Journal of Species Research 10(2):99-116, 2021

Eighteen unreported radiation-resistant bacterial species isolated from Korea in 2018

Soohyun Maeng[1], Yuna Park[1], Hyejin Oh[1], Tuvshinzaya Damdintogtokh[1], Minji Bang[1], Byoung-Hee Lee[2], Ki-eun Lee[2] and Myung Kyum Kim[1,*]

[1]*Department of Bio & Environmental Technology, College of Natural Science, Seoul Women's University, Seoul 01797, Republic of Korea*
[2]*Environmental Research Complex, National Institute of Biological Resources, Hwangyeong-ro 42, Seo-gu, Incheon 22689, Republic of Korea*

**Correspondent: biotech@swu.ac.kr*

In 2018, as a subset study to discover indigenous prokaryotic species in Korea, a total of 18 unreported bacterial strains were discovered. From the high 16S rRNA gene sequence similarity (>98.8%) and formation of a robust phylogenetic clade, it was determined that each strain belonged an independent and predefined bacterial species. There were no official report that these 18 species were previously described in Korea; therefore, one strain of *Williamsia*, one strain of *Rhodococcus*, three strains of *Microbacterium*, three strains of *Agromyces*, one strain of *Arthrobacter*, one strain of *Paeniglutamicibacter*, one strain of *Pseudarthrobacter*, one strain of *Nocardioides*, one strain of *Fibrella*, one strain of *Hymenobacter*, one strain of *Deinococcus*, two strains of *Fictibacillus*, and one strain of *Paenibacillus* are described as unreported bacterial species in Korea. Gram reaction, basic biochemical characteristics, and colony and cell morphologies are described in the species description section.

Keywords: 16S rRNA, bacterial diversity, *Bacteria*, unreported species

© 2021 National Institute of Biological Resources
DOI:10.12651/JSR.2021.10.2.99

Introduction

In 2018, 18 unreported bacterial species were isolated from diverse soil samples collected from Korea. The identified bacterial species belong to the phyla *Actinobacteria*, *Bacteriodetes*, *Deinococcus-Thermus*, and *Firmicutes*. This study focusses on the description of unrecorded bacterial species in the family *Nocardiaceae*, *Microbacteriaceae*, *Micrococcaceae*, *Nocardioidaceae*, *Cytophagaceae*, *Hymenobacteraceae*, *Deinococcaceae*, *Bacillaceae*, and *Paenibacillaceae*.

Firmicutes is a phylum of bacteria, of which most its species have Gram-stain-positive cell wall structure and produce endospores that are resistant to desiccation and can survive in the extreme conditions. At present, the phylum *Firmicutes* comprises 43 validated families according to the List of Prokaryotic Names with Standing in Nomenclature (LPSN) (http://www.bacterio.net/). Aside from gram-positive microbes, the octopus contains bacteria with phenomenological, phenological, and chemically specific properties. Therefore, the phylum *Firmicutes* is a fluid, and one of the incomplete taxonomic groups (Seong *et al*., 2018).

The phylum *Bacteroidetes* comprises of three large classes of bacteria that are Gram-stain-negative, non-spore forming, anaerobic or aerobic, and rod-shaped. The phylum *Bacteroides* comprises 34 validated families according to LPSN and the members are widely distributed in the diverse environment, including in soil, sediments, and sea water, as well as in the gut and on the skin of animals. The genus *Hymenobacter* was first proposed by Hirsch *et al*. (1998). and until now, the genus comprises of 67 species (http://www.bacterio.net/) that mostly shows radiation resistance property (Zhang *et al*., 2007; Su *et al*., 2014; Lee *et al*., 2014; 2017; Srinivasan *et al*., 2015).

Actinobacteria is one of the largest recently recognized major lineages within the bacterial domain, including five subclasses and six orders. The phylum *Actinobacteria* comprises 81 validated families according to LPSN. Most strains of *Actinobacteria* are free creatures that are widely distributed in in soil, stratosphere, marine and extreme dry environments (Miao and Davies, 2010). *Actinobacte-*

ria species are gram-positive filament bacteria with low GC content in the genome. *Actinobacteria* morphology includes coccoid (*Micrococcus*) and rod-coccoid (*Arthrobacter*) shaped, as well as fragmenting hyphal forms and forms with branched mycelia.

The phylum *Deinococcus-Thermus* represents an ancient lineage that contains some of the most conspicuous species within the domain Bacteria. The phyluem is divided into two orders, one that resists the deadly effects of ionizing radiation and UV exposure and one that thrives at high temperatures. *Deinococcus-Thermus* is comprised of two orders, the *Deinococcales* and the *Thermales*. The mostly mesophilic species of *Deinococcales* demonstrate uncommon resistance following exposure to electromagnetic radiation, tolerating doses that normally destroy vegetative bacteria (Battista, 2016). Also, *Deinococcus-Thermus* is gram positive and has high G+C content, which is characteristic of thermophilic rRNAs (Weisburg *et al*., 1989). Currently, the phylum *Deinococcus-Thermus* comprises three validated families according to the LPSN.

In this study, we describe 18 UV resistant bacterial strains isolated from a soil samples collected in Korea. UV radiation from sunlight is the most common environmental health danger, causing harmful effects (Yu and Lee, 2017) and ionizing radiation directly damages the DNA, which leads to mutation and cell death. More likely the radiation resistance bacteria evolved was in response to chronic exposure to radioactive forms of DNA damage (Jang *et al*., 2017; Choi *et al*., 2018). Thus, they provide a DNA repair system, which results in a better cell repair system and better UV resistance. The variety of other UV resistant bacteria were reported from previous studies including *Hymenobacter* sp. DG25A (Srinivasan *et al*., 2017), and complete genome were sequenced of *Hymenobacter sedentarius* DG5B^T (Kim *et al*., 2017a), *Spirosoma pulveris* JSH 5-14^T (Kim *et al*., 2017b), *Methylobacterium* sp. 17Sr1-43 (Srinivasan *et al*., 2018), *Nibribacter radioresistens* DG15C (Sathiyaraj *et al*., 2018a), and *Microvirga* sp. 17mud 1-3 (Sathiyaraj *et al*., 2018b).

Materials and Methods

Samples were isolated form soil collected from the Seogwipo-si, Jeju-do (N 33°14′40.1, E 126°34′59.1); Okcheon-gun, Chungcheongbuk-do (N 36°17′32.5, E 127°33′43.7); and Pyeongchang-gun, Gangwon-do (N 37°38′15.2, E 128°39′44.5) in South Korea. Samples were collected from less than 1 cm from the ground surface and were transported in sterilized 50 mL conical tubes. A soil suspension was prepared with a total volume of 10 mL using soil free of debris from the collected soil in 9 mL distilled water. The soil suspensions were serially diluted in distilled water. Depending on the culture environment of the strains, 100 μL aliquots of diluted soil suspensions was spread onto R2A medium or 1/10 LB agar medium, and incubated at 25°C for 3−4 days. The strain IDs, growth media, isolation sources, and incubation conditions are summarized in Table 1. The pure culture of the strains was stored using 20% glycerol suspension at −80°C as well as freeze-dried ampoules.

Cell morphology of strains were observed by transmission electron microscopy (JEOL, JEM1010) using cells grown for 3−4 days. Transmission electron microscopy images of the strains are shown in Figure 1. Gram reaction was performed using commercial kit, following manufacturer's instruction (BioMerieux). Biochemical characteristics were established by using Biolog Microstation with GEN III microplate system and API 20NE and 32GN strips. A single colony was selected and emulsified into 'inoculating fluid A' (Biolog) for subsequent inoculation on to the MicroPlate test plate (Biolog). More fastidious organisms, including capnophilic strains, were cultured on alternative media, according to the manufacturer's instructions, and inocula was prepared to a specified transmittance using a turbidimeter, as specified in the user's guide. For each isolate, 100 μL of the cell suspension was inoculated into each well of the MicroPlate, using a multichannel pipette and incubated at 37°C for 24 h, according to growth characteristics. MicroPlates were read in a MicroStation semi-automated reader after 24 h and results interpreted by the identification system's software (GEN III database, version 5.2.1). The system indicated which isolates could not be identified after 20 h and required further incubation. Such isolates were re-incubated and re-read 3 to 6 h later (Wragg *et al*., 2014).

Genomic DNA was extracted and 16S rRNA gene was amplified by PCR with 9F and 1492R universal bacterial primers (Weisburg *et al*., 1991). The 16SrRNA gene sequences of the closely related strains were obtained from EzBioCloud (https://www.ezbiocloud.net) (Kim *et al*., 2012) and edited using the BioEdit program (Hall, 1999). Multiple alignments were performed with the MUSCL program (Edgar, 2004). Using the two-parameter model (Kimura, 1983), evolutionary distances were calculated. Phylogenetic trees were constructed using the neighbor-joining (Saitou and Nei, 1987) in the MEGA7 program (Kumar *et al*., 2016) with bootstrap values based on 1,000 replications (Felsenstein, 1985). For UV radiation survival test, all strains were grown on R2A agar medium or 1/10 LB agar medium at 25°C for 3−4 days were irradiated with a UVC cross-linker (UVP, CX-2000, USA) at 254 nm (Im *et al*., 2013; Selvam *et al*., 2013). After being exposed to UV radiation, the survival rates of strain 18JY8-7^T, *Cohnella rhizosphaerae* CSE-5610^T and *Cohnella xylanilytica* MX15-2^T were measured on the cells in the early stationary phase ($\approx 10^9$c.f.u. mL^{-1}), in R2A agar medium or 1/10 LB agar medium at 25°C

Table 1. 16S rRNA gene sequence similarity, medium, and incubation conditions of unrecorded strains. All strains were isolated from soil.

Order	Family	Strain ID	NIBR ID	GenBank accession number	Most closely related species	Similarity (%)	Medium	Incubation conditions
Corynebacteriales	*Nocardiaceae*	BT115	NIBRBAC000502698	MK311241	*Williamsia spongiae*	99.80%	R2A	25°C, 3d
		BT120	NIBRBAC000501935	MK110482	*Rhodococcus kroppenstedtii*	100.00%	R2A	25°C, 3d
Micrococcales	*Microbacteriaceae*	BT109	NIBRBAC000501855	MK110420	*Microbacterium arthrosphaerae*	99.10%	R2A	25°C, 3d
		BT97	NIBRBAC000501852	MK101058	*Agromyces indicus*	99.60%	R2A	25°C, 3d
		BT98	NIBRBAC000501839	MK101067	*Agromyces arachidis*	99.20%	R2A	25°C, 3d
		BT102	NIBRBAC000501936	MK110483	*Agromyces binzhouensis*	98.70%	R2A	25°C, 3d
		BT89	NIBRBAC000501937	MK110422	*Microbacterium enclense*	99.90%	R2A	25°C, 3d
		BT119	NIBRBAC000501833	MK110481	*Microbacterium flavescens*	98.80%	R2A	25°C, 3d
		BT82	NIBRBAC000501851	MK192014	*Arthrobacter nitrophenolicus*	99.00%	R2A	25°C, 3d
	Micrococcaceae	BT53	NIBRBAC000502699	MK294306	*Paeniglutamicibacter sulfureus*	99.20%	1/10 LB	25°C, 3d
		BT92	NIBRBAC000502727	MK110378	*Pseudarthrobacter niigatensis*	99.90%	R2A	25°C, 3d
Propionibacteriales	*Nocardioidaceae*	BT84	NIBRBAC000502726	MK110421	*Nocardioides cavernae*	99.00%	R2A	25°C, 3d
Cytophagales	*Cytophagaceae*	BT100	NIBRBAC000501831	MK101050	*Fibrella aestuarina*	98.80%	R2A	25°C, 3d
	Hymenobacteraceae	BT99	NIBRBAC000501835	MK110423	*Hymenobacter monticola*	98.90%	R2A	25°C, 3d
Deinococcales	*Deinococcaceae*	BT95	NIBRBAC000501845	MK101062	*Deinococcus sonorensis*	99.60%	R2A	25°C, 3d
Bacillales	*Bacillaceae*	BT94	NIBRBAC000501846	MK101066	*Fictibacillus arsenicus*	99.60%	R2A	25°C, 3d
		BT96	NIBRBAC000501856	MK101065	*Fictibacillus phosphorivorans*	99.90%	R2A	25°C, 3d
	Paenibacillaceae	BT73	NIBRBAC000501826	MK110480	*Paenibacillus populi*	99.50%	R2A	25°C, 3d

(Difco). In the UV test, *Deinococcus radiodurans* R1^T (=DSM 20539^T) was used as a positive control, and *Escherichia coli* K-12 (=KCTC 1116) was used as a negative control. The numbers of colony-forming units (CFU) of the strains were counted, and the survival rate was calculated based on CFU value.

Results and Discussion

Based on 16S rRNA gene sequence similarity, 18 previously unreported bacterial species from Korea were identified. The taxonomic composition and identification results are summarized in Table 1. The strains BT115 (MK311241, GenBank accession number), and BT120 (MK110482) were assigned to the family Nocardiacea (2 strains); BT109 (MK110420), BT97 (MK101058), BT98 (MK101067), BT102 (MK110483), BT89 (MK110422), BT119 (MK110481), and BT82 (MK192014) were assigned to family Microbacteriaceae (7 strains); BT53 (MK294306), and BT92 (MK110378) were assigned to family Micrococcaceae (2 strains); BT84 (MK110421) was assigned to family Micrococcaceae (1 strain); BT100 (MK101050) was assigned to family Cytophagaceae (1 strain); BT99 (MK110423) was assigned to family Hymenobacteraceae (1 strain); BT95 (MK101062) was assigned to family Deinococcaceae (1 strain); BT94 (MK101066), and BT96 (MK101065) were assigned to family Bacillaceae (2 strains); BT73 (MK110480) was assigned to family Paenibacillaceae (1 strain); At the generic level, the strains belong to 13 different genera: *Williamsia* (1 species), *Rhodococcus* (1 species), *Microbacterium* (3 species), *Agromyces* (3 species), *Arthrobacter* (1 species), *Paeniglutamicibacter* (1 species), *Pseudarthrobacter* (1 species), *Nocardioides* (1 species), *Fibrella* (1 species), *Hymenobacter* (1 species), *Deinococcus* (1 species), *Fictibacillus* (1 species), and *Paenibacillus* (1 species).

The identification of the isolates based on sequence similarity was supported by the phylogenetic trees. The neighbor-joining trees inferred close relationships of the isolates and type strains of validly published species (Fig. 1). The detailed morphological and physiological characteristics are given in the strain descriptions.

As an outcome of this study, we report the diversity of radiation-resistant bacterial species in Korean ecosystems. The 18 isolates were identified as unreported species, and their phenotypic characteristics were examined through polyphasic study. Accordingly, the following 18 species are newly reported species in Korea.

Description of *Williamsia spongiae* BT115

Cells are Gram-stain-positive, non-flagellated, and rod-shaped. Colonies are pink colored after 3 days of incubation on R2A at 25°C. In the BIOLOG GEN III test, weak positive for dextrin, D-trehalose, D-turanose, 1% NaCl, D-mannose, D-fructose, D-galactose, L-rhamnose, 1% sodium lactate, D-mannitol, D-arabitol, tetrazolium violet, methyl pyruvate, D-lactic acid methyl ester, citric acid, L-malic acid, bromo-succinic acid, nalidixic acid, potassium tellurite, α-hydroxy-butyric acid, β-hydroxy-D, L-butyric acid, α-keto-butyric acid, acetic acid, aztreonam and sodium bromate are positive. D-fructose-6-PO, glucuronamide, and acetoacetic acid. In the API 20NE test, positive for urease, D-mannitol, and *N*-acetyl-D-glucosamin; weak positive for esculin hydrolysis, D-glucose, L-arabinose, D-mannose, D-maltose, and potassium gluconate; but negative for gelatin hydrolysis, β-galactosidase, malic acid, trisodium citratereduction of nitrates (NO_3) to nitrite (NO_2^-), reduction of nitrates (NO_3) to nitrogen (N_2), indole production on tryptophan, glucose fermentation, arginine dihydrolase, capric acid, adipic acid, and phenylacetic acid. In the API 32GN test, positive for D-saccharose (sucrose), D-maltose, sodium acetate, 3-hydroxybenzoic acid, D-mannitol, D-glucose, D-melibiose, L-arabinose, valeric acid, trisodium citrate, inositol, itaconic acid, sodium malonate, lactic acid, L-alanine, potassium 5-ketogluconate, L-serine, D-sorbitol, capric acid, L-histidine, potassium 2-ketogluconate, 3-hydroxybutyric acid, 4-hydroxybenzoic acid, and L-proline; but negative for L-rhamnose, salicin, *N*-acetyl-glucosamine, D-ribose, suberic acid, glycogen, D-fucose, and propionic acid. Strain BT115 (=NIBRBAC000502698) was isolated from a soil sample, Okcheon-gun, Chungcheongbuk-do, Korea.

Description of *Rhodococcus kroppenstedtii* BT120

Cells are Gram-stain-positive, non-flagellated, and rod-shaped. Colonies are light orange colored after 3 days of incubation on R2A at 25°C. In the BIOLOG GEN III test, positive for D-trehalose, sucrose, D-turanose, pH 6, *N*-acetyl-D-glucosamine, *N*-acetyl-D-galactosamine, 1% NaCl, 4% NaCl, α-D-glucose, D-fructose, D-fructose, 1% sodium lactate, D-sorbitol, D-mannitol, D-arabitol, myo-inositol, glycerol, D-glucose-6-PO, D-fructose-6-PO, D-aspartic acid, L-aspartic acid, L-glutamic acid, L-pyroglutamic acid, pectin, D-gluconic acid, citric acid, α-keto-glutaric acid, L-malic acid, bromo-succinic acid, lithium chloride, potassium tellurite, α-hydroxy-butyric acid, β-hydroxy-D, L-butyric acid, α-keto-butyric acid, acetoacetic acid, propionic acid, acetic acid, acetic acid, and sodium butyrate; and weak positive for dextrin, D-maltose, D-cellobiose, gentiobiose, stachyose, pH 5, D-raffinose, α-D-lactose, D-melibiose, β-methyl-D-glucoside, D-salicin, *N*-acetyl-β-D-mannosamine, *N*-acetyl-neuraminic acid, 8% NaCl, D-mannose, D-galactose, 3-methyl glucose, L-fucose, L-rhamnose, inosine, D-serine, D-serine, gelatin, glycyl-L-proline, L-arginine,

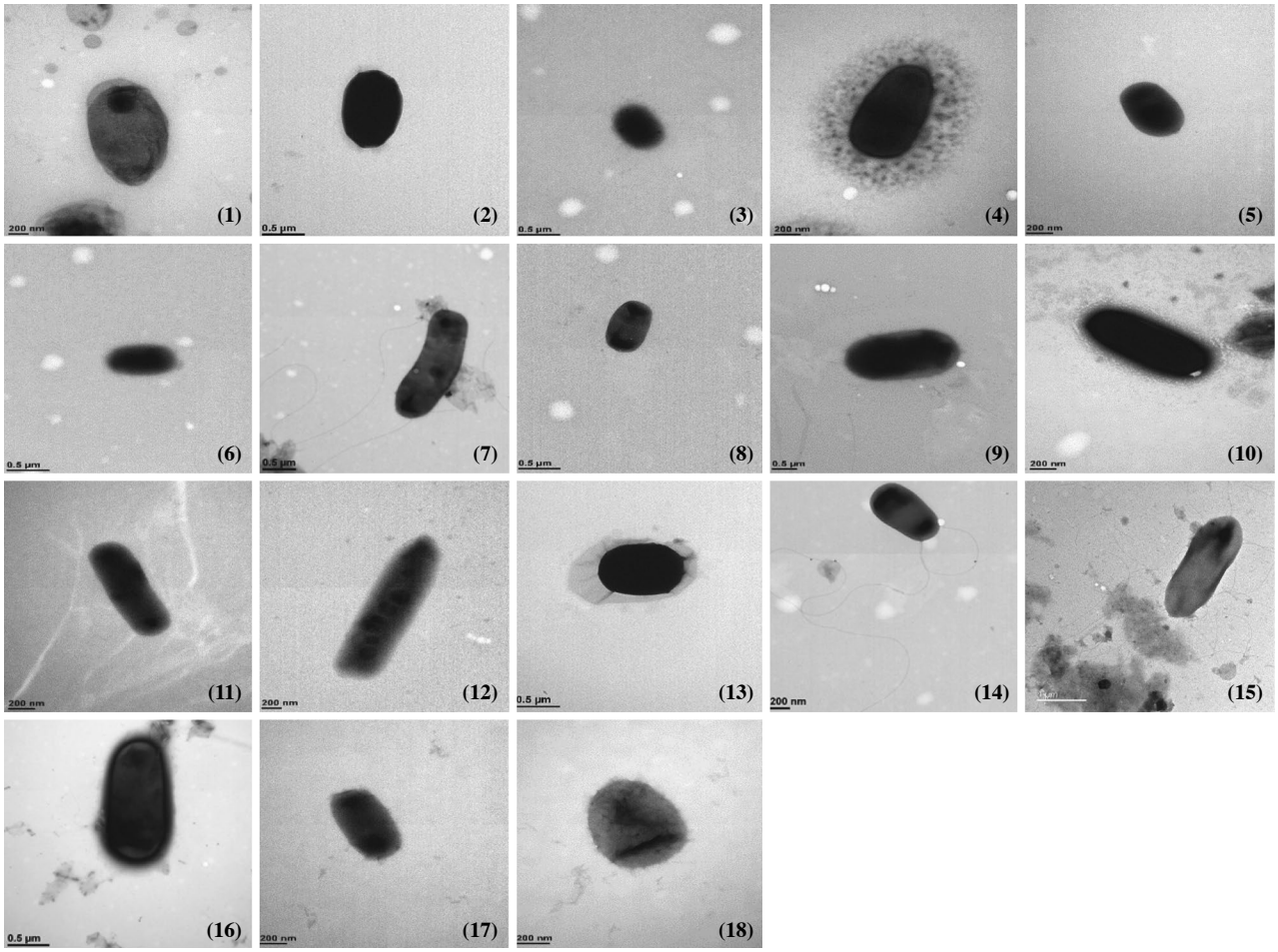

Fig. 1. Transmission electron micrographs of the strains isolated in this study. Strains: 1, BT100; 2, BT53; 3, BT92; 4, BT109; 5, BT97; 6, BT82; 7, BT94; 8, BT84; 9, BT95; 10, BT96; 11, BT98; 12, BT99; 13, BT115; 14, BT119; 15, BT73; 16, BT120; 17, BT102; 18, BT89.

L-histidine, L-serine, guanidine HCl, D-galacturonic acid, L-galactonic acid lactone, D-glucuronic acid, glucuronamide, mucic acid, quinic acid, D-saccharic acid, tetrazolium violet, methyl pyruvate, D-lactic acid methyl ester, L-lactic acid, D-malic acid, nalidixic acid, tween 40, γ-amino-butyric acid, formic acid and sodium bromate. In the API 20NE test, positive for D-mannitol, *N*-acetyl-D-glucosamine, potassium gluconate, malic acid, and trisodium citrate; weak positive for D-glucose, D-mannose, D-maltose, adipic acid, and phenylacetic acid; but negative for reduction of nitrates (NO_3) to nitrite (NO_2^-), reduction of nitrates (NO_3) to nitrogen (N_2), indole production on tryptophan, glucose fermentation, arginine dihydrolase, urease, esculin hydrolysis, gelatin hydrolysis, β-galactosidase, L-arabinose, and capric acids. In the API 32GN test, positive for inositol, D-saccharose (sucrose), D-mannitol, D-sorbitol, *N*-acetyl-glucosamine, suberic acid, sodium acetate, L-serine, D-glucose, propionic acid, valeric acid, trisodium citrate, 3-hydroxybutyric acid and L-proline; but negative for L-rhamnose, D-ribose, D-maltose, itaconic acid, sodium malonate, lactic acid, L-alanine, potassium 5-ketogluconate, glycogen, 3-hydroxybenzoic acid, salicin, D-melibiose, D-fucose, L-arabinose, capric acid, L-histidine, potassium 2-ketogluconate, and 4-hydroxybenzoic acid. Strain BT120 (=NIBRBAC000501935) was isolated from a soil sample, Okcheon-gun, Chungcheongbuk-do, Korea.

Description of *Microbacterium arthrosphaerae* BT109

Cells are Gram-stain-positive, non-flagellated, and rod-shaped. Colonies are yellow colored after 3 days of incubation on R2A at 25°C. In the BIOLOG GEN III test, positive for dextrin, D-maltose, D-trehalose, D-cellobiose, gentiobiose, sucrose, D-turanose, stachyose, pH 6, D-raffinose, α-D-lactose, D-melibiose, β-methyl-D-glucoside, D-salicin, *N*-acetyl-D-glucosamine, 1% NaCl, 4% NaCl, α-D-glucose, D-mannose, D-fructose, L-fucose, L-rhamnose, inosine, 1% sodium lactate, D-mannitol, glycerol, rifamycin SV, glycyl-L-proline, L-aspartic acid,

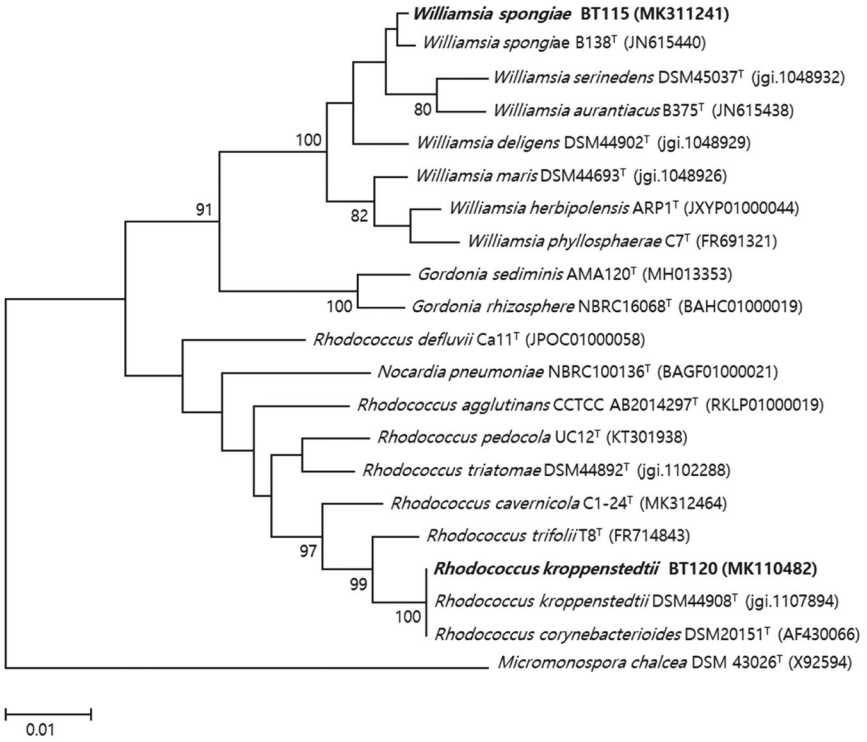

Fig. 2. Neighbor-joining phylogenetic tree based on 16S rRNA gene sequences shows the relationship between the strains isolated in this study and their relatives of the family *Nocardiaceae*. Strain: BT115, BT120. Bootstrap values (>80%) are shown above nodes for the neighbor-joining methods. Bar: 0.01 substitutions per nucleotide position.

L-glutamic acid, L-serine, guanidine HCl, pectin, D-gluconic acid, tetrazolium blue, p-hydroxy-phenylacetic acid, methyl pyruvate, L-lactic acid, citric acid, L-malic acid, bromo-succinic acid, nalidixic acid, lithium chloride, potassium tellurite, α-hydroxy-butyric acid, β-hydroxy-D, L-butyric acid, α-keto-butyric acid, acetoacetic acid, propionic acid, acetic acid, aztreonam, and sodium butyrate; and weak positive for 8% NaCl, D-galactose, D-sorbitol, L-alanine, D-saccharic acid, tetrazolium violet, D-lactic acid methyl ester, D-malic acid, tween 40, and sodium bromate. In the API 20NE test, positive for reduction of nitrates (NO_3) to nitrite (NO_2^-), reduction of nitrates (NO_3) to nitrogen (N_2), esculin hydrolysis, β-galactosidase, D-glucose, L-arabinose, D-mannose, D-mannitol, D-maltose and malic acid; weak positive for *N*-acetyl-D-glucosamine, potassium gluconate, and adipic acid; but negative for indole production on tryptophan, glucose fermentation, arginine dihydrolase, urease, gelatin hydrolysis, capric acid, trisodium citrate, and phenylacetic acid. In the API 32GN test, positive for L-rhamnose, *N*-acetyl-glucosamine, D-saccharose (sucrose), D-maltose, lactic acid, glycogen, L-serine, D-mannitol, D-glucose, D-melibiose, D-fucose, L-arabinose, inositol, sodium acetate, salicin, propionic acid, valeric acid, and 4-hydroxybenzoic acid; but negative for D-ribose, itaconic acid, suberic acid, sodium malonate, L-alanine, potassium 5-ketogluconate, 3-hydroxybenzoic acid, D-sorbitol, capric acid, trisodium citrate, L-histidine, potassium 2-ketogluconate, 3-hydroxybutyric acid, and L-proline. Strain BT109 (=NIBRBAC000501855) was isolated from a soil sample, Okcheon-gun, Chungcheongbuk-do, Korea.

Description of *Agromyces indicus* BT97

Cells are Gram-stain-positive, non-flagellated, and rod-shaped. Colonies are yellow colored after 3 days of incubation on R2A at 25°C. In the BIOLOG GEN III test, positive for dextrin, D-maltose, D-trehalose, D-cellobiose, sucrose, D-turanose, D-salicin, 1% NaCl, 4% NaCl, α-D-glucose, D-mannose, D-fructose, D-galactose, inosine, D-sorbitol, D-mannitol, glycerol, troleandomycin, rifamycin SV, gelatin, L-alanine, L-glutamic acid, pectin, D-gluconic acid, tetrazolium blue, p-hydroxy-phenylacetic acid, L-malic acid, nalidixic acid, lithium chloride, potassium tellurite, tween 40, β-hydroxy-D, L-butyric acid, acetoacetic acid, acetic acid, aztreonam, and sodium bromate; and weak positive for gentiobiose, stachyose, pH 6, D-melibiose, β-methyl-D-glucoside, *N*-acetyl-D-glucosamine, *N*-acetyl-β-D-mannosamine, *N*-acetyl-D-galactosamine, 3-methyl glucose, L-fucose, 1% sodium lactate, D-arabitol, myo-inositol, glycyl-L-proline, L-arginine, L-aspartic acid, L-pyroglutamic acid, L-serine, mucic

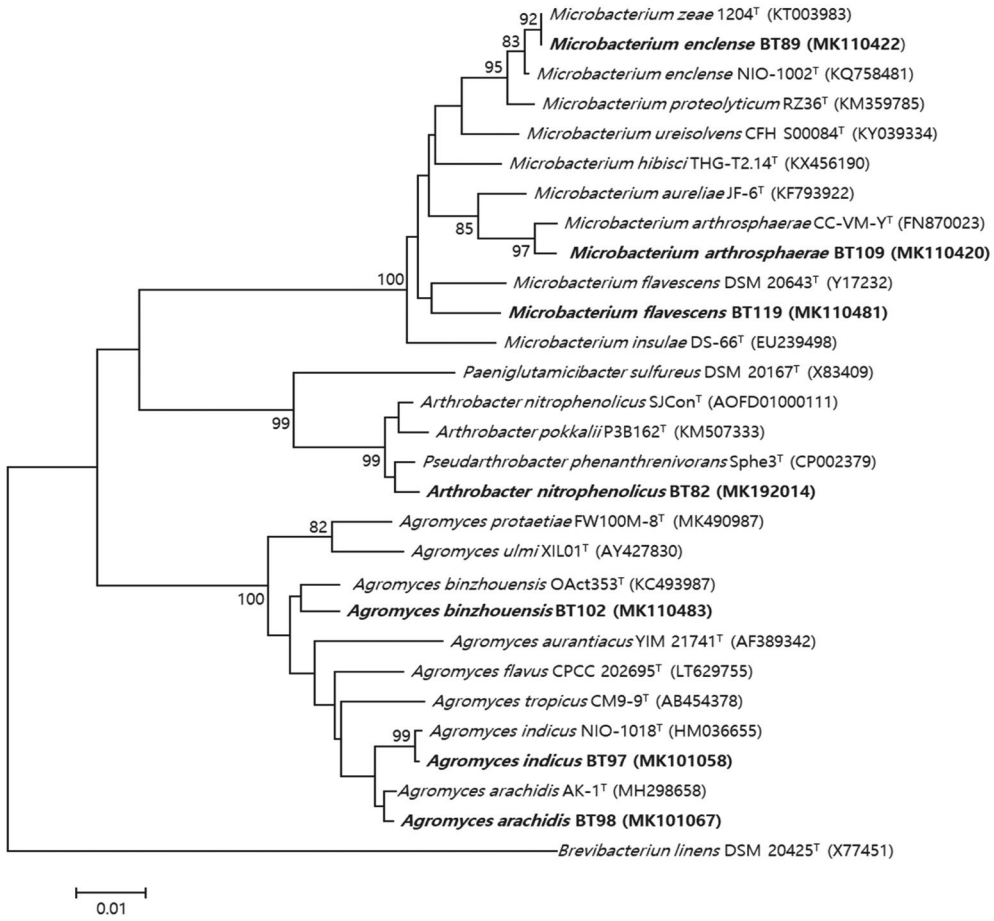

Fig. 3. Neighbor-joining phylogenetic tree based on 16S rRNA gene sequences shows the relationship between the strains isolated in this study and their relatives of the family *Microbacteriaceae*. Strains: BT109, BT97, BT98, BT102, BT89, BT119 and BT82. Bootstrap values (>80%) are shown above nodes for the neighbor-joining methods. Bar: 0.01 substitutions per nucleotide position.

acid, quinic acid, tetrazolium violet, D-lactic acid methyl ester, α-keto-glutaric acid, D-malic acid, and propionic acid. In the API 20NE test, positive for esculin hydrolysis, and β-galactosidase; weak positive for D-glucose, L-arabinose, D-mannitol, and capric acid; but negative for reduction of nitrates (NO_3) to nitrite (NO_2^-), reduction of nitrates (NO_3) to nitrogen (N_2), indole production on tryptophan, glucose fermentation, arginine dihydrolase, urease, gelatin hydrolysis, D-mannose, *N*-acetyl-D-glucosamine, D-maltose, potassium gluconate, adipic acid, malic acid, trisodium citrate, and phenylacetic acid. In the API 32 GN test, positive for D-saccharose (sucrose), D-maltose, glycogen, and L-arabinose; but negative for L-rhamnose, *N*-acetyl-glucosamine, D-ribose, inositol, itaconic acid, suberic acid, sodium malonate, sodium acetate, lactic acid, L-alanine, potassium 5-ketogluconate, 3-hydroxybenzoic acid, L-serine, D-mannitol, D-glucose, salicin, D-melibiose, D-fucose, D-sorbitol, propionic acid, capric acid, valeric acid, trisodium citrate, L-histidine, potassium 2-ketogluconate, 3-hydroxybutyric acid, 4-hydroxybenzoic acid, and L-proline. Strain BT97 (=NIBRBAC000501852) was isolated from a soil sample, Okcheon-gun, Chungcheongbuk-do, Korea.

Description of *Agromyces arachidis* BT98

Cells are Gram-stain-positive, non-flagellated, and rod-shaped. Colonies are yellow colored after 3 days of incubation on R2A at 25°C. In the BIOLOG GEN III test, positive for dextrin, D-maltose, sucrose, stachyose, pH 6, D-raffinose, 1% NaCl, 8% NaCl, D-fructose, inosine, 1% sodium lactate, D-mannitol, pectin, tetrazolium violet, tetrazolium blue, p-hydroxy-phenylacetic acid, L-malic acid, nalidixic acid, lithium chloride, potassium tellurite, and aztreonam; and weak positive for D-trehalose, D-cellobiose, gentiobiose, D-turanose, pH 5, D-salicin, 4% NaCl, α-D-glucose, fusidic acid, D-serine, glycerol, troleandomycin, rifamycin SV, minocycline, gelatin, L-glutamic acid, lincomycin, guanidine HCl, niaproof 4, D-gluconic acid, vancomycin, and sodium butyrate. In

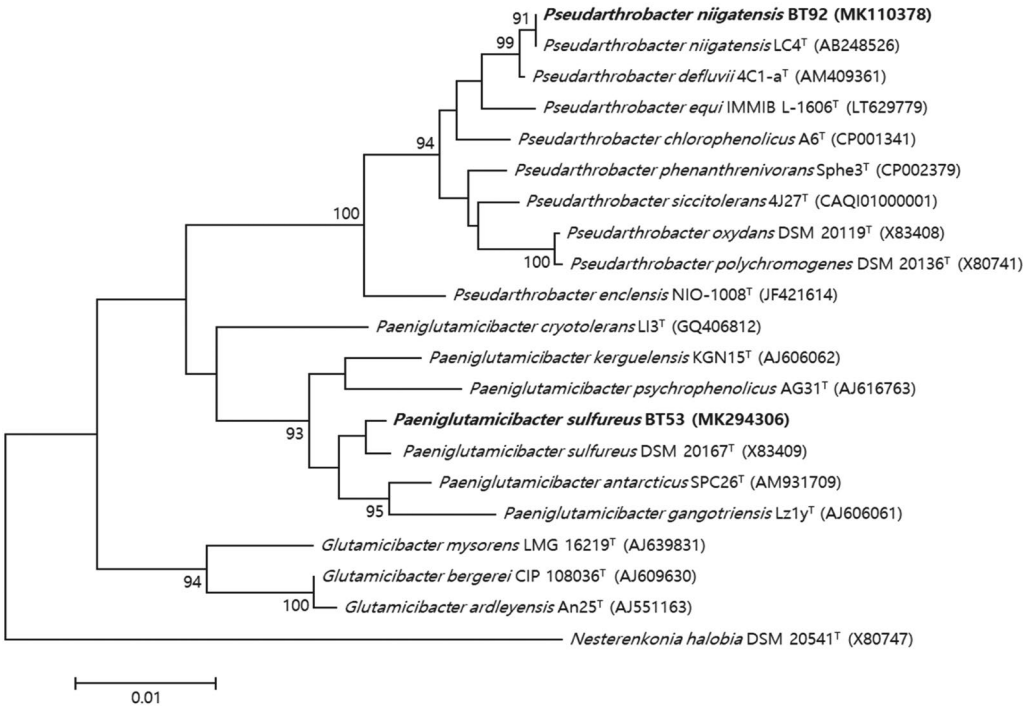

Fig. 4. Neighbor-joining phylogenetic tree based on 16S rRNA gene sequences shows the relationship between the strains isolated in this study and their relatives of the family *Micrococcaceae*. Strains: BT53 and BT92. Bootstrap values (>80%) are shown above nodes for the neighbor-joining methods. Bar: 0.01 substitutions per nucleotide position.

the API 20NE test, positive for β-galactosidase, D-mannitol and D-maltose. Weak positive for esculin hydrolysis, D-glucose, L-arabinose, D-mannose, potassium gluconate, adipic acid, malic acid, but negative for reduction of nitrates (NO_3) to nitrite (NO_2^-), reduction of nitrates (NO_3) to nitrogen (N_2), indole production on tryptophan, glucose fermentation, arginine dihydrolase, urease, gelatin hydrolysis, *N*-acetyl-D-glucosamine, capric acid, trisodium citrate and phenylacetic acid. In the API 32GN test, positive for 3-hydroxybutyric acid, D-saccharose (sucrose), D-maltose, glycogen, D-glucose, salicin and L-arabinose, but negative for L-rhamnose, *N*-acetyl-glucosamine, D-ribose, inositol, itaconic acid, suberic acid, sodium malonate, sodium acetate, lactic acid, L-alanine, potassium 5-ketogluconate 3-hydroxybenzoic acid, L-serine, D-mannitol, D-melibiose, D-fucose, D-sorbitol, propionic acid, capric acid, valeric acid, trisodium citrate, L-histidine, potassium 2-ketogluconate, 4-hydroxybenzoic acid and L-proline. Strain BT98 (=NIBRBAC000501839) was isolated from a soil sample, Okcheon-gun, Chungcheongbuk-do, Korea.

Description of *Agromyces binzhouensis* BT102

Cells are Gram-stain-positive, non-flagellated, and rod-shaped. Colonies are yellow colored after 3 days of incubation on R2A at 25°C. In the BIOLOG GEN III test, positive for dextrin, D-maltose, D-trehalose, D-cellobiose, gentiobiose, sucrose, D-turanose, stachyose, D-raffinose, α-D-lactose, D-melibiose, β-methyl-D-glucoside, D-salicin, 1% NaCl, α-D-glucose, D-mannose, D-fructose, D-galactose, L-rhamnose, inosine, D-mannitol, glycerol, rifamycin SV, L-glutamic acid, pectin, D-gluconic acid, D-glucuronic acid, glucuronamide, p-hydroxy-phenylacetic acid, L-lactic acid, L-malic acid, nalidixic acid, lithium chloride, potassium tellurite, tween 40, β-hydroxy-D, L-butyric acid, acetoacetic acid, acetic acid, and aztreonam. In the API 20NE test, positive for esculin hydrolysis, β-galactosidase, D-mannitol; weak positive for D-glucose, L-arabinose, D-mannose, *N*-acetyl-D-glucosamine, D-maltose, potassium gluconate, and trisodium citrate; but negative for reduction of nitrates (NO_3) to nitrite (NO_2^-), reduction of nitrates (NO_3) to nitrogen (N_2), indole production on tryptophan, glucose fermentation, arginine dihydrolase, urease, gelatin hydrolysis, capric acid, adipic acid, and phenylacetic acid. In the API 32GN test, positive for L-rhamnose, D-saccharose (sucrose), D-maltose, glycogen, D-mannitol, D-glucose, D-melibiose, L-arabinose and L-alanine; but negative for *N*-acetyl-glucosamine, D-ribose, inositol, itaconic acid, suberic acid, sodium malonate, sodium acetate potassium 5-ketogluconate, 3-hydroxybenzoic acid, L-serine, salicin,

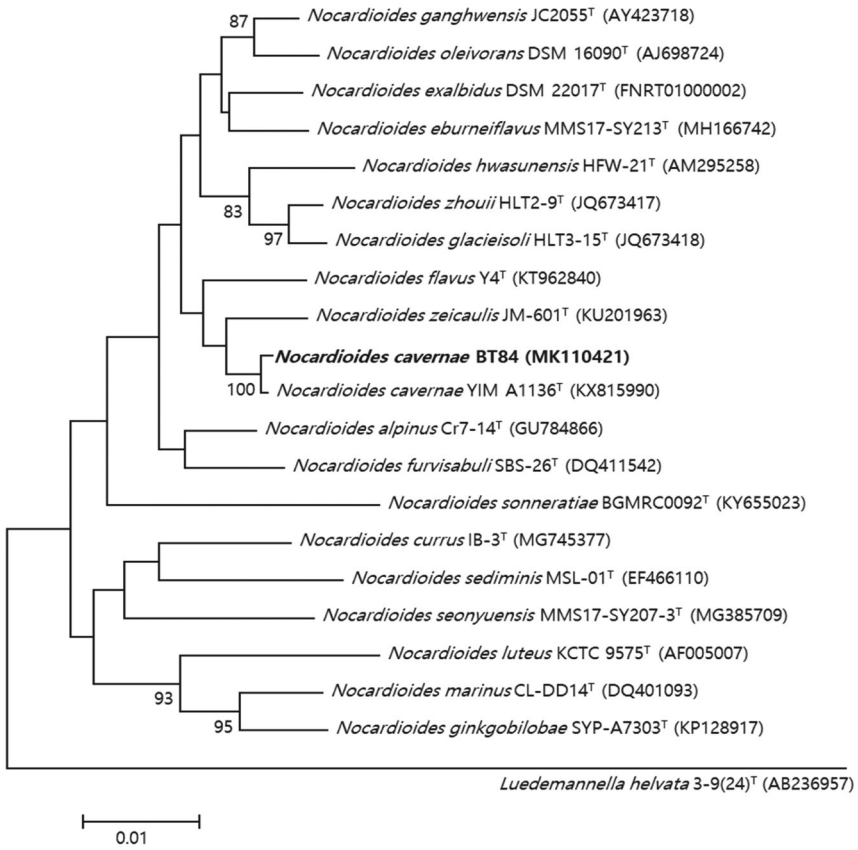

Fig. 5. Neighbor-joining phylogenetic tree based on 16S rRNA gene sequences shows the relationship between the strains isolated in this study and their relatives of the family *Nocardioidaceae*. Strains: BT84. Bootstrap values (>80%) are shown above nodes for the neighbor-joining methods. Bar: 0.01 substitutions per nucleotide position.

D-fucose, D-sorbitol, propionic acid, capric acid, valeric acid, trisodium citrate, L-histidine, potassium 2-ketogluconate, 3-hydroxybutyric acid, 4-hydroxybenzoic acid, and L-proline. Strain BT102 (=NIBRBAC000501936) was isolated from a soil sample, Okcheon-gun, Chungcheongbuk-do, Korea.

Description of *Microbacterium enclense* BT89

Cells are Gram-stain-positive, non-flagellated, and rod-shaped. Colonies are cream colored after 3 days of incubation on R2A at 25°C. In the BIOLOG GEN III test, positive for D-maltose, D-trehalose, D-cellobiose, gentiobiose, sucrose, D-turanose, pH 6, pH 5, β-methyl-D-glucoside, D-salicin, 1% NaCl, 4% NaCl, α-D-glucose, D-mannose, D-fructose, 1% sodium lactate, D-mannitol, D-gluconic acid, tetrazolium violet, nalidixic acid, lithium chloride, potassium tellurite, aztreonam, and sodium butyrate. In the API 20NE test, positive for esculin hydrolysis, gelatin hydrolysis, β-galactosidase, D-glucose, L-arabinose, D-mannose, D-mannitol, D-maltose, potassium gluconate, malic acid and trisodium citrate; and weak positive for phenylacetic acid, but negative for reduction of nitrates (NO_3) to nitrite (NO_2^-), reduction of nitrates (NO_3) to nitrogen (N_2), indole production on tryptophan, glucose fermentation, arginine dihydrolase, urease, *N*-acetyl-D-glucosamine, capric acid, and adipic acid. In the API 32GN test, positive for L-rhamnose, D-saccharose (sucrose), D-maltose, potassium 5-ketogluconate, D-mannitol, D-glucose, salicin, L-arabinose, potassium 2-ketogluconate, lactic acid, L-alanine, trisodium citrate, L-histidine; but negative for *N*-acetyl-glucosamine, D-ribose, inositol, itaconic acid, suberic acid, sodium malonate, sodium acetate, glycogen, 3-hydroxybenzoic acid, L-serine, D-melibiose, D-fucose, propionic acid, capric acid, valeric acid, 3-hydroxybutyric acid, 4-hydroxybenzoic acid, and L-proline. Strain BT89 (=NIBRBAC000501937) was isolated from a soil sample, Okcheon-gun, Chungcheongbuk-do, Korea.

Description of *Microbacterium flavescens* BT119

Cells are Gram-stain-positive, flagellated, and short rod-shaped. Colonies are yellow colored after 3 days of

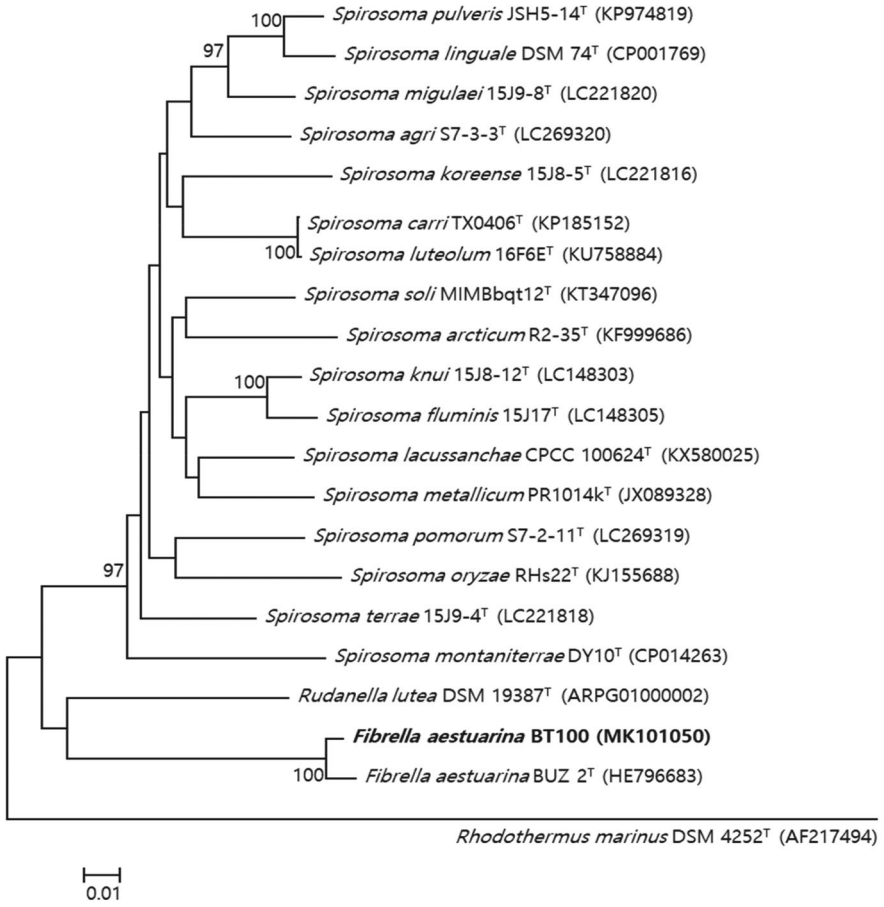

Fig. 6. Neighbor-joining phylogenetic tree based on 16S rRNA gene sequences shows the relationship between the strains isolated in this study and their relatives of the family *Cytophagaceae*. Strain: BT100. Bootstrap values (>80%) are shown above nodes for the neighbor-joining methods. Bar: 0.01 substitutions per nucleotide position.

incubation on R2A at 25°C. In the BIOLOG GEN III test, positive for dextrin, D-maltose, D-trehalose, D-cellobiose, gentiobiose, sucrose, D-turanose, pH 6, β-methyl-D-glucoside, D-salicin, 1% NaCl, 4% NaCl, α-D-glucose, D-mannose, D-fructose, D-galactose, 3-methyl glucose, L-fucose, L-rhamnose, inosine, 1% sodium lactate, D-mannitol, glycerol, gelatin, glycyl-L-proline, L-aspartic acid, L-glutamic acid, pectin, D-gluconic acid, p-hydroxy-phenylacetic acid, L-lactic acid, L-malic acid, bromo-succinic acid, nalidixic acid, lithium chloride, potassium tellurite, tween 40, α-hydroxy-butyric acid, β-hydroxy-D, L-butyric acid, α-keto-butyric acid, acetoacetic acid, propionic acid, acetic acid, aztreonam, sodium butyrate, and sodium bromate; and weak positive for D-raffinose, α-D-lactose, D-melibiose, *N*-acetyl-D-galactosamine, fusidic acid, D-sorbitol, D-glucose-6-PO, D-fructose-6-PO, troleandomycin, rifamycin SV, minocycline, L-arginine, L-pyroglutamic acid, L-serine, lincomycin, guanidine HCl, D-galacturonic acid, D-glucuronic acid, glucuronamide, quinic acid, vancomycin, tetrazolium violet, methyl pyruvate, D-lactic acid methyl ester, citric acid, α-keto-glutaric acid, D-malic acid, and γ-amino-butyric acid. In the API 20NE test, positive for esculin hydrolysis, β-galactosidase, D-glucose, D-mannitol, D-maltose, and potassium gluconate; weak positive for L-arabinose and D-mannose; but negative for reduction of nitrates (NO_3) to nitrite (NO_2^-), reduction of nitrates (NO_3) to nitrogen (N_2), indole production on tryptophan, glucose fermentation, arginine dihydrolase, urease, gelatin hydrolysis, *N*-acetyl-D-glucosamine, capric acid, adipic acid, and phenylacetic acid. In the API 32GN test, positive for D-saccharose (sucrose), D-maltose, D-mannitol, D-glucose, L-arabinose, trisodium citrate, glycogen, salicin, propionic acid, and valeric acid; but negative for L-rhamnose, *N*-acetyl-glucosamine, D-ribose, inositol, itaconic acid, suberic acid, sodium malonate, sodium acetate, lactic acid, L-alanine, potassium 5-ketogluconate, 3-hydroxybenzoic acid, L-serine, D-melibiose, D-fucose, D-sorbitol, capric acid, L-histidine, potassium 2-ketogluconate, 3-hydroxybutyric acid, 4-hydroxybenzoic acid,

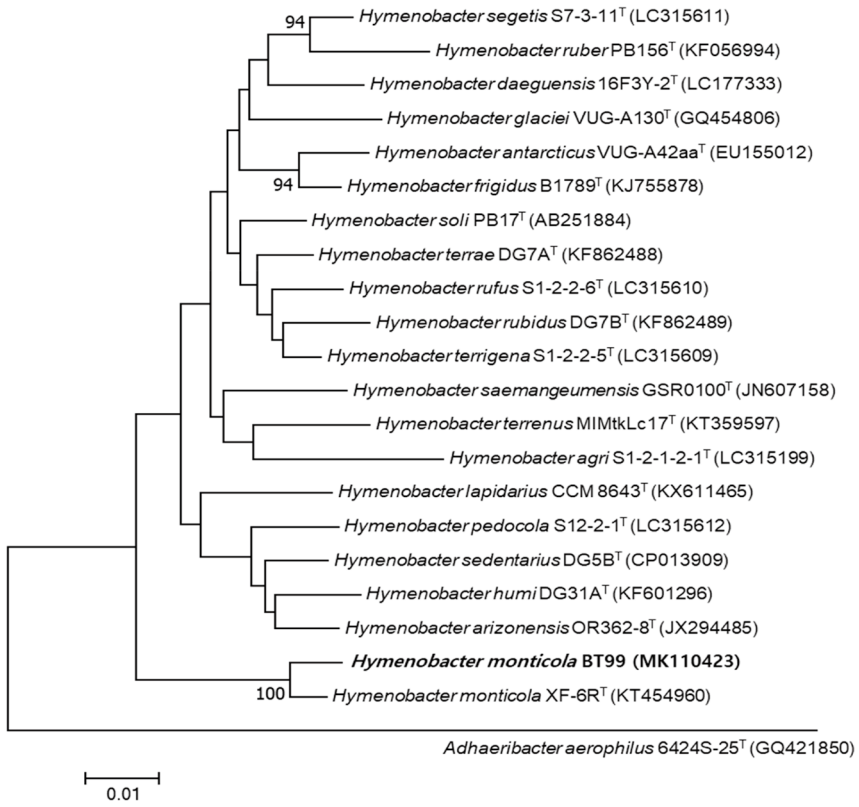

Fig. 7. Neighbor-joining phylogenetic tree based on 16S rRNA gene sequences shows the relationship between the strains isolated in this study and their relatives of the family *Hymenobacteraceae*. Strain: BT99. Bootstrap values (>80%) are shown above nodes for the neighbor-joining methods. Bar: 0.01 substitutions per nucleotide position.

and L-proline. Strain BT119 (=NIBRBAC000501833) was isolated from a soil sample, Okcheon-gun, Chungcheongbuk-do, Korea.

Description of *Arthrobacter nitrophenolicus* BT82

Cells are Gram-stain-positive, non-flagellated, and rod-shaped. Colonies are white colored after 3 days of incubation on R2A at 25°C. In the BIOLOG GEN III test, positive for glycerol, D-aspartic acid, L-alanine, L-aspartic acid, L-glutamic acid, L-histidine, L-pyroglutamic acid, D-gluconic acid, mucic acid, tetrazolium violet, L-lactic acid, citric acid, α-keto-glutaric acid, D-malic acid, γ-amino-butyric acid, α-hydroxy-butyric acid, β-hydroxy-D, L-butyric acid, α-keto-butyric acid, and propionic acid; and weak positive for pH 6, 1% sodium lactate, fusidic acid, troleandomycin, lincomycin, glucuronamide, vancomycin, tetrazolium blue, L-malic acid, nalidixic acid, acetic acid, and aztreonam. In the API 20NE test, positive for esculin hydrolysis, β-galactosidase, D-glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-D-glucosamine, D-maltose, potassium gluconate, adipic acid, malic acid, trisodium citrate, and phenylacetic acid; weak positive for urease; but negative for reduction of nitrates (NO_3) to nitrite (NO_2^-), reduction of nitrates (NO_3) to nitrogen (N_2), indole production on tryptophan, glucose fermentation, arginine dihydrolase, gelatin hydrolysis, and capric acid. In the API 32GN test, positive for *N*-acetyl-glucosamine, inositol, D-saccharose (sucrose), D-maltose, suberic acid, L-alanine, D-mannitol, D-glucose, salicin, D-melibiose, L-arabinose, L-histidine, potassium 2-ketogluconate, L-proline, L-rhamnose, D-ribose, sodium malonate, sodium acetate, lactic acid, potassium 5-ketogluconate, glycogen, 3-hydroxybenzoic acid, L-serine, propionic acid, valeric acid, trisodium citrate, 3-hydroxybutyric acid, and 4-hydroxybenzoic acid; but negative for itaconic acid, D-fucose, D-sorbitol, and capric acid. Strain BT82 (=NIBRBAC000501851) was isolated from a soil sample, Okcheon-gun, Chungcheongbuk-do, Korea.

Description of *Paeniglutamicibacter sulfureus* BT53

Cells are Gram-stain-positive, non-flagellated, and rod-shaped. Colonies are yellow colored after 3 days of incubation on 1/10 LB at 25°C. In the BIOLOG GEN III test, positive for dextrin, D-maltose, D-turanose, stachyose, pH 6, D-melibiose, *N*-acetyl-D-glucosamine, *N*-acetyl-D-galactosamine, *N*-acetyl neuraminic acid, 1%

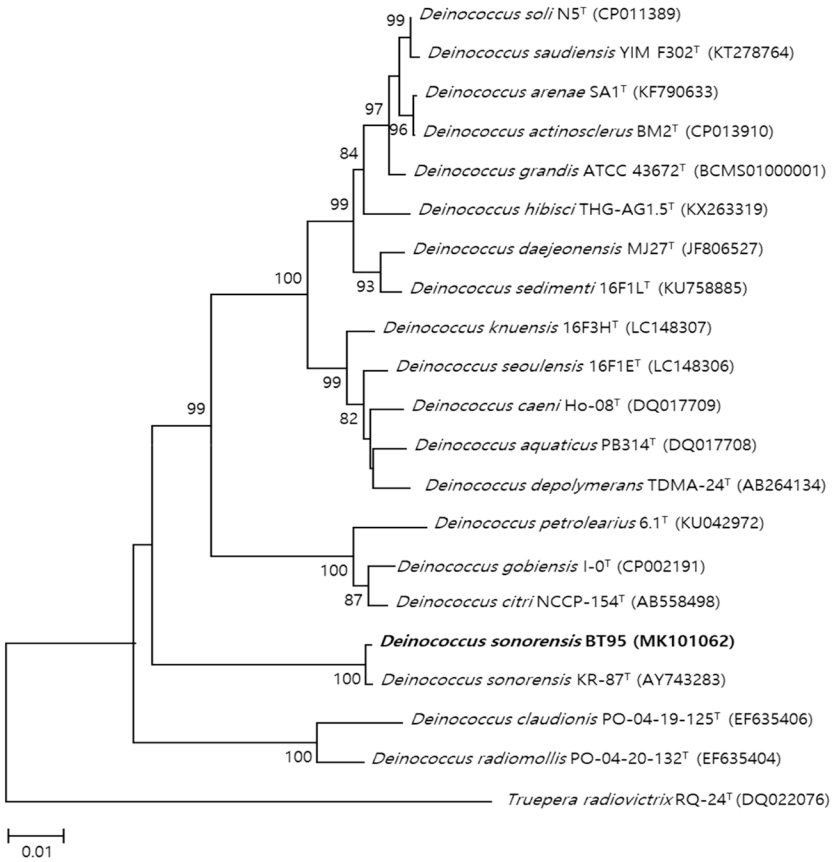

Fig. 8. Neighbor-joining phylogenetic tree based on 16S rRNA gene sequences shows the relationship between the strains isolated in this study and their relatives of the family *Deinococcaceae*. Strain: BT95. Bootstrap values (>80%) are shown above nodes for the neighbor-joining methods. Bar: 0.01 substitutions per nucleotide position.

NaCl, 4% NaCl, D-fructose, inosine, 1% sodium lactate, myo-inositol, D-glucose-6-PO_4, glycyl-L-proline, L-arginine, L-aspartic acid, L-glutamic acid, L-pyroglutamic acid, L-serine, guanidine HCl, D-gluconic acid, D-glucuronic acid, quinic acid, D-saccharic acid, L-lactic acid, citric acid, α-keto-glutaric acid, L-malic acid, bromo-succinic acid, nalidixic acid, lithium chloride, potassium tellurite, α-hydroxy-butyric acid, β-hydroxy-D, L-butyric acid, α-keto-butyric acid, acetoacetic acid, acetic acid, aztreonam, and sodium bromate. In the API 20NE test, positive for indole production on tryptophan, urease, D-glucose, D-maltose, potassium gluconate, malic acid, trisodium citrate and phenylacetic acid; weak positive for esculin hydrolysis and β-galactosidase; but negative for gelatin hydrolysis, D-glucose, L-arabinose, D-mannose, D-mannitol, reduction of nitrates (NO_3) to nitrite (NO_2^-), reduction of nitrates (NO_3) to nitrogen (N_2), glucose fermentation, arginine dihydrolase, *N*-acetyl-D-glucosamine, capric acid, and adipic acid. In the API 32GN test, positive for *N*-acetyl-glucosamine, D-saccharose (sucrose), D-maltose, sodium malonate, sodium acetate, lactic acid, L-alanine, potassium 5-ketogluconate, 3-hydroxybenzoic acid, L-serine, D-glucose, D-melibiose, propionic acid, 3-hydroxybutyric acid, D-ribose, suberic acid, glycogen, salicin, valeric acid, trisodium citrate, L-histidine, and L-proline; but negative for L-rhamnose, D-mannitol, L-arabinose, potassium 2-ketogluconate, inositol, itaconic acid, D-fucose, capric acid, and 4-hydroxybenzoic acid. Strain BT53 (=NIBRBAC000502699) was isolated from a soil sample, Pyeongchang-gun, Gangwon-do, Korea.

Description of *Pseudarthrobacter niigatensis* BT92

Cells are Gram-stain-positive, non-flagellated, and rod-shaped. Colonies are white colored after 3 days of incubation on R2A at 25°C. In the BIOLOG GEN III test, weak positive for D-maltose, Gentiobiose, D-turanose, stachyose, pH 6, D-raffinose, *N*-acetyl-neuraminic acid, 1% NaCl, D-galactose, D-fucose, inosine, 1% sodium lactate, D-sorbitol, myo-inositol, D-glucose-6-PO_4, D-fructose-6-PO_4, D-aspartic acid, L-aspartic acid, L-glutamic acid, L-pyroglutamic acid, L-serine, pectin, D-gluconic acid,

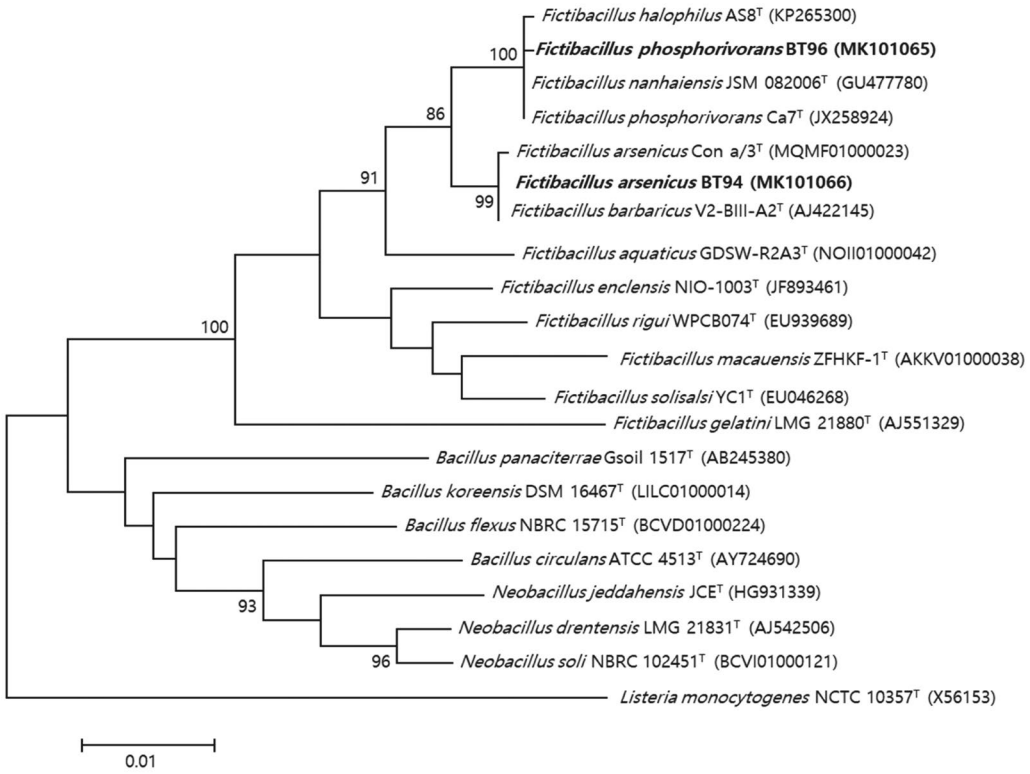

Fig. 9. Neighbor-joining phylogenetic tree based on 16S rRNA gene sequences shows the relationship between the strains isolated in this study and their relatives of the family *Bacillaceae*. Strain: BT94, BT96. Bootstrap values (>80%) are shown above nodes for the neighbor-joining methods. Bar: 0.01 substitutions per nucleotide position.

quinic acid, p-hydroxy-phenylacetic acid, methyl pyruvate, α-keto-glutaric acid, nalidixic acid, potassium tellurite, tween 40, γ-amino-butyric acid and aztreonam are positive. Dextrin, D-trehalose, D-cellobiose, sucrose, pH 5, α-D-lactose, D-melibiose, β-methyl-D-glucoside, D-salicin, *N*-acetyl-D-glucosamine, *N*-acetyl-β-D-mannosamine, *N*-acetyl-D-galactosamine, 4% NaCl, 8% NaCl, α-D-glucose, D-mannose, D-fructose, 3-methyl glucose, L-fucose, L-rhamnose, D-mannitol, D-arabitol, glycerol, gelatin, glycyl-L-proline, L-alanine, L-arginine, L-histidine, D-galacturonic acid, L-galactonic acid lactone, D-glucuronic acid, glucuronamide, mucic acid, D-saccharic acid, D-lactic acid methyl ester, L-lactic acid, citric acid, D-malic acid, L-malic acid, bromo-succinic acid, α-hydroxy-butyric acid, β-hydroxy-D, L-butyric acid, α-keto-butyric acid, acetoacetic acid, propionic acid, acetic acid, sodium butyrate, and sodium bromate. In the API 20NE test, positive for reduction of nitrates (NO_3) to nitrogen (N_2), reduction of nitrates (NO_3) to nitrite (NO_2^-), urease, esculin hydrolysis, β-galactosidase, D-glucose, L-arabinose, D-mannose, D-maltose, potassium gluconate, malic acid, trisodium citrate, phenylacetic acid; weak positive for D-mannitol; but negative for indole production on tryptophan, glucose fermentation, arginine dihydrolase, gelatin hydrolysis, *N*-acetyl-D-glucosamine, capric acid, and adipic acid. In the API 32GN test, positive for inositol, D-saccharose (sucrose), D-maltose, D-mannitol, D-glucose, D-melibiose, D-sorbitol, L-arabinose, D-mannitol, sodium malonate, D-ribose, sodium acetate, L-alanine, potassium 5-ketogluconate, L-serine, salicin, propionic acid, valeric acid, trisodium citrate, L-histidine, potassium 2-ketogluconate and 3-hydroxybutyric acid but negative for L-rhamnose, *N*-acetyl-D-glucosamine, itaconic acid, suberic acid, lactic acid, glycogen, 3-hydroxybenzoic acid, D-fucose, capric acid, 4-hydroxybenzoic acid, and L-proline. Strain BT92 (=NIBRBAC000502727) was isolated from a soil sample, Aewol-eup in Jeju Island, Korea.

Description of *Nocardioides cavernae* BT84

Cells are Gram-stain-positive, non-flagellated, and rod-shaped. Colonies are yellow colored after 3 days of incubation on R2A at 25°C. In the BIOLOG GEN III test, positive for dextrin, D-maltose, D-trehalose, D-cellobiose, sucrose, D-turanose, pH 6, D-raffinose, D-melibiose, D-salicin, *N*-acetyl-D-glucosamine, *N*-acetyl-β-D-mannosamine, 1% NaCl, α-D-glucose, D-mannose, D-fruc-

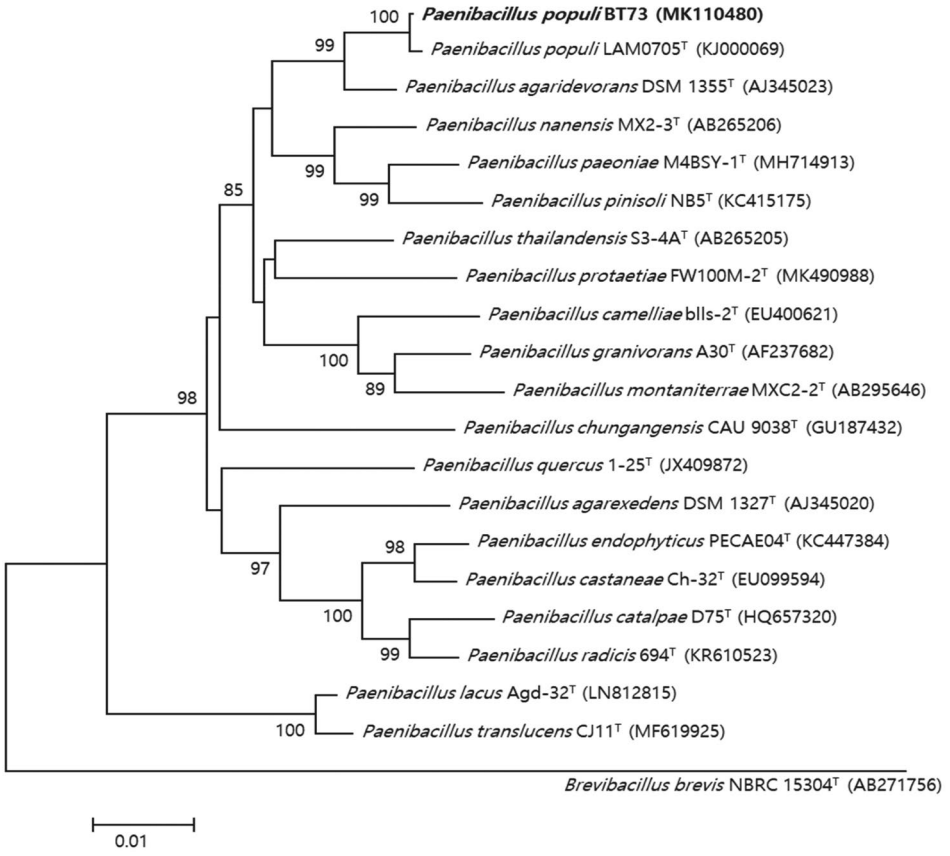

Fig. 10. Neighbor-joining phylogenetic tree based on 16S rRNA gene sequences shows the relationship between the strains isolated in this study and their relatives of the family *Paenibacillaceae*. Strain: BT73. Bootstrap values (>80%) are shown above nodes for the neighbor-joining methods. Bar: 0.01 substitutions per nucleotide position.

tose, D-galactose, D-fucose, L-fucose, L-rhamnose, inosine, 1% sodium lactate, D-sorbitol, D-mannitol, glycerol, D-glucose-6-PO, D-fructose-6-PO, rifamycin SV, gelatin, L-aspartic acid, L-glutamic acid, L-pyroglutamic acid, D-gluconic acid, L-malic acid, bromo-succinic acid, nalidixic acid, potassium tellurite, β-hydroxy-D, L-butyric acid, propionic acid, acetic acid, and aztreonam; and weak positive for gentiobiose, stachyose, α-D-lactose, β-methyl-D-glucoside, *N*-acetyl-D-galactosamine, *N*-acetyl-neuraminic acid, 4% NaCl, 8% NaCl, 3-methyl glucose, fusidic acid, D-arabitol, myo-inositol, D-aspartic acid, D-serine, glycyl-L-proline, L-alanine, L-arginine, L-histidine, L-serine, D-galacturonic acid, L-galactonic acid lactone, D-glucuronic acid, glucuronamide, mucic acid, quinic acid, D-saccharic acid, methyl pyruvate, D-lactic acid methyl ester, L-lactic acid, α-keto-glutaric acid, D-malic acid, lithium chloride, tween 40, γ-amino-butyric acid, α-hydroxy-butyric acid, α-keto-butyric acid, acetoacetic acid, odium butyrate, and sodium bromate. In the API 20NE test, positive for esculin hydrolysis, gelatin hydrolysis, β-galactosidase, D-glucose, D-mannitol, D-maltose, potassium gluconate, and malic acid; weak positive for L-arabinose, *N*-acetyl-D-glucosamine; but negative for reduction of nitrates (NO_3) to nitrite (NO_2^-), reduction of nitrates (NO_3) to nitrogen (N_2), indole production on tryptophan, glucose fermentation, arginine dihydrolase, urease, D-mannose, capric acid, adipic acid, trisodium citrate, and phenylacetic acid. In the API 32GN test, positive for L-rhamnose, D-saccharose (sucrose), D-mannitol, L-arabinose, propionic acid, *N*-acetyl-glucosamine, D-maltose, D-glucose, and valeric acid; but negative for D-ribose, inositol, itaconic acid, suberic acid, sodium malonate, sodium acetate, lactic acid, L-alanine, potassium 5-ketogluconate, glycogen, 3-hydroxybenzoic acid, L-serine, salicin, D-melibiose, D-fucose, D-sorbitol, capric acid, trisodium citrate, L-histidine, potassium 2-ketogluconate, 3-hydroxybutyric acid, 4-hydroxybenzoic, acid and L-proline. Strain BT84 (=NIBRBAC000502726) was isolated from a soil sample, Aewol-eup, Jeju Island, Korea.

Description of *Fibrella aestuarina* BT100

Cells are Gram-stain-negative, non-flagellated, and

rod-shaped. Colonies are red colored after 3 days of incubation on R2A at 25°C. In the BIOLOG GEN III test, positive for pH 6, α-D-glucose, D-mannose, D-fructose, gelatin, tetrazolium blue, nalidixic acid, and aztreonam; and weak positive dextrin, D-maltose, D-trehalose, D-cellobiose, gentiobiose, sucrose, D-turanose, α-D-lactose, D-melibiose, β-methyl-D-glucoside, D-salicin, *N*-acetyl-D-glucosamine, D-galactose, L-fucose, minocycline, glucuronamide, vancomycin, tetrazolium violet, and potassium tellurite. In the API 20NE test, positive for esculin hydrolysis, gelatin hydrolysis, β-galactosidase, D-glucose, D-mannose, and D-maltose; weak positive for *N*-acetyl-D-glucosamine; but negative for reduction of nitrates (NO_3) to nitrite (NO_2^-), reduction of nitrates (NO_3) to nitrogen (N_2), indole production on tryptophan, glucose fermentation, arginine dihydrolase, urease, L-arabinose, D-mannitol, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid. In the API 32GN test, positive for D-saccharose (sucrose), D-maltose, glycogen, D-glucose, D-melibiose and salicin, but negative for L-rhamnose, D-ribose, inositol, itaconic acid, suberic acid, sodium malonate, sodium acetate, lactic acid, L-alanine, potassium 5-ketogluconate, 3-hydroxybenzoic acid, L-serine, D-mannitol, D-fucose, D-sorbitol, L-arabinose, propionic acid, capric acid, valeric acid, trisodium citrate, L-histidine, potassium 2-ketogluconate, 3-hydroxybutyric acid, 4-hydroxybenzoic acid, and L-proline. Strain BT100 (=NIBRBAC000501831) was isolated from a soil sample, Okcheon-gun, Chungcheongbuk-do, Korea.

Description of *Hymenobacter monticola* BT99

Cells are Gram-stain-positive, non-flagellated, and rod-shaped. Colonies are red colored after 3 days of incubation on R2A at 25°C. In the BIOLOG GEN III test, positive for tetrazolium violet. In the API 20NE test, positive for β-galactosidase; weak positive for urease and esculin hydrolysis; but negative for reduction of nitrates (NO_3) to nitrite (NO_2^-), reduction of nitrates (NO_3) to nitrogen (N_2), indole production on tryptophan, glucose fermentation, arginine dihydrolase, gelatin hydrolysis, D-glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-D-glucosamine, D-maltose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid. In the API 32GN test, negative for L-rhamnose, *N*-acetyl-glucosamine, D-ribose, inositol, D-saccharose (sucrose), D-maltose, itaconic acid, suberic acid, sodium malonate, sodium acetate, lactic acid, L-alanine, potassium 5-ketogluconate, glycogen, 3-hydroxybenzoic acid, L-serine, D-mannitol, D-glucose, salicin, D-melibiose, D-fucose, D-sorbitol, L-arabinose, propionic acid, capric acid, valeric acid, trisodium citrate, L-histidine, potassium 2-ketogluconate, 3-hydroxybutyric acid, 4-hydroxybenzoic acid, and L-proline. Strain BT99 (=NIBRBAC000501835) was isolated from a soil sample, Okcheon-gun, Chungcheongbuk-do, Korea.

Description of *Deinococcus sonorensis* BT95

Cells are Gram-stain-negative, non-flagellated, and rod-shaped. Colonies are transparent white colored after 3 days of incubation on R2A at 25°C. In the BIOLOG GEN III test, positive for tetrazolium violet; and weak positive for dextrin, D-maltose, D-trehalose, D-cellobiose, α-D-lactose, β-methyl-D-glucoside, α-D-glucose, D-fructose, D-fructose, troleandomycin, rifamycin SV, gelatin, glucuronamide, tetrazolium blue, nalidixic acid, and aztreonam. In the API 20NE test, positive for β-galactosidase; weak positive for esculin hydrolysis; but negative for reduction of nitrates (NO_3) to nitrite (NO_2^-), reduction of nitrates (NO_3) to nitrogen (N_2), indole production on tryptophan, glucose fermentation, arginine dihydrolase, urease, gelatin hydrolysis, D-glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-D-glucosamine, D-maltose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid. In the API 32GN test, positive for D-maltose, but negative for L-rhamnose, *N*-acetyl-glucosamine, D-ribose, inositol, D-saccharose (sucrose), itaconic acid, suberic acid, sodium malonate, sodium acetate, lactic acid, L-alanine, potassium 5-ketogluconate, glycogen, 3-hydroxybenzoic acid, L-serine, D-mannitol, D-glucose, salicin, D-melibiose, D-fucose, D-sorbitol, L-arabinose, propionic acid, capric acid, valeric acid, trisodium citrate, L-histidine, potassium 2-ketogluconate, 3-hydroxybutyric acid, 4-hydroxybenzoic acid, and L-proline. Strain BT95 (=NIBRBAC000501845) was isolated from a soil sample, Okcheon-gun, Chungcheongbuk-do, Korea.

Description of *Fictibacillus arsenicus* BT94

Cells are Gram-stain-positive, flagellated, and rod-shaped. Colonies are light orange colored after 3 days of incubation on R2A at 25°C. In the BIOLOG GEN III test, positive for dextrin, D-maltose, D-trehalose, D-cellobiose, gentiobiose, sucrose, D-turanose, pH 6, β-methyl-D-glucoside, D-salicin, *N*-acetyl-D-glucosamine, *N*-acetyl-β-D-mannosamine, 1% NaCl, 8% NaCl, α-D-glucose, D-mannose, D-fructose, D-galactose, 3-methyl glucose, D-fucose, L-fucose, L-rhamnose, inosine, D-sorbitol, D-arabitol, D-glucose-6-PO_4, D-fructose-6-PO_4, D-aspartic acid, rifamycin SV, minocycline, gelatin, L-alanine, L-arginine, L-aspartic acid, L-glutamic acid, L-histidine, L-pyroglutamic acid, pectin, L-galactonic acid lactone, D-gluconic acid, D-glucuronic acid, quinic acid, D-saccharic acid, L-lactic acid, α-keto-glutaric acid, L-malic acid, acetoacetic acid, acetic acid, formic acid, aztreonam, and sodium butyrate; and weak positive for stachyose,

D-raffinose, α-D-lactose, D-melibiose, *N*-acetyl-D-galactosamine, *N*-acetyl neuraminic acid, 4% NaCl, 1% sodium lactate, D-serine, D-mannitol, myo-inositol, glycerol, glycyl-L-proline, L-serine, D-galacturonic acid, glucuronamide, mucic acid, tetrazolium blue, p-hydroxy-phenylacetic acid, D-lactic acid methyl ester, citric acid, D-malic acid, lithium chloride, potassium tellurite, tween 40, γ-amino-butyric acid, α-hydroxy-butyric acid, β-hydroxy-D, L-butyric acid, propionic acid, and sodium bromate. In the API 20NE test, positive for esculin hydrolysis, gelatin hydrolysis, D-glucose, D-maltose, and potassium gluconate; weak positive for D-mannitol, malic acid, and phenylacetic acid; but negative for reduction of nitrates (NO_3) to nitrite (NO_2^-), reduction of nitrates (NO_3) to nitrogen (N_2), indole production on tryptophan, glucose fermentation, arginine dihydrolase, urease, β-galactosidase, L-arabinose, D-mannose, *N*-acetyl-D-glucosamine, capric acid, adipic acid, and trisodium citrate. In the API 32GN test, positive for D-maltose, glycogen, and D-glucose; but negative for L-rhamnose, D-saccharose (sucrose), potassium 5-ketogluconate, D-mannitol, salicin, L-arabinose, potassium 2-ketogluconate, lactic acid, L-alanine, trisodium citrate, L-histidine, *N*-acetyl-glucosamine, D-ribose, inositol, itaconic acid, suberic acid, sodium malonate, sodium acetate, 3-hydroxybenzoic acid, L-serine, D-melibiose, D-fucose, propionic acid, capric acid, valeric acid, 3-hydroxybutyric acid, 4-hydroxybenzoic acid, and L-proline. Strain BT94 (=NIBRBAC000501846) was isolated from a soil sample, Okcheon-gun, Chungcheongbuk-do, Korea.

Description of *Fictibacillus phosphorivorans* BT96

Cells are Gram-stain-positive, non-flagellated, and rod-shaped. Colonies are yellow colored after 3 days of incubation on R2A at 25°C. In the BIOLOG GEN III test, positive for dextrin, D-maltose, D-trehalose, D-cellobiose, gentiobiose, sucrose, D-turanose, D-raffinose, D-melibiose, β-methyl-D-glucoside, D-salicin, *N*-acetyl-D-glucosamine, *N*-acetyl-β-D-mannosamine, 8% NaCl, α-D-glucose, D-mannose, D-fructose, 3-methyl glucose, D-fucose, L-fucose, L-rhamnose, inosine, 1% sodium lactate, D-sorbitol, D-arabitol, D-glucose-6-PO, D-fructose-6-PO_4, gelatin, glycyl-L-proline, L-aspartic acid, L-glutamic acid, L-histidine, pectin, D-gluconic acid, mucic acid, quinic acid, D-lactic acid methyl ester, α-keto-glutaric acid, L-malic acid, potassium tellurite, tween 40, acetoacetic acid, acetic acid, formic acid, and sodium butyrate; weak positive for stachyose, pH 6, α-D-lactose, *N*-acetyl-D-galactosamine, *N*-acetyl-neuraminic acid, 1% NaCl, 4% NaCl, D-galactose, D-serine, D-mannitol, myo-inositol, glycerol, D-aspartic acid, rifamycin SV, L-alanine, L-arginine, L-pyroglutamic acid, L-serine, lincomycin, D-galacturonic acid, L-galactonic acid lactone, D-glucuronic acid, glucuronamide, D-saccharic acid, tetrazolium blue, p-hydroxy-phenylacetic acid, methyl pyruvate, L-lactic acid, citric acid, D-malic acid, bromo-succinic acid, lithium chloride, γ-amino-butyric acid, α-hydroxy-butyric acid, β-hydroxy-D, L-butyric acid, α-keto-butyric acid, propionic acid, aztreonam, and sodium bromate. In the API 20NE test, positive for esculin hydrolysis, gelatin hydrolysis, D-glucose, D-mannose, D-maltose and potassium gluconate; weak positive for L-arabinose, D-mannitol, *N*-acetyl-D-glucosamine, malic acid, and phenylacetic acid.; but negative for reduction of nitrates (NO_3) to nitrite (NO_2^-), reduction of nitrates (NO_3) to nitrogen (N_2), indole production on tryptophan, glucose fermentation, arginine dihydrolase, urease, β-galactosidase, capric acid, adipic acid, and trisodium citrate. In the API 32GN test, positive for *N*-acetyl-glucosamine, D-ribose, D-saccharose (sucrose), D-maltose, sodium acetate, L-alanine, glycogen, and D-glucose; but negative for L-rhamnose, inositol, itaconic acid, suberic acid, sodium malonate, lactic acid, potassium 5-ketogluconate, 3-hydroxybenzoic acid, L-serine, D-mannitol, salicin, D-melibiose, D-fucose, D-sorbitol, L-arabinose, propionic acid, capric acid, valeric acid, trisodium citrate, L-histidine, potassium 2-ketogluconate, 3-hydroxybutyric acid, 4-hydroxybenzoic acid, and L-proline. Strain BT96 (=NIBRBAC000501856) was isolated from a soil sample, Okcheon-gun, Chungcheongbuk-do, Korea.

Description of *Paenibacillus populi* BT73

Cells are Gram-stain-positive, flagellated, and rod-shaped. Colonies are transparent white colored after 3 days of incubation on R2A at 25°C. In the BIOLOG GEN III test, positive for D-melibiose, D-sorbitol, and tetrazolium violet vancomycin. In the API 20NE test, positive for arginine dihydrolase, urease, D-glucose, L-arabinose, D-mannose, D-mannitol, potassium gluconate, adipic acid, malic acid, trisodium citrate, and phenylacetic acid; but negative for reduction of nitrates (NO_3) to nitrite (NO_2^-), reduction of nitrates (NO_3) to nitrogen (N_2), indole production on tryptophan, glucose fermentation, esculin hydrolysis, gelatin hydrolysis, β-galactosidase, *N*-Acetyl-D-glucosamine, D-maltose, and capric acid. In the API 32GN test, negative for inositol, D-saccharose (sucrose), D-mannitol, D-sorbitol, L-rhamnose, D-ribose, D-maltose, itaconic acid, sodium malonate, lactic acid, L-alanine, potassium 5-ketogluconate, glycogen, 3-hydroxybenzoic acid, salicin, D-melibiose, D-fucose, L-arabinose, capric acid, L-histidine, potassium 2-ketogluconate, 4-hydroxybenzoic acid, *N*-acetyl-glucosamine, suberic acid, sodium acetate, L-serine, D-glucose, propionic acid, valeric acid, trisodium citrate, 3-hydroxybutyric acid, and L-proline. Strain BT73 (=NIBRBAC000501826) was isolated from a soil sample, Pyeongchang-gun, Gangwon-do, Korea.

Acknowledgements

This work was supported by a research grant from Seoul Women's University (2018) and by a grant from the National Institute of Biological Resources (NIBR), funded by the Ministry of Environment (MOE) of the Republic of Korea (NIBR201801106).

References

Battista, J.R. 2016. *Deinococcus-ThermusGroup*. eLS, 1-12.

Choi, C.Y., J.Y. Choi, Y.J. Choi and J.H. Yoo. 2018. Physiological effects of various light spectra on oxidative stress by starvation in olive flounder, *Paralichthys olivaceus*. Mol Cell Toxicol 14:399-408.

Edgar, R.C. 2004. MUSCLE: multiple sequence alignment with high accuracy and high throughput. Nucleic Acids Res. 32:1792-1797.

Felsenstein, J. 1985. Confidence limits on phylogenies: an approach using the bootstrap. Evolution 39:783-791.

Hall, T.A. 1999. BioEdit: a user-friendly biological sequence alignment editor and analysis program for Windows 95/98/NT. In: Nucleic acids symposium series. vol 41. [London]: Information Retrieval Ltd., c1979-c2000, pp 95-98.

Hirsch, P., W. Ludwig, C. Hethke, M. Sittig, B. Hoffmann and C.A. Gallikowski. 1998. *Hymenobacter* roseosalivarius gen. nov., sp. nov. from continental Antartica soils and sandstone: bacteria of the *Cytophaga/Flavobacterium/Bacteroides* line of phylogenetic descent. Syst. Appl. Microbiol. 21:374-383.

Im, S., D. Song, M. Joe, D. Kim, D.-H. Park and S. Lim. 2013. Comparative survival analysis of 12 histidine kinase mutants of Deinococcus radiodurans after exposure to DNA-damaging agents. Bioprocess Biosyst Eng 36:781-789.

Jang, S.A., S.R. Lee, H.J. Koo, J.W. Lee, Y. Park, S. Namkoong, M.K. Kim, S.C. Kang and E.H. Sohn. 2017. Gamma irradiation-induced liver injury and its amelioration by red ginseng extract. Mol Cell Toxicol 13:461-469.

Kim, M.K., M.S. Kang, S. Srinivasan, D.H. Lee, S.-Y. Lee, H.-Y. Jung. 2017a. Complete genome sequence of *Hymenobacter sedentarius* DG5BT, a bacterium resistant to gamma radiation. Mol Cell Toxicol 13:199-205.

Kim, M.K., J.Y. Kim, S.J. Kim, M.J. Kim, J.Y. Lee, C.G. Kim and S. Srinivasan. 2017b. Complete genome sequence of *Spirosoma pulveris* JSH 5-14T, a bacterium isolated from a dust sample. Mol Cell Toxicol 13:373-378.

Kim, O.S., Y.J. Cho, K. Lee, S.H. Yoon, M. Kim, H. Na, S.C. Park, Y.S. Jeon, J.H. Lee, H. Yi, S. Won and J. Chun. 2012. Introducing EzTaxon-e: a prokaryotic 16S rRNA gene sequence database with phylotypes that represent uncultured species. International Journal of Systematic and Evolutionary Microbiology 62:716-721.

Kimura, M. 1983. The neutral theory of molecular evolution. Cambridge University Press.

Kumar, S., G. Stecher and K. Tamura. 2016. MEGA7: Molecular Evolutionary Genetics Analysis version 7.0 for bigger datadets. Molecular Biology and Evolution 33:1870-1874.

Lee, J.J., S.J. Park, Y.H. Lee, S.Y. Lee, L.N. Ten and H.Y. Jung. 2017. *Hymenobacter aquaticus* sp. nov., a radiation-resistant bacterium isolated from a river. International Journal of Systematic and Evolutionary Microbiology 67:1206-1211.

Lee, J.J., S. Srinivasan, S. Lim, M. Joe, S.H. Lee, S.A. Kwon, Y.J. Kwon, J. Lee, J.J. Choi, H.M. Lee, Y.K. Auh and M.K. Kim. 2014. *Hymenobacter swuensis* sp. nov., a gamma-radiation-resistant bacteria isolated from mountain soil. Current Microbiology 68:305-310.

Miao, V. and J. Davies. 2010. Actinobacteria: the good, the bad, and the ugly. Antonie Van Leeuwenhoek 98:143-150.

Saitou, N., M. Nei. 1987. The neighbor-joining method: a new method for reconstructing phylogenetic trees. Molecular Biology and Evolution 4:406-425.

Sathiyaraj, G., M.K. Kim, J.Y. Kim, S.J. Kim, J.H. Jang, S. Maeng, M.S. Kang and S. Srinivasan. 2018a. Complete genome sequence of *Microvirga* sp. 17 mud 1-3, a radiation-resistant bacterium. Mol Cell Toxicol 14:347-350.

Sathiyaraj, G., M.K. Kim, J.Y. Kim, S.J. Kim, J.H. Jang, S. Maeng, M.S. Kang and S. Srinivasan. 2018b. Complete genome sequence of *Nibribacter radioresistens* DG15C, a radiation resistant bacterium. Mol Cell Toxicol 14:323-328.

Selvam, K., J.R. Duncan, M. Tanaka and J.R. Battista. 2013. DdrA, DdrD, and PprA: components of UV and mitomycin C resistance in *Deinococcus radiodurans* R1. PLoS One 8(7):e69007.

Seong, C.N., J.W. Kang, J.H. Lee, S.Y. Seo, J.J. Woo, C. Park, K.S. Bae and M.S. Kim. 2018. Taxonomic hierarchy of the phylum *Firmicutes* and novel *Firmicutes* species originated from various environments in Korea. Journal of Microbiology 56(1):1-10.

Srinivasan, S., J.J. Lee, K.R. Park, S.H. Park, H.Y. Jung and M.K. Kim. 2015. *Hymenobacter terrae* sp. nov., a bacterium isolated from soil. Current Microbiology 70:643-650.

Srinivasan, S., S.Y. Lee, M.K. Kim and H.Y. Jung. 2017. Complete genome sequence of *Hymenobacter* sp. DG25 A, a gamma radiation-resistant bacterium isolated from soil. Mol Cell Toxicol 13:65-72.

Su, S., M. Chen, C. Teng, S. Jiang, C. Zhang, M. Lin and W. Zhang. 2014. *Hymenobacter kanuolensis* sp. nov., a novel radiationresistant bacterium. International Journal of Systematic and Evolutionary Microbiology 64:2108-2112.

Weisburg, W.G., S.J. Giovannoni and C.R. Woese. 1989.

The Deinococcus-Thermus Phylum and the Effect of rRNA Composition on Phylogenetic Tree Construction. Systematic and Applied Microbiology 11(2):128-134.

Weisburg, W.G., S.M. Barns, D.A. Pelletier and D.J. Lane. 1991. 16S ribosomal DNA amplification for phylogenetic study. Journal of Bacteriology 173:697-703.

Wragg, P., L. Randall and A.M. Whatmore. 2014. Comparison of Biolog GEN III MicroStation semi-automated bacterial identification system with matrix-assisted laser desorption ionization-time of flightmass spectrometry and 16S ribosomal RNA gene sequencing for the identification of bacteria of veterinary interest. Journal of Microbiological Methods 105:16-21.

Zhang, Q., C. Liu, Y. Tang, G. Zhou, P. Shen, C. Fang and A. Yokota. 2007. *Hymenobacter xinjiangensis* sp. nov., a radiation-resistant bacterium isolated from the desert of Xinjiang, China. International Journal of Systematic and Evolutionary Microbiology 57:1752-1756.

Submitted: July 2, 2019
Revised: April 14, 2021
Accepted: April 14, 2021