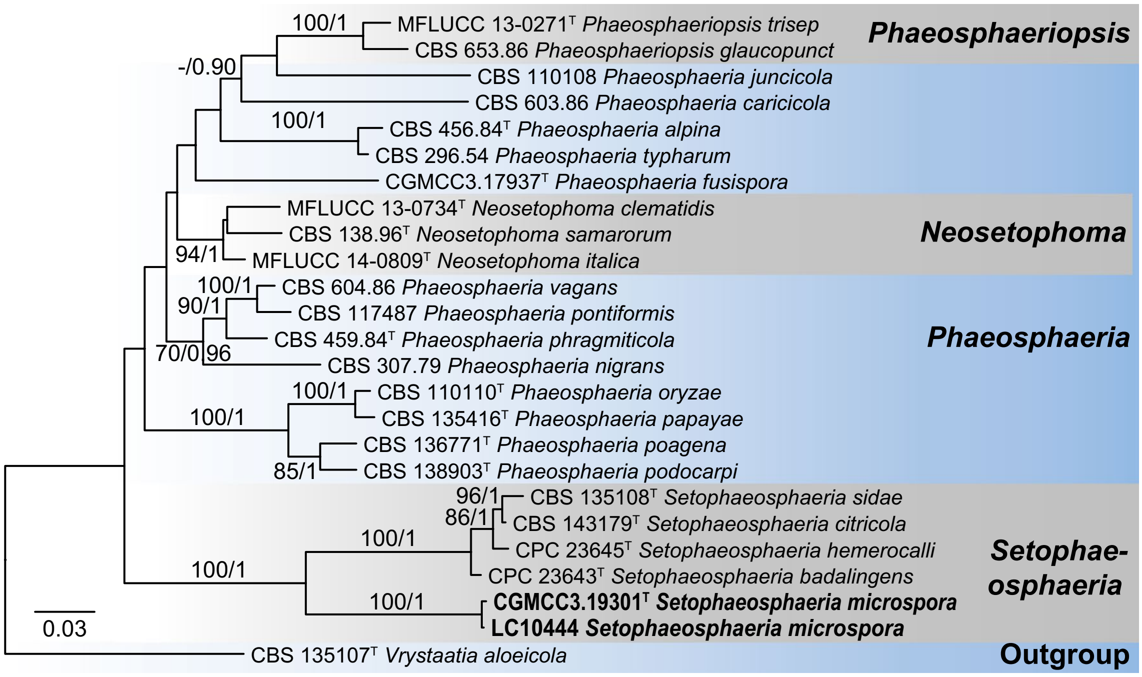


Fig. 7 Maximum likelihood (ML) tree of *Setophaeosphaeria* and allied genera based on ITS, LSU and TUB sequences. Twenty-five strains are used. The tree is rooted with *Vrystaatia aloeicola* (CBS 135107). Tree topology of the ML analysis was similar to the BI. The Best scoring RAxML tree with a final likelihood value of − 6493.809681. The matrix had 346 distinct alignment patterns, with 5.32 % of undetermined characters or gaps. Base frequencies estimated by jModelTest were as follows, A = 0.2352, C = 0.2241, G = 0.2578, T = 0.2829; substitution rates AC = 3.1633, AG = 6.7092, AT = 3.1633, CG = 1.0000, CT = 6.7092, GT = 1.0000; gamma shape = 0.6780. ML bootstrap values (≥ 70 %) and Bayesian posterior probability (≥ 90 %) are indicated along branches (ML/PP). Novel species are in bold font and "T" indicates type derived sequences

to *A. phialiformis* and *A. phialosimplex*. However, *A. limoniformis* can be distinguished from *A. phialiformis* and *A. phialosimplex* by the absence of globose conidia.

Aspergillus phialiformis Z.F. Zhang & L. Cai, ***sp. nov.***

Index Fungorum number: 556395, *Facesoffungi number:* FoF 08428; Fig. 11

Etymology: Referring to its phialidic conidiogenous cells.

Holotype: HMAS 248017.

Hyphae hyaline, septate, smooth, branched, 1.0–2.5 µm wide. **Asexual morph** *Conidiogenous cells* simple phialides arising laterally on vegetative hyphae. *Phialides* cylindrical or tapering with enlarged base, occasionally branched, smooth, hyaline, variable in length, 4.0–12.0 µm long, 1.0–4.0 µm diam at base, tapering to 1.0–2.0 µm diam. at apex. *Conidia* formed in long chains, limoniform, subglobose or globose, apiculate, thick-walled, rough initially, then becoming smooth with age, hyaline, 2.5–4.0 µm ($\bar{x} \pm$ SD = 3.3 ± 0.28, n = 60). **Sexual morph** not observed.

Culture characteristics—Colonies on PDA attaining 36–41 mm diam. after 4 weeks, flat, margin fimbriate, cream yellow (4A2) at fruiting region, white to pale brown (5A2) from middle to aging region, with brown, radially striate and lobate ring, aerial mycelia sparse. Reverse cream-yellow (4A2) to brown (5C7). Colonies on OA attaining 31–36 mm diam. after 4 weeks, flat, margin undulate, aerial mycelia sparse, pulverulent in center, white. Reverse floralwhite (4A2). Colonies on SNA attaining 43–47 mm diam. after 4 weeks, flat, pulverulent, white. Reverse white. Sporulation within 3 weeks.

Material examined: CHINA, Yunnan, Yiliang, Sanjiao Cave, N 25.134°, E 103.383°, on rock, May 2016, Z.F. Zhang, HMAS 248017 (holotype designated here), ex-type living culture CGMCC3.19314 = LC12536; ibid., LC12537.

Notes: *Aspergillus phialiformis* is phylogenetically closely related to *A. phialosimplex* (Fig. 9). While, phialides of *A. phialiformis* are cylindrical or basal enlarged, which are mostly cylindrical in *A. phialosimplex*. Meanwhile, limoniform conidia are not observed in *A. phialosimplex* and color of *A. phialosimplex* and *A. phialiformis* on PDA and OA are different.

Aspergillus phialosimplex Z.F. Zhang & L. Cai, ***sp. nov.***

Index Fungorum number: 556396, *Facesoffungi number:* FoF 08429; Fig. 12

Etymology: Referring to its phialosimplex-like morphology.

Holotype: HMAS 248007.

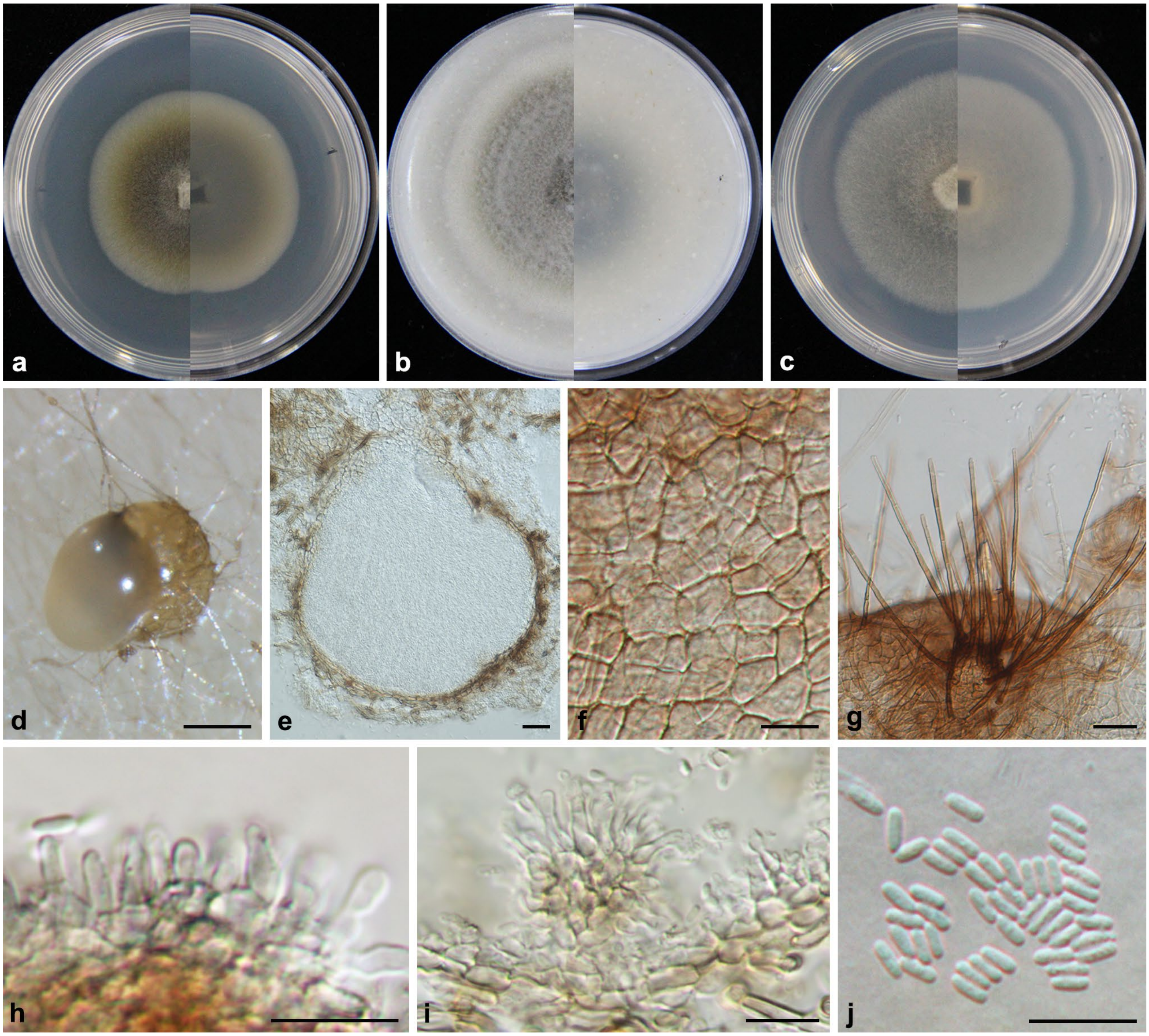


Fig. 8 *Setophaeosphaeria microspora* (from ex-holotype CGMCC3.19301). **a**–**c** Upper and reverse views of cultures on PDA, OA and SNA 14 d after inoculation; **d** pycnidia on SNA; **d** section of pycnidia; **f** pycnidial wall; **g** setae; **h**–**i** conidiogenous cells; **j** conidia. Scale bars: **d** 100 µm; **e**, **g** 20 µm; **f**, **h**–**j** 10 µm

Hyphae hyaline, septate, smooth, branched, 1.0–3.5 µm wide, sometimes swollen, up to 7.0 µm. **Asexual morph** *Conidiogenous cells* simple phialides arising laterally on vegetative hyphae. *Phialides* cylindrical, occasionally ampulliform, variable in length, smooth, hyaline, 2.5–8.5 µm long, 1.0–2.0 µm diam. *Conidia* formed in long chains, subglobose to globose, thick-walled, rough initially, then becoming smooth with age, hyaline, 3.5–5.5 µm ($\bar{x} \pm$ SD = 4.7 ± 0.42, n = 60). **Sexual morph** not observed.

Culture characteristics—Colonies on PDA attaining 20–29 mm diam. after 4 weeks, flat, felty to pulverulent, margin slightly undulate, brown (7C5) to dark brown (7F7) from margin to center. Reverse pale brown (6B3) to dark brown (7F8). Colonies on OA attaining 20–28 mm diam. after 4 weeks, flat, margin entire, white to pale lavender (6B2), aerial mycelia sparse. Reverse white to pale brown. Colonies on SNA attaining 42–46 mm diam. after 4 weeks, flat, pulverulent, margin unclear, white. Reverse white. Sporulation within 3 weeks.

Material examined: CHINA, Sichuan, Huaying, Liujia Cave, N 30.41°, E 106.878°, on plant debris, May 2016, Z.F. Zhang, HMAS 248007 (holotype designated here), ex-type living culture CGMCC3.19637 = LC12578; Guangxi, Guilin, E'gu Cave, N 24.942°, E 110.511°, on animal faeces,

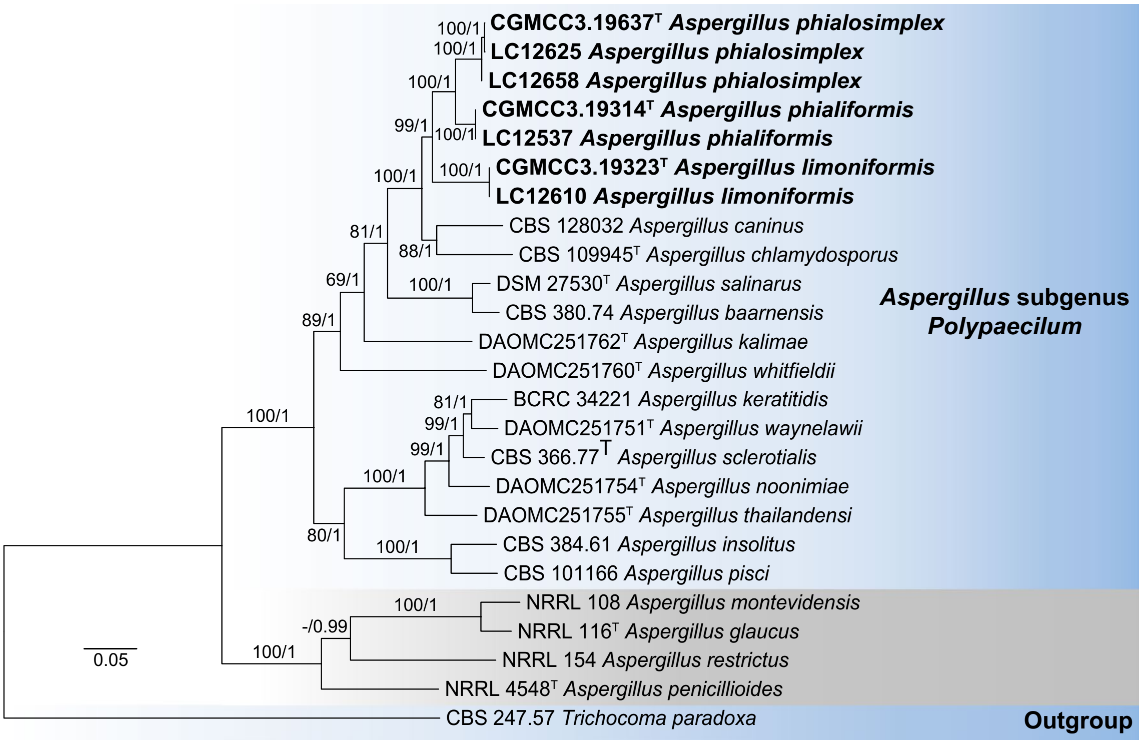


Fig. 9 Maximum likelihood (ML) tree of phialosimplex-like *Aspergillus* and several other *Aspergillus* species based on ITS, RPB2, Tsr and TUB sequences. Twenty-five strains are used. The tree is rooted with *Trichocoma paradoxa* (CBS 247.57). Tree topology of the ML analysis was similar to the BI. The Best scoring RAxML tree with a final likelihood value of − 19500.215104. The matrix had 1225 distinct alignment patterns, with 11.99 % of undetermined characters or gaps. Base frequencies estimated by jModelTest were as follows, A = 0.2187, C = 0.2928, G = 0.2635, T = 0.2250; substitution rates AC = 0.9532, AG = 3.3181, AT = 0.9699, CG = 0. 7315, CT = 4.0026, GT = 1.0000; gamma shape = 1.5800. ML bootstrap values (≥ 70 %) and Bayesian posterior probability (≥ 90 %) are indicated along branches (ML/PP). Novel species are in bold font and “T” indicates type derived sequences

May 2016, Z.F. Zhang, LC12658; Yunnan, Yuxi, Niumo Cave, N 28.192°, E 102.842°, on plant root, May 2016, Z.F. Zhang, LC12625.

Notes: *Aspergillus phialosimplex* is phylogenetically allied to *A. phialiformis* (Fig. 9), but they can be easily distinguished (see notes of *A. phialiformis*).

Onygenales Cif. ex Benny & Kimbr.

The *Onygenales* in Eurotiomycetes is characterized by smooth or appendiculate ascomata, with pseudoparenchymatous, membranous cleistoperidium or filamentous gymnoperidium of loosely interwoven hyphae, centrum of globose, irregularly disposed, pseudoprototunicate asci, and one-celled, hyaline or pale coloured ascospores (Currah 1985, Doveri et al. 2012). Species of *Onygenales* are usually keratinophilic, keratinolytic, cellulolytic or chitinoclastic (Doveri et al. 2012).

Gymnoascaceae Baran.

The family *Gymnoascaceae* was firstly established by Baranetzky 1872, with *Gymnoascus* and *G. reessii* as type genus and species respectively. Members of this family are often isolated from soil, plant debris, dung or animal components (Doveri et al. 2012).

Gymnoascus Baran.

The genus *Gymnoascus* was classified in *Gymnoascaceae*, *Onygenales*, with *G. reesii* as generic type (Baranetzky 1872). In the most recent treatment, genera *Arachniotus* Arachniotus J. Schröt., *Gymnascella* Peck, *Gymnoascoideus* G.F. Orr, K. Roy & G.R. Ghosh and *Narasimhella* Thirum. & P.N. Mathur have been synonymized with *Gymnoascus* based on the morphological and molecular evidences, marking *Gymnoascus* one of the largest genera in the order *Onygenales* (Solé et al. 2002). *Gymnoascus* is characterized by spherical, yellowish to brownish ascomata with peridium composed of a loose network of hyaline or pigmented hyphae, with or without appendages, and by oblate and pigmented ascospores and chrysosporium-like conidia (von Arx 1977; Solé et al. 2002; Sharma and Singh 2013; Zhou et al. 2016). The genus currently comprises 22 species (Zhou et al. 2016). In this study, one new species is described as *Gymnoascus flavus* (Fig. 13).

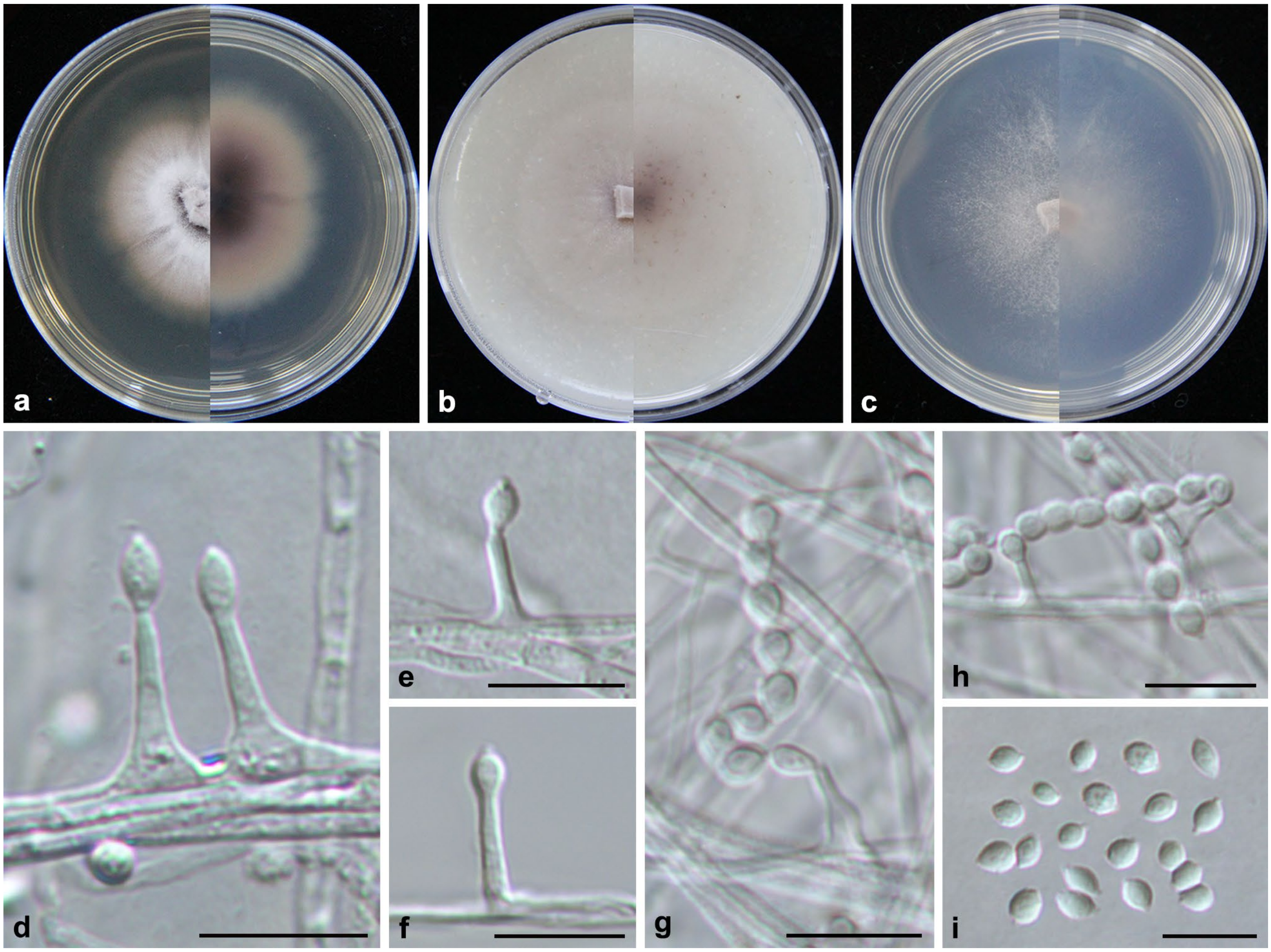


Fig. 10 *Aspergillus limoniformis* (from ex-holotype CGMCC3.19323). **a**–**c** Upper and reverse views of cultures on PDA, OA and SNA 4 weeks after inoculation; **d**–**h** phialides and conidia; **i** conidia. Scale bars: **d**–**i** 10 µm

Gymnoascus flavus Z.F. Zhang & L. Cai, ***sp. nov.***

Index Fungorum number: 556397, *Facesoffungi number:* FoF 08430; Fig. 14

Etymology: Referring to the color of its conidia, yellow.

Holotype: HMAS 248010.

Hyphae pale yellow to yellow, septate, branched, smooth or slightly rough, 1.5–5.0 µm diam.; racquet hyphae present, 'racquet' up to 11.0 µm wide. **Asexual morph** Fertile mycelia usually gathered into special, superficial yellow structure, where conidia borne mostly. *Conidia* mostly terminal or lateral, occasionally intercalary, sessile or borne on short protrusions or side branches, unicellular, pyriform, ellipsoidal or globose, smooth, thick-walled, hyaline initially, then becoming yellow, 4.5–7.0 × 4–6 µm ($\bar{x} \pm$ SD = 6.0 ± 0.62 × 5.1 ± 0.64 µm, n = 60), with truncated base. **Sexual morph** not observed.

Culture characteristics—Colonies on PDA attaining 26–34 mm diam. after 3 weeks, coriarious, plicated in center, margin entire, beige (1A2) to salmon (6A3), aerial mycelia sparse. Reverse beige (1A2) to orange (6A3). Colonies on OA not growing. Colonies on SNA attaining 24–27 mm diam. after 10 days, powdery, margin rhizoids, white initially, becoming light yellow (2A3-2A5) when sporulation, aerial mycelia sparse. Reverse white to pale yellow (2A3). Sporulation within 2 weeks on SNA.

Material examined: CHINA, Sichuan, Xingwen, Feng Cave, N 28.186°, E 105.148°, on soil, May 2016, Z.F. Zhang, HMAS 248010 (holotype designated here), ex-type living culture CGMCC3.19574 = LC12500; Sichuan, Xingwen, Tianliang Cave, N 28.19°, E 105.139°, on soil, May 2016, Z.F. Zhang, LC12511.

Notes: Phylogenetically, *Gymnoascus flavus* forms a distinct clade sister to *G. exasperates* Z.F. Zhang, F. Liu & L. Cai, *G. reessii* and *G. uncinatus* Eidam based on ITS and LSU sequences (Fig. 13). However, dissimilar to *G. reessii* and *G. uncinatus*, the sexual morph of *G. flavus* was not observed despite repeated attempts using OA, PDA and SNA media, as well as horse hair and chicken feather as inducers

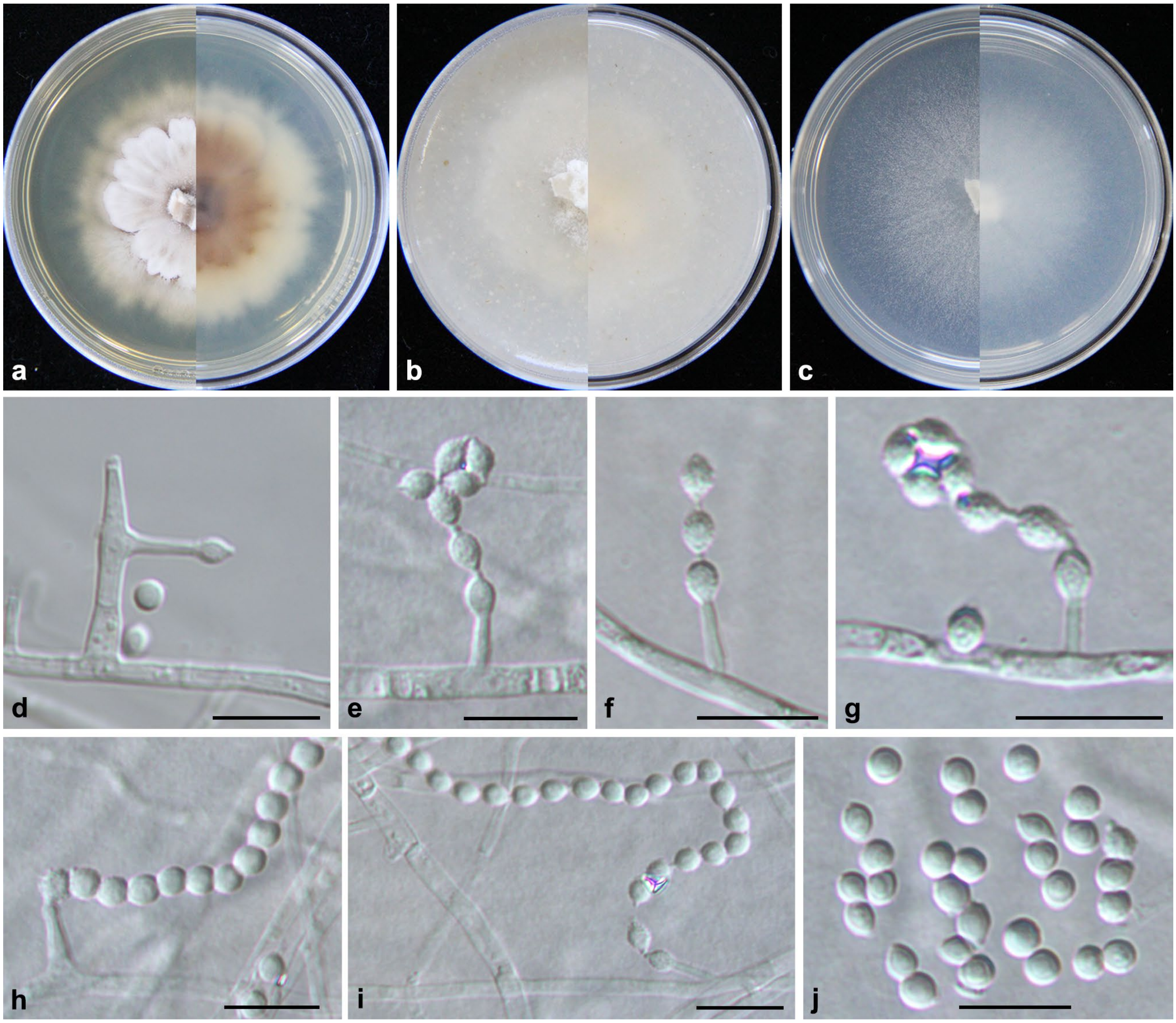


Fig. 11 *Aspergillus phialiformis* (from ex-holotype CGMCC3.19314). **a**–**c** Upper and reverse views of cultures on PDA, OA and SNA 4 weeks after inoculation; **d**–**i** phialides and conidia; **j** conidia. Scale bars: **d**–**j** 10 µm

(Orr and Kuehn 1972). Conidia of *Gymnoascus flavus* are mostly terminal or lateral, as compared to the abundant intercalary conidia of *G. exasperates*.

Onygenaceae Berk.

The *Onygenaceae* is characterised by pseudoparenchymatous cleistothecia or hyphal gymnothecia with a structure similar to *Gymnoascaceae*. The ascospores of *Onygenaceae* are oblate, discoidal, or spherical, sometimes reniform or allantoid, punctate, pitted or pitted-reticulate, and the anamorphs are predominantly one-celled arthro- and aleurioconidia (Doveri et al. 2012).

Auxarthron G.F. Orr & Kueh

The *Auxarthron* was placed in *Gymnoascaceae* when established (Orr et al. 1963), while subsequent studies based on molecular data showed its actual affinity to *Onygenaceae* (Sugiyama et al. 1999; Sigler et al. 2002). Hitherto, *Auxarthron* encompasses 18 species. In this study, two new species are described as *Auxarthron chinense* and *A. guangxiense* (Fig. 15).

Auxarthron chinense Z.F. Zhang & L. Cai, ***sp. nov.***

Index Fungorum number: 556412, *Facesoffungi number:* FoF 08431; Fig. 16

Etymology: Referring to the country where this fungus was firstly isolated.

Holotype: HMAS 247999.

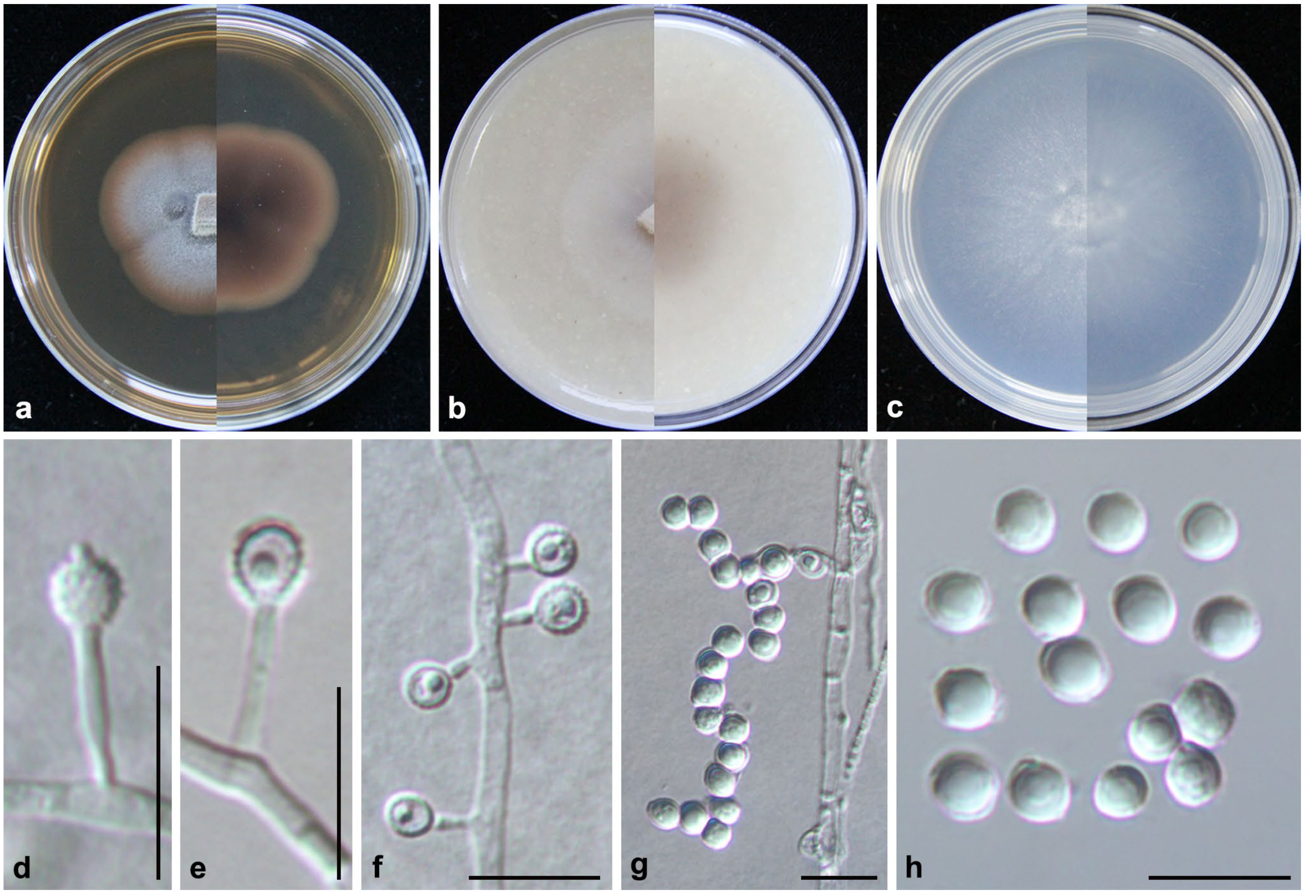


Fig. 12 *Aspergillus phialosimplex* (from ex-holotype CGMCC3.19637). **a**–**c** upper and reverse views of cultures on PDA, OA and SNA 4 weeks after inoculation; **d**–**g** phialides and conidia; h. conidia. Scale bars: **d**–**h** 10 µm

Hyphae hyaline, septate, branched, smooth, 1.5–3.5 µm wide, sometimes swollen, up to 10.0 µm wide; racquet hyphae present, 'racquet' 4–5 µm wide. **Asexual morph** *Conidia* arthroconidial, abundant, mostly intercalary, few lateral and terminal, unicellular, cylindrical, ellipsoidal or clavate with one or two truncated bases, smooth, hyaline, 4.0–7.0 (–8.0) × 2.0–3.5 µm ($\bar{x} \pm$ SD = 5.3 ± 0.92 × 2.6 ± 0.25 µm, n = 50), frequently separated by 1–3 autolytic connective cells. **Sexual morph** not observed.

Culture characteristics—Colonies on PDA 18–23 mm diam. after 4 weeks, flat, annular, margin dentate, cottony and white at center, pulverulent to felty and light yellow (1A2) at margin. Reverse orange (5A5) to pale orange (4A5). Colonies on OA 18–23 mm diam. after 4 weeks, flat, pulverulent, margin unclear, white, aerial mycelia sparse. Reverse beige (28A3). Colonies on SNA 21–25 mm diam. after 4 weeks, flat, powdery, margin crenate, cream-yellow. Reverse cream-yellow (1A2) to white. Sporulation within 3 weeks.

Material examined: CHINA, Guangxi, Guilin, Luotian Cave, N 24.948°, E 110.524°, on soil, May 2016, Z.F. Zhang, HMAS 247999 (holotype designated here), ex-type living culture CGMCC3.19572 = LC12475; ibid., LC12477; ibid., LC12550; ibid., LC12580 (animal faeces); Guangxi, Guilin, E'gu Cave, N 24.942°, E 110.511°, on soil, May 2016, Z.F. Zhang, LC12473; ibid., LC12474; Yunnan, Mengzi, Mingjiu old Cave, N 23.487°, E 103.619°, on soil, May 2016, Z.F. Zhang, LC12463.

Notes: Morphological and phylogenetic data (Figs. 15, 16) support our strains as new species of *Auxarthron*. *Auxarthron chinense* is phylogenetically closely related to *A. alboluteum* Sigler, Hambl. & Flis, *A. compactum* G.F. Orr & Plunkett and *A. zuffianum* (Morini) G.F. Orr & Kuehn (Fig. 15). However, *A. chinense* can be distinguished from *A. alboluteum* by less lateral and terminal conidia; from *A. compactum* by the hyaline conidia rather than pale yellow of *A. compactum*; from *A. zuffianum* by wider conidia (2.0–3.5 µm vs. 1.2–1.6 µm).

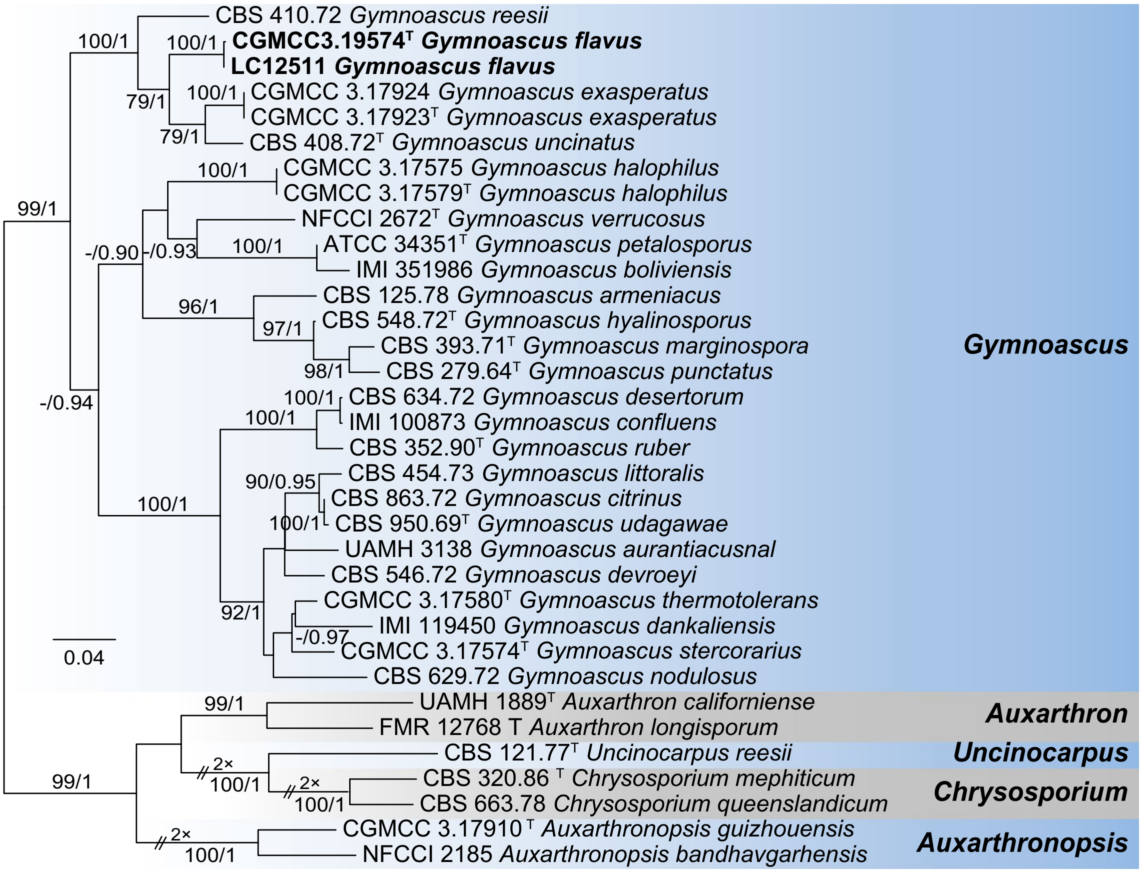


Fig. 13 Maximum likelihood (ML) tree of *Gymnoascus* and allied genera based on ITS and LSU sequences. Thirty-four strains are used. Tree topology of the ML analysis was similar to the BI. The Best scoring RAxML tree with a final likelihood value of − 9224.916077. The matrix had 579 distinct alignment patterns, with 22.64 % of undetermined characters or gaps. Base frequencies estimated by jModelTest were as follows, A = 0.2064, C = 0.2679, G = 0.2988, T = 0.2269; substitution rates AC = 1.5486, AG = 2.9623, AT = 2.4354, CG = 0.9897, CT = 5.0848, GT = 1.0000; gamma shape = 1.0300. ML bootstrap values (≥ 70 %) and Bayesian posterior probability (≥ 90 %) are indicated along branches (ML/PP). Novel species are in bold font and "T" indicates type derived sequences

Auxarthron guangxiense Z.F. Zhang & L. Cai, ***sp. nov.***

Index Fungorum number: 556413, *Facesoffungi number:* FoF 08432; Fig. 17

Etymology: Referring to the province where the type strain was isolated.

Holotype: HMAS 247993.

Hyphae hyaline, septate, branched, smooth, 1.5–2.5 µm diam. **Sexual morph** *Ascomata* abundant, solitary or in clusters, subglobose to globose, white at first, becoming orange-brown at maturity, 250–380 µm diam. *Peridial hyphae* rough, thick-walled, septate, pale brown, branched and anastomosed to form a reticuloperidium, terminated by spine-like or blunt prominences, sometimes dichotomously branched, 1.5–2.5 µm diam, appendages not observed. *Asci* 8-spored, pyriform, subglobose or globose, hyaline, 8.5–12.0 × 6.5–9.0 µm. *Ascospores* oblate, smooth, hyaline, 2.5–3.5 µm ($\bar{x} \pm$ SD = 3.1 ± 0.22 µm, n = 40). **Asexual morph** not observed.

Culture characteristics—Colonies on PDA attaining 26–31 mm diam. after 4 weeks, flat, margin crenate, cottony, cream-white (2A1) to yellow (2A3) at fruiting region, floralwhite at aging region. Reverse pale yellow (1A2) to goldenrod (2A3) at margin, dark brown (4D8) at center. Colonies on OA attaining 32–40 mm diam. after 4 weeks, flat, annular, cottony at middle, white to pale yellow (2A3) from margin to center. Reverse pale yellow (2A3). Colonies on SNA attaining 28–32 mm diam. after 4 weeks, flat, white to pale yellow (1B3), aerial mycelia sparse, with ascomata scattered. Reverse white to pale yellow (1B3). Sporulation within 3 weeks on SNA.

Material examined: CHINA, Guangxi, Guilin, E'gu Cave, N 24.942°, E 110.511°, on soil, May 2016, Z.F. Zhang, HMAS 247993 (holotype designated here), ex-type living culture CGMCC3.19634 = LC12464; ibid., LC12465.

Notes: Phylogenetically, *Auxarthron guangxiense* is close to *A. pseudauxarthron* G.F. Orr & Kuehn (Fig. 15), but differs in the absence of ascomatal appendages.

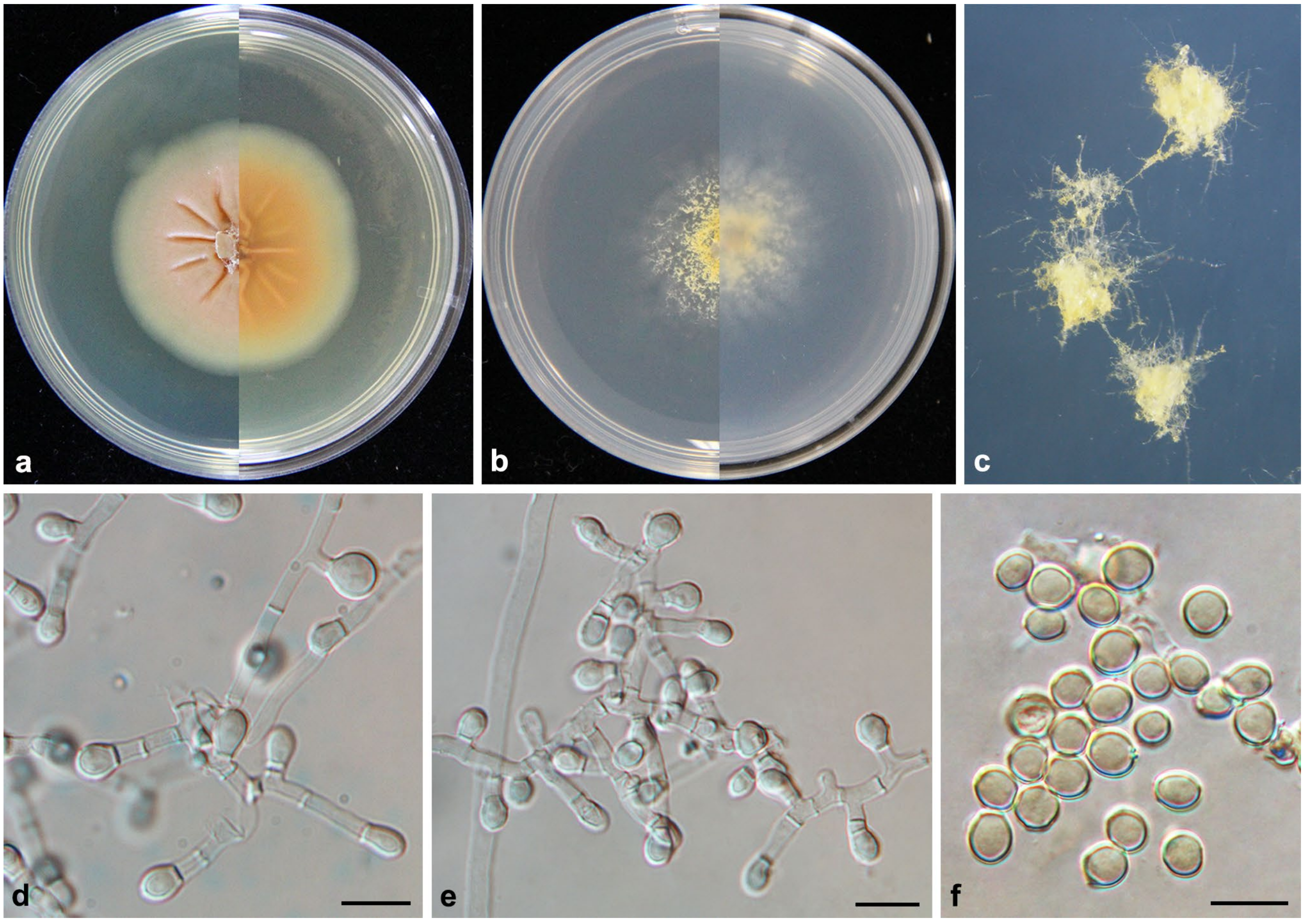


Fig. 14 *Gymnoascus flavus* (from ex-holotype CGMCC3.19574). **a**, **b** Upper and reverse views of cultures on PDA and SNA 4 weeks after inoculation; **c** fertile mycelia on SNA; **d**, **e** terminal and lateral conidia; **f** conidia. Scale bars: **d**–**f** 10 μm

Morphologically, *A. guangxiense* is similar to *A. zuffianum*, whereas, the asci of *A. guangxiense* are larger than those of *A. zuffianum* (8.5–12.0 × 6.5–9.0 μm vs. 7.0–8.4 × 5.6–7.0 μm). In addition, sexual stage of *A. guangxiense* is absent.

Auxarthronopsis Rahul Sharma, Y. Gräser & S.K. Singh

The genus *Auxarthronopsis* was established by Sharma et al. (2013) and previously comprises only two species, *A. bandhavgarhensis* Rah. Sharma, Y. Gräser & S.K. Singh and *A. guizhouensis* Z.F. Zhang & L. Cai (Zhang et al. 2017). Species of *Auxarthronopsis* are characterized by interlaced peridium, tapering appendages with multiple swollen septa, oblate ascospores with finely punctate walls, and asexual morphs of terminal and intercalary arthro- and aleurioconidia (Sharma et al. 2013). In this study, four new species *A. globiasca*, *A. pedicellaris*, *A. pulverea* and *A. stercicola* are described (Fig. 15).

Auxarthronopsis globiasca Z.F. Zhang & L. Cai, ***sp. nov.***

Index Fungorum number: 556414, *Facesoffungi number:* FoF 08433; Fig. 18

Etymology: Referring to its globose asci.

Holotype: HMAS 247994.

Hyphae hyaline, septate, branched, smooth, 1.5–3.0 μm diam., sometimes cross connected, racquet hyphae present, up to 6 μm wide. **Sexual morph** *Ascomata* abundant, solitary or in clusters, surface powdery, subglobose to globose, pale yellow, 270–450 μm diam. *Peridial hyphae* septate, rough, thick-walled, pale brown, branched and anastomosed to form a reticuloperidium, terminated by short blunt prominences, 1.5–3.0 μm diam. *Asci* 8-spored, subglobose or globose, hyaline, 5.5–8.0 × 5.5–7.5 μm. *Ascospores* oblate, ellipsoidal, subglobose or globose in front view, smooth, hyaline, 2.5–3.5 × 2.0–3.0 μm ($\bar{x} \pm SD = 2.9 \pm 0.21 \times 2.0 \pm 0.24$ μm, n = 50). **Asexual morph** *Arthroconidia* presented, abundant, mostly intercalary, few terminal and lateral, unicellular, cylindrical, ellipsoidal or clavate with truncated base, smooth, hyaline, 3.5–6.5 × 2.0–3.5 μm ($\bar{x} \pm SD = 4.8 \pm 0.73 \times 2.7 \pm 0.34$ μm, n = 50), frequently separated by 1–3 autolytic connective cells.

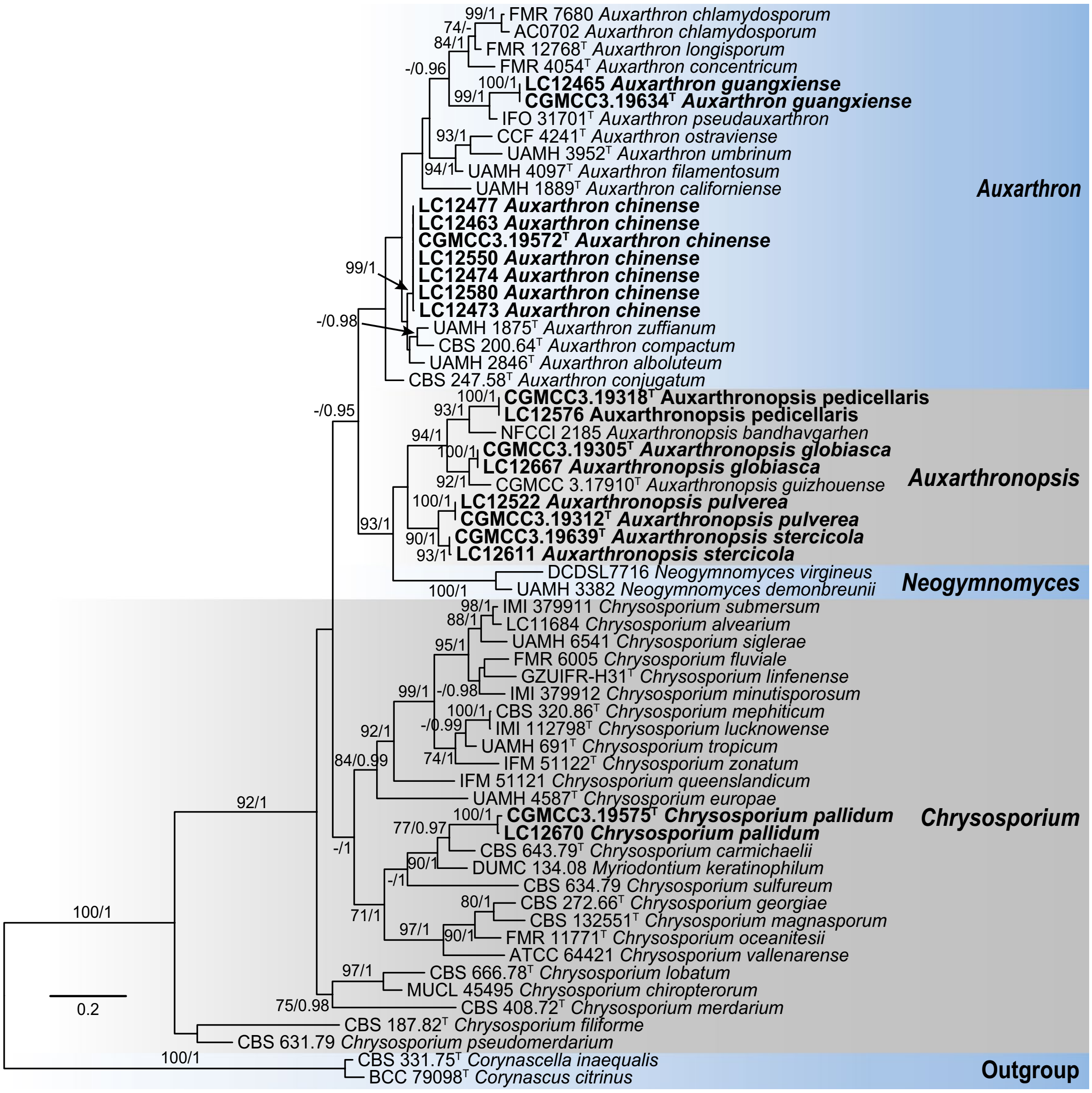


Fig. 15 Maximum likelihood (ML) tree of *Auxarthron*, *Auxarthronopsis*, *Chrysosporium* and allied genera based on ITS sequences. Sixty-two strains are used. The tree is rooted with *Corynascus citrinus* (BCC 79098) and *Corynascella inaequalis* (CBS 331.75). Tree topology of the ML analysis was similar to the BI. The Best scoring RAxML tree with a final likelihood value of − 10475.385887. The matrix had 390 distinct alignment patterns, with 13.25 % of undetermined characters or gaps. Base frequencies estimated by jModelTest were as follows, A = 0.2136, C = 0.2792, G = 0.2575, T = 0.2497; substitution rates AC = 1.1074, AG = 2.0735, AT = 2.1813, CG = 0.8592, CT = 3.5964, GT = 1.0000; gamma shape = 0.9040. ML bootstrap values (≥ 70 %) and Bayesian posterior probability (≥ 90 %) are indicated along branches (ML/PP). Novel species are in bold font and "T" indicates type derived sequences

Culture characteristics—Colonies on PDA attaining 31–36 mm diam. after 4 weeks, flat, felty, annular, margin fimbriate, seashell (5A2) to light yellow (4A3) from margin to center. Reverse cream-yellow (4A2) to orange at margin, brown (6D8) at middle, black (6F1) at center. Colonies on OA attaining 46–48 mm diam. after 4 weeks, flat, beige (4A1), aerial mycelia extremely sparse. Reverse beige (3A2). Colonies on SNA attaining 23–30 mm diam. after 4 weeks, margin rhizoids, aerial mycelia sparse, with floralwhite (30A2) ascomata scattered. Reverse ivory. Sporulation within 25 days on SNA.

Material examined: CHINA, Guangxi, Guilin, Luotian Cave, N 24.948°, E 110.524°, on soil, May 2016, Z.F. Zhang, HMAS 247994 (holotype designated here), ex-type living culture CGMCC3.19305 = LC12472; Guangxi, Guilin, E'gu Cave, N 24.942°, E 110.511°, on soil, May 2016, Z.F. Zhang, LC12667.

Notes: Our strains form a well supported distinct clade with *Auxarthronopsis* species (Fig. 15). *Auxarthronopsis*

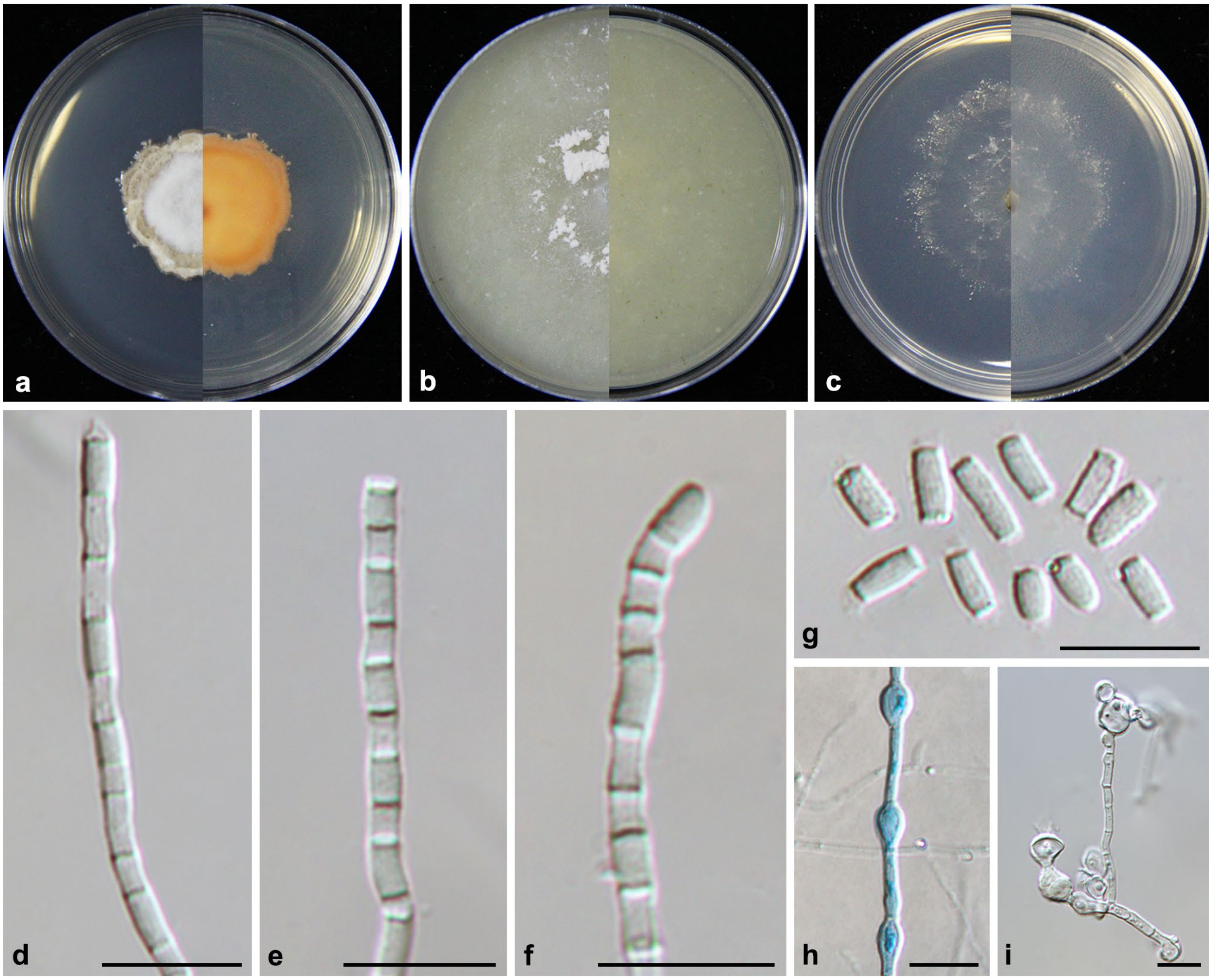


Fig. 16 *Auxarthron chinense* (from ex-holotype CGMCC3.19572). **a**–**c** Upper and reverse views of cultures on PDA, OA and SNA 4 weeks after inoculation; **d**–**g** arthroconidia; **h** racquet hyphae; **i** swollen hyphae. Scale bars: **d**–**i** 10 µm

globiasca is phylogenetically allied with *A. bandhavgarhensis*, *A. guizhouensis* and *A. pedicellaris*. Ascomata of *A. bandhavgarhensis* are white and much larger than those of *A. globiasca* (500–1000 µm vs. 270–450 µm). *A. globiasca* differs from *A. guizhouensis* by the presence of asexual morph. In contrast to *A. globiasca*, conidia of *A. pedicellaris* are lateral or terminal.

Auxarthronopsis pedicellaris Z.F. Zhang & L. Cai, ***sp. nov.***

Index Fungorum number: 556415, *Facesoffungi number:* FoF 08434; Fig. 19

Etymology: Referring to the stalk-bearing arthroconidia.

Holotype: HMAS 248012.

Hyphae hyaline, septate, branched, smooth, 1.5–3.0 µm diam. **Asexual morph** Conidiophore-like stalk cylindrical, erect, straight or curved, septate, branched, smooth, thick-walled, hyaline, various in length, 1.0–2.5 µm wide. *Arthroconidia* abundant, lateral or terminal, stalked, occasionally sessile, unicellular, pyriform, ellipsoidal or globose with truncate base, smooth, hyaline, 3.5–6.5 × 2.0–3.5 µm ($\bar{x}$ ± SD = 4.8 ± 0.73 × 2.7 ± 0.34 µm, n = 50). **Sexual morph** not observed.

Culture characteristics—Colonies on PDA attaining 26–32 mm diam. after 4 weeks, flat, felty, annular, margin dentate, floralwhite (30A2). Reverse floralwhite (30A2) to bisque (7A2). Colonies on OA attaining 30–33 mm diam. after 4 weeks, flat, margin lobate, white. Reverse white. Colonies on SNA attaining 26–29 mm diam. after 4 weeks, margin entire, white, aerial mycelia sparse. Reverse white. Sporulation within 3 weeks.

Material examined: CHINA, Chongqing, Wulong, Erwang Cave, N 29.585°, E 108.001°, on rock, May 2016, Z.F. Zhang, HMAS 248012 (holotype designated here),

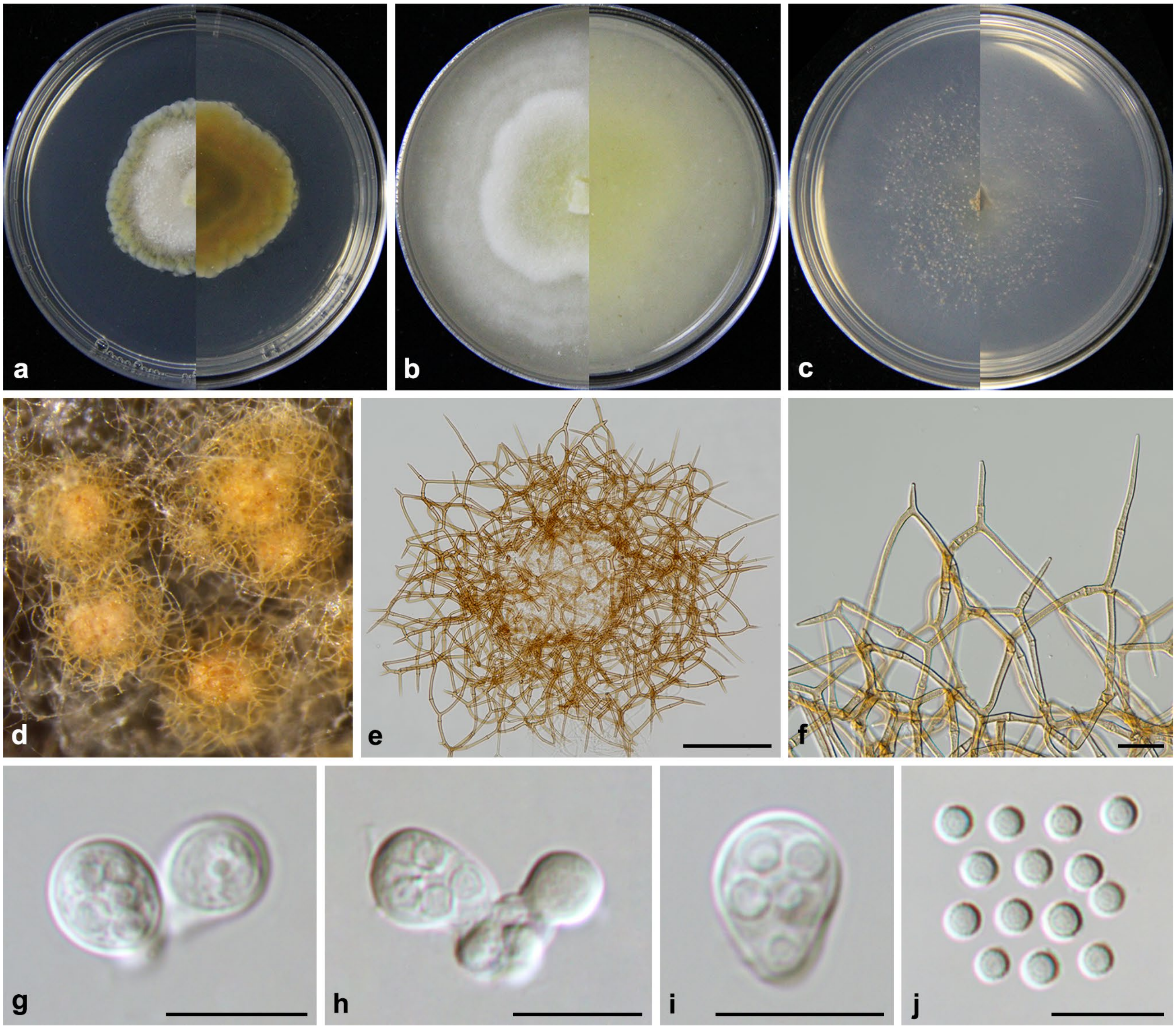


Fig. 17 *Auxarthron guangxiense* (from ex-holotype CGMCC3.19634). **a–c** Upper and reverse views of cultures on PDA, OA and SNA 4 weeks after inoculation; **d** ascomata; **e**, **f** peridial hyphae; **g–i** asci; **j** ascospores. Scale bars: **e** 50 µm; **f** 20 µm; **g–j** 10 µm

ex-type living culture CGMCC3.19318 = LC12575; ibid., LC12576.

Notes: *Auxarthronopsis pedicellaris* is phylogenetically allied to *A. bandhavgarhensis*, *A. guizhouensis* and *A. globiasca* (Fig. 15), but can be distinguished by its lateral or terminal conidia and absence of intercalary conidia.

Auxarthronopsis pulverea Z.F. Zhang & L. Cai, ***sp. nov.***

Index Fungorum number: 556416, *Facesoffungi number:* FoF 08435; Fig. 20

Etymology: Referring to the powdery conidia on OA medium.

Holotype: HMAS 248008.

Hyphae hyaline, septate, branched, smooth. **Asexual morph** *Arthroconidia* abundant, mostly intercalary or terminal, few lateral, unicellular, solitary, straight or slightly curved, hyaline, intercalary conidia cylindrical, terminal and lateral conidia cylindrical or ellipsoidal with truncated base, sessile or short stalked, frequently separated by 1–3 autolytic connective cells, 3.0–6.0 × 2.0–3.5 µm ($\bar{x}$ ± SD = 4.5 ± 0.76 × 2.6 ± 0.36 µm, n = 50). **Sexual morph** not observed.

Culture characteristics—Colonies on PDA attaining 25–28 mm diam. after 4 weeks, flat, felty, annular, margin radially striate with lobate edge, beige (2A2) at margin, yellow (3A3-3B5) at middle, white to pale orange (3A2) in center. Reverse beige (2A2) to brown (4B8), with pale yellow (3A5) ring at middle. Colonies on OA attaining 29–34

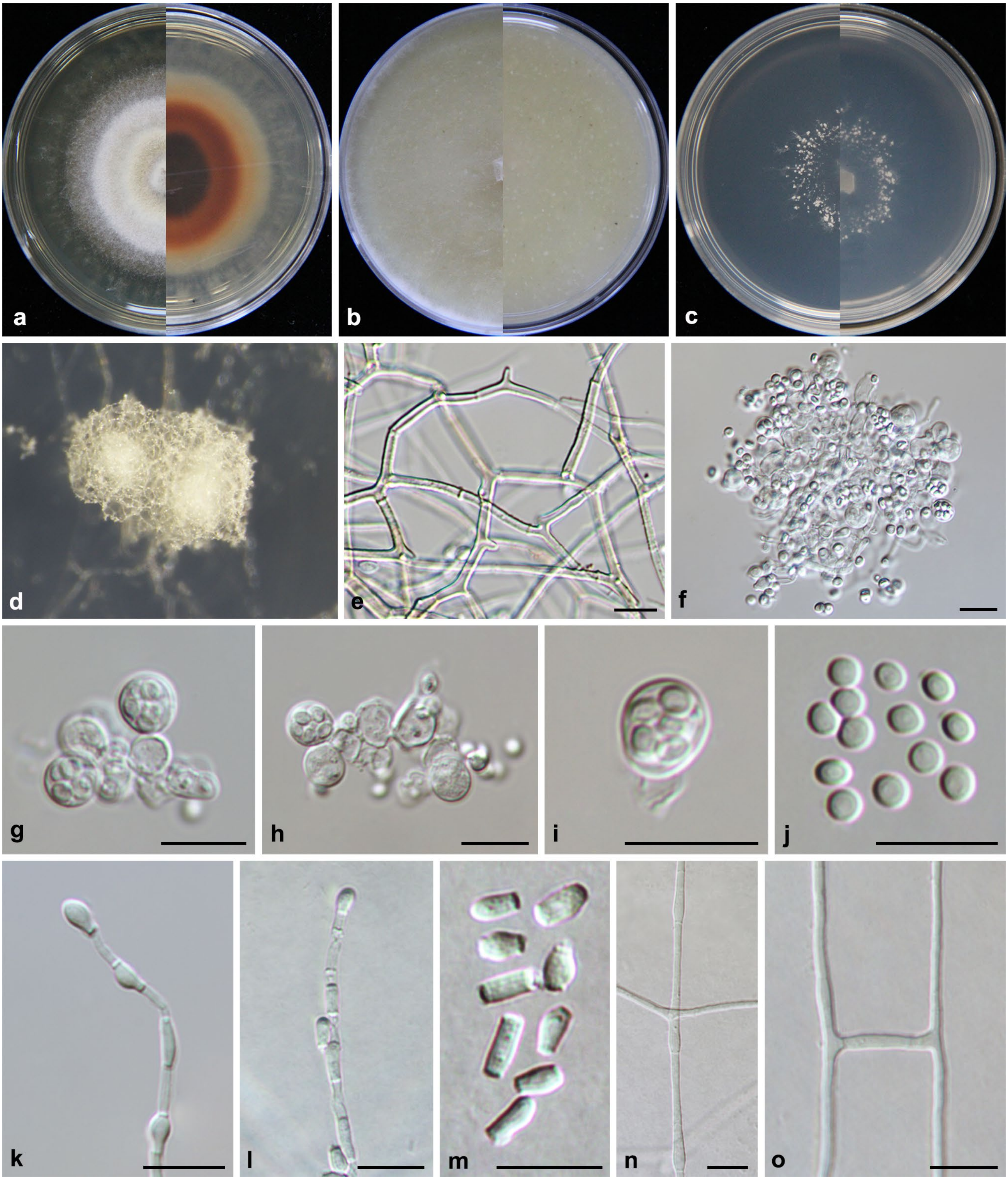


Fig. 18 *Auxarthronopsis globiasca* (from ex-holotype CGMCC3.19305). **a–c** Upper and reverse views of cultures on PDA, OA and SNA 4 weeks after inoculation; **d** ascomata; **e** peridial hyphae; **f–i** asci; **j** ascospores; **k–m** arthroconidia; **n** racquet hyphae; **o** connected hyphae. Scale bars: **e–o** 10 µm

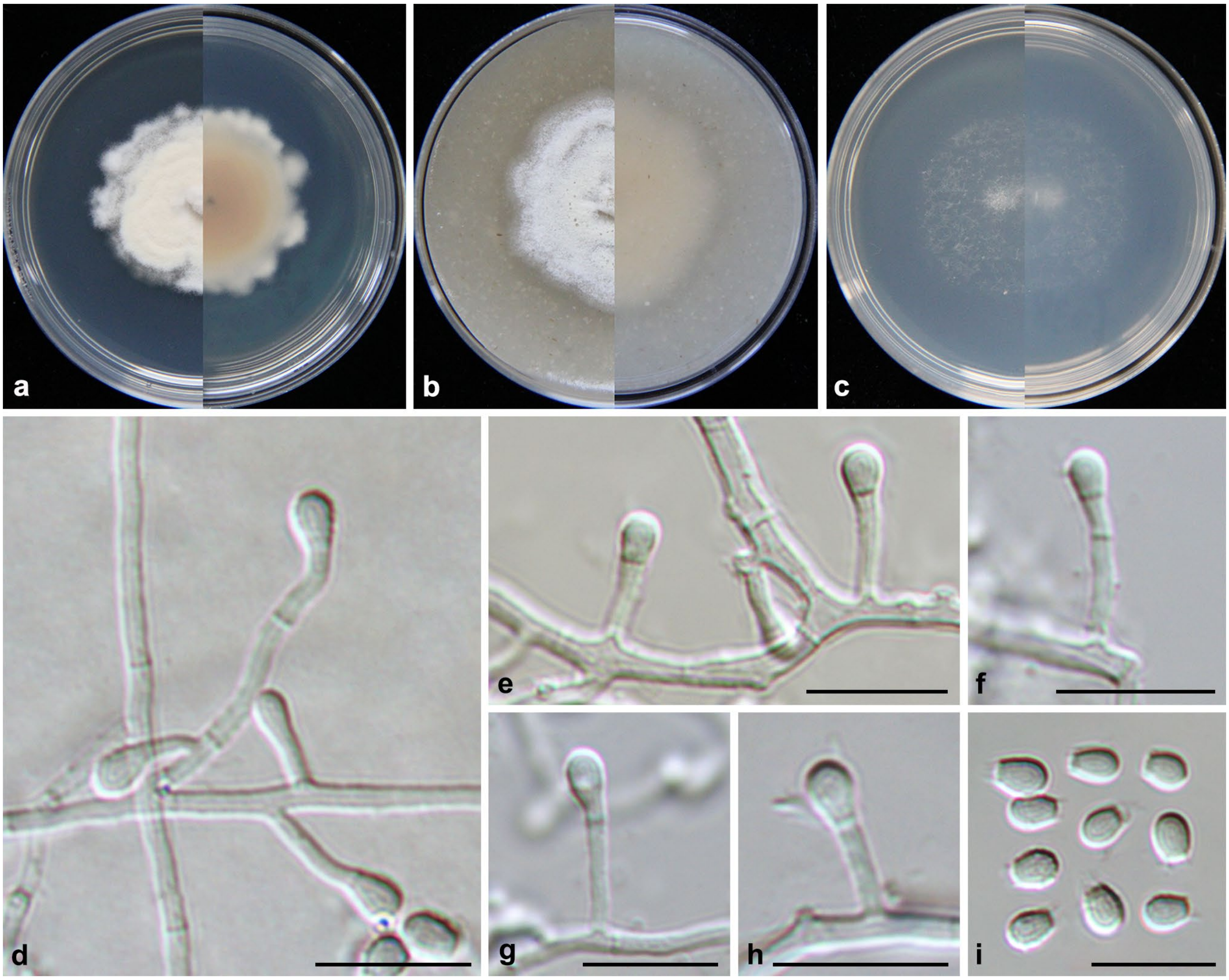


Fig. 19 *Auxarthronopsis pedicellaris* (from ex-holotype CGMCC3.19318). **a**–**c** Upper and reverse views of cultures on PDA, OA and SNA 4 weeks after inoculation; **d**–**h** stalk-bearing arthroconidia; **i** arthroconidia. Scale bars: **d**–**i** 10 μm

mm diam. after 4 weeks, flat, powdery, white. Reverse white to beige (30A2). Sporulation within 3 weeks on OA. Colonies on SNA attaining 24–29 mm diam. after 4 weeks, margin rhizoids, white, aerial mycelia sparse. Reverse white.

Material examined: CHINA, Sichuan, Huaying, Liujia Cave, N 30.41°, E 106.878°, on plant debris, May 2016, Z.F. Zhang, HMAS 248008 (holotype designated here), ex-type living culture CGMCC3.19312 = LC12521; ibid., LC12522.

Notes: *Auxarthronopsis pulverea* is phylogenetically closely related to *A. stercicola* (Fig. 15). However, terminal and lateral conidia of *A. stercicola* are much more abundant than those of *A. pulverea*.

Auxarthronopsis stercicola Z.F. Zhang & L. Cai, ***sp. nov.***

Index Fungorum number: 556417, *Facesoffungi number:* FoF 08436; Fig. 21

Etymology: Referring to the substrate in which this species was isolated.

Holotype: HMAS 248015.

Hyphae hyaline, septate, branched, smooth, 1.0–3.0 μm wide. **Asexual morph** *Arthroconidia* abundant, intercalary, terminal, or lateral, unicellular, solitary, straight or curved, hyaline, intercalary conidia cylindrical, terminal and lateral conidia cylindrical or ellipsoidal with truncated base, sometimes irregularly swollen, sessile or short stalked, 2.5–5.0 × 2.0–3.0 μm ($\bar{x} \pm$ SD = 3.7 ± 0.56 × 2.4 ± 0.24 μm, n = 60), frequently separated by 1–3 autolytic connective cells. **Sexual morph** not observed.

Culture characteristics—Colonies on PDA attaining 21–26 mm diam. after 4 weeks, flat, felty, annular, margin undulate, beige (30A2) at margin, white to pale orange (3A2) in center. Reverse annular, beige (30A2) to pale brown (4B6). Colonies on OA attaining 25–28 mm diam.

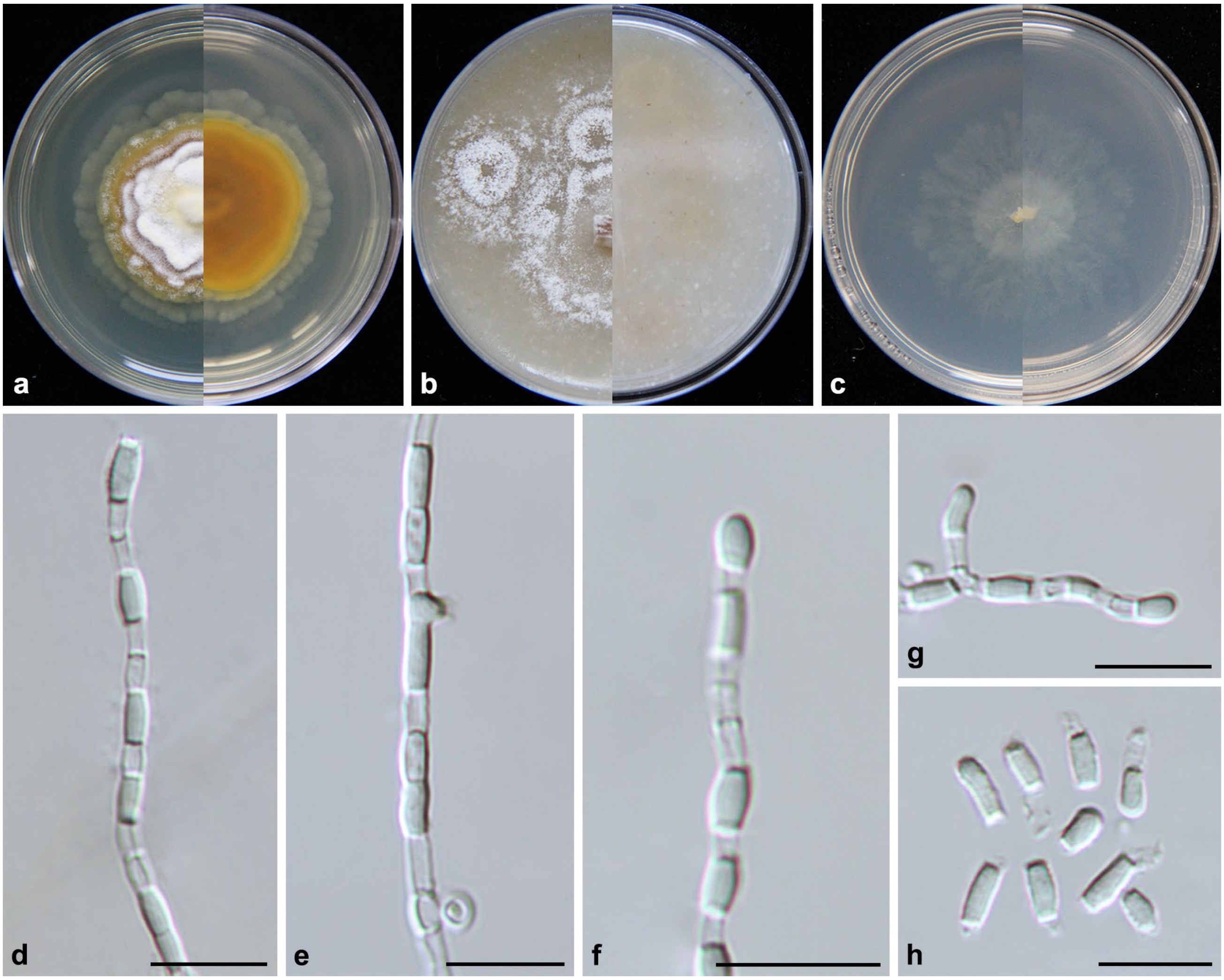


Fig. 20 *Auxarthronopsis pulverea* (from ex-holotype CGMCC3.19312). **a**–**c** Upper and reverse views of cultures on PDA, OA and SNA 4 weeks after inoculation; **d**–**h** arthroconidia. Scale bars: **d**–**h** 10 µm

after 4 weeks, flat, pulverulent, margin undulate, white. Reverse floralwhite (1A2). Sporulation within 3 weeks on OA. Colonies on SNA attaining 16–18 mm diam. after 4 weeks, radially striate with rhizoid margin, white. Reverse white.

Material examined: CHINA, Yunan, Yiliang Sanjiao Cave, N 25.134°, E 103.383°, on animal faeces, May 2016, Z.F. Zhang, HMAS 248015 (holotype designated here), ex-type living culture CGMCC3.19639 = LC12635; Guilin, Luotian Cave, N 24.948°, E 110.524°, on animal faeces, May 2016, Z.F. Zhang, LC12611.

Notes: *Auxarthronopsis stercicola* is phylogenetically closely related to *A. pulverea* (Fig. 15), but can be easily distinguished (see notes of *A. pulverea*).

Chrysosporium Corda

Chrysosporium was introduced by Corda (1833), and revealed to be polyphyletic based on ITS phylogeny (Vidal et al. 2000). The genus currently comprises 66 species (Wijayawardene et al. 2020), most of which are saprophytic and keratinolytic isolated from various habitats such as air, sea, sludge, waste water (Zhang et al. 2016). In this study, one new species is described as *Chrysosporium pallidum* (Fig. 15).

Chrysosporium pallidum Z.F. Zhang & L. Cai, ***sp. nov.***

Index Fungorum number: 556418, *Facesoffungi number:* FoF 08437; Fig. 22

Etymology: Referring to the color of ascomata, white to pale yellow.

Holotype: HMAS 247992.

Hyphae hyaline, septate, branched, smooth, 2.0–3.0 µm diam., racquet hyphae present, up to 6 µm wide. **Sexual**

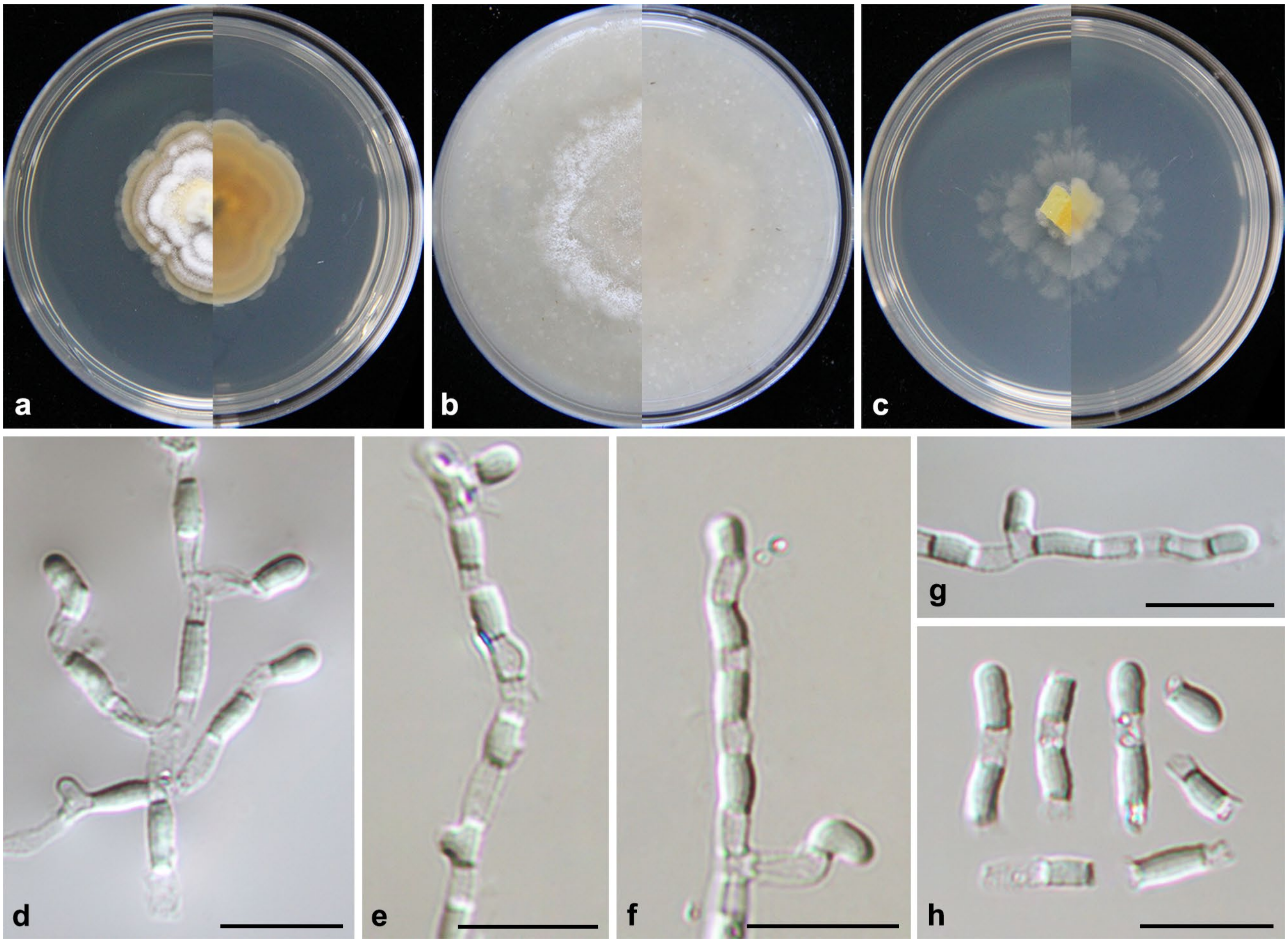


Fig. 21 *Auxarthronopsis stercicola* (from ex-holotype CGMCC3.19639). **a**–**c** Upper and reverse views of cultures on PDA, OA and SNA 4 weeks after inoculation; **d**–**h** arthroconidia. Scale bars: **d**–**h** 10 µm

morph *Ascomata* abundant, solitary, or in clusters, cottony, globose, white initially, becoming pale yellow when aging, with conidia produced on surface, up to 750 µm diam. *Peridial hyphae* difficult to distinguished from aerial hyphae, septate, branched and anastomosed, terminated by short blunt prominences, smooth, thick-walled, hyaline, 2.5–4.0 µm diam. *Asci* 8-spored, pyriform, subglobose or globose, hyaline, 8.0–13.0 × 7.5–10.5 µm. *Ascospores* oblate, globose in front view, hyaline, smooth, 2.5–3.5 µm ($\bar{x}$ ± SD = 3.0 ± 0.21 µm, n = 70). **Sexual morph** *Arthroconidia* abundant, intercalary, lateral or terminal, unicellular, hyaline; intercalary conidia cylindrical or ellipsoidal with truncated base, 3.5–6.5 × 2.0–3.5 µm (mean = 6.6 ± 1.28 × 2.9 ± 0.46 µm, n = 40); lateral or terminal conidia arising from aerial hyphae directly, pyriform or clavate with truncated base, 4.0–7.0 × 2.5–4.0 µm (mean = 5.3 ± 0.73 × 3.4 ± 0.43 µm, n = 40).

Culture characteristics—Colonies on PDA attaining 28–34 mm diam. after 4 weeks, flat, felty, annular, margin with fimbriate, ivory (1A1) to white from margin to center. Reverse ivory (1A1) to yellow (2A2) from margin to center. Colonies on OA attaining 27–30 mm diam. after 4 weeks, flat, felty, annular, white. Reverse white to beige (30A2). Colonies on SNA attaining 26–29 mm diam. after 4 weeks, margin rhizoids, floralwhite (1A2), aerial mycelia sparse. Reverse floralwhite (1A2). Sporulation within 3 weeks on SNA.

Material examined: CHINA, Guangxi, Guilin, E'gu Cave, N 24.942°, E 110.511°, on animal faeces, May 2016, Z.F. Zhang, HMAS 247992 (holotype designated here), ex-type living culture CGMCC3.19575 = LC12583; ibid., LC12670.

Notes: *Chrysosporium pallidum* is phylogenetically allied to *C. carmichaelii* Oorschot and *Myriodontium keratinophilum* Samson & Polon (Fig. 15). *C. pallidum* differs from *C. carmichaelii* by its more abundant intercalary conidia and sessile lateral conidia. Conidia of *Myriodontium keratinophilum* are lateral with short stem (conidiogenous cell), comparing with sessile lateral conidia and the presence of intercalary, lateral or terminal of *C. pallidum*. In addition,

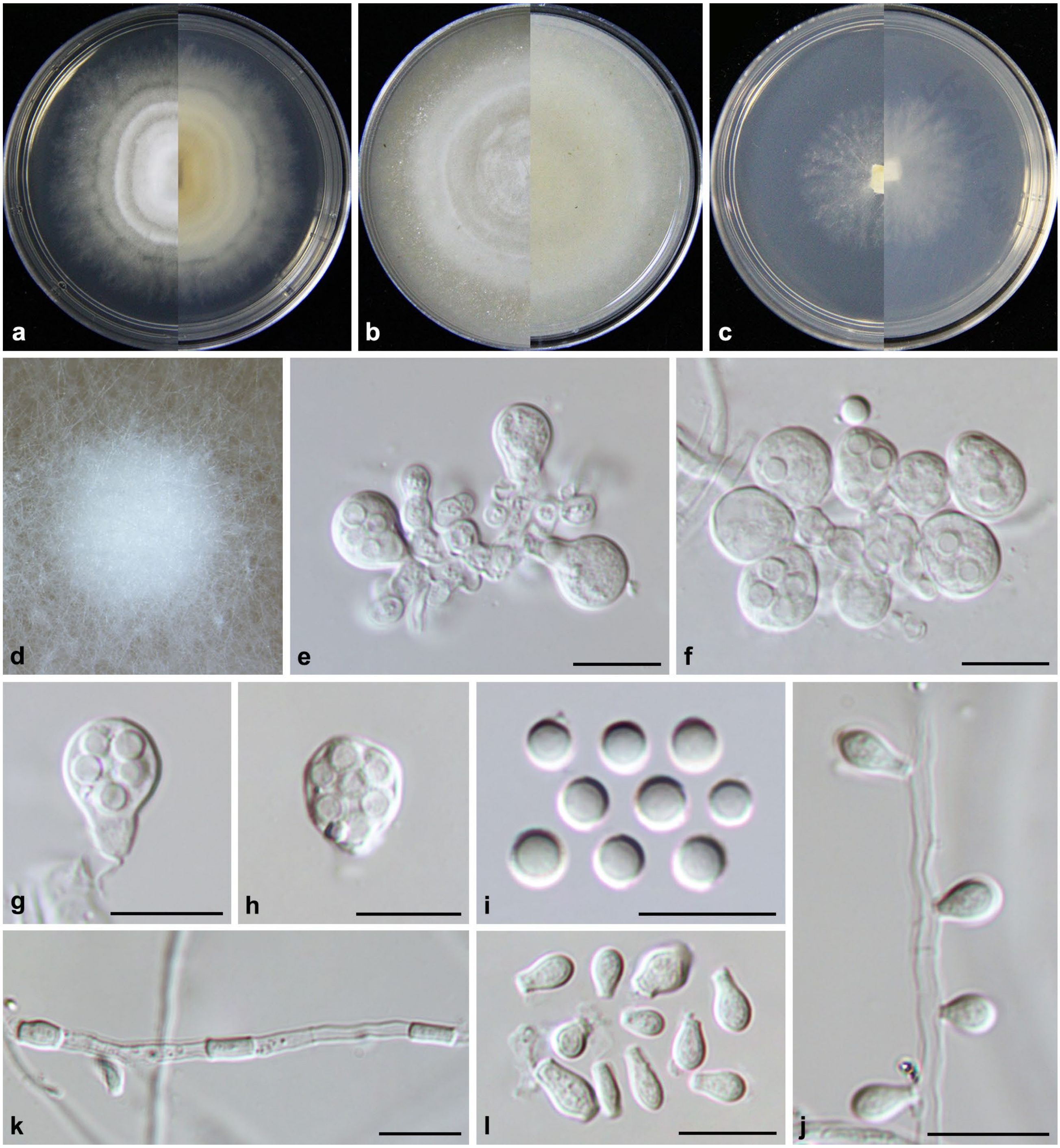


Fig. 22 *Chrysosporium pallidum* (from ex-holotype CGMCC3.19575). **a–c** Upper and reverse views of cultures on PDA, OA and SNA 4 weeks after inoculation; **d** ascomata; **e–h** asci; **i** ascospores; **j–l** arthroconidia. Scale bars: **e–l** 10 µm

neither *C. carmichaelii* nor *myriodontium keratinophilum* produces sexual stage.

Class Sordariomycetes O.E. Erikss. & Winka

The classification of Sordariomycetes follw the latest treatment by Hongsanan et al. (2017) and Wijayawardene et al. (2017, 2018, 2020)

Subclass Hypocreomycetidae O.E. Erikss. & Winka

Hypocreales Lindau

Hypocreales is characterized by pigment producing, brightly coloured perithecial ascomata, and typically ostiolate perithecial fruiting body (Rehner and Samuels 1995). Asexual morphs of *Hypocreales*, the form most frequently encountered in nature, are moniliaceous and phialidic (Lombard et al. 2015). *Hypocreales* are highly diverse and currently comprise 14 families (Wijayawardene et al. 2020)

Cordycipitaceae Kreisel ex G.H. Sung et al.

Cordycipitaceae was validated by Sung et al. (2007a) to accommodate species of *Cordyceps* forming brightly coloured, fleshy stromata. Species of *Cordycipitaceae* are known as obligate saprotrophs, parasites and symbionts with insects and fungi or grasses, rushes or sedges (Phookamsak et al. 2019).

Amphichorda Fr.

Amphichorda was established by Fries (1825) with *A. felina* (DC.) Fr. as type. The genus is morphologically similar to *Beauveria* except its regular conidiogenous cells without elongate denticulate rachis. Currently there are two species in *Amphichorda,* and both of them are coprophilous (Zhang et al. 2017; Xu et al. 2018). We described *Amphichorda cavernicola* sp. nov. in this study (Fig. 23).

Amphichorda cavernicola Z.F. Zhang & L. Cai, ***sp. nov.***

Index Fungorum number: 556419, *Facesoffungi number:* FoF 08438; Fig. 24

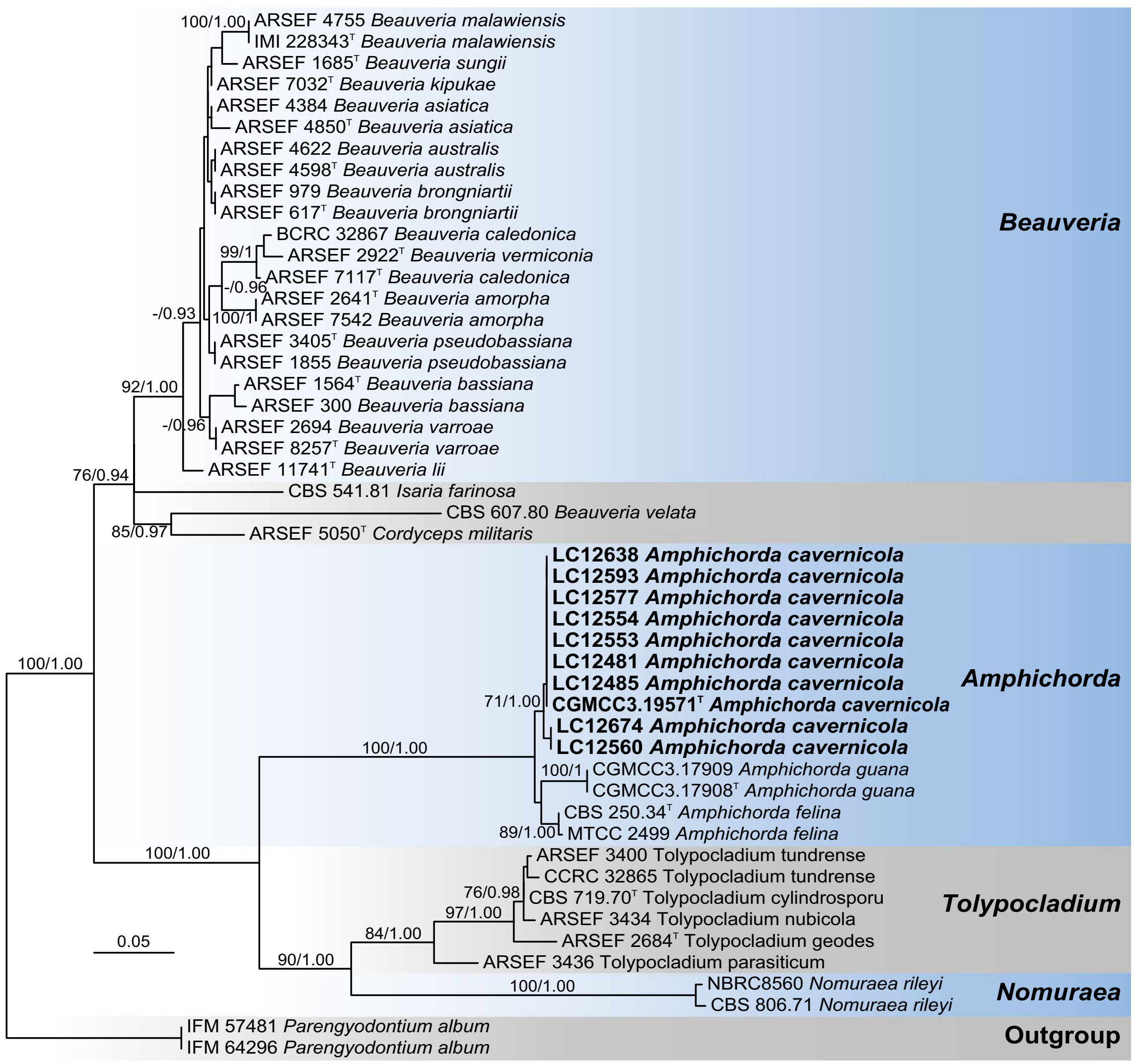


Fig. 23 Maximum likelihood (ML) tree of *Amphichorda* and allied genera based on ITS sequences. Forty-nine strains are used. The tree is rooted with *Parengyodontium album* (IFM 57481 and IFM 64296). Tree topology of the ML analysis was similar to the BI. The Best scoring RAxML tree with a final likelihood value of – 3338.441281. The matrix had 298 distinct alignment patterns, with 16 % of undetermined characters or gaps. Base frequencies estimated by jModelTest were as follows, A = 0.2103, C = 0.3352, G = 0.2666, T = 0.1878; substitution rates AC = 1.0000, AG = 2.2239, AT = 1.0000, CG = 1.0000, CT = 3.4151, GT = 1.0000; gamma shape = 0.4260. ML bootstrap values (≥ 70 %) and Bayesian posterior probability (≥ 90 %) are indicated along branches (ML/PP). Novel species are in bold font and “T” indicates type derived sequences

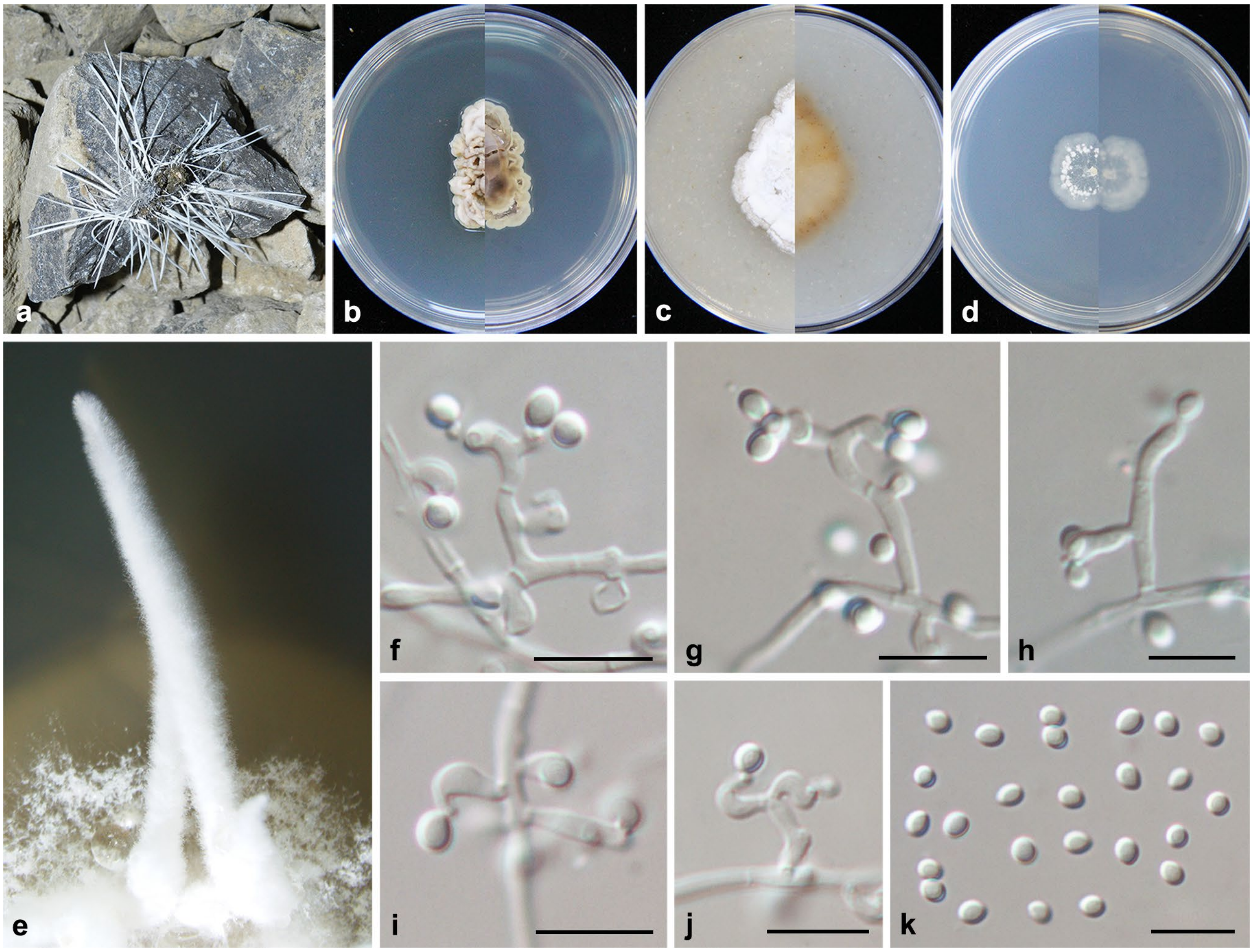


Fig. 24 *Amphichorda cavernicola* (from ex-holotype CGMCC3.19571). **a** *A. cavernicola* on bird faeces; **b–d** upper and reverse views of cultures on PDA, OA and SNA 14 days after inoculation; **e** synnemata; **f–j** conidiophores, conidiogenous cells and conidia; **k** conidia. Scale bars: **f–k** 10 µm

Etymology: Referring to the cavernicolous habitat it was isolated.

Holotype: HMAS 248011.

Hyphae hyaline, septate, smooth-walled, 1.5–2.5 µm diam. **Asexual morph** *Synnemata* arising in the center part of colonies on OA or PDA with peptone, cylindrical with apical apex, tomentose, white. *Conidiophores* arising laterally from hyphae, cylindrical, straight or slightly curved, occasionally branched, hyaline. *Conidiogenous cells* bone on conidiophores or mycelia, fusiform or ellipsoidal, straight or irregularly bent, 4.5–8.0 × 2.0–3.0 µm. *Conidia* holoblastic, solitary or clumped, unicellular, broadly ellipsoidal to subglobose, smooth, hyaline, 2.5–4.0 × 2.0–3.5 µm ($\bar{x} \pm$ SD = 3.4 ± 0.36 × 2.8 ± 0.24 µm, n = 60). Chlamydospores and **Sexual morph** not observed.

Culture characteristics—Colonies on PDA attaining 9–15 mm diam. after 14 days, irregular, compact, extremely plicated and crack, cream-yellow (4A1) to seashell (30A2) in fruiting zone and tan (5A2) in aging zone, aerial mycelia sparse. Reserve compact and crack, cream-yellow (1A2) to brown from fruiting zone and tan (4E8) in aging zone. Colony on OA attaining 18–22 mm diam. after 14 days, dense, compact and plicated, margin radially striate with lobate edge, white to milk-white, with synnemata in center. Reserve pale yellow (4A2) with yellow-brown (4B8) margin. Colonies on SNA slowly growing, attaining 9–13 mm diam. after 14 days, margin entire, white, mycelia sparse, with white hyphae body. Reverse white. Sporulation within 10 days on OA and SNA.

Material examined: CHINA, Sichuan, Xingwen, Feng Cave, N28.186°, E105.148°, on bird faeces, May 2016, Z.F. Zhang, HMAS 248011 (holotype designated here), ex-type living culture CGMCC3.19571 = LC12448; ibid., LC12554; ibid., LC12577; Chongqing, Wulong, Sanwang Cave, N29.591°, E108.001°, on soil, May 2016, Z.F. Zhang, LC12481; Guangxi, Guilin, E'gu Cave, N24.942°, E110.511°, on plant debris, May 2016, Z.F. Zhang, LC12674; Sichuan, Xinwen, Yuguan Cave, N28.179°, E105.143°, on soil, May 2016, Z.F. Zhang, LC12485; Sichuan, Xinwen, Tianliang Cave, N28.19°, E105.139°, on animal faeces, May 2016, Z.F. Zhang, LC12553; Sichuan, Huaying, Liujia Cave, N30.41°, E106.878°, on bat guano, May 2016, Z.F. Zhang, LC12638; ibid., LC12593; Sichuan, Huaying, Bijia Cave, N 30.43°, E 106.898°, on animal faeces, May 2016, Z.F. Zhang, LC12560.

Note: This new species is morphologically and phylogenetically allied to *Amphichorda* (Fig. 23). *Amphichorda cavernicola* differs from *A. guana* Z.F. Zhang, F. Liu & L. Cai in its smaller conidia (2.5–4.0 × 2.0–3.5 µm vs. 4.5–5.5 ×3.5–4.5 µm) and low sequence similarity (96.8% similarity, 16 base pairs (bp) difference in 504 bp of ITS; 99.2% similarity, 6 bp difference in 849 bp of LSU; 99% similarity, 7 bp difference in 884 bp of TEF; 97% similarity, 10 bp difference in 290 bp of TUB); from *A. felina* (DC.) Fr. in its fusiform or ellipsoidal conidiogenous cells, which are flask shaped in *A. felina*, and the colonies on PDA medium are also obviously different.

Gamszarea Z.F. Zhang & L. Cai, ***gen. nov.***

Index Fungorum number: 556420, *Facesoffungi number:* FoF 08439

Etymology: "*Gamszarea*" named in honour of Walter Gams and Rasoul Zare, for their contributions to the taxonomic study of *Lecanicillium* W. Gams & Zare.

Asexual morph *Conidiophores* commonly arising from aerial hyphae, erect, hyaline. *Conidiogenous cells* discrete aculeate phialides, usually solitary or verticillate, sometimes branched. *Conidia* adhering in more or less globose slimy heads and of two types, macroconidia first usually and then microconidia, aseptate. *Macroconidia* fusiform or falcate with more or less pointed ends; *microconidia* ellipsoidal, falcate, lunate or reniform. Crystals occasionally observed. **Sexual morph** only observed in *Gamszarea wallacei* on the pupal host. *Perithecium* hyaline, delicate, smooth, obclavate to naviculate. *Asci* 8-spored, with a prominent cap, narrowly cylindrical with an inflated vase. *Ascospores* hyaline, filiform, spirally twisted in the ascus, approximately the same length as the ascus, slender, indistinctly septate.

Type: *Gamszarea wallacei* (H.C. Evans) Z.F. Zhang & L. Cai

Notes: *Lecanicillium* was introduced by Gams and Zare (2001) to accommodate the taxa with aculeate phialides that cannot be classified in the genera such as *Beauveria*, *Isaria* Pers and *Microhilum* H.Y. Yip & A.C. Rath, with *L. lecanii* (Zimm.) Zare & W. Gams as the generic type (Sung et al. 2007a; Park et al. 2015; Huang et al. 2018). While, previous studies of *Cordycipitaceae* based on multi-locus phylogeny showed that *Lecanicillium* is polyphyly (Sung et al. 2007a; Sanjuan et al. 2014; Chiriví-Salomón et al. 2015; Kepler et al. 2017), and several species of *Lecanicillium*, including the type *L. lecanii*, were transferred to genus *Akanthomyces* Lebert (Kepler et al. 2017). Nevertheless, several distinctly separate clades remained (Figs. 25, 26). Three of our new species clustered with *L. wallacei* (H.C. Evans) H.C. Evans & Zare (teleomorph synonym: *Torrubiella wallacei* H.C. Evans), *L. kalimantanense* Kurihara & Sukarno, *Verticillium indonesiacum* Kurihara & Sukarno and several new *Lecanicillium* species published recently in a single clade in *Cordycipitaceae*, which represented a new genus, herein named as *Gamszarea* (Figs. 25, 26). The most closely related genus to *Gamszarea* is *Simplicillium* Zare & W. Gams. Species of *Simplicillium* usually have discrete solitary phialides arising from prostrate hyphae and short-ellipsoidal to subglobose or obclavate conidia (Zare and Gams 2008). On contrary, phialides of *Gamszarea* are aculeate, solitary or verticillate and the dimorphic conidia are lunate, fusiform or falcate.

Gamszarea wallacei (H.C. Evans) Z.F. Zhang & L. Cai, ***comb. nov.***

Index Fungorum number: 556421, *Facesoffungi number:* FoF 08440

Basionym: *Simplicillium wallacei* H.C. Evans, Nova Hedwigia 73 (1–2): 43 (2001).

Synonym: *Torrubiella wallacei* H.C. Evans, Nova Hedwigia 73 (1–2): 46 (2001).

Lecanicillium wallacei (H.C. Evans) H.C. Evans & Zare, Mycological Research 112 (7): 816 (2008).

Holotype: Indonesia, Sulawesi, Dumoga Bone forest, on lepidopteran larva, IMI 331549, ex-type living culture, CBS 101237.

Notes: This species was first described as *Simplicillium wallacei* by Gams and Zare (2001) based on morphological features, and then transferred to *Lecanicillium* based on ITS analyses (Zare and Gams 2008). While, in the cladogram of Zare and Gams (2008), *Lecanicillium wallacei* clustered in a distinct clade between *Lecanicillium* and *Simplicillium*, which was consistent with our multi-locus analyses (Figs. 25, 26). Therefore, a new combination is proposed here, as *Gamszarea wallacei*.

Gamszarea indonesiaca (Kurihara & Sukarno) Z.F. Zhang & L. Cai, ***comb. nov.***

Index Fungorum number: 556422, *Facesoffungi number:* FoF 08441

Basionym: *Verticillium indonesiacum* Kurihara & Sukarno, Mycoscience 50 (5): 377 (2009).

Holotype: Indonesia, East Kalimantan, Kutai National Park, on synnemata growing on a spider, BO22577, ex-type living culture, BTCC-F36 = NBRC 105408 = ID06-F0380.

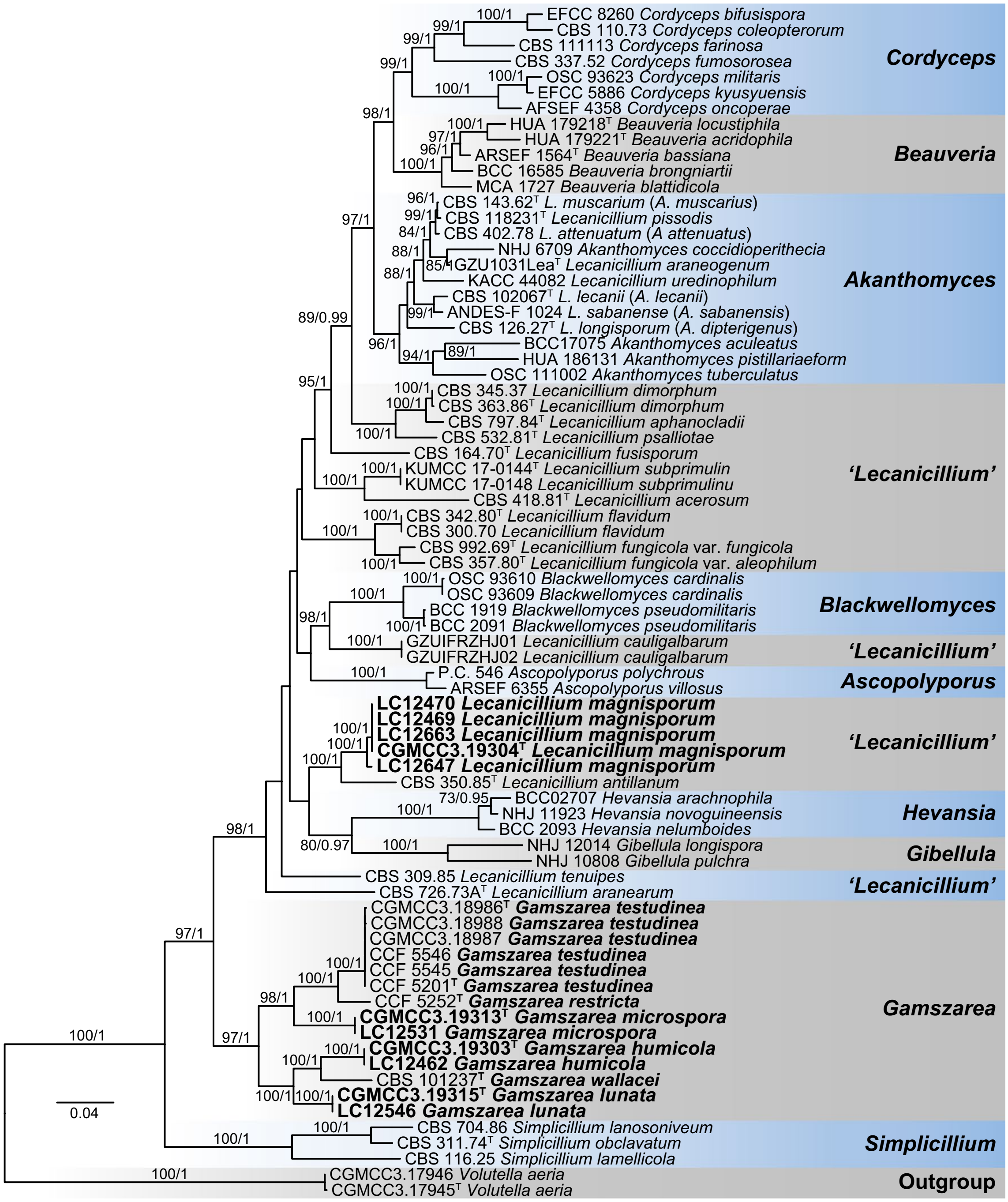


Fig. 25 Maximum likelihood (ML) tree of *Gamszarea*, *Lecanicillium* and allied genera in *Cordycipitaceae* based on ITS, LSU, SSU, EF1-α, RPB1 and RPB2 sequences. Seventy-six strains are used. The tree is rooted with *Volutella aeria* (CGMCC3.17945 and CGMCC3.17946). Tree topology of the ML analysis was similar to the BI. The Best scoring RAxML tree with a final likelihood value of − 41813.806368. The matrix had 2082 distinct alignment patterns, with 17.94 % of undetermined characters or gaps. Base frequencies estimated by jModelTest were as follows, A = 0.2338, C = 0.2762, G = 0.2605, T = 0.2295; substitution rates AC = 1.4660, AG = 3.7913, AT = 0.9486, CG = 0.9281, CT = 7.8283, GT = 1.0000; gamma shape = 0.5830. ML bootstrap values (≥ 70 %) and Bayesian posterior probability (≥ 90 %) are indicated along branches (ML/PP). Novel species are in bold font and "T" indicates type derived sequences

Notes: *Verticillium indonesiacum* was introduced as a species of *Verticillium* Nees (*Plectosphaerellaceae*) based on morphological characters (Sukarno et al. 2009). However, ITS-based phylogeny suggested a close affinity to *Lecanicillium* (Sukarno et al. 2009), despite its verticillate phialides with branches that is more similar to *Verticillium* (Sukarno et al. 2009). In our phylogenetic tree of *Cordycipitaceae*, *V. indonesiacum* clustered within *Gamszarea* clade

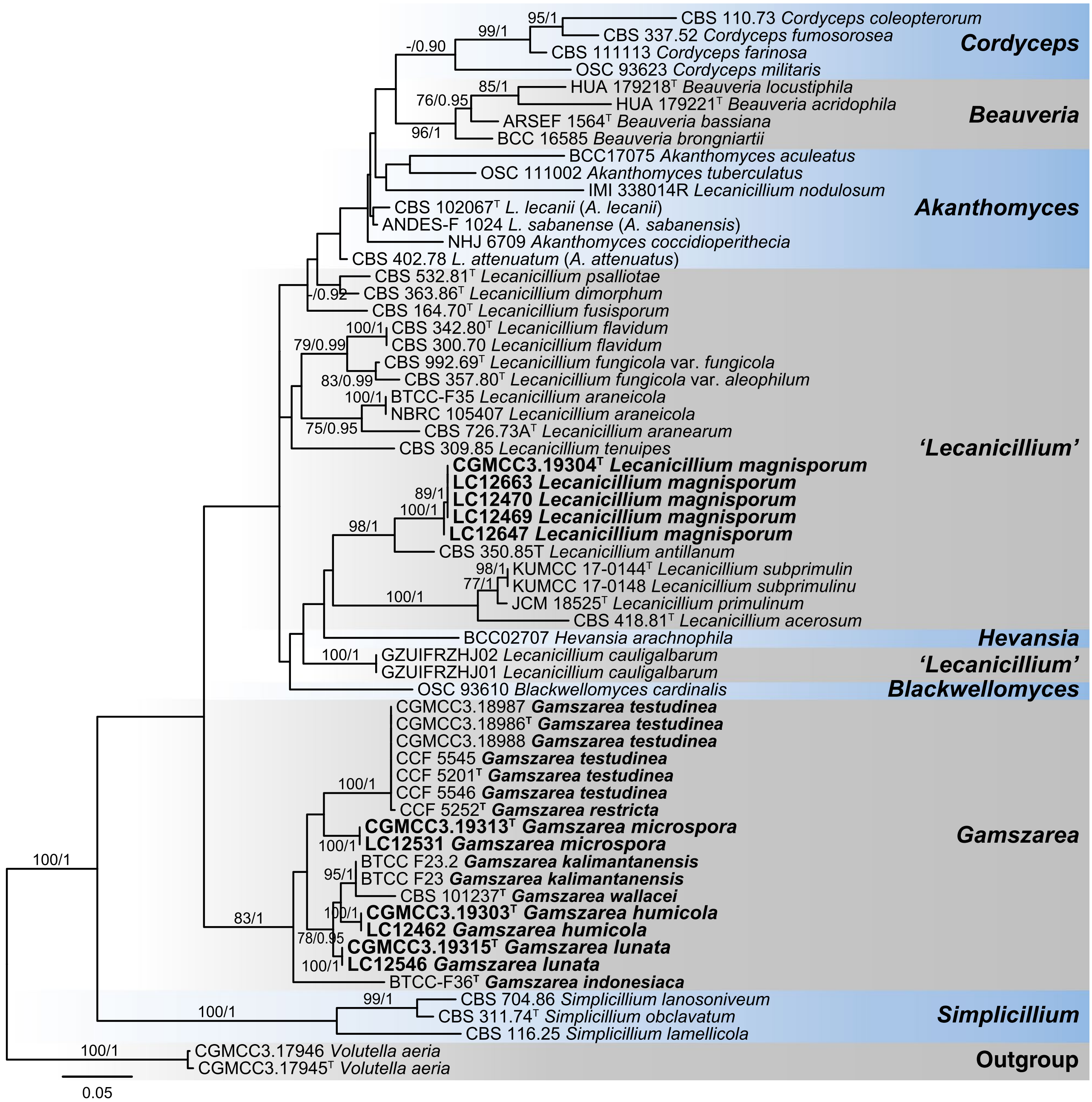


Fig. 26 Maximum likelihood (ML) tree of *Gamszarea*, *Lecanicillium* and allied genera in *Cordycipitaceae* based on ITS sequences. Sixty-two strains are used. The tree is rooted with *Volutella aeria* (CGMCC3.17945 and CGMCC3.17946). Tree topology of the ML analysis was similar to the BI. The Best scoring RAxML tree with a final likelihood value of − 5440.348928. The matrix had 347 distinct alignment patterns, with 14.62 % of undetermined characters or gaps. Base frequencies estimated by jModelTest were as follows, A = 0.2220, C = 0.3155, G = 0.2645, T = 0.1980; substitution rates AC = 2.3755, AG = 2.4987, AT = 1.5316, CG = 0.9389, CT = 5.6398, GT = 1.0000; gamma shape = 0.5370. ML bootstrap values (≥ 70 %) and Bayesian posterior probability (≥ 90 %) are indicated along branches (ML/PP). Novel species are in bold font and "T" indicates type derived sequences

(Figs. 25, 26), and its solitary or verticillate phialides and the mostly falcate conidia fit well to the general features of *Gamszarea*, which are distinctly different from *Verticillium* species with mainly verticillate phialides arising below the transverse septum along conidiophores and the cylindrical to oval conidia (Inderbitzin et al. 2011). Although macroconidia and microconidia can be easily distinguished in Fig. 2i, j (Sukarno et al. 2009), condia were too few to measure the size. *Gamszarea indonesiaca*can be easily distinguished from other *Gamszarea* species by its more abundant verticillate phialides on the erect, septate and branched hyphae.

Gamszarea kalimantanensis (Kurihara & Sukarno) Z.F. Zhang & L. Cai, ***comb. nov.***

Index Fungorum number: 556423, *Facesoffungi number:* FoF 08442

Basionym: *Lecanicillium kalimantanense* Kurihara & Sukarno, Mycoscience 50 (5): 376 (2009).

Holotype: Indonesia, East Kalimantan, Kutai National Park, on exoskeleton of staphylinid-like beetle, BO22579, ex-type living culture, BTCC-F23 = NBRC 105406 = ID06-F0406.

Notes: Although the conidia of *Lecanicillium kalimantanense* varied significantly in size (Sukarno et al. 2009), macroconidia and microconidia can be easily distinguished (Fig. 2e–g in Sukarno et al. 2009). Based on the provided scale bars, we managed to measure the conidial size using Fig. 2g in Sukarno et al. (2009), 9.0–12.0 × 1.0–2.0 µm for macroconidia, and 4.5–7.5 × 1.0–2.0 µm for microconidia, which fitted well to the generic features of *Gamszarea*. Combining with phylogenetic data (Figs. 25, 26), we proposed this species as a new combination, *G. kalimantanensis*. It differs from other *Gamszarea* species in its longer conidia and more abundant verticillate phialides along the prostrate aerial hyphae.

Gamszarea restricta (Hubka, Kubátová, Nonaka, Čmoková & Řehulka) Z.F. Zhang & L. Cai, ***comb. nov.***

Index Fungorum number: 557629, *Facesoffungi number:* FoF 08443

Basionym: *Lecanicillium restrictum* Hubka, Kubátová, Nonaka, Čmoková & Řehulka, Persoonia 40: 291 (2018).

Holotype: Czech Republic, Starý Bohumín, surface of the wooden barrel found during archaeological excavations, PRM 946543, ex-type living culture, CCF 5252 = CBS 143072.

Notes: *Lecanicillium restrictum* and *L. testudineum* Hubka, Kubátová, Schauflerová, Déniel & Jany were published by Crous et al. (2018), while only *Lecanicillium* species and two loci, ITS and EF1-α, were used in their study phylogenetic study. However, both the single and six-locus phylogeny (Figs. 25, 26) presented a highly support clade of *L. restrictum* and *L. testudineum* within the new genus *Gamszarea*. Meanwhile, morphological features of *L. restrictum*

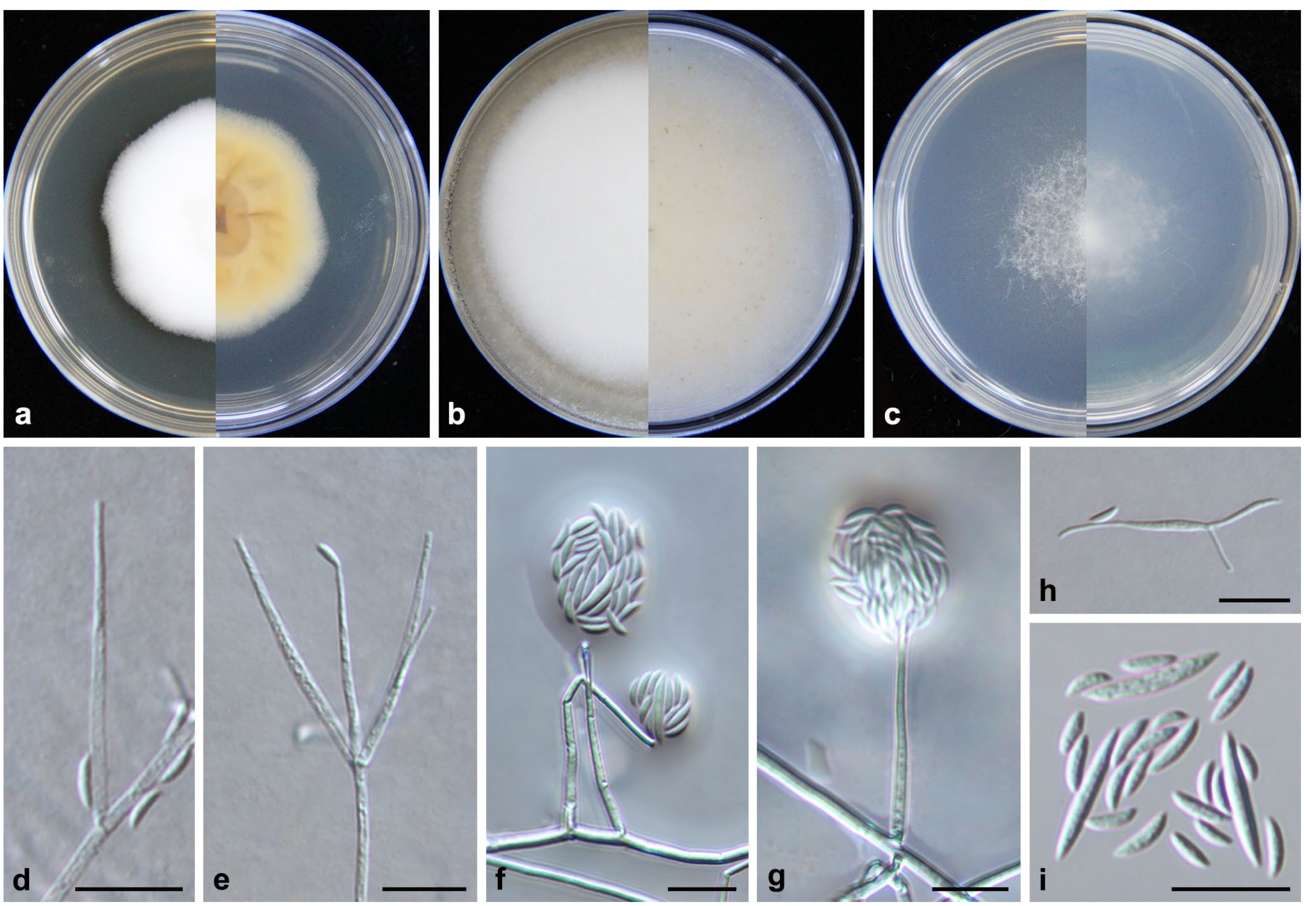


Fig. 27 *Gamszarea humicola* (from ex-holotype CGMCC3.19303). **a**–**c** Upper and reverse views of cultures on PDA, OA and SNA 4 weeks after inoculation; **d**–**e** conidiophores and phialides; **f**–**g** conidia in globose heads; **h** germinated conidia; **i** macroconidia and microconidia. Scale bars: **d**–**i** 10 µm

and *L. testudineum*, such as solitary or verticillate phialides produced on aerial hyphae, dimorphic conidia, fusiform or falcate macroconidia with pointed ends, and curved reniform with rounded ends, were consistent with the generic concept of *Gamszarea*. Therefore, they were proposed as new combinations, *G. restricta* and *G. testudinea*. *G. restricta* can be distinguished from other *Gamszarea* species by it lager macroconidia but smaller microconidia.

Gamszarea testudinea (Hubka, Kubátová, Nonaka, Čmoková & Řehulka) Z.F. Zhang & L. Cai, ***comb. nov.***

Index Fungorum number: 557630, *Facesoffungi number:* FoF 08444

Basionym: *Lecanicillium testudineum* Hubka, Kubátová, Schauflerová, Déniel & Jany, Persoonia 40: 293 (2018).

Synonym: *Lecanicillium coprophilum* Lei Su, Hua Zhu & C. Qin, Phytotaxa 387 (1): 58 (2019).

Holotype: Czech Republic, Prague, scales from the carapace of the captive red-eared slider, PRM 935078, ex-type living culture, CCF 5201 = CBS 141096.

Notes: See note of *Gamszarea restricta*. Blastn search with ITS sequence gave an almost 100% similarity between *Lecanicillium testudineum* and *L. coprophilum*, which was supported by our phylogenetic analyses (Figs. 25, 26). Morphological features of *L. testudineum* and *L. coprophilum* were very similar, except macroconidia, pointed ends in *L. testudineum* but rounded ends in *L. coprophilum*. However, it can be clearly noticed in Fig. 2e, g, h in Su's article that the end of macroconidia *L. coprophilum* were slightly pointed more than that rounded. *L. coprophilum* was introduced by Su et al. in (2019), a bit later than *L. testudineum* (Crous et al. 2018). Therefore they were combined to *Gamszarea testudinea* here. *G. testudinea* morphological differed from other species of *Gamszarea* by its smaller conidia (macroconidia 3.5–6 × 1.0–1.5 µm, microconidia 2.5–3 × 1.0–1.5 µm for *G. testudinea*; 8.5–10.5 × 1.0–1.5 µm and 4.0–5.5 × 0.7–1.2 µm for *G. wallacei*; 9.0–12.0 × 1.0–2.0 µm and 4.5–7.5 × 1.0–2.0 µm for *G. kalimantanensis*; 9.0–13.0 × 1.5–2.5 µm and 3.5–6.5 × 1.0–1.5 for *G. humicola*; 7.0–9.5 × 1.5–2.5 µm and 3.0–5.0 × 1.5–2.0 µm for *G. lunata*; 6.0–10 × 1.0–1.5 µm and 2.5–3 × 1.0–1.5 µm for *Gamszarea restricta*) and the present of prismatic crystals (Crous et al. 2018; Su et al. 2019).

Gamszarea humicola Z.F. Zhang & L. Cai, ***sp. nov.***

Index Fungorum number: 557631, *Facesoffungi number:* FoF 08445; Fig. 27

Etymology: Referring to the substrate where this fungus was isolated.

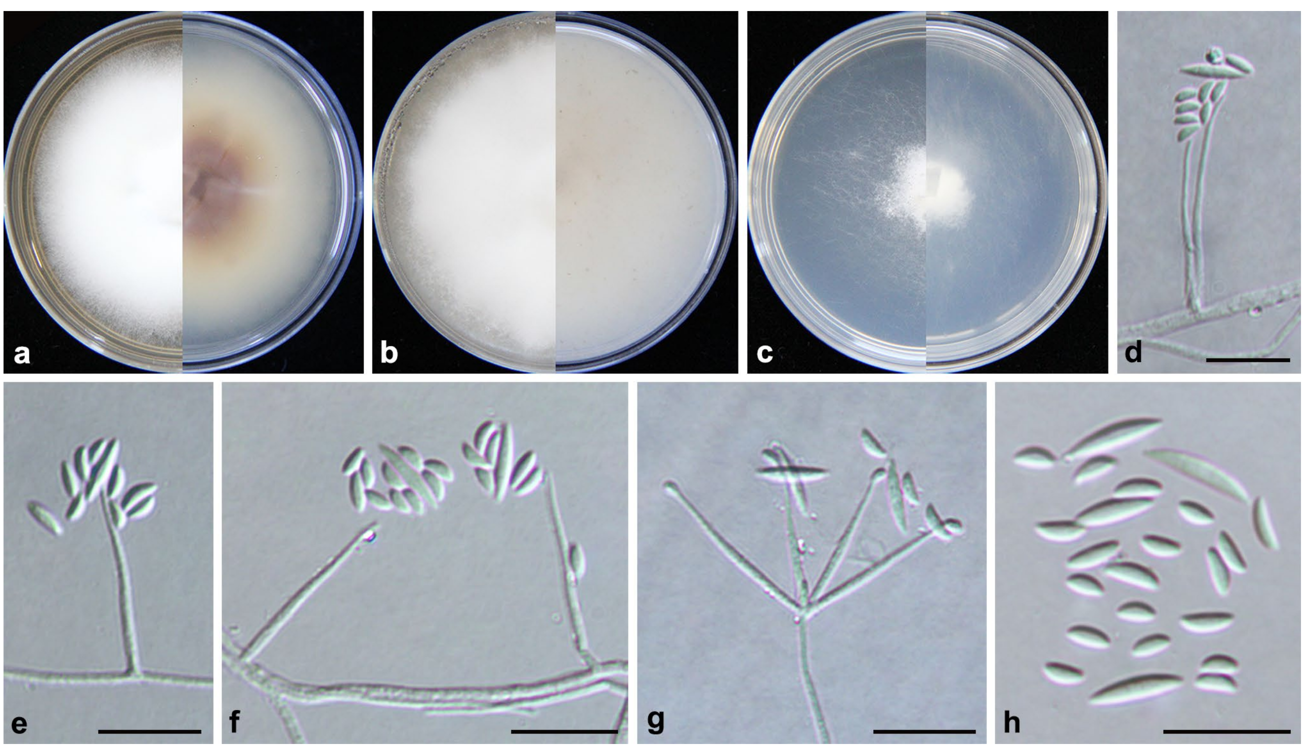


Fig. 28 *Gamszarea lunata* (from ex-holotype CGMCC3.19315). **a–c** Upper and reverse views of cultures on PDA, OA and SNA 4 weeks after inoculation; **d–f** phialides and conidia in globose heads; **g** conidiophores and phialides; **h** macroconidia and microconidia. Scale bars: **d–h** 10 µm

Holotype: HMAS 247987.

Hyphae hyaline, septate, smooth, 1.5–2.5 µm wide. **Asexual morph** *Conidiophores* arising from prostrate aerial hyphae, erect, hyaline, 1.0–2.5 µm diam. *Phialides* arising from prostrate aerial hyphae solitary, or in whorls of 2–6 at the apex of conidiophores, erect, aculeate, tapering to the apex, hyaline, 14.0–34.0 µm long, 1.0–2.5 µm diam. at base. *Conidia* unicellular, long fusiform, or curved to falcate, smooth, hyaline, each phialide producing one macroconidia and several microconidia, variable in size, aggregated in slimy head; *macroconidia* 9.0–13.0 × 1.5–2.5 µm ($\bar{x}$ ± SD = 10.7 ± 1.1 × 2.0 ± 0.19 µm, n = 35); *microconidia* 3.5–6.5 × 1.0–1.5 µm ($\bar{x}$± SD = 5.1 ± 0.88 × 1.3 ± 0.15 µm, n = 50). **Sexual morph** not observed.

Culture characteristics—Colonies on PDA attaining 31–40 mm diam. after 4 weeks, flat, cottony, margin slightly undulate, white. Reverse plicate, cream yellow (4A1) to light yellow (3A3). Colonies on OA attaining 44–48 mm diam. after 4 weeks, flat, cottony, margin entire, white. Reverse cream-white. Colonies on SNA attaining 46–50 mm diam. after 4 weeks, flocculent, margin unclear, white. Reverse white. Sporulation within 20 days.

Material examined: CHINA, Guangxi, Guilin, E'gu Cave, N 24.942°, E 110.511°, on soil, May 2016, Z.F. Zhang, HMAS 247987 (holotype designated here), ex-type living culture CGMCC3.19303 = LC12461; ibid., LC12462.

Notes: *Gamszarea humicola* is phylogenetically close to *G. kalimantanensis*, *G. lunata* and *G. wallacei* (Fig. 25). Morphologically, *G. humicola* differs from *G. kalimantanensis* by its mostly solitary phialides; from *G. lunata* by its longer macroconidia (9.0–13.0 µm vs. 7.0–9.5 µm); from *G. wallacei* in its wider phialides (1.0–2.5 µm vs. 0.7–1.2 µm) and macroconidia (1.5–2.5 µm vs. 1.0–1.5 µm).

Gamszarea lunata Z.F. Zhang & L. Cai, ***sp. nov.***

Index Fungorum number: 557632, *Facesoffungi number:* FoF 08446; Fig. 28

Etymology: Referring to the shape of its microconidia.

Holotype: HMAS 247996.

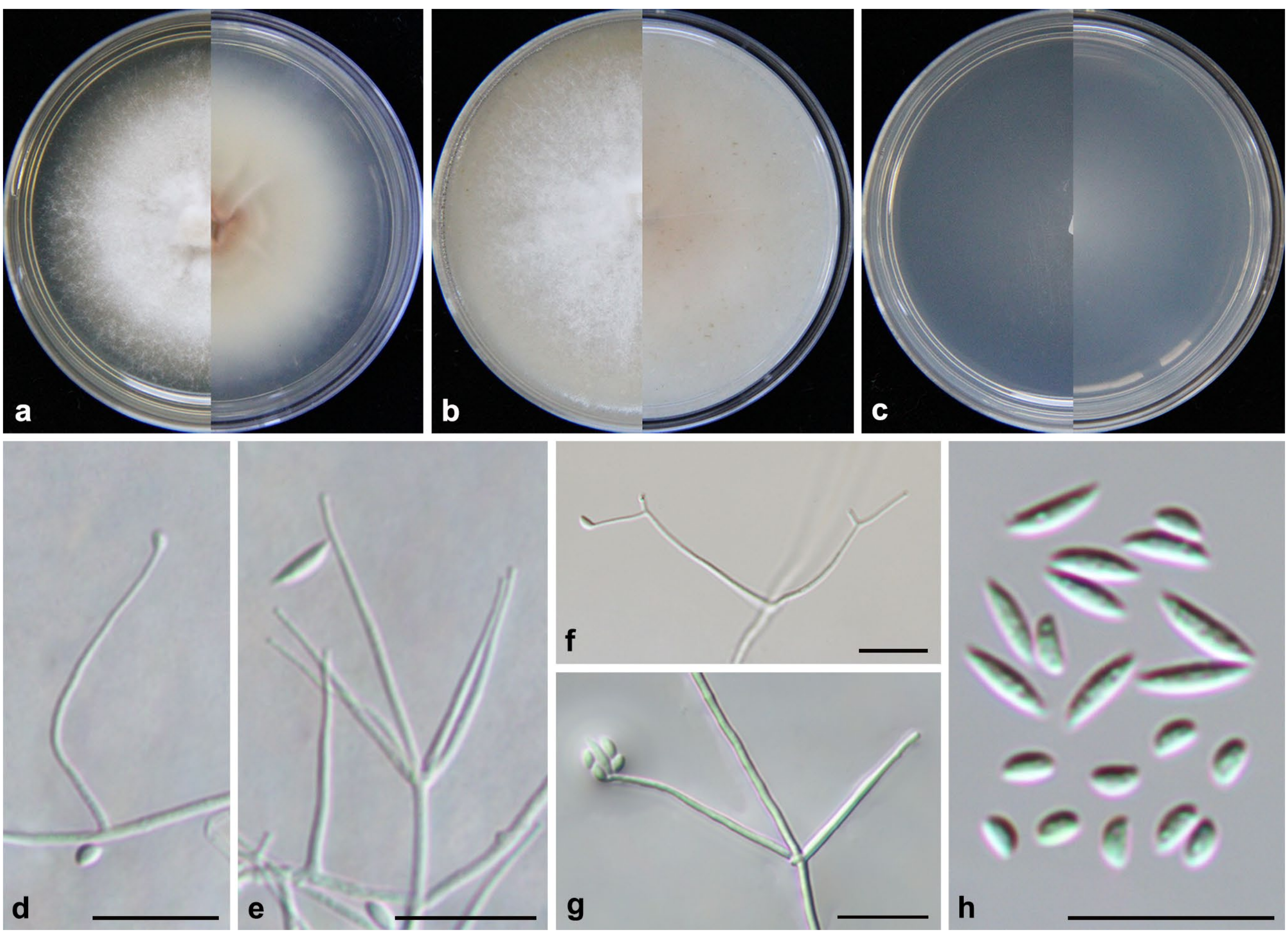


Fig. 29 *Gamszarea microspora* (from ex-holotype CGMCC3.19313). **a**–**c** Upper and reverse views of cultures on PDA, OA and SNA 4 weeks after inoculation; **e** conidiophores and phialides; **d**, **f**, **g** phialides and conidia (**f** branched phialides); **h** macroconidia and microconidia. Scale bars: **d**–**h** 10 µm

Hyphae hyaline, septate, smooth, 1.0–2.5 µm wide. **Asexual morph** *Conidiophores* arising from prostrate aerial hyphae, erect, hyaline, 1.0–2.0 µm diam. *Phialides* arising from prostrate aerial hyphae solitary, or in whorls of 2–4 at the apex of conidiophores, straight or slightly curved, tapering toward the apex, smooth, hyaline, 15.0–28.0 µm long, 1.0–2.0 µm diam. at base. *Conidia* unicellular, smooth, hyaline, each phialide producing one macroconidia and several microconidia, variable in size, aggregated in slimy head; *macroconidia* long fusiform or falcate, 7.0–9.5 × 1.5–2.5 µm ($\bar{x}$ ± SD = 8.3 ± 0.77 × 2.0 ± 0.19 µm, n = 30); *microconidia* mostly lunate, 3.0–5.0 × 1.5–2.0 µm ($\bar{x}$± SD = 3.8 ± 0.49 × 1.7 ± 0.14 µm, n = 60). **Sexual morph** not observed.

Culture characteristics—Colonies on PDA attaining 45–48 mm diam. after 4 weeks, cottony to pulverulent, slightly convex, margin entire, white. Reverse plicated, cream white to brown (7C6). Colonies on OA attaining 46–49 mm diam. after 4 weeks, flat, cottony, margin entire, white. Reverse white. Colonies on SNA attaining 47–49 mm diam. after 4 weeks, flat, pulverulent at center, aerial mycelia sparse, white. Reverse white. Sporulation within 3 weeks.

Material examined: CHINA, Guangxi, Guilin, E'gu Cave, N 24.942°, E 110.511°, on rock, May 2016, Z.F. Zhang, HMAS 247996 (holotype designated here), ex-type living culture CGMCC3.19315 = LC12545; ibid., LC12546.

Notes: *Gamszarea lunata* can be easily distinguished from *G. humicola* (see notes of *G. humicola*). Macroconidia of *G. lunata* is wider than *G. wallacei* (1.5–2.5 µm vs. 1.0–1.5 µm). In addition, microconidia of *G. lunata* is lunate rather than ellipsoidal to slightly falcate in *G. wallacei*. Conidia of *G. kalimantanensis* are much longer than *G. lunata* (macroconidia: 9.0–12.0 µm vs. 7.0–9.5 µm, microconidia: 4.5–7.5 µm vs. 3.0–5.0 µm). Meanwhile, ITS sequences of *G. kalimantanensis* has 98% similarity to *G. lunata* (nine bp difference in 515 bp).

Gamszarea microspora Z.F. Zhang & L. Cai, ***sp. nov.***

Index Fungorum number: 557633, *Facesoffungi number:* FoF 08447; Fig. 29

Etymology: Referring to its smaller conidia than other species in this genus.

Holotype: HMAS 248009.

Hyphae hyaline, septate, branched, smooth, 1.0–2.5 µm wide. **Asexual morph** *Conidiophores* arising from prostrate aerial hyphae, erect, hyaline, 1.0–2.5 µm diam. *Phialides* arising from hyphae solitary or in whorls of 2–3, or in whorls of 2–4 lateral or at the apex of conidiophores, straight or slightly curved, tapering to the apex, sometimes branched, smooth, hyaline, 11.0–22.0 (–35.0) µm long, 1.0–1.5 µm diam. at base. *Conidia* unicellular, smooth, hyaline, each phialide producing one macroconidia and several microconidia, variable in size, aggregated in slimy head; *macroconidia* long fusiform or falcate, 4.5–6.0 × 1.5–2.0 µm ($\bar{x}$ ± SD = 5.1 ± 1.1 × 1.7 ± 0.15 µm, n = 50); *microconidia* short lunate, 2.0–3.5 × 1.0–2.0 µm ($\bar{x}$± SD = 2.7 ± 0.33 × 1.6 ± 0.12 µm, n = 60). **Sexual morph** not observed.

Culture characteristics—Colonies on PDA attaining 42–47 mm diam. after 4 weeks, plicated, flocculent to pulverulent, margin entire, white. Reverse plicated, cream white to pale brown (7B4). Colonies on OA attaining 43–47 mm diam. after 4 weeks, flat, felty, white. Reverse cream-white to pale salmon (6A2). Colonies on SNA attaining 44–48 mm diam. after 4 weeks, flat, colorless, aerial mycelia extremely sparse. Reverse colorless. Sporulation within 3 weeks on PDA and OA.

Material examined: CHINA, Sichuan, Xingwen, Tianliang Cave, N 28.19°, E 105.139°, on rock, May 2016, Z.F. Zhang, HMAS 248009 (holotype designated here), ex-type living culture CGMCC3.19313 = LC12530; ibid., LC12531.

Notes: *Gamszarea microspora* can be easily distinguished from most species of *Gamszarea* by its significantly smaller conidia and the occasionally branched phialides. *G. microspora* differs from *G. indonesiaca* in the phialides which are mostly produced on prostrating aerial hyphae, while that of *G. indonesiaca* are mostly at the apex of the erect hyphae (Sukarno et al. 2009).

Lecanicillium W. Gams & Zare

See short notes of *Gamszarea.*

Lecanicillium magnisporum Z.F. Zhang & L. Cai, ***sp. nov.***

Index Fungorum number: 557634, *Facesoffungi number:* FoF 08448; Fig. 30

Etymology: Referring to its larger conidia than other species in this genus.

Holotype: HMAS 248013.

Hyphae hyaline, septate, smooth, 0.5–2.5 µm wide. **Asexual morph** *Conidiophores* arising from aerial hyphae, erect, smooth, hyaline, 1.0–1.5 µm diam. *Phialides* arising from aerial hyphae solitary, or in whorls of 2–5 at the apex of conidiophores, straight or slightly curved, tapering to the apex, smooth, hyaline, 17.0–37.0 µm long, 1.0–1.5 µm diam. at base. *Conidia* rare, unicellular, smooth, hyaline, variable in size; *macroconidia* long fusiform or falcate, 9.0–16.0 × 2.0–3.0 µm ($\bar{x}$ ± SD = 12.3 ± 2.0 × 2.5 ± 0.29 µm, n = 45); *microconidia* much fewer than macroconidia, 5.0–7.0 × 1.5–2.5 µm ($\bar{x}$ ± SD = 5.94 ± 0.75 × 1.9 ± 0.41 µm, n = 20). **Sexual morph** not observed.

Culture characteristics—Colonies on PDA attaining 44–48 mm diam. after 4 weeks, flat, felty, margin fimbriate, white. Reverse plicate, light yellow (4A2) to yellow (4A5). Colonies on OA attaining 38–40 mm diam. after 4 weeks, flat, cottony, margin entire, white. Reverse cream-white in center, pale rosybrown (6B3) at margin. Colonies on SNA attaining 45–47 mm diam. after 4 weeks, flat, tomentose, white, aerial mycelia sparse. Reverse white. Sporulation within 18 days.

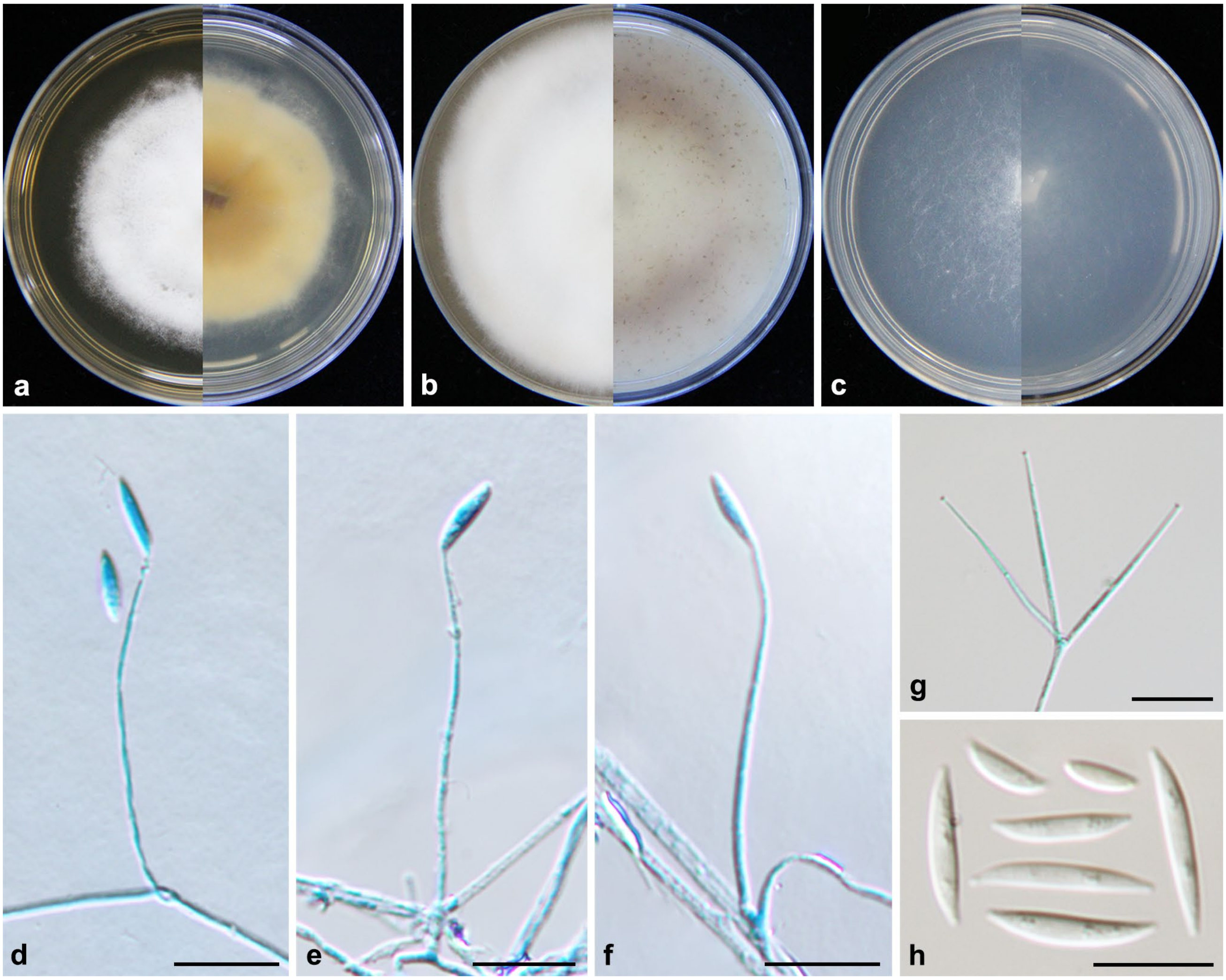


Fig. 30 *Lecanicillium magnisporum* (from ex-holotype CGMCC3.19304). **a**–**c** Upper and reverse views of cultures on PDA, OA and SNA 4 weeks after inoculation; **d**–**f** phialides and conidia; **g** conidiophores and phialides; **h** macroconidia and microconidia. Scale bars: **d**–**h** 10 µm

Material examined: CHINA, Chongqing, Wulong, Erwang Cave, N 29.585°, E 108.001°, on soil, May 2016, Z.F. Zhang, HMAS 248013 (holotype designated here), ex-type living culture CGMCC3.19304 = LC12468; ibid., LC12469; ibid., LC12470; Chongqing, Wulong, Sanwang Cave, N 29.591°, E 108.001°, on soil, May 2016, Z.F. Zhang, LC12647; ibid., LC12663.

Notes: *Lecanicillium magnisporum* is phylogenetically allied to *L. antillanum* (R.F. Castañeda & G.R.W. Arnold) Zare & W. Gams, which belongs to one of the remaining clades of *Lecanicillium* (Fig. 25), but can be distinguished by the larger conidia (2.0–3.0 µm vs. 0.5–1.5 µm wide for marcoconidia, 5.0–7.0 × 1.5–2.5 µm vs. 2.0–3.5 × 0.5–1.5 µm for microconidia) and low sequence similarities (96% similarity, 23 bp difference in 524 bp of ITS; 99% similarity, 6 bp difference in 823 bp of LSU; 91% similarity, 73 bp difference in 820 bp of RPB2; 96% similarity, 38 bp difference in 912 bp of EF1-α). However, further revisions of the remaining species of *Lecanicillium* are required (see notes of *Gamszarea*).

Simplicillium W. Gams & Zare

The genus *Simplicillium* was introduced by Zare and Gams (2001) with *S. lanosoniveum* (J. F. H. Beyma) Zare & W. Gams as the type species. The genus is characterised by predominantly solitary phialides, conidial masses either in globose slimy heads, short chains, or in sympodial succession (Zare and Gams 2001; Nonaka et al. 2013). *Simplicillium* species are widely distributed and considered as mammal- and plant-parasitic, symbiotic, entomopathogenic, fungicolous and nematophagous fungi (Wei et al. 2019). In this study, two new species are described as *Simplicillium album* and *S. humicola* (Fig. 31).

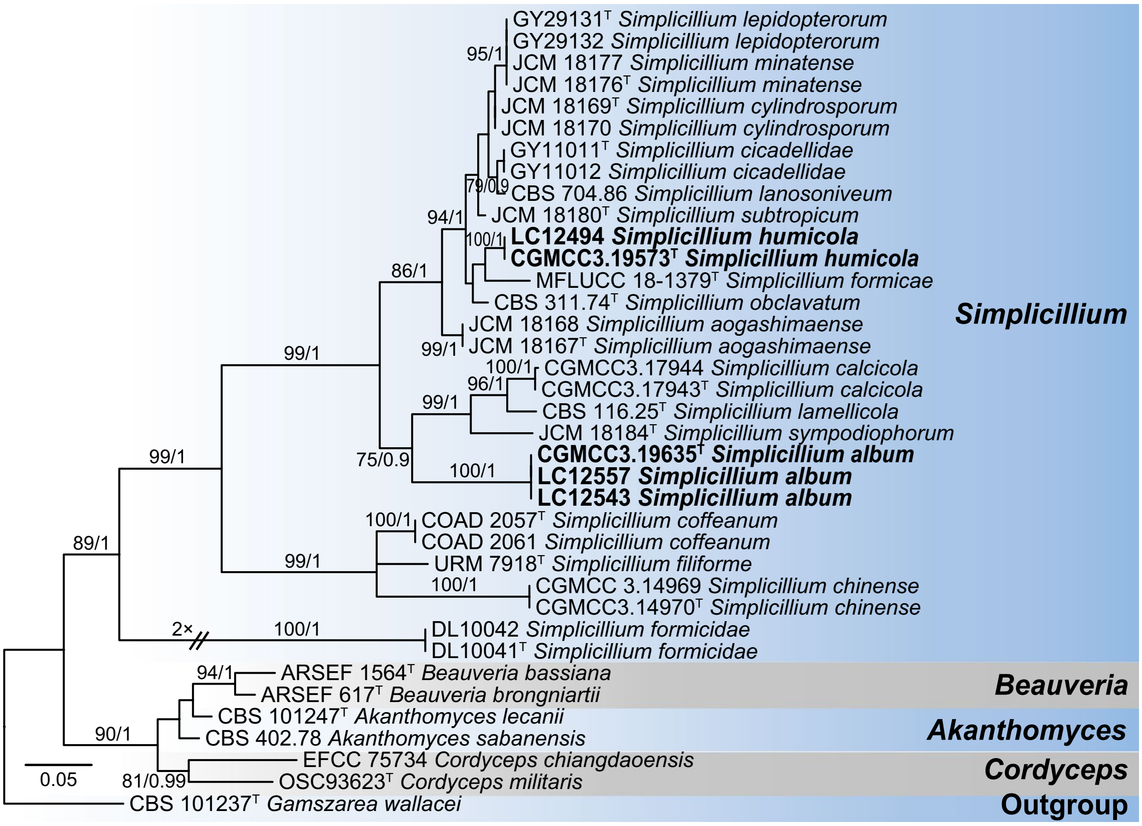


Fig. 31 Maximum likelihood (ML) tree of *Simplicillium* and allied genera based on ITS sequences. Thirty-seven strains are used. The tree is rooted with *Gamszarea wallacei* (CBS 101237). Tree topology of the ML analysis was similar to the BI. The Best scoring RAxML tree with a final likelihood value of − 3470.407859. The matrix had 262 distinct alignment patterns, with 11.19 % of undetermined characters or gaps. Base frequencies estimated by jModelTest were as follows, A = 0.2158, C = 0.3110, G = 0.2557, T = 0.2175; substitution rates AC = 1.5516, AG = 2.4182, AT = 1.5516, CG = 1.0000, CT = 4.4767, GT = 1.0000; gamma shape = 0.2860. ML bootstrap values (≥ 70 %) and Bayesian posterior probability (≥ 90 %) are indicated along branches (ML/PP). Novel species are in bold font and "T" indicates type derived sequences

Simplicillium album Z.F. Zhang & L. Cai, ***sp. nov.***

Index Fungorum number: 557740, *Facesoffungi number:* FoF 08449; Fig. 32

Etymology: Referring to the color of its white colonies on plates.

Holotype: HMAS 248003.

Hyphae hyaline, septate, smooth, 1.5–3.5 μm wide. **Asexual morph** *Conidiophores* simple, erect, cylindrical, smooth, hyaline. *Phialides* arising from prostrate aerial hyphae solitary, or in whorls of 2–3 at the apex of conidiophores, erect, tapering to the apex, with basal septum, smooth, hyaline, 13.0–40.0 μm long, 1.5–3.0 μm wide at base. *Conidia* variable in size and shape, 1-celled, smooth, hyaline; *microconidia* oblong or ellipsoidal, 3.0–4.0 × 1.5–2.0 μm ($\bar{x} \pm SD = 3.6 \pm 0.37 \times 1.7 \pm 0.18$ μm, n = 40), *macroconidia* fusiform or falcate, 8.0–11.0 (–13.0) × 2.0–3.5 μm ($\bar{x} \pm SD = 9.7 \pm 0.86 \times 2.9 \pm 0.31$ μm, n = 20). Octahedral crystals presented. **Sexual morph** not observed.

Culture characteristics—Colonies on PDA attaining 27–29 mm diam. after 10 days, flat, cottony, margin entire, white, light yellow secretions exuded. Reverse plicate, beige (1A1) to bisque (4A2). Colonies on OA attaining 28–31 mm diam. after 10 days, flat, cottony, margin entire, white. Reverse seashell (5A3) to wheat. Colonies on SNA attaining 30–34 mm diam. after 10 days, cottony, margin entire, white, aerial mycelia sparse. Reverse white. Sporulation within 10 days.

Material examined: CHINA, Guangxi, Laibin, Sanshan Cave, N 23.41°, E 108.931°, on soil, May 2016, Z.F. Zhang, HMAS 248003 (holotype designated here), ex-type living culture CGMCC3.19635 = LC12442; Guangxi, Guilin, E'gu Cav, N 24.942°, E 110.511°, on animal faeces, May 2016, Z.F. Zhang, LC12543; ibid., LC12557.

Notes: *Simplicillium album* is phylogenetically close to *S. calcicola* Z.F. Zhang, F. Liu & L. Cai, *S. lamellicola* (F.E.V. Sm.) Zare & W. Gams and *S. sympodiophorum* Nonaka, Kaifuchi & Masuma (Fig. 31), while *S. sympodiophorum* is distinguishable in producing monomorphic sympodial conidia. *S. album* shares similar morphological characters with *S. calcicola* and *S. lamellicola* in producing dimorphic

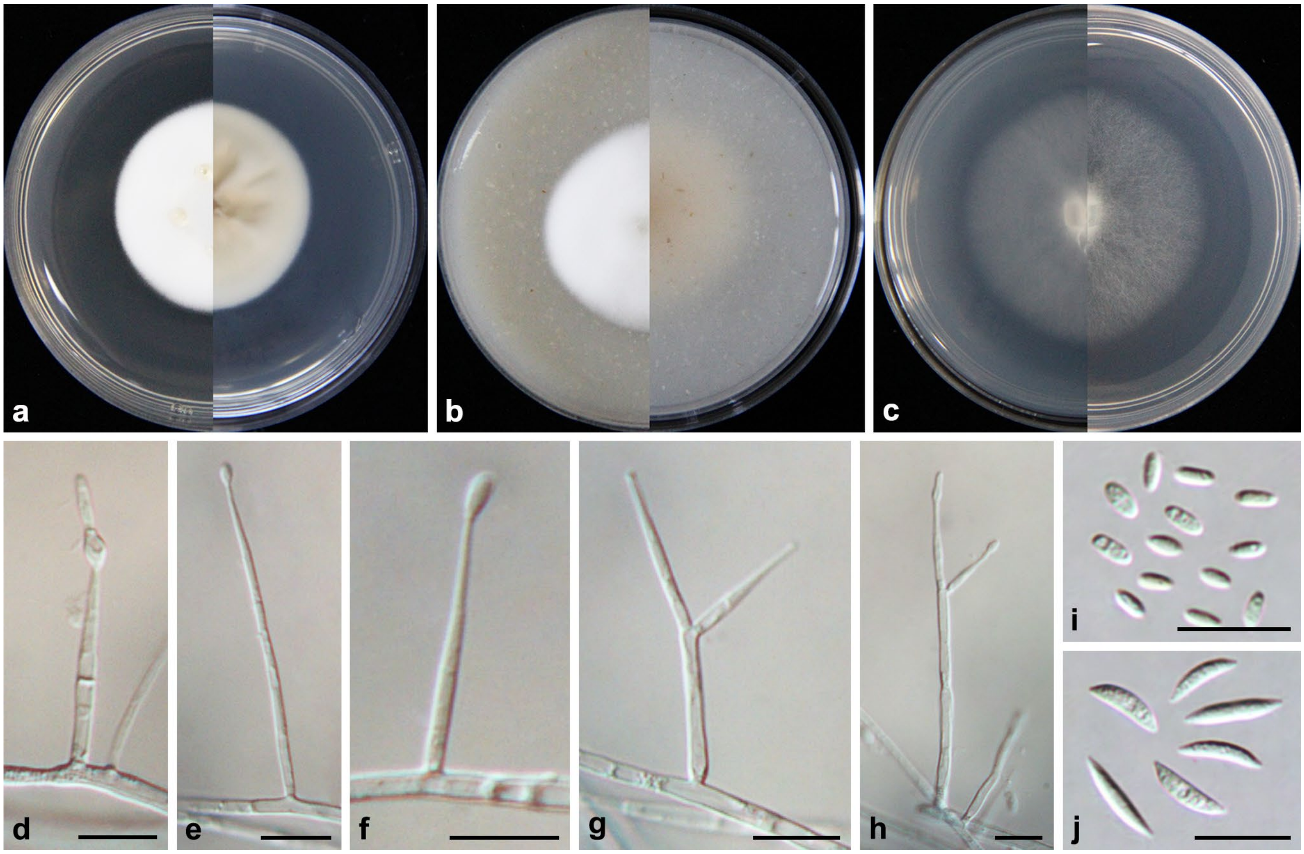


Fig. 32 *Simplicillium album* (from ex-holotype CGMCC3.19635). **a–c** Upper and reverse views of cultures on PDA, OA and SNA 10 days after inoculation; **d–h** conidiophores and phialides; **i**, **j** microconidia and macroconidia. Scale bars: d–j = 10 µm

conidia. However, *S. album* produces larger macroconidia (8.0–11.0 (–13.0) × 2.0–3.5 µm) than *S. calcicola* (4.5–8.0 × 1.0–2.0 µm) and *S. lamellicola* (4.5–9.0 × 0.8–1.2 µm). In addition, the octahedral crystals of *S. calcicola* are absent.

Simplicillium humicola Z.F. Zhang & L. Cai, ***sp. nov.***

Index Fungorum number: 557741, *Facesoffungi number:* FoF 08450; Fig. 33

Etymology: Referring to the substrate in which this fungus was isolated.

Holotype: HMAS 247991.

Hyphae hyaline, septate, smooth, 1.5–3.5 µm wide. **Asexual morph** *Phialides* arising from prostrate aerial hyphae solitary, or up to 2–3 in whorls, sometimes with short stalks, erect, tapering to the apex, straight or slightly curved, with basal septum, smooth, hyaline, 20.0–35.0 (–47.0) µm long, 1.5–3.0 µm wide at base. *Conidia* 1-celled, oblong or ellipsoidal, smooth, hyaline, 3.0–5.0 × 1.5–3.0 µm ($\bar{x} \pm$ SD = 3.7 ± 0.56 × 2.3 ± 0.3 µm, n = 60). Octahedral crystals presented. **Sexual morph** not observed.

Culture characteristics—Colonies on PDA attaining 28–31 mm diam. after 15 days, plicate, felty, margin entire, white, light yellow secretions exuded. Reverse plicate, light yellow (4A2) to brown (5C8). Colonies on OA attaining 30–36 mm diam. after 15 days, aerial mycelia abundant, fluffy, cottony, margin entire, white. Reverse floralwhite (4A2) to pale brown (7B4). Colonies on SNA attaining 30–38 mm diam. after 15 days, flat, ulotrichy, margin entire, white. Reverse white. Sporulation within 10 days.

Material examined: CHINA, Guangxi, Guilin, E'gu Cav, N 24.942°, E 110.511°, on soil, May 2016, Z.F. Zhang, HMAS 247991 (holotype designated here), ex-type living culture CGMCC3.19573 = LC12493; ibid., LC12494.

Notes: *Simplicillium humicola* is phylogenetically allied to *S. formicae* Nonaka, Kaifuchi & Masuma and *S. obclavatum* Nonaka, Kaifuchi & Masuma (Fig. 31), but morphologically differs in conidial shape and size (globose to ellipsoidal, 2.0–3.5 µm long in *S. formicae*; 2.5–3.5 µm long in *S. obclavatum*). Meanwhile, phialides of *S. obclavatum* are always solitary.

Nectriaceae Tul. & C. Tul.

The family *Nectriaceae* is characterised by uniloculate, white, yellow, orange-red or purple ascomata that change colour in KOH. The asexual morphs of *Nectriaceae* are phialidic, producing amerosporous to phragmosporous conidia.

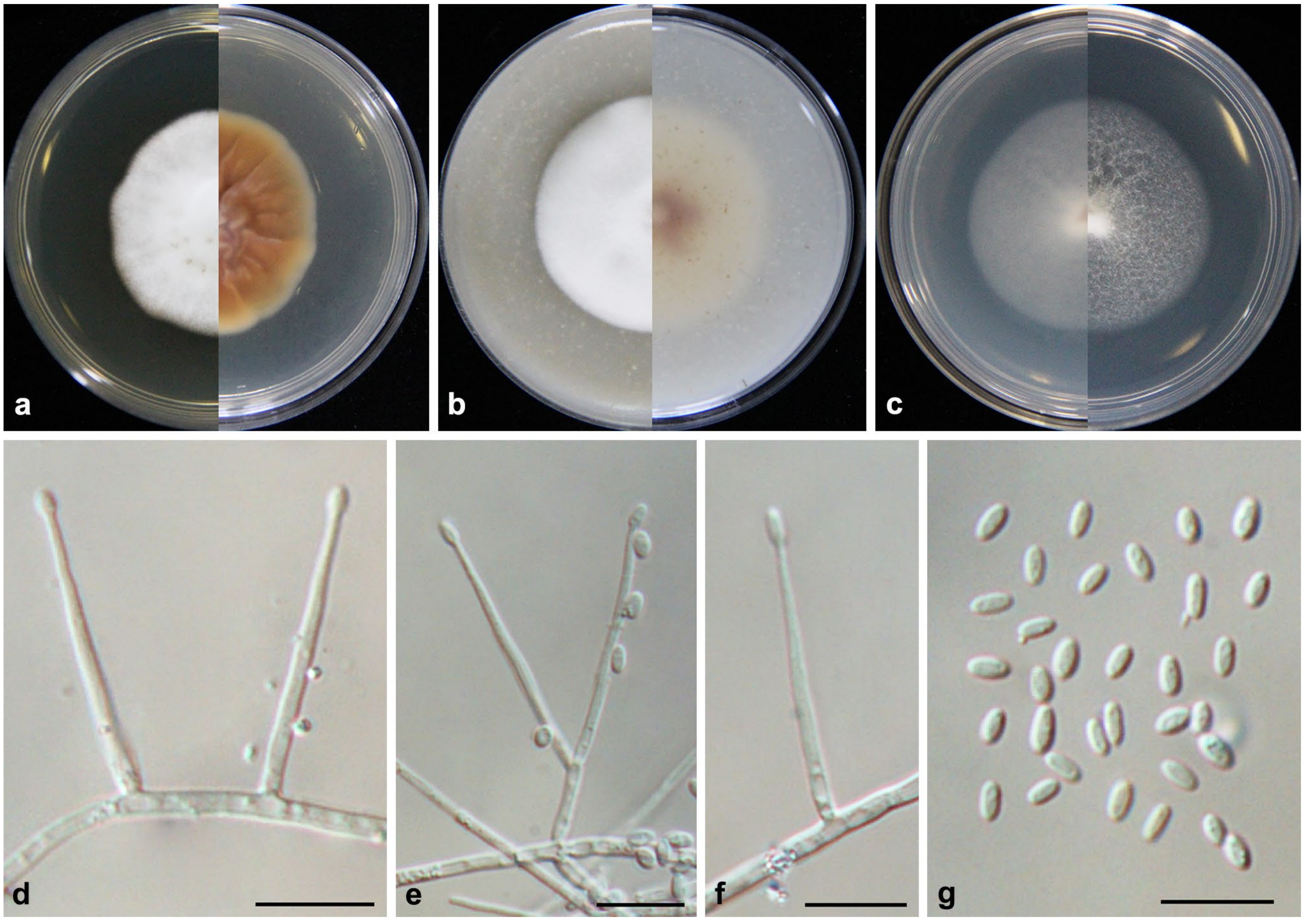


Fig. 33 *Simplicillium humicola* (from ex-holotype CGMCC3.19573). **a**–**c** Upper and reverse views of cultures on PDA, OA and SNA 15 days after inoculation; **d**–**f** conidiophores and phialides; **g** conidia. Scale bars: **d**–**g** 10 µm

The majority of species are soil-borne saprobes or weak to virulent, facultative or obligate plant pathogens (Lombard et al. 2015).

Paracremonium L. Lombard & Crous

The genus *Paracremonium* was established to accommodate *Acremonium recifei* and could be distinguished from other acremonium-like genera by the formation of sterile coils from which conidiophores radiate with inconspicuously swollen septa in the hyphae (Lombard et al. 2015). However, among the currently accepted six species, *P. binnewijzendii* Houbraken, van der Kleij & L. Lombard, *P. contagium* L. Lombard & Crous, *P. inflatum* L. Lombard & Crous, *P. moubasheri* Al-Bedak & M.A. Ismail, *P. pembeum* S.C. Lynch & Eskalen and *P. variiforme* Z.F. Zhang, F. Liu & L. Cai, only *P. inflatum* produces sterile coils (Lombard et al. 2015; Lynch et al. 2016; Crous et al. 2017; Zhang et al. 2017; Al-Bedak et al. 2019). Sterile coils is thus no longer a significant distinguishing character of the genus from allied genera. In this study, two new species named as *Paracremonium apiculatum* and *P. ellipsoideum* are described (Fig. 34).

Paracremonium apiculatum Z.F. Zhang & L. Cai, ***sp. nov.***

Index Fungorum number: 557742, *Facesoffungi number:* FoF 08451; Fig. 35

Etymology: Referring to its terminally apiculate conidia.

Holotype: HMAS 248078.

Hyphae hyaline, smooth, thick-walled, septate, branched, 2.0–7.0 µm diam. **Asexual morph** *Conidiophores* arising from vegetative hyphae solitary or tightly aggregated in cream-white, slimy sporulation, erect, simple or mostly branched, septate, bearing whorls of 2–6 conidiogenous cells. *Conidiogenous cell* terminal or lateral, straight, acicular, tapering towards apex, smooth, hyaline, 14–24 µm long, 1.5–3.0 µm wide at base, with prominent periclinal thickening and inconspicuous collarette, 1.0–1.5 µm diam. *Conidia* abundant, unicellular, subglobose to globose, apiculate, smooth, thick-walled, hyaline, 3.5–5.0 µm ($\bar{x} \pm$ SD =

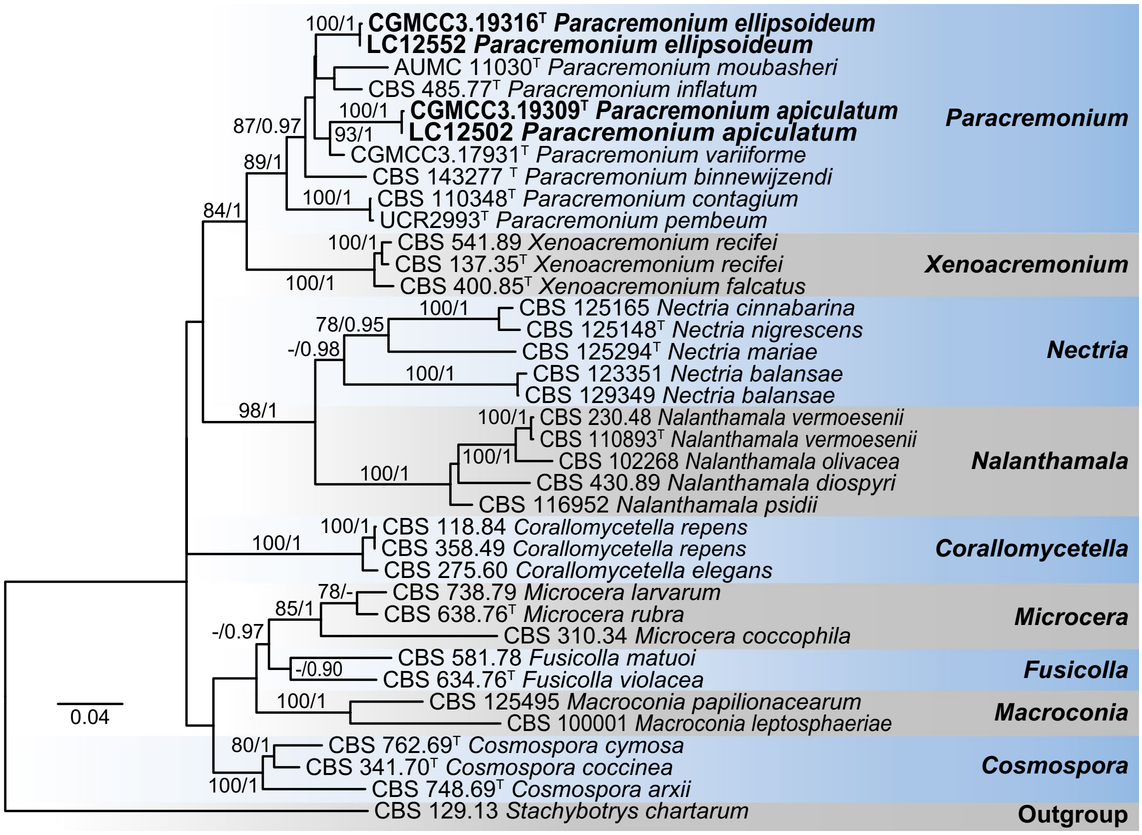


Fig. 34 Maximum likelihood (ML) tree of *Paracremonium* and allied genera based on ITS, LSU and TUB sequences. Thirty-seven strains are used. The tree is rooted with *Stachybotrys chartarum* (CBS 129.13). Tree topology of the ML analysis was similar to the BI. The Best scoring RAxML tree with a final likelihood value of − 11533.136016. The matrix had 731 distinct alignment patterns, with 15.39 % of undetermined characters or gaps. Base frequencies estimated by jModelTest were as follows, A = 0.2113, C = 0.2875, G = 0.2614, T = 0.2397; substitution rates AC = 0.8788, AG = 2.3877, AT = 1.0307, CG = 0.5837, CT = 4.6222, GT = 1.0000; gamma shape = 0.4430. ML bootstrap values (≥ 70 %) and Bayesian posterior probability (≥ 90 %) are indicated along branches (ML/PP). Novel species are in bold font and "T" indicates type derived sequences

4.13 ± 0.3 µm, n = 60). Chlamydospores and **Sexual morph** not observed.

Culture characteristics—Colonies on PDA attaining 25–30 mm diam. after 15 days, flat, felty, margin entire, cream-white (1A1), aerial mycelia sparse. Reverse white to beige (30A1). Colonies on OA attaining 24–33 mm diam. after 15 days, flat, margin unclear, aerial mycelia extremely sparse, with cream-white and slimy sporulation in center. Reverse floralwhite (1A2). Colonies on SNA attaining 28–33 mm diam. after 15 days, flat, annular, margin entire, white to floralwhite, aerial mycelia extremely sparse with slimy sporulation scattered. Reverse annular, white to floralwhite (1A2). Sporulation within 10 days.

Material examined: CHINA, Yunnan, Yiliang, Sanjiao Cave, N 25.134°, E 103.383°, on soil, May 2016, Z.F. Zhang, HMAS 248078 (holotype designated here), ex-type living culture CGMCC3.19309 = LC12501; ibid., LC12502.

Notes: *P. apiculatum* can be easily distinguished from phylogenetically allied species (Fig. 34), *P. variiforme*, by its smaller ellipsoidal conidia with apiculate bases, which are ovoid or elliptical in *P. variiforme* (3.5–5.0 µm vs. 9.0–14.5 µm). Moreover, its conidiogenous cells are much shorter than those of *P. variiforme* (14–24 µm vs. 18–41 µm).

Paracremonium ellipsoideum Z.F. Zhang & L. Cai, ***sp. nov.***

Index Fungorum number: 557743, *Facesoffungi number:* FoF 08452; Fig. 36

Etymology: Referring to the ellipsoidal conidia of this species.

Holotype: HMAS 248016.

Hyphae hyaline, smooth, thick-walled, septate, branched. **Asexual morph** *Sporulation* abundant, white, slimy. *Conidiophores* arising from vegetative hyphae solitary or in clusters, erect, branched, septate, thick-walled, hyaline, apex slightly swollen. *Conidiogenous cells* borne on aerial hyphae solitary or in whorls of 2–6 at apex of conidiophores, straight, acicular, tapering towards apex, smooth, hyaline, 22–38 µm long, 2.5–3.5 µm wide at base, with prominent

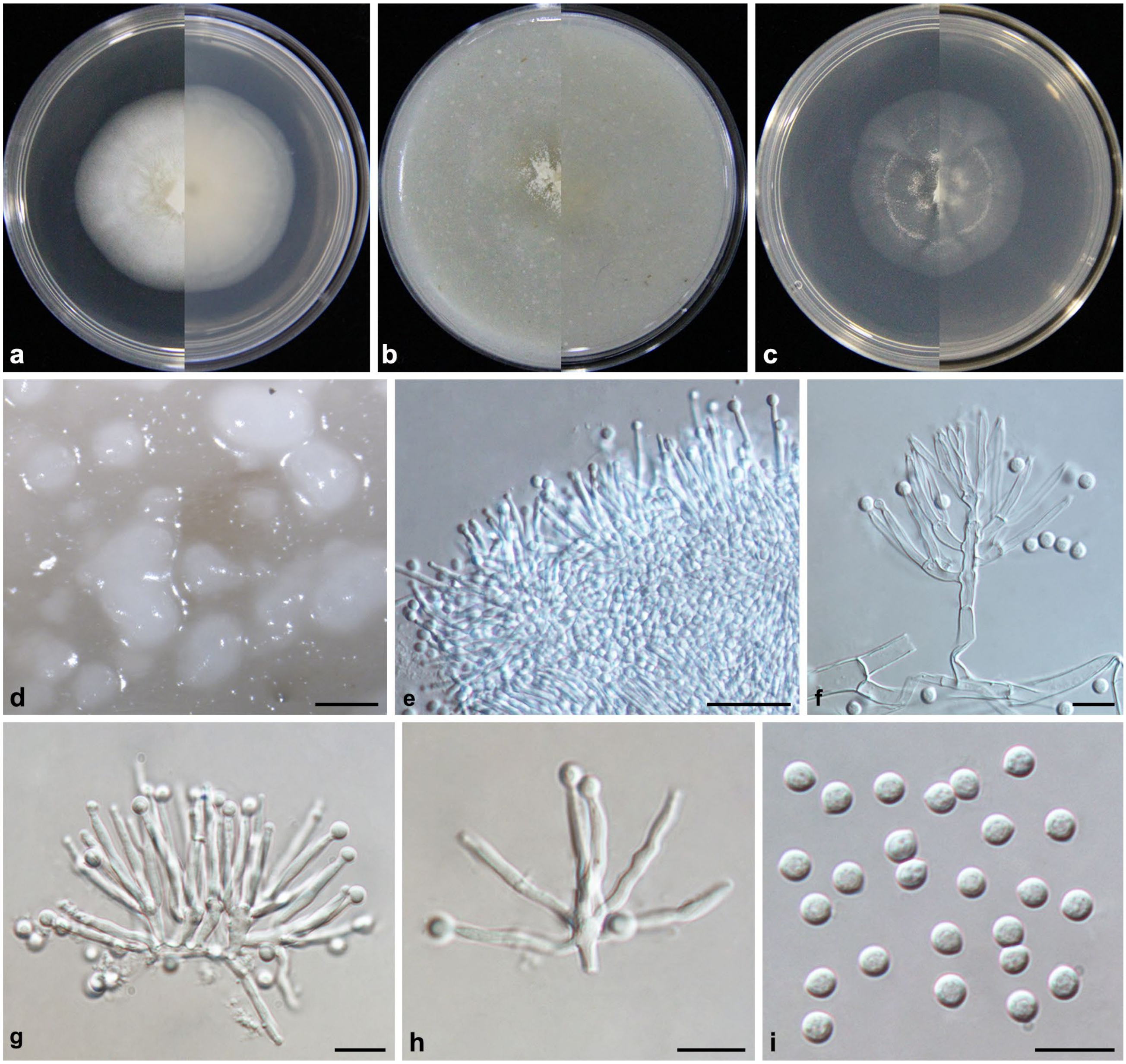


Fig. 35 *Paracremonium apiculatum* (from ex-holotype CGMCC3.19309). **a–c** Upper and reverse views of cultures on PDA, OA and SNA 15 days after inoculation; **d** sporulation on PDA under stereomicroscope; **e–h** conidiophores, phialides and conidia; **i** conidia. Scale bars: **d** 100 μm; **e** 20 μm; **f–i** 10 μm

periclinal thickening and inconspicuous collarette, 1.5–2.0 μm diam. *Conidia* in slimy head, abundant, unicellular, ellipsoidal with apiculate bases, smooth, thick-walled, hyaline, 5.5–8.0 × 3.5–5.0 μm ($\bar{x}$ ± SD = 6.5 ± 0.62 × 4.2 ± 0.28 μm, n = 60). Chlamydospores and not observed.

Culture characteristics—Colonies on PDA attaining 33–37 mm diam. after 15 days, flat, felty, margin entire, white to cream-yellow (30A2), aerial mycelia sparse. Reverse white to bisque (5A2). Colonies on OA attaining 33–37 mm diam. after 15 days, flat, margin unclear, aerial mycelia extremely sparse, with cream-white and slimy sporulation in center. Reverse light yellow (1A2). Colonies on SNA attaining 32–39 mm diam. after 15 days, flat, annular, margin entire, white to light yellow (1A2), aerial mycelia extremely sparse, with slimy sporulation scattered. Reverse annular, white to light yellow (1A2). Sporulation within 10 days.

Material examined: CHINA, Yunnan, Yiliang, Sanjiao Cave, N 25.134°, E 103.383°, on sewage, May 2016, Z.F. Zhang, HMAS 248016 (holotype designated here), ex-type living culture CGMCC3.19316 = LC12551; ibid., LC12552.

Notes: Phylogenetic analysis based on ITS, LSU and TUB sequences showed that new species *Paracremonium*

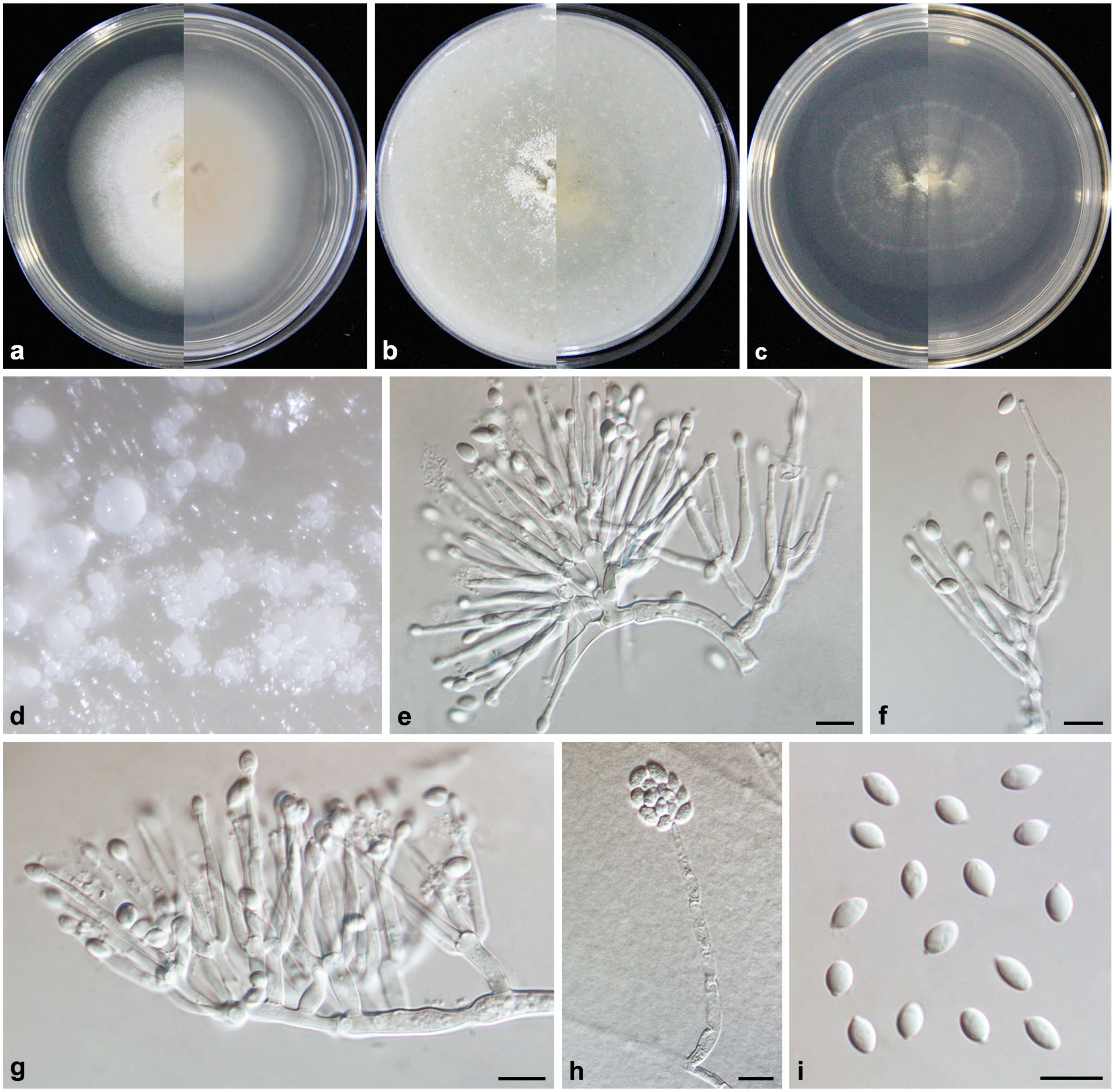


Fig. 36 *Paracremonium ellipsoideum* (from ex-holotype CGMCC3.19316). **a–c** Upper and reverse views of cultures on PDA, OA and SNA 15 days after inoculation; **d** sporulation on PDA under stereomicroscope; **e–g** conidiophores, phialides and conidia; **h** phialides borne on aerial hyphae and conidia in globose head. **i** conidia. Scale bars: **e–i** 10 μm

*ellipsoideum*was closely related to *Paracremonium inflatum* and *P. moubasheri* (Fig. 34), but could be easily differentiated by its ellipsoidal conidia with apiculate bases, rather than the curved ellipsoidal to fusiform conidia in *P. inflatum*. In addition, conidiophores of *P. inflatum* are unbranched or rarely branched, differed from other species in *Paracremonium* by its branched conidiophores and ellipsoidal conidia with apiculate bases.

Microascales Luttr. ex Benny & Kimbr.

The order is characterized by nonstromatic black perithecial ascomata with long necks or rarely with cleistothecial ascomata that lack paraphyses, and globose and evanescent asci, developing singly or in chains (Réblová et al. 2011). Currently, *Microascales* comprise four families, i.e. *Ceratocystidaceae*, *Chadefaudiellaceae*, *Halosphaeriaceae*, and *Microascaceae* (Kirk et al. 2008; Réblová et al. 2011).

Microascaceae Luttr. ex Malloch

Microascaceae was established by Luttrell (Malloch 1970) to accommodate a morphologically heterogeneous group of fungi. Species of the family are characterised by the presence of mostly annellidic asexual morphs with dry aseptate conidia and by sexual morphs that form cleistothecial or perithecial, carbonaceous ascomata producing reniform, lunate or triangular ascospores with or without germ pores. Most species of *Microascaceae* are reported as saprobiont or plant pathogens, and others are opportunistic pathogens of humans and show intrinsic resistance to antifungal agents (Sandoval-Denis et al. 2016b).

Microascus Zukal

The genus *Microascus* was established by Zukal (1985) with *M. longirostris* Zukal as the type species, and the asexual morphs were traditionally included in *Scopulariopsis* Bainier. Several authors subsequently demonstrated by culturing, mating studies and molecular methods, that the sexual morphs of *Scopulariopsis* belong to the ascomycete genus *Microascus* (Morton and Smith 1963; Issakainen et al. 2003). Sandoval-Denis et al. (2016a) refined the generic delimitations in *Microascaceae* and updated their circumscriptions based on multi-locus phylogeny. Members of the newly refined *Microascus* were characterised by dark-coloured colonies, mostly brown to green-brown mycelia, solitary conidiogenous cells (annellides) with long and narrow annelated zone, smooth to roughened conidia, mostly ostiolate ascomata with papillate or long cylindrical necks, coloured ascospores with a single, mostly inconspicuous germ pore (Sandoval-Denis et al. 2016a). In this study, five new species named as *Microascus collaris*, *M. levis*, *M. sparsimycelialis*, *M. superficialis* and *M. trigonus* are described (Fig. 37).

Microascus collaris Z.F. Zhang & L. Cai, ***sp. nov.***

Index Fungorum number: 557744, *Facesoffungi number:* FoF 08453; Fig. 38

Etymology: Referring to its long neck of ascomata.

Holotype: HMAS 248018.

hyphae hyaline to pale brown, septate, branched, thin- and smooth-walled 1.5–2.5 µm. **Sexual morph** *Ascomata* abundant, ostiolate, immersed or semi-immersed, subglobose or globose, black, 190–280 µm diam., 200–340 µm high, glabrous, with 1–2 cylindrical ostiolar neck, up to 250 µm, peridium with a textura angularis. *Asci* 8-spored, ovate to globose, hyaline, 9.0–13.5 × 8.5–12.5 µm. *Ascospores* triangular to lunate, smooth, thick-walled, pale yellow, 4.5–7.0 × 3.5–5.5 µm ($\bar{x} \pm$ SD = 6.0 ± 0.59 × 4.4 ± 0.54 µm, n = 50). **Asexual morph** *conidiophores* indistinctive or simple, cylindrical, smooth-walled, pale yellow. *Conidiogenous cells* solitary on aerial hyphae, or clustered on conidiophores, cylindrical to ampulliform, slightly curved, smooth, pale yellow, 7.5–14.0 × 2.5–3.5 µm, with conspicuous collarette. *Conidia* aggregated in slimy head, ellipsoidal, smooth, hyaline to pale yellow, 4.0–6.0 × 3.0–4.0 µm ($\bar{x} \pm$ SD = 4.9 ± 0.56 × 3.4 ± 0.32 µm, n = 50), with truncated base.

Culture characteristics—Colonies on PDA attaining 10–13 mm diam. after 4 weeks, compact, convex with papillate surface, margin dentate, black, aerial mycelia extremely sparse. Reverse crack, black. Colonies on OA attaining 25–26 mm diam. after 4 weeks, surface undulate, margin entire, dark brown (5A8) to black, with black ascomata scattered. Reverse cream-colored. Colonies on SNA attaining 18–22 mm diam. after 4 weeks, flat, margin entire with rhizoids, white to grey-yellow (4A2), with black ascomata scattered. Sporulation within 20 days.

Material examined: CHINA, Guangxi, Laibin, Sanshan Cave, N 23.41°, E 108.931°, on plant debris, May 2016, Z.F. Zhang, HMAS 248018 (holotype designated here), ex-type living culture CGMCC3.19321 = LC12598; ibid., LC12599.

Notes: Phylogenetically, our strains nested within the *Microascus* clade based on ITS, LSU, TUB and EF1-α sequences (Fig. 37) and its morphological characteristics fit well to this genus, i.e. ampulliform or lageniform conidiogenous cells and smooth- and thin-walled or finely rough- and thick-walled conidia (Sandoval-Denis et al. 2016a).

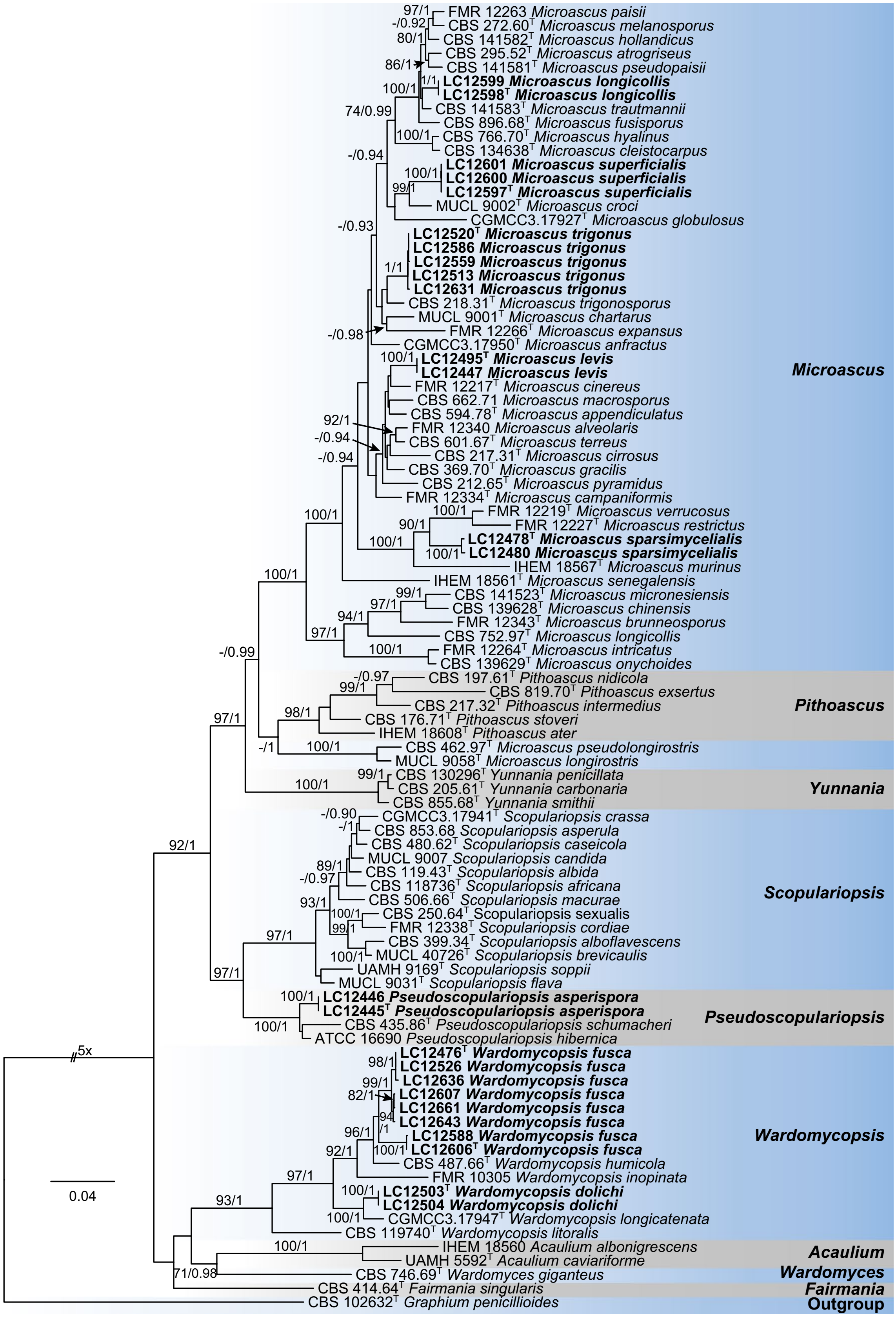
Microascus collaris is phylogenetically closely related to *M. trautmannii* Woudenb. & Samson (Fig. 37). However, *M. collaris* can be distinguished from *M. trautmannii* by the presence of sexual stage, shorter conidiogenous cells (7.5–14.0 µm vs. 16.0–22.0 µm) and wider conidia (3.0–4.0 µm vs. 2.5–3.0 µm). In morphology, *M. pyramidus* resembles *M. collaris* but can be differentiated by its longer asci (13.0–18.0 µm vs. 9.0–13.4 µm) and wider ascospores (5.0–6.5 µm vs. 3.5–5.5 µm).

Microascus levis Z.F. Zhang & L. Cai, ***sp. nov.***

Index Fungorum number: 557745, *Facesoffungi number:* FoF 08454; Fig. 39

Etymology: Referring to its smooth conidia.

Holotype: HMAS 248002.


FMR 12263 Microascus paisii
CBS 272.60T Microascus melanosporus
CBS 141582T Microascus hollandicus
CBS 295.52T Microascus atrogriseus
CBS 141581T Microascus pseudopaisii
LC12599 Microascus longicollis
LC12598T Microascus longicollis
CBS 141583T Microascus trautmannii
CBS 896.68T Microascus fusisporus
CBS 766.70T Microascus hyalinus
CBS 134638T Microascus cleistocarpus
LC12601 Microascus superficialis
LC12600 Microascus superficialis
LC12597T Microascus superficialis
MUCL 9002T Microascus croci
CGMCC3.17927T Microascus globulosus
LC12520T Microascus trigonus
LC12586 Microascus trigonus
LC12559 Microascus trigonus
LC12513 Microascus trigonus
LC12631 Microascus trigonus
CBS 218.31T Microascus trigonosporus
MUCL 9001T Microascus chartarus
FMR 12266T Microascus expansus
CGMCC3.17950T Microascus anfractus
LC12495T Microascus levis
LC12447 Microascus levis
FMR 12217T Microascus cinereus
CBS 662.71 Microascus macrosporus
CBS 594.78T Microascus appendiculatus
FMR 12340 Microascus alveolaris
CBS 601.67T Microascus terreus
CBS 217.31T Microascus cirrosus
CBS 369.70T Microascus gracilis
CBS 212.65T Microascus pyramidus
FMR 12334T Microascus campaniformis
FMR 12219T Microascus verrucosus
FMR 12227T Microascus restrictus
LC12478T Microascus sparsimycelialis
LC12480 Microascus sparsimycelialis
IHEM 18567T Microascus murinus
IHEM 18561T Microascus senegalensis
CBS 141523T Microascus micronesiensis
CBS 139628T Microascus chinensis
FMR 12343T Microascus brunneosporus
CBS 752.97T Microascus longicollis
FMR 12264T Microascus intricatus
CBS 139629T Microascus onychoides
Microascus
CBS 197.61T Pithoascus nidicola
CBS 819.70T Pithoascus exsertus
CBS 217.32T Pithoascus intermedius
CBS 176.71T Pithoascus stoveri
IHEM 18608T Pithoascus ater
Pithoascus
CBS 462.97T Microascus pseudolongirostris
MUCL 9058T Microascus longirostris
CBS 130296T Yunnania penicillata
CBS 205.61T Yunnania carbonaria
CBS 855.68T Yunnania smithii
Yunnania
CGMCC3.17941T Scopulariopsis crassa
CBS 853.68 Scopulariopsis asperula
CBS 480.62T Scopulariopsis caseicola
MUCL 9007 Scopulariopsis candida
CBS 119.43T Scopulariopsis albida
CBS 118736T Scopulariopsis africana
CBS 506.66T Scopulariopsis macurae
CBS 250.64T Scopulariopsis sexualis
FMR 12338T Scopulariopsis cordiae
CBS 399.34T Scopulariopsis alboflavescens
MUCL 40726T Scopulariopsis brevicaulis
UAMH 9169T Scopulariopsis soppii
MUCL 9031T Scopulariopsis flava
Scopulariopsis
LC12446 Pseudoscopulariopsis asperispora
LC12445T Pseudoscopulariopsis asperispora
CBS 435.86T Pseudoscopulariopsis schumacheri
ATCC 16690 Pseudoscopulariopsis hibernica
Pseudoscopulariopsis
LC12476T Wardomycopsis fusca
LC12526 Wardomycopsis fusca
LC12636 Wardomycopsis fusca
LC12607 Wardomycopsis fusca
LC12661 Wardomycopsis fusca
LC12643 Wardomycopsis fusca
LC12588 Wardomycopsis fusca
LC12606T Wardomycopsis fusca
CBS 487.66T Wardomycopsis humicola
FMR 10305 Wardomycopsis inopinata
LC12503T Wardomycopsis dolichi
LC12504 Wardomycopsis dolichi
CGMCC3.17947T Wardomycopsis longicatenata
CBS 119740T Wardomycopsis litoralis
Wardomycopsis
IHEM 18560 Acaulium albonigrescens
UAMH 5592T Acaulium caviariforme
Acaulium
CBS 746.69T Wardomyces giganteus
Wardomyces
CBS 414.64T Fairmania singularis
Fairmania
CBS 102632T Graphium penicillioides
Outgroup
5x
0.04

◂**Fig. 37** Maximum likelihood (ML) tree of *Microascaceae* based on ITS, LSU, EF1-α and TUB sequences. Ninety-five strains are used. The tree is rooted with *Graphium penicillioides* (CBS 102632). Tree topology of the ML analysis was similar to the BI. The Best scoring RAxML tree with a final likelihood value of − 26065.467269. The matrix had 1186 distinct alignment patterns, with 10.4 % of undetermined characters or gaps. Base frequencies estimated by jModelTest were as follows, A = 0.1959, C = 0.3221, G = 0.2677, T = 0.2142; substitution rates AC = 0.8077, AG = 2.3643, AT = 1.5854, CG = 1.0723, CT = 4.6528, GT = 1.0000; gamma shape = 0.7390. ML bootstrap values (≥ 70 %) and Bayesian posterior probability (≥ 90 %) are indicated along branches (ML/PP). Novel species are in bold font and "T" indicates type derived sequences

Hyphae pale brown to brown, septate, branched, smooth- or rough-walled, 1.5–3.5 µm diam. **Asexual morph** *Conidiophores* simple, cylindrical, smooth, hyaline to pale brown. *Conidiogenous cell* borne laterally on aerial hyphae, or lateral or at the apex of conidiophores, ampulliform or irregular shapes, sometimes curved, smooth-walled, pale brown, 6.0–12.5×2.5–5.0 µm. *Conidia* arranged in chains, subglobose to globose, smooth- and thick-walled, pale brown, 5.5–8.5(− 9.5) × 5.0–8.5 µm ($\bar{x}$± SD = 6.8 ± 0.83 × 6.2 ± 0.79 µm, n = 55). **Sexual morph** not observed.

Culture characteristics—Colonies on PDA attaining 23–25 mm diam. after 3 weeks, felty, compact, plicated, convex, margin entire to undulate, gray-yellow (4A2) to dark green (28E2) from margin to center, with light-colored margin. Reverse plicated, sunken, gray-yellow (4A2) to dark green (28E2). Colonies on OA attaining 32–40 mm diam. after 3 weeks, flat, white to cream-colored, margin entire, aerial mycelia sparse. Reverse white to cream-colored. Colonies on SNA attaining 30–34 mm diam. after 3 weeks, flat, margin entire, pale grey (30B2) to grey-yellow (30B3). Reverse pale grey (30B2) to grey-yellow (30B3). Sporulation within 15 days.

Material examined: CHINA, Guangxi, Guilin, Luotian Cave, N 24.948°, E 110.524°, on soil, May 2016, Z.F. Zhang, HMAS 248002 (holotype designated here), ex-type living culture CGMCC3.19308 = LC12495; ibid., LC12447.

Notes: *Microascus levis* is phylogenetically closely related to *M. cirrosus* Curzi. Whereas, the conidia of *M. levis* are subglobose to globose, rather than subglobose to obovate in *M. cirrosus*. In addition, the sexual stage of *M. levis* is absent. In morphology, *M. levis* is similar to *M. restrictus* Sand.-Den., Gené & Deanna A. Sutton and *M. verrucosus* Sand.-Den., Gené & Cano. While *M. levis* has larger conidia than *M. restrictus* (5.5–8.5(–9.5) × 5.0–8.5 vs. 4.5–6.0 × 4.0–5.5) and the conidiogenous cell of *M. levis* is smooth-walled rather than typically warted in *M. verrucosus*. Meanwhile, colonies of these three closely related species on OA are obviously different (white to cream-colored with entire and flat margin for *M. levis*, olive brown to brown with an irregular undulate margin for *M. restrictus*, olive grey with an immersed and slightly undulated margin for *M. verrucosus*).

Microascus sparsimycelialis Z.F. Zhang & L. Cai, ***sp. nov.***

Index Fungorum number: 557746, *Facesoffungi number:* FoF 08455; Fig. 40

Etymology: Referring to its sparse aerial mycelia on media.

Holotype: HMAS 248006.

Hyphae pale brown to brown, septate, branched, thick-walled, 1.5–3.5 µm diam, swollen to globose sometimes, up to 10 µm diam., aerial hyphae becoming dark brown and clustered when aging. **Asexual morph** *Conidiophores* simple, cylindrical to ellipsoidal, smooth, pale brown to brown. *Conidiogenous cells* solitary on aerial hyphae, or in whorls of 2–3 at apex of conidiophores, ellipsoidal, ampulliform or irregular shapes, straight or slightly curved, smooth or finely roughened, pale brown to brown, 5.0–10.0 (− 14.0) × 3.0–5.0 µm, with conspicuous collarette. *Conidia* in long chains, ovoid to globose, smooth or finely roughened, thick-walled, pale brown, 3.5–6.0 × 3.0–5.5 µm ($\bar{x}$ ± SD = 4.8 ± 0.58 × 4.31 ± 0.55 µm, n = 60), with apical base. **Sexual morph** not observed.

Culture characteristics—Colonies on PDA attaining 9–13 mm diam. after 3 weeks, compact, convex with crack surface, margin crenate, cream-white to grey-yellow (29D3), aerial mycelia sparse. Reverse crack, pale yellow-green (29A2) with dark green (29E3) patches. Colonies on OA attaining 28–35 mm diam. after 3 weeks, flat, margin entire, dark green (28F8) with white margin, aerial mycelia sparse. Reverse dark green (28F8) with white margin. Colonies on SNA attaining 34–36 mm diam. after 3 weeks, flat, margin radially striate with lobate edge, pale grey-green (28A2) to olive (30E4). Reverse light gainsboro (30E4) to dark olive (30E8). Sporulation within 15 days on OA and SNA.

Material examined: CHINA, Guangxi, Laibin, Sanshan Cave, N 23.41°, E 108.931°, on animal faeces, May 2016, Z.F. Zhang, HMAS 248006 (holotype designated here), ex-type living culture CGMCC3.19307 = LC12478; ibid., LC12480.

Notes: *Microascus sparsimycelialis* is phylogenetically and morphologically closely related to *M. restrictus* and *M. verrucosus* (Fig. 37). Colonies of *M. sparsimycelialis* on OA are dark green with entire margin, while these of *M. restrictus* are olive green with irregular margin. *M. sparsimycelialis* differs from *M. verrucosus* by its smooth conidiogenous cells, rather than sparsely warted in *M. verrucosus*. Moreover, conidia of *M. sparsimycelialis* are pale brown with apical base, comparing to that being dark brown with truncate base in *M. restrictus* and *M. verrucosus*. In addition, both of *M. restrictus* and *M. verrucosus* produce solitary conidia laterally from vegetative hyphae, which is not the case in *M. sparsimycelialis*.

Microascus superficialis Z.F. Zhang & L. Cai, ***sp. nov.***

Index Fungorum number: 557747, *Facesoffungi number:* FoF 08456; Fig. 41

Etymology: Referring to its superficial ascomata.

Holotype: HMAS 248005.

Hyphae hyaline to pale brown, septate, branched, smooth. **Sexual morph** *Ascomata* black, superficial or semi-immersed, glabrous, ostiolate, subglobose to globose, 215–350 µm diam., with a short cylindrical ostiolar neck, peridium with a textura angularis. *Asci* hyaline, 8-spored, irregularly ellipsoidal to subglobose, 12.0–15.0 × 9.0–11.5 µm. *Ascospores* triangular, yellow-brown, smooth, thick-walled, 5.5–7.0 × 4.0–5.5 µm ($\bar{x} \pm$ SD = 6.4 ± 0.41 × 4.8 ± 0.34 µm, n = 50). **Asexual morph** not observed.

Culture characteristics —Colonies on PDA attaining 12–17 mm diam. after 4 weeks, compact, rugged, crack, margin undulate, cream-yellow (5A2) to red-brown (6C8), aerial mycelia sparse. Reverse crack, cream-yellow (5A2) to pale red-brown (6B5). Colonies on OA attaining 30–32 mm diam. after 4 weeks, plicated, margin undulate, white to beige (4A1) with dark-grey (7C1) circle, aerial mycelia sparse. Reverse white to pale salmon (5A2). Colonies on SNA attaining 17–19 mm diam. after 4 weeks, flat, compact, margin fimbriate, beige (30A2) to pale grey (30C4). Reverse beige to pale grey. Sporulation within 20 days on OA and SNA.

Material examined: CHINA, Guangxi, Laibin, Sanshan Cave, N 23.41°, E 108.931°, on animal faeces, May 2016, Z.F. Zhang, HMAS 248005 (holotype designated here), ex-type living culture CGMCC3.19638 = LC12597; ibid., LC12600; ibid., LC12601.

Notes: *Microascus superficialis* is phylogeneticly closely related to *M. croci* (J.F.H. Beyma) Sand.-Den., Gené & Guarro (Fig. 37), while contrast to *M. superficialis*, no sexual morph was observed in *M. croci.* Morphologically, *M. superficialis* shares similar sexual morph with *M. pyramidus* G.L. Barron & J.C. Gilman. However, ascospores of *M. pyramidus* have attenuated ends and often acquire a nearly square shape (Sandoval-Denis et al. 2016a). Meanwhile, *M. pyramidus* grows faster (40–50 mm in 4 weeks) than our new species on PDA (Barron et al. 1961).

Microascus trigonus Z.F. Zhang & L. Cai, ***sp. nov.***

Index Fungorum number: 557748, *Facesoffungi number:* FoF 08457; Fig. 42

Etymology: Referring the shape of the ascospores.

Holotype: HMAS 248001.

hyphae hyaline, septate, branched, smooth, thin-walled, 1.5–3.0 µm diam. **Sexual morph** *Ascomata* abundant, black, superficial, glabrous, subglobose to globose, 182–294 µm diam, with a short cylindrical ostiolar neck; peridium with a textura angularis. *Asci* short clavate, subglobose to globose, hyaline, 8-spored, 9.0–17 × 8.0–12 µm. *Ascospores* triangular, smooth, thick-walled, pale brown, 4.5–6.0 × 3.5–5.5 µm ($\bar{x} \pm$ SD = 5.7 ± 0.43 × 4.3 ± 0.53 µm, n = 50). **Asexual morph** *conidiophores* simple, straight, septate, occasionally branched, hyaline. *Conidiogenous cells* solitary on aerial hyphae, or in whorls of 2–3 on apex of conidiophores, lageniform to ampulliform, straight or slightly curved, pale brown, 4.5–10.0 (−14.5) × 2.5–4.5 µm. *Conidia* in long chains, ellipsoidal to globose, smooth, thick-walled, hyaline to pale brown, 3.5–5.5 × 3.0–4.5 µm ($\bar{x} \pm$ SD = 4.5 ± 0.47 × 3.8 ± 0.29 µm, n = 70).

Culture characteristics—Colonies on PDA attaining 26–30 mm diam after 3 weeks, felty, compact, plicated, convex, margin undulate, beige (30A2) to whitesmoke (4A2) with lightgrey (1C4) ring. Reverse plicated, crack, beige (30A2) to oldlace (5A2) with lightgray ring (1C4). Colonies on OA attaining 34–36 mm diam after 3 weeks, flat, margin entire, white to dark brown (5F8). Reverse white to pale brown (5B3). Colonies on SNA attaining 28–36 mm diam after 3 weeks, flat, margin fimbriate, floralwhite (1A2) to yellow-green (2A2). Reverse floralwhite (1A2) to pale yellow-green (2A2). Sporulation within 15 days.

Material examined: CHINA, Guangxi, Guilin, Luotian Cave, N 24.948°, E 110.524°, on soil, May 2016, Z.F. Zhang, HMAS 248001 (holotype designated here), ex-type living culture CGMCC3.19636 = LC12520; ibid., LC12513; Guangxi, Guilin, E'gu Cave, N 24.942°, E 110.511°, animal

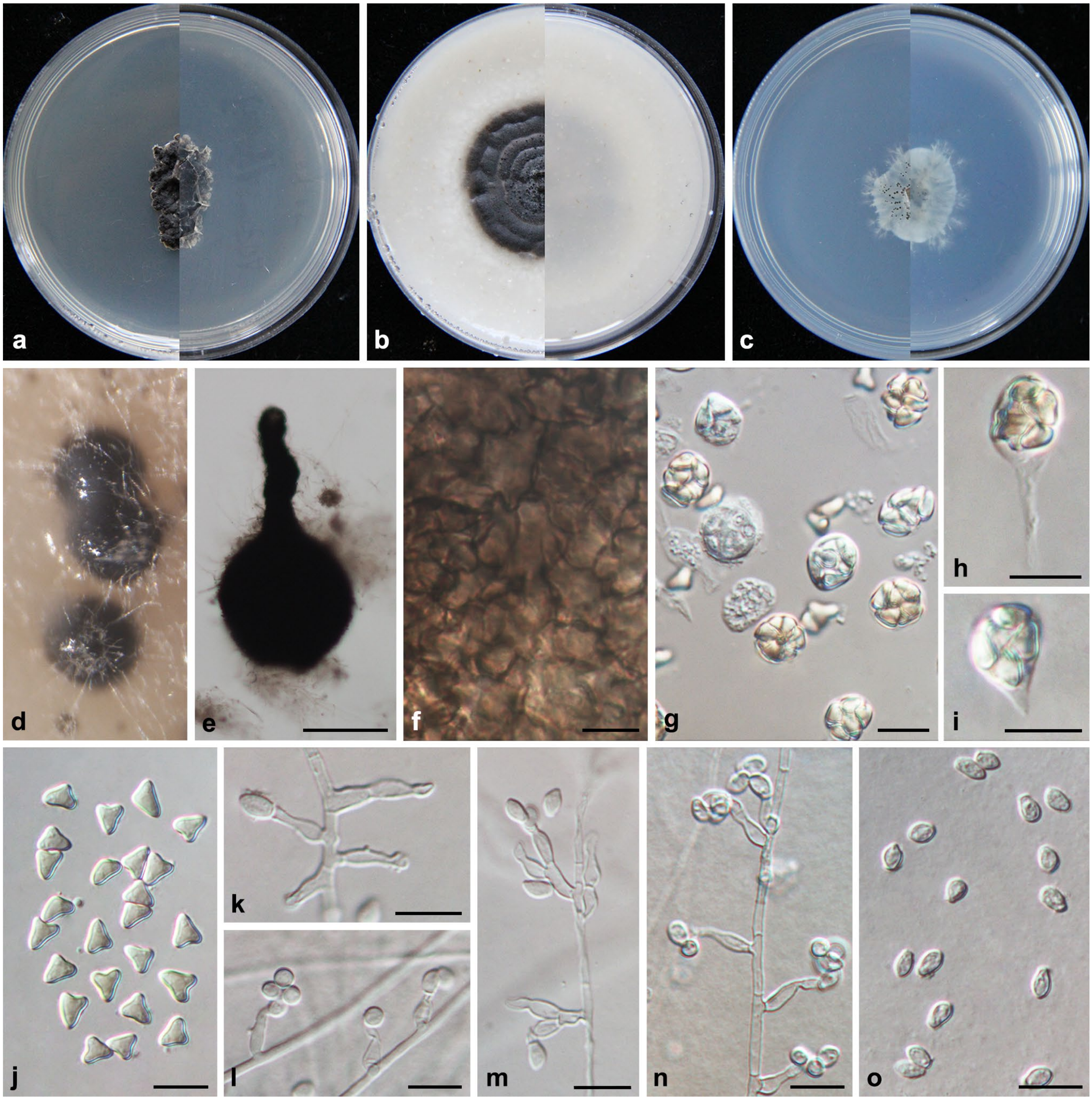


Fig. 38 *Microascus collaris* (from ex-holotype CGMCC3.19321). **a**–**c** Upper and reverse views of cultures on PDA, OA and SNA 3 weeks after inoculation; **d** immersed ascoma; **e** ascoma; **f** peridium; **g**–**i** asci; **j** ascospores; **k**–**n** conidiogenous cells and conidia; **o** conidia. Scale bars: **e** 100 µm; **f**–**o** 10 µm

faeces, May 2016, Z.F. Zhang, LC12559; ibid., LC12586; ibid., LC12631.

Notes: *Microascus trigonus* is phylogenetically closely allied to *M. chartarus* (G. Sm.) Sand.-Den. (Fig. 37), but can be distinguished by the absence of sexual morph with ovate, green-brown, and frequently pointed conidia. Morphologically, *M. alveolaris* resembles *M. trigonus*. However, the conidia in *M. alveolaris* are ellipsoidal, navicular or bullet-shaped rather than ellipsoidal to globose in *M. trigonus*.

Pseudoscopulariopsis Sand.-Den., Gené & Guarro

Pseudoscopulariopsis was established to accommodate species that are generally similar to *Scopulariopsis*, but differs in the gray or olivaceaous colonies, ampulliform annellides and navicular to fusiform ascospores without germ

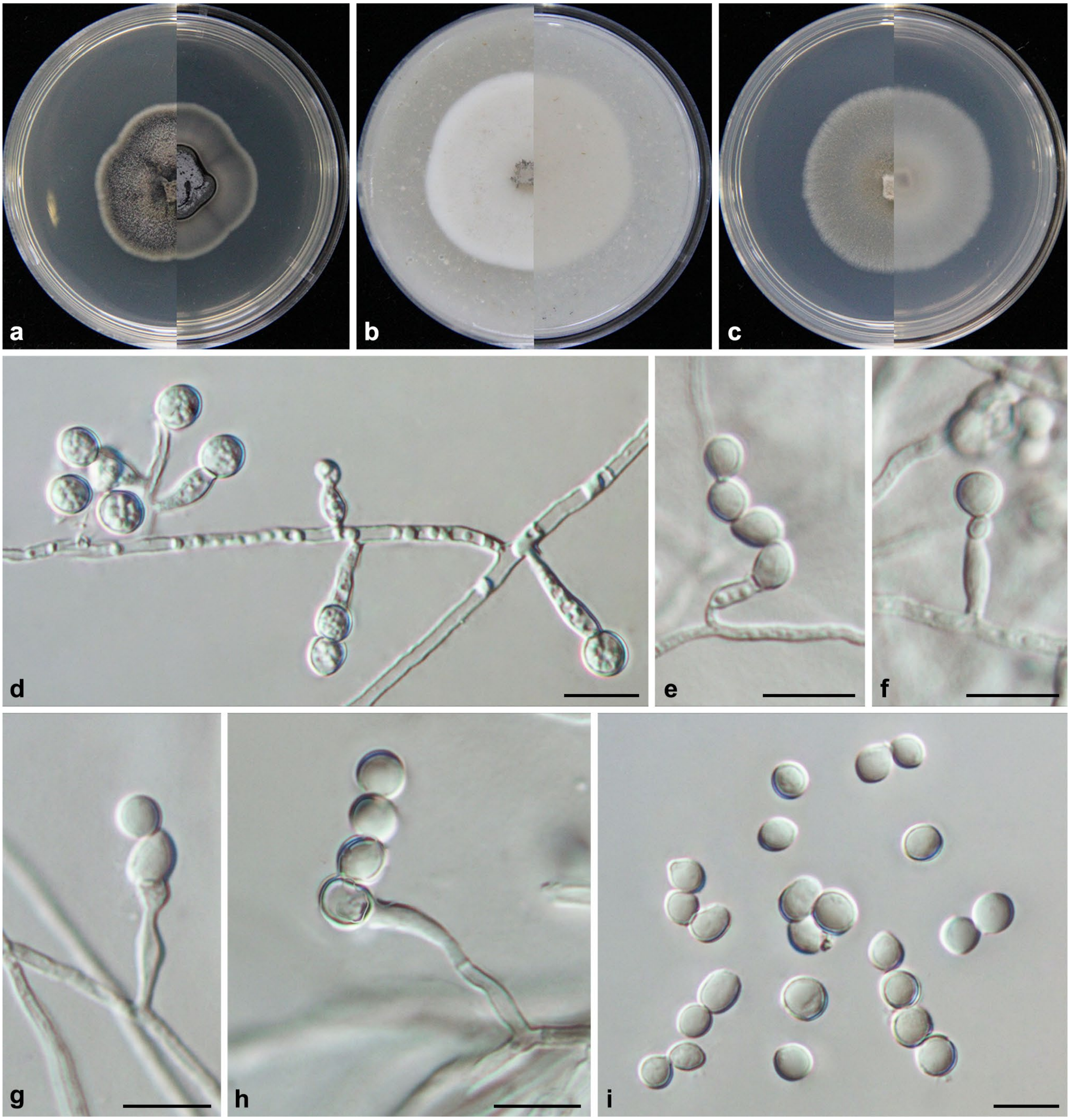


Fig. 39 *Microascus levis* (from ex-holotype CGMCC3.19308). **a**–**c** Upper and reverse views of cultures on PDA, OA and SNA 3 weeks after inoculation; **d**–**h** conidiogenous cells and conidia; **i** conidia. Scale bars: **d**–**i** 10 µm

pores (Sandoval-Denis et al. 2016a). Currently, this genus contains only two species. *Pseudoscopulariopsis asperispora* sp. nov. is described below (Fig. 37).

Pseudoscopulariopsis asperispora **Z.F. Zhang & L. Cai, *sp. nov.***

Index Fungorum number: 557749, *Facesoffungi number*: FoF 08458; Fig. 43

Etymology: Referring to its rough-walled conidia.

Holotype: HMAS 247989.

Hyphae pale brown to brown, septate, branched, rough- and thick-walled, 1.5–3.5 µm diam. **Asexual morph** *Conidiophores* arising from hyphae, irregularly cylindrical,

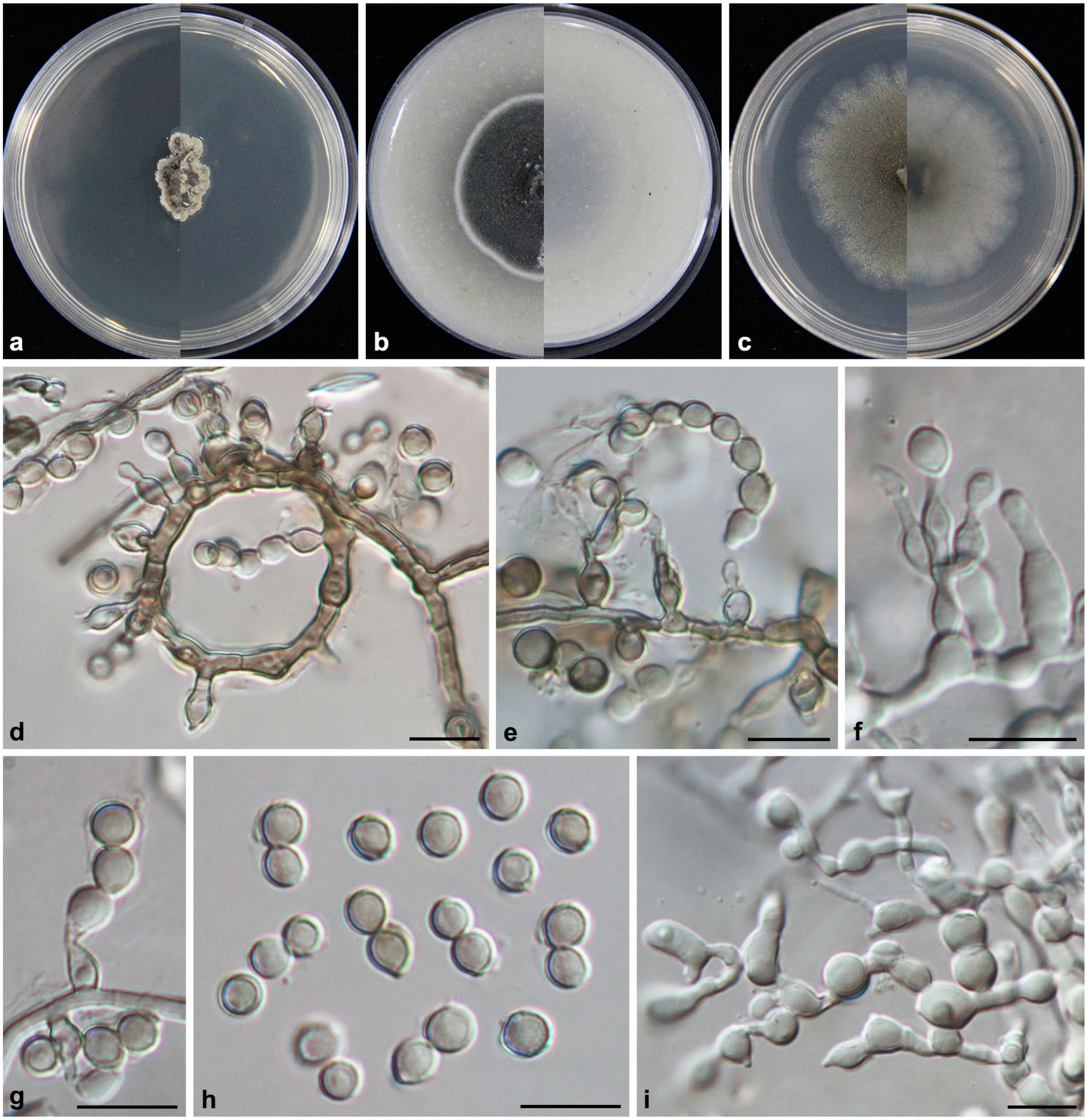


Fig. 40 *Microascus sparsimycelialis* (from ex-holotype CGMCC3.19307). **a**–**c** Upper and reverse views of cultures on PDA, OA and SNA 3 weeks after inoculation; **d**–**g** conidiogenous cells and conidia in chains; **h** conidia; **i** swollen hyphae. Scale bars: **d**–**i** 10 µm

branched 1–3 times, smooth or slightly rough, thick-walled, hyaline to pale brown, 2.0–4.0 µm diam. at base, swollen at apex, up to 6.5 µm diam. *Conidiogenous cells* in whorls of 2–6 at apex of conidiophores, ampulliform or cylindrical, straight or slightly curved, smooth, thin-walled, pale brown, 5.5–10.0 (−12.0) × 2.5–4.5 µm, with inconspicuous annellidic. *Conidia* in long chains, subglobose to globose, rough, thick-walled, brown, 4.5–7.5 × 4.5–7.0 µm ($\bar{x} \pm SD = 6.0 \pm 0.67 \times 5.6 \pm 0.66$ µm, n = 60), with truncated base. **Sexual morph** not observed.

Culture characteristics—Colonies on PDA attaining 21–25 mm diam. after 3 weeks, low convex, margin erose, pale yellow-green (29D5) to olive (29F4), with ivory (29A2) margin. Reverse yellow-green (29D5) to olive (29F4) with ivory (29A2) margin. Colonies on OA attaining 42–45 mm diam. after 3 weeks, flat, slightly raised at center, margin erose, dark-brown (5F8) to black, aerial mycelia sparse. Reverse yellow-green (29A5). Colonies on SNA attaining 18–22 mm diam. after 3 weeks, flat, margin radially striate with lobate edge, dark olive with yellow-green (29C4) margin. Reverse dark olive (29E5) with yellow-green (29C4) margin. Sporulation within 15 days.

Material examined: CHINA, Guangxi, Guilin, Luotian Cave, N 24.948°, E 110.524°, on animal faeces, May 2016, Z.F. Zhang, HMAS 247989 (holotype designated here), ex-type living culture CGMCC3.19302 = LC12445; ibid., LC12446.

Notes: *Pseudoscopulariopsis asperispora* clustered within *Pseudoscopulariopsis* in a distinct clade with high support value based on the ITS, LSU, TUB, and EF1-α sequence analysis (Fig. 37). *P. asperispora* can be easily distinguished from *P. schumacheri* (E.C. Hansen) Sand.-Den., Gené & Guarro by its subglobose to globose conidia rather than obovate or short clavate in *P. schumacheri*; from *P.*

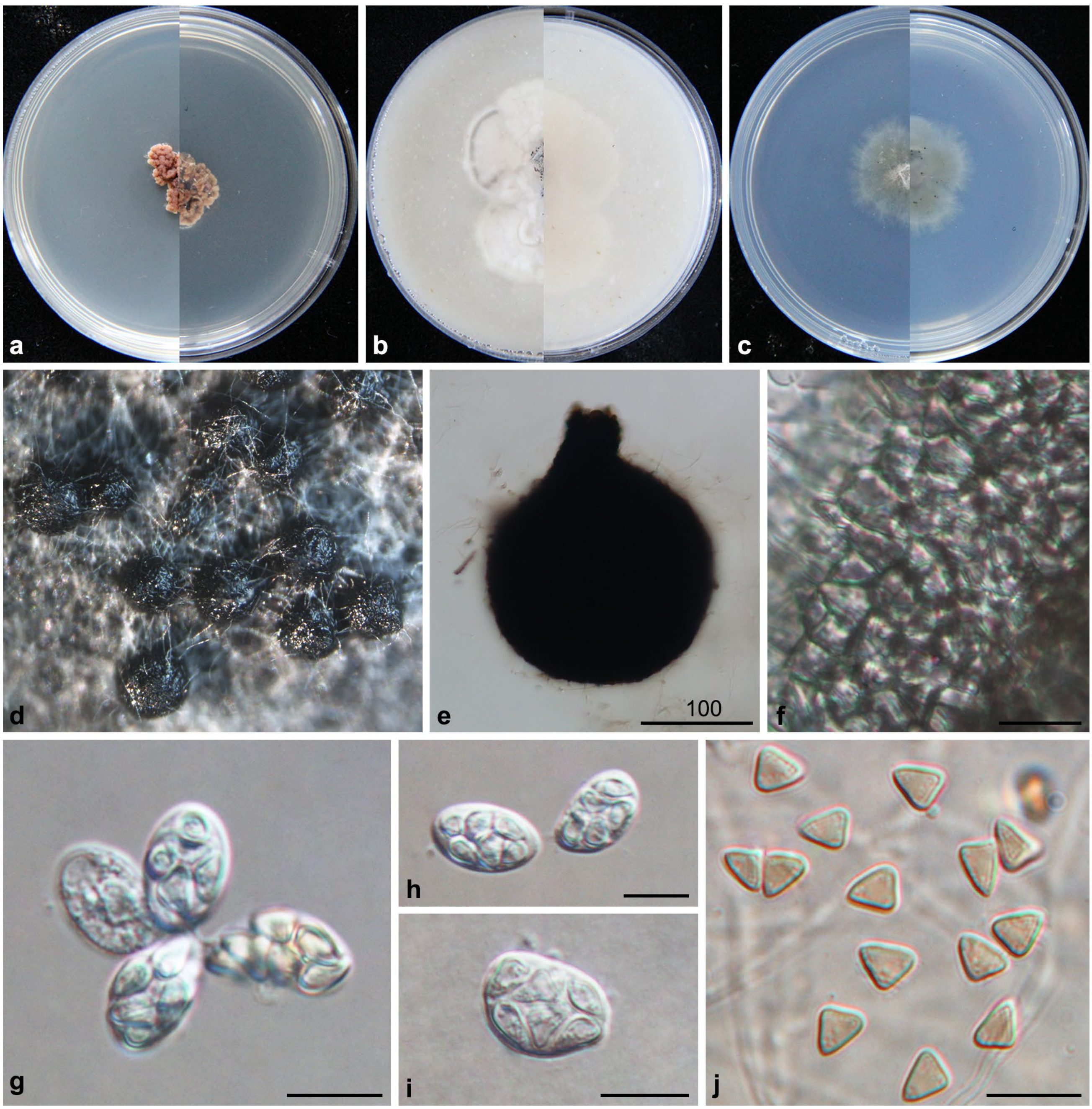


Fig. 41 *Microascus superficialis* (from ex-holotype CGMCC3.19638). **a**–**c** Upper and reverse views of cultures on PDA, OA and SNA 3 weeks after inoculation; **d**, **e** ascoma; **f** peridium; **g**–**i** asci; **j** ascospores. Scale bars: **e** 100 µm; **f**–**j** 10 µm

hibernica (A. Mangan) Sand.-Den., Gené & Cano by shorter conidiogenous cells (5.5–10.0 µm vs. 9.0–15.0 µm).

Wardomycopsis Udagawa & Furuya

Wardomycopsis was introduced as one of the anamorph-typified genera related to *Microascus*, characterised by dark, globose, thick-walled conidia with germ slits that form short chains on annellidic conidiogenous cells (Udagawa and Furuya 1978; Silvera-Simón et al. 2008). Recent phylogenetic analyses demonstrated that *Wardomycopsis* is monophyletic (Sandoval-Denis et al. 2016a; Zhang et al. 2017). Currently, *Wardomycopsis* comprises fives species and we herein add three new species named as *W. dolichi*, *W. ellipsoconidiophora* and *W. fusca* (Fig. 37).

Wardomycopsis dolichi Z.F. Zhang & L. Cai, ***sp. nov.***

Index Fungorum number: 557750, *Facesoffungi number:* FoF 08459; Fig. 44

Etymology: Referring to its long conidiophore.

Holotype: HMAS 247998.

Hyphae hyaline to pale olive, septate, smooth or finely verrucose, thick-walled, 1.5–3.5 µm diam., sometimes swollen, up to 7.0 µm diam. **Asexual morph** *Conidiophores* cylindrical or long ellipsoidal, septate, branched 1–3 times, smooth, hyaline. *Conidiogenous cells* solitary on aerial hyphae, or in whorls of 1–3 at apex of conidiophores, ellipsoidal or ampulliform, hyaline, 3.5–7.5 × 2.5–4.0 µm. *Conidia* mostly borne from conidiogenous cells, occasionally observed on aerial hyphae directly, ellipsoidal or clavate, thick-walled, brown, 4.5–7.0 × 2.5–4.0 µm ($\bar{x} \pm$ SD = 5.7 ± 0.72 × 3.3 ± 0.33 µm, n = 50), with truncated base and median longitudinal germ slit. **Sexual morph** not observed.

Culture characteristics—Colonies on PDA attaining 24–28 mm diam. after 3 weeks, compact, slightly plicated, margin entire, white at margin, black at center. Reverse cream-yellow (30A2) to black. Colonies on OA attaining 28–34 mm diam. after 3 weeks, ulotrichy, low convex, margin entire, white to gray (27E1) from margin to center. Reverse white to pale gray (25B1). Colonies on SNA attaining 24–29 mm diam. after 3 weeks, ulotrichy, margin crenate, beige (2A2) to pale olive (30D8). Reverse beige (2A2) to dark olive (30E8). Sporulation within 15 days on OA and SNA.

Material examined: CHINA, Guangxi, Guilin, E'gu Cave, N 24.942°, E 110.511°, on soil, May 2016, Z.F. Zhang, HMAS 247998 (holotype designated here), ex-type living culture CGMCC3.19310 = LC12503; ibid., LC12504.

Notes: Our strains clustered within *Wardomycopsis* and formed a distinct clade with high support value based on the multi-locus analysis (Fig. 37). *W. dolichi* is phylogenetically allied to *W. longicatenata* Z.F. Zhang, F. Liu & L. Cai, but differs in its wider conidiogenous cells (2.5–4.0 µm vs. 1.5–2.5 µm) and conidia (2.5–4.0 µm vs. 1.5–2.5 µm), color on PDA and SNA media, and the absence of sexual morph, which is observed in *W. longicatena*.

Wardomycopsis ellipsoconidiophora Z.F. Zhang & L. Cai, ***sp. nov.***

Index Fungorum number: 557751, *Facesoffungi number:* FoF 08460; Fig. 45

Etymology: Referring to its ellipsoidal conidiophores.

Holotype: HMAS 248004.

Hyphae hyaline, septate, smooth, thick-walled, 1.5–2.5 µm diam. **Asexual morph** *Conidiophores* arising from hyphae, ellipsoidal, septate, branched 1–3 times, smooth, thick-walled, hyaline to pale olive. *Conidiogenous cells* solitary on aerial hyphae, or in whorls of 1–5 at apex of conidiophores, ellipsoidal, smooth, thick-walled, pale olive, 3.0–6.0 × 2.5–3.0 µm. *Conidia* mostly borne from conidiogenous cells, occasionally observed on aerial hyphae directly, ellipsoidal or clavate, thick-walled, olive-brown, 4.0–6.0 (− 7.5) × 2.5–4.0 µm ($\bar{x} \pm$ SD = 5.1 ± 0.68 × 3.3 ± 0.30 µm, n = 30), with truncated base and median longitudinal germ slit. **Sexual morph** not observed.

Culture characteristics—Colonies on PDA attaining 23–29 mm diam. after 3 weeks, compact, plicated, low convex, margin entire, white at margin, becoming tan (4C8) to cream-yellow (4A2) from middle to center. Reverse plicated, light yellow (2A1) to dark khaki (2C8). Colonies on OA attaining 29–31 mm diam. after 3 weeks, ulotrichy, flat, margin lobate, white to pale gray (1B2). Reverse pale white to pale tan (3A2). Colonies on SNA attaining 25–28 mm diam. after 3 weeks, flat, slightly plicated, margin undulate, oldlace (3A2). Reverse oldlace (3A2). Sporulation within 3 weeks on OA and SNA.

Material examined: CHINA, Guangxi, Laibin, Sanshan Cave, N 23.41°, E 108.931°, on animal faeces, May 2016, Z.F. Zhang, HMAS 248004 (holotype designated here), ex-type living culture CGMCC3.19322 = LC12606; ibid., LC12588.

Notes: *Wardomycopsis ellipsoconidiophora* is phylogenetically closely allied to *W. fusca* and *W. humicola* (Fig. 37), while they are morphologically distinguishable. Conidiophores of *W. ellipsoconidiophora* are ellipsoidal and branched, comparing to ellipsoidal to globose and unbranched in *W. fusca*. *W. ellipsoconidiophora* differs from *W. humicola* (G.L. Barron) Udagawa & Furuya in its slightly wider conidia (2.5–3.0 µm vs. 1.5–2.5 µm) and low sequence similarities (98% similarity, 7 bp difference in 416 bp of ITS; 99% similarity, 5 bp difference in 842 bp of LSU; 96% similarity, 35 bp difference in 928 bp of EF1-α; 95% similarity, 22 bp difference in 475 bp of TUB).

Wardomycopsis fusca Z.F. Zhang, F. Liu & L. Cai, ***sp. nov.***

Index Fungorum number: 557752, *Facesoffungi number:* FoF 08461; Fig. 46

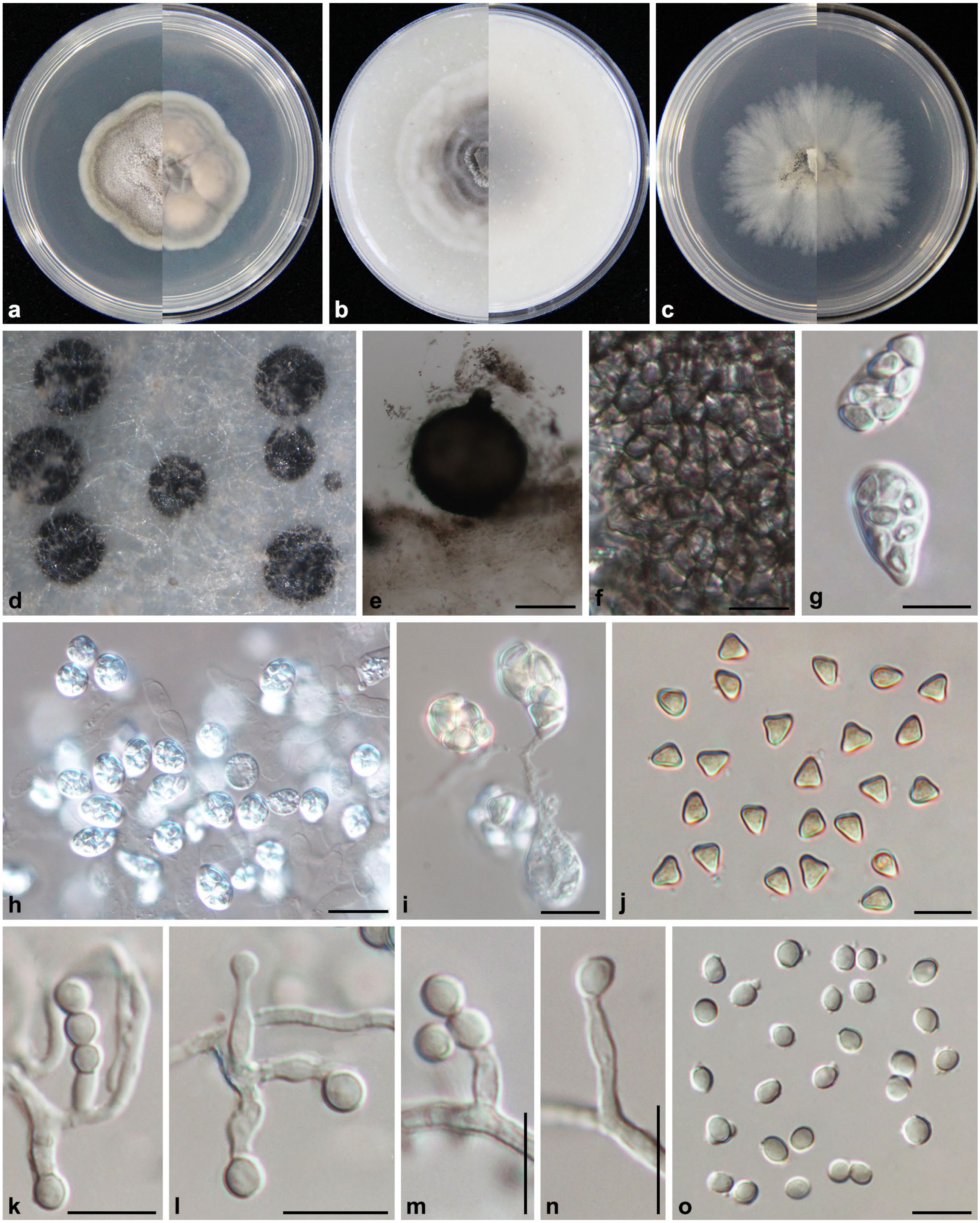


Fig. 42 *Microascus trigonus* (from ex-holotype CGMCC3.19636). **a**–**c** Upper and reverse views of cultures on PDA, OA and SNA 3 weeks after inoculation; **d**, **e** ascoma; **f** peridium; **g**–**i** asci; **j** ascospore; **k**–**n** conidiogenous cells and conidia; **o** conidia. Scale bars: **e** 100 μm; **h** 20 μm; **f**, **g**, **i**–**o** 10 μm

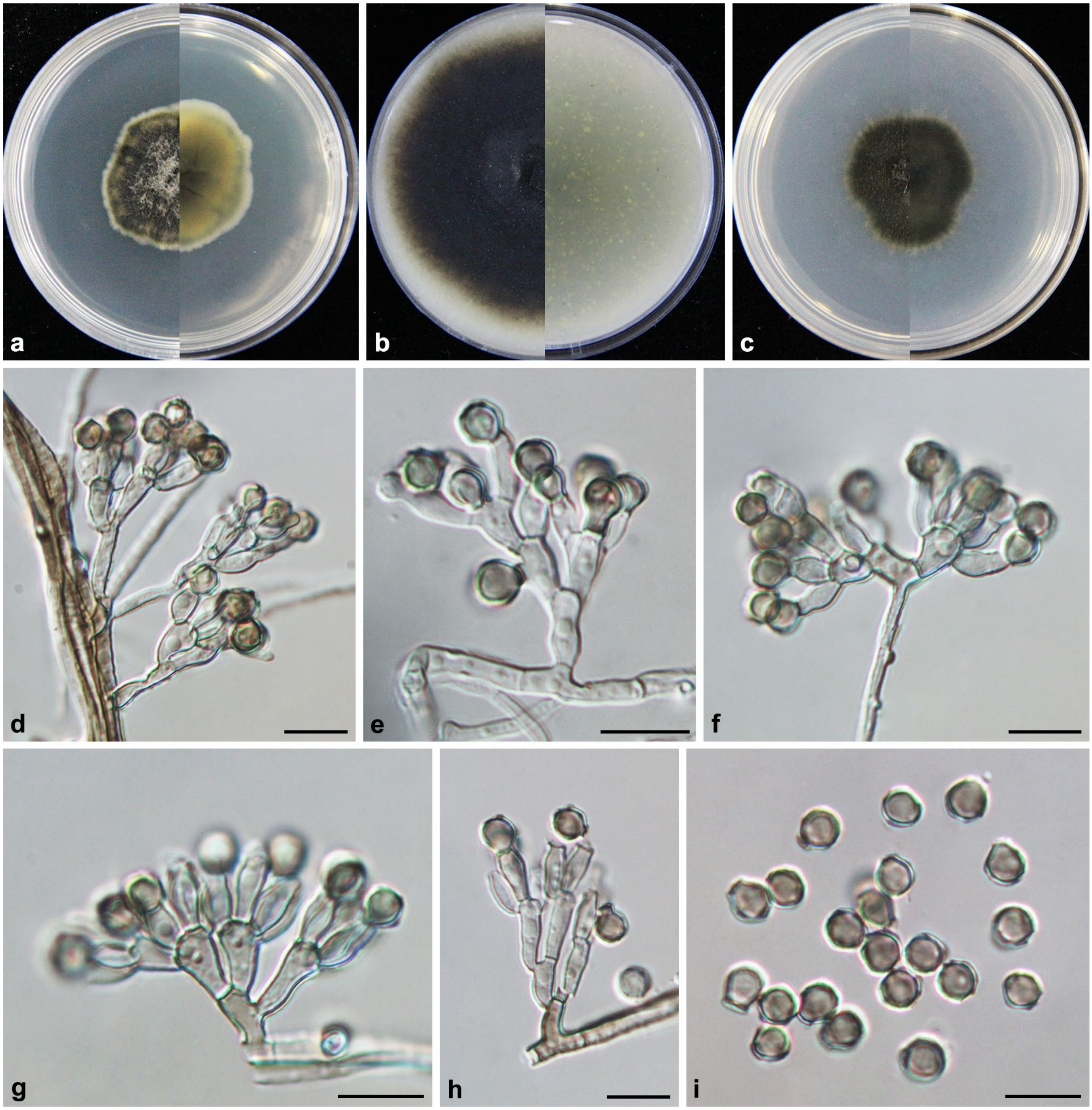


Fig. 43 *Pseudoscopulariopsis asperispora* (from ex-holotype CGMCC3.19302). **a**–**c** Upper and reverse views of cultures on PDA, OA and SNA 14 days after inoculation; **d**–**h** conidiophores and conidiogenous cells; **i** conidia. Scale bars: **d**–**i** 10 μm

Etymology: Referring to the brown color of its conidia.

Holotype: HMAS 247997.

Hyphae hyaline to pale olive, septate, smooth, thin-walled, 1.5–2.5μm diam. **Asexual morph** *Sporulation* abundant on SNA, brown, slimy. *Conidiophores* arising from hyphae, ellipsoidal to globose, occasionally branched one times, smooth, thick-walled, pale olive-brown, 3.0–7.5 × 2.5–5.0 μm. *Conidiogenous cells* solitary on aerial hyphae, ellipsoidal, or clustered on conidiophores, ampulliform, smooth, thick-walled, pale olive-brown, 3.0–5.0 (−6.0) × 2.5–3.5 μm. *Conidia* ellipsoidal, thick-walled, brown, 4.0–6.5 × 2.5–3.5 μm ($\bar{x}$± SD = 5.1 ± 0.62 × 3.0 ± 0.32 μm, n = 30), with truncated base and median longitudinal germ slit. **Sexual morph** not observed.

Culture characteristics—Colonies on PDA attaining 25–31 mm diam. after 3 weeks, felty, compact, convex, margin entire, pale olive (29A3) to grey (28B3), with light colored margin. Reverse sunken in center, cream-yellow (29A3) to olive (29D4). Colonies on OA attaining 26–28 mm diam after 3 weeks, flat, margin entire, white to dark olive (29F5), with olive rings (29F5). Reverse white to pale olive (29B2). Colonies on SNA attaining 23–28 mm diam after 3 weeks, flat, slightly plicated, margin entire, beige (28A2) to pale olive (29D4). Reverse beige (28A2) to dark olive (29F6). Sporulation within 15 days.

Material examined: CHINA, Guangxi, Guilin, Luotian Cave, N 24.948°, E 110.524°, on soil, May 2016, Z.F. Zhang, HMAS 247997 (holotype designated here), ex-type living culture CGMCC3.19306 = LC12476; ibid., LC12526; Guangxi, Guilin, E'gu Cave, N 24.942°, E 110.511°, on animal faeces, May 2016, Z.F. Zhang, LC12636; Yunnan, Mengzi, Mingjiu old Cave, N 23.487°, E 103.619°, on animal faeces, May 2016, Z.F. Zhang, LC12607; ibid., LC12661; Yunnan, Yiliang, Sanjiao Cave, N 25.134°, E 103.383°, on soil, May 2016, Z.F. Zhang, LC12643.

Notes: *Wardomycopsis fusca* is phylogenetically and morphologically closely related to *W. ellipsoconidiophora* and *W. humicola* (Fig. 37), but differs in ellipsoidal or globose and mostly unbranched conidiophores. Contrast to *W. fusca*, *W. ellipsoconidiophora* and *W. humicola* have cylindrical to ellipsoidal and branched conidiophores.

Subclass Sordariomycetidae O.E. Erikss. & Winka

Calosphaeriales M.E. Barr

The *Calosphaeriales* is an order of perithecial ascomycetous fungi with allantoid to suballantoid ascospores and

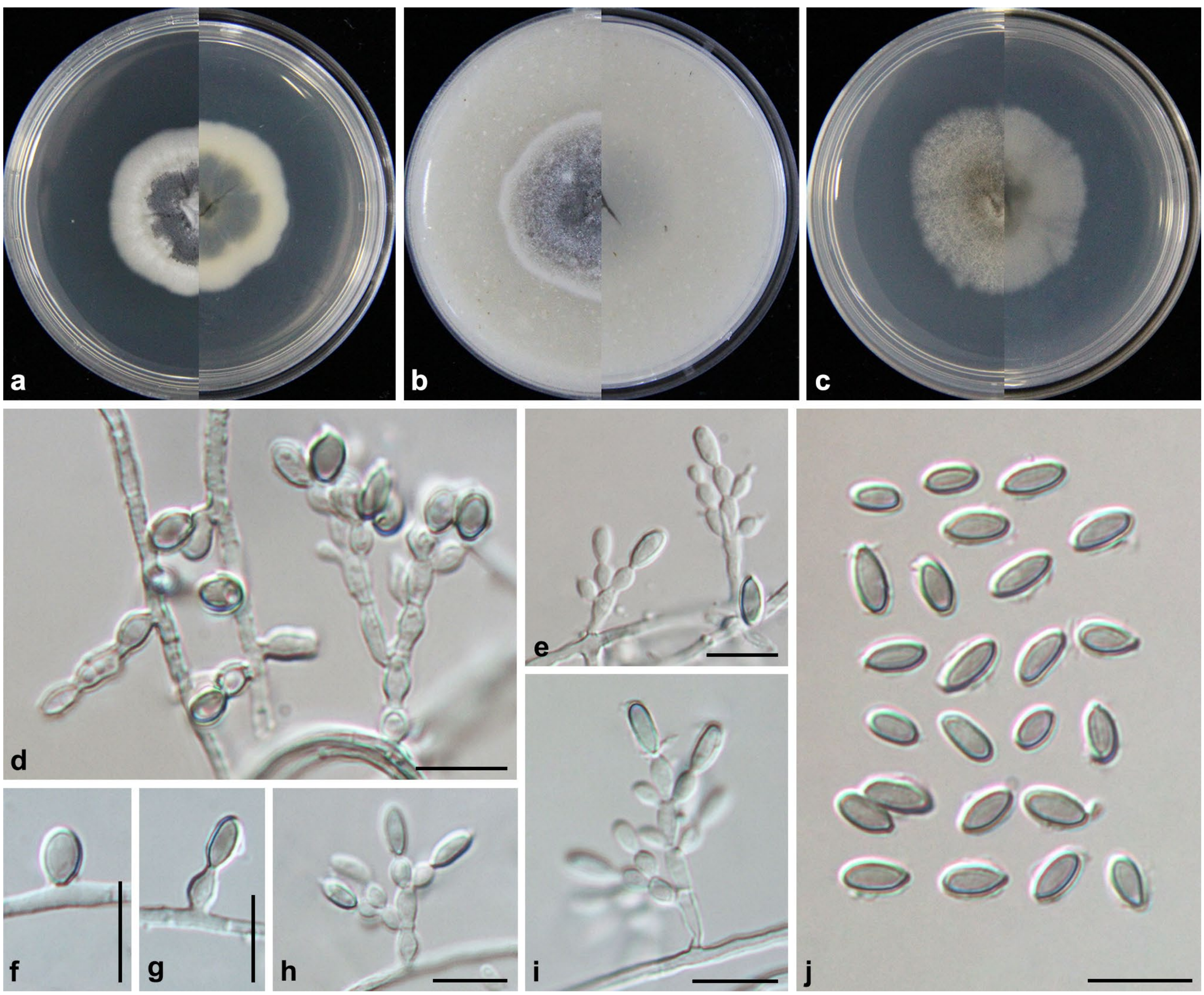


Fig. 44 *Wardomycopsis dolichi* (from ex-holotype CGMCC3.19310). **a**–**c** Upper and reverse views of cultures on PDA, OA and SNA 14 days after inoculation; **d**, **e**, **g**–**i** conidiophores and conidiogenous cells; **f** conidia borne on hypha; **j** conidia. Scale bars: **d**–**j** 10 µm

characteristic ascogenous hyphae, ascogenous cells and centrum, considered unique among the ascomycetes (Réblová et al. 2015). The order traditionally comprises wood-inhabiting perithecial ascomycetes that occupy specialized habitats between wood and periderm (Réblová et al. 2015).

Calosphaeriaceae Munk

The family was introduced by Munk (1957), followed by several recent revisions (Damm et al. 2008). Members of the *Calosphaeriaceae* share a set of typical characters such as globose to subglobose dark ascomata with a central neck, hyaline, non-septate or one to several transverse septa, 8-spored, clavate, tapering, stipitate asci. The asci have a conspicuous, symmetrical thickening at the apex, which lacks a visible discharge mechanism (Réblová et al. 2015). *Calosphaeriaceae* members are typical inhabitants of wood and bark of a broad spectrum of trees and shrubs worldwide, including *Prunus* wood (Barr 1985).

Jattaea Berl.

Berlese (1900) introduced genus *Jattaea* with *J. algeriensis* Berl. as generic type. *Jattaea* was recently revised based on a five-locus phylogeny (Réblová et al. 2015) and 18 species are currently accepted (Réblová et al. 2015; Dayarathne et al. 2017). The members of *Jattaea* are characterized by non-stromatic perithecial ascomata, clavate and stipitate asci with a thickened apex and distinct sporiferous part, persistent paraphyses and allantoid, 1-septate, hyaline ascospores. Asexual morphs of *Jattaea* are phialophora-like, i.e. short-ampulliform to elongate-ampulliform phialides or adelo-phialides with funnel-shaped collarettes (Réblová et al. 2015; Dayarathne et al. 2017). In this study, one new species *Juttaea reniformis* is described (Fig. 47).

Jattaea reniformis Z.F. Zhang & L. Cai, ***sp. nov.***, Fig. 48

Index Fungorum number: 557753, *Facesoffungi number:* FoF 08462; Fig. 48

Etymology: Referring to its reniform conidia.

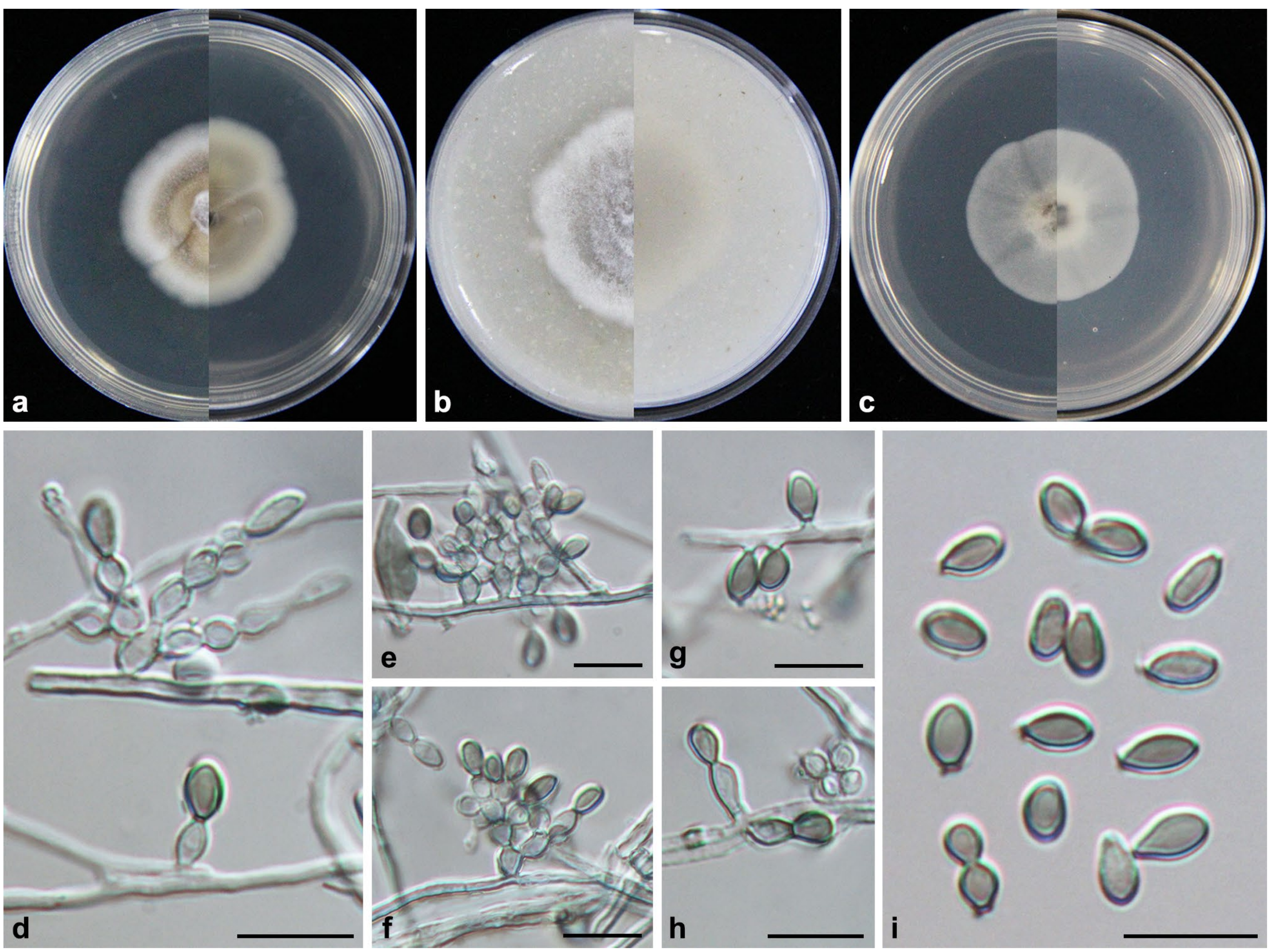


Fig. 45 *Wardomycopsis ellipsoconidiophora* (from ex-holotype CGMCC3.19322). **a**–**c** Upper and reverse views of cultures on PDA, OA and SNA 14 days after inoculation; **d**–**f**, **h** conidiophores and conidiogenous cells; **g** conidia borne on hyphae; **i** conidia. Scale bars: **d**–**i** 10 μm

Holotype: HMAS 247995.

Hyphae hyaline, septate, branched, smooth, 1.5–3.5 µm wide. **Asexual morph** *Conidiophores* micronematous, reduced to conidiogenous cells. *Phialides* arise from prostrate aerial hyphae solitary, lateral, monophialidic, long ampulliform to tapering, smooth to slightly granulate, hyaline, various in length, 4.5–11.5 µm long, 1.5–3.0 µm diam. at base, with conspicuous collarette, tapering to 1.0–1.5 µm below the collarette; adelophialides subcylindrical or ampulliform, 1.5–3.0 µm × 1.0–2.0 µm. *Conidia* aggregated in globose heads, cylindrical to reniform, unicellular, smooth, hyaline, various in size, 3.0–6.0 × 1.0–2.0 µm ($\bar{x} \pm$ SD = 4.2 ± 0.66 × 1.5 ± 0.21 µm, n = 60). **Sexual morph** not observed.

Culture characteristics—Colonies on PDA attaining 32–38 mm diam. after 4 weeks, plicated, margin entire, pale linen (5A2), aerial mycelia sparse. Reverse plicated, cream-white to yellow (4A7). Colonies on OA attaining 32–36 mm diam. after 4 weeks, flat, margin entire, white at margin, light gray (4B2) at middle, gainsboro (4A2) in center, aerial mycelia sparse. Reverse white to gainsboro (4B2) with gray ring (4B2). Colonies on SNA attaining 35–38 mm diam. after 4 weeks, flat, margin erose, white, aerial mycelia extremely sparse. Reverse white. Sporulation within 3 weeks.

Material examined: CHINA, Yunnan, Yiliang, Sanjiao Cave, N 25.134°, E 103.383°, on soil, May 2016, Z.F. Zhang, HMAS 247995 (holotype designated here), ex-type living culture CGMCC3.19311 = LC12509; ibid., LC12510.

Notes: This species should be classified into genus *Jattaea*, because it fits well to the asexual morphs of *Jattaea*, i.e. short-ampulliform to elongate-ampulliform to cylindrical phialides or adelo-phialides, tapering, with a more or less conspicuous funnel-shaped collarette (Réblová 2011; Réblová et al. 2015). Meanwhile, our strains are phylogenetically allied with *Jattaea* species based on ITS, LSU and TUB sequences (Fig. 47). *Jattaea reniformis* is currently known only for its asexual morph and comparable with *J.*

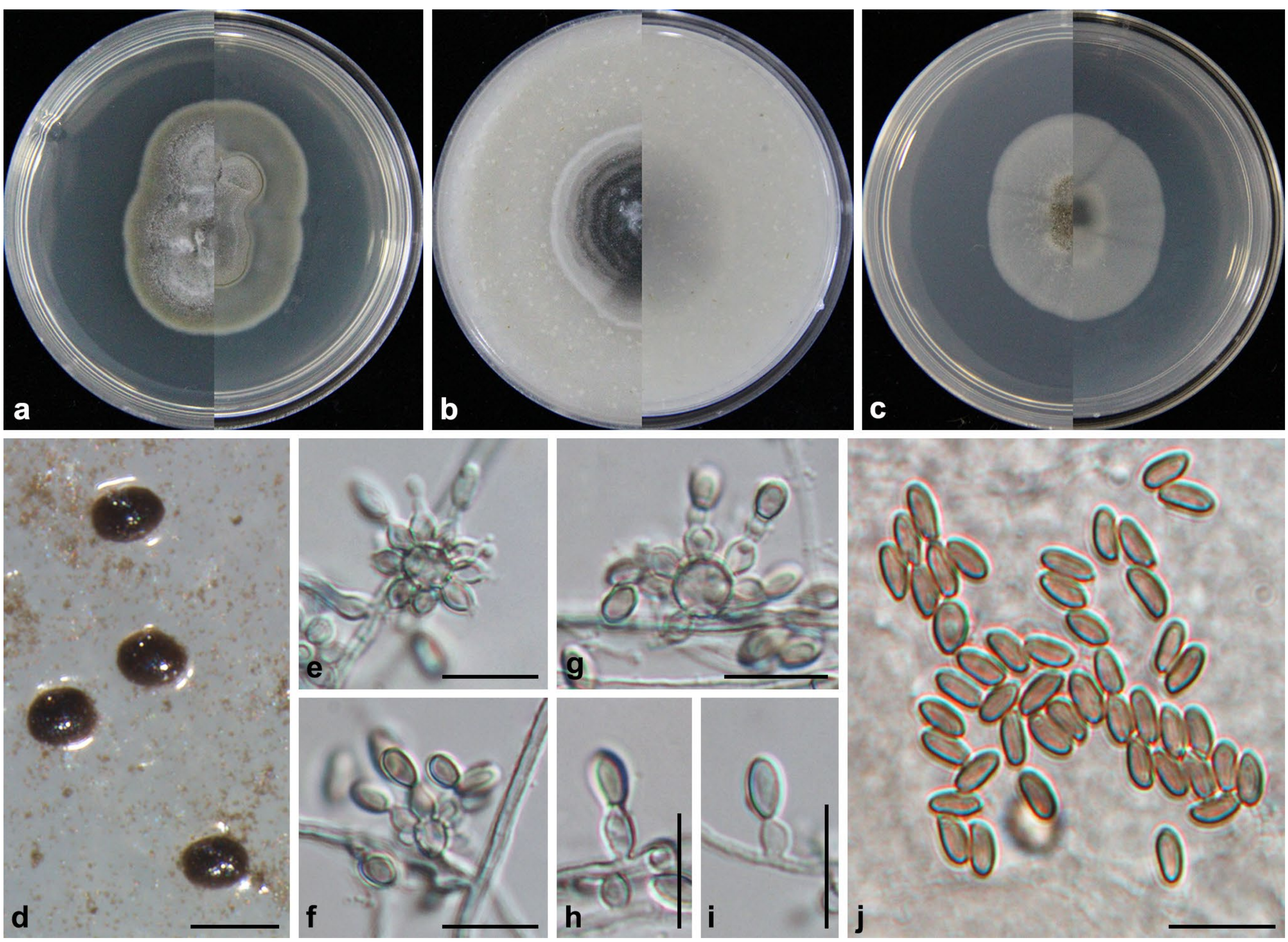


Fig. 46 *Wardomycopsis fusca* (from ex-holotype CGMCC3.19306). **a–c** Upper and reverse views of cultures on PDA, OA and SNA 14 days after inoculation; **d** sporulation on SNA under stereomicroscope; **e–i** conidiophores and conidiogenous cells; **j** conidia. Scale bars: **d** 100 µm; **e–j** 10 µm

aphanospora Réblová & J. Fourn., *J. ribicola* Réblová & Jaklitsch and *J. tumidula* (Sacc.) Réblová. While *J. reniformis* differs from *J. aphanospora* and *J. ribicola* by the presence of phialides and adelophialides, whereas only adelophialides are observed in *J. aphanospora* and *J. ribicola*. *J. reniformis* differs from *J. tumidula* by its subcylindrical or ampulliform adelophialides and wider conidia (1.0–2.0 μm vs. 1.0–1.2 μm); meanwhile only subcylindrical adelophialides was observed in *J. tumidula*. Generally *J. reniformis* is well distinguishable from other species in *Jattaea* by the absence of conidiophores.

Subclass Xylariomycetidae O.E. Erikss. & Winka

Xylariales Nannf.

The order *Xylariales* was established by Nannfeldt (1932), and have been revised in several recent studies (Daranagama et al. 2018; Voglmayr et al. 2018; Wendt et al. 2018), with three families *Barrmaeliaceae* Voglmayr & Jaklitsch, *Graphostromataceae* M.E. Barr, J.D. Rogers & Y.M. Ju and *Hypoxylaceae* DC. included and revised. *Xylariales* is one of the largest order of the subclass Xylariomycetidae, which currently comprises 22 families (Wijayawardene et al. 2020).

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

Apiosporaceae was introduced by Hyde et al. (1998) and confirmed as a family within *Xylariales*, closely related to *Amphisphaeriaceae* (Crous and Groenewald 2013).

Nigrospora Zimm.

Nigrospora was introduced by Zimmerman (1902) and most recently revised by Wang et al. (2017). *Nigrospora* is characterized by branched micronematons or semi-macronematous conidiophores, monoblastic condiogenous cells and black, shiny, aseptate condia. Sexual morphs comprise perithecial ascomata, short-stalked asci with biseriated ascopsores (Wang et al. 2017). Species of *Nigrospora* are cosmopolitans with wide host range, and reported as endophytes, saprobes, or pathogens on crops or humans (Wang et al. 2017; Raza et al. 2019). In this study, one new species *Nigrospora globosa* is described based on ITS, EF1-α and TUB phylogeny (Fig. 49).

Nigrospora globosa Z.F. Zhang & L. Cai, ***sp. nov.***

Index Fungorum number: 557754, *Facesoffungi number:* FoF 08463; Fig. 50

Etymology: Referring to its globose conidia.

Holotype: HMAS 248000.

Hyphae hyaline to pale brown, septate, branched, smooth, 1.5–8.0 μm wide. **Asexual morph** *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* arising from aerial hyphae solitary or aggregated in clusters, cylindrical, ampulliform, ellipsoidal or subglobose, straight or curved, smooth, hyaline to pale brown, 8.5–22.0 × 5.0–9.0 μm. *Conidia* solitary, unicellular, subglobose to globose, smooth, dark brown to black, shiny, 11.0–14.5 × 9.0–13.0 μm ($\bar{x} \pm SD = 13.0 \pm 0.84 \times 11.3 \pm 1.0$ μm, n = 60). Sterile cells and **Sexual morph** not observed.

Culture characteristics—Colonies on PDA attaining 38–41 mm diam. after 6 days, flat, floccose, radially striate with lobate edge, white initially, becoming pale gray with age. Reverse white to light yellow (2A2) initially, becoming pink (5A2) to brown (5B3) with age. Colonies on OA attaining 50 mm diam. after 4 days, flat, aerial mycelia abundant, floccose, margin entire, white initially, becoming gray (4B2) with age. Reverse white initially, becoming pink (5A2) with age. Colonies on SNA attaining 38–41 mm diam. after 6 days, flat, margin entire, white to pale yellow (3A3) initially, then becoming pale gray with gray (4B2) sporulation patches. Reverse white to pale yellow (4A1-4A2). Sporulation within 7 days.

Material examined: CHINA, Guangxi, Guilin, Luotian Cave, N 24.948°, E 110.524°, on soil, May 2016, Z.F. Zhang, HMAS 248000 (holotype designated here), ex-type living culture CGMCC3.19633 = LC12440; ibid., LC12441.

Notes: Our two strains representing *N. globosa* clustered with *N. chinensis* Mei Wang & L. Cai in a distinct clade (Fig. 49). Morphologically, *N. globosa* differs from *N. chinensis* by its larger conidiogenous cells (8.5–22.0 × 5.0–9.0 μm vs. 5.0–9.5 × 4.0–7.0 μm), and the absence of sterile cells in *N. globosa*.

Discussion

Karst area covers ca. 20% of the terrestrial area on the earth (Ford and Williams 2013), and there are more than a half million karst caves in China (Chen 2006; Zhang and Zhu 2012). According to Hawksworth and Lücking (2017), there are more than 120,000 hitherto described fungal species, but the estimation of global fungal diversity on the earth is 2.2 to 3.8 million. However, only 1626 fungal species were documented from caves and mines worldwide. Our study revealed that karst caves encompass a high fungal diversity, with a number of undescribed species.

Up to now, nine phyla have been reported in cave environments, and five phyla were obtained in this study. The proportion of species of Ascomycota, 88.0 % in this study, and 75.8 % in caves worldwide, is much higher than other phyla including Basidiomycota (Fig. 3a, e). In addition, the majority of genera with high species diverse (> 10 species) in caves are Ascomycota (Fig. 3f). In cave Basidiomycota is rare possibly because they are difficult to culture and often need to be associated with nutrient rich substrates such as

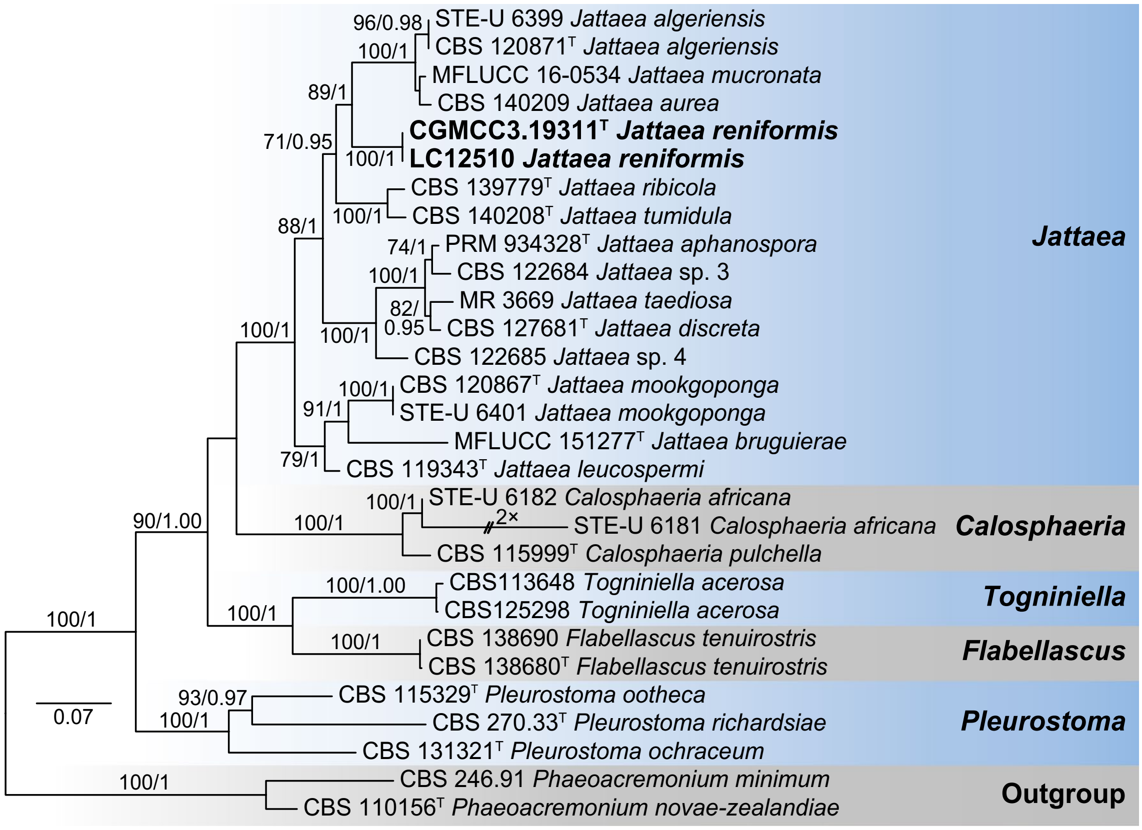


Fig. 47 Maximum likelihood (ML) tree of *Jattaea* and allied genera based on ITS, LSU and TUB sequences. Twenty-nine strains are used. The tree is rooted with *Phaeoacremonium minimum* (CBS 246.91) and *P. novae-zealandiae* (CBS 110156). Tree topology of the ML analysis was similar to the BI. The Best scoring RAxML tree with a final likelihood value of − 12288.310004. The matrix had 764 distinct alignment patterns, with 21.23 % of undetermined characters or gaps. Base frequencies estimated by jModelTest were as follows, A = 0.2144, C = 0.3000, G = 0.2795, T = 0.2061; substitution rates AC = 1.3366, AG = 2.3273, AT = 1.3366, CG = 1.0000, CT = 4.0395, GT = 1.0000; gamma shape = 0.4960. ML bootstrap values (≥ 70 %) and Bayesian posterior probability (≥ 90 %) are indicated along branches (ML/PP). Novel species are in bold font and "T" indicates type derived sequences

wood and dung (Vanderwolf et al. 2013), while these organic matters are much exiguous compared to a regular terrestrial environment. Glomeromycota, a phylum of arbuscular mycorrhizal (AM) fungi (Schüßler et al. 2001) never reported from caves in previous studies, was obtained in this study from soil sample of Sanjiao Cave (Table S1). Meanwhile, in our another study on fungal community based on high-throughput sequencing (HTS), Glomeromycota accounts for ca. 0.3% of all fungal OTUs in caves, and soil and water samples encompass more abundant reads of Glomeromycota than air and rock samples (Zhang and Cai 2019), which might due to the higher nutrient concentrations in soils (Vanderwolf et al. 2013) and a better link of water sample inside caves and the forest reservoir outside the caves (Voříšková and Baldrian 2013).

The most commonly recorded fungal genera in worldwide caves are cosmopolitan ones, especially *Penicillium* and *Aspergillus*, two genera discovered in all the caves investigated (Fig. 3c, f). Due to their diverse physiological features, species of *Penicillium* and *Aspergillus* are ubiquitous and can grow on almost all types of habitat, including the subsurface environments (Houbraken et al. 2014). Although *Mortierella* and *Mucor* had been reported from many caves, Vanderwolf et al. (2013) suggested that the incidence of Zygomycota, mainly *Mortierella* and *Mucor*, in caves might be overestimated due to the bias of detecting method. However, several studies using metabarcoding method did detect high relative abundance of Zygomycota (up to 49.8% when endogenous carbon available) in tourism caves and pristine caves (Cloutier et al. 2017; Pfendler et al. 2019; Zhang and Cai 2019). Therefore, the culture-based method may not be as biased as previously speculated (Zhang and Cai 2019). Several studies demonstrated that fungi in caves with fast growth and abundant spore production, including

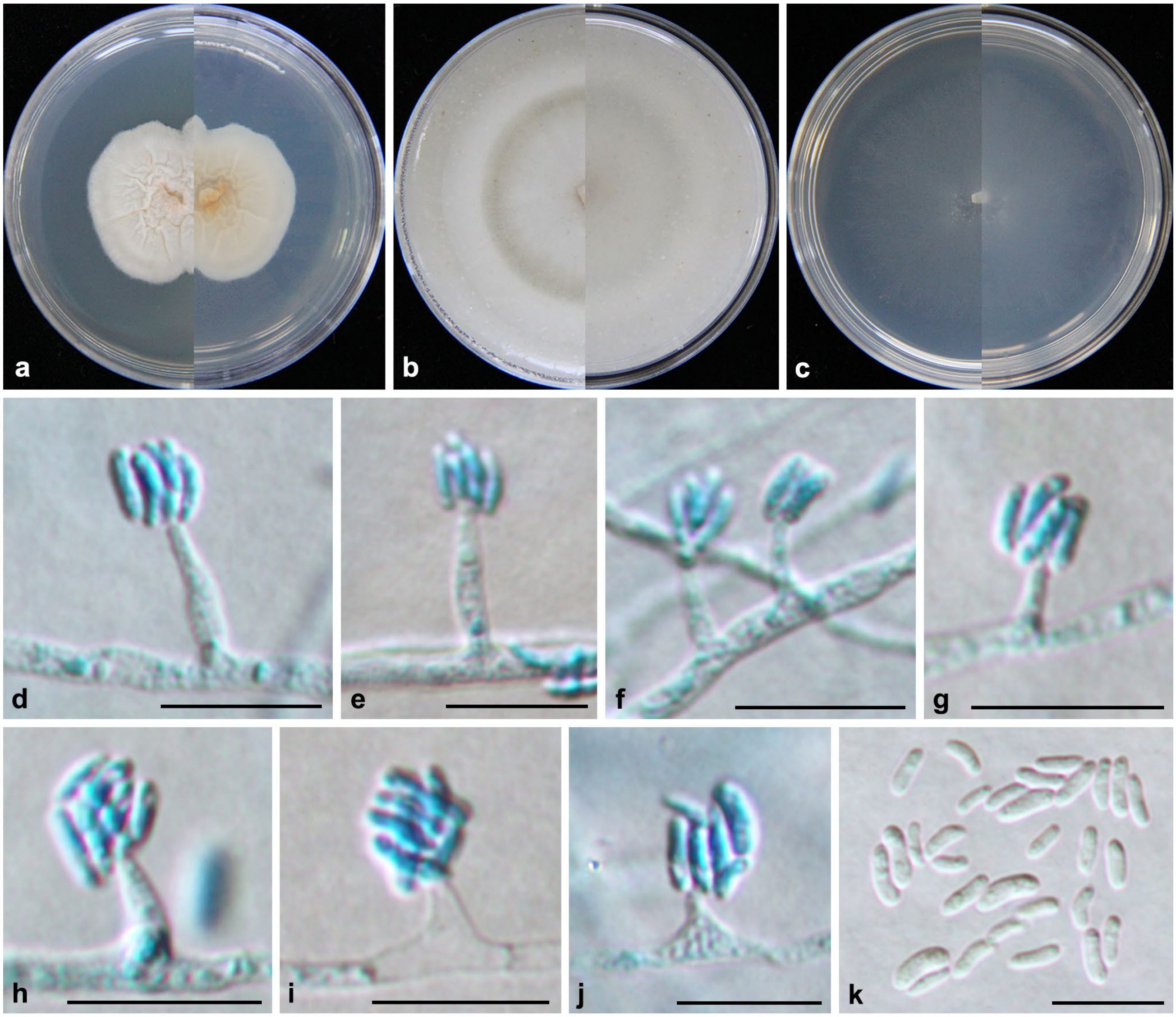


Fig. 48 *Jattaea reniformis* (from ex-holotype CGMCC3.19311). **a–c** Upper and reverse views of cultures on PDA, OA and SNA 4 weeks after inoculation; **d–j** phialides and conidia in globose heads; **k** conidia. Scale bars: **d–k** 10 µm

Penicillium, *Aspergillus*, *Mortierella* and *Mucor*, were sensitive to the changes of organic matters or human activates (Min 1988; Docampo et al. 2010, 2011; Jurado et al. 2010; Vanderwolf et al. 2013), indicating a predominantly saprobic lifestyle and potentially exogenous origin. According to the summary of Vanderwolf et al. (2013), *Rhachomyces* was widespread and thirty-two species, as insect coloniners, had been reported in caves, which was however, not recorded here possibly because only very few insect samples were collected in this study.

Cave systems were suggested to be a good harbour for the development and preservation of allochthonous microorganisms, such as mycorrhizal and pathogenic fungi (Kuzmina et al. 2012; Vanderwolf et al. 2013; Zhang et al. 2017; Zhang and Cai 2019). Many fungi obtained in this study are plant endophytic or pathogenic. For example, *Entrophospora* R.N. Ames & R.W. Schneid., isolated from soil in Sanjiao Cave, was reported as an AM fungi (Schüßler et al. 2001; Palenzuela et al. 2010). *Fusarium graminearum* Schwabe, a plant pathogen that causes head blight of wheat (Bai and Shaner 2004), was isolated from soil and water samples of Mingjiu Old Cave and Tianliang Cave. Many species of *Colletotrichum* Corda, *Diaporthe* Nitschke, *Fusarium* and *Phoma* Sacc. complexes obtained in this study

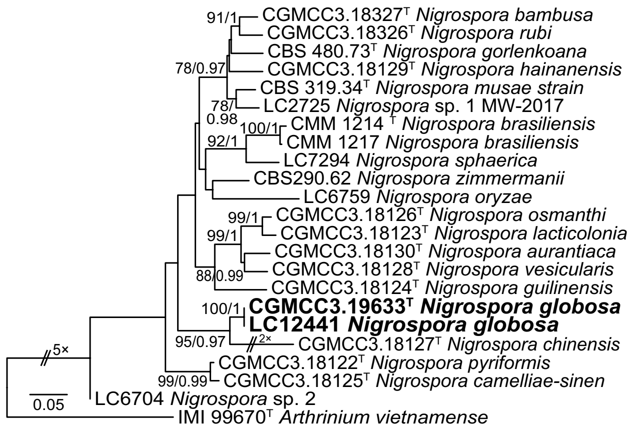


Fig. 49 Maximum likelihood (ML) tree of *Nigrospora* based on ITS, EF1-α and TUB sequences. Twenty-three strains are used. The tree is rooted with *Arthrinium vietnamense* (IMI 99670). Tree topology of the ML analysis was similar to the BI. The Best scoring RAxML tree with a final likelihood value of − 8201.629166. The matrix had 573 distinct alignment patterns, with 12.71 % of undetermined characters or gaps. Base frequencies estimated by jModelTest were as follows, A = 0.1979, C = 0.3209, G = 0.2348, T = 0.2463; substitution rates AC = 1.0000, AG = 3.4930, AT = 1.0000, CG = 1.0000, CT = 4.4017, GT = 1.0000; gamma shape = 0.2080. ML bootstrap values (≥ 70 %) and Bayesian posterior probability (≥ 90 %) are indicated along branches (ML/PP). Novel species are in bold font and "T" indicates type derived sequences

are also known as plant pathogenic fungi. *Myriodontium keratinophilum*, an occasional human and animal pathogen widely spread in nature (Maran et al. 1985; Domsch et al. 2007), was isolated not only in this study, but also from several other caves in previous studies (Man et al. 2015; Zhang et al. 2017; Nováková et al. 2018). Many of these fungi may not grow in the cave environment, but are present rarely or regularly as spores, carried in by water, air currents, or animals (Vanderwolf et al. 2013; Zhang et al. 2017).

Studies had revealed that fungi in caves might be originated from outside environments, since the majority of fungi documented in caves have been reported from other environments such as soil and forest (Vanderwolf et al. 2013; Zhang et al. 2017). All genera and most species recorded in this study have also been reported from other environments. Although there are several suspected obligate troglobitic fungi exist in caves, and several were also observed in this study, such as *Aspergillus spelunceus* Raper & Fennell, *A. thesauricus* Hubka & A. Nováková, *Trichosporon akiyoshidainum* Sugita, Takshima & Kikuchi and *T. chiropterorum* Sugita, Takshima & Kikuchi, it needs further investigation to confirm if these have a troglobitic nature (Vanderwolf et al. 2013; Zhang et al. 2017, 2018). Although a number of new species have been discovered in caves, no new genera or families were reported (Zhang et al. 2017). Zhang et al. (2018) estimated the divergence time of suspected obligate troglobitic fungi and found that they were obviously much older than the cave formation geologic age. In other words, the geologic age of caves is too short for fungal speciation and these fungi are unlikely troglobitic fungi but travelers from other environments.

Caves are special environments with a number of potentially highly valuable fungal species that have been the targets for drug discovery (Cheeptham 2012; Rawat et al. 2017). According to Vanderwolf et al. (2013), there are still 14 potential troglobitic cave fungi. Four new oligotrophic fungi using carbon free silica gel medium (SGM) and 20 new fungal taxa from two caves in Guizhou, China were published by Jiang et al. (2017a, b) and Zhang et al. (2017), respectively. *Amphichorda felina* (syn. *Beauveria felina* (DC.) J.W. Carmich., *Isaria felina* (DC.) Fr.), a species known in producing insecticidal cyclodepsipeptide (Baute et al. 1981; Langenfeld et al. 2011; Seifert et al. 2011) and Cyclosporin C (Xu et al. 2018), is widely distributed in caves (Vanderwolf et al. 2013; Zhang et al. 2017; Belyagoubi et al. 2018), as well as this study. Meanwhile, the other two coprophilous species in *Amphichorda* were isolated in this study, and they may have good potential for the investigation of bioactive natural products. *Trichoderma harzianum*, a species that has been used as biocontrol agents against fungal diseases of plants (Elad et al. 1982; Felse and Panda 1999), was isolated from soil and organic matters. Another example is *Beauveria bassiana* (Bals.-Criv.) Vuill. isolated from four caves in this study and several times in other studies (Ogórek et al. 2013, 2014b, Vanderwolf et al. 2013; Zhang et al. 2014; Yoder et al. 2015), is a species widely used as insecticide (Feng et al. 1994; Zimmermann 2007; Xiao et al. 2012).

Conclusions

Our investigation reveals that karst caves from southwest China encompass a high fungal diversity, with a number of previously undescribed species. Most species identified in this study have been reported from other environments, indicating that the outside environment is likely a major source of mycobiota in caves. Based on morphological and phylogenetic distinctions, 33 new species scattered in seven different orders were identified and described. One new genus is proposed. This study significantly improved our understanding on fungal species diversity in caves. Further studies incorporating metagenomics and culture method could possibly provide broader and more comprehensive overview on fungal communities and their ecological roles in caves.

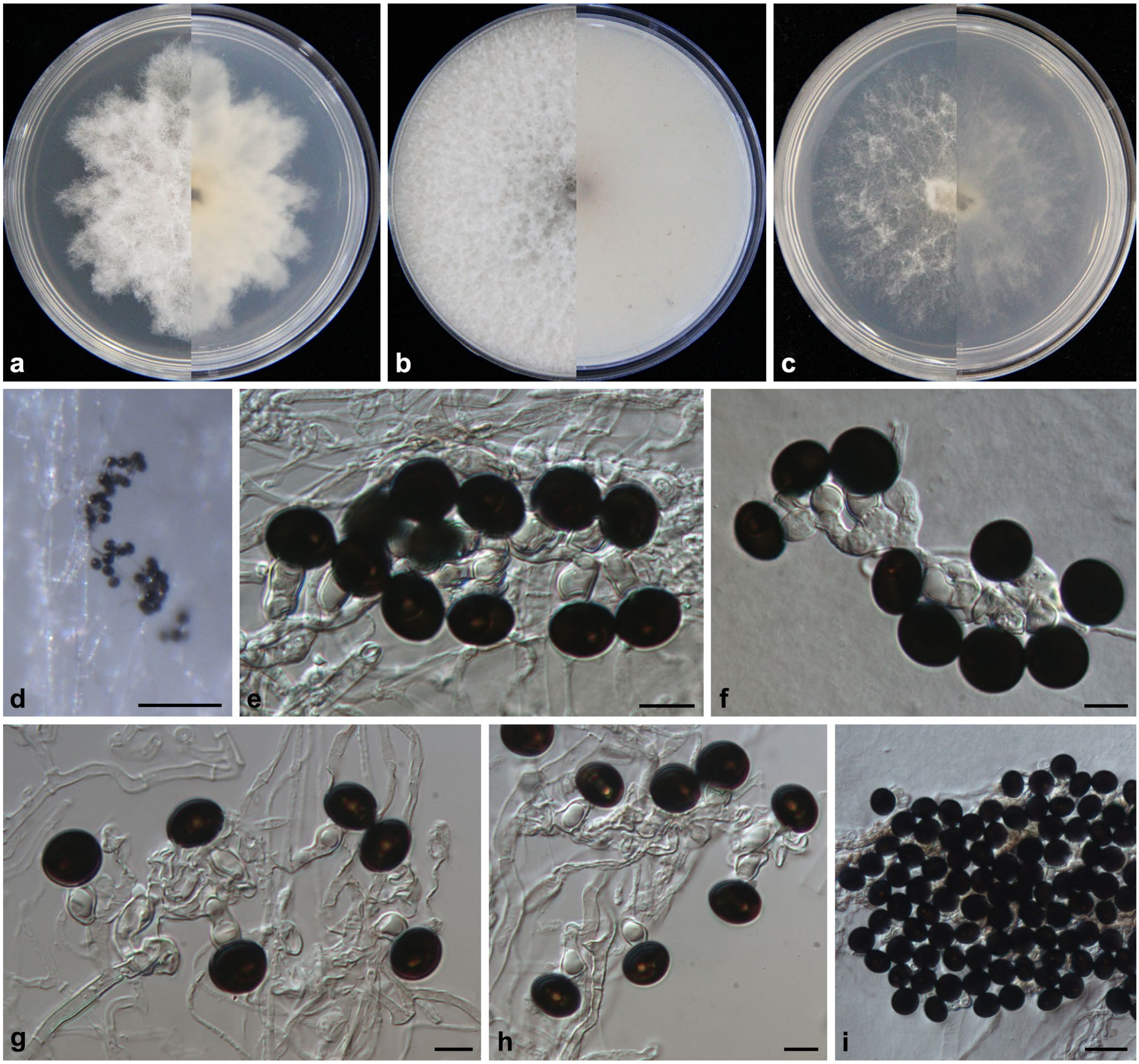


Fig. 50 *Nigrospora globosa* (from ex-holotype CGMCC3.19633). **a**–**c** Upper and reverse views of cultures on PDA, OA and SNA 6 days after inoculation; **d** condia under stereomicroscope; **e**–**h** conidiogenous cells and conidia; **i** conidia. Scale bars: **d** 100 µm; **i** 20 µm; **e**–**h** 10 µm

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Author contributions ZFZ: Designed the work, conducted the experiment, and drafted the manuscript; SYZ: Part of the fungal isolation, and data submission; LE, SI, MR, and FL: Revised the manuscript; PZ, and QC: Help for the sample collection; LC: Conceived the work, and revised manuscript.

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