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Twelve unrecorded UV-resistant bacterial species isolated in 2020

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In 2020, a total of 12 bacterial strains were isolated from soil after a comprehensive investigation of indigenous prokaryotic species in Korea. It was determined that each strain belonged to independent and predefined bacterial species, with high 16S rRNA gene sequence similarity (>98.7%) and formation of a robust phylogenetic clade with the closest species. This study identified four families in the phylum *Actinobacteria*, two families in the phylum *Proteobacteria*, one family in the phylum *Bacteroidetes* one family in the phylum *Firmicutes*; and four species in the family *Nocardiaceae*, two species in the family *Nocardioidaceae*, one species in the family *Cellulomonadaceae*, one species in the family *Hymenobacter*, one species in the family *Methylobacteriaceae*, one species in the family *Microbacteriaceae*, one species in the family *Bacillaceae* and one species in the family *Sphingomonadaceae*. There is no official report of these 12 species in Korea, so they are described as unreported bacterial species in Korea in this study. Gram reaction, basic biochemical characteristics, colony, and cell morphology are included in the species description section.

Keywords: 16S rRNA, bacteria, bacterial diversity, unreported species

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Introduction

We collected soil samples in Korea from different locations for the isolation of various novel and unrecorded bacterial species during a research program supported by NIBR of Korea in 2020, such as Guri-si, Gwangju-si, Namhan-sanseong, Gyeongju-si, Wonju-si, Uijeongbu-si and Jeongseon-gun. From this study we report 12 strains belonging to various genera in the phyla *Actinobacteria*, *Proteobacteria*, *Bacteroidetes* and *Firmicutes*. The isolates belonged to these phyla in Korea are significant due to their tremendous application. At present, the phylum *Actinobacteria* primarily comprises Gram positive bacteria with a high G+C content (>55 mol% in genomic DNA), and is one of the largest phyla within *Bacteria* (Gao and Gupta, 2012); the phylum *Bacteroidetes* is Gram-stain-negative, rod-shaped, and does not form endospores (Ludwig *et al*., 2010); the phylum *Firmicutes* is gram-positive, has low G+C content containing rod/coccus bacteria that are found in diverse environmental habitats; and the phylum *Proteobacteria* are Gram-negative and is largest and most phenotypically diverse division among prokaryotes (Gupta, 2000a; 2000b).

Materials and methods

A total of 12 bacterial strains were isolated from soil samples collected in Korea. The soil samples were serially diluted in distilled water and the aliquot was spread onto R2A medium and 1/10 LB agar medium, incubated at 25°C for 3−4 days. The strain IDs, growth media, isolation sources and incubation conditions are summarized in Table 1. All strains were purified as single strain and stored using 20% glycerol suspension at −80°C as well as freeze-dried ampoules. Morphology of strains was examined by transmission electron microscopy (JEOL, JEM1010) using cells grown for 3−4 days on R2A agar medium. Transmission electron micrograph of the strains are shown in Fig. 1. Gram staining tests were performed using a commercial kit, according to the manufacturer's instruction (bioMérieux). Biochemical characteristics were evaluated using Biolog Microstation with GEN III microplate system, API 20NE and API 32GN strips ac-

Table 1. 16S rRNA gene sequence similarity, isolation source, medium, and incubation conditions of unrecorded strains.

Order	Family	Strain ID	NIBRBAC	Most closely related species	16S rRNA similarity	Isolation source	Medium
Propionibacteriales	*Nocardioidaceae*	BT578	NIBRBAC000506206	*Aeromicrobium choanae*	99.5%	Soil	R2A at 25°C, 3 days
		BT579	NIBRBAC000506207	*Aeromicrobium massiliense*	99.9%	Soil	R2A at 25°C, 3 days
Mycobacteriales	*Nocardiaceae*	BT623	NIBRBAC000506216	*Rhodococcus gordoniae*	99.9%	Soil	R2A at 25°C, 3 days
		BT581	NIBRBAC000506217	*Rhodococcus sovatensis*	99.0%	Soil	R2A at 25°C, 3 days
		BT582	NIBRBAC000506218	*Rhodococcus yunnanensis*	99.3%	Soil	R2A at 25°C, 3 days
		BT474	NIBRBAC000506215	*Nocardia asiatica*	99.0%	Soil	R2A at 25°C, 3 days
Micrococcales	*Cellulomonadaceae*	BT580	NIBRBAC000506208	*Cellulomonas rhizosphaerae*	99.1%	Soil	R2A at 25°C, 3 days
	Microbacteriaceae	BT558	NIBRBAC000506214	*Microbacterium proteolyticum*	99.9%	Soil	R2A at 25°C, 3 days
Rhizobiales	*Methylobacteriaceae*	BT455	NIBRBAC000506213	*Methylobacterium phyllostachyos*	99.8%	Soil	R2A at 25°C, 3 days
Sphingomonadales	*Sphingomonadaceae*	BT653	NIBRBAC000506219	*Sphingomonas adhaesiva*	100.0%	Soil	R2A at 25°C, 3 days
Cytophagales	*Hymenobacteraceae*	BT183	NIBRBAC000506210	*Hymenobacter edaphi*	98.8%	Soil	R2A at 25°C, 3 days
Bacillales	*Bacillaceae*	BT649	NIBRBAC000506220	*Peribacillus muralis*	100.0%	Soil	R2A at 25°C, 3 days

cording to manufacturer instruction (bioMérieux). For BIOLOG GEN III test, a single colony was selected and emulsified into 'inoculating fluid A' (Biolog) for subsequent inoculation on to the test plate (Biolog) and we followed the procedure described by 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 16S rRNA gene sequences of the closely related strains were obtained from EzBiocloud (https://www.ezbiocloud.net/identify) (Yoon *et al*., 2017) and edited using the BioEdit program (Hall, 1999). Multiple alignments were performed with the Clustal X program (Thompson *et al*., 1997). Using the two-parameter model (Kimura, 1983) the evolutionary distances was 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 1000 replications (Felsenstein, 1985). For UV radiation survival test, the cells are irradiated with a UVC cross-linker (UVP, CX-2000, USA) at 254 nm and was used with different dose adjustments as described previously (Im *et al*., 2013; Selvam *et al*., 2013). After the UV radiation treatment, the survival rates of strains were measured on the cells in the early stationary phase ($\approx 10^9$ c.f.u. mL^{-1}), in R2A agar medium (Difco). During 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

The 12 strains were distributed into three orders of *Actinobacteria* (two strains in *Propionibacteriales*, four strain in *Mycobacteriales* and two strains in *Micrococcales*) and two orders of *Proteobacteria* (one strain in *Rhizobiales* and one strain in *Sphingomonadales*), one order of *Bacteroidetes* and one order of *Firmicutes* (Table 1). These strains are all rod-shaped (Fig. 1). The detailed morphological and physiological characteristics are given in the strain descriptions. Based on 16S rRNA gene sequence similarity, 12 strains of previously unreported bacterial species were identified. The neighbor-joining trees showed the close relationship between the isolates and their type strains of validly published species (Figs. 2−10). In the order *Propionibacteriales*, strains BT578 and BT579, belonging to the family *Nocardioidaceae*, were closely related to *Aeromicrobium choanae* (MT992768; 99.5%) and *Aeromicrobium massiliense* (MT992767; 99.9%), respectively. In the order *Mycobacteriales*, strain BT623, BT581, BT582 and BT474, belong-

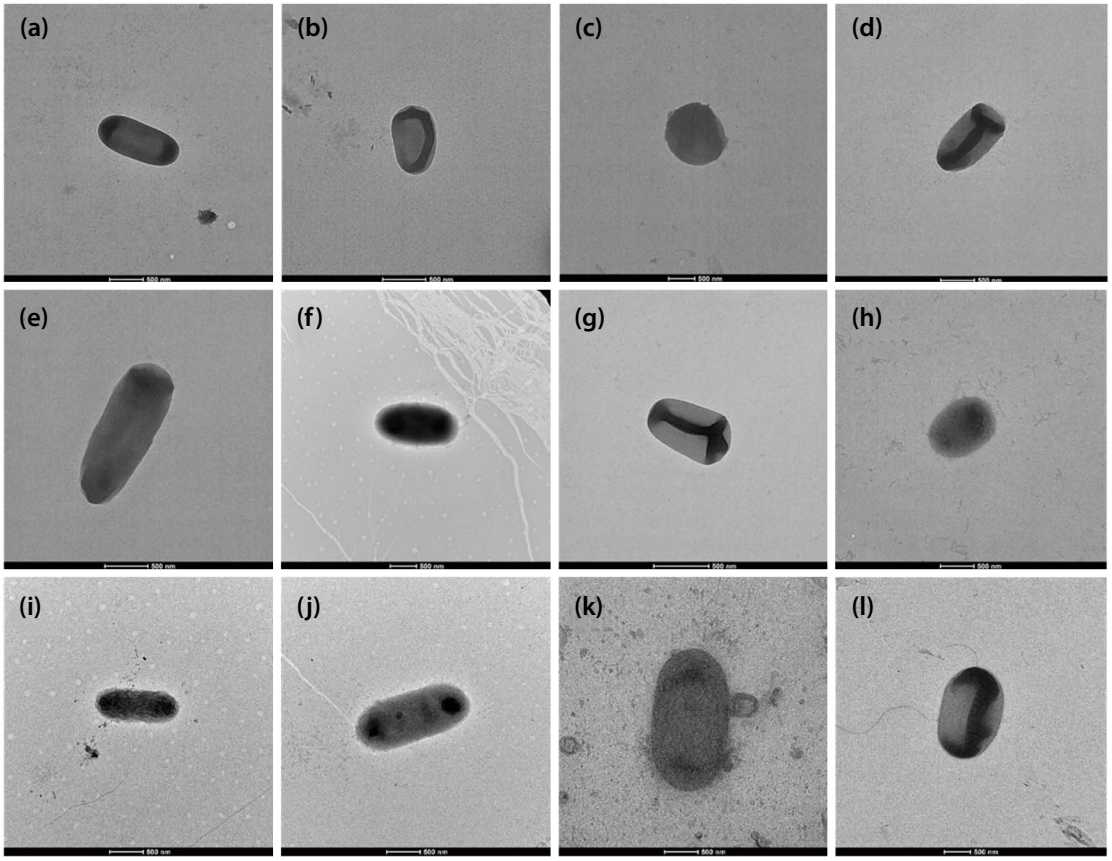

Fig. 1. Transmission electron micrographs of the strains isolated in this study. Strains: a, BT578; b, BT579; c, BT623; d, BT581; e, BT582; f, BT474; g, BT580; h, BT558; i, BT455; j, BT653; k, BT183; l, BT649.

ing to the family *Nocardiaceae*, was closely related to *Rhodococcus gordoniae* (MT993421; 99.9%) *Rhodococcus sovatensis* (MT993416; 99.0%), *Rhodococcus yunnanensis* (MT993385; 99.3%) and *Nocardia asiatica* (MT99 2799; 99.0%), respectively. In the order *Micrococcales*, strain BT580, belonging to the family *Cellulomonadaceae*, was closely related to *Cellulomonas rhizosphaerae* (MT992755; 99.1%) and strain BT558, belonging to the family *Microbacteriaceae*, was closely related to *Microbacterium proteolyticum* (MT993604; 99.9%). In the order *Rhizobiales*, strain BT455 belonging to the family *Methylobacteriaceae*, was closely related to *Methylobacterium phyllostachyos* (MT992795; 99.8%). In the order *Sphingomonadales*, strain BT653, belonging to the family *Sphingomonadaceae*, was closely related to *Sphingomonas adhaesiva* (MT992785; 99.8%). In the order *Cytophagales*, strain BT183, belonging to the family *Hymenobacteraceae*, were closely related to *Hymenobacter edaphi* (MT993359; 98.8%). In the order *Bacillales*, strain BT649, belonging to the family *Bacillaceae*, was closely related to *Peribacillus muralis* (MT993387; 100.0%). The 12 isolates were identified as previously unreported species in Korea, and their phenotypic characteristics were examined through polyphasic study. The UV-radiation resistance tests were done to all the 12 unreported species and the results are given in Fig. 11. Here we report 12 unrecorded bacterial species to Korea belonging to four families of three orders in *Actinobacteria*, two families of two orders in *Proteobacteria*, one family of one order in *Bacteroidetes* and one familiy of one order in the *Firmicutes*.

Description of *Aeromicrobium choanae* BT578

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-cellobiolose, gentiobiose, sucrose, D-turanose, pH 6, D-salicin, 1% NaCl, 4% NaCl, α-D-glucose, D-fructose, D-galactose, 6-methyl-glucose, L-rhamnose, inosine, sodium lactate, glycerol, D-glucose, D-fructose, gelatin, glyctl-L-proline, L-alanine, L-aspartic acid, L-glutamic acid, L-serine, pectin, D-gluconic acid, quinic acid, methyl pyruvate, L-lactic acid, nalidixic acid, lithium chloride, potassium tellurite, β-butryric acid, α-butyric acid, acetoacetic acid,

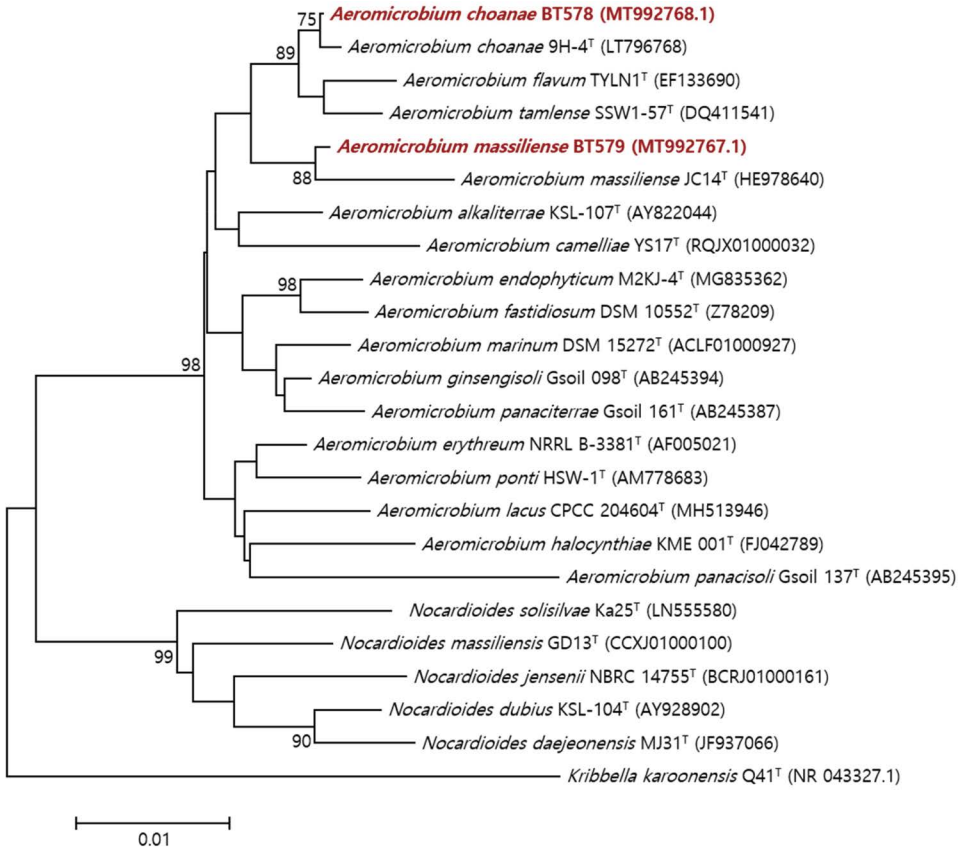

Fig. 2. Neighbor-joining phylogenetic tree based on 16S rRNA gene sequences shows the relationship between the strains isolated in this study and their relatives of the genus *Aeromicrobium* BT578 and BT579. Bootstrap values (>70%) are shown above nodes. Bar: 0.01 substitutions per nucleotide position.

propionic acid, acetic acid, aztreonam, sodium butyrate and sodium bromate; weak positive for stachyose, D-raffinose, α-D-lactose, D-melibiose, β-D-glucoside, *N*-glucosamine, β-mannosamin, *N*-galactosamin, neuraminic acid, D-mannose, D-fucose, L-fucose, D-serine, D-sorbitol, D-mannitol, D-arabitol, myo-inositol, D-aspartic acid, rifamycin SV, pyroglutamic acid, lincomycin, galacturonic acid, galactonic lactone, D-glucuronic acid, mucic acid, D-saccharic acid, vancomycin, tetrazolium violet, D-lactic acid, citric acid, α-glutaric acid, D-malic acid, L-malic acid, succinic acid, Tween 40, γ-butryric acid and α-butryric acid; but negative for pH 5, 8% NaCl, fusidic acid, D-serine, troleandomycin, minocycline, L-arginine, L-histidine, guanidine HCl, Niaproof 4, glucuronamide, tetrazolium blue, ppheylacetic acid and formic acid. In API 20NE, esculin hydrolysis, β-galactosidase, D-glucose, D-maltose, potassium gluconate and adipic acid were utilized; whereas 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, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-D-glucosamine, capric acid, malic acid, trisodium citrate and phenylacetic acid were not utilized. In the API 32GN test, L-rhamnose, D-saccharose (sucrose), D-maltose, sodium acetate, glycogen, D-glucose, propionic acid, valeric acid and 4-hydroxybenzoic acid were utilized; while *N*-acetyl-glucosamine, D-ribose, inositol, itaconic acid, suberic acid, sodium malonate, lactic acid, L-alanine, potassium 5-ketogluconate, 3-hydroxybenzoic acid, L-serine, D-mannitol, salicin, D-melibiose, D-fucose, D-sorbitol, L-arabinose, capric acid, trisodium citrate, L-histidine, potassium 2-ketogluconate, 3-hydroxybutyric acid and L-proline were not utilized. Strain BT578 (=NIBRBAC000506206) was isolated from a soil sample from Guri-si, Gyeonggi-do, Korea.

Description of *Aeromicrobium massiliense* BT579

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-cellobiolose, gentiobiose, sucrose, D-turanose, positive control,

pH 6, D-salicin, 1% NaCl, α-D-glucose, D-fructose, L-rhamnose, inosine, D-serine, glycerol, rifamycin SV, L-glutamic acid, pectin, D-gluconic acid, tetrazolium blue, methyl pyruvate, nalidixic acid, lithium chloride, Tween 40, β-butryric acid, acetoacetic acid, propionic acid, acetic acid, aztreonam and sodium butyrate; weak positive for stachyose, D-raffinose, β-D-glucoside, *N*-glucosamine, β-mannosamin, *N*-galactosamin, neuraminic acid, 4% NaCl, sodium lactate, D-sorbitol, D-mannitol, D-arabitol, myo-inositol, D-glucose, gelatin, glyctl-L-proline, L-aspartic acid, pyroglutamic acid, guanidine HCl, galacturonic acid and D-glucuronic acid; but negative for pH 5, α-D-lactose, D-melibiose, 8% NaCl, D-mannose, D-galactose, 6-methyl-glucose, D-fucose, L-fucose, fusidic acid, D-fructose, D-aspartic acid, D-serine, troleandomycin, minocycline, L-alanine, L-arginine, L-histidine, L-serine, lincomycin, Niaproof 4, galactonic lactone, glucuronamide, pheylacetic acid, succinic acid, γ-butryric acid, formic acid and sodium bromate. In API 20NE, reduction of nitrates (NO_3^-) to nitrite (NO_2^-), reduction of nitrates (NO_3^-) to nitrogen (N_2), esculin hydrolysis, β-galactosidase, D-glucose and D-maltose were utilized; potassium gluconate was weakly utilized; whereas, indole production on tryptophan, glucose fermentation, arginine dihydrolase, urease, gelatin hydrolysis, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-D-glucosamine, capric acid, adipic acid, malic acid, trisodium citrate and phenylacetic acid were not utilized. In the API 32GN test, L-rhamnose, D-saccharose (sucrose), D-maltose, sodium acetate, D-glucose, propionic acid, valeric acid and 3-hydroxybutyric acid were utilized; while *N*-acetyl-glucosamine, D-ribose, inositol, itaconic acid, suberic acid, sodium malonate, lactic acid, L-alanine, potassium 5-ketogluconate, glycogen, 3-hydroxybenzoic acid, L-serine, D-mannitol, salicin, D-melibiose, D-fucose, D-sorbitol, L-arabinose, capric acid, trisodium citrate, L-histidine, potassium 2-ketogluconate, 4-hydroxybenzoic acid and L-proline were not utilized. Strain BT579 (=NIBRBAC000506207) was isolated from a soil sample from Guri-si, Gyeonggi-do, Korea.

Description of *Rhodococcus gordoniae* BT623

Cells are Gram-stain-positive, non-flagellated and rod-shaped. Colonies are orange colored after 3 days of incubation on R2A at 25°C. In the BIOLOG GEN III test, positive for pH 6, 1% NaCl, 4% NaCl, 8% NaCl, D-fructose, sodium lactate, D-sorbitol, D-mannitol, D-arabitol, quinic acid, L-lactic acid, L-malic acid, succinic acid, nalidixic acid, lithium chloride, potassium tellurite, Tween 40, α-butryric acid, β-butryric acid, acetoacetic acid, propionic acid, acetic acid, aztreonam and sodium butyrate; weak positive for dextrin, D-trehalose, D-cellobiolose, gentiobiose, sucrose, D-turanose, D-raffinose, D-melibiose, neuraminic acid, α-D-glucose, D-mannose, D-galactose, D-fucose, L-fucose, L-rhamnose, D-serine, L-histidine, guanidine HCl, galactonic lactone, D-glucuronic acid, glucuronamide, tetrazolium violet, D-lactic acid, D-malic acid, α-butyric acid and sodium bromate; but negative for D-maltose, stachyose, pH 5, α-D-lactose, β-D-glucoside, D-salicin, *N*-glucosamine, β-mannosamin, *N*-galactosamin, 6-methyl-glucose, inosine, fusidic acid, myo-inositol, D-aspartic acid, D-serine, troleandomycin, rifamycin SV, minocycline, gelatin, glyctl-L-proline, L-alanine, L-arginine, L-aspartic acid, L-glutamic acid, pyroglutamic acid, L-serine, lincomycin, niaproof 4, pectin, D-gluconic acid, mucic acid, D-saccharic acid, vancomycin, tetrazolium blue, pheylacetic acid, methyl pyruvate, citric acid, α-glutaric acid, γ-butryric acid and formic acid. In API 20NE, reduction of nitrates (NO_3^-) to nitrite (NO_2^-), reduction of nitrates (NO_3^-) to nitrogen (N_2), esculin hydrolysis, D-mannitol, adipic acid and malic acid were utilized; D-glucose and potassium gluconate were weakly utilized; whereas indole production on tryptophan, glucose fermentation, arginine dihydrolase, urease, gelatin hydrolysis, β-galactosidase, L-arabinose, D-mannose, *N*-acetyl-D-glucosamine, D-maltose, capric acid, trisodium citrate and phenylacetic acid were not utilized. In the API 32GN test, L-rhamnose, inositol, D-saccharose (sucrose), D-maltose, itaconic acid, suberic acid, sodium malonate, sodium acetate, lactic acid, potassium 5-ketogluconate, glycogen, 3-hydroxybenzoic acid, L-serine, D-mannitol, D-glucose, D-fucose, D-sorbitol, L-arabinose, propionic acid, valeric acid, trisodium citrate, L-histidine, potassium 2-ketogluconate and 3-hydroxybutyric acid were utilized; while *N*-acetyl-glucosamine, D-ribose, L-alanine, salicin, D-melibiose, capric acid, 4-hydroxybenzoic acid and L-proline were not utilized. Strain BT623 (=NIBRBAC000506216) was isolated from a soil sample from Gwangju, Gyeonggi-do Korea.

Description of *Rhodococcus sovatensis* BT581

Cells are Gram-stain-positive, non-flagellated and rod-shaped. Colonies are pale yellow colored after 3 days of incubation on R2A at 25°C. In the BIOLOG GEN III test, positive for D-trehalose, sucrose, D-turanose, α-D-glucose, D-mannose, D-fructose, D-galactose, L-rhamnose, sodium lactate, D-sorbitol, D-mannitol, D-arabitol, myo-inositol, rifamycin SV, L-glutamic acid, pectin, D-gluconic acid, quinic acid, tetrazolium violet, citric acid, α-glutaric acid, D-malic acid, L-malic acid, succinic acid, lithium chloride, potassium tellurite, Tween 40, β-butryric acid, α-butyric acid, acetoacetic acid, propionic acid, acetic acid and aztreonam; weak positive for dextrin, D-maltose, D-cellobiolose, gentiobiose, stachyose, pH 6, D-raffinose, α-D-lactose, D-melibiose, β-D-glucoside, *N*-glucosamine, β-mannosamin, *N*-galactosamin,

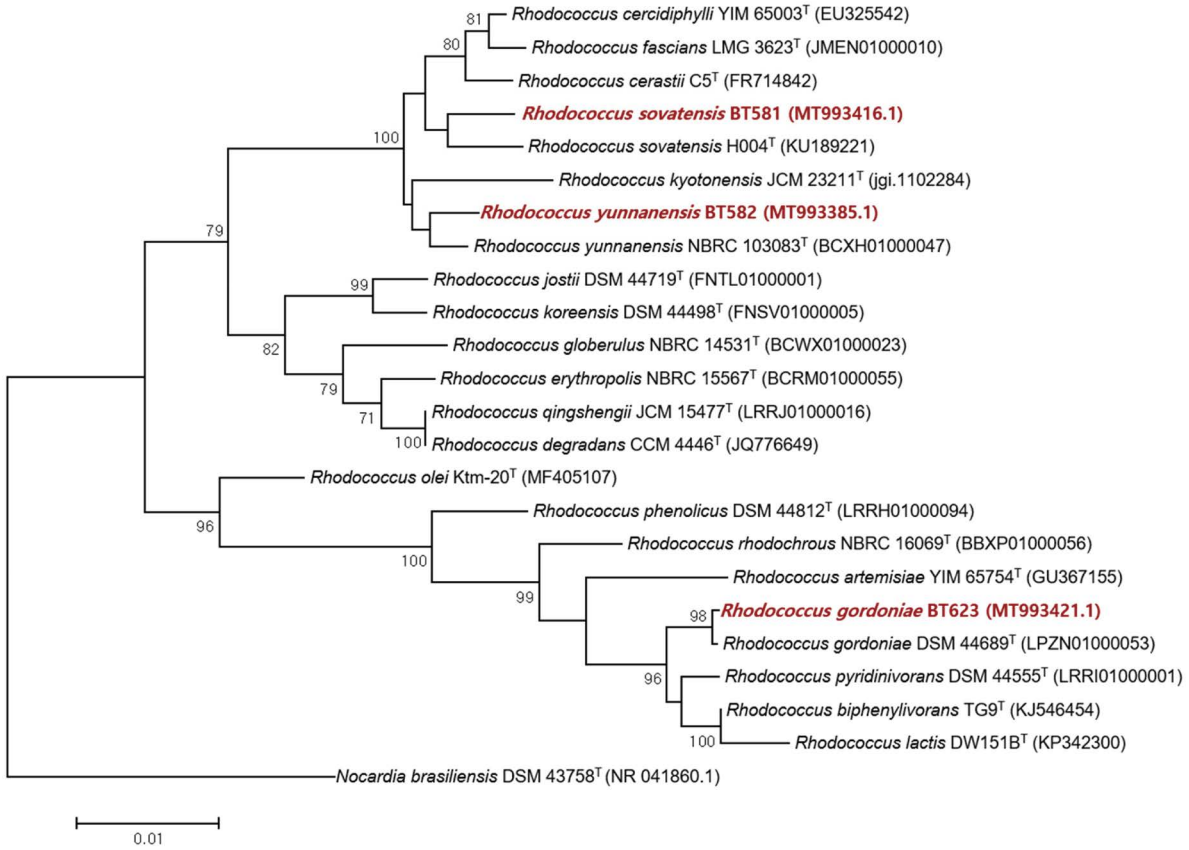

Fig. 3. Neighbor-joining phylogenetic tree based on 16S rRNA gene sequences shows the relationship between the strains isolated in this study and their relatives of the genus *Rhodococcus* BT623, BT581 and BT582. Bootstrap values (>70%) are shown above nodes. Bar: 0.01 substitutions per nucleotide position.

neuraminic acid, 8% NaCl, 6-methyl-glucose, D-fucose, L-fucose, D-serine, glycerol, D-gluose, D-aspartic acid, gelatin, glyctl-L-proline, L-alanine, L-arginine, L-aspartic acid, L-histidine, pyroglutamic acid, L-serine, guanidine HCl, galacturonic acid, galactonic lactone, D-glucuronic acid, mucic acid, D-saccharic acid, tetrazolium blue, methyl pyruvate, D-lactic acid, L-lactic acid, nalidixic acid, γ-butryric acid, α-butryric acid, sodium butyrate and sodium bromate; but negative for pH 5, D-salicin, 1% NaCl, 4% NaCl, 8% NaCl, inosine, fusidic acid, D-serine, troleandomycin, minocycline, lincomycin, Niaproof 4, glucuronamide, vancomycin, pheylacetic acid and formic acid. In API 20NE, urease, D-mannitol, malic acid and trisodium citrate were utilized; D-glucose, D-mannose, potassium gluconate, adipic acid and phenylacetic acid were weakly utilized; whereas 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, esculin hydrolysis, gelatin hydrolysis, β-galactosidase, L-arabinose, *N*-acetyl-D-glucosamine, D-maltose and capric acid were not utilized. In the API 32GN test, L-rhamnose, inositol, D-saccharose (sucrose), sodium acetate, D-mannitol, D-sorbitol, valeric acid, trisodium citrate and 4-hydroxybenzoic acid were utilized; while *N*-acetyl-glucosamine, D-ribose, D-maltose, itaconic acid, suberic acid, sodium malonate, lactic acid, L-alanine, potassium 5-ketogluconate, glycogen, 3-hydroxybenzoic acid, L-serine, D-glucose, salicin, D-melibiose, D-fucose, L-arabinose, propionic acid, capric acid, L-histidine, potassium 2-ketogluconate, 3-hydroxybutyric acid and L-proline were not utilized. Strain BT581 (=NIBRBAC000506217) was isolated from a soil sample from Guri-si, Gyeonggi-do, Korea.

Description of *Rhodococcus yunnanensis* BT582

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 D-maltose, D-trehalose, D-cellobiolose, gentiobiose, sucrose, D-turanose, D-raffinose, α-D-lactose, D-melibiose, β-D-glucoside, D-salicin, *N*-glucosamine, β-mannosamin, *N*-galactosamin, neuraminic acid, 1% NaCl, α-D-glucose, D-mannose, D-fructose, D-galactose, 6-me-

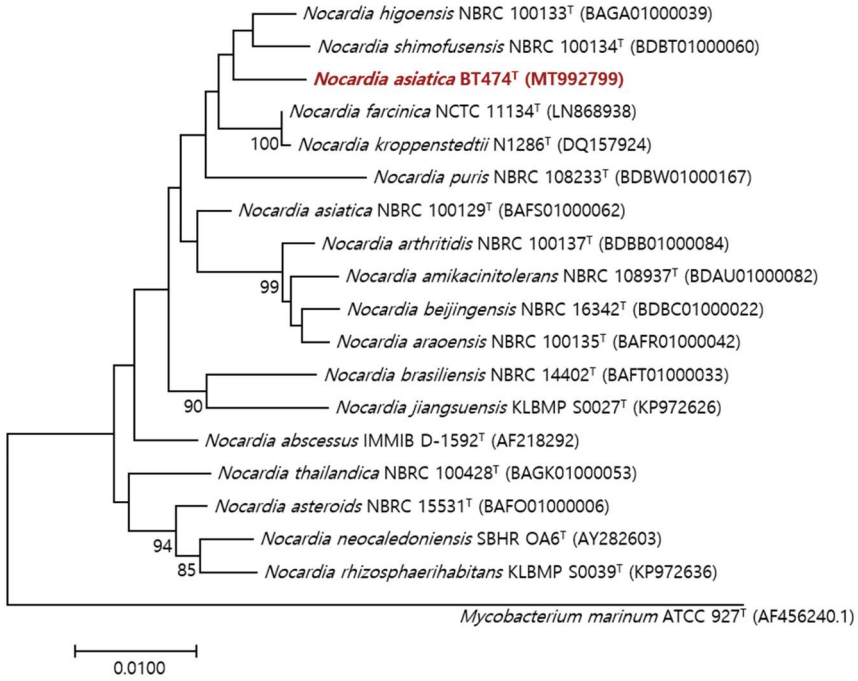

Fig. 4. Neighbor-joining phylogenetic tree based on 16S rRNA gene sequences shows the relationship between the strains isolated in this study and their relatives of the genus *Nocardia* BT474. Bootstrap values (>70%) are shown above nodes. Bar: 0.01 substitutions per nucleotide position.

thyl-glucose, D-fucose, L-fucose, D-galactose, sodium lactate, D-sorbitol, D-mannitol, D-arabitol, myo-inositol, glycerol, D-gluose, D-aspartic acid, L-alanine, L-aspartic acid, L-glutamic acid, pyroglutamic acid, pectin, galactonic lactone, D-gluconic acid, D-glucuronic acid, D-saccharic acid, methyl pyruvate, D-lactic acid, citric acid, α-glutaric acid, D-malic acid, L-malic acid, succinic acid, lithium chloride, potassium tellurite, Tween 40, α-butryric acid, β-butryric acid, α-butyric acid, acetoacetic acid, propionic acid, acetic acid and aztreonam; weak positive for dextrin, stachyose, pH 6, 4% NaCl, 8% NaCl, inosine, D-serine, D-fructose, rifamycin SV, gelatin, glyctl-L-proline, L-arginine, L-histidine, L-serine, guanidine HCl, galacturonic acid, glucuronamide, mucic acid, quinic acid, tetrazolium violet, L-lactic acid, nalidixic acid, γ-butryric acid, formic acid, sodium butyrate and sodium bromate; but negative for pH 5, fusidic acid, D-serine, troleandomycin, minocycline, lincomycin, Niaproof 4, vancomycin, tetrazolium blue and pheylacetic acid. In API 20NE, urease, esculin hydrolysis, D-mannitol, potassium gluconate, malic acid and trisodium citrate were utilized;adipic acid were weakly utilized; whereas 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, β-galactosidase, D-glucose, L-arabinose, D-mannose, *N*-acetyl-D-glucosamine, D-maltose, capric acid and phenylacetic acid were not utilized. In the API 32GN test, glycogen and L-histidine were utilized; while 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, 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, potassium 2-ketogluconate, 3-hydroxybutyric acid, 4-hydroxybenzoic acid and L-proline were not utilized. Strain BT582 (=NIBRBA C000506218) was isolated from a soil sample from Gurisi, Gyeonggi-do, Korea.

Description of *Nocardia asiatica* BT474

Cells are Gram-stain-positive, non-flagellate, 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 methyl pyruvate, L-malic acid, Tween 40, β-butryric acid, acetoacetic acid, propionic acid and acetic acid; weak positive for D-trehalose, gentiobiose, D-melibiose, neuraminic acid, 1% NaCl, D-mannose, D-fructose, D-galactose, 6-methyl-glucose, D-fucose, L-fucose, D-galactose, D-arabitol, D-gluose, D-fructose, rifamycin SV, L-histidine, guanidine HCl, galacturonic acid, galactonic lactone, D-glucuronic acid, glucuronamide, D-saccharic

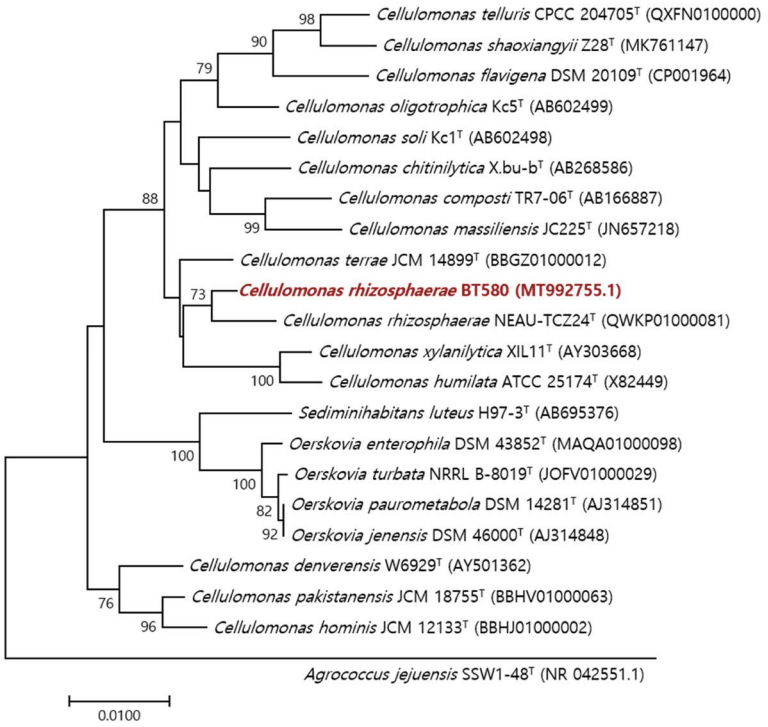

Fig. 5. Neighbor-joining phylogenetic tree based on 16S rRNA gene sequences shows the relationship between the strains isolated in this study and their relatives of the genus *Cellulomonas* BT580. Bootstrap values (>70%) are shown above nodes. Bar: 0.01 substitutions per nucleotide position.

acid, tetrazolium violet, tetrazolium blue, D-lactic acid, α-glutaric acid, D-malic acid, nalidixic acid, potassium tellurite and aztreonam; but negative for dextrin, D-maltose, D-cellobiolose, sucrose, D-turanose, stachyose, pH 6, pH 5, D-raffinose, α-D-lactose, β-D-glucoside, D-salicin, *N*-glucosamine, β-mannosamin, *N*-galactosamin, 4% NaCl, 8% NaCl, α-D-glucose, inosine, sodium lactate, fusidic acid, D-serine, D-sorbitol, D-mannitol, myo-inositol, glycerol, D-aspartic acid, D-serine, troleandomycin, minocycline, gelatin, glyctl-L-proline, L-alanine, L-arginine, L-aspartic acid, L-glutamic acid, pyroglutamic acid, L-serine, lincomycin, Niaproof 4, pectin, D-gluconic acid, mucic acid, quinic acid, vancomycin, pheylacetic acid, L-lactic acid, citric acid, succinic acid, lithium chloride, γ-butryric acid, α-butryric acid, α-butyric acid, formic acid, sodium butyrate and sodium bromate. In API 20NE, 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 and gelatin hydrolysis were utilized; β-galactosidase, 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 were not utilized. In the API 32GN test, 3-hydroxybenzoic acid, propionic acid and valeric acid were utilized; while 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, L-serine, D-mannitol, D-glucose, salicin, D-melibiose, D-fucose, D-sorbitol, L-arabinose, capric acid, trisodium citrate, L-histidine, potassium 2-ketogluconate, 3-hydroxybutyric acid, 4-hydroxybenzoic acid and L-proline were not utilized. Strain BT474 (=NIBRBAC000506215) was isolated from a soil sample from Namhansanseong, Gyeonggi-do, Korea.

Description of *Cellulomonas rhizosphaerae* BT580

Cells are Gram-stain-positive, non-flagellate, 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 D-maltose, D-trehalose, D-cellobiolose, gentiobiose, sucrose, D-turanose, α-D-glucose, D-mannose, D-fructose, inosine, glycerol, lithium chloride, Tween 40, acetoacetic acid, propionic acid, acetic acid, formic acid and sodium butyrate; weak positive for dextrin, D-raffinose, α-D-lactose, D-melibiose, β-D-glucoside, D-salicin, *N*-glucosamine, β-mannosamin, 1% NaCl, D-galactose, 6-methyl-glucose, fusidic acid, D-serine, D-sorbitol, D-mannitol, myo-inositol, D-gluose, D-serine, troleandomycin, rifamycin SV, minocycline, gelatin, L-argi-

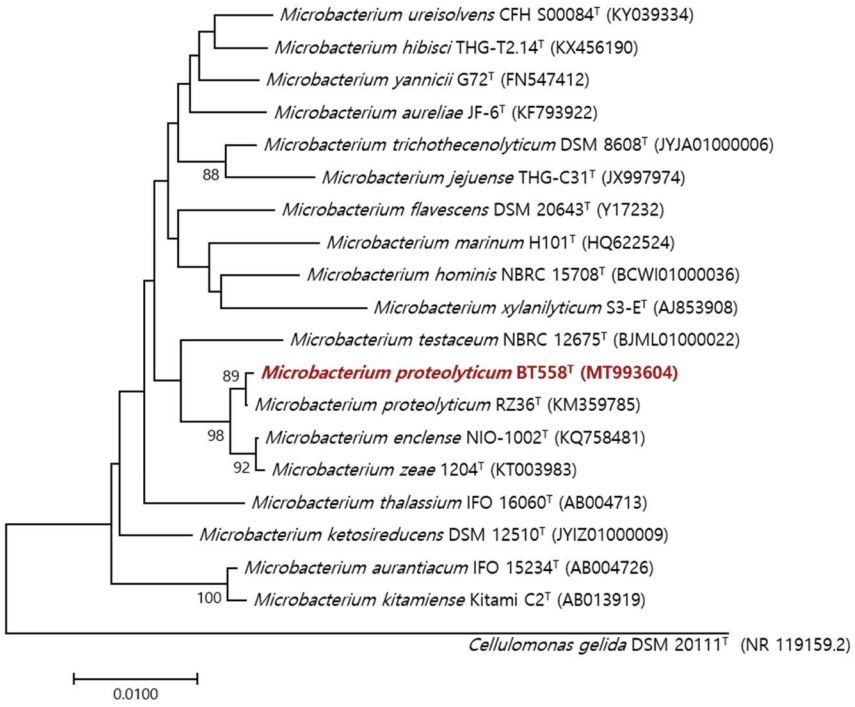

Fig. 6. Neighbor-joining phylogenetic tree based on 16S rRNA gene sequences shows the relationship between the strains isolated in this study and their relatives of the genus *Microbacterium* BT558. Bootstrap values (>70%) are shown above nodes. Bar: 0.01 substitutions per nucleotide position.

nine, L-aspartic acid, L-serine, lincomycin, Niaproof 4, pectin, galacturonic acid, galactonic lactone, D-gluconic acid, mucic acid, vancomycin, tetrazolium violet, tetrazolium blue, methyl pyruvate, D-lactic acid, α-glutaric acid, nalidixic acid, potassium tellurite and aztreonam; but negative for stachyose, pH 6, pH 5, *N*-galactosamin, neuraminic acid, 4% NaCl, 8% NaCl, D-fucose, L-fucose, D-galactose, sodium lactate, D-arabitol, D-fructose, D-aspartic acid, glyctl-L-proline, L-alanine, L-glutamic acid, L-histidine, pyroglutamic acid, guanidine HCl, D-glucuronic acid, glucuronamide, quinic acid, D-saccharic acid, pheylacetic acid, L-lactic acid, citric acid, D-malic acid, L-malic acid, succinic acid, γ-butryric acid, α-butryric acid, β-butryric acid, α-butyric acid and sodium bromate. In API 20NE, urease, esculin hydrolysis and β-galactosidase were utilized;whereas 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 were not utilized. In the API 32GN test, 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 and D-sorbitol were utilized; while L-arabinose, propionic acid, capric acid, valeric acid, trisodium citrate, L-histidine, potassium 2-ketogluconate, 3-hydroxybutyric acid, 4-hydroxybenzoic acid and L-proline were not utilized. Strain BT580 (=NIBRBAC000506208) was isolated from a soil sample from Guri-si, Gyeonggi-do, Korea.

Description of *Microbacterium proteolyticum* BT558

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-cellobiolose, gentiobiose, sucrose, D-turanose, pH 6, β-D-glucoside, D-salicin, 1% NaCl, 4% NaCl, α-D-glucose, D-mannose, D-fructose, D-galactose, inosine, sodium lactate, D-mannitol, glycerol, gelatin, L-alanine, L-aspartic acid, L-glutamic acid, L-serine, pectin, D-gluconic acid, quinic acid, tetrazolium blue, pheylacetic acid, methyl pyruvate, L-lactic acid, α-glutaric acid, L-malic acid, nalidixic acid, lithium chloride, potassium tellurite, β-butryric acid, acetoacetic acid, propionic acid, acetic acid, formic acid, aztreonam and sodium butyrate; weak positive for stachyose, D-raffinose, *N*-glucosamine, β-mannosamin, *N*-galactosamin, neuraminic acid, D-arabitol, myo-inositol, D-gluose, D-fructose, D-aspartic acid, glyctl-L-proline, L-arginine,

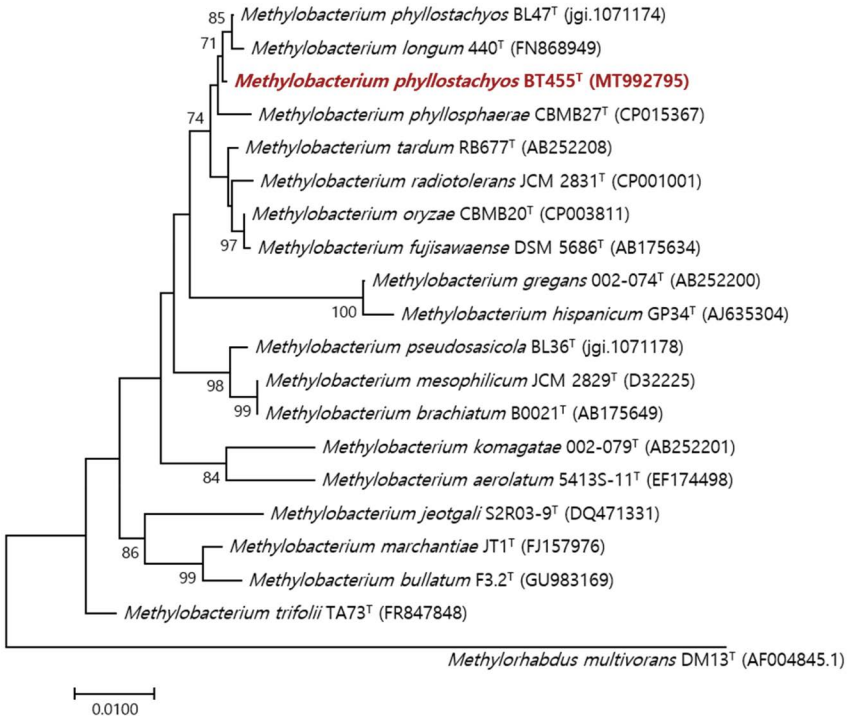

Fig. 7. Neighbor-joining phylogenetic tree based on 16S rRNA gene sequences shows the relationship between the strains isolated in this study and their relatives of the genus *Methylobacterium* BT455. Bootstrap values (>70%) are shown above nodes. Bar: 0.01 substitutions per nucleotide position.

L-histidine, pyroglutamic acid, galacturonic acid, mucic acid, D-saccharic acid, tetrazolium violet, D-lactic acid, D-malic acid, Tween 40, γ-butryric acid, α-butryric acid, α-butyric acid and sodium bromate; but negative for pH 5, α-D-lactose, D-melibiose, 8% NaCl, 6-methyl-glucose, D-fucose, L-fucose, D-galactose, fusidic acid, D-serine, D-serine, troleandomycin, rifamycin SV, minocycline, lincomycin, guanidine HCl, Niaproof 4, galactonic lactone, D-glucuronic acid, glucuronamide, vancomycin, citric acid and succinic acid. In API 20NE, esculin hydrolysis, gelatin hydrolysis, β-galactosidase, D-glucose and D-mannitol were utilized; L-arabinose, D-mannose, D-maltose and potassium gluconate were weakly utilized; whereas 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, adipic acid, malic acid, trisodium citrate and phenylacetic acid were not utilized. In the API 32GN test, D-ribose, D-saccharose (sucrose), potassium 5-ketogluconate, salicin, L-arabinose and potassium 2-ketogluconate were utilized; while L-rhamnose, *N*-acetyl-glucosamine, inositol, D-maltose, itaconic acid, suberic acid, sodium malonate, sodium acetate, lactic acid, L-alanine, glycogen, 3-hydroxybenzoic acid, L-serine, D-mannitol, D-glucose, D-melibiose, D-fucose, D-sorbitol, propionic acid, capric acid, valeric acid, trisodium citrate, L-histidine, 3-hydroxybutyric acid, 4-hydroxybenzoic acid and L-proline were not utilized. Strain BT558 (=NIBRBAC000506214) was isolated from a soil sample from Namhansanseong, Gyeonggi-do, Korea.

Description of *Methylobacterium phyllostachyos* BT455

Cells are Gram-stain-negative, flagellated and rod-shaped. Colonies are pink colored after 3 days of incubation on R2A at 25°C. In the BIOLOG GEN III test, positive for tetrazolium violet; weak positive for pH 6, glycerol, D-fructose, D-aspartic acid, L-aspartic acid, L-glutamic acid, lincomycin, glucuronamide, mucic acid, D-saccharic acid, vancomycin, tetrazolium blue, methyl pyruvate, L-lactic acid, α-glutaric acid, L-malic acid, succinic acid, β-butryric acid, acetic acid and aztreonam; but negative for dextrin, D-maltose, D-trehalose, D-cellobiolose, gentiobiose, sucrose, D-turanose, stachyose, pH 5, D-raffinose, α-D-lactose, D-melibiose, β-D-glucoside, D-salicin, *N*-glucosamine, β-mannosamin, *N*-galactosamin, neuraminic acid, 1% NaCl, 4% NaCl, 8% NaCl, α-D-glucose, D-mannose, D-fructose, D-galactose, 6-methyl-glucose, D-fucose, L-fucose, D-galactose, inosine, sodium lactate, fusidic acid, D-serine, D-sorbitol, D-mannitol,

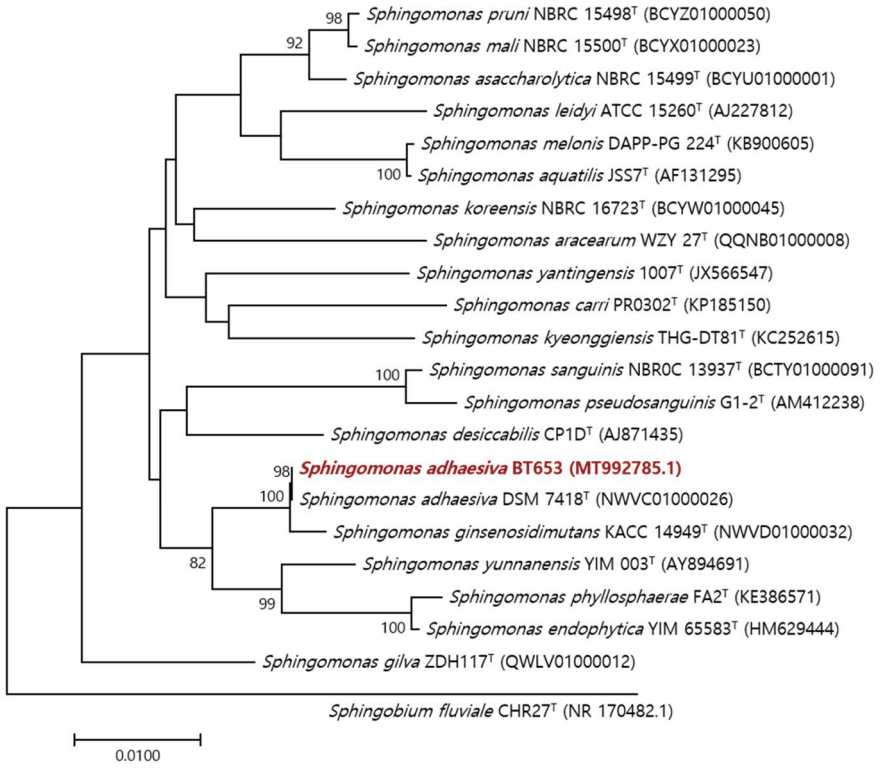

Fig. 8. Neighbor-joining phylogenetic tree based on 16S rRNA gene sequences shows the relationship between the strains isolated in this study and their relatives of the genus *Sphingomonas* BT653. Bootstrap values (>70%) are shown above nodes. Bar: 0.01 substitutions per nucleotide position.

D-arabitol, myo-inositol, D-gluose, D-serine, troleandomycin, rifamycin SV, minocycline, gelatin, glyctl-L-proline, L-alanine, L-arginine, L-histidine, pyroglutamic acid, L-serine, guanidine HCl, Niaproof 4, pectin, galacturonic acid, galactonic lactone, D-gluconic acid, D-glucuronic acid, quinic acid, pheylacetic acid, D-lactic acid, citric acid, D-malic acid, nalidixic acid, lithium chloride, Tween 40, γ-butryric acid, α-butryric acid, α-butyric acid, acetoacetic acid, propionic acid, formic acid, sodium butyrate and sodium bromate. In API 20NE, reduction of nitrates (NO_3^-) to nitrite (NO_2^-), reduction of nitrates (NO_3^-) to nitrogen (N_2) and urease were utilized; esculin hydrolysis were weakly utilized; whereas indole production on tryptophan, glucose fermentation, arginine dihydrolase, gelatin hydrolysis, β-galactosidase, 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 were not utilized. In the API 32GN test, 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 were not utilized. Strain BT455 (=NIBRBAC00050 6213) was isolated from a soil sample from Gyeongju, Gyeongsangbuk-do Korea.

Description of *Sphingomonas adhaesiva* BT653

Cells are Gram-stain-negative, non-flagellated and rod-shaped. Colonies are pale 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-cellobiolose, sucrose, D-turanose, stachyose, Positive control, pH 6, D-melibiose, *N*-glucosamine, 1% NaCl, α-D-glucose, D-mannose, D-fructose, D-galactose, sodium lactate, glycerol, D-gluose, D-fructose, troleandomycin, rifamycin SV, glyctl-L-proline, L-alanine, L-glutamic acid, lincomycin, pectin, D-glucuronic acid, tetrazolium blue and α-glutaric acid; weak positive for gentiobiose, D-raffinose, α-D-lactose, β-D-glucoside, D-salicin, β-mannosamin, *N*-galactosamin, neuraminic acid, 4% NaCl, D-arabitol, myo-inositol, minocycline, gelatin, L-aspartic acid, pyroglutamic acid, galacturonic acid, glucuronamide, D-saccharic acid, tetrazolium violet, methyl pyruvate, D-lactic acid, citric acid, D-malic acid, acetoacetic acid, formic acid,

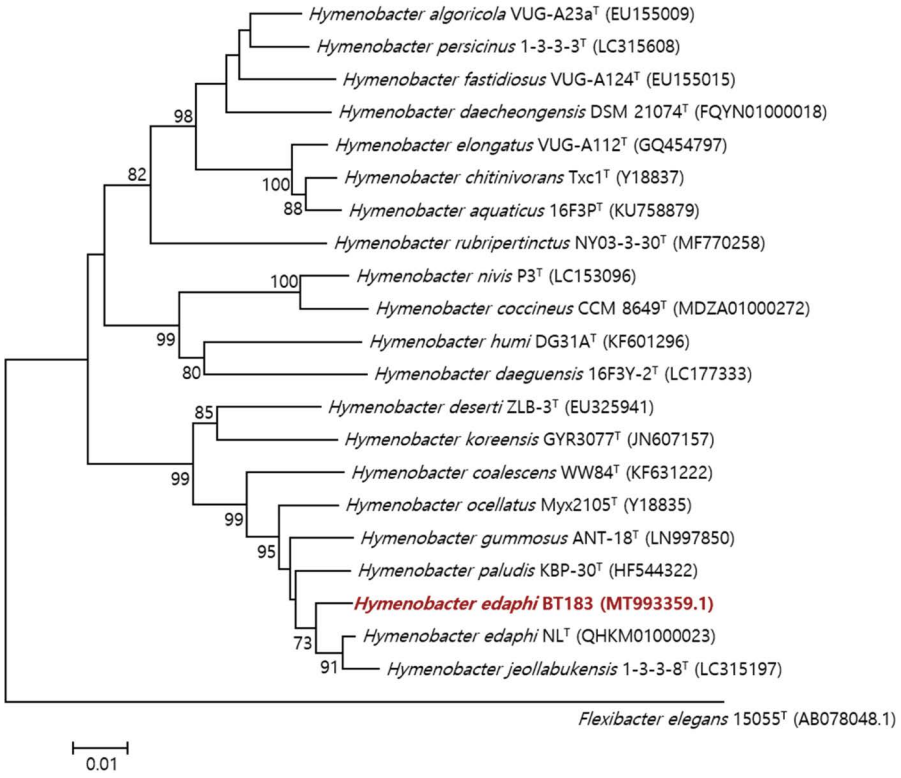

Fig. 9. Neighbor-joining phylogenetic tree based on 16S rRNA gene sequences shows the relationship between the strains isolated in this study and their relatives of the genus *Hymenobacter* BT183. Bootstrap values (> 70%) are shown above nodes. Bar: 0.01 substitutions per nucleotide position.

sodium butyrate and sodium bromate; but negative for pH 5, 8% NaCl, D-sorbitol, D-mannitol, 6-methyl-glucose, inosine, D-serine, D-aspartic acid, D-serine, L-arginine, L-histidine, L-serine, guanidine HCl, Niaproof 4, pheylacetic acid, L-lactic acid, γ-butryric acid, α-butryric acid, β-butryric acid, α-butyric acid and propionic acid. In API 20NE, esculin hydrolysis, D-glucose and D-mannose were utilized; β-galactosidase, D-maltose, malic acid and trisodium citrate were weakly utilized; whereas 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, L-arabinose, D-mannitol, *N*-acetyl-D-glucosamine, potassium gluconate, capric acid, adipic acid and phenylacetic acid were not utilized. In the API 32GN test, D-saccharose (sucrose), D-maltose, glycogen, D-glucose and L-proline were utilized; while 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, 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 and 4-hydroxybenzoic acid were not utilized. Strain BT653 (=NIBRBAC00050 6219) was isolated from a soil sample from Wonju, Gangwon-do, Korea.

Description of *Hymenobacter edaphi* BT183

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 tetrazolium violet; weak positive for lincomycin, D-fructose, glucuronamide and tetrazolium blue; but negative for dextrin, D-maltose, D-trehalose, D-cellobiolose, gentiobiose, sucrose, D-turanose, stachyose, Positive control, pH 6, pH 5, D-raffinose, α-D-lactose, D-melibiose, β-D-glucoside, D-salicin, *N*-glucosamine, β-mannosamin, *N*-galactosamin, neuraminic acid, 1% NaCl, 4% NaCl, 8% NaCl, α-D-glucose, D-mannose, D-fructose, D-galactose, 6-methyl-glucose, D-fucose, L-fucose, D-galactose, inosine, sodium lactate, fusidic acid, D-serine, D-sorbitol, D-mannitol, D-arabitol, myo-inositol, glycerol, D-gluose, D-aspartic acid, D-serine, troleandomycin, rifamycin SV, minocycline, gelatin, glyctl-L-proline, L-alanine, L-arginine, L-aspartic acid, L-glutamic acid, L-histidine, pyroglutamic acid, L-serine, guanidine HCl, Niaproof 4, pec-

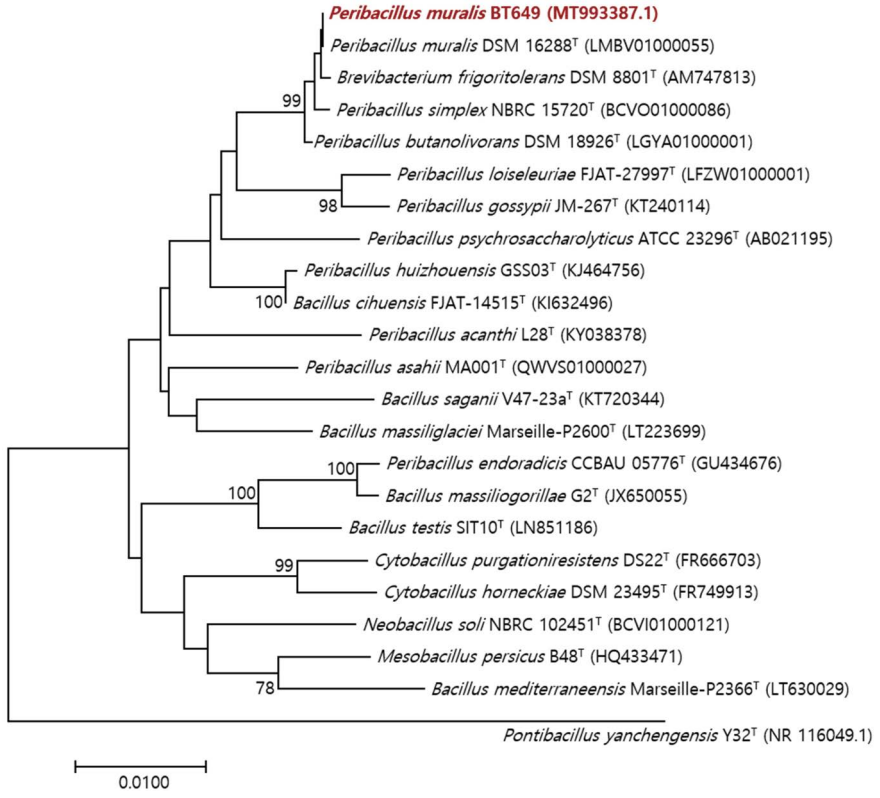

Fig. 10. Neighbor-joining phylogenetic tree based on 16S rRNA gene sequences shows the relationship between the strains isolated in this study and their relatives of the genus *Peribacillus* BT649. Bootstrap values (>70%) are shown above nodes. Bar: 0.01 substitutions per nucleotide position.

tin, galacturonic acid, galactonic lactone, D-gluconic acid, D-glucuronic acid, mucic acid, quinic acid, D-saccharic acid, vancomycin, pheylacetic acid, methyl pyruvate, D-lactic acid, L-lactic acid, citric acid, α-glutaric acid, D-malic acid, L-malic acid, succinic acid, nalidixic acid, lithium chloride, potassium tellurite, Tween 40, γ-butryric acid, α-butryric acid, β-butryric acid, α-butyric acid, acetoacetic acid, propionic acid, acetic acid, formic acid, aztreonam, sodium butyrate and sodium bromate. In API 20NE, reduction of nitrates (NO_3^-) to nitrogen (N_2), indole production on tryptophan and gelatin hydrolysis were utilized; esculin hydrolysis, D-glucose, D-maltose were weakly utilized; whereas reduction of nitrates (NO_3^-) to nitrite (NO_2^-), glucose fermentation, arginine dihydrolase, urease, β-galactosidase, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-D-glucosamine, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate and phenylacetic acid were not utilized. In the API 32GN test, glycogen and trisodium citrate were utilized; while 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, 3-hydroxybenzoic acid, L-serine, D-mannitol, D-glucose, salicin, D-melibiose, D-fucose, D-sorbitol, L-arabinose, propionic acid, capric acid, valeric acid, L-histidine, potassium 2-ketogluconate, 3-hydroxybutyric acid, 4-hydroxybenzoic acid and L-proline were not utilized. Strain BT183 (=NIBRBAC00050 6210) was isolated from a soil sample from Uijeongbu, Gyeonggi, Korea.

Description of *Peribacillus muralis* BT649

Cells are Gram-stain-positive, flagellated and circle-shaped. Colonies are 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-cellobiolose, gentiobiose, sucrose, stachyose, pH 6, D-melibiose, β-D-glucoside, D-salicin, *N*-glucosamine, β-mannosamin, *N*-galactosamin, 1% NaCl, 4% NaCl, D-mannose, D-fructose, D-galactose, D-galactose, inosine, sodium lactate, D-mannitol, glycerol, rifamycin SV, L-alanine, L-arginine, L-glutamic acid, L-histidine, L-serine, galacturonic acid, D-gluconic acid, D-glucuronic acid, quinic acid, L-lactic acid, citric acid, nalidixic acid, potassium tellurite, β-butryric acid, acetoacetic acid, acetic acid, formic acid, aztreonam and sodium butyrate; weak positive for D-turanose, α-D-lactose, neuraminic acid, 8% NaCl, α-D-glucose,

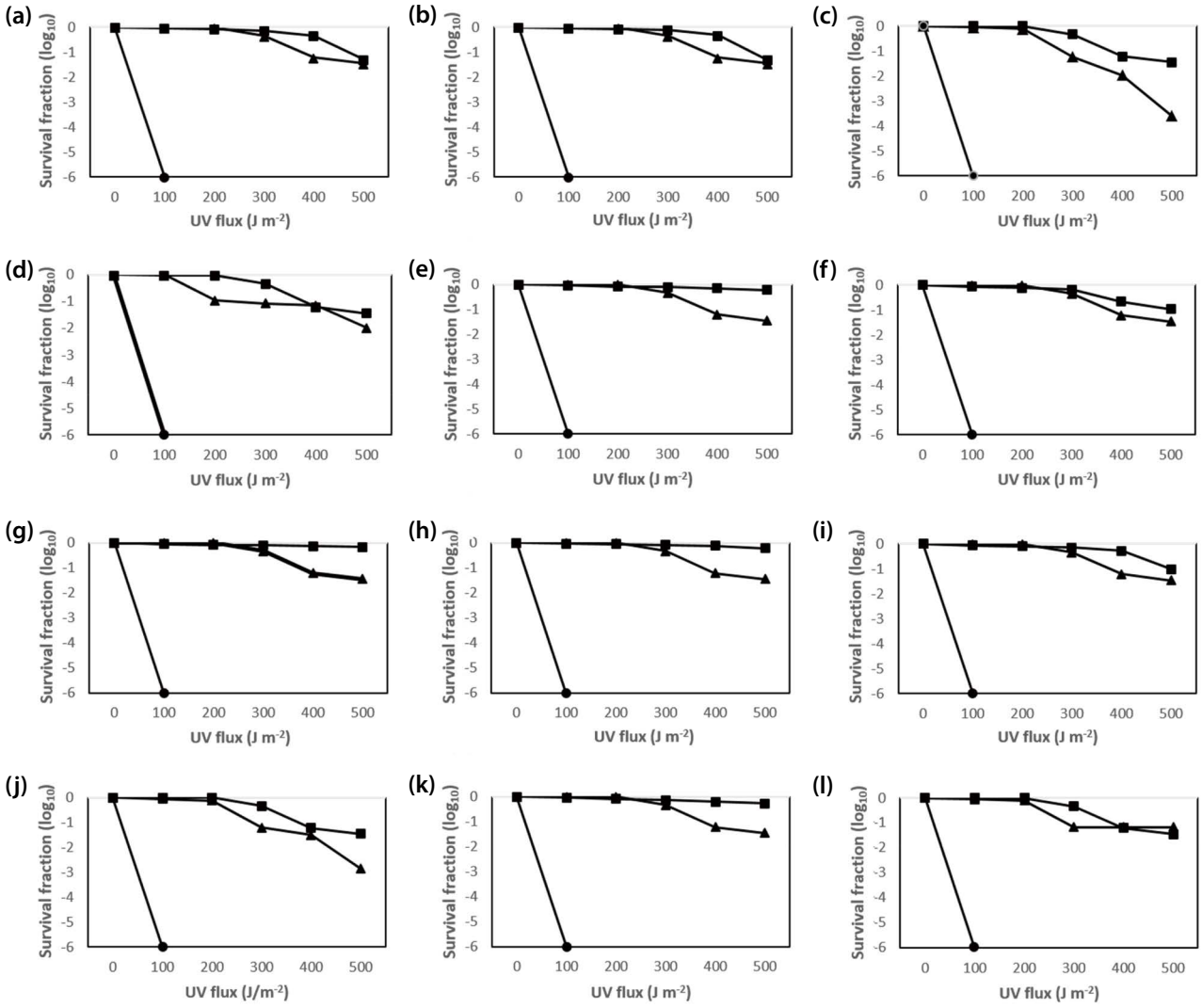

Fig. 11. UV resistance graph of the strains isolated in this study. Survival rates of *D. radiodurans* R1^{T} (■), strains (●) and *E. coli* K12 (◆) are also shown. Strains: a, BT578; b, BT579; c, BT623; d, BT581; e, BT582; f, BT474; g, BT580; h, BT558; i, BT455; j, BT653; k, BT183; l, BT649.

6-methyl-glucose, D-fucose, L-fucose, D-arabitol, myo-inositol, D-gluose, D-fructose, D-aspartic acid, glyctl-L-proline, L-aspartic acid, pyroglutamic acid, galactonic lactone, glucuronamide, mucic acid, D-saccharic acid, tetrazolium violet, D-lactic acid, α-glutaric acid, D-malic acid, L-malic acid, Tween 40, γ-butryric acid, α-butryric acid, propionic acid and sodium bromate; but negative for pH 5, D-raffinose, fusidic acid, D-serine, D-sorbitol, D-serine, troleandomycin, minocycline, gelatin, lincomycin, guanidine HCl, Niaproof 4, pectin, vancomycin, tetrazolium blue, pheylacetic acid, methyl pyruvate, succinic acid, lithium chloride and α-butyric acid. In API 20NE, reduction of nitrates (NO_3^-) to nitrogen (N_2), esculin hydrolysis, gelatin hydrolysis, β-galactosidase, D-glucose, D-mannitol, *N*-acetyl-D-glucosamine, D-maltose, potassium gluconate and trisodium citrate were utilized; D-mannose, adipic acid and phenylacetic acid were weakly utilized; whereas reduction of nitrates (NO_3^-) to nitrite (NO_2^-), indole production on tryptophan, glucose fermentation, arginine dihydrolase, urease, L-arabinose and capric acid, malic acid were not utilized. In the API 32GN test, *N*-acetyl-glucosamine, D-saccharose (sucrose), D-maltose, sodium acetate, glycogen, D-mannitol, D-glucose, salicin, L-histidine and 3-hydroxybutyric acid were utilized; while L-rhamnose, D-ribose, inositol, itaconic acid, suberic acid, sodium malonate, lactic acid, L-alanine, potassium 5-ketogluconate, 3-hydroxybenzoic acid, L-serine, D-melibiose, D-fucose, D-sorbitol, L-arabinose, propionic acid, capric acid, valeric acid, trisodium citrate, potassium 2-ketogluconate, 4-hydroxybenzoic acid

and L-proline were not utilized. Strain BT649 (=NIBR BAC000506220) was isolated from a soil sample from Jeongseon-gun, Gangwon-do, Korea.

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