



Article

Unveiling Species Diversity Within Early-Diverging Fungi from China XIII: Four New Species of *Absidia* (Cunninghamellaceae, Mucoromycota)

Wen-Xiu Liu ¹, Fei Li ¹, Shu-Ting Geng ¹, Hong-Yu Zou ¹, Heng Zhao ^{2,*}  and Xiao-Yong Liu ^{1,3,*} 

¹ College of Life Sciences, Shandong Normal University, Jinan 250358, China; 18054356852@163.com (W.-X.L.)

² CAS Key Laboratory of Forest Ecology and Silviculture, Institute of Applied Ecology, Chinese Academy of Sciences, Shenyang 110016, China

³ Institute of Microbiology, Chinese Academy of Sciences, Beijing 100101, China

* Correspondence: zhaoheng181@mails.ucas.ac.cn (H.Z.); liuxy@sdnu.edu.cn (X.-Y.L.)

Abstract

The genus *Absidia* is predominantly distributed in soil habitats. During the fungal investigation of soil collected from China (Guangxi, Yunnan, and Chongqing), four novel species of *Absidia* were identified, namely *Absidia brunneola* sp. nov., *A. digitata* sp. nov., *A. exilis* sp. nov., and *A. tumida* sp. nov. This identification was based on morphological characteristics and molecular analyses of the internal transcribed spacer (ITS), small subunit (SSU) and large subunit of ribosomal RNA gene (LSU rDNA), actin gene (ACT), and translation elongation factor 1-alpha gene (TEF1 α). *Absidia brunneola* sp. nov. is sister to *A. jiangxiensis*, which is characterized by the production of light brown sporangia. *Absidia digitata* sp. nov. and *A. tumida* sp. nov. are sister to each other with the former species developing digitiform rhizoids and the latter swollen in sporangiophores. *Absidia exilis* sp. nov. is closely related to *A. oblongispora*, exhibiting poorly developed sporangiophores. To date, the total number of recognized species within the genus *Absidia* has increased to 66, including the four new ones herein.

Keywords: Mucorales; taxonomy; morphology; molecular phylogeny; fungal diversity

1. Introduction

The genus *Absidia* was first formally proposed by van Tieghem in 1876 and typified by *A. reflexa* [1], and it currently belongs to Cunninghamellaceae, Mucorales, Mucoromycetes, and Mucoromycota. It is widely distributed and has been reported in all continents except Antarctica [2–4]. Over the past decade, at least 20 species have been successively reported in countries around the world, mainly including Brazil, China, South Korea, and Thailand [5–16]. In China, this genus was mainly found in southern hot areas, such as Yunnan, Hainan, and Sichuan provinces; it can also be sporadically found in certain regions with low temperatures, including northeast and northwest provinces [7]. As a saprophytic fungal group, it is primarily isolated from soil samples, and it is also distributed in herbivorous animal feces, decaying materials, and air [5,9,14,17–19]. Being a fungal genus of significant research value, *Absidia* holds important applications in industrial and medicinal fields. It can produce various secondary metabolites including α -galactosidase, steroids, and fatty acids [5,20–24], and some species are capable of participating in the biotransformation of natural products such as flavones, flavanones, and cresol red [23,25].



Academic Editor: Gary A. Strobel

Received: 2 January 2026

Revised: 21 January 2026

Accepted: 31 January 2026

Published: 2 February 2026

Copyright: © 2026 by the authors.

Licensee MDPI, Basel, Switzerland.

This article is an open access article distributed under the terms and conditions of the [Creative Commons Attribution \(CC BY\)](https://creativecommons.org/licenses/by/4.0/) license.

The taxonomic status of the genus *Absidia* has long been controversial. Initially assigned to the family Absidiaceae [26] upon its proposal, it was subsequently classified under Mucoraceae [27]. At present, it is placed within Cunninghamellaceae [28]. Drawing upon phylogenetic and morphological evidence, recent studies have demonstrated that *Absidia* sensu lato encompasses three genera, namely *Absidia* sensu stricto, *Lentamyces*, and *Lichtheimia* [29–31]. Species of the genus *Absidia* exhibit distinct morphological characteristics, which are mainly manifested as follows: sporangiophores are scattered along the stolons, showing an asymmetrical distribution relative to rhizoids, and they can be solitary, paired, clustered, or verticillate; rhizoids occur on stolons; sporangia mostly pyriform to subglobose with deliquescent walls and distinct apophyses; columellae usually bear apical protrusions. Studies conducted by Ding et al. [32] and Ji et al. [33] indicated that the number of recognized species within this genus has reached 62 to date.

Based on molecular phylogenetic and morphological characteristics, this paper presents a thorough characterization of four new *Absidia* species isolated and verified from soil specimens sampled in the Guangxi Zhuang Autonomous Region, Yunnan Province, and Chongqing Municipality, China. This constitutes the thirteenth report in a serial study focusing on the diversity of early-diverging fungi in China [32–38].

2. Materials and Methods

2.1. Sample Collection and Strain Isolation

In 2025, we collected soil samples from the Guangxi Zhuang Autonomous Region, Yunnan Province, and Chongqing Municipality of China, following the methodologies outlined by Liu et al. [39] and Zou et al. [40]. Roughly 50 g of each sample was placed into a sterile sealed bag with labels indicating the sample number, vegetation type, collection date, longitude, latitude, and altitude. After collection, all samples were transported back to the laboratory and stored at 4 °C (Cat. No.: LSC-650E, Zhejiang Xingxing Cold Chain Integration Co., Ltd., Taizhou, China). Fungal isolation and purification were performed using a combination of the single-spore isolation method and the serial dilution plate method [40,41] with a detailed procedures as follows: Approximately 1 g of soil sample was weighed and transferred to a test tube containing 9 mL of sterile water. After shaking thoroughly, a 10^{-1} soil suspension was prepared. An aliquot of 1 mL of the initial suspension was transferred to another test tube with 9 mL of sterile water, and then it was fully mixed to obtain a 10^{-2} suspension. This serial dilution step was repeated sequentially to prepare 10^{-3} and 10^{-4} suspensions. An aliquot of 200 μ L from each of the 10^{-3} and 10^{-4} dilutions was pipetted onto the surface of Rose Bengal Chloramphenicol Agar (RBC) (Cat. No.: HB0237-3, Qingdao Hope Bio-Technology Co., Ltd., Qingdao, China) plates [42] supplemented with 0.03% streptomycin sulfate. The RBC medium composition was as follows: peptone 5.00 g/L, glucose 10.00 g/L, $\text{MgSO}_4 \cdot 7\text{H}_2\text{O}$ 0.50 g/L, KH_2PO_4 1.00 g/L, rose bengal 0.05 g/L, chloramphenicol 0.10 g/L, and agar 15.00 g/L. Each inoculated plate was then uniformly spread using a sterile glass spreader. The inoculated plates were incubated in a 25 °C incubator in the dark for 3 d. Subsequently, under a stereomicroscope (Olympus SZX10, Tokyo, Japan), sporangia of the target strains were picked using a sterile inoculating loop and transferred onto Potato Dextrose Agar (PDA) (Cat. No.: HB0233, Qingdao Hope Bio-Technology Co., Ltd., Qingdao, China) plates with the following medium composition: 6.00 g/L potato infusion powder, 20.00 g/L dextrose, and 20.00 g/L agar, which was followed by incubation in the dark at 25 °C Incubator (Cat. No.: 1010159, Ningbo Jiangnan Instrument Factory, Taizhou, China). After purification, the strains were preserved with 10% glycerol at 4 °C refrigerator (Cat. No.: LSC-650E, Zhejiang Xingxing Cold Chain Integration Co., Ltd., Taizhou, China).

The dried type specimens were preserved in the Herbarium Mycologicum Academiae Sinicae (HMAS; Beijing, China). The ex-type strains were deposited at the China General Microbiological Culture Collection Center (CGMCC; Beijing, China). Replicated experiments were performed at Shandong Normal University (XG; Jinan, China). Taxonomic details pertaining to the novel taxa have been submitted to the Fungal Names database (<https://nmdc.cn/fungalnames/>, accessed on 15 January 2026).

2.2. Morphological Observation

Macroscopic morphological traits were recorded via photography using a high-definition color digital camera (DP80, Olympus, Tokyo, Japan). Simultaneously, the microscopic morphological features of the fungal isolates were examined with a stereomicroscope (Olympus SZX10; Olympus, Tokyo, Japan) and a light microscope (BX53; Olympus, Tokyo, Japan). Subsequently, Digimizer software v 6.0.0 (<https://www.digimizer.com/>, accessed on 2 November 2025) was used for microstructure measurements with each characteristic (sporangiphores, columellae, sporangiospores, and so on) measured at least 50 times. Finally, Adobe Photoshop CC 2019 (<https://www.adobe.com/products/photoshop.html>, accessed on 8 November 2025) was employed for image typesetting of the captured microstructures.

2.3. DNA Extraction, PCR Amplification, and Sequencing

We inoculated the strain onto PDA medium and incubated in a 25 °C incubator under dark conditions for 3–5 d; then, fungal genomic DNA was extracted using either the Beaver Beads Plant DNA Kit (BEAVER Biomedical Engineering Co., Ltd., Cat. No.: 70409-20, Suzhou, China) or the CTAB method [43,44]. Polymerase chain reaction (PCR) was employed to amplify the ITS, LSU rDNA, TEF-1 α , ACT, and SSU gene regions with the primer pairs ITS4/ITS5 [45], LR0R/LR5 [46], EF1-983F/TEF1LLerev [47,48], ACT-1/ACT-4R [49], and NS1/NS4 [45] utilized for each respective region (Table 1). The PCR amplification was carried out in a total volume of 25 μ L, which contained 12.5 μ L of 2 $\times$ Hieff Canace[®] Plus PCR Master Mix (Yeasen Biotechnology, Shanghai, China; Cat. No.: 10154ES03), 9.5 μ L of double-distilled water (ddH₂O), 1 μ L each of the forward and reverse primers (10 μ M, TsingKe Biotechnology Co., Ltd., Beijing, China), and 1 μ L of fungal DNA template. Upon completion of amplification, the resulting products were separated via 1% agarose gel electrophoresis and visualized under ultraviolet light [50]. Target bands were excised and purified using a Gel Extraction Kit (Cat. No.: AE0101-C; Shandong Sparkjade Biotechnology Co., Ltd., Jinan, China), and subsequent DNA sequencing was conducted by Sangon Biotech (Shanghai, China) Co., Ltd. Consensus sequences were assembled using Geneious Prime 2025.0.2 software (<https://www.geneious.com>, accessed on 14 July 2025). All sequences were deposited at the National Microbiology Data Center (<https://nmdc.cn/>, accessed on 6 December 2025) with the accession numbers provided in Table S1.

2.4. Phylogenetic Analyses

All sequences were retrieved from the National Center for Biotechnology Information (<https://www.ncbi.nlm.nih.gov/>, accessed on 9 October 2025) with reference to recently published articles on the genus *Absidia* [32,33], and detailed information of all sequences is provided in Table S1. Sequence alignment and concatenation were performed using Geneious Prime 2025.0.2 software. Based on the combined ITS-SSU-LSU-ACT-TEF1 α sequence dataset, phylogenetic trees were constructed using two methods: maximum likelihood (ML) and Bayesian inference (BI). The ML analysis was conducted on the CIPRES Science Gateway (<https://www.phylo.org/>, accessed on 15 October 2025) using RAxML 8.2.4 software with 1000 bootstrap replicates [51]. For the Bayesian inference analysis, the GTR + I + G model was utilized with sampling conducted at intervals of 1000 gen-

erations. Eight cold Markov chains were operated concurrently for a total of 2,000,000 generations [51,52]. The generated phylogenetic tree was optimized through the iTOL web platform (<https://itol.embl.de>, 17 October 2025) and visually polished using Adobe Illustrator CC 2019 software (<https://adobe.com/products/illustrator>, 18 October 2025).

Table 1. PCR primers and amplification programs employed in this study.

Loci	PCR Primers	Primer Sequence (5'–3')	PCR Cycles	References
ITS	ITS5	GGA AGT AAA AGT CGT AAC AAG G	95 °C 5 min; (95 °C 30 s, 55 °C 30 s, 72 °C 1 min) × 35 cycles; 72 °C 10 min	[45]
	ITS4	TCC TCC GCT TAT TGA TAT GC		
LSU	LR0R	GTA CCC GCT GAA CTT AAG C	95 °C 5 min; (95 °C 50 s, 47 °C 30 s, 72 °C 1.5 min) × 35 cycles; 72 °C 10 min	[46]
	LR5	TCC TGA GGG AAA CTT CG		
TEF1 α	EF1-983F	GCYCCYGGHCAYCGTGAYTTYAT	95 °C 5 min; (95 °C: 30 s, 55 °C: 60s, 72 °C: 60 s) × 30 cycles; 72 °C 10 min	[47,48]
	TEF1LLev	AAC TTG CAG GCA ATG TGG		
ACT	ACT-1	TGG GAC GAT ATG GAI AAI ATC TGG CA	95 °C 3 min; (95 °C: 60 s, 55 °C: 60 s, 72 °C: 1 min) × 30 cycles; 72 °C 10 min	[49]
	ACT-4R	TC ITC GTA TIC TIG CTH IGA IAT CCA CA T		
SSU	NS1	GTA GTC ATA TGC TTG TCT CC	95 °C 5 min; (94 °C: 60 s, 54 °C: 50 s, 72 °C: 1 min) × 37 cycles; 72 °C 10 min	[45]
	NS4	CTT CCG TCA ATT CCT TTA AG		

3. Results

3.1. Phylogeny

Phylogenetic analysis was performed based on a molecular dataset including 109 strains, comprising 66 species of the genus *Absidia*, as well as two taxa selected as outgroups (i.e., *Cunninghamella blakesleeana* and *Cunninghamella elegans*). The dataset consisted of a total of 5189 concatenated characters, covering five fragments ITS (positions 1–1236), SSU (1237–2344), LSU (2345–3413), ACT (3414–4335), and TEF1 α (4336–5189). Among these characters, 2901 were constant characters, 563 were variable but parsimony-uninformative characters, and 1725 were parsimony-informative characters. The maximum likelihood (ML) tree and Bayesian inference (BI) tree exhibited topological congruence, so the ML tree was selected for comprehensive visualization (Figure 1). Eight *Absidia* strains obtained in the present study formed four well-defined clades, each receiving full statistical support in the phylogenetic tree.

3.2. Taxonomy

Absidia brunneola W.X. Liu, H. Zhao & X.Y. Liu, sp. nov., Figure 2.

Fungal Names: FN 573310.

Type: China, Guangxi Zhuang Autonomous Region, Fangchenggang City, Shangsi County, Shiwanda Mountain National Forest Park. (21°90'58" N, 107°90'36" E, altitude 277.0 m), from soil, 9 February 2025, W. X. Liu, holotype HMAS 354234, ex-holotype living culture CGMCC 3.29490 (=XG12984-12-1).

Etymology: The epithet *brunneola* (Lat.) refers to the light brown sporangia.

Description: Colonies on PDA at 25 °C for 4 d, reaching 73 mm in diameter, fast growing with a rate of 18.3 mm/d. Mycelium grows on the surface of the agar medium. Hyphae initially white, gradually turning brown with age, aseptate when young and septate at maturity, 3.9–19.0 μ m wide. Stolons septate, branched, hyaline or slightly brownish, 3.3–10.2 μ m wide. Rhizoids well developed, hyaline, root-like. Sporangiphores arising from stolons, erect or slightly bent, mostly unbranched or with simple branches, single or 2–5 in whorls, 19.6–281.0 μ m long, 1.8–5.6 μ m wide with a septum 12.4–23.4 μ m below the apophysis. Sporangia globose or pyriform, light brown, smooth-walled, deliquescent, 12.9–49.6 μ m long, 10.9–49.6 μ m wide. Columellae globose or subglobose, hyaline or subhyaline, smooth walled, 7.6–25.3 μ m long, 7.1–21.4 μ m wide. Projections present or

absent; if present, solitary and crystal-like. Apophyses present, funnel shaped, 6.1–23.1 μm high, 2.6–6.8 μm wide at the base, and 10.6–30.2 μm wide at the top. Collars present or absent. Sporangiospores ovoid, hyaline, smooth walled, 2.3–4.5 μm long and 1.9–2.5 μm wide. Chlamydospores absent. Zygospores unknown.

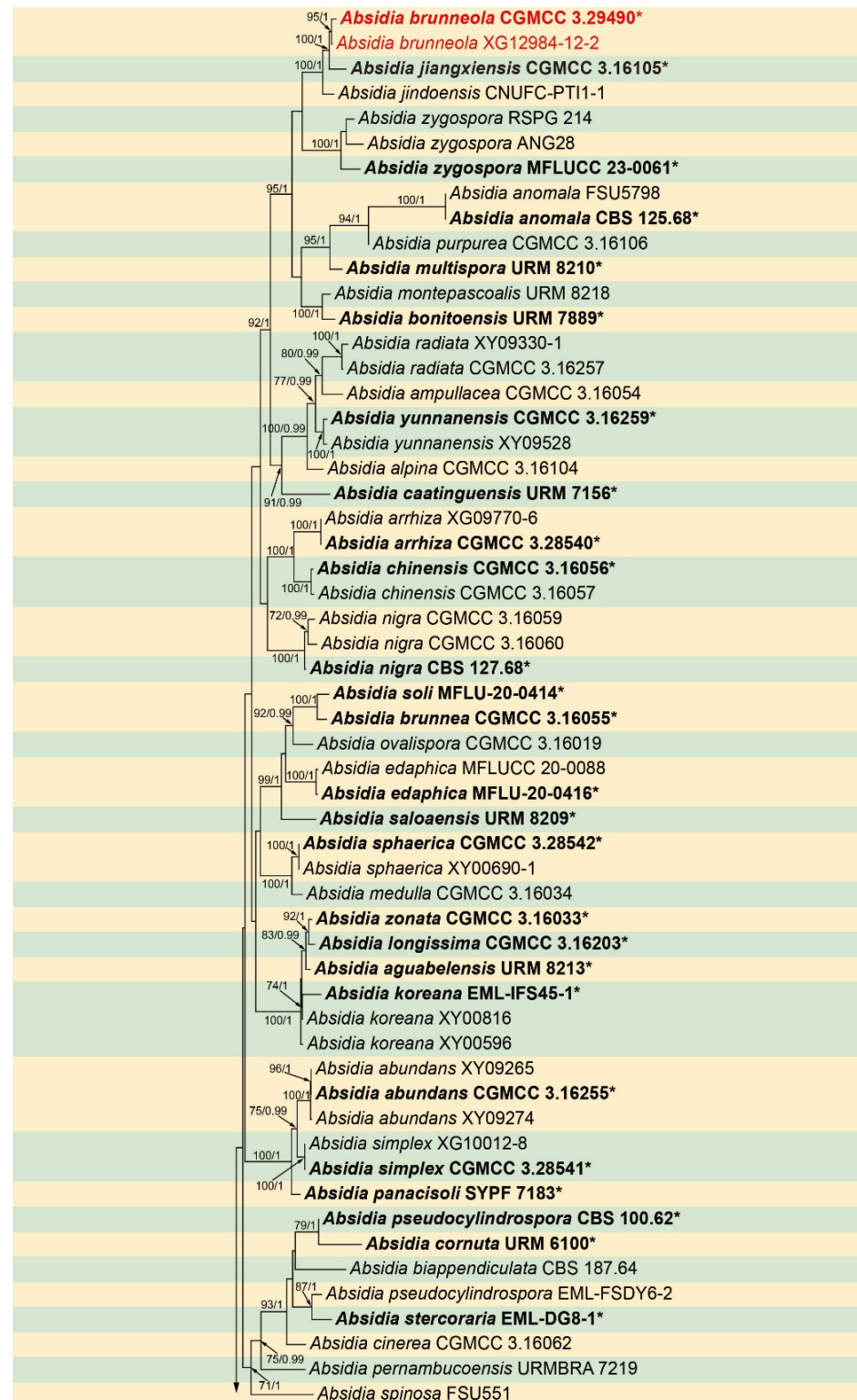


Figure 1. Cont.

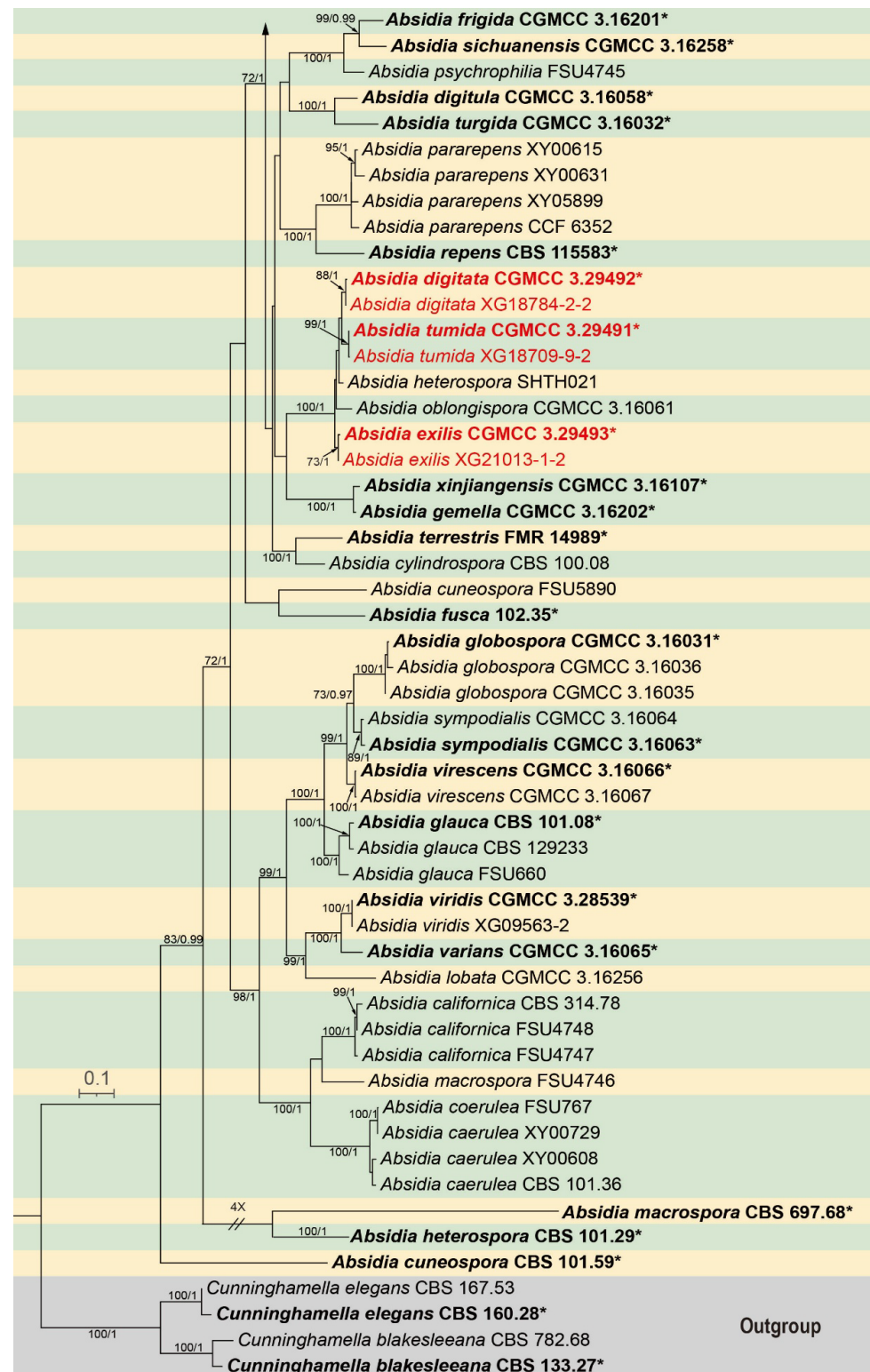


Figure 1. The ML phylogenetic tree of *Absidia* was constructed using concatenated ITS, SSU, LSU, ACT, and TEF-1 α sequences with *Cunninghamella blakesleeana* and *C. elegans* as outgroups. Node support is shown as ML bootstrap values ($\geq 70\%$)/Bayesian posterior probabilities (≥ 0.90). Ex-type/ex-holotype strains are highlighted in bold black font with an asterisk (*); the eight novel species strains isolated in this study are highlighted in red. Branches that have been shortened are denoted by a double slash “//” with “x” indicating the shortening fold. The phylogenetic tree is split into two parts, which are connected by an arrow at the top and bottom. The scale bar represents the number of substitutions per site.

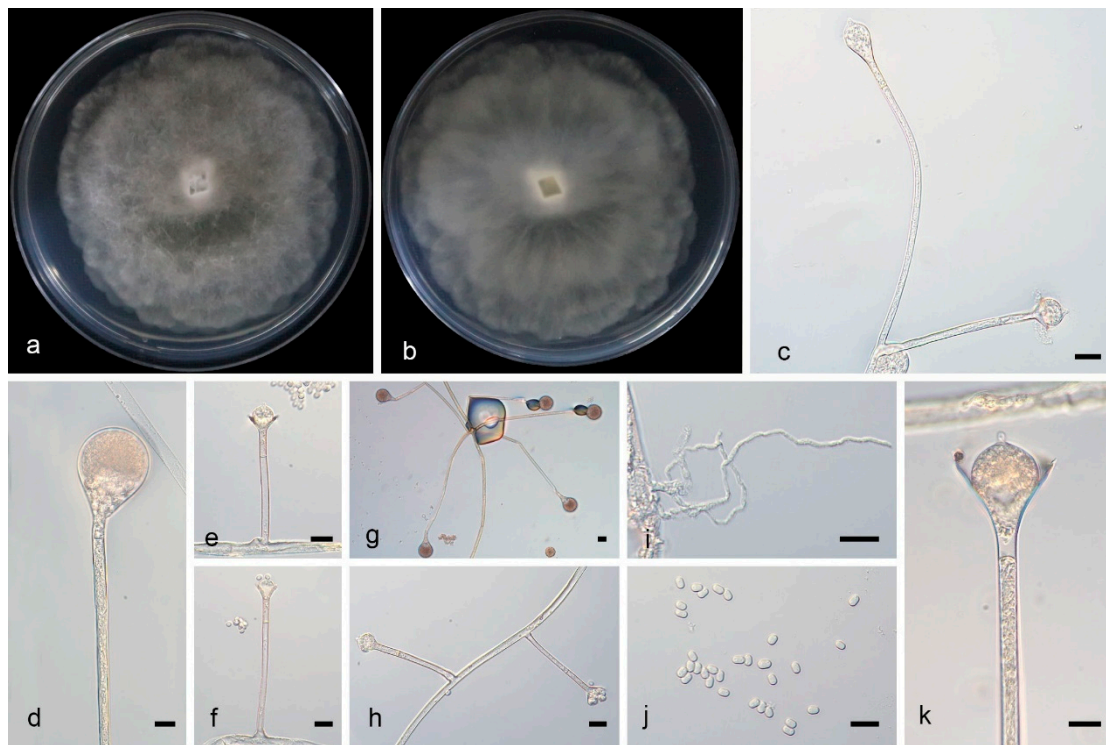


Figure 2. Morphologies of *Absidia brunneola* ex-holotype CGMCC 3.29490. (a,b) Colonies on PDA: (a) obverse, (b) reverse; (c,d,g) sporangia; (e,f,h,k) columellae; (i) rhizoids; (j) sporangiospores. Scale bars: (c–f,h–k) 10 µm; (g) 20 µm.

Additional strains examined. China, Guangxi Zhuang Autonomous Region, Fangchenggang City, Shangsi County, Shiwanda Mountain National Forest Park (21°90'58" N, 107°90'36" E, altitude 277.0 m), from soil, 9 February 2025, W. X. Liu, living culture XG12984-12-2.

Notes. On the phylogenetic tree constructed from the concatenated ITS–SSU–LSU–ACT–TEF1 α sequences, strains CGMCC 3.29490 and XG12984-12-2 cluster together to form a single clade with a support value of MLBS/BIPP = 95/1.00 (Figure 1), sister to *Absidia jiangxiensis* [19]. Morphologically, the sporangiophores of these two strains exhibit simple branches with up to five in a whorls arrangement, and their sporangia are light brown. In contrast, the sporangiophores of *A. jiangxiensis* are unbranched with up to six in a whorls arrangement. Based on molecular phylogenetic analyses and morphological observations, these two strains are proposed as a novel species *A. brunneola*.

Absidia digitata W.X. Liu, H. Zhao & X.Y. Liu, sp. nov., Figure 3.

Fungal Names: FN 573311.

Type. China, Yunnan Province, Xishuangbanna Dai Autonomous Prefecture, Mengla County, Mengla Town, G213. (21°51'58" N, 101°50'77" E, altitude 878.19 m), from soil, 19 May 2025, W. X. Liu, holotype HMAS 354235, ex-holotype living culture CGMCC 3.29492 (=XG18784-2-1).

Etymology: The epithet *digitata* (Lat.) refers to the species producing digitiform rhizoids.

Description. Colonies on PDA at 25 °C for 4 d, reaching 56 mm in diameter, fast growing with a rate of 14 mm/d. Mycelium grows on the surface of the agar medium. Hyphae are initially white, gradually becoming grayish-brown with age, aseptate when young and septate when mature, 3.9–15.8 µm wide. Stolons septate, branched, hyaline or slightly brownish with a diameter of 2.9–12.7 µm. Rhizoids well developed, hyaline, and finger-shaped. Sporangiophores arising from stolons, erect or slightly bent, occasionally swollen, mostly unbranched or with simple branches, single or 2–3 in whorls, 23.9–165.1 µm long, 2.7–4.3 µm wide with a septum 11.5–19 µm below the apophysis. Sporangia pyriform, rarely

globose, hyaline, smooth-walled, deliquescent walled, 19.1–33.5 μm long, 17.7–26.2 μm wide. Columella globose, hyaline, smooth walled, 6.6–17.8 μm long, 6.3–12.7 μm wide. Projections present, pacifier shaped. Apophysis distinct, funnel-shaped, hyaline and slightly light brown, 6.4–12.9 μm high, 2.7–5.2 μm wide at the base and 8.6–25 μm wide at the top. Collars present. Sporangiospores oval, smooth walled, hyaline, 2.4–4.9 μm long, 1.8–3.1 μm wide. Chlamydospores not found. Zygospores unknown.

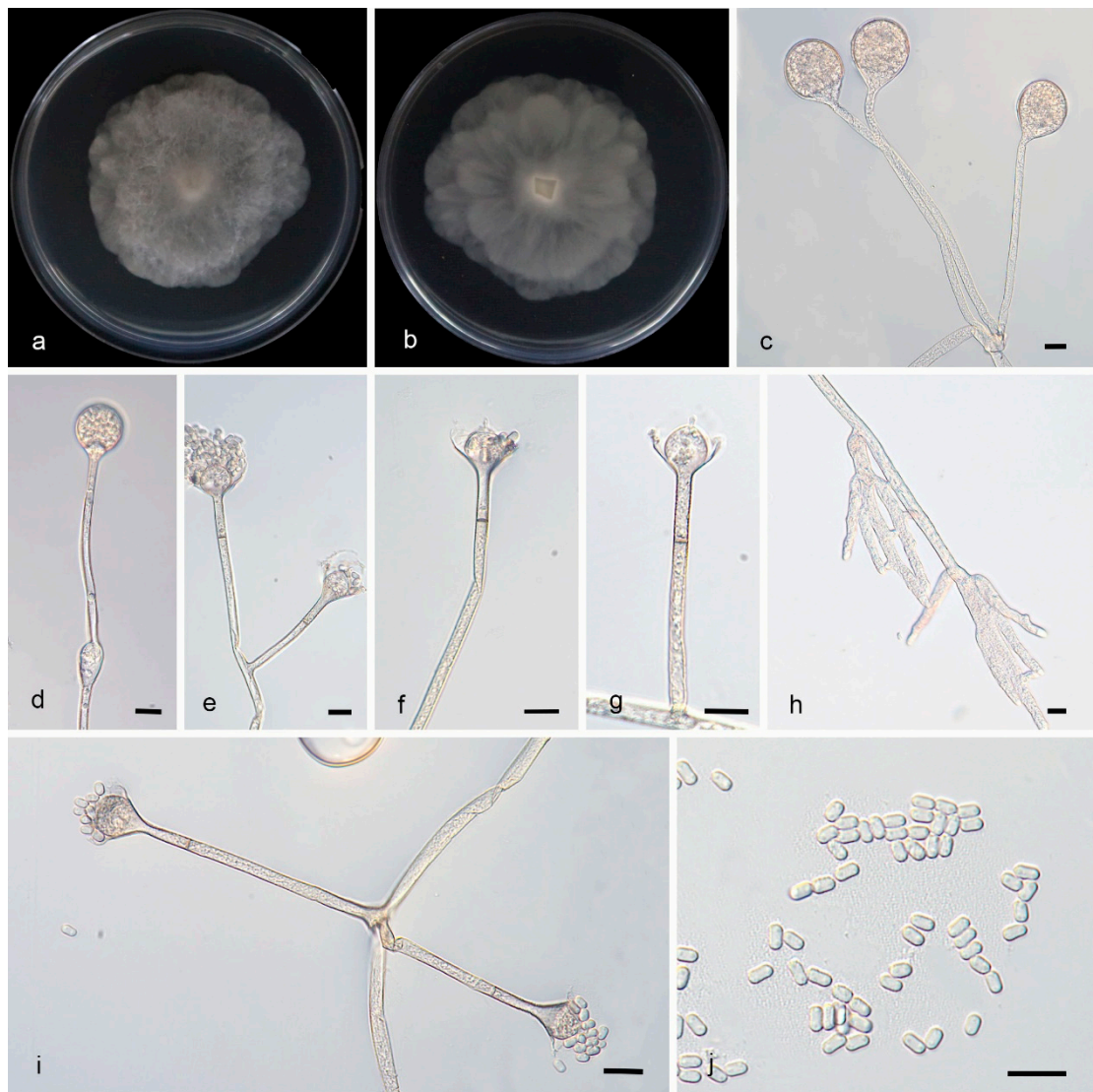


Figure 3. Morphologies of *Absidia digitata* ex-holotype CGMCC 3.29492. (a,b) Colonies on PDA: (a) obverse, (b) reverse; (c,d) sporangia; (e–g,i) columellae; (h) rhizoids; (j) sporangiospores. Scale bars: (c–j) 10 μm .

Additional strains examined. China, Yunnan Province, Xishuangbanna Dai Autonomous Prefecture, Mengla County, Mengla Town, G213 (21°51'58" N, 101°50'77" E, altitude 878.19 m), from soil, 19 May 2025, W. X. Liu, living culture XG18784-2-2.

Notes. On the phylogenetic tree constructed from the concatenated ITS–SSU–LSU–ACT–TEF1 α sequences, strains CGMCC 3.29492 and XG18784-2-2 cluster together to form a single clade with a support value of MLBS/BIPP = 88/1.00 (Figure 1), sister to *Absidia tumida*. Morphologically, the sporangiophores of these two strains were at most three in whorls, producing digitiform rhizoids. However, the sporangiophores of *A. tumida* were at most four in whorls, and rhizoids are root-like. Based on molecular phylogenetic

analyses and morphological observations, these two strains are proposed as a novel species *A. digitata*.

Absidia exilis W.X. Liu, H. Zhao & X.Y. Liu, sp. nov., Figure 4.

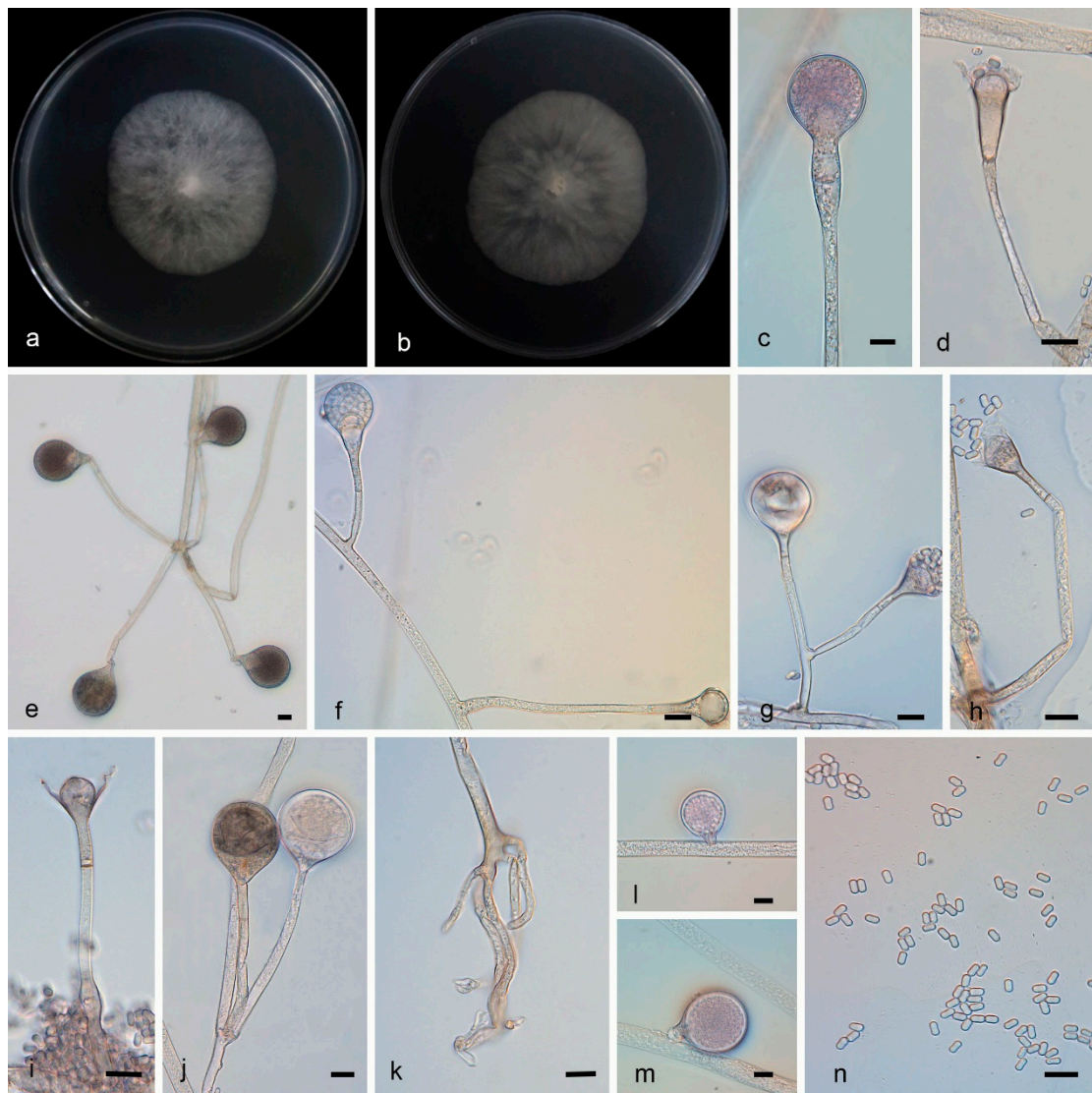


Figure 4. Morphologies of *Absidia exilis* ex-holotype CGMCC 3.29493. (a,b) Colonies on PDA: (a) obverse, (b) reverse; (c,e–g,j,l,m) sporangia; (d,h,i) columellae; (k) rhizoids; (n) sporangiospores. Scale bars: (c–n) 10 µm.

Fungal Names: FN 573312.

Type. China, Chongqing, Xiushan Tujia and Miao Autonomous County, 242 National Road, near Bapai Village. (28°42'33" N, 109°14'17" E, altitude 421.65 m), from soil, 14 November 2025, W. X. Liu, holotype HMAS 354236, ex-holotype living culture CGMCC 3.29493 (=XG21013-11-1)

Etymology: The epithet *exilis* (Lat.) refers to the poorly developed sporangiophores.

Description. Colonies on PDA at 25 °C for 3 d, reaching 47 mm in diameter, fast growing with a rate of 15.7 mm/d. Mycelium grows on the surface of the agar medium. Hyphae initially white, gradually turning tawny-brown with age, aseptate when young and septate at maturity, 2.1–21.1 µm wide. Stolons septate, branched, hyaline or subhyaline, 2.5–9.3 µm wide. Rhizoids well developed, hyaline, root-like. Sporangiohphores arising from stolons, erect or slightly bent, usually accompanied by a swelling, mostly unbranched

or with simple branches, solitary or 2–4 in whorls, 42.0–197.9 µm long and 1.5–6.1 µm wide with a septum 7.1–18.5 µm below the apophysis. Sporangia globose, rarely pyriform, dark brown, sometimes laterally borne on stolons, smooth walled, deliquescent, 15.9–37.1 µm long, 10.5–33.1 µm wide. Columellae globose, subglobose, or rarely ellipsoidal, hyaline, smooth walled, 8.9–20.9 µm long, 7.9–17.6 µm wide. Projections present or absent, pacifier shaped. Apophyses present, funnel shaped, 7.4–17.9 µm high, 2.9–8.0 µm wide at the base and 13.5–29.5 µm wide at the top. Collars present or absent. Sporangiospores ovoid, hyaline, smooth walled, 2.8–4.8 µm long and 1.5–2.7 µm wide. Chlamydospores absent. Zygosporangia unknown.

Additional strains examined. China, Chongqing, Xiushan Tujia and Miao Autonomous County, 242 National Road, near Bapai Village (28°42'33" N, 109°14'17" E, altitude 421.65 m) from soil, 14 November 2025, W. X. Liu, living culture XG21013-11-2.

Notes. On the phylogenetic tree constructed from the concatenated ITS–SSU–LSU–ACT–TEF1α sequences, strains CGMCC 3.29493 and XG21013-11-2 cluster together to form a single clade with a support value of MLBS/BIPP = 73/1.00 (Figure 1), and they are closely related to *Absidia oblongispora* [19]. Morphologically, the sporangiophores of these two strains are commonly swollen and sometimes poorly developed, whereas those of *A. oblongispora* are well developed with no swelling observed. Based on molecular phylogenetic analyses and morphological observations, these two strains are proposed as a novel species *A. exilis*.

Absidia tumida W.X. Liu, H. Zhao & X.Y. Liu, sp. nov., Figure 5.

Fungal Names: FN 573313.

Type. China, Yunnan Province, Xishuangbanna Dai Autonomous Prefecture, Jinghong City, Mengyang Town, G8511 (22°21'66" N, 100°88'59" E, altitude 804.28 m), from soil, 25 July 2025, W. X. Liu, holotype HMAS 354237, ex-holotype living culture CGMCC 3.29491 (=XG18709-9-1)

Etymology: The epithet *tumida* (Lat.) refers to the swollen sporangiophores.

Description. Colonies on PDA at 25 °C for 4 d, reaching 60 mm in diameter, fast growing with a rate of 15 mm/d. Mycelium grows on the surface of the agar medium. Hyphae initially white, gradually turning dark brown with age, aseptate when young and septate at maturity, 3.5–14.2 µm wide. Stolons septate, branched, hyaline or subhyaline, 1.8–5.8 µm wide. Rhizoids well developed, hyaline, root-like. Sporangiophores arising from stolons, erect or slightly bent, sometimes swollen, mostly unbranched or with simple branches, solitary or 2–4 in whorls, 19.5–180.6 µm long, 1.3–5 µm wide with a septum 6.1–18.5 µm below the apophysis. Sporangia globose to pyriform, hyaline or brown, smooth walled, deliquescent, 12.1–37.4 µm long and 13.2–33.5 µm wide. Columellae globose or ovoid, hyaline, smooth walled, 4.2–17.7 µm long and 2.7–15 µm wide. Projections present or absent; if present, distinct and pacifier shaped. Apophyses distinct and conspicuous, funnel shaped, 3.4–15.7 µm high, 1.9–5.1 µm wide at the base, and 8.9–23.3 µm wide at the top. Collars present. Sporangiospores ovoid, hyaline, smooth walled, 2.6–4.7 µm long and 1.6–3.0 µm wide. Chlamydospores not observed. Zygosporangia unknown.

Additional strains examined. China, Yunnan Province, Xishuangbanna Dai Autonomous Prefecture, Jinghong City, Mengyang Town, G8511 (22°21'66" N, 100°88'59" E, altitude 804.28 m), from soil, 25 July 2025, W. X. Liu, living culture XG18709-9-2.

Notes. On the phylogenetic tree constructed from the concatenated ITS–SSU–LSU–ACT–TEF1α sequences, strains CGMCC 3.29491 and XG18709-2-2 cluster together to form a single clade with a support value of MLBS/BIPP = 99/1.00 (Figure 1), sister to *A. digitata*. In terms of morphology, sporangiophores of the two strains formed whorls with a maximum number of four per whorl, and the sporangia are brown. In contrast, the sporangiophores of *A. digitata* were at most three in whorls, and the sporangia are hyaline. Based on molecular

phylogenetic analyses and morphological observations, these two strains are proposed as a novel species *A. tumida*.

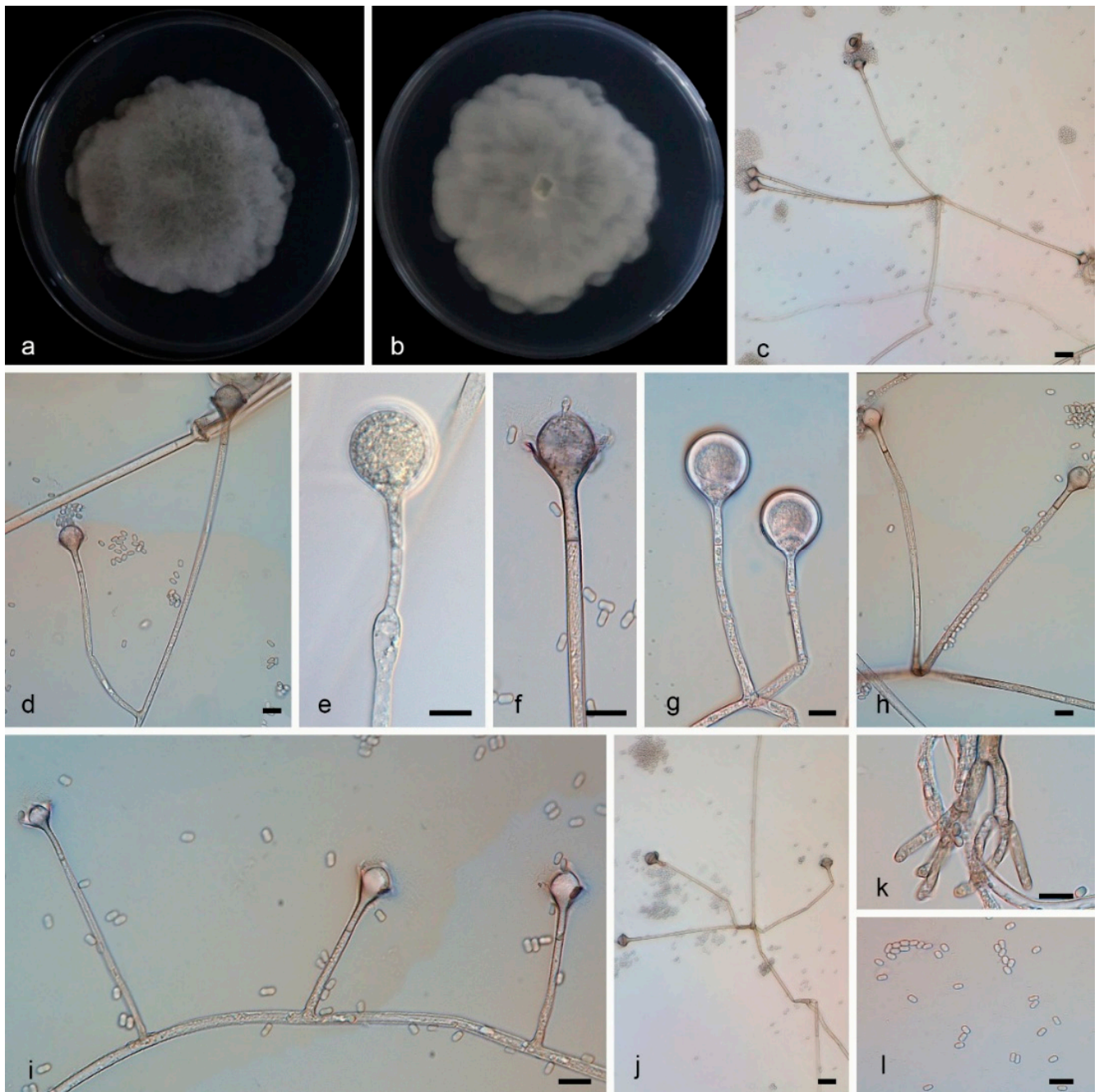


Figure 5. Morphologies of *Absidia tumida* ex-holotype CGMCC 3.29491. (a,b) Colonies on PDA: (a) obverse, (b) reverse; (e,g) sporangia; (c,d,f,h–j) columellae; (k) rhizoids; (l) sporangiospores. Scale bars: (d–i,k–l) 10 µm; (c,j) 20 µm.

4. Discussion

In the multi-locus phylogenetic tree, all these four new species each formed a well-supported clade (Figure 1). A comparative analysis of morphological characteristics between these four novel species and their closely related taxa was conducted (Table 2).

Table 2. Comparisons for morphological characteristics of *Absidia* species proposed in this study and their allies.

Species	Colonies	Sporangiophores	Sporangia	Columellae	Collars	Sporangiospores	References
<i>A. brunneola</i>	PDA: 25 °C 4 d, 73 mm in diameter	unbranched or simple branched, 2–5 in whorls	globose or pyriform, light brown, 12.9–49.6 × 10.9–49.6 µm	globose or subglobose, 7.6–25.3 × 7.1–21.4 µm	present or absent	ovoid, 2.3–4.5 × 1.9–2.5 µm	This study
<i>A. digitata</i>	PDA: 25 °C 4 d, 56 mm in diameter	unbranched or simple branched, 2–3 in whorls	pyriform, rarely globose, hyaline, 19.1–33.5 × 17.7–26.2 µm	globose, 6.6–17.8 × 6.3–12.7 µm	present	oval, 2.4–4.9 × 1.8–3.1 µm	This study
<i>A. exilis</i>	PDA: 25 °C 3 d, 47 mm in diameter	unbranched or simple branched, 2–4 in whorls	globose, rarely pyriform, dark brown, 15.9–37.1 × 10.5–33.1 µm	globose, subglobose, ellipsoidal, 8.9–20.9 × 7.9–17.6 µm	present or absent	ovoid, 2.8–4.8 × 1.5–2.7 µm	This study
<i>A. jiangxiensis</i>	MEA: 27 °C 5 d, 68 mm in diameter	unbranched, single or 2–6 in whorls	globose to pyriform, 16.5–48.0 × 16.5–44.0 µm	subspherical to hemispherical, sometimes conical, 10.0–30.0 × 10.5–34.0 µm	distinct if present	ovoid to cylindrical, sometimes globose to subglobose, 3.5–4.5 × 2.5–3.0 µm	[19]
<i>A. oblongispora</i>	MEA: 27 °C 10 d, 90 mm in diameter	mostly unbranched, rarely simple or monopodial, single or 2–5 in whorls	globose, 13.5–31.0 µm in diameter	conical, hemispherical, 7.0–15.0 × 8.5–16.5 µm	present or absent	oblong, 3.5–4.5 × 2.5–3.0 µm	[19]
<i>A. tumida</i>	PDA: 25 °C 4 d, 60 mm in diameter	unbranched or simple branched, 2–4 in whorls	globose to pyriform, hyaline or brown, 12.1–37.4 × 13.2–33.5 µm	globose, ovoid, 4.2–17.7 × 2.7–15.0 µm	present	ovoid, 2.6–4.7 × 1.6–3.0 µm	This study

Absidia brunneola is sister to *A. jiangxiensis* [19]. Compared with *A. jiangxiensis*, *A. brunneola* exhibits a faster colony growth rate with a daily average of 18.3 mm. Its sporangia are colored light brown and the apophyses are hyaline, whereas the sporangia of *A. jiangxiensis* are hyaline and its apophyses are slightly greenish. *Absidia digitata* and *A. tumida* are sister groups. A comparative analysis revealed that *A. digitata* produces finger-shaped rhizoids with sporangiophores arranged in whorls of up to three at most, which are fewer in number. Projections are always present. In contrast, *A. tumida* has root-like rhizoids, the projections are present or absent, and its sporangia are brown. *Absidia exilis* is closely related to *A. oblongispora* [19]. In comparison, the sporangiophores of *A. exilis* are usually swollen and sometimes poorly developed, and its sporangia are dark brown and globose with a special lateral attachment pattern on the stolons. By contrast, the sporangiophores of *A. oblongispora* are well developed without swellings, and its sporangia are hyaline.

The genus *Absidia* is widely distributed across the globe with the highest prevalence in Europe and extreme rarity in Antarctica [2–4]. It is commonly found in tropical, subtropical, and temperate regions. In China, it is mainly distributed in areas such as Yunnan Province, the Xinjiang Uygur Autonomous Region, and Taiwan Region, and it has also been reported in other countries with similar climates, including Brazil and Thailand [8–10,13,14,18]. This genus inhabits diverse habitats such as soil, herbivore dung, decaying substrates, air, and insect remains [5,9,14,17–19], among which soil is its primary habitat. The four novel species described in this study were all isolated from soil, further confirming that *Absidia* is most extensively distributed in soil environments [53]. Species of *Absidia* can produce various secondary metabolites such as α -galactosidase, steroids, and fatty acids [22–24], and some species are capable of participating in biotransformation [23,25], laying an important foundation for their development and application. The four novel species reported in this study increase the total number of globally recognized *Absidia* species to 66, which enriches

the species diversity of the genus and provides new and significant strain resources for exploring fungal secondary metabolites.

Supplementary Materials: The following supporting information can be downloaded at <https://www.mdpi.com/article/10.3390/microorganisms14020348/s1>, Table S1: GenBank accession numbers of sequences used in this study.

Author Contributions: W.-X.L. performed DNA sequencing, photo editing and manuscript drafting; F.L. conducted data analysis; S.-T.G. and H.-Y.Z. were in charge of soil sample collection; H.Z. participated in study conception and manuscript revision; X.-Y.L. undertook the naming of the new species, participated in study conception and manuscript revision, and provided financial support. All authors have read and agreed to the published version of the manuscript.

Funding: This study was supported by the National Natural Science Foundation of China (Nos. 32170012, 32470004 and 32300011), Ji'nan City's 'New University 20 Policies' Initiative for Innovative Research Teams Project (202228028), Innovative Agricultural Application Technology Project of Jinan City (CX202210) and Key Technological Innovation Program of Shandong Province, China (2022CXGC020710).

Institutional Review Board Statement: Not applicable.

Informed Consent Statement: Not applicable.

Data Availability Statement: All original contributions from this study are contained within the main article and its Supplementary Materials. For further questions, please contact the corresponding authors.

Conflicts of Interest: The authors have no conflicts of interest to declare.

References

1. Tieghem, P. Troisième mémoire sur les Mucorinées. *Ann. Sci. Nat. Bot.* **1878**, *4*, 312–399.
2. Ellis, J.; Hesseltine, C. The genus *Absidia*: Globose-spored species. *Mycologia* **1965**, *57*, 222–235. [CrossRef]
3. Tran, N.T.; Miles, A.K.; Dietzgen, R.G.; Drenth, A. *Phyllosticta capitalensis* and *P. paracapitalensis* are endophytic fungi that show potential to inhibit pathogenic *P. citricarpa* on citrus. *Australas. Plant Pathol.* **2019**, *48*, 281–296. [CrossRef]
4. Větrovský, T.; Morais, D.; Kohout, P.; Lepinay, C.; Algora, G.C.; Awokunle, H.S.; Baldrian, P.; Bahnmann, B.D.; Bílohněd, K.; Brabcová, V.; et al. GlobalFungi, a global database of fungal occurrences from high-throughput-sequencing metabarcoding studies. *Sci. Data* **2020**, *7*, 228. [CrossRef] [PubMed]
5. Zhao, H.; Zhu, J.; Zong, T.K.; Liu, X.L.; Ren, L.Y.; Lin, Q.; Qiao, M.; Nie, Y.; Zhang, Z.D.; Liu, X.Y. Two new species in the family Cunninghamellaceae from China. *Mycobiology* **2021**, *49*, 142–150. [CrossRef]
6. Zong, T.K.; Zhao, H.; Liu, X.L.; Ren, L.Y.; Zhao, C.L.; Liu, X.Y. Taxonomy and phylogeny of four new species in *Absidia* (Cunninghamellaceae, Mucorales) from China. *Front. Microbiol.* **2021**, *12*, 2181. [CrossRef]
7. Zhao, H.; Nie, Y.; Zong, T.K.; Dai, Y.C.; Liu, X.Y. Three new species of *Absidia* (Mucoromycota) from China based on phylogeny, morphology and physiology. *Diversity* **2022**, *14*, 132. [CrossRef]
8. Cordeiro, L.; Lee, H.B.; Nguyen, T.T.T.; Gurgel, L.M.S.; de Azevedo, A.L.C.M. *Absidia bonitoensis* (Mucorales, Mucoromycota), a new species isolated from the soil of an upland Atlantic forest in Northeastern Brazil. *Nova Hedwig.* **2021**, *112*, 241–251. [CrossRef]
9. Cordeiro, T.R.L.; Nguyen, T.T.T.; Lima, D.X.; da Silva, S.B.G.; de Lima, C.F.; Leitão, J.D.; Gurgel, L.M.S.; Lee, H.B.; de Santiago, A.L.M.A. Two new species of the industrially relevant genus *Absidia* (Mucorales) from soil of the Brazilian Atlantic Forest. *Acta Bot. Bras.* **2020**, *34*, 549–558. [CrossRef]
10. Crous, P.W.; Cowan, D.A.; Maggs-Kölling, G.; Yilmaz, N.; Thangavel, R.; Wingfield, M.J.; Noordeloos, M.E.; Dima, B.; Brandrud, T.E.; Jansen, G.M.; et al. Fungal planet description sheets: 1182–1283. *Persoonia* **2021**, *46*, 313–528. [CrossRef]
11. Crous, P.W.; Luangsa-Ard, J.J.; Wingfield, M.J.; Carnegie, A.J.; Hernández-Restrepo, M.; Lombard, L.; Roux, J.; Barreto, R.W.; Baseia, I.G.; Cano-Lira, J.F.; et al. Fungal Planet description sheets: 785–867. *Persoonia* **2018**, *41*, 238–417. [CrossRef] [PubMed]
12. Crous, P.W.; Wingfield, M.J.; Chooi, Y.H.; Gilchrist, C.L.; Lacey, E.; Pitt, J.I.; Roets, F.; Swart, W.J.; Cano-Lira, J.F.; Valenzuela-Lopez, N.; et al. Fungal planet description sheets: 1042–1111. *Persoonia* **2020**, *44*, 301–459. [CrossRef] [PubMed]
13. Leitao, J.D.; Cordeiro, T.R.; Nguyen, T.T.T.; Lee, H.B.; Gurgel, L.M.; de Santiago, A.L.D.A. *Absidia aguabelensis* sp. nov.: A new mucoralean fungi isolated from a semiarid region in Brazil. *Phytotaxa* **2021**, *516*, 83–91. [CrossRef]

14. Lima, D.X.; Cordeiro, T.R.; de Souza, C.A.; de Oliveira, R.J.; Lee, H.B.; Souza-Motta, C.M.; de Santiago, A.L.A. Morphological and molecular evidence for two new species of *Absidia* from Neotropical soil. *Phytotaxa* **2020**, *446*, 61–71. [\[CrossRef\]](#)
15. Urquhart, A.S.; Idnurm, A. *Absidia healeyae*: A new species of *Absidia* (Mucorales) isolated from Victoria, Australia. *Mycoscience* **2021**, *62*, 331–335. [\[CrossRef\]](#)
16. Wanasinghe, D.N.; Phukhamsakda, C.; Hyde, K.D.; Jeewon, R.; Lee, H.B.; Jones, E.G.; Tibpromma, S.; Tennakoon, D.S.; Dissanayake, A.J.; Jayasiri, S.C.; et al. Fungal diversity notes 709–839: Taxonomic and phylogenetic contributions to fungal taxa with an emphasis on fungi on *Rosaceae*. *Fungal Divers.* **2018**, *89*, 1–236. [\[CrossRef\]](#)
17. Zhang, T.Y.; Yu, Y.; Zhu, H.; Yang, S.Z.; Yang, T.M.; Zhang, M.Y.; Zhang, Y.X. *Absidia panacisoli* sp. nov., isolated from rhizosphere of *Panax notoginseng*. *Int. J. Syst. Evol. Microbiol.* **2018**, *68*, 2468–2472. [\[CrossRef\]](#)
18. Hurdeal, V.G.; Gentekaki, E.; Lee, H.B.; Jeewon, R.; Hyde, K.D.; Tibpromma, S.; Mortimer, P.E.; Xu, J. Mucoralean fungi in Thailand: Novel species of *Absidia* from tropical forest soil. *Cryptogam. Mycol.* **2021**, *42*, 39–61. [\[CrossRef\]](#)
19. Zhao, H.; Nie, Y.; Zong, T.K.; Wang, K.; Lv, M.L.; Cui, Y.J.; Tohtirjap, A.; Chen, J.J.; Zhao, C.L.; Wu, F.; et al. Species diversity, updated classification and divergence times of the phylum Mucoromycota. *Fungal Divers.* **2023**, *123*, 49–157. [\[CrossRef\]](#)
20. Kaczmarek, M.B.; Struszczyk-Swita, K.; Li, X.; Szczesna-Antczak, M.; Daroch, M. Enzymatic modifications of chitin, chitosan, and chitoooligosaccharides. *Front. Bioeng. Biotechnol.* **2019**, *7*, 243. [\[CrossRef\]](#)
21. Chen, J.; Fan, F.; Qu, G.; Tang, J.; Xi, Y.; Bi, C.; Sun, Z.; Zhang, X. Identification of *Absidia orchidis* steroid 11- β -hydroxylation system and its application in engineering *Saccharomyces cerevisiae* for one-step biotransformation to produce hydrocortisone. *Metab. Eng.* **2020**, *57*, 31–42. [\[CrossRef\]](#)
22. Davoust, N.; Persson, A. Effects of growth morphology and time of harvesting on the chitosan yield of *Absidia repens*. *Appl. Microbiol. Biotechnol.* **1992**, *37*, 572–575. [\[CrossRef\]](#)
23. Kristanti, R.A.; Zubir, M.M.F.A.; Hadibarata, T. Biotransformation studies of cresol red by *Absidia spinosa* M15. *J. Environ. Manag.* **2016**, *172*, 107–111. [\[CrossRef\]](#) [\[PubMed\]](#)
24. Kitahata, S.; Ishikawa, H.; Miyata, T.; Tanaka, O. Production of rubusoside derivatives by transgalactosylation of various α -galactosidases. *Agric. Biol. Chem.* **1989**, *53*, 2929–2934. [\[CrossRef\]](#)
25. Sordon, S.; Popłowski, J.; Tronina, T.; Huszcza, E. Regioselective O-glycosylation of flavonoids by fungi *Beauveria bassiana*, *Absidia coerulea* and *Absidia glauca*. *Bioorganic Chem.* **2019**, *93*, 102750. [\[CrossRef\]](#) [\[PubMed\]](#)
26. von Arx, J.A. On Mucoraceae s. str. and other families of the Mucorales. *Sydowia* **1982**, *35*, 10–26.
27. Benny, G.L.; Humber, R.A.; Morton, J.B. Zygomycota: Zygomycetes. In *Systematics and Evolution; The Mycota (A Comprehensive Treatise on Fungi as Experimental Systems for Basic and Applied Research)*; McLaughlin, D.J., McLaughlin, E.G., Lemke, P.A., Eds.; Springer: Berlin/Heidelberg, Germany, 2001; Volume 7A, pp. 113–146. [\[CrossRef\]](#)
28. Ashton, H. Ainsworth and Bisby's Dictionary of the Fungi (10th edition). *Ref. Rev.* **2009**, *23*, 42. [\[CrossRef\]](#)
29. Hoffmann, K.; Discher, S.; Voigt, K. Revision of the genus *Absidia* (Mucorales, Zygomycetes) based on physiological, phylogenetic, and morphological characters; thermotolerant *Absidia* spp. form a coherent group *Mycocladiaceae* fam. nov. *Mycol. Res.* **2007**, *111*, 1169–1183. [\[CrossRef\]](#)
30. Hoffmann, K.; Voigt, K. *Absidia parvicida* plays a dominant role in biotrophic fusion parasitism among mucoralean fungi (Zygomycetes): *Lentamyces*, a new genus for *A. parvicida* and *A. zychae*. *Plant Biol.* **2009**, *11*, 537–554. [\[CrossRef\]](#)
31. Hoffmann, K. Identification of the genus *Absidia* (Mucorales, Zygomycetes): A comprehensive taxonomic revision. In *Molecular Identification of Fungi*; Gherbawy, Y., Voigt, K., Eds.; Springer: Berlin/Heidelberg, Germany, 2010; pp. 439–460. [\[CrossRef\]](#)
32. Ding, Z.Y.; Ji, X.Y.; Tao, M.F.; Jiang, Y.; Liu, W.X.; Wang, Y.X.; Meng, Z.; Liu, X.Y. Unveiling species diversity within early-diverging fungi from China IV: Four new species of *Absidia* (Cunninghamellaceae, Mucoromycota). *MycoKeys* **2025**, *119*, 29–46. [\[CrossRef\]](#)
33. Ji, X.Y.; Ding, Z.Y.; Nie, Y.; Zhao, H.; Wang, S.; Huang, B.; Liu, X.Y. Unveiling species diversity within early-diverging fungi from China V: Five new species of *Absidia* (Cunninghamellaceae, Mucoromycota). *MycoKeys* **2025**, *117*, 267–288. [\[CrossRef\]](#) [\[PubMed\]](#)
34. Tao, M.F.; Ding, Z.Y.; Wang, Y.X.; Zhang, Z.X.; Zhao, H.; Meng, Z.; Liu, X.Y. Unveiling species diversity within early-diverging fungi from China II: Three new species of *Absidia* (Cunninghamellaceae, Mucoromycota) from Hainan Province. *MycoKeys* **2024**, *110*, 255–272. [\[CrossRef\]](#) [\[PubMed\]](#)
35. Wang, Y.X.; Ding, Z.Y.; Ji, X.Y.; Meng, Z.; Liu, X.Y. Unveiling species diversity within early-diverging fungi from China VI: Four *Absidia* sp. nov. (Mucorales) in Guizhou and Hainan. *Microorganisms* **2025**, *13*, 1315. [\[CrossRef\]](#)
36. Ji, X.Y.; Ding, Z.Y.; Liu, W.X.; Li, F.; Zhao, H.; Wang, S.; Liu, X.Y. Unveiling species diversity within early-diverging fungi from China X: Three new species in *Linnemannia* and one in *Mortierella*. *MycoKeys* **2025**, *125*, 245–262. [\[CrossRef\]](#)
37. Jiang, Y.; Zhao, H.; Ji, X.Y.; Ding, Z.Y.; Liu, W.X.; Li, F.; Wang, S.; Liu, X.Y.; Meng, Z. Unveiling species diversity within early-diverging fungi from China XI: Nine new species of *Cunninghamella* (Mucoromycota). *Microorganisms* **2025**, *13*, 2508. [\[CrossRef\]](#)
38. Liu, W.X.; Li, F.; Ding, Z.Y.; Ji, X.Y.; Geng, S.T.; Zou, H.Y.; Zhao, H.; Wang, S.; Liu, X.Y. Unveiling Species Diversity Within Early-Diverging Fungi from China XII: Six New Species of *Mucor* (Mucoromycota). *J. Fungi* **2026**, *12*, 98. [\[CrossRef\]](#)

39. Liu, P.; Zou, Y.; Li, S.; Stephenson, S.L.; Wang, Q.; Li, Y. Two new species of dictyostelid cellular slime molds in high-elevation habitats on the Qinghai-Tibet Plateau, China. *Sci. Rep.* **2019**, *9*, 5. [\[CrossRef\]](#)
40. Zou, Y.; Hou, J.; Guo, S.; Li, Z.; Stephenson, S.L.; Pavlov, I.N.; Liu, P.; Li, Y. Diversity of dictyostelid cellular slime molds, including two species new to science, in forest soils of Changbai Mountain, China. *Microbiol. Spectr.* **2022**, *10*, e02402-22. [\[CrossRef\]](#)
41. Li, W.X.; Wei, Y.H.; Zou, Y.; Liu, P.; Li, Z.; Gontcharov, A.A.; Stephenson, S.L.; Wang, Q.; Zhang, S.H.; Li, Y. Dictyostelid cellular slime molds from the Russian Far East. *Protist* **2020**, *171*, 125756. [\[CrossRef\]](#)
42. Corry, J.E.L. Rose bengal chloramphenicol (RBC) agar. In *Progress in Industrial Microbiology*; Elsevier: Amsterdam, The Netherlands, 1995; pp. 431–433.
43. Doyle, J.J.; Doyle, J.L.; Brown, A.H.D. Chloroplast DNA phylogenetic affinities of newly described species in *Glycine* (Leguminosae: Phaseoleae). *Syst. Bot.* **1990**, *15*, 466–471. [\[CrossRef\]](#)
44. Guo, L.D.; Hyde, K.D.; Liew, E.C.Y. Identification of endophytic fungi from *Livistona chinensis* based on morphology and rDNA sequences. *New Phytol.* **2000**, *147*, 617–630. [\[CrossRef\]](#)
45. White, T.J.; Bruns, T.; Lee, S.; Taylor, J. Amplification and direct sequencing of fungal ribosomal RNA genes for phylogenetics. In *PCR Protocols: A Guide to Methods and Applications*; Innis, M.A., Gelfand, D.H., Sninsky, J.J., White, T.J., Eds.; Academic Press, Inc.: New York, NY, USA, 1990; pp. 315–322. [\[CrossRef\]](#)
46. Hurdeal, V.G.; Jones, E.B.G.; Gentekaki, E. *Absidia zygospora* (Mucoromycetes), a new species from nan province, Thailand. *Stud. Fungi* **2023**, *8*, 15. [\[CrossRef\]](#)
47. Rehner, S.A.; Buckley, E. A *Beauveria* phylogeny inferred from nuclear ITS and EF1- α sequences: Evidence for cryptic diversification and links to *Cordyceps* teleomorphs. *Mycologia* **2005**, *97*, 84–98. [\[CrossRef\]](#)
48. Jaklitsch, W.M.; Komon, M.; Kubicek, C.P.; Druzhinina, I.S. *Hypocrea voglmayrii* sp. nov. from the Austrian Alps represents a new phylogenetic clade in *Hypocrea/Trichoderma*. *Mycologia* **2005**, *97*, 1365–1378. [\[CrossRef\]](#) [\[PubMed\]](#)
49. Voigt, K.; Wöstemeyer, J. Reliable amplification of actin genes facilitates deep-level phylogeny. *Microbiol. Res.* **2000**, *155*, 179–195. [\[CrossRef\]](#) [\[PubMed\]](#)
50. Zhang, Z.; Liu, R.; Liu, S.; Mu, T.; Zhang, X.; Xia, J. Morphological and phylogenetic analyses reveal two new species of Sporocadaceae from Hainan, China. *MycoKeys* **2021**, *88*, 171–192. [\[CrossRef\]](#) [\[PubMed\]](#)
51. Stamatakis, A. RAxML Version 8: A tool for phylogenetic analysis and post-analysis of large phylogenies. *Bioinformatics* **2014**, *30*, 1312–1313. [\[CrossRef\]](#)
52. Ronquist, F.; Teslenko, M.; Van Der Mark, P.; Ayres, D.L.; Darling, A.; Höhna, S.; Larget, B.; Liu, L.; Suchard, M.A.; Huelsenbeck, J.P. MrBayes 3.2: Efficient Bayesian phylogenetic inference and model choice across a large model space. *Syst. Biol.* **2021**, *61*, 539–542. [\[CrossRef\]](#)
53. Richardson, M. The ecology of the Zygomycetes and its impact on environmental exposure. *Clin. Microbiol. Infect.* **2009**, *15*, 2–9. [\[CrossRef\]](#)

Disclaimer/Publisher’s Note: The statements, opinions and data contained in all publications are solely those of the individual author(s) and contributor(s) and not of MDPI and/or the editor(s). MDPI and/or the editor(s) disclaim responsibility for any injury to people or property resulting from any ideas, methods, instructions or products referred to in the content.