MYCOBIOLOGY
2020, VOL. 48, NO. 2, 81–94
https://doi.org/10.1080/12298093.2020.1726563

RESEARCH ARTICLE

OPEN ACCESS Check for updates

Five New Records of the Family Aspergillaceae in Korea, *Aspergillus europaeus*, *A. pragensis*, *A. tennesseensis*, *Penicillium fluviserpens*, and *P. scabrosum*

Thuong T. T. Nguyen, Monmi Pangging, Naila Khan Bangash and Hyang Burm Lee

Environmental Microbiology Lab, Department of Agricultural Biological Chemistry, College of Agriculture & Life Sciences, Chonnam National University, Gwangju, Korea

ABSTRACT

During an investigation of the fungi from the Aspergillaceae family obtained from different environmental sources in Korea, we isolated six strains, including CNUFC WJC9-1, CNUFC BPM36-33, CNUFC MSW6, CNUFC ESW1, CNUFC TM6-2, and CNUFC WD17-1. The morphology and phylogeny of these isolates were analyzed based on their partial β-tubulin (*BenA*) and calmodulin (*CaM*) gene sequences. Based on the morphological characteristics and sequence analyses, the isolates CNUFC WJC9-1, CNUFC BPM36-33, CNUFC TM6-2, and CNUFC WD17-1 were identified as *A. europaeus*, *A. pragensis*, *Penicillium fluviserpens*, and *P. scabrosum*, respectively, and isolates CNUFC MSW6 and CNUFC ESW1 were identified as *A. tennesseensis*. To the best of our knowledge, the species *A. europaeus*, *A. pragensis*, *A. tennesseensis*, *P. fluviserpens*, and *P. scabrosum* have not been previously reported in Korea.

ARTICLE HISTORY
Received 19 August 2019
Revised 30 January 2020
Accepted 2 February 2020

KEYWORDS
Aspergillus; Aspergillaceae; morphology; *Penicillium*; phylogeny

1. Introduction

Aspergillus and *Penicillium* are genera within the phylum Ascomycota (class: Eurotiomycetes; order: Eurotiales; family: Aspergillaceae). Species belonging to these two genera are mainly environmental saprobes, which act as decomposers of organic materials [1,2]. They can be found in water, soil, vegetation, fruits, foods, indoor environments, and air [2–4]. Several species are considered beneficial for their commercial, economic, or medical uses; they are used in enzyme production, and in the fermentation of foods such as soy sauce (e.g., *Aspergillus oryzae* and *A. sojae*), cheese (e.g., *Penicillium roqueforti*), and sausages (e.g., *P. nalgiovense*). These species also produce a wide range of secondary metabolites that can be used as drugs and antibiotics [5–7], while others can cause diseases in both humans and animals and can also act as plant pathogens [8–10].

The genus *Aspergillus* was first described by Micheli in 1729 [11] as asexual fungi whose conidiophores resemble an aspergillum. This genus consists of 339 species, which are classified into four subgenera (*Aspergillus*, *Circumdati*, *Fumigati*, and *Nidulantes*) and 20 sections [2,3,12,13]. Identification of *Aspergillus* species has been revised, and now relies on standardized methods based on morphological characteristics, extrolite characterization, and multi-locus DNA sequence analyses. Molecular DNA markers used for *Aspergillus* involved sequencing of the internal transcribed spacer (ITS), calmodulin (*CaM*), β-tubulin (*BenA*), and the RNA polymerase II second largest subunit (*RPB2*) sequences. Due to the well-established *CaM* database, and the relative ease of locus amplification and adequate polymorphism, the *CaM* marker is being used for the identification of *Aspergillus* species [2,14]. About 56 species of *Aspergillus* have been reported from Korea [15]. Recently, a new *Aspergillus* species, *A. koreanus*, has been described [16]. Six more species were recorded recently from Korea, *A. allahabadii* and *A. caninus* from soil, *A. sojae* from meju, and *A. montenegroi*, *A. rhizopodus*, and *A. tabacinus* from tidal mudflats and sea sand [17–20].

The genus *Penicillium* was first described by Link in 1809 [21]. This genus is subdivided into two subgenera (*Aspergilloides* and *Penicillium*) and 26 sections [1,22]. Species of *Penicillium* can be isolated from different environmental sources including air, soil, indoor environments, and food products [1,23]. *Penicillium* species are also identified in a manner similar to *Aspergillus* species, through the use of morphological characteristics, multi-locus DNA sequencing, and extrolite analyses. The *BenA* marker appears to be suitable for their identification [2,14]. This genus includes 354 accepted species according

CONTACT Hyang Burm Lee hblee@jnu.ac.kr

to Visagie et al. [24]. Approximately 100 *Penicillium* species have been reported from Korea [15,16,25–27]. Twelve species of *Penicillium* are currently reported as new from Korea (Source: www.indexfungorum.org as of July 2019).

The aims of this study were to identify five previously unrecorded fungal species in Korea, *A. europaeus*, *A. pragensis*, *A. tennesseensis*, *P. fluviserpens*, and *P. scabrosum* based on morphological and molecular analyses and to contribute to the knowledge about biodiversity in Korea.

2. Materials and methods

2.1. Sampling and isolation

Commercial corn grain was collected from Wanju, Korea in August 2016. Tomato (*Solanum lycopersicum* L.) fruits were purchased from markets in Gwangju, Korea in July 2017. Death moths (Lepidoptera; Sphingidae) were collected from a garden at Chonnam National University located in Gwangju, Korea in January 2018. By-products of rice bran were collected from Daejeon, Korea in August 2017. Water samples were collected from Eulsukdo Island located in Busan and from a reservoir at Wando island, Korea in August 2017 and 2018, respectively. The samples were collected in sterile plastic bags or sterile 50-mL Falcon tubes and transferred to the laboratory.

To isolate fungi from corn grain, 7–10 corn grains were plated directly onto malt extract agar (MEA) (Difco™, Sparks, MD) adjusted with NaCl, glycerol, or glucose to a water activity range of 0.9–0.85. The plates were incubated at 25 °C in the dark for 7–21 d. Hyphal tips were transferred to potato dextrose agar (PDA; Difco™, Sparks, MD) media using the tips of heat-stretched capillary tubes under a stereomicroscope.

For death moths and tomato fruits, samples were examined under a stereomicroscope to detect any fungal infection. Hyphal tips or spore were transferred to PDA media using the tips of heat-stretched capillary tubes. The plates were incubated at 25 °C in the dark for 7 d.

For by-products of rice bran and water samples, we used the serial dilution plating method as described by Nguyen and Lee [28] and Nguyen et al. [29]. Individual colonies with various morphologies were collected, transferred to PDA, and subcultured until pure mycelia were obtained.

For stock storage, pure isolates were maintained in PDA slant tubes in 20% glycerol at −80 °C at the Environmental Microbiology Laboratory Fungarium, Chonnam National University, Gwangju, Korea as CNUFC WJC9-1, CNUFC BPM36-33, CNUFC MSW6, CNUFC ESW1, CNUFC TM6-2, and CNUFC WD17-1. CNUFC WJC9-1, CNUFC BPM36-33, CNUFC MSW6, and CNUFC TM6-2 were also deposited at the Collection of National Institute of Biological Resources (NIBR), Incheon, Korea. CNUFC WD17-1 was deposited at the Culture Collection of the Nakdonggang National Institute of Biological Resources (NNIBR), Sangju, Korea. Information on all isolates used in this study was shown in Table 1.

2.2. Morphological studies

The strains were three-point inoculated onto Czapek yeast extract agar (CYA), MEA, yeast extract sucrose agar (YES), and PDA [25]. The plates were incubated at 25 °C in the dark for 7 d. Fragments of mycelia were removed from the cultures and placed on microscope slides with lactic acid (60%). An Olympus BX51 microscope with differential interference contrast optics (Olympus, Tokyo, Japan) was used to capture digital images. The size and shape of the microscopic features were recorded.

2.3. DNA extraction, PCR, and sequencing

Fungal isolates were cultured on PDA overlaid with cellophane at 25 °C for 5–7 d. Genomic DNA was extracted using the Solg TM Genomic DNA preparation Kit (Solgent Co. Ltd., Daejeon, Korea). The *BenA* was amplified using the primer pairs Bt2a/Bt2b, and T10/Bt2b [30]. *CaM* gene was amplified using the primer pairs CMD5/CMD6, and CF1/CF4 [31,32], respectively. PCR amplification was

Table 1. Information on all isolates used in this study.

Species	Culture no.	Substrate	Geographic origin
A. europaeus	CNUFC WJC9-1	Corn grain	Wanju, Korea (35°40′0.12″N 126°00′0.00″E)
A. pragensis	CNUFC BPM36-33	By-product rice bran	Daejeon, Korea (36°19′17.00″ N 127°25′ 10.99″E)
A. tennesseensis	CNUFC MSW6	Death moth	Gwangju, Korea (35°09′60.00″N 126°54′ 59.99″E)
A. tennesseensis	CNUFC ESW1	Sea water	Eulsukdo, Busan, Korea (35°06′10.01″N 129°02′25.01″E)
P. fluviserpens	CNUFC TM6-2	Tomato fruit	Gwangju, Korea (35°09′60.00″N 126°54′ 59.99″E)
P. scabrosum	CNUFC WD17-1	Freshwater	Wando, Korea (34°19′1.20″ N 126°45′0.00″ E)

Table 2. Accession numbers for fungal strains used for the phylogenetic analysis.

Species	Collection no.	GenBank accession no. BenA	CaM
Aspergillus amoenus	NRRL 4838 (T)	EF652304	EF652392
A. austroafricanus	NRRL 233 (T)	JN853963	JN854025
A. brunneo-uniseriatus	NRRL 4273 (T)	EF652123	EF652138
A. campestris	CBS 348.81 (T)	EU014091	EF669535
A. candidus	CBS 566.65 (NT)	EU014089	EF669550
A. chrysellus	NRRL 5084 (T)	EF652109	EF652136
A. creber	NRRL 58592 (T)	JN853980	JN854043
A. cvjetkovicii	NRRL 227 (T)	EF652264	EF652352
A. dimorphicus	NRRL 3650 (T)	EF652111	EF652135
A. dobrogensis	CBS 143370 (T)	LT627027	LT558722
A. europaeus	CBS 140936	LN909018	LN909019
A. europaeus	CBS 134392	LN909004	LN909005
A. europaeus	NRRL 66252 (T)	LN909006	LN909007
A. europaeus	**CNUFC WJC9-1**	**MN337608**	**MN894576**
A. europaeus	**CNUFC WJC9-2**	**MN337609**	**MN894577**
A. flaschentraegeri	NRRL 5042 (T)	EF652113	EF652130
A. flavus	NRRL 1957 (T)	EF661485	EF661508
A. fructus	NRRL 239 (T)	EF652273	EF652361
A. fruticans	CBS 486.65 (T)	EF652307	EF652395
A. griseoaurantiacus	CBS 138191 (T)	KJ775086	KJ775357
A. jensenii	NRRL 58600	JN854007	JN854046
A. penicillioides	NRRL 4548 (T)	EF651928	EF652024
A. pragensis	CBS 135591 (T)	HE661604	FR751452
A. pragensis	CCF 4654	HG916673	HG916680
A. pragensis	**CNUFC BPM36-33**	**MN337604**	**MN337610**
A. pragensis	**CNUFC BPM36-34**	**MN337605**	**MN337611**
A. protuberus	NRRL 3505 (T)	EF652284	EF652372
A. pseudonomius	NRRL 3353	EF661495	EF661529
A. pulvinus	CBS 578.65 (T)	FJ531013	FJ531086
A. puulaauensis	NRRL 35641 (T)	JN853979	JN854034
A. restrictus	NRRL 154 (T)	EF651880	EF652029
A. subalbidus	CBS 567.65 (T)	KP987050	EF669551
A. subversicolor	NRRL 58999 (T)	JN853970	JN854010
A. sydowii	NRRL 250 (T)	EF652274	EF652362
A. tabacinus	NRRL 4791 (T)	EF652302	EF652390
A. taichungensis	IBT 19404 (T)	EU076297	HG916679
A. tamarii	NRRL 20818	EF661474	EF661526
A. tritici	CBS 266.81 (T)	EU076293	HG916678
A. tennesseensis	NRRL 13150 (T)	JN853976	JN854017
A. tennesseensis	LEMI875	KJ766999	KJ766995
A. tennesseensis	LEMI917	KJ766998	KJ766994
A. tennesseensis	**CNUFC ESW1**	**MN337606**	**MN337612**
A. tennesseensis	**CNUFC MSW6**	**MN337607**	**MN337613**
A. venenatus	NRRL 13147 (T)	JN854003	JN854014
A. versicolor	CBS 583.65 (T)	EF652266	EU076368
A. wentii	NRRL 375 (T)	EF652106	EF652131
Penicillium alfredii	CBS138224 (T)	KJ775177	KJ775411
P. atrovenetum	CBS241.56 (T)	JX140944	KJ867004
P. astrolabium	CBS122427 (T)	DQ645793	DQ645808
P. brevicompactum	NRRL 2011	DQ645784	AY484817
P. cinnamopurpureum	NRRL162 (T)	EF626948	EF626949
P. colei	NRRL13013 (T)	KF932926	KF932942
P. coralligerum	CBS123.65 (T)	KJ834444	KJ866994
P. crystallinum	CBS479.65 (T)	EF669682	FJ530973
P. cvjetkovicii	NRRL35841 (T)	KF932931	KF932948
P. ellipsoideosporeum	CBS112493 (T)	JQ965104	AY678559
P. fluviserpens	NRRL35838 (T)	KF932929	KF932946
P. fluviserpens	NRRL35844	KF932933	KF932950
P. fluviserpens	**CNUFC TM6-2**	**MN894578**	**MN317092**
P. fluviserpens	**CNUFC TM6-3**	**MN894579**	**MN317093**
P. gravinicasei	NRRL66733 (T)	MG600565	MG600570
P. idahoense	NRRL5274 (T)	EF626953	EF626954
P. incoloratum	CBS101753 (T)	KJ834457	KJ866984
P. jamesonlandense	CBS102888 (T)	DQ309448	KJ866985
P. janczewskii	CBS221.28 (T)	KJ834460	KJ867001
P. kojigenum	CBS345.61 (T)	KJ834463	KJ867011
P. lanosum	CBS106.11 (T)	DQ285627	FJ530974
P. lemhiflumine	NRRL35843 (T)	KF932932	KF932949
P. lenticrescens	CBS138215 (T)	KJ775168	KJ775404
P. malacaense	NRRL35754 (T)	EU427268	KJ866997
P. mexicanum	CBS138227 (T)	KJ775178	KJ775412
P. monsgalena	NRRL22302 (T)	KF932927	KF932943
P. monsserratidens	NRRL35884 (T)	KF932930	KF932947
P. nodulum	CBS227.89 (T)	KJ834475	KJ867003
P. novae-zeelandiae	CBS137.41 (T)	KJ834477	KJ866996
P. paradoxum	NRRL2162 (T)	EF669683	EF669692
P. parvulum	NRRL35504 (T)	EF506218	EF506225
P. pusillum	NRRL2498 (T)	KF932925	KF932941
P. raistrickii	CBS261.33 (T)	KJ834485	KJ867006
P. ribeum	CBS127809 (T)	DQ285625	KJ866995
P. sajarovii	CBS277.83 (T)	KJ834489	KJ867007
P. salmoniflumine	NRRL35837 (T)	KF932928	KF932945
P. scabrosum	CBS683.89 (T)	DQ285610	FJ530987
P. scabrosum	**CNUFC WD17-1**	**MN317088**	**MN317090**
P. scabrosum	**CNUFC WD17-2**	**MN317089**	**MN317091**
P. shennangjianum	CBS228.89 (T)	KJ834491	AY678561
P. simile	CBS129191 (T)	FJ376595	GQ979710
P. soppii	CBS226.28 (T)	DQ285616	KJ867002
P. swiecickii	CBS119391 (T)	KJ834494	KJ866993
P. virgatum	CBS114838 (T)	KJ834500	KJ866992
Talaromyces flavus	NRRL2098 (T)	EU021663	EU021694

Bold letters indicate isolates and accession numbers determined in our study.
CBS: Westerdijk Fungal Biodiversity Institute, Utrecht, The Netherlands; CCF: Culture Collection of Fungi, Charles University, Prague, Czech Republic; CNUFC: Chonnam National University Fungal Collection (Gwangju, South Korea); NRRL: ARS culture collection, Peoria, IL, USA; T: ex-type strain; NT: neo-type.

performed according to the conditions described in Visagie et al. [24] and Yilmaz et al. [33]. PCR products were purified with an Accuprep PCR Purification Kit (Bioneer Corp., Daejeon, South Korea). Sequencing was performed using the same primers pairs and analyzed using the ABI PRISM 3730XL Genetic Analyzer (Applied Biosystems, Foster City, CA).

2.4. Phylogenetic analysis

Sequences for selected strains were aligned with reference sequences obtained from GenBank using Clustal_X version 2.1 [34] and were edited manually with Bioedit version 7.2.6.0 [35]. Maximum likelihood (ML) phylogenies were constructed using MEGA version 6 [36]. The sequence of *Talaromyces flavus* was used as an out group. The sequences of the isolates in this study were deposited in the NCBI database under the accession numbers shown in Table 2.

3. Results

3.1. Phylogenetic analysis

A BLASTn search of the BenA regions of CNUFC WJC9-1, CNUFC BPM36-33, CNUFC ESW1, CNUFC TM6-2, and CNUFC WD17-1 showed similarities of 100% (405/405 bp), 100% (447/447 bp), 100% (399/399 bp), 99.6% (559/561 bp), and 99.6% (551/553 bp), with *A. europaeus* (LN909018), *A. pragensis* (HG916673), *A. tennesseensis* (KJ76999), *P. fluviserpens* (KF932929), and *P. scabrosum* (DQ285610), respectively. Similarly, CaM regions of

CNUFC WJC9-1, CNUFC BPM36-33, CNUFC ESW1, CNUFC TM6-2, and CNUFC WD17-1, showed similarities of 99.6% (507/509 bp), 100% (590/590 bp), 100% (642/642 bp), 100% (632/632 bp), and 99.3% (421/424 bp), with *A. europaeus* (LN909019), *A. pragensis* (FR751452), *A. tennesseensis* (KJ766995), *P. fluviserpens* (KF932946), and *P. scabrosum* (FJ530987), respectively. ML gene trees for BenA and CaM revealed that the strains, CNUFC WJC9-1, CNUFC BPM36-33, CNUFC ESW1, CNUFC TM6-2, and CNUFC WD17-1 were identical to *A. europaeus*, *A. pragensis*, *A. tennesseensis*, *P. fluviserpens*, and *P. scabrosum*, respectively (Figures 1 and 2).

3.2. Taxonomy

3.2.1. Taxonomy of CNUFC WJC9-1

A. europaeus Hubka, A. Nováková, Samson, Houbraken, Frisvad, M. Kolařík, Plant Systematics and Evolution 302: 645 (2016) (Table 3; Figure 3).

Colony characteristics: Colonies on CYA were floccose, pale yellow to dark brown, with yellowish white mycelium, no soluble pigment, moderate sporulation, reverse yellow, and reached 11–13 mm in diameter after 7 d at 25 °C. On MEA, colonies were floccose, with a raised colony center, no soluble pigment, the reverse was pale yellow, and reached 20–22 mm in diameter after 7 d at 25 °C. On PDA, colonies were plane, floccose in the colony center, with strong sporulation, no soluble pigment, reverse light olive, and reached 21–23 mm in diameter after 7 d at 25 °C.

Micromorphology: Conidiophores were smooth-walled, 6.5–11.5 µm wide. Vesicles were pyriform or globose, and were 11–32 µm in diameter. Metulae were broadened toward the top, 6–13.5 × 3–4.5 µm. Phialides were ampulliform, 6–9.2 × 2.4–3.9 µm. Conidia were globose to subglobose, roughened, and yellow-brown to brown at maturity, 3.1–4.6 × 3.2–4.2 µm.

3.2.2. Taxonomy of CNUFC BPM36-33

A. pragensis V. Hubka, J. C. Frisvad & M. Kolařík, Medical Mycology 52: 565–576 (2014) (Table 4; Figure 4).

Colony characteristics: Colonies on CYA were white, with a floccose surface, reverse light brown, and no diffusible pigment, and reached 10–13 mm in diameter after 7 d at 25 °C. On MEA, colonies were pinkish white, with a floccose surface, slightly raised at the center, no diffusible pigment, the reverse was puff brown, and reached 5–8 mm in diameter after 7 d at 25 °C. On PDA, colonies were white, slightly raised at the center, no sporulation, and reached 4–6 mm in diameter after 7 d at 25 °C.

Micromorphology: Conidiophores were smooth-walled, and were 89–400 µm in diameter. Vesicles were pyriform or globose, and were 9–23 µm in diameter. Metulae were cylindrical or wedge-shaped, 3.8–11.4 × 2.6–3.3 µm. Phialides were ampulliform, 4–8 × 2.6–4.1 µm. Conidia were globose with rough echinulate walls, and were 2.6–3.4 µm in diameter.

3.2.3. Taxonomy of CNUFC ESW1

A. tennesseensis Jurjević, S.W. Peterson & B.W. Horn, IMA Fungus 3 (1): 73 (2012) (Table 5; Figure 5).

Colony characteristics: Colonies on CYA were radially sulcate, centrally raised, pea-green in color, with central sporulation, no soluble pigments, and exudates were observed in some isolates, the reverse was brown-yellow in color, and reached 19–22 mm in diameter after 7 d at 25 °C. On MEA, colonies were plane, mycelia green white at the margins to dark green color at the centers, no soluble pigments or exudates, reverse gray-green or pale lemon yellow, and reached 12–14 mm in diameter after 7 d at 25 °C. On YES, colonies were floccose, mycelial pale white at margins to gray-green at the center, centrally sparse sporulation, no soluble pigments, no exudates, reverse dull orange to pale brown, and reached 23–26 mm in diameter after 7 d at 25 °C.

Micromorphology: Conidial heads biseriate, conidiophores greenish, smooth-walled stipes typically yellow to brown, sometimes hyaline to brownish shades, 18.5–413.5 × 4.2–7.3 µm. Vesicles were pyriform, 7.5–17.6 µm in diameter. Metulae were 4–7.1 × 2.4–4.1 µm. Phialides forming chains resembling penicillate fructifications, 5.5–11.4 × 2.1–3 µm. Conidia were globose, spherical, and finely roughened, and were 2.4–5.1 µm in diameter.

3.2.4. Taxonomy of CNUFC TM6-2

P. fluviserpens S. W. Peterson, Z. Jurjevic & J.C. Frisvad, PloS One 10: 1–28 (2015) (Table 6; Figure 6).

Colony characteristics: Colonies on CYA were velutinous, pale gray-green, radially sulcate at margins and sulcate to wrinkled centrally, white mycelium, abundant sporulation, no soluble pigment, reverse pale caramel brown, and reached 21–23 mm in diameter after 7 d at 25 °C. On MEA, colonies were calendine green, velutinous, lightly sulcate, with moderate sporulation, reverse was pale green, and reached 24–25 mm in diameter after 7 d at 25 °C. On PDA, colonies were moderately deep, with white mycelia, pale gray-green at the center, no sporulation, no soluble pigment, and reached 23–27 mm in diameter after 7 d at 25 °C.

Micromorphology: Conidiophores were monoverticillate, 17–110 µm. Phialides were ampulliform,

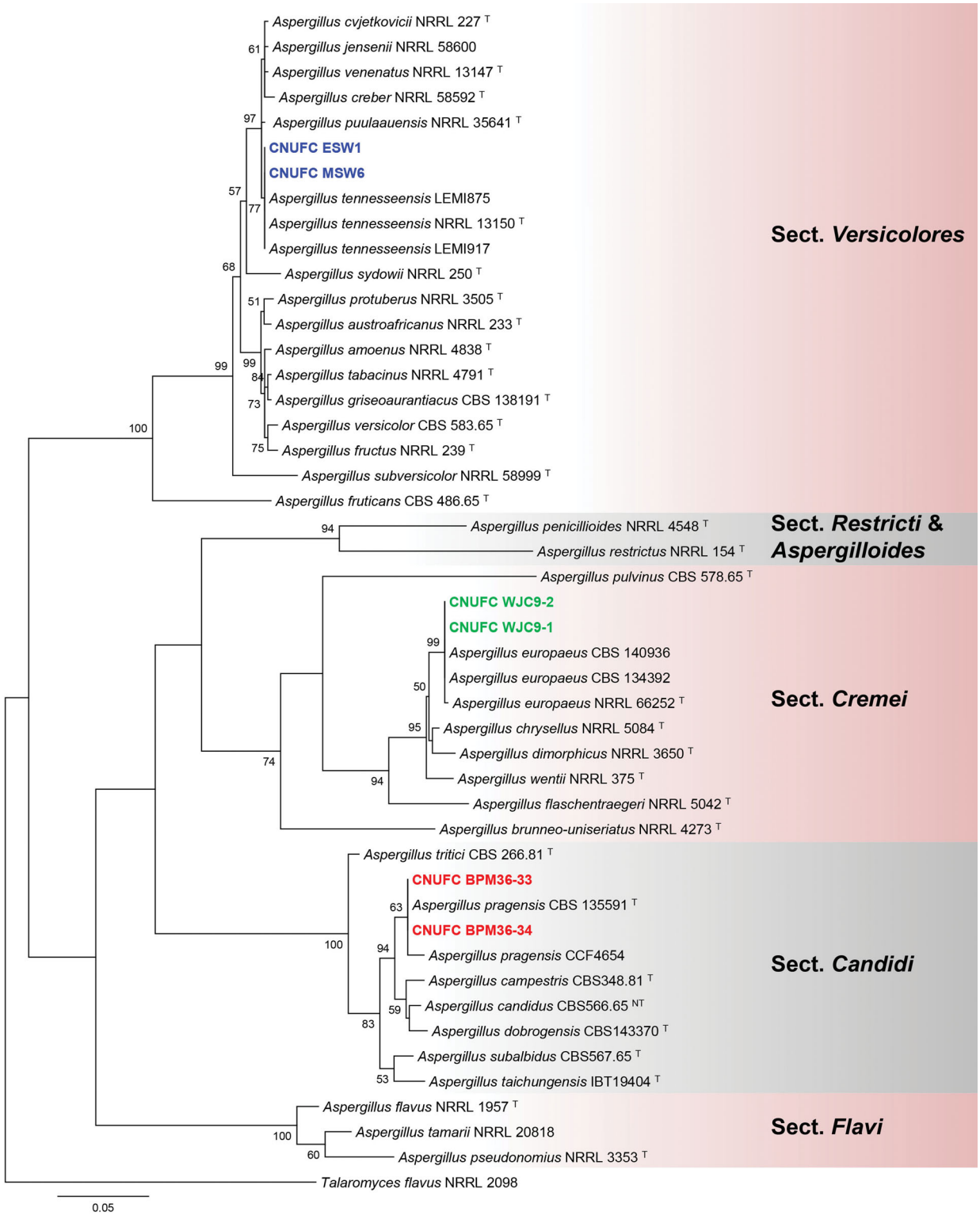

Figure 1. Phylogenetic tree of *Aspergillus europaeus* CNUFC WJC9-1 and CNUFC WJC9-2, *A. pragensis* CNUFC BPM36-33 and CNUFC BPM36-34, *A. tennesseensis* CNUFC ESW1 and CNUFC MSW6, and related species based on maximum likelihood analysis of the combined *BenA* and *CaM* sequences. The sequence of *Talaromyces flavus* was used as an out group. Numbers at the nodes indicate the bootstrap values (>50%) from 1000 replicates. The bar indicates the number of substitutions per nucleotide. The study isolates are shown in bold blue, green, and red.

5.5–9 × 2–3.2 µm. Conidia were sub-spherical to ellipsoidal, and were 2.5–3.3 µm in diameter.

3.2.5. Taxonomy of CNUFC WD17-1

P. scabrosum Frisvad, Samson & Stolk, Persoonia 14 (2): 177 (1990) (Table 7; Figure 7).

Colony characteristics: Colonies on CYA were plane, radially wrinkled, with good sporulation, white or green mycelium, green conidia, no soluble pigment, reverse bright yellow, and reached 13–16 mm in diameter after 7 d at 25 °C. On MEA, colonies were velutinous, with good sporulation,

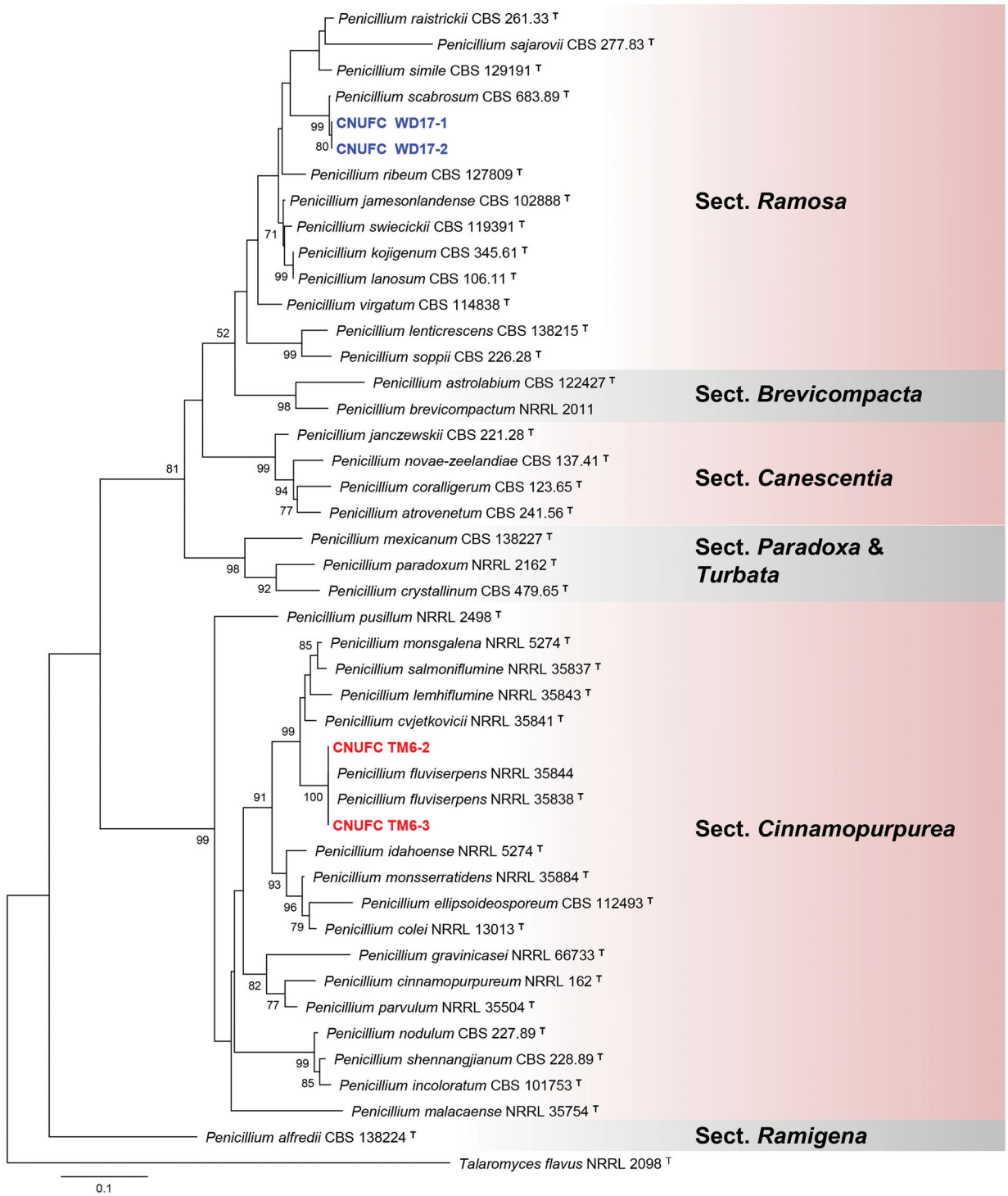

Figure 2. Phylogenetic tree of *Penicillium fluviserpens* CNUFC TM6-2 and CNUFC TM6-3, *P. scabrosum* CNUFC WD17-1 and CNUFC WD17-2 and related species, based on the maximum likelihood analysis of the combined *BenA* and *CaM* sequences. Sequence of *Talaromyces flavus* was used as an out group. Numbers at the nodes indicate the bootstrap values (>50%) from 1000 replicates. The bar indicates the number of substitutions per nucleotide. The study isolates are shown in bold blue and red.

green conidia, no soluble pigments, radially sulcate at margins, and the reverse was yellow, and reached 14–17 mm in diameter after 7 d at 25 °C. On YES, colonies were radially wrinkled, centrally floccose, no soluble pigment, reverse yellow, and reached 24–27 mm in diameter after 7 d at 25 °C.

Micromorphology: Conidiophores were biverticillate, 2.9–4.5 µm. Metulae were 10.3–18.5 × 2.3–4.1 µm, 2–4. Phialides were ampulliform, 4–8 per metula, 8.6–11.8 × 2.1–3.1 µm. Conidia were globose to subglobose, and were 2.3–3.2 µm in diameter.

Table 3. Morphological characteristics of CNUFC WJC9-1 compared with those of the reference strain, *Aspergillus europaeus*.

Character	CNUFC WJC9-1	*Aspergillus europaeus*[a]
Conidiophores	Smooth-walled, 6.5–11.5 µm wide	300–750 × 7–13(−15) µm
Vesicle	Pyriform or globose, 11–32 µm diam.,	Pyriform or globose, 11–44 µm diam.,
Metuale	Broadening toward the top, 6–13.5 × 3–4.5 µm	Broadening toward the top, 6–25 × 5–9 µm
Phialides	Ampulliform, 6–9.2 × 2.4–3.9 µm	Ampuliform, 6–11.5 × 3–6 µm
Conidia	Globose to subglobse, 3.1–4.6 × 3.2–4.2 µm	Globose to subglobse, 3.5–5 × 3–4.5 µm

[a]From the description by Hubka et al. [37].

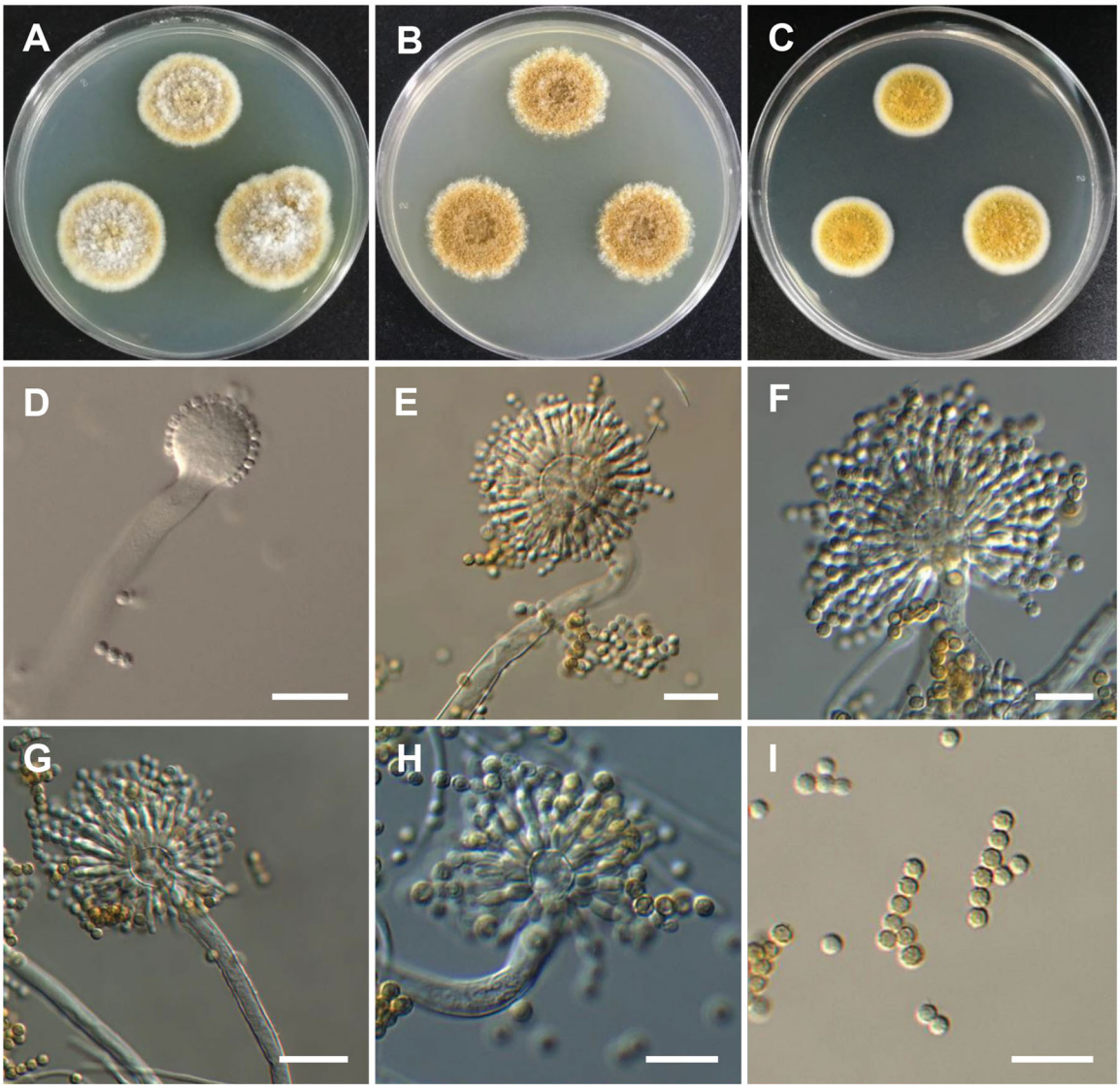

Figure 3. Morphology of *Aspergillus europaeus*. (A) Colonies on Potato dextrose agar (PDA); (B) Colonies on Blakeslee's malt extract agar (MEA); (C) Czapek yeast autolysate agar (CYA); (D–H) Conidiophores; (I) Conidia (scale bars: D–I = 20 µm).

4. Discussion

Species of *Aspergillus* and *Penicillium* belonging to the sections *Cremei*, *Candidi*, *Versicolores*, *Cinnamopurpurea*, and *Ramosa*, were discovered during a survey on the biodiversity of Aspergillaceae inhabiting different substrates. Here, three *Aspergillus* and two *Penicillium* species in five different sections were identified and compared to their most closely related species.

Analysis of the combined *BenA* and *CaM* datasets showed that the strains CNUFC WJC9-1 and CNUFC WJC9-2 were clustered within the same clade as *A. europaeus* NRRL 66252 (ex-type strain), belonging to the section *Cremei* (Figure 1). The isolate CNUFC WJC9-1 is morphologically similar to *A. europaeus* previously described by Hubka et al. [37] with respect to producing globose to subglobose coarsely roughened conidia, with a yellow-brown to brown color at maturity. However, the sizes of metuale reported in the literature (6–25 × 5–9 µm) are bigger than those of our isolate. *Aspergillus* section *Cremei* (known as the

Table 4. Morphological characteristics of CNUFC BPM36-33 compared with those of the reference strain *Aspergillus pragensis*.

Character	CNUFC BPM36-33	*Aspergillus pragensis*[a]
Conidiophores	Smooth-walled, 89–400 µm long	Hyaline, smooth-walled, usually 90–600 µm (but up to 1200 µm)
Vesicle	Pyriform or globose, 9–23 µm	Predominantly globose, 9–21 µm
Metuale	Cylindrical or wedge-shaped, measured 3.8–11.4 × 2.6–3.3 µm	Wedge-shaped or cylindrical, 4.5–10.5 × 3.5–5.5 µm
Phialides	Ampulliform, 4–8 × 2.6–4.1 µm	Ampuliform, 6–8.5 × 2.5–3.5 µm
Conidia	Globose with rough echinulate walls, 2.6–3.4 µm	Globose, 2.5–3.5 µm, smooth

[a]From the description by Hubka et al. [41].

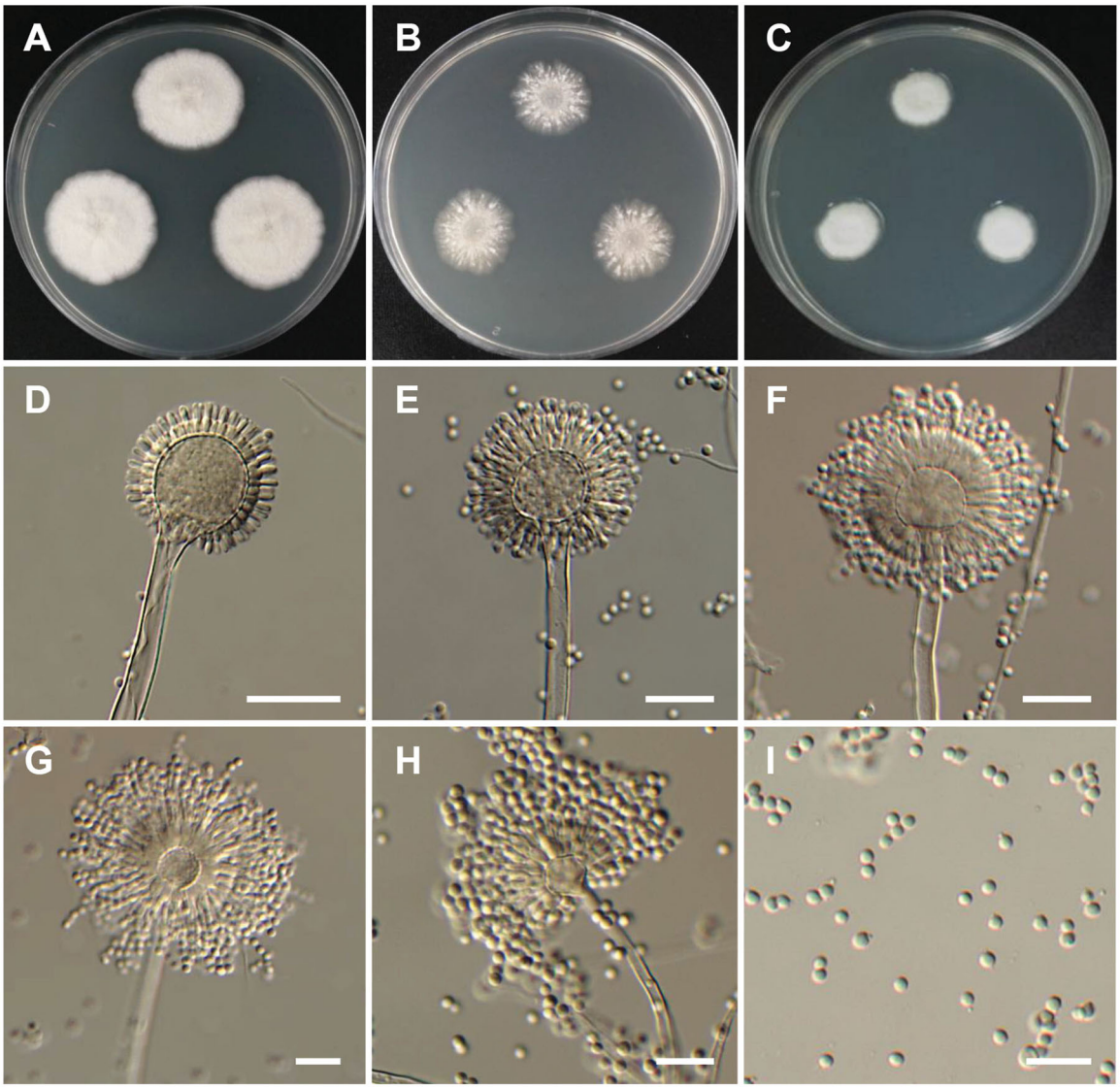

Figure 4. Morphology of *Aspergillus pragensis*. (A) Colonies on Czapek yeast autolysate agar (CYA); (B) Colonies on Blakeslee's malt extract agar (MEA); (C) Colonies on Potato dextrose agar (PDA); (D–H) Conidiophores; (I) Conidia (scale bars: D–I = 20 µm).

A. cremeus group) was first described by Raper and Fennell [38] and included five species, *A. itaconicus*, *A. flaschentraegeri*, *A. stromatoides*, *A. chrysella*, and *A. cremea*. The species belonging to this section are characterized by their yellowish-brown to brown or gray-green colony color, with biseriate conidial heads and long conidiophores [2]. Several fungal species belonging to the section *Cremi* are frequently found in soil and foods where they can cause spoilage of cereals and nuts; they are found less frequently in indoor environments or in clinical material [37,39]. *A. europaeus* was earlier reported from soil samples in European caves and several steppe-like localities in the Czech Republic [37]. In this study, *A. europaeus* was isolated from corn grains. *A. europaeus* shares the production of 3-O-methylsulochrin and 3-O-demethylsulochrin with *A. wentii* [37,40].

The strains CNUFC BPM36-33 and CNUFC BPM36-34 reside in a well-supported clade with *A. pragensis* CBS 135591 (ex-type strain), belonging to the section *Candidi* (Figure 1). The morphological characteristics of the isolate *A. pragensis* in this study were similar to those previously described

Table 5. Morphological characteristics of CNUFC ESW1 compared with those of the reference strain *Aspergillus tennesseensis*.

Character	CNUFC ESW1	*Aspergillus tennesseensis*[a]
Conidiophores	Greenish smooth walled, yellow to brown, sometimes hyaline to brownish shades 18.5–413.5 × 4.2–7.3 µm	Smooth walled, hyaline to yellowish with brownish shades (35–)100–300(–400) × 4–7 µm
Vesicle	Pyriform, 7.5–17.6 µm	Pyriform (7–)10–16(–18) µm
Metulae	4–7.1 × 2.4–4.1 µm	(4–)6– (–8) × 2.5–4 µm
Phialides	Forming chains resembling penicillate fructifications, 5.5–11.4 × 2.1–3 µm	Fragmentary heads resembling penicillate fructifications, 5–8(–11) × 2–3 µm
Conidia	Conidia globose, spherical, finely roughened, 2.4–5.1 µm	Spherical to subspherical, ellipsiodal to pyriform (2.5–)3–4(–8) µm, roughened wall

[a]From the description by Jurjevic et al. [50].

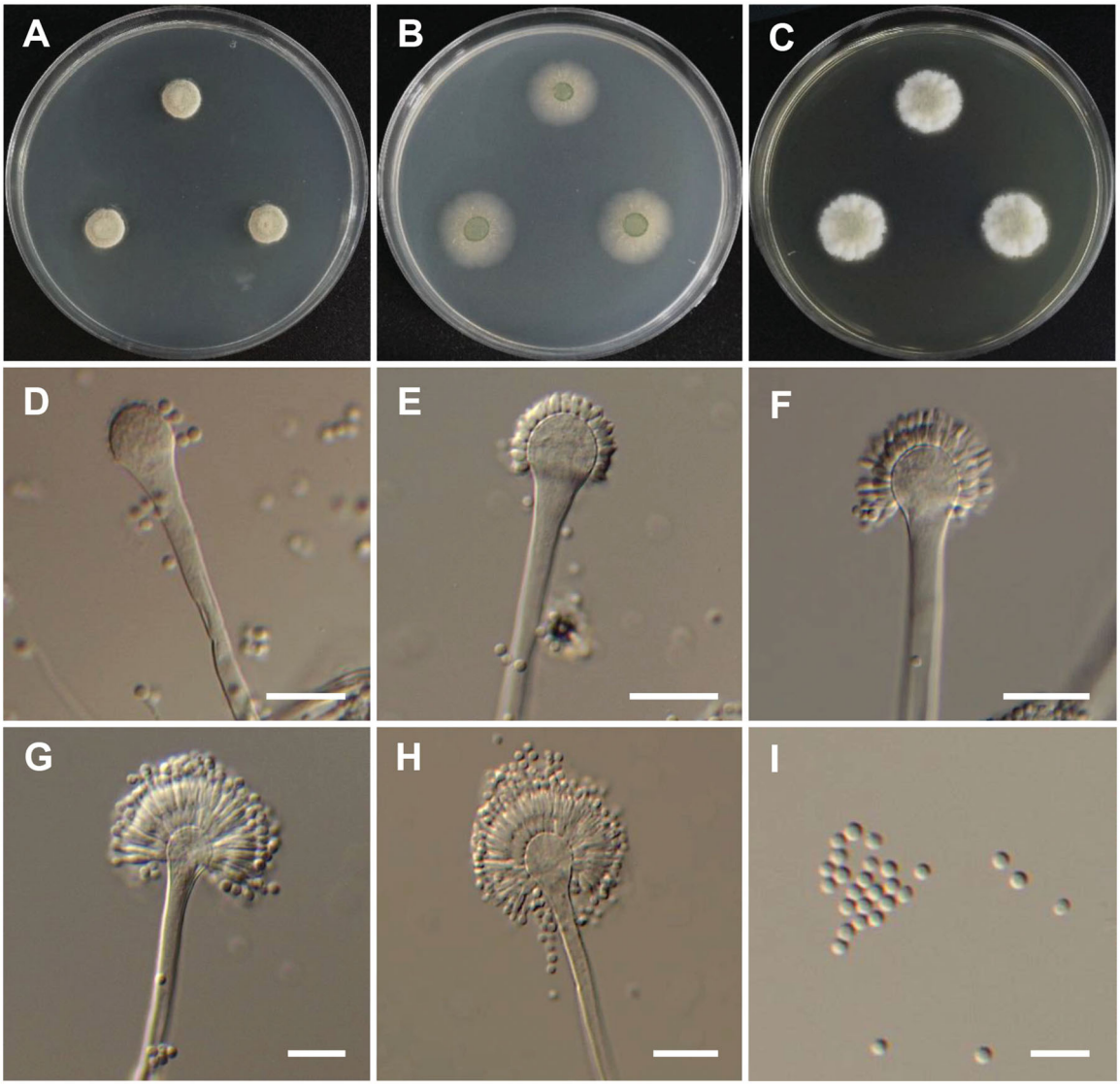

Figure 5. Morphology of *Aspergillus tennesseensis*. (A) Colonies on Czapek yeast autolysate agar (CYA); (B) Colonies on Blakeslee's malt extract agar (MEA); (C) Colonies on yeast malt extract agar (YES); (D–H) Conidiophores. (I) Conidia (scale bars: D–I = 20 µm).

by Hubka et al. [41]. Colony diameter on CYA was similar to that of the previously described *A. pragensis* type species (CYA: 22–24 mm after 14 d); however, differences in colony diameter were observed on MEA (MEA: 16–18 mm after 14 d). No growth was observed for the isolate CNUFC BPM36-33 on MEA at 37 °C. The *Aspergillus* section *Candidi* was established by Gams et al. [42] for the previous *A. candidus* group based on the criterion proposed by Thom and Raper [43]. Currently, this section includes seven species [41,44], isolated from dust, cave air, carpet, mouse dung, herbivore dung, cave sediment, bat droppings and guano, indoor environments, and clinical samples [44,45]. These are economically significant species, which are used in biotechnology sectors; these species are used as starter cultures for the production of food sauces, alcoholic beverages, production of extracellular

Table 6. Morphological characteristics of CNUFC TM6-2 compared with those of the reference strain *Penicillium fluviserpens*.

Character	CNUFC TM6-2	*Penicillium fluviserpens*[a]
Conidiophores	Monoverticillate, 17–110 µm	Smooth to finely roughened, monoverticillate (5–) 30–130 (–180) µm
Phialides	Ampulliform, 5.5–9 × 2–3.2 µm	Ampulliform (5–) 6–8 (–32) × 2–3.5 µm
Conidia	Ellipsoidal to sub-spherical, 2.5–3.3 µm in diameter	Ellipsoidal to sub-spherical 2.5–3.5(–7) µm

[a]From the description by Peterson et al. [63].

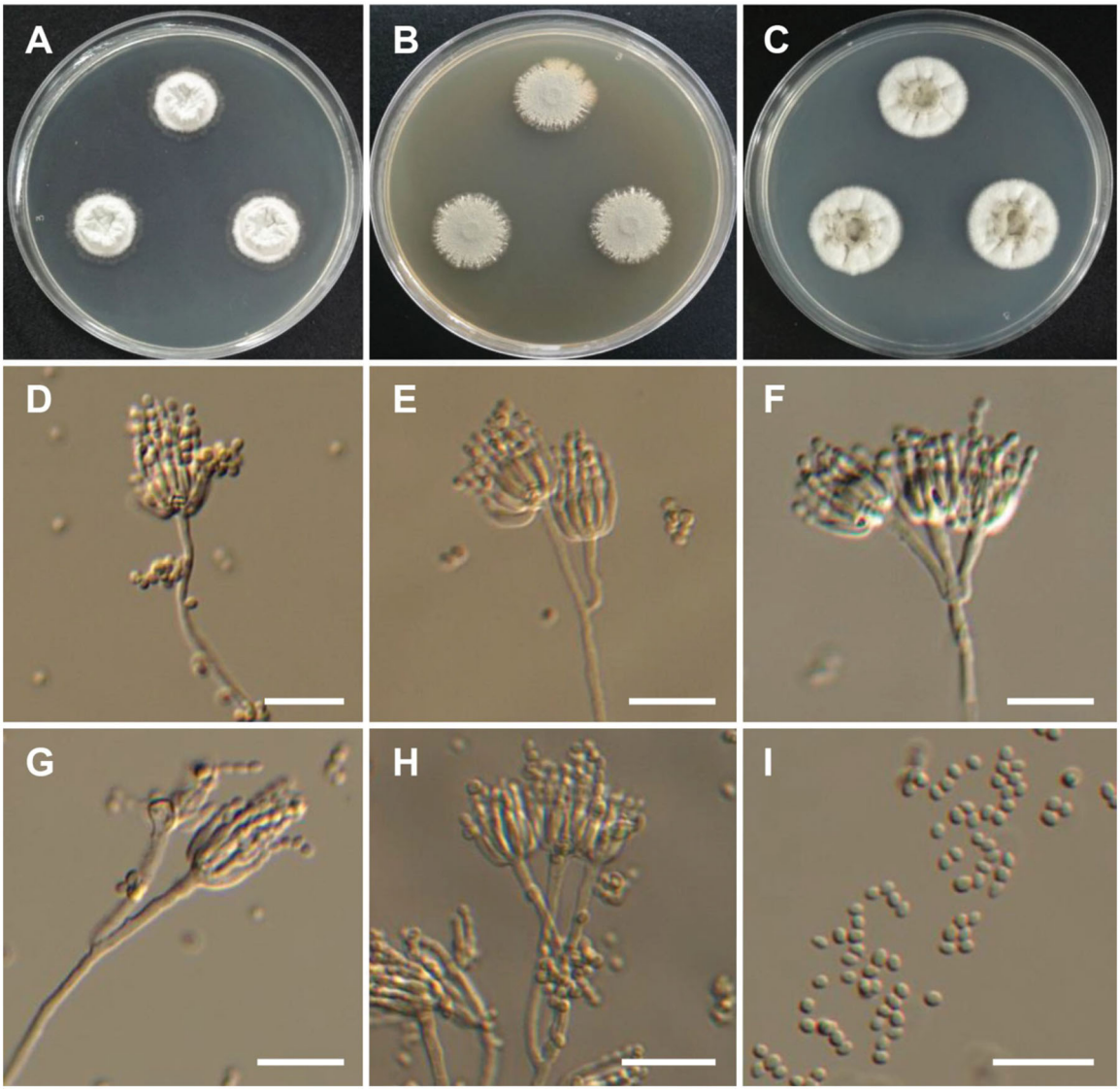

Figure 6. Morphology of *Penicillium fluviserpens*. (A) Colonies on Czapek yeast autolysate agar (CYA); (B) Colonies on Blakeslee's malt extract agar (MEA); (C) Colonies on Potato dextrose agar (PDA); (D–H) Conidiophores; (I) Conidia (scale bars: D–I = 20 µm).

enzymes, and waste degradation. They are also known to produce many bioactive compounds including antimicrobial, anti-oxidative, antitumor, and cytotoxic compounds [44]. In addition, these species are also known to cause human infection, namely, onychomycosis, invasive aspergillosis, otomycosis, and pulmonary aspergilloma [46,47]. Two species, *A. candidus* and *A. tritici* were isolated from Meju samples in Korea [48]. *A. pragensis* was recovered from human clinical material (nail) and was found to be responsible for causing onychomycosis in the Czech Republic [41]; it has also been isolated from rock samples from unnamed Karst caves in Suiyang located beside the Kuankuoshui National Natural Reserve, China [49]. In this study, *A. pragensis* was isolated from a by-product of rice bran.

The strains CNUFC MSW6 and CNUFC ESW1 were clustered within the same clade as *A. tennesseensis* NRRL 13150 (ex-type strain) in the section *Versicolores* (Figure 1). The isolate CNUFC ESW1 was morphologically most similar to *A. tennesseensis* as described by Jurjevic et al. [50], although there were differences in the length and color of conidiophores. The conidiophores described by Jurjevic et al. [50] were (35–)100–300(–400) µm in length, while our isolates were 18.5–413.5 µm in length. The *Aspergillus* section *Versicolores* was first described by Thom and Church [51]. Members of this section are

Table 7. Morphological characteristics of CNUFC WD17-1 compared with those of the reference strain *Penicillium scabrosum*.

Character	CNUFC WD17-1	*Penicillium scabrosum*[a]
Conidiophores	Biverticillate, 2.9–4.5 μm	Biverticillate, 200–400 × 3–4 μm
Metulae	2–4, 10.3–18.5 × 2.3–4.1 μm	10–20 × 2.5–4.0 μm
Phialides	Ampulliform, 4–8 per metula, 8.6–11.8 × 2.1–3.1 μm.	5–12 per metula, 7–11 × 2.0–2.5 μm
Conidia	Globose to subglobose, 2.3–3.2 μm	Globose to subglobose, 2.4–3.2 μm

[a]From the description by Frisva et al. [67].

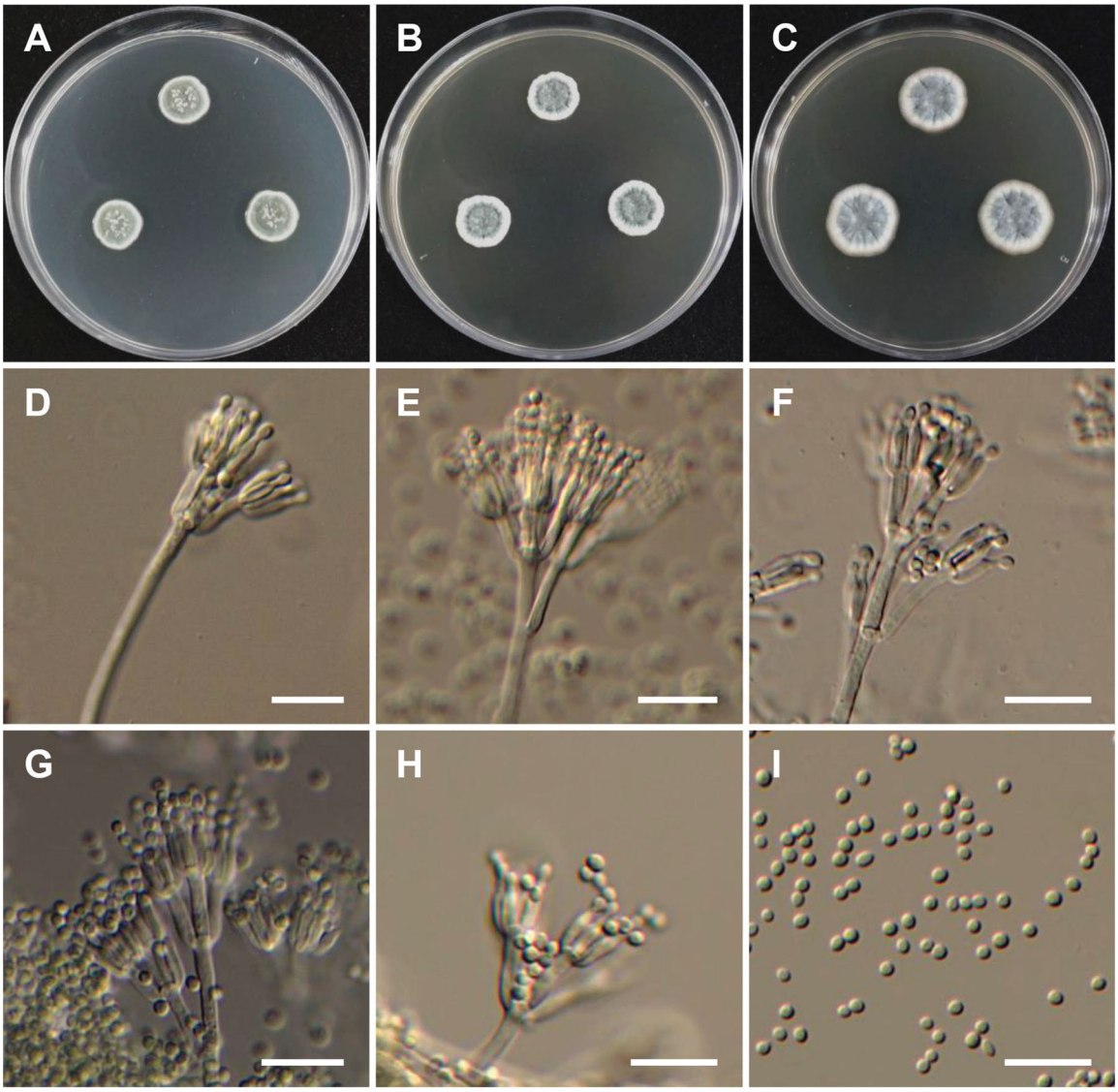

Figure 7. Morphology of *Penicillium scabrosum*. (A) Colonies on Czapek yeast autolysate agar (CYA); (B) Colonies on Blakeslee's malt extract agar (MEA); (C) Colonies on yeast malt extract agar (YES); (D–H) Conidiophores; (I) Conidia (scale bars: D–*I* = 20 μm).

found in soil, foods items [45], toxic dairy feed [50], and indoor environments [4,52,53], and can cause diseases in humans and animals [54,55]. Some species of this section produce kipukasins, nucleoside derivates, and the mycotoxin, sterigmatocystin [56–58]. *A. tennesseensis* has been reported to produce various compounds such as versicoamides F–H, prenylated indole alkaloids, diorcinol L, and (*R*)-diorcinol B [59,60]. In Korea, there are only six species reported to belong to the section *Versicolores*, including *A. creber*, *A. jensenii*, *A. nidulans, A. sydowii*, *A. tabacinus*, and *A. versicolor*. These were isolated from different sources including meju [48], chronic granulomatous patient [61], poultry farming soil [62], tidal mudflats, and sea sand [17]. In this study, *A. tennesseensis* was isolated from sea water and dead moths.

The strains CNUFC TM6-2 and CNUFC TM6-3 are well placed with other species in the *Penicillium* section *Cinnamopurpurea* as shown in Figure 2. The morphological features of our isolates were in line with the description of *P. fluviserpens* by Peterson et al. [63]. However, the isolate CNUFC TM6-2 exhibited a colony measurement which differed

from that of the description of *P. fluviserpens* on CYA (10–12 mm), MEA (8–11 mm), and PDA (10–12 mm) by Peterson et al. [63]. Members of this section are slow-growing, often with brown reverse on some media and mostly produce colonies with similar morphologies, subglobose to ellipsoidal, smooth to finely roughened spores, and have monoverticillate to divaricate biverticillate smooth-walled conidiophores. This section contains about 16 species [24,63,64]. Only two species, *P. chermesinum* (recently found to have phylogeny similar to *P. cvjetkovicii*) and *P. malacaense* were reported from meju samples in Korea with no detailed description [65]. Species in this section are known to produce the human lung tumor inhibitor compound, citreoviridin, and are commonly isolated from pecans, moldy nuts, air samples and hospital environments [63]. *P. fluviserpens* was previously isolated from air sampler from different locations, USA, California, Pennsylvania [63] and as endophytes from coffee plants in Colombia [66]. Interestingly, the present isolates in our study are from a tomato sample.

The strains CNUFC WD17-1 and CNUFC WD17-2 were grouped with *P. scabrosum* CBS 683.89 (ex-type strain) in the phylogenetic analysis of *BenA* and *CaM* sequences, and belong to the section *Ramosa* (Figure 2). There were differences observed with respect to the number of phialides per metula and colony diameter for the isolate *P. scabrosum* in comparison to previous descriptions by Frisvad et al. [67]. However, the size and shape of phialides and conidia were similar to those of the described species. *Penicillium* species in this section are characterized by biverticillate or terverticillate conidiophores [1]. They are commonly isolated from soil [67,68], but it is also found in sea water, fruiting bodies of *Chroogomphus rutilus*, and Tunisian orchard apples [69–71]. *P. scabrosum* has been reported to produce cyclopenin, cyclopenol, viridicatin, fumagillin, as well as a large number of unknown metabolites [67]. Larsen et al. [72] found two metabolites produced by *P. scabrosum* to be penigequinolone A and B. To the best of our knowledge, this is the first report of isolation of *P. scabrosum* from a freshwater sample.

Different species of the genus *Penicillium* have been reported to produce a variety of bioactive extrolites, including mycotoxins citrinin and patulin. Andersen and Frisvad [73] showed that *P. tularense* isolated from tomato fruit could produce janthitrems, paspalinine, paxilline, and 3-O-acetoxypaxilline. Harwig et al. [74] have reported that *P. expansum* is capable of producing patulin and citrinin in tomato fruit. Our strain *P. fluviserpens* was also isolated from tomato fruit. Therefore, it suggested that the strain may also produce mycotoxins as well as secondary metabolites. Interestingly, in this study, strains of *A. tennesseensis* found on the moths may be a potential as new biopesticide. Isolation and descriptions of new record from specific substrates and habitats, like freshwater, sea water, and dead moths, will be added to our knowledge on fungal diversity. Further studies are needed to better understand the ecological roles of both *Aspergillus* and *Penicillium* on different substrates. More studies on extrolites production and their ecological roles, the production of extracellular enzymes and antimicrobial compounds are needed.

Disclosure statement

No potential conflict of interest was reported by the author(s).

Funding

This study was financially supported by Chonnam National University [Grant number: 2017-2827]. This work was in part supported by the Graduate Program for the Undiscovered Taxa of Korea, the Project on Survey and Discovery of Indigenous Fungal Species of Korea funded by NIBR, and the Project on Discovery of Fungi from Freshwater and Collection of Fungarium, funded by NNIBR of the Ministry of Environment (MOE).

References

[1] Houbraken J, Samson RA. Phylogeny of *Penicillium* and the segregation of *Trichocomaceae* into three families. Stud Mycol. 2011;70:1–51.
[2] Samson RA, Visagie CM, Houbraken J, et al. Phylogeny, identification and nomenclature of the genus *Aspergillus*. Stud Mycol. 2014;78:141–173.
[3] Houbraken J, de Vries RP, Samson RA, et al. Modern taxonomy of biotechnologically important *Aspergillus* and *Penicillium* species. Adv Appl Microbiol. 2014;86:199–249.
[4] Visagie CM, Hirooka Y, Tanney JB, et al. *Aspergillus*, *Penicillium* and *Talaromyces* isolated from house dust samples collected around the world. Stud Mycol. 2014;78:63–139.
[5] Frisvad JC, Smedsgaard J, Larsen TO. Mycotoxins, drugs and other extrolites produced by species in *Penicillium* subgenus *Penicillium*. Stud Mycol. 2004;49:201–241.
[6] Chávez R, Bull P, Eyzaguirre J. The xylanolytic enzyme system from the genus *Penicillium*. J Biotechnol. 2006;123:413–433.
[7] Ichishima E. Development of enzyme technology for *Aspergillus oryzae*, *A. sojae*, and *A. luchuensis*, the national microorganisms of Japan. Biosci Biotechnol Biochem. 2016;80:1681–1692.
[8] Latgé JP. *Aspergillus fumigatus* and aspergillosis. Clin Microbiol Rev. 1999;12:310–350.
[9] Kwon-Chung KJ, Sugui JA. *Aspergillus fumigatus*—what makes the species a ubiquitous human fungal pathogen? PLoS Pathog. 2013;9:e1003743.

[10] Chan JFW, Lau SKP, Yuen KY, et al. *Talaromyces* (*Penicillium) marneffei* infection in non-HIV-infected patients. Emerg Microbes Infect. 2016;5: e19–9.
[11] Micheli PA. Nova Plantarum Genera juxta Tournefortii methodum disposita. Florence (Italy): Typis Bernardi Paperinii; 1729.
[12] Hubka V, Nováková A, Kolařík M, et al. Revision of *Aspergillus* section *Flavipedes*: seven new species and proposal of section *Jani* sect. nov. Mycologia. 2015;107:169–208.
[13] Gautier M, Normand AC, Ranque S. Previously unknown species of *Aspergillus*. Clin Microbiol Infect. 2016;22:662–669.
[14] Raja HA, Miller AN, Pearce CJ, et al. Fungal identification using molecular tools: a primer for the natural products research community. J Nat Prod. 2017;80:756–770.
[15] Kim HJ, Kim JS, Cheon KH, et al. Species list of *Aspergillus*, *Penicillium* and *Talaromyces* in Korea, based on 'One Fungus One Name' System. Kor J Mycol. 2016;44:207–219.
[16] Hyde KD, Hongsanan S, Jeewon R, et al. Fungal diversity notes 367-491: taxonomic and phylogenetic contributions to fungal taxa. Fungal Divers. 2016;80:1–270.
[17] Lee S, Park MS, Lim YW. Diversity of marine-derived *Aspergillus* from tidal mudflats and sea sand in Korea. Mycobiology. 2016;44:237–247.
[18] Kim KM, Lim J, Lee JJ, et al. Characterization of *Aspergillus sojae* isolated from Meju, Korean traditional fermented soybean brick. J Microbiol Biotechnol. 2017;27:251–261.
[19] Tagele SB, Adhikari M, Gurung SK, et al. New records of *Aspergillus allahabadii* and *Penicillium sizovae* from crop field soil in Korea. Mycobiology. 2018;46:297–304.
[20] Adhikari M, Gurung SK, Kim SW, et al. *Aspergillus caninus* (Syn: *Phialosimplex caninus*): a new isolate from field soils in Korea. Kor J Mycol. 2018;46:383–392.
[21] Link HF. Observationes in ordines plantarum naturales. Dissertatio 1. Mag Ges Naturf Freunde Berlin. 1809;3:3–42.
[22] Houbraken J, Wang L, Lee HB, et al. New sections in *Penicillium* containing novel species producing patulin, pyripyropens or other bioactive compounds. Pers Int Mycol J. 2016;36:299–314.
[23] Diao YZ, Chen Q, Jiang XZ, et al. *Penicillium* section *Lanata-divaricata* from acidic soil. Cladistics. 2018;35:514–549.
[24] Visagie CM, Houbraken J, Frisvad JC, et al. Identification and nomenclature of the genus *Penicillium*. Stud Mycol. 2014;78:343–371.
[25] Pangging M, Nguyen TTT, Lee HB. New records of four species belonging to Eurotiales from soil and freshwater in Korea. Mycobiology. 2019;47: 154–164.
[26] Park MS, Chung D, Baek K, et al. Three unrecorded species belonging to *Penicillium* section *Sclerotiora* from marine environments in Korea. Mycobiology. 2019;47:165–172.
[27] Phookamsak R, Hyde KD, Jeewon R, et al. Fungal diversity notes 929–1035: taxonomic and phylogenetic contributions on genera and species of fungi. Fungal Divers. 2019;95:1–273.
[28] Nguyen TTT, Lee HB. Isolation and characterization of three Zygomycetous fungi in Korea: *Backusella circina*, *Circinella muscae*, and *Mucor ramosissimus*. Mycobiology. 2018;46:317–327.
[29] Nguyen TT, Choi YJ, Lee HB. Isolation and characterization of three unrecorded Zygomycete fungi in Korea: *Cunninghamella bertholletiae*, *Cunninghamella echinulata*, and *Cunninghamella elegans*. Mycobiology. 2017;45:318–326.
[30] Glass NL, Donaldson GC. Development of primer sets designed for use with the PCR to amplify conserved genes from filamentous ascomycetes. Appl Environ Microbiol. 1995;61:1323–1330.
[31] Hong SB, Cho HS, Shin HD, et al. Novel *Neosartorya* species isolated from soil in Korea. Int J Syst Evol Microbiol. 2006;56:477–486.
[32] Peterson SW, Vega F, Posada F, et al. *Penicillium coffeae*, a new endophytic species isolated from a coffee plant and its phylogenetic relationship to *P. fellutanum*, *P. thiersii* and *P. brocae* based on parsimony analysis of multilocus DNA sequences. Mycologia. 2005;97:659–666.
[33] Yilmaz N, Visagie CM, Houbraken J, et al. Polyphasic taxonomy of the genus *Talaromyces*. Stud Mycol. 2014;78:175–341.
[34] Thompson JD, Gibson TJ, Plewniak F, et al. The CLUSTAL_X windows interface: flexible strategies for multiple sequence alignment aided by quality analysis tools. Nucleic Acids Res. 1997;25: 4876–4882.
[35] Hall TA. BioEdit: a user-friendly biological sequence alignment editor and analysis program for Windows 95/98/NT. Nucleic Acids Symp Ser. 1999;41:95–98.
[36] Tamura K, Stecher G, Peterson D, et al. MEGA6: molecular evolutionary genetics analysis version 6.0. Mol Biol Evol. 2013;30:2725–2729.
[37] Hubka V, NováKová A, Samson RA, et al. *Aspergillus europaeus* sp. nov., a widely distributed soil-borne species related to *A. wentii* (section *Cremei*). Plant Syst Evol. 2016;302:641–650.
[38] Raper KB, Fennell DI. The genus *Aspergillus*. Baltimore (MD): Williams & Wilkins; 1965.
[39] Rainer J, Peintner U, Pöder R. Biodiversity and concentration of airborne fungi in a hospital environment. Mycopathologia. 2001;149:87–97.
[40] Rabie C, Terblanche M. Influence of temperature on the toxicity of different isolates of *Aspergillus wentii* Wehm. S Afr J Agr Sci. 1967;10:263–266.
[41] Hubka V, Lyskova P, Frisvad JC, et al. *Aspergillus pragensis* sp. nov. discovered during molecular reidentification of clinical isolates belonging to *Aspergillus* section *Candidi*. Med Mycol. 2014;52: 565–576.
[42] Gams W, Christensen M, Onions AH, et al. Infrageneric taxa of *Aspergillus*. In: Samson RA, Pitt JI, editors. Advances in *Penicillium* and *Aspergillus* systematics. New York (NY): Plenum Press; 1985. p. 55–62.
[43] Thom C, Raper KB. A manual of the aspergilli. Baltimore(MD): Williams & Wilkins; 1945.
[44] Hubka V, Nováková A, Jurjević Ž, et al. Polyphasic data support the splitting of *Aspergillus candidus* into two species; proposal of *Aspergillus dobrogensis* sp. nov. Int J Syst Evol Microbiol. 2018;68:995–1011.

[45] Pitt JI, Hocking AD. Fungi and food spoilage. 3rd ed. New York (NY): Springer; 2009.
[46] de Hoog GS, Guarro J, Gené J, et al. Atlas of clinical fungi. 3rd ed. Utrecht (the Netherlands): CBS-KNAW Fungal Biodiversity Centre; 2009.
[47] Hubka V, Kubatova A, Mallatova N, et al. Rare and new aetiological agents revealed among 178 clinical *Aspergillus* strains obtained from Czech patients and characterized by molecular sequencing. Med Mycol. 2012;50:601–610.
[48] Hong SB, Kim DH, Samson RA. *Aspergillus* associated with Meju, a fermented soybean starting material for traditional soy sauce and soybean paste in Korea. Mycobiology. 2015;43:218–224.
[49] Zhang ZF, Liu F, Zhou X, et al. Culturable mycobiota from Karst caves in China with descriptions of 20 new species. Persoonia. 2017;39:1–31.
[50] Jurjevic Z, Peterson SW, Horn BW. *Aspergillus* section *Versicolores*: nine new species and multilocus DNA sequence based phylogeny. IMA Fungus. 2012;3:59–79.
[51] Thom C, Church MB. The Aspergilli. Baltimore (MD): Williams and Wilkins Co.; 1926.
[52] Samson R, Houbracken K, Summerbell RC, et al. Common and important species of *Actinomycetes* and fungi in indoor environments. In: Flannigan B, Samson R, Miller JD, editors. Microorganisms in home and indoor work environments. New York (NY): Taylor & Francis; 2001. 287 − 293.
[53] Andersen B, Frisvad JC, Søndergaard I, et al. Associations between fungal species and water-damaged building materials. Appl Environ Microbiol. 2011;77:4180–4188.
[54] Baddley JW, Marr KA, Andes DR, et al. Patterns of susceptibility of *Aspergillus* isolates recovered from patients enrolled in the transplant-associated infection surveillance network. J Clin Microbiol. 2009;47:3271–3275.
[55] Moreno G, Arenas R. Other fungi causing onychomycosis. Clin Dermatol. 2010;28:160–163.
[56] Jiao P, Mudur SV, Gloer JB, et al. Kipukasins, nucleoside derivatives from *Aspergillus versicolor*. J Nat Prod. 2007;70:1308–1311.
[57] Veršilovskis A, De Saeger S. Sterigmatocystin: occurrence in foodstuffs and analytical methods–an overview. Mol Nutr Food Res. 2010;54:136–147.
[58] Kobayashi N, Kubosaki A, Takahashi Y, et al. Distribution of sterigmatocystin-producing *Aspergilli* in Japan. Food Safety. 2018;6:67–73.
[59] Liu L, Wang L, Bao L, et al. Versicoamides F–H, prenylated indole alkaloids from *Aspergillus tennesseensis*. Org Lett. 2017;19:942–945.
[60] Li ZX, Wang XF, Ren GW, et al. Prenylated diphenyl ethers from the marine algal-derived endophytic fungus *Aspergillus tennesseensis*. Molecules. 2018;23:2368.
[61] Kim M, Shin JH, Suh SP, et al. *Aspergillus nidulans* infection in a patient with chronic granulomatous disease. J Kor Med Sci. 1997;12:244–248.
[62] Kim JD. Keratinolytic activity of five *Aspergillus* species isolated from poultry farming soil in Korea. Mycobiology. 2003;31:157–161.
[63] Peterson SW, Jurjević Ž, Frisvad JC. Expanding the species and chemical diversity of *Penicillium* section *Cinnamopurpurea*. PLoS One. 2015;10:e0121987.
[64] Anelli P, Peterson SW, Haidukowski M, et al. *Penicillium gravinicasei*, a new species isolated from cave cheese in Apulia, Italy. Int J Food Mcirobiol. 2018;282:66–70.
[65] Kim DH, Kim SH, Kwon SW, et al. The Mycobiota of air inside and outside the Meju fermentation room and the origin of Meju fungi. Mycobiology. 2015;43:258–265.
[66] Vega FE, Simpkins A, Aime MC, et al. Fungal endophyte diversity in coffee plants from Colombia, Hawai'i, Mexico and Puerto Rico. Fungal Ecol. 2010;3:122–138.
[67] Frisvad JC, Samson RA, Stolk AC. A new species of *Penicillium*, *P. scabrosum*. Persoonia. 1990;14:177–182.
[68] Frisvad JC, Larsen TO, Dalsgaard PW, et al. Four psychrotolerant species with high chemical diversity consistently producing cycloaspeptide A, *P. jamesonlandense* sp. nov., *P. ribium* sp. nov., *P. soppii* and *P. lanosum*. Int J Syst Evol Microbiol. 2006;56:1427–1437.
[69] Rong C, Ma Y, Liu Y, et al. *Penicillium chroogomphum*, a new species in *Penicillium* section *Ramosa* isolated from fruiting bodies of *Chroogomphus rutilus* in China. Mycoscience. 2016;57:79–84.
[70] Ouhibi S, Santos C, Ghali R, et al. *Penicillium tunisiense* sp. nov., a novel species of *Penicillium* section *Ramosa* discovered from Tunisian orchard apples. Int J Syst Evol Microbiol. 2018;68:3217–3225.
[71] Gonçalves MFM, Santos L, Silva BMV, et al. Biodiversity of *Penicillium* species from marine environments in Portugal and description of *Penicillium lusitanum* sp. nov., a novel species isolated from sea water. Int J Syst Evol Microbiol. 2019;69:3014–3021.
[72] Larsen TO, Smedsgaard J, Frisvad JC, et al. Consistent production of penigequinolone A and B by *Penicillium scabrosum*. Biochem Syst Ecol. 1999;27:329–332.
[73] Andersen B, Frisvad JC. Natural occurrence of fungi and fungal metabolites in moldy tomatoes. J Agric Food Chem. 2004;52:7507–7513.
[74] Harwig J, Scott PM, Stoltz DR, et al. Toxins of molds from decaying tomato fruit. Appl Environ Microbiol. 1979;38:267–274.