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Identification of 12 radiation-resistant bacterial species in the phylum *Proteobacteria* new to Korea

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In 2019, after a comprehensive investigation of indigenous prokaryotic species in Korea, a total of 12 bacterial strains assigned to the phylum *Proteobacteria* were isolated from soil. With the high 16S rRNA gene sequence similarity (>98.8%) and formation of a robust phylogenetic clade with the closest species, it was determined that each strain belonged to independent, predefined bacterial species. This study identified two species in the family *Burkholderiaceae*, one species in the family *Comamonadaceae*, two species in the family *Oxalobacteraceae*, one species in the family *Micrococcaceae*, one species in the family *Bradyrhizobiaceae*, one species in the family *Methylobacteriaceae*, one species in the family *Rhizobiaceae*, one species in the family *Rhodocyclaceae*, and one species in the family *Sphingomonadaceae*. There is no official report about these 12 species in Korea, so are described as unreported bacterial species in Korea in this study. Gram reaction, basic biochemical characteristics, colony, and cell morphology are also described in the species description section.

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

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Introduction

Proteobacteria is a major phylum of Gram-negative bacteria constituting the largest and phenotypically most diverse division among prokaryotes (Gupta, 2000). Carl Woese established this grouping in 1987, calling it informally the "purple bacteria and their relatives" (Woese, 1987). Later, Stackebrandt *et al*. (1988) named the *Proteobacteria* after the Greek god Proteus, who could assume many different shapes, to reflect the enormous diversity of morphologies and physiologies observed within this bacterial phylum. At present, the phylum *Proteobacteria* contains 8 class, 58 orders, and 173 families as per List of prokaryotic names with standing in nomenclature (LPSN) (http://www.bacterio.net/-classifphyla.html). All *Proteobacteria* are Gram-negative, with an outer membrane mainly composed of lipopolysaccharides (Garrity *et al*., 2005). The members of *Proteobacteria* show extreme metabolic diversity, as they include strains useful for medicine, veterinary medicine, and industry (Kersters *et al*., 2006).

In 2019, we collected soil samples in Korea from different locations (Ganghwa Island, Gyeongju City, Pocheon City, Namyangju City, Seogwipo City, and Uijeongbu City) for the isolation of various novel and unrecorded bacterial species through a research program supported by the National Institute of Biological Resources (NIBR) of Korea. From this study, we report 12 strains belonging to various genera in the phylum *Proteobacteria*. Isolating the members of *Proteobacteria* in Korea is significant due to their application in medicine and industry.

Materials and Methods

A total of 12 bacterial strains assigned to the phylum *Proteobacteria* 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

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
Burkholderiales	*Burkholderiaceae*	BT434	NIBRBAC000503050	*Caballeronia cordobensis*	99.6%	Soil	R2A at 25°C, 3 days
	Burkholderiaceae	BT368	NIBRBAC000503025	*Paraburkholderia kirstenboschensis*	99.4%	Soil	R2A at 25°C, 3 days
	Comamonadaceae	BT370	NIBRBAC000503024	*Variovorax gossypii*	99.7%	Soil	R2A at 25°C, 3 days
	Oxalobacteraceae	BT239	NIBRBAC000503018	*Massilia neuiana*	99.9%	Soil	R2A at 25°C, 3 days
	Oxalobacteraceae	BT339	NIBRBAC000503036	*Novitherbaspirillum canariense*	99.8%	Soil	R2A at 25°C, 3 days
Micrococcales	*Micrococcaceae*	BT427	NIBRBAC000503047	*Arthrobacter nitrophenolicus*	99.3%	Soil	R2A at 25°C, 3 days
Rhizobiales	*Bradyrhizobiaceae*	BT362	NIBRBAC000503041	*Pseudomonas reidholzensis*	99.3%	Soil	R2A at 25°C, 3 days
	Methylobacteriaceae	BT250	NIBRBAC000503027	*Microvirga lotononidis*	99.1%	Soil	R2A at 25°C, 3 days
	Rhizobiaceae	BT338	NIBRBAC000503035	*Rhizobium alamii*	99.9%	Soil	R2A at 25°C, 3 days
Rhodocyclales	*Rhodocyclaceae*	BT344	NIBRBAC000503015	*Oryzomicrobium terrae*	99.4%	Soil	R2A at 25°C, 3 days
Sphingomonadales	*Sphingomonadaceae*	BT346	NIBRBAC000503016	*Sphingomonas sanguinis*	99.2%	Soil	R2A at 25°C, 3 days
	Sphingomonadaceae	BT364	NIBRBAC000503043	*Sphingomonas azotifigens*	100.0%	Soil	R2A at 25°C, 3 days

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 according to manufacturer instruction (bioMérieux). For Biolog GEN III, a single colony was selected and emulsified into 'inoculating fluid A' (Biolog) for subsequent inoculation on to the test plate (Biolog) and 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 EzTaxon-e server (http://eztaxon-e.ezbiocloud.net) (Kim *et al*., 2012) 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 1,000 replicates (Felsenstein, 1985).

For UV radiation survival test, the cells were 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 five orders of *Proteobacteria*: five strains in the *Burkholderiales*, one strain in *Micrococcales*, three strains in *Rhizobiales*, one strain in the *Rhodocyclales*, and two strains in *Sphingomonadales* (Table 1). These strains are Gram-negative and rod-shaped (Fig. 1). The detailed morphological and physiological characteristics are given in the strain descriptions.

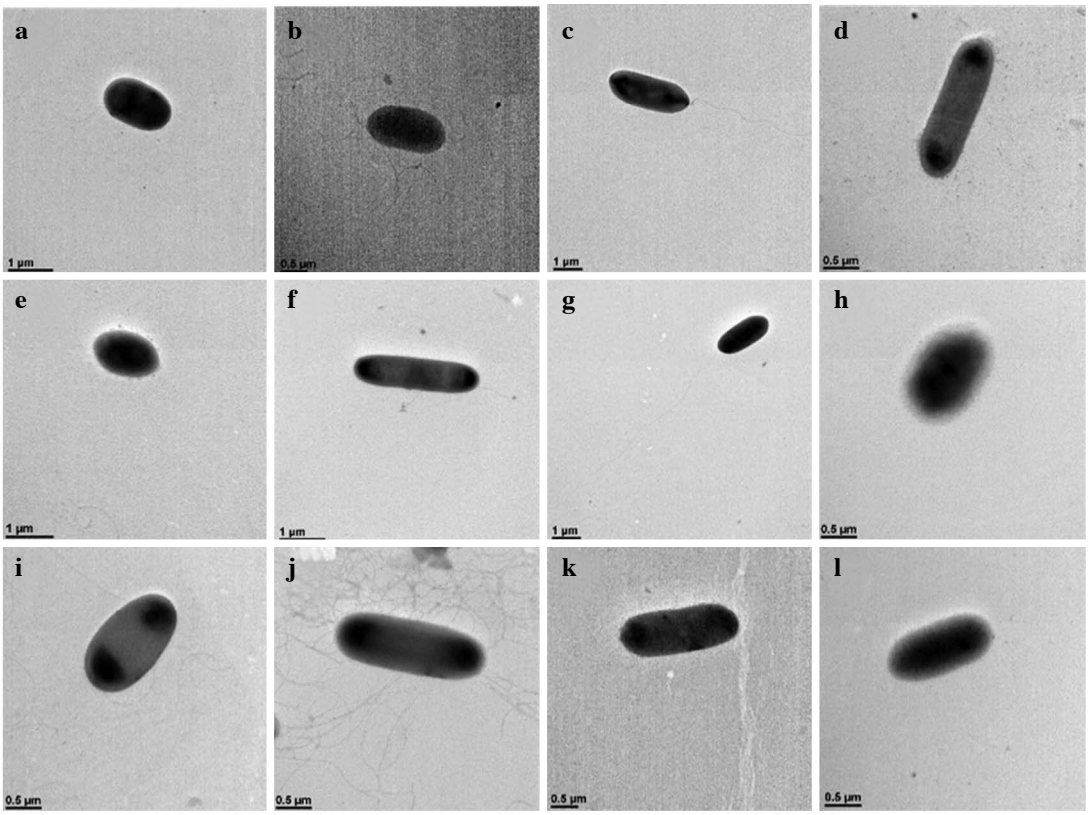


Fig. 1. Transmission electron micrographs of the strains isolated in this study. Strains: a, BT434; b, BT368; c, BT370; d, BT239; e, BT339; f, BT427; g, BT362; h, BT250; i, BT338; j, BT344; k, BT346; l, BT364.

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. 2−7). In the order *Burkholderiales*, strains BT434 and BT368 belonging to the family *Burkholderiacea*, were closely related to *Caballeronia cordobensis* (MN204472; 99.6%) and *Paraburkholderia kirstenboschensis* (MN204221; 99.40%), respectively; strain BT370 belonging to the family *Comamonadaceae*, was closely related to *Variovorax gossypii* (MN204216; 99.4%); strains BT239 and BT339 belonging to the family *Oxalobacteraceae*, were closely related to *Massilia neuiana* (MN204043; 99.9%) and *Noviherbaspirillum canariense* (MN204069; 99.8%), respectively. In the order *Micrococcales*, strain BT427 belonging to the family *Micrococcaceae*, was closely related to *Arthrobacter nitrophenolicus* (MN204223; 99.3%). In the order *Rhizobiales*, strain BT362 belonging to the family *Bradyrhizobiaceae*, was closely related to *Pseudomonas reidholzensis* (MN204213; 99.3%); strain BT250 belonging to the family *Methylobacteriaceae*, was closely related to *Microvirga lotononidis* (MN204051; 99.1%); strain BT338 belonging to the family *Rhizobiaceae*, was closely related to *Rhizobium alamii* (MN204070; 99.9%). In the order *Rhodocyclales*, strain BT344 belonging to the family *Rhodocyclaceae*, was closely related to *Oryzomicrobium terrae* (MN204072; 99.4%). In the order *Sphingomonadales*, strains BT346 and BT364 belonging to the family *Sphingomonadaceae*, were most closely related to *Sphingomonas sanguinis* (MN204210; 99.2%) and *Sphingomonas azotifigens* (accession number MN204209; 100.0%), respectively.

The 12 isolates were identified as unreported species to Korea, and their phenotypic characteristics were examined through polyphasic study. The UV radiation resistance tests were done on all the 12 unreported species and the results were given in Fig. 14. Here we report 12 unrecorded bacterial species belonging to nine families of five orders in *Proteobacteria*, which were isolated in Korea.

Description of *Caballeronia cordobensis* BT434

Cells are Gram-stain-negative, non-flagellated, and cocci-shaped. Colonies are white-colored after 3 days of incubation on R2A at 25°C. In the BIOLOG GEN III, positive for pH 6, 1% NaCl, α-D-glucose, D-mannose, D-fructose, D-galactose, L-rhamnose, 1% sodium lactate,

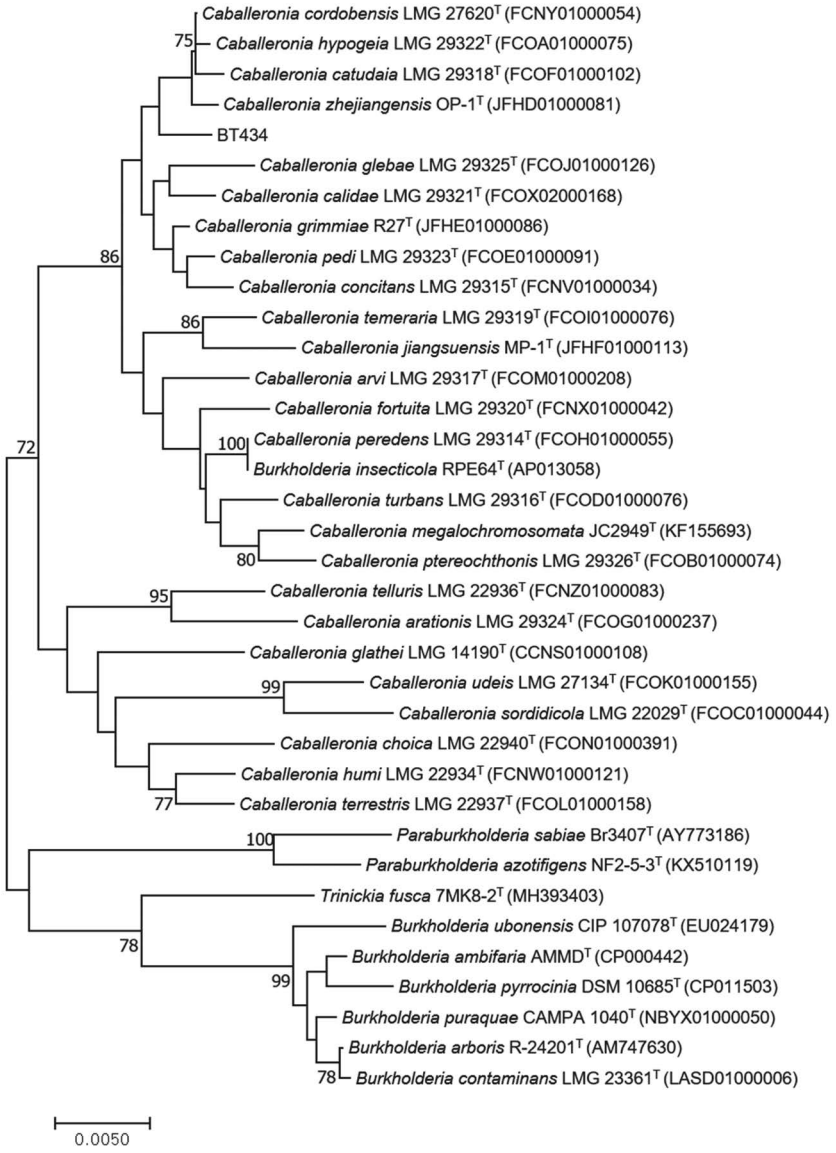


Fig. 2. Neighbor-joining phylogenetic tree based on 16S rRNA gene sequences shows the relationship between the strains isolated in this study and their relatives of the species *Caballeronia cordobensis*. Bootstrap values (>70%) are shown above nodes for the neighbor-joining methods. Bar: 0.01 and 0.02 substitutions per nucleotide position, respectively.

myo-inositol, D-glucose-6-PO_4, D-fructose-6-PO_4, D-aspartic acid, lincomycin, D-galacturonic acid, D-glucuronic acid, mucic acid, quinic acid, D-saccharic acid, tetrazolium violet, tetrazolium blue, β-hydroxy-D, L-butyric acid, propionic acid and acetic acid; weak positive for pH 5, *N*-acetyl-D-glucosamine, L-fucose, D-sorbitol, D-mannitol, D-arabitol, rifamycin SV, glyctl-L-proline, L-arginine, L-aspartic acid, L-glutamic acid, L-histidine, L-pyroglutamic acid, guanidine HCl, L-galactonic acid lactone, D-gluconic acid, vancomycin, *p*-hydroxy-pheylacetic acid, methyl pyruvate, L-lactic acid, citric acid, L-malic acid, bromo-succinic acid, potassium tellurite, tween 40, γ-amino-butryric acid, α-keto butyric acid and aztreonam; but negative for dextrin, D-maltose, D-trehalose, D-cellobiolose, gentiobiose, sucrose, D-turanose, stachyose, D-raffinose, α-D-lactose, D-melibiose, β-methyl-D-glucoside, D-salicin, *N*-acetyl-β-mannosamin, *N*-acetyl-D-galactosamin, *N*-acetyl neuraminic acid, 4% NaCl, 8% NaCl, 3-methyl-glucose, D-fucose, inosine, fusidic acid, D-serine, glycerol, D-serine, troleandomycin, minocycline, gelatin, L-alanine, L-serine, niaproof 4, pectin, glucuronamide, D-lactic acid methyl ester, α-keto-glutaric acid, D-malic acid, nalidixic acid, lithium chloride, α-hydroxy-butyric acid, acetoacetic acid, formic acid, sodium butyrate and sodium bromate. In API 20NE test, positive for reduction of nitrates (NO_3) to nitrite (NO_2^-) and reduction of nitrates (NO_3) to

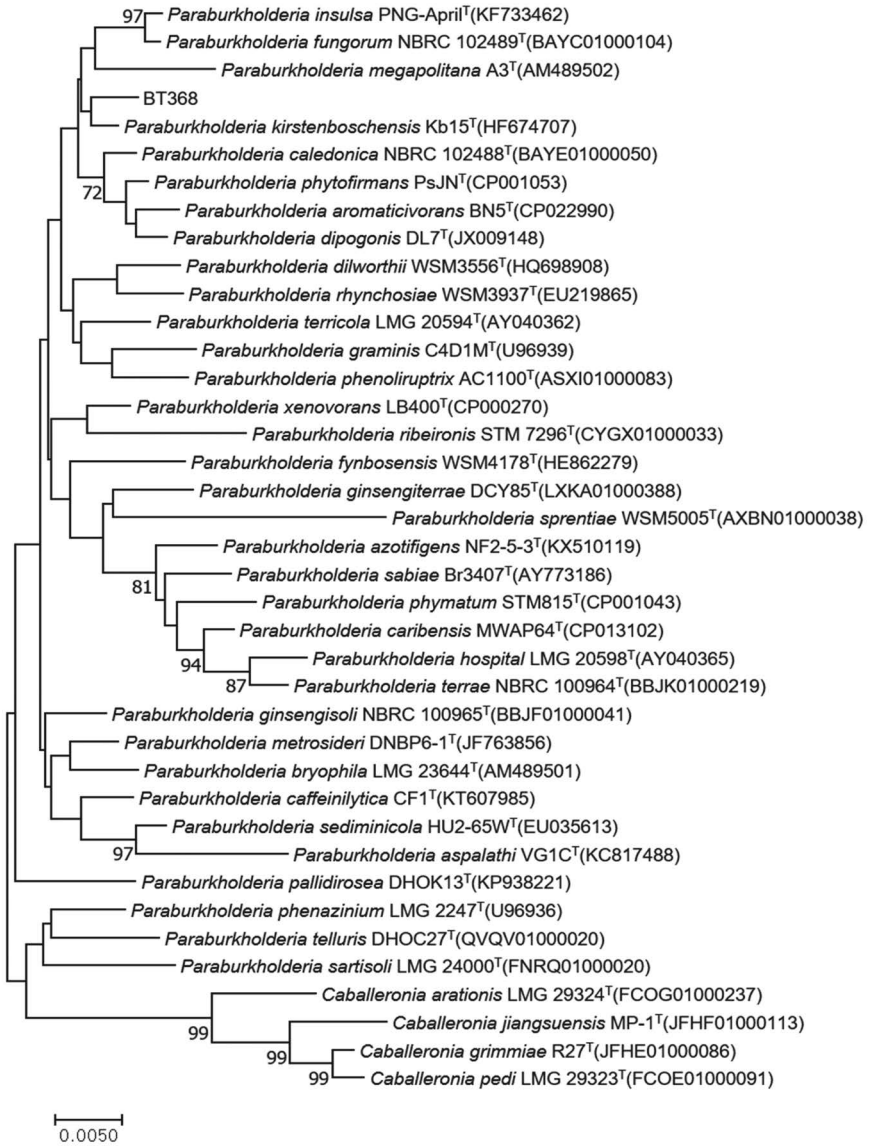


Fig. 3. Neighbor-joining phylogenetic tree based on 16S rRNA gene sequences shows the relationship between the strains isolated in this study and their relatives of the species *Paraburkholderia kirstenboschensis*. Bootstrap values (>70%) are shown above nodes for the neighbor-joining methods. Bar: 0.01 and 0.02 substitutions per nucleotide position, respectively.

nitrogen (N_2); weak positive for urease, esculin hydrolysis and gelatin hydrolysis; but negative for indole production on tryptophan, glucose fermentation, arginine dihydrolase and β-galactosidase. D-Glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-D-glucosamine, malic acid, phenylacetic acid (weak), potassium gluconate (weak) and trisodium citrate (weak) were utilized whereas, D-maltose, capric acid and adipic acid were not utilized. In API 32GN test, L-rhamnose, *N*-acetyl-glucosamine, inositol, sodium acetate, lactic acid, L-alanine, potassium 5-ketogluconate, 3-hydroxybenzoic acid, L-serine, D-mannitol, D-glucose, L-arabinose, propionic acid, L-histidine, potassium 2-ketogluconate, 3-hydroxybutyric acid, 4-hydroxybenzoic acid and L-proline were utilized; D-ribose, D-saccharose (sucrose), D-maltose, itaconic acid, suberic acid, sodium malonate, D-fucose, D-sorbitol, capric acid, valeric acid and trisodium citrate were weak utilized whereas, glycogen, salicin and D-melibiose were utilized.

Strain BT434 (=NIBRBAC000503050) was isolated from a soil sample, Ganghwa Island in Incheon City, Korea.

Description of *Paraburkholderia kirstenboschensis* BT368

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

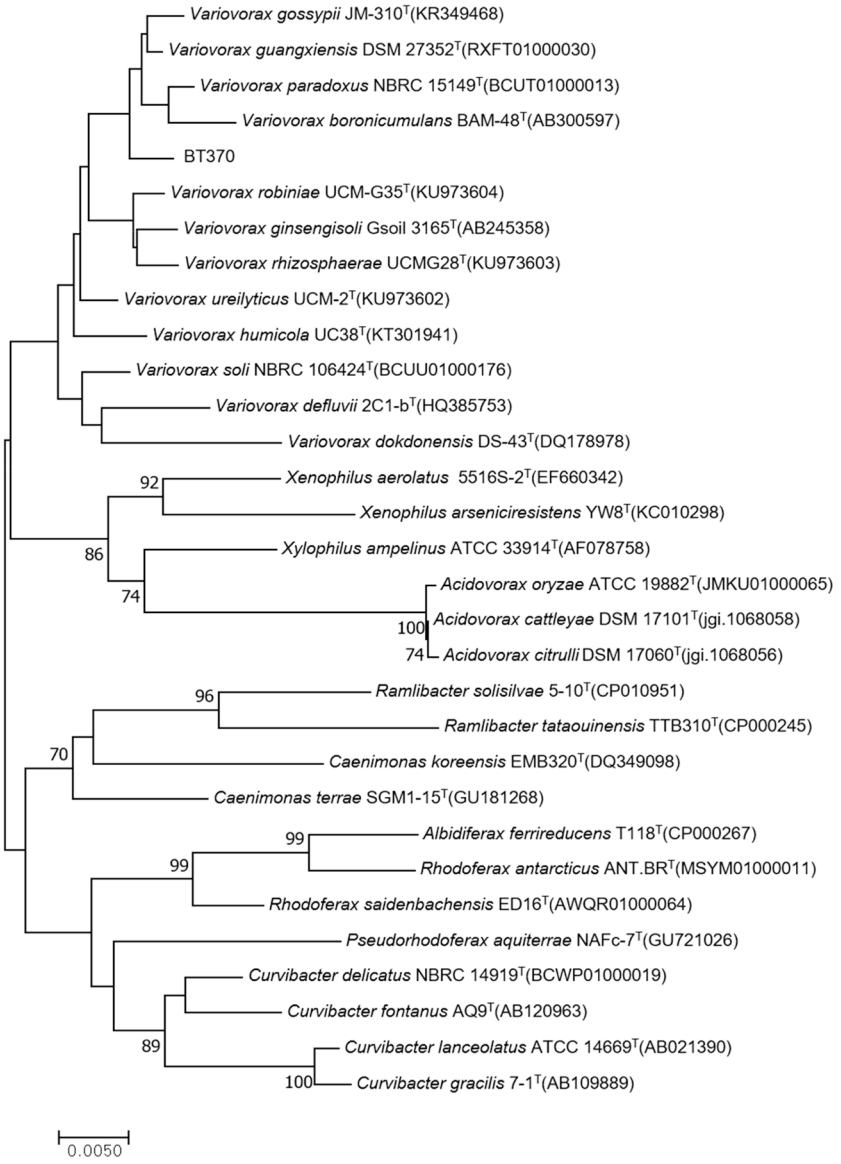


Fig. 4. Neighbor-joining phylogenetic tree based on 16S rRNA gene sequences shows the relationship between the strains isolated in this study and their relatives of the species *Variovorax gossypii*. Bootstrap values (>70%) are shown above nodes for the neighbor-joining methods. Bar: 0.01 and 0.02 substitutions per nucleotide position, respectively.

rod-shaped. Colonies are white-colored after 3 days of incubation on R2A at 25°C. In the BIOLOG GEN III, positive for D-trehalose, pH 6, pH 5, *N*-acetyl-D-glucosamine, *N*-acetyl-D-galactosamin, 1% NaCl, α-D-glucose, D-mannose, D-galactose, L-fucose, L-rhamnose, 1% sodium lactate, D-sorbitol, D-mannitol, D-arabitol, glycerol, troleandomycin, rifamycin SV, glyctl-L-proline, L-alanine, L-arginine, L-aspartic acid, L-glutamic acid, L-histidine, L-pyroglutamic acid, L-serine, lincomycin, D-galacturonic acid, L-galactonic acid lactone, D-gluconic acid, D-glucuronic acid, mucic acid, quinic acid, D-saccharic acid, vancomycin, tetrazolium violet, tetrazolium blue, *p*-hydroxy-pheylacetic acid, L-lactic acid, citric acid, D-malic acid, L-malic acid, bromo-succinic acid, γ-amino-butryric acid, β-hydroxy-D, L-butyric acid, propionic acid, acetic acid, formic acid and aztreonam; weak positive for D-fructose, D-fucose, fusidic acid, D-serine, myo-inositol, D-glucose-6-PO_4, D-fructose-6-PO_4, guanidine HCl, niaproof 4, methyl pyruvate, α-keto-glutaric acid, potassium tellurite, tween40, α-hydroxy-butyric acid and acetoacetic acid; but negative for dextrin, D-maltose, D-cellobiolose, gentiobiose, sucrose, D-turanose, stachyose, D-raffinose, α-D-lactose, D-melibiose, β-methyl-D-glucoside, D-salicin, *N*-acetyl-β-mannosamin, *N*-acetyl neuraminic acid,

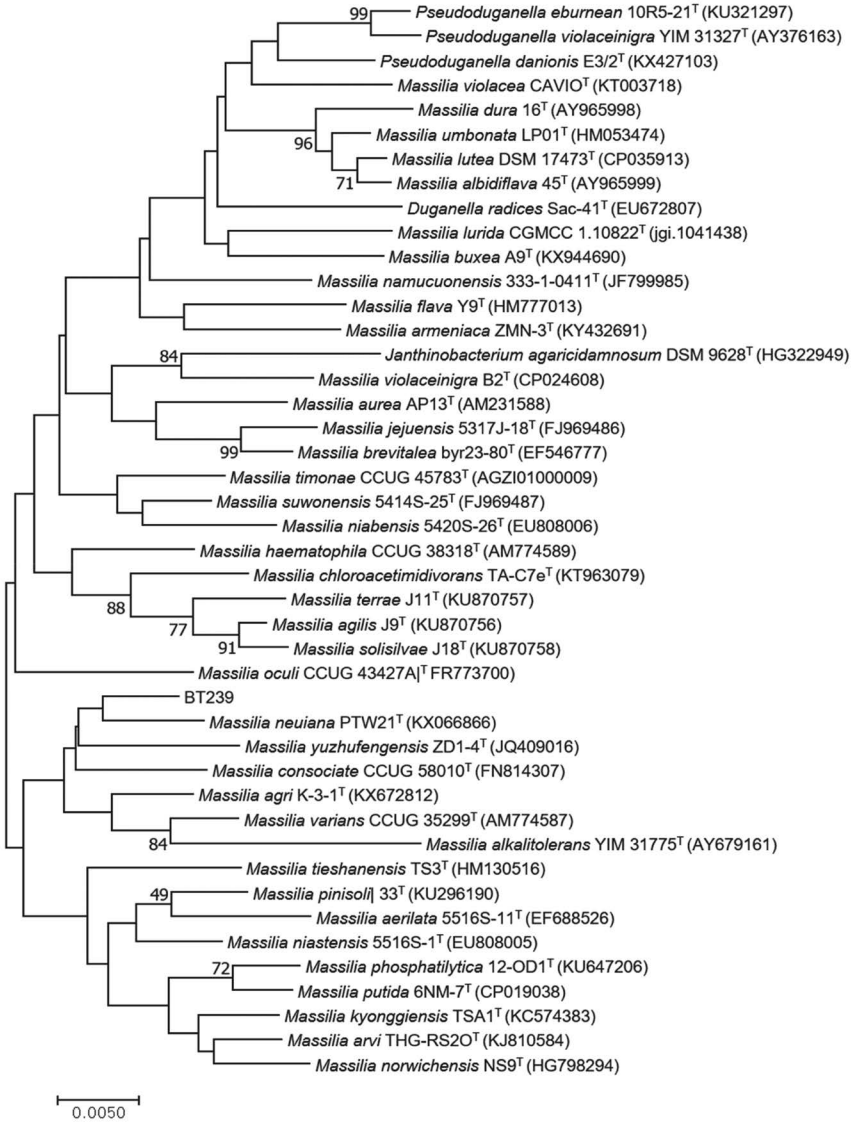


Fig. 5. Neighbor-joining phylogenetic tree based on 16S rRNA gene sequences shows the relationship between the strains isolated in this study and their relatives of the species *Massilia neuiana*. Bootstrap values (>70%) are shown above nodes for the neighbor-joining methods. Bar: 0.01 and 0.02 substitutions per nucleotide position, respectively.

4% NaCl, 8% NaCl, 3-methyl-glucose, inosine, D-aspartic acid, D-serine, minocycline, gelatin, pectin, glucuronamide, D-lactic acid methyl ester, nalidixic acid, lithium chloride, α-keto butyric acid, sodium butyrate and sodium bromate. In API 20NE test, positive for urease; weak positive for β-galactosidase; 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 and arginine dihydrolase. D-Glucose, L-arabinose, D-mannose, D-mannitol, potassium gluconate, adipic acid, malic acid, trisodium citrate and phenylacetic acid were utilized whereas, *N*-acetyl-D-glucosamine (weak), capric acid (weak) were utilized; but D-maltose were not utilized. In API 32GN test, L-rhamnose, *N*-acetyl-glucosamine, D-ribose, inositol, D-mannitol, D-glucose, D-fucose, D-sorbitol, L-arabinose, L-histidine, potassium 2-ketogluconate, L-proline, sodium acetate, lactic acid, L-alanine, potassium 5-ketogluconate, L-serine, propionic acid, capric acid, valeric acid, 3-hydroxybutyric acid, 4-hydroxybenzoic acid were utilized, D-saccharose (sucrose), D-maltose, itaconic acid, suberic acid, sodium malonate, glycogen, 3-hydroxybenzoic acid, salicin, D-melibiose, trisodium citrate were not utilized.

Strain BT368 (=NIBRBAC000503025) was isolated from a soil sample, Gyeongju City in Gyeongsangbuk Province, Korea.

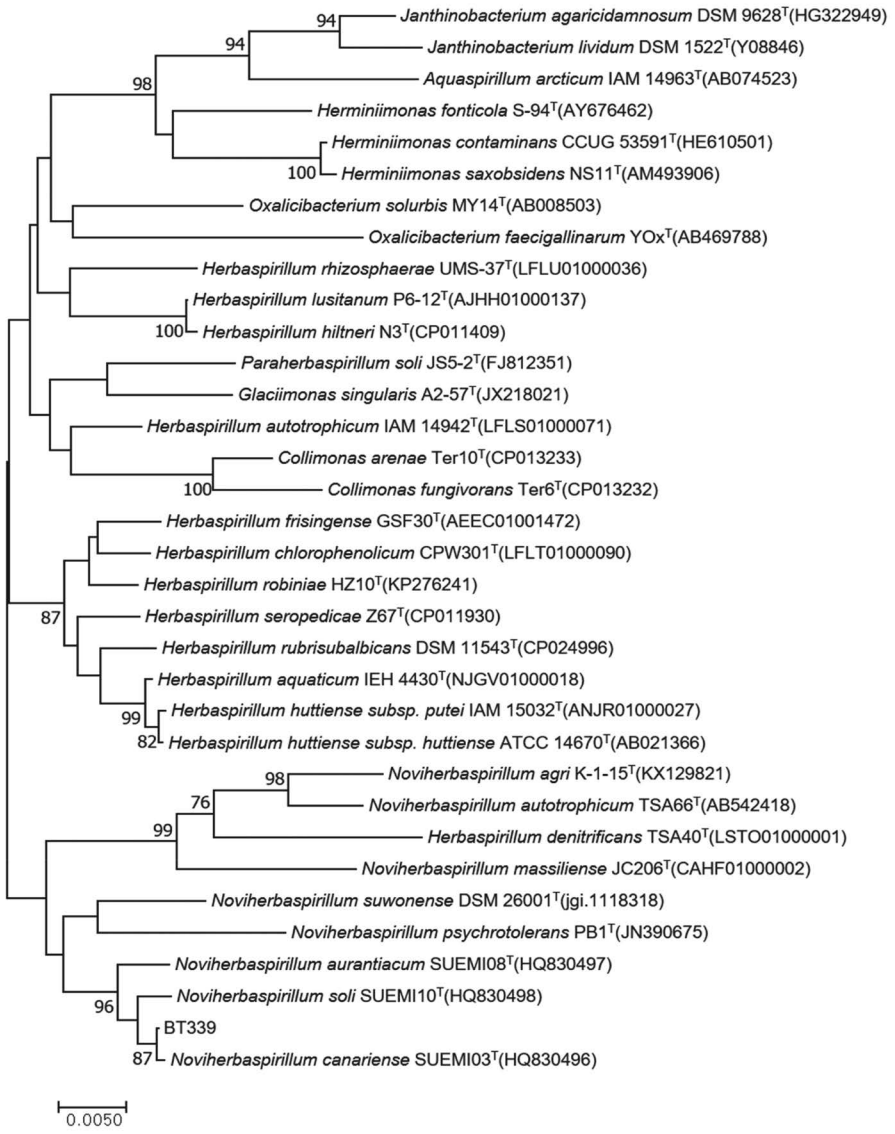


Fig. 6. Neighbor-joining phylogenetic tree based on 16S rRNA gene sequences shows the relationship between the strains isolated in this study and their relatives of the species *Noviherbaspirillum canariense*. Bootstrap values (>70%) are shown above nodes for the neighbor-joining methods. Bar: 0.01 and 0.02 substitutions per nucleotide position, respectively.

Description of *Variovorax gossypii* BT370

Cells are Gram-stain-negative, flagellated, and rod-shaped. Colonies are white-colored after 3 days of incubation on R2A at 25°C. In the BIOLOG GEN III, positive for sodium bromate, pH 6, pH 5, *N*-acetyl-D-glucosamine, *N*-acetyl-D-galactosamin, 1% NaCl, α-D-glucose, D-mannose, D-galactose, L-fucose, L-rhamnose, 1% sodium lactate, D-sorbitol, D-mannitol, D-arabitol, glycerol, troleandomycin, rifamycin SV, glyctl-L-proline, L-alanine, L-arginine, L-aspartic acid, L-glutamic acid, L-histidine, L-pyroglutamic acid, L-serine, lincomycin, D-galacturonic acid, L-galactonic acid lactone, D-gluconic acid, D-glucuronic acid, mucic acid, quinic acid, D-saccharic acid, vancomycin, tetrazolium violet, tetrazolium blue, *p*-hydroxy-pheylacetic acid, L-lactic acid, citric acid, D-malic acid, L-malic acid, bromo-succinic acid, γ-amino-butryric acid, β-hydroxy-D, L-butyric acid, propionic acid, acetic acid, formic acid and aztreonam; weak positive for D-fructose, D-fucose, fusidic acid, D-serine, myo-inositol, D-glucose-6-PO_4, D-fructose-6-PO_4, guanidine HCl, niaproof 4, methyl pyruvate, α-keto-glutaric acid, potassium tellurite, tween 40, α-hydroxy-butyric acid and acetoacetic acid; but negative for dextrin, D-maltose, D-cellobiolose, gentiobiose, sucrose, D-turanose, stachyose, D-raffinose, α-D-lactose, D-melibiose, β-methyl-D-glucoside, D-sali-

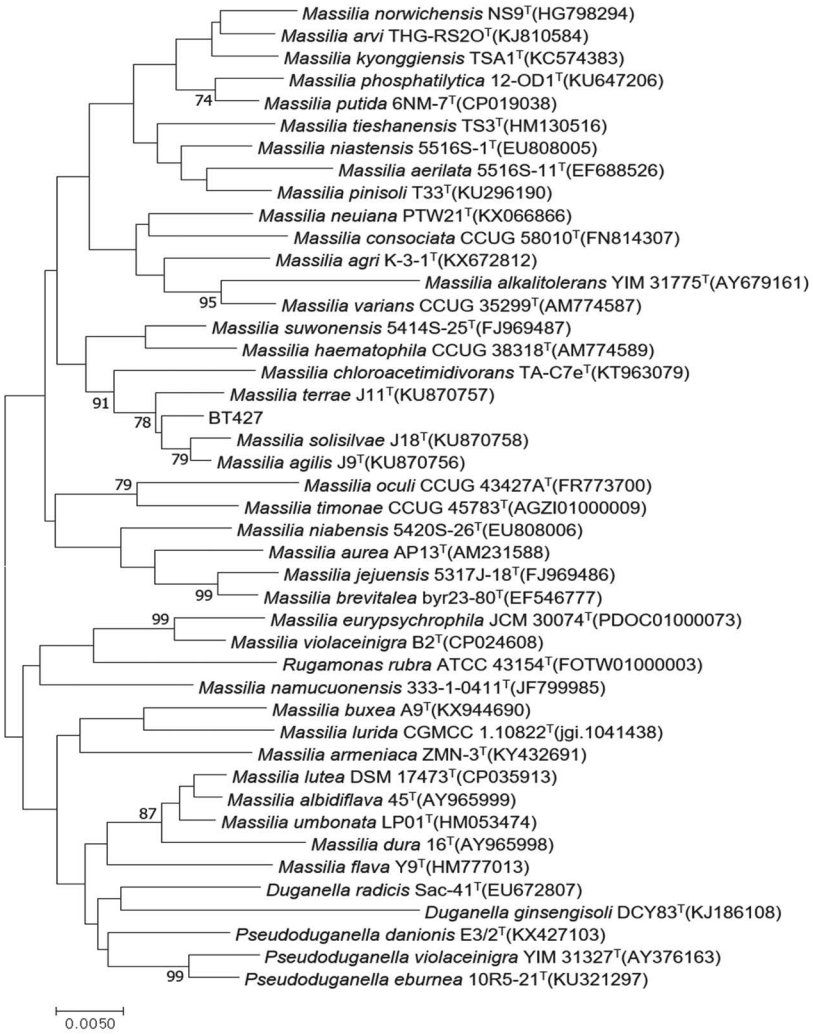


Fig. 7. Neighbor-joining phylogenetic tree based on 16S rRNA gene sequences shows the relationship between the strains isolated in this study and their relatives of the species *Arthrobacter nitrophenolicus*. Bootstrap values (>70%) are shown above nodes for the neighbor-joining methods. Bar: 0.01 and 0.02 substitutions per nucleotide position, respectively.

cin, *N*-acetyl-β-mannosamin, *N*-acetyl neuraminic acid, 4% NaCl, 8% NaCl, 3-methyl-glucose, inosine, D-aspartic acid, D-aerine, minocycline, gelatin, pectin, glucuronamide, D-lactic acid methyl ester, nalidixic acid, lithium chloride, α-keto butyric acid, sodium butyrate and sodium bromate. In 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 and gelatin hydrolysis. D-Mannitol, D-maltose, D-glucose, L-arabinose (weak), D-mannose (weak), potassium gluconate (weak), adipic acid (weak), malic acid (weak) were utilized whereas, *N*-acetyl-D-glucosamine, capric acid, trisodium citrate and phenylacetic acid were not utilized. In API 32GN test, *N*-acetyl-glucosamine, D-ribose, inositol, D-saccharose (sucrose), D-maltose, glycogen, D-mannitol, D-glucose, D-melibiose, L-arabinose, sodium acetate, lactic acid, L-alanine, salicin, trisodium citrate, potassium 2-ketogluconate and L-proline were utilized whereas, L-rhamnose, itaconic acid, suberic acid, sodium malonate, potassium 5-ketogluconate, 3-hydroxybenzoic acid, L-serine, D-fucose, D-sorbitol, propionic acid, capric acid, valeric acid, L-histidine, 3-hydroxybutyric acid and 4-hydroxybenzoic acid were not utilized.

Strain BT370 (=NIBRBAC000503024) was isolated from a soil sample, Gyeongju City in Gyeongsangbuk Province, Korea.

Description of *Massilia neuiana* BT239

Cells are Gram-stain-positive, non-flagellated, and rod-

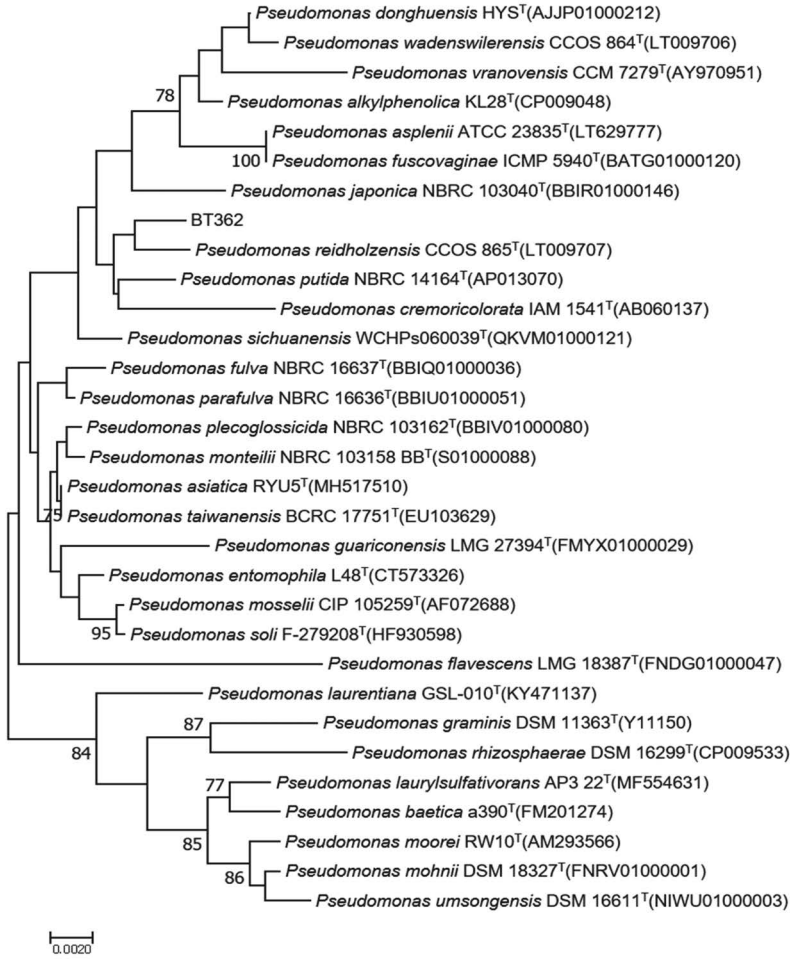


Fig. 8. Neighbor-joining phylogenetic tree based on 16S rRNA gene sequences shows the relationship between the strains isolated in this study and their relatives of the species *Pseudomonas reidholzensis*. Bootstrap values (>70%) are shown above nodes for the neighbor-joining methods. Bar: 0.01 and 0.02 substitutions per nucleotide position, respectively.

shaped. Colonies are pale yellow-colored after 3 days of incubation on R2A at 25°C. In the BIOLOG GEN III, positive for dextrin, D-maltose, gentiobiose, pH 6, L-rhamnose, gelatin, glyctl-L-proline, L-aspartic, L-glutamic acid, lincomycin, D-galacturonic acid, L-galactonic acid lactone, D-glucuronic acid, tetrazolium blue, D-malic acid, L-malic acid, propionic acid, acetic acid and aztreonam; weak positive for D-glucose, D-fructose, D-galactose, D-fucose, 1% sodium lactate, D-fructose-6-PO_4, L-histidine, pectin, glucuronamide, tetrazolium violet, tween 40, β-hydroxy-D, L-butyric acid, acetoacetic acid and formic acid; but negative for D-trehalose, D-cellobiolose, sucrose, D-turanose, stachyose, pH 5, D-raffinose, α-D-lactose, D-melibiose, β-methyl-D-glucoside, D-salicin, *N*-acetyl-D-glucosamine, *N*-acetyl-β-mannosamin, *N*-acetyl-D-galactosamin, *N*-acetyl neuraminic acid, 1% NaCl, 4% NaCl, 8% NaCl, D-mannose, 3-methyl-glucose, L-fucose, inosine, fusidic acid, D-serine, D-sorbitol, D-mannitol, D-arabitol, myo-inositol, glycerol, D-glucose-6-PO_4, D-aspartic acid, D-serine, troleandomycin, rifamycin SV, minocycline, L-alanine, L-arginine, L-pyroglutamic acid, L-serine, guanidine HCl, niaproof 4, D-gluconic acid, mucic acid, quinic acid, D-saccharic acid, bancomycin, *p*-hydroxy-pheylacetic acid, methyl pyruvate, D-lactic acid methyl ester, L-lactic acid, citric acid, α-keto-glutaric acid, bromo-succinic acid, nalidixic acid, lithium chloride, potassium tellurite, γ-amino-butryric acid, α-hydroxy-butyric acid, α-keto butyric acid, sodium butyrate and sodium bromate. In API 20NE test, positive for arginine dihydrolase, 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, gelatin hydrolysis, β-galactosidase and D-maltose (weak) were utilized. D-Glucose, 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 API 32GN test, *N*-acetyl-glucosamine, D-ribose, inositol,

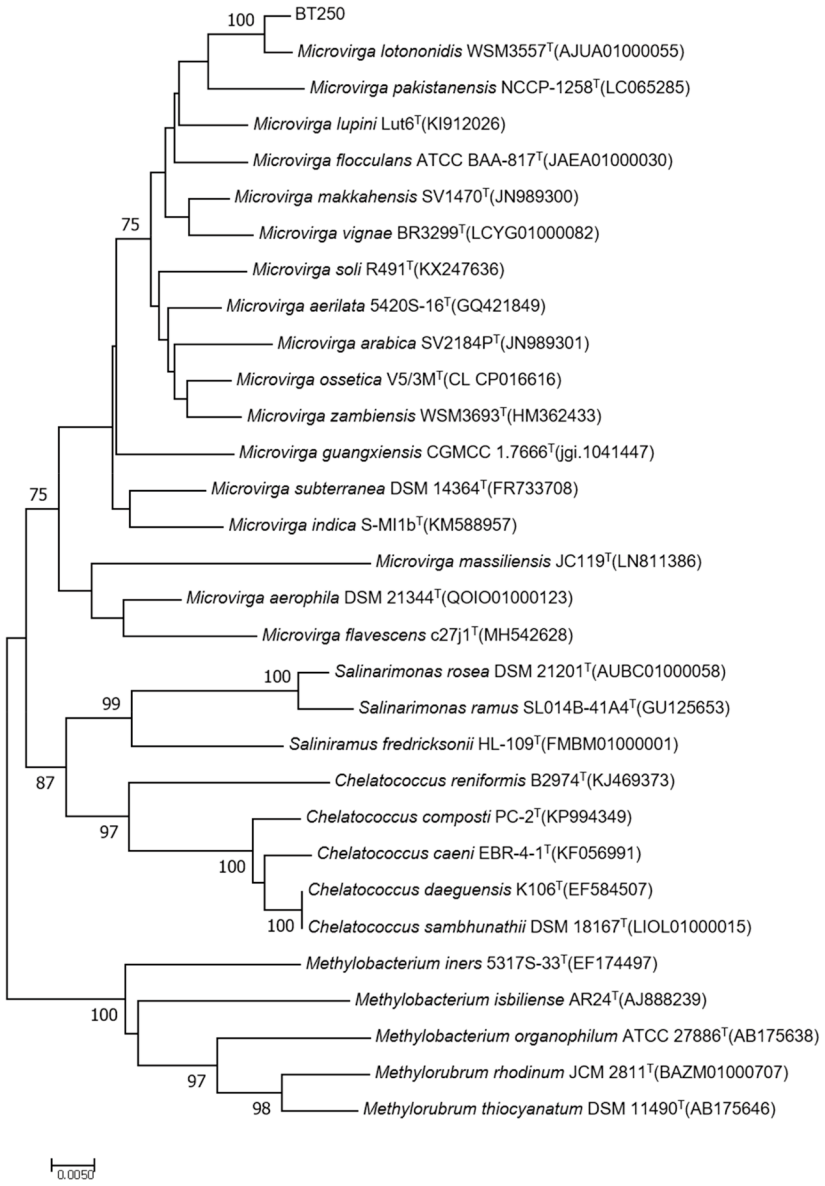


Fig. 9. Neighbor-joining phylogenetic tree based on 16S rRNA gene sequences shows the relationship between the strains isolated in this study and their relatives of the species *Microvirga lotononidis*. Bootstrap values (>70%) are shown above nodes for the neighbor-joining methods. Bar: 0.01 and 0.02 substitutions per nucleotide position, respectively.

D-saccharose (sucrose), itaconic acid, suberic acid, sodium malonate, lactic acid, potassium 5-ketogluconate, 3-hydroxybenzoic acid, D-mannitol, D-glucose, salicin, D-melibiose, D-fucose, D-sorbitol, capric acid, valeric acid, trisodium citrate, L-histidine, potassium 2-ketogluconate and 4-hydroxybenzoic acid were utilized whereas, L-rhamnose, D-maltose, glycogen, L-serine and L-arabinose were not utilized.

Strain BT239 (=NIBRBAC000503018) was isolated from a soil sample, Pocheon City in Gyeonggi Province, Korea.

Description of *Noviherbaspirillum canariense* BT339

Cells are Gram-stain-negative, non-flagellated, and rod-shaped. Colonies are Yellow-colored after 3 days of incubation on R2A at 25°C. In the BIOLOG GEN III, positive for pH 6, L-aspartic acid, L-glutamic acid, lincomycin, quinic acid, tetrazolium blue, L-lactic acid, D-malic acid, L-malic acid, acetic acid and aztreonam; weak positive for 1% sodium lactate, rifamycin SV, D-gluconic acid, glucuronamide, D-saccharic acid, tetrazolium violet, *p*-hydroxy-pheylacetic acid, methyl pyruvate, citric acid, α-keto-glutaric acid, nalidixic acid, α-hydroxy-bu-

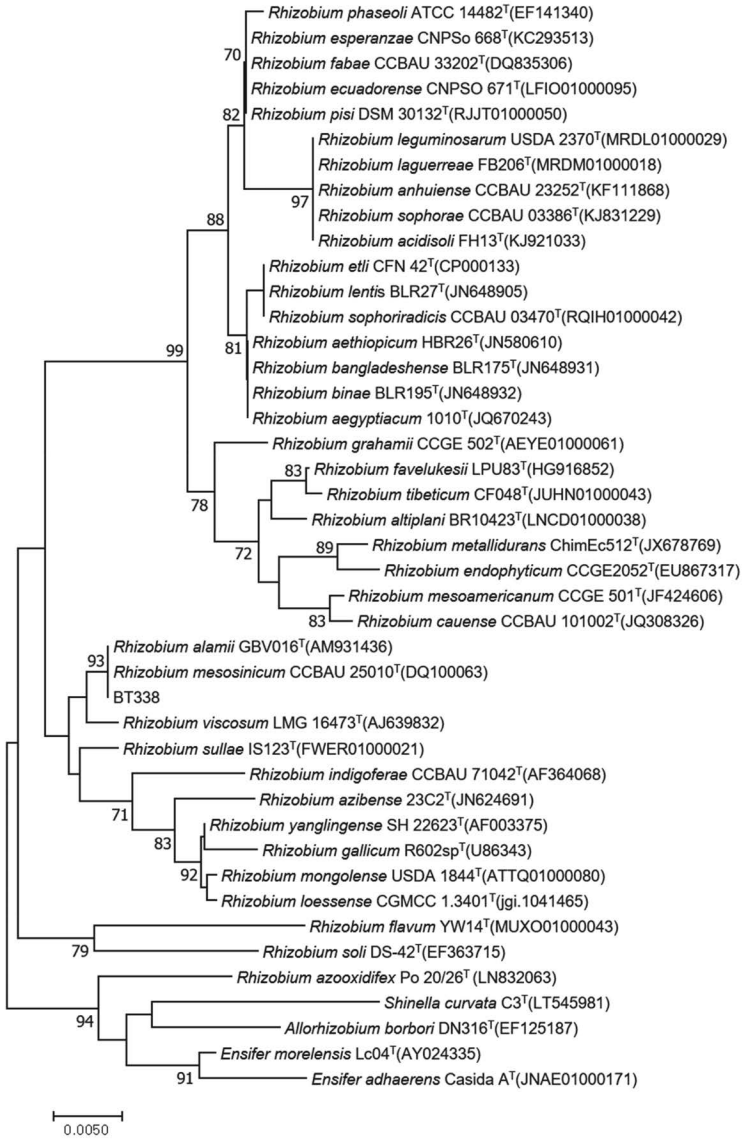


Fig. 10. Neighbor-joining phylogenetic tree based on 16S rRNA gene sequences shows the relationship between the strains isolated in this study and their relatives of the species *Rhizobium alamii*. Bootstrap values (>70%) are shown above nodes for the neighbor-joining methods. Bar: 0.01 and 0.02 substitutions per nucleotide position, respectively.

tyric acid, β-hydroxy-D, L-butyric acid, α-keto butyric acid, acetoacetic acid and propionic acid; 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-methyl-D-glucoside, D-salicin, *N*-acetyl-D-glucosamine, *N*-acetyl-β-mannosamin, *N*-acetyl-D-galactosamin, *N*-acetyl neuraminic acid, 1% NaCl, 4% NaCl, 8% NaCl, α-D-glucose, D-mannose, D-fructose, D-galactose, 3-methyl-glucose, D-fucose, L-fucose, L-rhamnose, inosine, fusidic acid, D-serine, D-sorbitol, D-mannitol, D-arabitol, myo-inositol, glycerol, D-glucose-6-PO_4, D-fructose-6-PO_4, D-aspartic acid, D-serine, troleandomycin, minocycline, gelatin, glyctl-L-proline, L-alanine, L-arginine, L-histidine, L-pyroglutamic acid, L-serine, guanidine HCl, niaproof 4, pectin, D-galacturonic acid, L-galactonic acid lactone, D-glucuronic acid, mucic acid, vancomycin, D-lactic acid methyl ester, bromo-succinic acid, lithium chloride, potassium tellurite, tween 40, γ-amino-butryric acid, formic acid, sodium butyrate and sodium bromate. In API 20NE test, positive for potassium gluconate and malic acid; weak positive for indole production on tryptophan, esculin hydrolysis; but negative for reduction of nitrates (NO_3) to nitrite (NO_2^-), reduction of nitrates (NO_3) to nitrogen (N_2), glucose fermentation, arginine dihydrolase, urease, gelatin hydrolysis (weak) and adipic acid (weak) were utilized. β-Galactosidase,

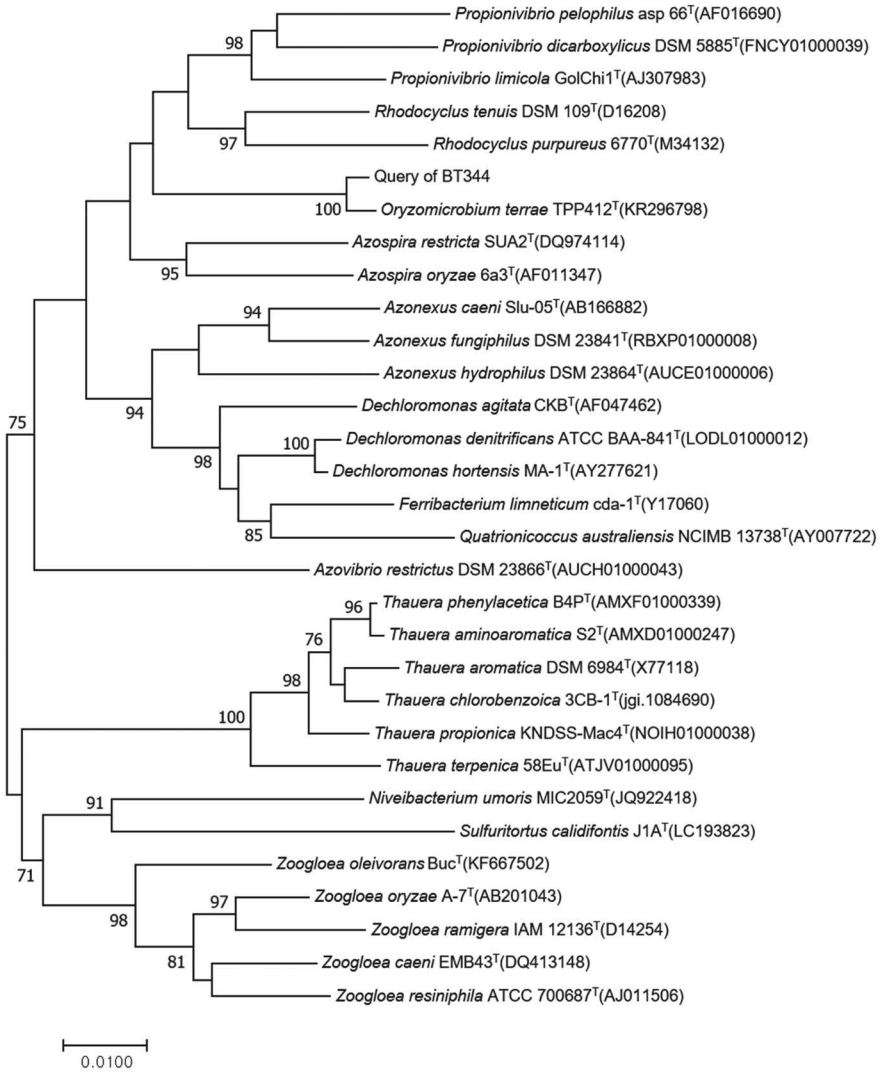


Fig. 11. Neighbor-joining phylogenetic tree based on 16S rRNA gene sequences shows the relationship between the strains isolated in this study and their relatives of the species *Oryzomicrobium terrae*. Bootstrap values (>70%) are shown above nodes for the neighbor-joining methods. Bar: 0.01 and 0.02 substitutions per nucleotide position, respectively.

D-glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-D-glucosamine, D-maltose, capric acid, trisodium citrate and phenylacetic acid were not utilized. In API 32GN test, itaconic acid, suberic acid, sodium acetate, lactic acid, propionic acid, valeric acid, 3-hydroxybutyric acid, 3-hydroxybenzoic acid, trisodium citrate and 4-hydroxybenzoic acid were utilized whereas, L-rhamnose, *N*-acetyl-glucosamine, D-ribose, inositol, D-saccharose (sucrose), D-maltose, sodium malonate, L-alanine, potassium 5-ketogluconate, glycogen, L-serine, D-mannitol, D-glucose, salicin, D-melibiose, D-fucose, D-sorbitol, L-arabinose, capric acid, L-histidine, potassium 2-ketogluconate and L-proline were not utilized.

Strain BT339 (=NIBRBAC000503036) was isolated from a soil sample, Namyangju City in Gyeonggi Province, Korea.

Description of *Massilia agilis* BT427

Cells are Gram-stain-negative, non-flagellated, and rod-shaped. Colonies are white-colored after 3 days of incubation on R2A at 25°C. In the BIOLOG GEN III, negative for pH 6, L-aspartic acid, L-glutamic acid, lincomycin, quinic acid, tetrazolium blue, L-lactic acid, D-malic acid, L-malic acid, acetic acid, aztreonam, 1% sodium lactate, rifamycin SV, D-gluconic acid, glucuronamide, D-saccharic acid, tetrazolium violet, *p*-hydroxy-pheylacetic acid, methyl pyruvate, citric acid, α-keto-glutaric acid, nalidixic acid, α-hydroxy-butyric acid, β-hydroxy-D, L-butyric acid, α-keto butyric acid, acetoacetic acid, propionic acid,

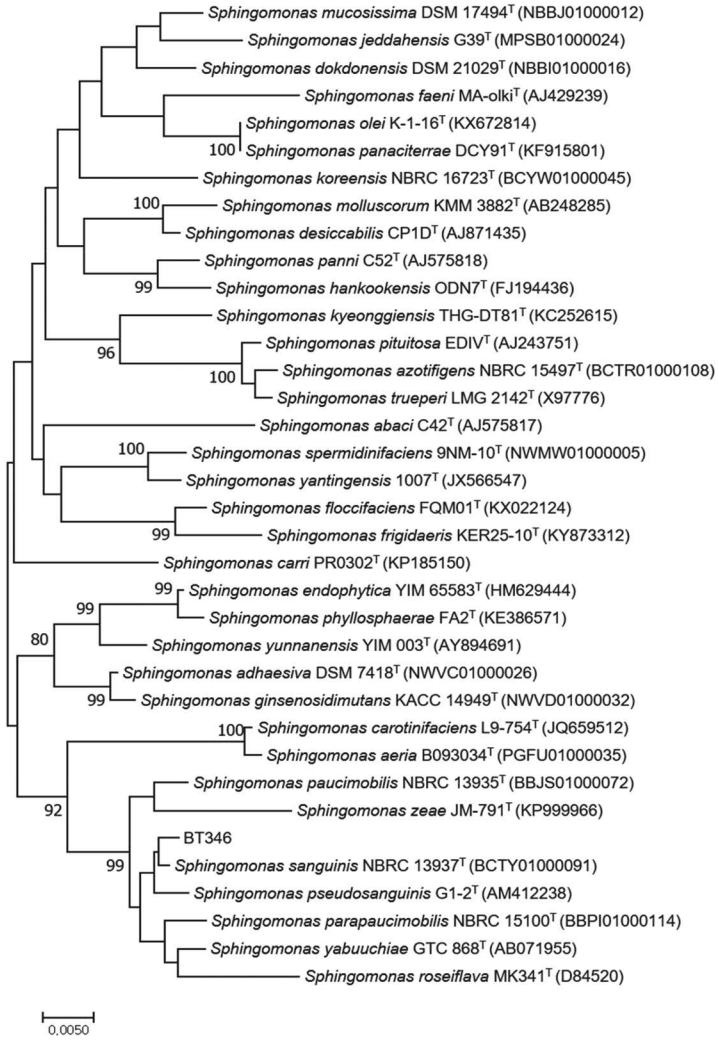


Fig. 12. Neighbor-joining phylogenetic tree based on 16S rRNA gene sequences shows the relationship between the strains isolated in this study and their relatives of the species *Sphingomonas sanguinis*. Bootstrap values (>70%) are shown above nodes for the neighbor-joining methods. Bar: 0.01 and 0.02 substitutions per nucleotide position, respectively.

dextrin, D-maltose, D-trehalose, D-cellobiolose, gentiobiose, sucrose, D-turanose, stachyose, pH 5, D-raffinose, α-D-lactose, D-melibiose, β-methyl-D-glucoside, D-salicin, *N*-acetyl-D-glucosamine, *N*-acetyl-β-mannosamin, *N*-acetyl-D-galactosamin, *N*-acetyl neuraminic acid, 1% NaCl, 4% NaCl, 8% NaCl, α-D-glucose, D-mannose, D-fructose, D-galactose, 3-methyl-glucose, D-fucose, L-fucose, L-rhamnose, inosine, fusidic acid, D-serine, D-sorbitol, D-mannitol, D-arabitol, myo-inositol, glycerol, D-glucose-6-PO_4, D-fructose-6-PO_4, D-aspartic acid, D-serine, troleandomycin, minocycline, gelatin, glyctl-L-proline, L-alanine, L-arginine, L-histidine, L-pyroglutamic acid, L-serine, guanidine HCl, niaproof 4, pectin, D-galacturonic acid, L-galactonic acid lactone, D-glucuronic acid, mucic acid, vancomycin, D-lactic acid methyl ester, bromo-succinic acid, lithium chloride, potassium tellurite, tween 40, γ-amino-butryric acid, formic acid, sodium butyrate and sodium bromate. In API 20NE test, 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, esculin hydrolysis, gelatin hydrolysis and β-galactosidase. D-Maltose (weak) and malic acid (weak) were utilized whereas, D-glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-D-glucosamine, potassium gluconate, capric acid, adipic acid, trisodium citrate and phenylacetic acid were not utilized. In API 32GN test, D-maltose are weakly utilized whereas, 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

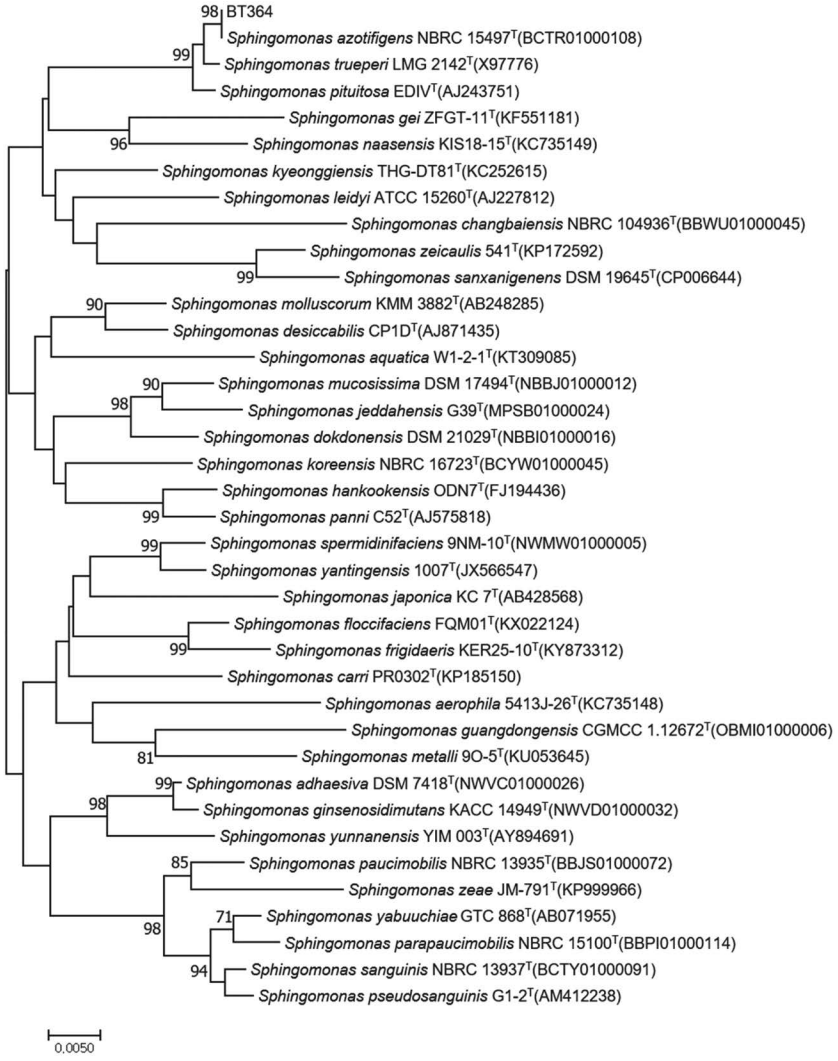


Fig. 13. Neighbor-joining phylogenetic tree based on 16S rRNA gene sequences shows the relationship between the strains isolated in this study and their relatives of the species *Sphingomonas azotifigens*. Bootstrap values (>70%) are shown above nodes for the neighbor-joining methods. Bar: 0.01 and 0.02 substitutions per nucleotide position, respectively.

acid, trisodium citrate, L-histidine, potassium 2-ketogluconate, 3-hydroxybutyric acid, 4-hydroxybenzoic acid and L-proline were not utilized.

Strain BT427 (=NIBRBAC000503047) was isolated from a soil sample, Ganghwa Island in Incheon City, Korea.

Description of *Pseudomonas reidholzensis* BT362

Cells are Gram-stain-negative, flagellate, and rod-shaped. Colonies are yellow-colored after 3 days of incubation on R2A at 25°C. In the BIOLOG GEN III, positive for pH 6, pH 5, 1% NaCl, 4% NaCl, α-D-glucose, D-mannose, D-fructose, 1% sodium lactate, fusidic acid, glycerol, troleandomycin, rifamycin SV, L-alanine, L-arginine, L-aspartic acid, L-glutamic acid, L-histidine, L-serine, lincomycin, guanidine HCl, niaproof 4, D-galacturonic acid, D-gluconic acid, D-glucuronic acid, mucic acid, quinic acid, vancomycin, tetrazolium violet, tetrazolium blue, L-lactic acid, citric acid, L-malic acid, nalidixic acid, lithium chloride, potassium tellurite, γ-amino-butryric acid, β-hydroxy-D, L-butyric acid, propionic acid and acetic acid; weak positive for 8% NaCl, inosine, D-serine, D-fructose-6-PO_4, glyctl-L-proline, L-galactonic acid lactone, glucuronamide, D-saccharic acid, methyl pyruvate, α-keto-glutaric acid, bromo-succinic acid, α-keto butyric acid, formic acid and aztreonam; but negative for dextrin, D-maltose, D-trehalose, D-trehalose, gentiobiose, sucrose, D-turanose, stachyose, D-raffinose, α-D-lactose, D-melibiose, β-methyl-D-glucoside, D-salicin, *N*-acetyl-D-glucosamine, *N*-acetyl-β-mannosamin, *N*-acetyl-D-galactosamin, *N*-acetyl *N*-acetyl neuraminic acid, D-galactose, 3-meth-

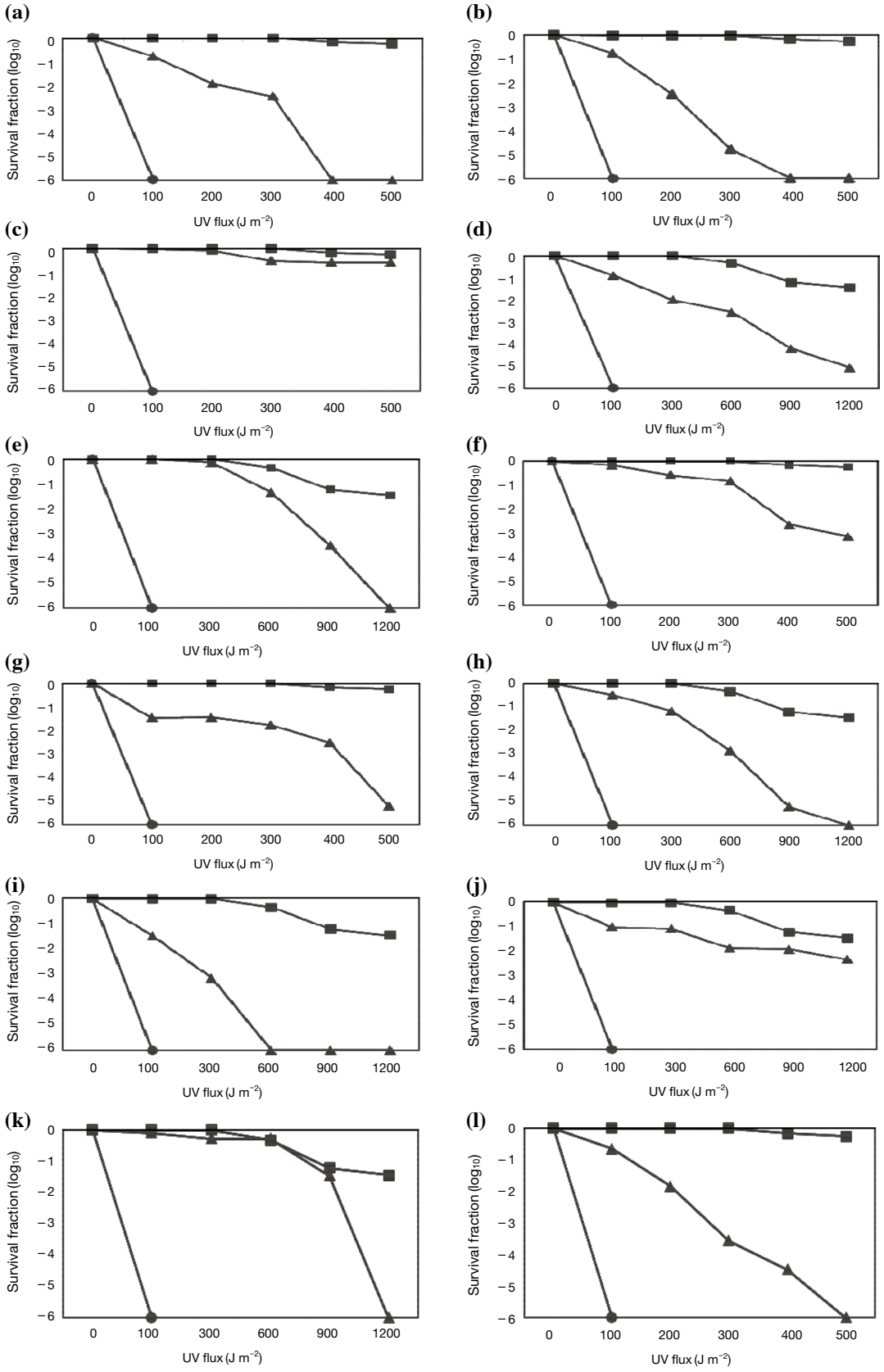


Fig. 14. UV resistance graph of the strains isolated in this study. Survival rates of *D. radiodurans* R1^T (■), strains (●) and *E. coli* K12 (◆) are also shown. Strains: a, BT434; b, BT368; c, BT370; d, BT239; e, BT339; f, BT427; g, BT362; h, BT250; i, BT338; j, BT344; k, BT346; l, BT364.

yl-glucose, D-fucose, L-fucose, L-rhamnose, D-sorbitol, D-mannitol, D-arabitol, myo-inositol, D-glucose-6-PO_4, D-aspartic acid, D-serine, minocycline, gelatin, L-pyroglutamic acid, pectin, *p*-hydroxy-pheylacetic acid, D-lactic acid methyl ester, D-malic acid, tween 40, α-hydroxy-butyric acid, acetoacetic acid, sodium butyrate and sodium bromate. In 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-Mannitol and D-maltose, D-glucose (weak), L-arabinose (weak), D-mannose, potassium gluconate (weak), adipic acid (weak) and malic acid (weak) were utilized whereas, *N*-acetyl-D-glucosamine, capric acid, trisodium citrate and phenylacetic acid were not utilized. In API 32GN test, L-alanine, L-serine, D-glucose, propionic acid, capric acid, valeric acid, trisodium citrate, L-histidine, potassium 2-ketogluconate, 3-hydroxybutyric acid, 4-hydroxybenzoic acid, L-proline, D-ribose, sodium malonate, sodium acetate, lactic acid and 3-hydroxybenzoic acid were utilized whereas, L-rhamnose, *N*-acetyl-glucosamine, inositol, D-saccharose (sucrose), D-maltose, itaconic acid, suberic acid, potassium 5-ketogluconate, glycogen, potassium 5-ketogluconate, glycogen, D-mannitol, salicin, D-melibiose, D-fucose, D-sorbitol and L-arabinose were not utilized.

Strain BT362 (=NIBRBAC000503041) was isolated from a soil sample, Seogwipo City in Jeju Island, Korea.

Description of *Microvirga lotononidis* BT250

Cells are Gram-stain-negative, non-flagellated, and rod-shaped. Colonies are white-colored after 3 days of incubation on R2A at 25°C. In the BIOLOG GEN III, positive for tetrazolium violet; weak positive for pH 6, 1% sodium lactate, fusidic acid, D-fructose, troleandomycin, rifamycin SV, L-glutamic acid, lincomycin, glucuronamide, tetrazolium blue, acetoacetic acid and acetic acid; 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-methyl-D-glucoside, D-salicin, *N*-acetyl-D-glucosamine, *N*-acetyl-β-mannosamin, *N*-acetyl-D-galactosamin, *N*-acetyl *N*-acetyl neuraminic acid, 1% NaCl, 4% NaCl, 8% NaCl, α-D-glucose, D-mannose, D-fructose-6-PO_4, D-galactose, 3-methyl-glucose, D-fucose, L-fucose, L-rhamnose, inosine, D-serine, D-sorbitol, D-mannitol, D-arabitol, myo-inositol, glycerol, D-glucose-6-PO_4, D-aspartic acid, D-serine, minocycline, gelatin, glyctl-L-proline, L-alanine, L-arginine, L-aspartic acid, L-histidine, L-pyroglutamic acid, L-serine, guanidine HCl, niaproof 4, pectin, D-galacturonic acid, L-galactonic acid lactone, D-gluconic acid, D-glucuronic acid, mucic acid, quinic acid, D-saccharic acid, vancomycin, *p*-hydroxy-pheylacetic acid, methyl pyruvate, D-lactic acid methyl ester, L-lactic acid, citric acid, α-keto-glutaric acid, D-malic acid, L-malic acid, bromo-succinic acid, nalidixic acid, lithium chloride, potassium tellurite, tween 40, γ-amino-butryric acid, α-hydroxy-butyric acid, β-hydroxy-D, L-butyric acid, α-keto butyric acid, propionic acid, formic acid, aztreonam, sodium butyrate and sodium bromate. In API 20NE test, 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, esculin hydrolysis, gelatin hydrolysis, β-galactosidase. D-Glucose, L-arabinose (weak), D-mannose (weak) and phenylacetic acid (weak) were utilized whereas, D-mannitol, *N*-acetyl-D-glucosamine, D-maltose, potassium gluconate, capric acid, adipic acid, malic acid and trisodium citrate were not utilized. In API 32GN test, glycogen, L-arabinose and 3-hydroxybutyric acid were utilized whereas, 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, 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 BT250 (=NIBRBAC000503027) was isolated from a soil sample, Uijeongbu City in Gyeonggi Province, Korea.

Description of *Rhizobium alamii* BT338

Cells are Gram-stain-negative, non-flagellated, and rod-shaped. Colonies are white-colored after 3 days of incubation on R2A at 25°C. In the BIOLOG GEN III positive for D-maltose, D-trehalose, D-cellobiolose, gentiobiose, sucrose, D-turanose, pH 6, α-D-lactose, D-melibiose, *N*-acetyl-D-glucosamine, *N*-acetyl-β-mannosamin, 1% NaCl, α-D-glucose, D-mannose, D-fructose, D-galactose, L-fucose, L-rhamnose, 1% sodium lactate, D-mannitol, D-arabitol, myo-inositol, glycerol, glycerol, rifamycin SV, L-glutamic acid, lincomycin, quinic acid, tetrazolium violet, tetrazolium blue, methyl pyruvate, L-malic acid, nalidixic acid, potassium tellurite and acetic acid; weak positive for dextrin, D-raffinose, β-methyl-D-glucoside, D-salicin, *N*-acetyl-D-galactosamin, *N*-acetyl *N*-acetyl neuraminic acid, D-fucose, D-sorbitol, glycyl-L-proline, L-alanine, L-aspartic acid, L-histidine, L-serine, pectin, D-glucuronic acid, D-malic acid, bromo-succinic acid, acetoacetic acid, formic acid and aztreonam; but negative for stachyose, pH 5, 4% NaCl, 8% NaCl, 3-methyl-glucose, inosine, fusidic acid, D-serine, D-glucose-6-PO_4, D-fructose-6-PO_4, D-aspartic acid, D-serine, minocycline,

gelatin, L-arginine, L-pyroglutamic acid, guanidine HCl, niaproof 4, D-galacturonic acid, L-galactonic acid lactone, D-gluconic acid, glucuronamide, mucic acid, D-saccharic acid, vancomycin, *p*-hydroxy-pheylacetic acid, D-lactic acid methyl ester, L-lactic acid, citric acid, α-keto-glutaric acid, lithium chloride, tween 40, γ-amino-butryric acid, α-hydroxy-butyric acid, β-hydroxy-D, L-butyric acid, α-keto butyric acid, propionic acid, sodium butyrate and sodium bromate. In API 20NE test, positive for esculin hydrolysis; weak positive for β-galactosidase; but negative for 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, D-maltose and malic acid, *N*-acetyl-D-glucosamine (weak) were utilized; but potassium gluconate, capric acid, adipic acid, trisodium citrate and phenylacetic acid were not utilized. In API 32 GN test, glycogen, salicin, D-fucose, D-sorbitol, 4-hydroxybenzoic acid, L-rhamnose, *N*-acetyl-glucosamine, inositol, D-saccharose (sucrose), D-maltose, L-serine, D-mannitol, salicin and D-sorbitol were utilized whereas, D-ribose, itaconic acid, suberic acid, sodium malonate, sodium acetate, lactic acid, L-alanine, potassium 5-ketogluconate, 3-hydroxybenzoic acid, L-serine, propionic acid, capric acid, valeric acid, trisodium citrate, L-histidine, potassium 2-ketogluconate, 3-hydroxybutyric acid and L-proline were not utilized.

Strain BT338 (=NIBRBAC000503035) was isolated from a soil sample, Uijeongbu City in Gyeonggi Province, Korea.

Description of *Oryzomicrobium terrae* BT344

Cells are Gram-stain-negative, flagellated, and rod-shaped. Colonies are pale yellow-colored after 3 days of incubation on R2A at 25°C. In the BIOLOG GEN III, positive for pH 6, *N*-acetyl neuraminic acid, 1% NaCl, 4% NaCl, 1% sodium lactate, D-serine, glyctl-L-proline, L-alanine, L-aspartic acid, L-glutamic acid, L-histidine, L-serine, guanidine HCl, methyl pyruvate, L-lactic acid, citric acid, L-malic acid, nalidixic acid, lithium chloride, potassium tellurite, tween 40, α-hydroxy-butyric acid, α-hydroxy-butyric acid, β-hydroxy-D, L-butyric acid, α-keto butyric acid, acetoacetic acid, propionic acid, acetic acid, formic acid, aztreonam, sodium butyrate and sodium bromate; weak positive for dextrin, D-maltose, D-trehalose, D-cellobiolose, gentiobiose, sucrose, D-turanose, stachyose, D-raffinose, D-melibiose, β-methyl-D-glucoside, D-salicin, *N*-acetyl-D-glucosamine, *N*-acetyl-β-mannosamin, α-D-glucose, D-mannose, D-fructose, D-galactose, 3-methyl-glucose, D-fucose, L-fucose, L-rhamnose, D-sorbitol, D-mannitol, D-arabitol, myo-inositol, glycerol, D-glucose-6-PO_4, D-fructose-6-PO_4, D-serine, L-arginine, L-pyroglutamic acid, D-galacturonic acid, D-gluconic acid, D-glucuronic acid, quinic acid, D-saccharic acid, bromo-succinic acid and γ-amino-butryric acid; but negative for pH 5, α-D-lactose, *N*-acetyl-D-galactosamin, 8% NaCl, inosine, fusidic acid, D-aspartic acid, troleandomycin, rifamycin SV, minocycline, gelatin, lincomycin, niaproof 4, pectin, L-galactonic acid lactone, glucuronamide, mucic acid, vancomycin, tetrazolium violet, tetrazolium blue, *p*-hydroxy-pheylacetic acid, D-lactic acid methyl ester, α-keto-glutaric acid and D-malic acid. In API 20NE test, weak positive for indole production on tryptophan and esculin hydrolysis; but negative for reduction of nitrates (NO_3) to nitrite (NO_2^-), reduction of nitrates (NO_3) to nitrogen (N_2), glucose fermentation, arginine dihydrolase, urease, gelatin hydrolysis, β-galactosidase. Potassium gluconate and malic acid adipic acid (weak) were utilized whereas, D-glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-D-glucosamine, D-maltose, capric acid, trisodium citrate and phenylacetic acid were not utilized. In API 32GN test, inositol, sodium acetate, lactic acid, L-alanine, L-serine, propionic acid, valeric acid, trisodium citrate, L-histidine, 3-hydroxybutyric acid were utilized whereas, L-rhamnose, *N*-acetyl-glucosamine, D-ribose, D-saccharose (sucrose), D-maltose, itaconic acid, suberic acid, sodium malonate, potassium 5-ketogluconate, glycogen, 3-hydroxybenzoic acid, D-mannitol, D-glucose, salicin, D-melibiose, D-fucose, D-sorbitol, L-arabinose, capric acid, potassium 2-ketogluconate, 4-hydroxybenzoic acid and L-proline were not utilized.

Strain BT344 (=NIBRBAC000503015) was isolated from a soil sample from Jeju Island, Korea.

Description of *Sphingomonas sanguinis* BT346

Cells are Gram-stain-negative, non-flagellated, and rod-shaped. Colonies are yellow-colored after 3 days of incubation on R2A at 25°C. In the BIOLOG GEN III, positive for D-maltose, D-trehalose, D-cellobiolose, 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, α-D-glucose, D-mannose, D-fructose, D-galactose, 1% sodium lactate, rifamycin SV, gelatin, L-aspartic acid, L-glutamic acid, lincomycin, pectin, tetrazolium blue, citric acid, α-keto-glutaric acid, L-malic acid, nalidixic acid, tween 40, β-hydroxy-D, L-butyric acid, acetic acid and aztreonam; weak positive for *N*-acetyl-β-mannosamin, 4% NaCl, D-fucose, L-fucose, L-rhamnose, D-sorbitol, D-mannitol, D-arabitol, myo-inositol, glycerol, D-glucose-6-PO_4, D-fructose, troleandomycin, glyctl-L-proline, L-pyroglutamic acid, L-serine, guanidine HCl, D-galacturonic acid, L-galactonic acid lactone, D-glucuronic acid, tetrazolium violet, methyl pyruvate, D-lactic acid methyl ester, bromo-succinic acid, potassium tellurite, α-keto butyric acid, acetoacetic acid, propionic acid and sodium bro-

mate; but negative for pH 5, *N*-acetyl-D-galactosamin, *N*-acetyl neuraminic acid, 8% NaCl, 3-methyl-glucose, inosine, fusidic acid, D-serine, D-aspartic acid, D-serine, minocycline, L-alanine, L-arginine, L-histidine, niaproof 4, D-gluconic acid, glucuronamide, mucic acid, quinic acid, D-saccharic acid, vancomycin, *p*-hydroxy-pheylacetic acid, L-lactic acid, D-malic acid, lithium chloride, γ-amino-butryric acid, α-hydroxy-butyric acid and formic acid, sodium butyrate. In API 20NE test, positive for esculin hydrolysis and β-galactosidase; 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 and gelatin hydrolysis. D-Glucose, L-arabinose, D-mannose, *N*-acetyl-D-glucosamine, D-maltose and malic acid were weakly utilized whereas, D-mannitol, potassium gluconate, capric acid, adipic acid, trisodium citrate and phenylacetic acid were not utilized. In API 32GN test, D-saccharose (sucrose), D-maltose, D-glucose, salicin, D-melibiose, L-arabinose, *N*-acetyl-glucosamine, sodium acetate, trisodium citrate and 4-hydroxybenzoic acid were utilized whereas, L-rhamnose, D-ribose, inositol, itaconic acid, suberic acid, sodium malonate, lactic acid, L-alanine, potassium 5-ketogluconate, glycogen, 3-hydroxybenzoic acid, L-serine, D-mannitol, D-fucose, D-sorbitol, propionic acid, capric acid, valeric acid, L-histidine, potassium 2-ketogluconate, 3-hydroxybutyric acid and L-proline were not utilized.

Strain BT346 (=NIBRBAC000503016) was isolated from a soil sample from Jeju Island, Korea.

Description of *Sphingomonas azotifigens* BT364

Cells are Gram-stain-negative, non-flagellated, and rod-shaped. Colonies are Yellow-colored after 3 days of incubation on R2A at 25°C. In the BIOLOG GEN III, positive for dextrin, D-maltose, D-cellobiolose, gentiobiose, sucrose, D-raffinose, α-D-lactose, D-melibiose, *N*-acetyl-D-glucosamine, 1% NaCl, α-D-glucose, D-mannose, D-fructose-6-PO_4, D-galactose, L-fucose, L-rhamnose, 1% sodium lactate, D-glucose-6-PO_4, troleandomycin, rifamycin SV, L-alanine, L-aspartic acid, L-glutamic acid, lincomycin, D-glucuronic acid, tetrazolium blue, nalidixic acid, potassium tellurite, β-hydroxy-D, L-butyric acid, propionic acid, acetic acid and aztreonam; weak positive for pH 6, 4% NaCl, 3-methyl-glucose, myo-inositol, D-fructose-6-PO_4, gelatin, glyctl-L-proline, pectin, D-galacturonic acid, L-galactonic acid lactone, glucuronamide, tetrazolium violet, L-lactic acid, citric acid, L-malic acid, tween 40, α-keto butyric acid and acetoacetic acid; but negative for D-trehalose, D-turanose, stachyose, pH 5, β-methyl-D-glucoside, D-salicin, *N*-acetyl-β-mannosamin, *N*-acetyl-D-galactosamin, *N*-acetyl neuraminic acid, 8% NaCl, D-fucose, inosine, fusidic acid, D-serine, D-sorbitol, D-mannitol, D-arabitol, glycerol, D-aspartic acid, D-serine, minocycline, L-arginine, L-histidine, L-pyroglutamic acid, L-serine, guanidine HCl, niaproof 4, D-gluconic acid, mucic acid, quinic acid, D-saccharic acid, vancomycin, methyl pyruvate, D-lactic acid methyl ester, α-keto-glutaric acid, D-malic acid, bromo-succinic acid, lithium chloride, γ-amino-butryric acid, α-hydroxy-butyric acid, formic acid, sodium butyrate and sodium bromate. In 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-Mannitol, D-maltose, D-glucose (weak), L-arabinose (weak), D-mannose (weak), potassium gluconate (weak), adipic acid (weak) and malic acid (weak) were utilized whereas, *N*-acetyl-D-glucosamine, capric acid, trisodium citrate and phenylacetic acid were not utilized. In API 32GN test, *N*-acetyl-glucosamine, D-saccharose (sucrose), D-maltose, D-glucose, D-melibiose, D-fucose, L-arabinose, L-rhamnose, sodium acetate, salicin, propionic acid and 4-hydroxybenzoic acid were utilized whereas, D-ribose, inositol, itaconic acid, suberic acid, sodium malonate, lactic acid, L-alanine, potassium 5-ketogluconate, glycogen, 3-hydroxybenzoic acid, L-serine, D-mannitol, D-sorbitol, capric acid, valeric acid, trisodium citrate, L-histidine, potassium 2-ketogluconate, 3-hydroxybutyric acid and L-proline were not utilized.

Strain BT364 (=NIBRBAC000503043) was isolated from a soil sample from Jeju Island, Korea.

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References

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

Garrity, G.M., J.A. Bell and T. Lilburn. 2005. Phylum XIV. Proteobacteria phyl. nov. In: Bergey's Manual of Systematic Bacteriology Springer, New York, NY.

Gupta, R.S. 2000. The phylogeny of proteobacteria: relationships to other eubacterial phyla and eukaryotes. FEMS Microbiology Review 24(4):367-402.

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 Information Retrieval Ltd, London.

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. Systamatic Applied Microbiology 21:374-383.

Im, W.T., H.M. Jung, L.N. Ten, M.K. Kim, N. Bora, M. Goodfellow, S. Lim, J. Jung and S.T. Lee 2008. *Deinococcus aquaticus* sp. nov., isolated from fresh water, and *Deinococcus caeni* sp. nov., isolated from activated sludge. International Journal of Systematic and Evolutionary Microbiology 58:2348-2353.

Kersters, K., P. De Vos, M. Gillis, J. Swings, P. Vandamme and E. Stackebrandt. 2006. Introduction to the *Proteobacteria*. In: The Prokaryotes Springer, New York, NY.

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.

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

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.

Stackebrandt, E., R.G.E. Murray and H.G. Trüper. 1988b Proteobacteria classis nov., a name for the phylogenetic taxon that includes the "purple bacteria and their relatives." Int. J. Syst. Bacteriol. 38 321-325.

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.

Woese, CR. 1987. "Bacterial evolution". Microbiological Reviews 51(2):221-271.

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.

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