

# A report of 35 unrecorded bacterial species isolated from sediment in Korea

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A total of 35 bacterial strains were isolated from various sediment samples. From 16S rRNA gene sequence similarities higher than 98.7% and the formation of a robust phylogenetic clade with the closest species, it was determined that each strain belonged to independent and predefined bacterial species. No previous official reports have described these 35 species in Korea. The unrecorded species were assigned to 6 phyla, 10 classes, 18 orders, 23 families, and 31 genera. At the genus level, the unrecorded species were affiliated with *Terriglobus* of the phylum *Acidobacteria*, as well as with *Mycobacterium*, *Rhodococcus*, *Kineococcus*, *Phycococcus*, *Agromyces*, *Cryobacterium*, *Microbacterium*, and *Arthrobacter*; *Catellatospora* of the class *Actinomycetia*; *Lacibacter* of the class *Chitinophagia*; *Algoriphagus* and *Flectobacillus* of the class *Cytophagia*; *Flavobacterium* and *Maribacter* of the class *Flavobacteriia*; *Bacillus*, *Cohnella*, *Fontibacillus*, *Paenibacillus*, *Lysinibacillus*, and *Paenisporosarcina* of the class *Bacilli*; *Bradyrhizobium*, *Gemmobacter*, *Loktanella*, and *Altererythrobacter* of the class *Alphaproteobacteria*; *Acidovorax* of the class *Betaproteobacteria*; *Aliiglaciecola*, *Cellvibrio*, *Arenimonas*, and *Lysobacter* of class *Gammaproteobacteria*; and *Roseimicrobium* of the class *Verrucomicrobia*. The selected strains were subjected to further taxonomic characterization, including Gram reaction, cellular and colonial morphology, and biochemical properties. This paper provides detailed descriptions of the 35 previously unrecorded bacterial species.

Keywords: 16S rRNA gene, freshwater, sediment, unrecorded bacteria

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## INTRODUCTION

Aquatic sediment is one of the largest ecosystems on Earth. In general, sediments are overlaid by a permanent water body, such as an ocean, lake, river, or reservoir, and share the property of being continuously wet (Nealson, 1997). Sediment-dwelling microbes are key players in biogeochemical cycling and have potential for the bioremediation of undesirable compounds from sediments. Microbial communities can be responsible for 76–96% of the total sediment respiration, and the communities are generally known as a dominant driving force in the transformation of complex organic compounds (Craft *et al.*, 2002; Zhang *et al.*, 2015). Therefore, investigations into the microbial structure and function of sediment is indispensable to obtain a better understanding of aquatic

ecosystems.

Culture-independent molecular approaches based on 16S rRNA have been used for microbial ecology studies of sediments and the biomass and taxon richness of microbes in sediments are known to be much higher than those of the corresponding water bodies (Wang *et al.*, 2012). Although previous studies have been conducted on the basis of traditional cultivation methods, it is now widely recognized that only 0.001–15% (0.25% in sediments) of the total cell counts in environmental samples can be cultured (Amann *et al.*, 1995). However, cultivation-based study remains important because the ecological role of bacteria in natural environments and the industrial application of bacterial resources can be revealed only when they are successfully cultivated and characterized.

Since 2015, we have isolated a great number of unre-

corded prokaryotic species from the sediments of diverse freshwater environments in the Republic of Korea. The isolated strains were found to belong to six phyla: *Acidobacteria*, *Actinobacteria*, *Bacteroidetes*, *Firmicutes*, *Proteobacteria*, and *Verrucomicrobia*. The present report focuses on the descriptions of 35 strains that have not been previously isolated in Korea.

## MATERIALS AND METHODS

Sediment samples were collected from the Nakdonggang River, Seomjingang River, Taehwagang River, Gyeongpo Lake, Hyang Lake, Chodang Cave, and Moojehineup Wetland (Table 1). Each sediment sample was processed separately by spreading onto diverse culture agar media: Reasoner's 2A agar, humic acid vitamin agar, International *Streptomyces* Project 4 agar, marine agar, trypticase soy agar, nutrient agar, and 1/10 diluted agar of each of these media. After incubation at 15–30°C for 7–14 days, bacterial strains were purified by subculturing a single colony on fresh media and pure cultures were preserved at –80°C in 20% (w/v) glycerol suspension.

For bacterial identification, PCR amplification with universal primers 27F and 1492R and 16S rRNA gene sequencing with primers 518F and 800R were performed using standard procedures. The 16S rRNA gene sequences of the bacterial strains were compared with other bacterial strains using the EZ Biocloud server (Yoon *et al.*, 2017). Bacterial strains showing 98.7% or higher sequence similarity with validly published species that had not previously been reported in Korea were selected as unrecorded bacterial species. For phylogenetic analysis, 16S rRNA gene sequence alignment between isolated

strains and those of closely related strains was carried out using EZ Editor (Jeon *et al.*, 2014). Phylogenetic trees were constructed using neighbor-joining (Saitou and Nei, 1987), maximum parsimony (Fitch, 1971), and maximum likelihood (Felsenstein, 1981) methods and evolutionary distances were calculated using the Jukes and Cantor one-parameter model (Jukes and Cantor, 1969) with the MEGA package ver. 7.0 (Kumar *et al.*, 2016). Bootstrap analysis was carried out using 1,000 resampled datasets (Felsenstein, 1985), which were also used to test the topology of the phylogenetic tree.

The colony morphology of the strains was observed on agar plates with a magnifying glass after the cells grew to stationary phase. Cellular morphology and cell size were examined by transmission electron microscopy (CM200, Philips or HT7700, Hitachi). Gram staining was performed using a Gram staining kit (Sigma) and oxidase activity was determined using 1% (w/v) tetramethyl *p*-phenylenediamine. Biochemical characteristics were tested by using API-20NE galleries (bioMérieux) according to the manufacturers' instructions.

## RESULTS AND DISCUSSION

On the basis of the 16S rRNA gene sequence comparison and phylogenetic analysis, a total of 35 strains were assigned to six phyla: one strain to the phylum *Acidobacteria*, 10 strains to the phylum *Actinobacteria*, seven strains to the phylum *Bacteroidetes*, six strains to the phylum *Firmicutes*, 10 strains to the phylum *Proteobacteria*, and one strain to the phylum *Verrucomicrobia*. The strain information and identification results are summarized in Table 1.

A phylogenetic tree of the 17 bacterial strains assigned

**Table 1.** GPS information of sampling site for sediment sample collected.

	Sampling site	Sample code	GPS
Lagoon	Gyeongpo Lake	LS1	N 37°47'49.5", E 128°53'52.4"
	Hyang Lake	LS2	N 37°54'30.3", E 128°48'27.1"
Lime stone cave	Chodang Cave	CCS	N 37°22'47.26", E 129°10'53.26"
River	Nakdonggang River	SS	N 36°26'4.11", E 128°15'4.37"
		GS	N 35°6'4.03", E 128°56'49.39"
		AS	N 36°41'38.4", E 128°48'44.24"
		ES	N 35°6'42.04", E 128°56'59.28"
	Seomjingang River	HS, SJS	N 35°3'48.18", E 127°44'29.21"
	Taehwagang River	UTS2	N 35°33'7.32", E 129°19'9.05"
		UTS5	N 35°33'5.17", E 129°18'17.26"
Wetland	Moojehineup Wetland	UMS	N 35°45'91.27", E 129°13'3.04"

**Table 2.** Summary of isolated strains from the freshwater sediment and their taxonomic affiliation.

Sampling site	Class	Order	Family	Most closely related species	Strain ID	NNIBR No.	Sim. (%)	Accession no.	Medium	Incubation condition
Gyeongpo Lake	Flavobacteria	Flavobacteriales	Flavobacteriaceae	<i>Maribacter antarcticus</i>	LS1-46	NNIBR2017301BA33	98.97	MG780329	MA	15°C, 3-4 days
	Bacilli	Bacillales	Paenibacillaceae	<i>Fontibacillus solani</i>	LS1-27	NNIBR2017301BA32	99.06	MG780328	TSA	30°C, 2-3 days
				<i>Cohnella rhizosphaerae</i>	LS1-26	NNIBR2018141BA3	98.97	MK396575	NA	30°C, 2-3 days
Hyang Lake	Gammaaproteobacteria	Celviribronales	Celviribronaceae	<i>Celviribrio gandavensis</i>	LS2-11	NNIBR2018141BA4	99.80	MK396576	R2A	30°C, 2-3 days
Chodang Cave	Bacilli	Bacillales	Bacillaceae	<i>Bacillus niacini</i>	CCS-46	NNIBR2017301BA43	99.04	MG780339	TSA	30°C, 2-3 days
Nakdonggang River	Actinomycetia	Corynebacteriales	Mycobacteriaceae	<i>Mycobacterium rifium</i>	SS1-64	NNIBR2015296BA10	99.59	KU341399	R2A	25°C, 5 days
			Kineosporiaceae	<i>Kineococcus endophytica</i>	SS1-41	NNIBR2015296BA9	99.64	KU984671	R2A	25°C, 2-3 days
			Intrasporangiaceae	<i>Phycococcus ginsenosidimitans</i>	AS4-17	NNIBR2016301BA21	99.93	KY012263	R2A	20°C, 2-3 days
			Microbacteriaceae	<i>Cryobacterium psychrotolerans</i>	GS1-31	NNIBR2015296BA38	99.00	KU984675	R2A	20°C, 3 days
				<i>Microbacterium hydrothermale</i>	SS2-77	NNIBR2015296BA15	99.38	KU341402	R2A	25°C, 2-3 days
	Bacilli	Bacillales	Micrococcaceae	<i>Microbacterium kitamiense</i>	ES2-36	NNIBR2016301BA27	100.00	KY012260	R2A	25°C, 3-4 days
				<i>Arthrobacter enclensis</i>	SS5-09	NNIBR2018141BA5	98.78	MK396577	TSA	30°C, 3-4 days
			Paenibacillaceae	<i>Paenibacillus gorillae</i>	SS1-12	NNIBR2015296BA4	99.73	KU341394	R2A	30°C, 2-3 days
			Planococcaceae	<i>Lysinibacillus parvivoronicaptiens</i>	SS1-02	NNIBR2015296BA2	99.18	KU341392	R2A	30°C, 2-3 days
				<i>Paenisporosarcina macmurdoensis</i>	ES1-24	NNIBR2016301BA24	99.93	KY012258	R2A	25°C, 2-3 days
Alphaproteobacteria	Rhodobacteriales	Rhodobacteraceae	<i>Gemmobacter aquaticus</i>	OSSS-25	NNIBR2017301BA44	99.85	MG780340	R2A	30°C, 2-3 days	
	Sphingomonadales	Erythrobacteraceae	<i>Altererythrobacter buctensis</i>	SS12-22	NNIBR2018141BA9	99.57	MK396581	R2A	30°C, 2-3 days	
Gammaaproteobacteria	Lysobacteriales	Lysobacteraceae	<i>Arenimonas maotaiensis</i>	SS7-26	NNIBR2018141BA7	99.80	MK396579	R2A	37°C, 2-3 days	
			<i>Arenimonas taoyuanensis</i>	SS7-18	NNIBR2018141BA6	99.45	MK396578	TSA	30°C, 2-3 days	
Verrucomicrobiae	Verrucomicrobiales	Verrucomicrobiaceae	<i>Roseimicrobium gellanilyticum</i>	GS1-01	NNIBR2015296BA35	98.97	KU984672	R2A	25°C, 2-3 days	
Seomjingang River	Cytophagia	Cytophagales	Cyclobacteriaceae	<i>Algoriphagus ratkowskyi</i>	HS1-69	NNIBR2017301BA28	99.22	KX809752	MA	10°C, 5 days
		Flavobacteriales	Flavobacteriaceae	<i>Flavobacterium degerlachei</i>	SIS1-74	NNIBR2017301BA40	99.65	MG780336	R2A	20°C, 2-3 days
	Alphaproteobacteria	Rhodobacteriales	Rhodobacteraceae	<i>Maribacter arcticus</i>	SIS1-42-1	NNIBR2017301BA39	99.86	MG780335	MA	15°C, 3-4 days
				<i>Loktanella atrilutea</i>	HS1-70	NNIBR2017301BA29	99.49	KX809753	MA	30°C, 2-3 days
	Betaproteobacteria	Burkholderiales	Comamonadaceae	<i>Acidovorax defluvi</i>	HS1-68	NNIBR2018141BA2	99.93	MK396574	NA	30°C, 2-3 days
	Gammaaproteobacteria	Alteromonadales	Alteromonadaceae	<i>Aliiglaciecola litoralis</i>	SIS3-28	NNIBR2017301BA41	99.18	MG780337	MA	25°C, 2-3 days
Lysobacteriales			Lysobacteraceae	<i>Lysobacter caeni</i>	SS12-55	NNIBR2017301BA42	99.73	MG780338	R2A	30°C, 2-3 days
Taehwagang River	Actinomycetia	Corynebacteriales	Nocardiaceae	<i>Rhodococcus coprophilus</i>	UTS6-49	NNIBR2017301BA36	99.72	MG780332	R2A	30°C, 2-3 days
			Micrococcaceae	<i>Agromyces ramosus</i>	UTS5-20	NNIBR2018141BA12	99.17	MK396584	R2A	30°C, 2-3 days
	Chitinophagia	Chitinophagales	Micromonosporales	<i>Catillatospora chokortensis</i>	UTS5-15	NNIBR2018141BA11	99.51	MK396583	R2A	30°C, 2-3 days
				<i>Lactibacter caeniensis</i>	UTS2-06	NNIBR2017301BA34	99.86	MG780330	R2A	25°C, 2-3 days
	Cytophagia	Cytophagales	Cytophagaceae	<i>Flectobacillus major</i>	UTS5-52	NNIBR2017301BA35	99.72	MG780331	R2A	25°C, 2-3 days
Flavobacteria	Flavobacteriales	Flavobacteriaceae	<i>Flavobacterium caeniense</i>	UTS2-20	NNIBR2018141BA10	100.00	MK396582	R2A	30°C, 2-3 days	
Moojehineup Wetland	Acidobacteria	Acidobacteriales	Acidobacteriaceae	<i>Terriglobus roseus</i>	UMS-18	NNIBR2017301BA37	100.00	MG780333	R2A	30°C, 2-3 days
			Rhizobiales	Nitrobacteraceae	<i>Bradyrhizobium canariense</i>	UMS-61	NNIBR2017301BA38	99.29	MG780334	R2A

to phyla *Actinobacteria*, *Firmicutes*, and *Verrucomicrobia* is shown in Figure 1. Strains in the phylum *Actinobacteria*, *Firmicutes*, and *Verrucomicrobia* were assigned to the classes *Actinomycetia* (10 strains), *Bacilli* (six strains) and *Verrucomicrobiae* (one strain), respectively. At the genus and family level, 17 strains belonged to 16 genera of 11 families: *Mycolicibacterium* of *Mycobacteriaceae*, *Rhodococcus* of *Nocardiaceae*; *Kineococcus* of *Kineosporiaceae*; *Phycococcus* of *Intrasporangiaceae*; *Agromyces*, *Cryobacterium*, and *Microbacterium* of *Microbacteriaceae*; *Arthrobacter* of *Micrococcaceae*; *Catellatospora* of *Micromonosporaceae*; *Bacillus* of *Bacillaceae*; *Cohnella*, *Fontibacillus*, and *Paenibacillus* of *Paenibacillaceae*; *Lysinibacillus* and *Paenisporosarcina* of *Planococcaceae*; and *Roseimicrobium* of *Verrucomicrobiaceae*.

The phylogenetic assignments of the strains in the phyla *Acidobacteria*, *Bacteroidetes*, and *Proteobacteria* are shown in Figure 2. These 18 strains are belonged to seven classes, including *Actinomycetia*, *Chitinophagia*, *Cytophagia*, *Flavobacteriia*, *Alphaproteobacteria*, *Betaproteobacteria*, and *Gammaproteobacteria*. At the generic and family level, 17 strains belonged to 15 genera of 12 families; *Terriglobus* of *Acidobacteriaceae*, *Lacibacter* of *Chitinophagaceae*, *Algoriphagus* of *Cyclobacteriaceae*, *Flectobacillus* of *Cytophagaceae*, *Flavobacterium* and *Maribacter* of *Flavobacteriaceae*, *Bradyrhizobium* of *Nitrobacteriaceae*, *Gemmobacter* and *Loktanella* of *Rhodobacteraceae*, *Altererythrobacter* of *Erythrobacteriaceae*, *Acidovorax* of *Comamonadaceae*, *Aliiglaciicola* of *Alteromonadaceae*, *Cellvibrio* of *Cellvibrionaceae*, and *Arenimonas* and *Lysobacter* of *Lysobacteriaceae*.

These 35 unrecorded species showed diverse cellular morphologies, including rods, short rods, and cocci (Fig. 3). The colony colors were white, cream, ivory, yellow, orange, or pink. All species grew aerobically and some strains produced spores. The enzymatic and physiological properties examined by API 20NE kits were variable depending on species. Detailed cultural, morphological, and biochemical characteristics are also shown in the species description section.

From the sediments of lagoons, caves, rivers, and wetlands in Korea, 35 species were found and examined taxonomically. The presence of these 35 species have been reported in overseas, but not previously in Korea. Thus, the following 35 species are unrecorded species in Korea and their phenotypic properties are given.

## Phylum *Acidobacteria*

### Description of *Terriglobus roseus* UMS-18

Cells are Gram-stain-negative, non-flagellated, and short-rod shaped. Colonies grown on Reasoner's 2A agar (R2A) are circular, convex, smooth, and pink colored af-

ter incubation for 2–3 days at 30°C. Positive for esculin hydrolysis and  $\beta$ -galactosidase, but negative for oxidase, reduction of nitrates, indole production, glucose fermentation, arginine dihydrolase, urease, and gelatin hydrolysis. Does not utilize D-glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, D-maltose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid as sole carbon sources. Strain UMS-18 (= NNIBR2017301BA37) was isolated from sediment of Moojehchineup Wetland, Ulsan, Korea. The GenBank accession number of 16S rRNA gene sequence is MG780333.

## Phylum *Actinobacteria*

### Description of *Mycolicibacterium rufum* SS1-64

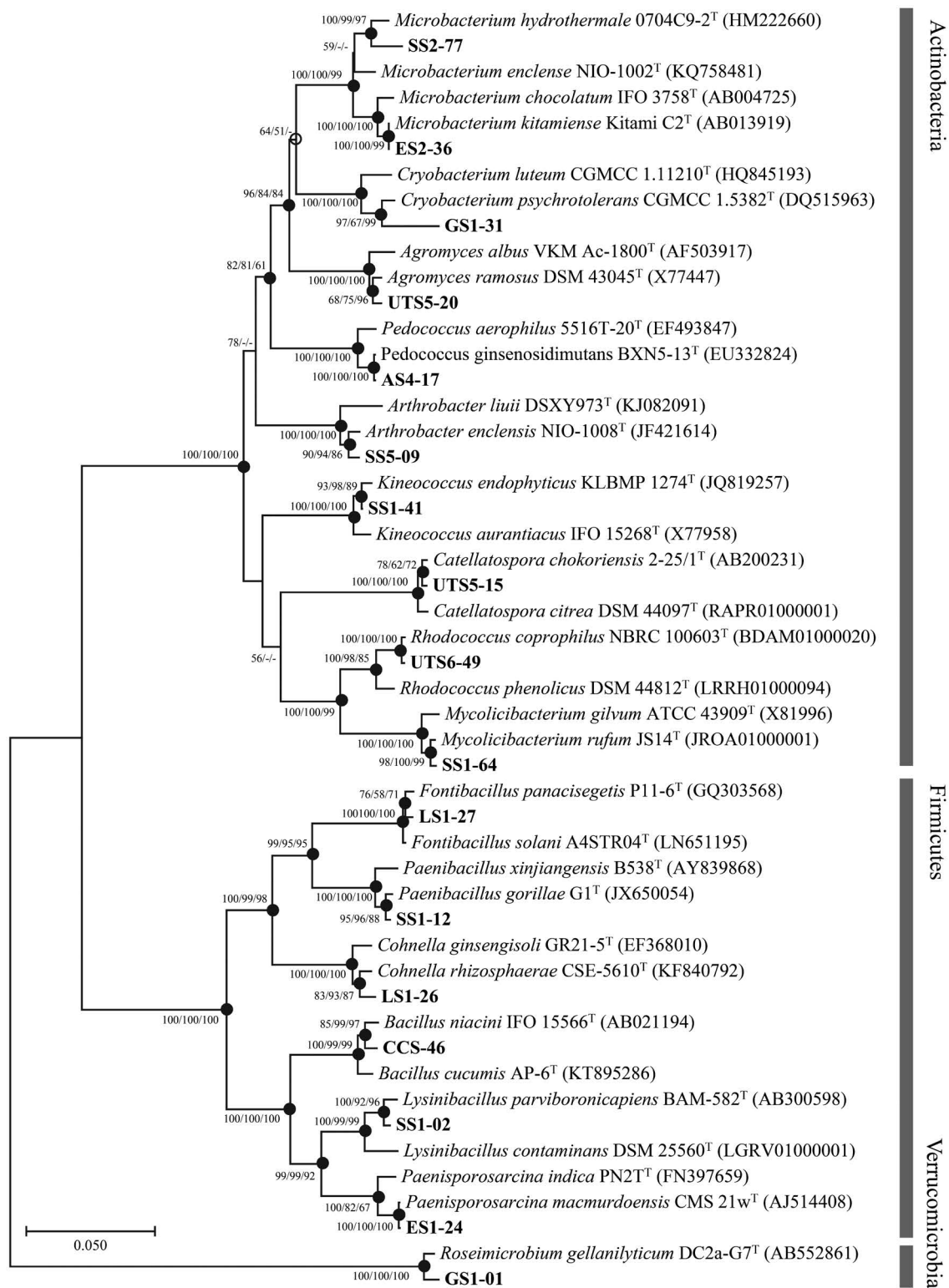
Cells are Gram-stain-positive, non-flagellated, and rod-shaped. Colonies grown on Reasoner's 2A agar (R2A) are circular, raised, dry with smooth border, and yellow colored after incubation for 5 days at 25°C. Positive for oxidase, reduction of nitrates, and urease, but negative for indole production, glucose fermentation, arginine dihydrolase, esculin hydrolysis, and gelatin hydrolysis. D-Mannitol, L-arabinose (weakly), D-maltose (weakly), potassium gluconate (weakly), and malic acid are utilized as sole carbon sources, but not D-glucose, D-mannose, *N*-acetyl-glucosamine, capric acid, adipic acid, trisodium citrate, and phenylacetic acid. Strain SS1-64 (= NNIBR2015296BA10) was isolated from sediment of the Nakdonggang River, Sangju-si, Gyeongsangbuk-do, Korea. The GenBank accession number of 16S rRNA gene sequence is KU341399.

### Description of *Rhodococcus coprophilus* UTS6-49

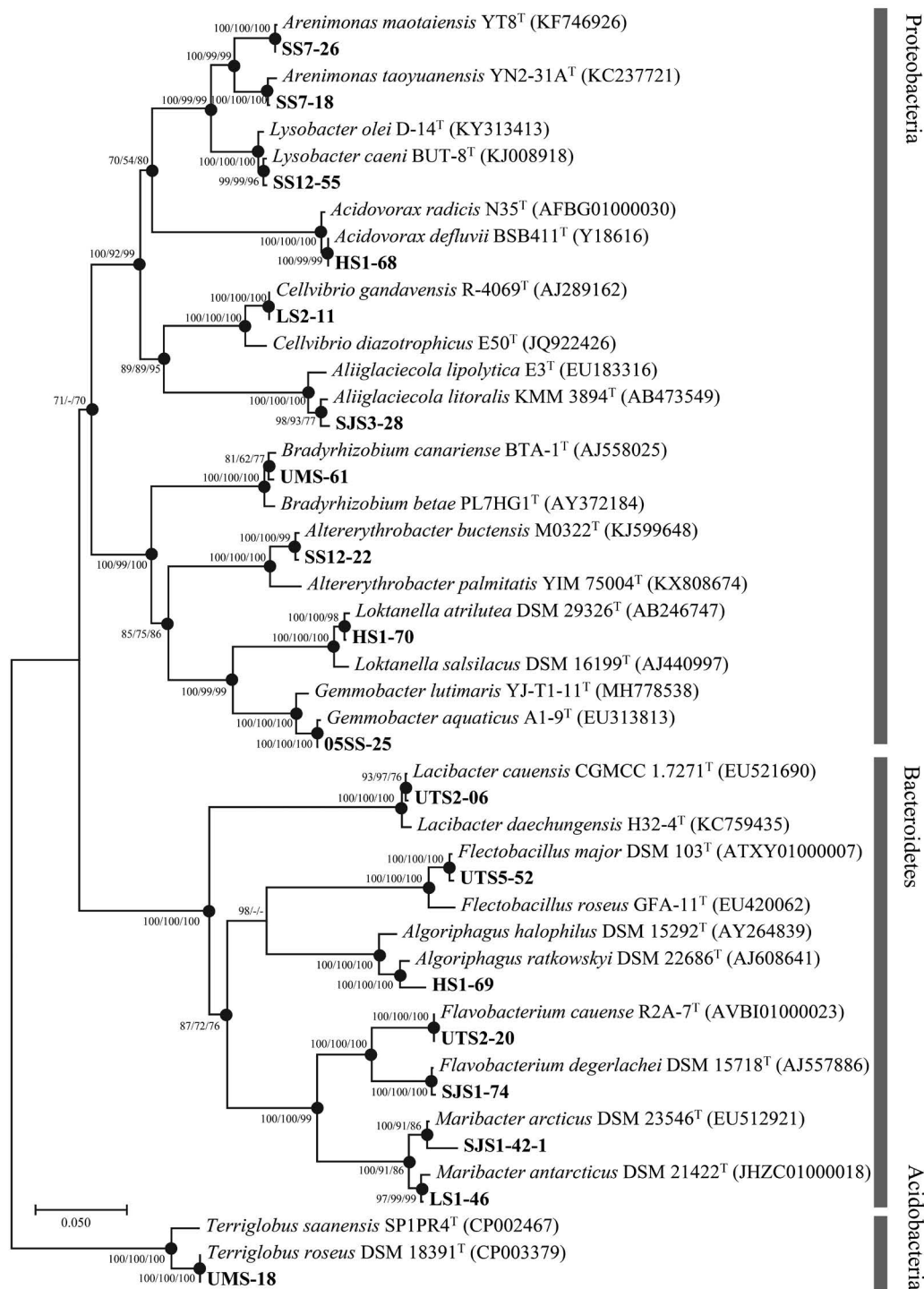
Cells are Gram-stain-positive, non-flagellated, spore forming, and rod-shaped. Colonies grown on Reasoner's 2A agar (R2A) are circular, crateriform, and pinkish-orange colored after incubation 2–3 days at 30°C. Positive for reduction of nitrates, and urease in API 20NE, but negative for oxidase, indole production, glucose fermentation, arginine dihydrolase, esculin hydrolysis, gelatin hydrolysis, and  $\beta$ -galactosidase. D-Glucose, and D-mannose are utilized as sole carbon sources, but not L-arabinose, D-mannitol, *N*-acetyl-glucosamine, D-maltose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid. Strain UTS6-49 (= NNIBR2017301BA36) was isolated from sediment of the Taehwagang River, Ulsan, Korea. The GenBank accession number of 16S rRNA gene sequence is MG780332.

### Description of *Kineococcus endophytica* SS1-41

Cells are Gram-stain-positive, flagellated, and coc-



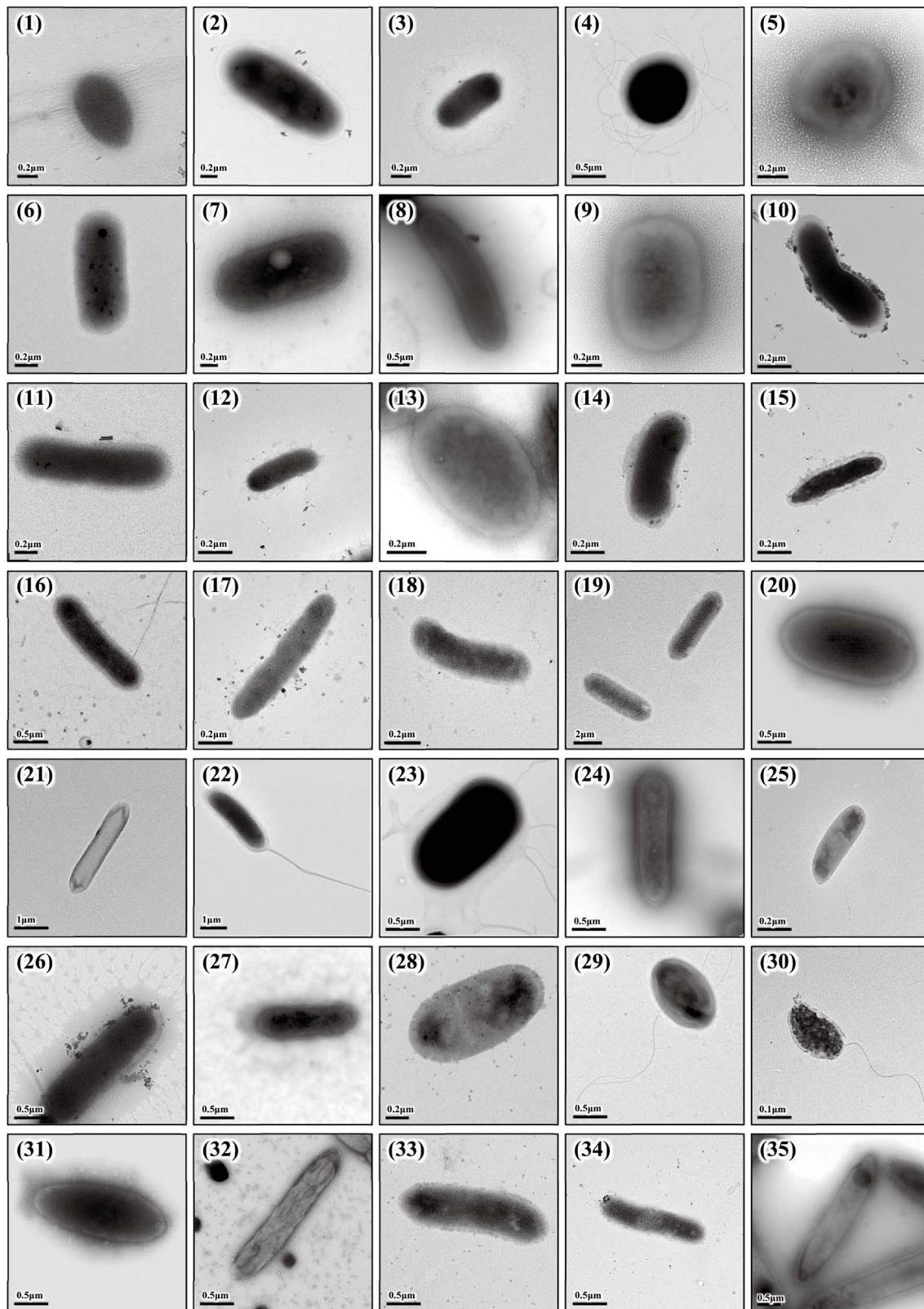
**Fig. 1.** Neighbor-joining phylogenetic tree based on 16S rRNA gene sequences showing the relationship between the strains isolated in this study and their relatives of the phyla *Actinobacteria*, *Firmicutes* and *Verrucomicrobia*. Bootstrap values (expressed as percentages of 1,000 replication) over 50% are shown at node for neighbor-joining, maximum parsimony, maximum likelihood, respectively. Filled circles indicate that the corresponding nodes were also recovered in the trees generated with the maximum likelihood and maximum parsimony algorithms, while open circles indicate that the corresponding nodes were also recovered in the tree generated with one of these algorithms. Bar, 0.05 substitutions per nucleotide position.



**Fig. 2.** Neighbor-joining phylogenetic tree based on 16S rRNA gene sequences showing the relationship between the strains isolated in this study and their relatives of the phyla Acidobacteria, Bacteroidetes and Proteobacteria. Bootstrap values (expressed as percentages of 1,000 replication) over 50% are shown at node for neighbor-joining, maximum parsimony, maximum likelihood, respectively. Filled circles indicate that the corresponding nodes were also recovered in the trees generated with the maximum likelihood and maximum parsimony algorithms, while open circles indicate that the corresponding nodes were also recovered in the tree generated with one of these algorithms. Bar, 0.05 substitutions per nucleotide position.

cus-shaped. Colonies grown on Reasoner's 2A agar (R2A) are circular, smooth, and pale pink to orange colored

after incubation 2–3 days at 25°C. Positive for esculin hydrolysis and  $\beta$ -galactosidase, but negative for reduc-



**Fig. 3.** Transmission electron micrographs of cells of the strains isolated in this study. Strains: 1, UMS-18; 2, SS1-64; 3, UTS6-49; 4, SS1-41; 5, AS4-17; 6, UTS5-20; 7, GS1-31; 8, SS2-77; 9, ES2-36; 10, SS5-09; 11, UTS5-15; 12, UTS2-06; 13, HS1-69; 14, UTS5-52; 15, SJS1-74; 16, UTS2-20; 17, LS1-46; 18, SJS1-42-1; 19, CCS-46; 20, LS1-26; 21, LS1-27; 22, SS1-12; 23, SS1-02; 24, ES1-24; 25, UMS-61; 26, 05SS-25; 27, HS1-70; 28, SS12-22; 29, HS1-68; 30, SJS3-28; 31, LS2-11; 32, SS7-26; 33, SS7-18; 34, SS12-55; 35, GS1-01.

tion of nitrates, indole production, glucose fermentation, gelatin hydrolysis, and oxidase. D-Glucose, L-arabinose, D-mannose, D-maltose, and trisodium citrate are utilized as sole carbon sources, but not D-mannitol, *N*-acetyl-glucosamine, potassium gluconate, capric acid, adipic acid, malic acid, and phenylacetic acid. Strain SS1-41 (= NNIBR2015296BA9) was isolated from sediment of the Nakdonggang River, Sangju-si, Gyeongsangbuk-do, Korea. The GenBank accession number of 16S rRNA gene sequence is KU984671.

#### **Description of *Phycoccus ginsenosidimutans* AS4-17**

Cells are Gram-stain-positive, non-flagellated, and coccus-shaped. Colonies grown on Reasoner's 2A agar (R2A) are circular, convex, smooth, and ivory colored after incubation 2–3 days at 20°C. Positive for reduction of nitrates, esculin hydrolysis, gelatin hydrolysis, and  $\beta$ -galactosidase, but negative for oxidase, indole production, glucose fermentation, arginine dihydrolase, and urease. D-Glucose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, D-maltose, potassium gluconate, and malic acid are utilized as sole carbon sources, but not L-arabinose, capric acid, adipic acid, trisodium citrate, and phenylacetic acid. Strain AS4-17 (= NNIBR2016301BA21) was isolated from sediment of the Nakdonggang River, Andong-si, Gyeongsangbuk-do, Korea. The GenBank accession number of 16S rRNA gene sequence is KY012263.

#### **Description of *Agromyces ramosus* UTS5-20**

Cells are Gram-stain-positive, non-flagellated, and rod-shaped. Colonies grown on Reasoner's 2A agar (R2A) are circular, convex, smooth, and light-yellow colored after incubation 2–3 days at 30°C. Positive for esculin hydrolysis, and  $\beta$ -galactosidase, but negative for oxidase, reduction of nitrates, indole production, glucose fermentation, arginine dihydrolase, urease, and gelatin hydrolysis. L-Arabinose, D-mannitol, and D-maltose are utilized as sole carbon sources, but not D-glucose, D-mannose, *N*-acetyl-glucosamine, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid. Strain UTS5-20 (= NNIBR2018141BA12) was isolated from sediment of the Taehwagang River, Ulsan, Korea. The GenBank accession number of 16S rRNA gene sequence is MK396584.

#### **Description of *Cryobacterium psychrotolerans* GS1-31**

Cells are Gram-stain-positive, non-flagellated, and rod-shaped. Colonies grown on Reasoner's 2A agar (R2A) are circular, convex with entire edge, and yellow colored after incubation 3 days at 20°C. Positive for reduction of nitrates, esculin hydrolysis, and gelatin hydrolysis, but negative for oxidase, indole production, glucose fermenta-

tion, arginine dihydrolase, urease, and  $\beta$ -galactosidase. D-Glucose, L-arabinose, D-mannose, and D-maltose are utilized as sole carbon sources, but not D-mannitol, *N*-acetyl-glucosamine, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid. Strain GS1-31 (= NNIBR2015296BA38) was isolated from sediment of the Nakdonggang River, Gumi-si, Gyeongsangbuk-do, Korea. The GenBank accession number of 16S rRNA gene sequence is KU984675.

#### **Description of *Microbacterium hydrothermale* SS2-77**

Cells are Gram-stain-positive, non-flagellated, and rod-shaped. Colonies grown on Reasoner's 2A agar (R2A) are circular, opaque, and yellow colored after incubation 2–3 days at 25°C. Positive for reduction of nitrates, esculin hydrolysis, gelatin hydrolysis, and  $\beta$ -galactosidase, but negative for oxidase, indole production, glucose fermentation, arginine dihydrolase, and urease. D-Glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, D-maltose, and potassium gluconate as sole carbon sources, but not capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid. Strain SS2-77 (= NNIBR2015296BA15) was isolated from sediment of the Nakdonggang River, Sangju-si, Gyeongsangbuk-do, Korea. The GenBank accession number of 16S rRNA gene sequence is KU341402.

#### **Description of *Microbacterium kitamiense* ES2-36**

Cells are Gram-stain-positive, non-flagellated, and rod-shaped. Colonies grown on Reasoner's 2A agar (R2A) are circular, convex, smooth, and yellow colored after incubation 3–4 days at 25°C. Positive for esculin hydrolysis, and  $\beta$ -galactosidase, but negative for oxidase, reduction of nitrates, indole production, glucose fermentation, arginine dihydrolase, urease, and gelatin hydrolysis. D-Glucose, D-mannose, D-mannitol, D-maltose, potassium gluconate as sole carbon sources, but not L-arabinose, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid. Strain ES2-36 (= NNIBR2016301BA27) was isolated from sediment of the Nakdonggang River, Eulsukdo Island, Busan, Korea. The GenBank accession number of 16S rRNA gene sequence is KY012260.

#### **Description of *Arthrobacter enclensis* SS5-09**

Cells are Gram-stain-positive, non-flagellated, rod-, and curved rod-shaped. Colonies grown on Trypticase soy agar (TSA) are circular with entire margin and cream to light-yellow colored after incubation 3–4 days at 30°C. Positive for oxidase, reduction of nitrates, esculin hydrolysis, and  $\beta$ -galactosidase, but negative for indole production, glucose fermentation, arginine dihydrolase, urease, and gelatin hydrolysis. D-Glucose, L-arabinose,



D-mannose, and D-mannitol are utilized as sole carbon sources, but not *N*-acetyl-glucosamine, D-maltose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid. Strain SS5-09 (= NNIBR2018141BA5) was isolated from sediment of the Nakdonggang River, Sangju-si, Gyeongsangbuk-do, Korea. The GenBank accession number of 16S rRNA gene sequence is MK396577.

#### Description of *Catellatospora chokoriensis* UTS5-15

Cells are Gram-stain-positive, non-flagellated, spore-forming, and rod-shaped. Colonies grown on Reasoner's 2A agar (R2A) are circular, convex, smooth, and light-yellow colored after incubation 2–3 days at 30°C. Positive for esculin hydrolysis, gelatin hydrolysis, and  $\beta$ -galactosidase, but negative for oxidase, reduction of nitrates, indole production, glucose fermentation, arginine dihydrolase, and urease. D-Glucose, L-arabinose, D-mannose, and D-maltose are utilized as sole carbon sources, but not D-mannitol, *N*-acetyl-glucosamine, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid. Strain UTS5-15 (= NNIBR2018141BA11) was isolated from sediment of the Taehwagang River, Ulsan, Korea. The GenBank accession number of 16S rRNA gene sequence is MK396583.

#### Phylum *Bacteroidetes*

##### Description of *Lacibacter cauensis* UTS2-06

Cells are Gram-stain-negative, non-flagellated, and rod-shaped. Colonies grown on Reasoner's 2A agar (R2A) are circular, convex, smooth, and orange colored after incubation 2–3 days at 25°C. Positive for oxidase, esculin hydrolysis, gelatin hydrolysis, and  $\beta$ -galactosidase, but negative for reduction of nitrates, indole production, glucose fermentation, arginine dihydrolase, and urease. D-Glucose, D-mannose, *N*-acetyl-glucosamine, and D-maltose are utilized as sole carbon sources, but not L-arabinose, D-mannitol, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid. Strain UTS2-06 (= NNIBR2017301BA34) was isolated from sediment the Taehwagang River, Ulsan, Korea. The GenBank accession number of 16S rRNA gene sequence is MG780330.

##### Description of *Algoriphagus ratkowskyi* HS1-69

Cells are Gram-stain-negative, non-flagellated, and short rod-shaped. Colonies grown on Marine agar (MA) are circular, convex, smooth, and orange colored after incubation 5 days at 10°C. Positive for oxidase, esculin hydrolysis, gelatin hydrolysis, and  $\beta$ -galactosidase, but negative for reduction of nitrates, indole production, glucose

fermentation, arginine dihydrolase, and urease. Does not utilize D-glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, D-maltose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid as sole carbon sources. Strain HS1-69 (= NNIBR2017301BA28) was isolated from sediment of the Seomjingang River, Hadong-gun, Gyeongsangnam-do, Korea. The GenBank accession number of 16S rRNA gene sequence is KX809752.

##### Description of *Flectobacillus major* UTS5-52

Cells are Gram-stain-negative, non-flagellated, and rod-shaped. Colonies grown on Reasoner's 2A agar (R2A) are irregular, convex, smooth, mucoid, and light-pink colored after incubation 2–3 days at 25°C. Positive for oxidase, reduction of nitrates, esculin hydrolysis, and  $\beta$ -galactosidase, but negative for indole production, glucose fermentation, arginine dihydrolase, urease, and gelatin hydrolysis. D-Glucose, L-arabinose, D-mannose, *N*-acetyl-glucosamine, D-maltose, and potassium gluconate as sole carbon sources, but not D-mannitol, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid. Strain UTS5-52 (= NNIBR2017301BA35) was isolated from sediment of the Taehwagang River, Ulsan, Korea. The GenBank accession number of 16S rRNA gene sequence is MG780331.

##### Description of *Flavobacterium degerlachei* SJS1-74

Cells are Gram-stain-negative, non-flagellated, and rod-shaped. Colonies grown on Reasoner's 2A agar (R2A) are circular, convex, smooth, and yellow colored after incubation 2–3 days at 20°C. Positive for esculin hydrolysis and gelatin hydrolysis, but negative for oxidase, reduction of nitrates, indole production, glucose fermentation, arginine dihydrolase, and  $\beta$ -galactosidase. D-Glucose, D-mannose, and D-maltose are utilized as sole carbon sources, but not L-arabinose, D-mannitol, *N*-acetyl-glucosamine, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid. Strain SJS1-74 (= NNIBR2017301BA40) was isolated from sediment of the Seomjingang River, Hadong-gun, Gyeongsangnam-do, Korea. The GenBank accession number of 16S rRNA gene sequence is MG780336.

##### Description of *Flavobacterium cauense* UTS2-20

Cells are Gram-stain-negative, flagellated, and rod-shaped. Colonies grown on Reasoner's 2A agar (R2A) are circular, convex, smooth, and yellow colored after incubation 2–3 days at 30°C. Positive for arginine dihydrolase, esculin hydrolysis (weakly), gelatin hydrolysis, and  $\beta$ -galactosidase (weakly), but negative for oxidase, reduction of nitrates, indole production, glucose fermentation, and

urease. Does not utilize D-glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, D-maltose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid as sole carbon sources. Strain UTS2-20 (= NNIBR2018141BA10) was isolated from sediment the Taehwagang River, Ulsan, Korea. The GenBank accession number of 16S rRNA gene sequence is MK396582.

#### **Description of *Maribacter antarcticus* LS1-46**

Cells are Gram-stain-negative, non-flagellated, and rod-shaped. Colonies grown on Marine agar (MA) are circular, convex, smooth, and yellow colored after incubation 3–4 days at 15°C. Positive for glucose fermentation, esculin hydrolysis, and  $\beta$ -galactosidase, but negative for oxidase, reduction of nitrates, indole production, arginine dihydrolase, urease, and gelatin hydrolysis. Does not utilize D-glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, D-maltose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid as sole carbon sources. Strain LS1-46 (= NNIBR2017301BA33) was isolated from sediment of the Gyeongpo Lake, Gangneung-si, Gangwon-do, Korea. The GenBank accession number of 16S rRNA gene sequence is MG780329.

#### **Description of *Maribacter arcticus* SJS1-42-1**

Cells are Gram-stain-negative, non-flagellated, and rod-shaped. Colonies grown on Marine agar (MA) are circular, convex, smooth, and yellow colored after incubation 3–4 days at 15°C. Positive for glucose fermentation, arginine dihydrolase, esculin hydrolysis, and  $\beta$ -galactosidase, but negative for oxidase, reduction of nitrates, indole production, urease, and gelatin hydrolysis. D-Glucose, D-mannose, *N*-acetyl-glucosamine, D-maltose, potassium gluconate, adipic acid (weakly), and malic acid are utilized as sole carbon sources, but not L-arabinose, D-mannitol, capric acid, trisodium citrate, and phenylacetic acid. Strain SJS1-42-1 (= NNIBR2017301BA39) was isolated from sediment of the Seomjingang River, Hadong-gun, Gyeongsangnam-do, Korea. The GenBank accession number of 16S rRNA gene sequence is MG780335.

### **Phylum *Firmicutes***

#### **Description *Bacillus niacini* CCS-46**

Cells are Gram-stain-positive, non-flagellated, and rod-shaped. Colonies grown on Trypticase soy agar (TSA) are circular, convex, smooth, and greyish-ivory colored after incubation 2–3 days at 30°C. Positive for reduction of nitrates, urease, esculin hydrolysis (weakly), and  $\beta$ -galactosidase, but negative for oxidase, indole production,

glucose fermentation, arginine dihydrolase, and gelatin hydrolysis. D-Glucose, *N*-acetyl-glucosamine (weakly), D-maltose, and potassium gluconate are utilized as sole carbon sources, but not L-arabinose, D-mannose, D-mannitol, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid. Strain CCS-46 (= NNIBR2017301BA43) was isolated from sediment of the Chodang Cave, Samcheok-si, Gangwon-do, Korea. The GenBank accession number of 16S rRNA gene sequence is MG780339.

#### **Description of *Cohnella rhizosphaerae* LS1-26**

Cells are Gram-stain-positive, non-flagellated, and rod-shaped. Colonies grown on Nutrient agar (NA) are circular, convex, and ivory colored after incubation 2–3 days at 30°C. Positive for oxidase, reduction of nitrates, esculine hydrolysis, and  $\beta$ -galactosidase, but negative for indole production, glucose fermentation, arginine dihydrolase, urease, and gelatin hydrolysis. D-Glucose, L-arabinose, D-mannose, and D-mannitol are utilized as sole carbon sources, but not *N*-acetyl-glucosamine, D-maltose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid. Strain LS1-26 (= NNIBR2018141BA3) was isolated from sediment of the Gyeongpo Lake, Gangneung-si, Gangwon-do, Korea. The GenBank accession number of 16S rRNA gene sequence is MK396575.

#### **Description of *Fontibacillus solani* LS1-27**

Cells are Gram-stain-positive, non-flagellated, and rod-shaped. Colonies grown on trypticase soy agar (TSA) are circular, convex, smooth, and ivory colored after incubation 2–3 days at 30°C. Positive for glucose fermentation, esculin hydrolysis, and  $\beta$ -galactosidase, but negative for oxidase, reduction of nitrates, indole production, arginine dihydrolase, urease, and gelatin hydrolysis. L-Arabinose and D-maltose are utilized as sole carbon sources, but not D-glucose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid. Strain LS1-27 (= NNIBR2017301BA32) was isolated from sediment of the Gyeongpo Lake, Gangneung-si, Gangwon-do, Korea. The GenBank accession number of 16S rRNA gene sequence is MG780328.

#### **Description of *Paenibacillus gorillae* SS1-12**

Cells are Gram-stain-positive, flagellated, and rod-shaped. Colonies grown on Reasoner's 2A agar (R2A) are irregular and white-cream colored after incubation 2–3 days at 30°C. Positive for urease, esculin hydrolysis, and  $\beta$ -galactosidase, but negative for oxidase, reduction of nitrates, indole production, glucose fermentation, ar-

ginine dihydrolase, and gelatin hydrolysis. D-Glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, D-maltose, and potassium gluconate are utilized as sole carbon sources, but not capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid. Strain SS1-12 (= NNIBR2015296BA4) was isolated from sediment of the Nakdonggang River, Sangju-si, Gyeongsangbuk-do, Korea. The GenBank accession number of 16S rRNA gene sequence is KU341394.

#### **Description of *Lysinibacillus parvivoronicapiens* SS1-02**

Cells are Gram-stain-positive, non-flagellated, and rod-shaped. Colonies grown on Reasoner's 2A agar (R2A) are circular with entire edges, opaque, and cream colored after incubation 2–3 days at 30°C. Positive for arginine dihydrolase, urease, and gelatin hydrolysis, but negative for oxidase, reduction of nitrates, indole production, glucose fermentation, esculin hydrolysis, and  $\beta$ -galactosidase. *N*-Acetyl-glucosamine, malic acid, and phenylacetic acid are utilized as sole carbon sources, but not D-glucose, A-arabinose, D-mannose, D-mannitol, D-maltose, potassium gluconate, capric acid, adipic acid, and trisodium citrate. Strain SS1-02 (= NNIBR2015296BA2) was isolated from sediment of the Nakdonggang River, Sangju-si, Gyeongsangbuk-do, Korea. The GenBank accession number of 16S rRNA gene sequence is KU341392.

#### **Description of *Paenisporosarcina macmurdoensis* ES1-24**

Cells are Gram-stain-positive, non-flagellated, and rod-shaped. Colonies grown on Reasoner's 2A agar (R2A) are circular, flat, irregular, opaque, and cream colored after incubation 2–3 days at 25°C. Positive for oxidase, esculin hydrolysis, and gelatin hydrolysis, but negative for reduction of nitrates, indole production, glucose fermentation, arginine dihydrolase, urease, and  $\beta$ -galactosidase. D-Glucose, and potassium gluconate are utilized as sole carbon sources, but not L-arabinose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, D-maltose, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid. Strain ES1-24 (= NNIBR2016301BA24) was isolated from sediment of the Nakdonggang River, Eulsukdo Island, Busan, Korea. The GenBank accession number of 16S rRNA gene sequence is KY012258.

### **Phylum *Proteobacteria***

#### **Description of *Bradyrhizobium canariense* UMS-61**

Cells are Gram-stain-negative, non-flagellated, and rod-shaped. Colonies grown on Reasoner's 2A agar (R2A) are circular, convex, smooth, and white colored after incubation 2–3 days at 25°C. Positive for oxidase, reduction of

nitrates, arginine dihydrolase, urease, esculin hydrolysis, and  $\beta$ -galactosidase, but negative for indole production, glucose fermentation, and gelatin hydrolysis. D-Glucose, L-arabinose, D-mannose, D-mannitol, potassium gluconate, adipic acid, malic acid, and trisodium citrate, but not *N*-acetyl-glucosamine, D-maltose, capric acid, and phenylacetic acid. Strain UMS-61 (= NNIBR2017301BA38) was isolated from sediment of the Moojehineup Wetland, Ulsan, Korea. The GenBank accession number of 16S rRNA gene sequence is MG780334.

#### **Description of *Gemmobacter aquaticus* 05SS-25**

Cells are Gram-stain-negative, non-flagellated, and rod-shaped. Colonies grown on Reasoner's 2A agar (R2A) are circular, convex, smooth, and cream colored after incubation 2–3 days at 30°C. Positive for reduction of nitrates to nitrogen, arginine dihydrolase, urease, esculin hydrolysis, and  $\beta$ -galactosidase, but negative for oxidase, indole production, glucose fermentation, and gelatin hydrolysis. *N*-Acetyl-glucosamine, D-maltose, potassium gluconate, adipic acid, malic acid, trisodium citrate, and phenylacetic acid are utilized as sole carbon sources, but not D-glucose, L-arabinose, D-mannose, D-mannitol, and capric acid. Strain 05SS-25 (= NNIBR2017301BA44) was isolated from sediment of the Nakdonggang River, Sangju-si, Gyeongsangbuk-do, Korea. The GenBank accession number of 16S rRNA gene sequence is MG780340.

#### **Description of *Loktanella atrilutea* HS1-70**

Cells are Gram-stain-negative, non-flagellated, and rod-shaped. Colonies grown on marine agar (MA) are circular, convex, smooth, and ivory colored after incubation 2–3 days at 30°C. Positive for oxidase, glucose fermentation, urease, esculin hydrolysis, and  $\beta$ -galactosidase, but negative for reduction of nitrates, indole production, arginine dihydrolase, and gelatin hydrolysis. D-Glucose, L-arabinose, D-mannose, D-mannitol (weakly), and D-maltose are utilized as sole carbon sources, but not *N*-acetyl-glucosamine, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid. Strain HS1-70 (= NNIBR2017301BA29) was isolated from sediment of the Seomjingang River, Hadong-gun, Gyeongsangnam-do, Korea. The GenBank accession number of 16S rRNA gene sequence is KX809753.

#### **Description of *Altererythrobacter buctensis* SS12-22**

Cells are Gram-stain-negative, non-flagellated, and rod-shaped. Colonies grown on Reasoner's 2A agar (R2A) are circular, convex, smooth, mucoid, and yellow colored after incubation 2–3 days at 30°C. Positive for oxidase, esculin hydrolysis, and  $\beta$ -galactosidase, but negative for reduction of nitrates, indole production, glucose ferment-

tation, arginine dihydrolase, urease, and gelatin hydrolysis. D-Glucose, L-arabinose, D-mannose, and D-maltose are utilized as sole carbon sources, but not D-mannitol, *N*-acetyl-glucosamine, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid. Strain SS12-22 (=NNIBR2018141BA9) was isolated from sediment of the Nakdonggang River, Sangju-si, Gyeongsangbuk-do, Korea. The GenBank accession number of 16S rRNA gene sequence is MK396581.

#### **Description of *Acidovorax defluvii* HS1-68**

Cells are Gram-stain-negative, flagellated, and rod-shaped. Colonies grown on nutrient agar (NA) are circular with entire margin, convex, smooth and cream-white colored after incubation 2–3 days at 30°C. Positive for oxidase, reduction of nitrates to nitrogen, urease, and esculin hydrolysis (weakly), but negative for indole production, glucose fermentation, arginine dihydrolase, gelatin hydrolysis, and  $\beta$ -galactosidase. D-Mannitol, *N*-acetyl-glucosamine, potassium gluconate, capric acid, adipic acid, and malic acid are utilized as sole carbon sources, but not D-glucose, L-arabinose, D-mannose, D-maltose, trisodium citrate, and phenylacetic acid. Strain HS1-68 (=NNIBR2018141BA2) was isolated from sediment of the Seomjingang River, Hadong-gun, Gyeongsangnam-do, Korea. The GenBank accession number of 16S rRNA gene sequence is MK396574.

#### **Description of *Aliiglaciecola litoralis* SJS3-28**

Cells are Gram-stain-negative, flagellated, and rod-shaped. Colonies grown on marine agar (MA) are circular, convex, smooth and ivory colored after incubation 2–3 days at 25°C. Positive for esculin hydrolysis, gelatin hydrolysis, and  $\beta$ -galactosidase, but negative for oxidase, reduction of nitrates, indole production, glucose fermentation, and arginine dihydrolase. D-Glucose, L-arabinose, D-mannose, D-mannitol, D-maltose, potassium gluconate, adipic acid, malic acid, and trisodium citrate are utilized as sole carbon sources, but not *N*-acetyl-glucosamine, capric acid, and phenylacetic acid. Strain SJS3-28 (=NNIBR2017301BA41) was isolated from sediment of the Seomjingang River, Hadong-gun, Gyeongsangnam-do, Korea. The GenBank accession number of 16S rRNA gene sequence is MG780337.

#### **Description of *Cellvibrio gandavensis* LS2-11**

Cells are Gram-stain-negative, non-flagellated, and rod-shaped. Colonies grown on Reasoner's 2A agar (R2A) are irregular, convex, opaque, shiny, mucoid, and ivory colored after incubation 2–3 days at 30°C. Positive for esculin hydrolysis and  $\beta$ -galactosidase, but negative for

oxidase, reduction of nitrates, indole production, glucose fermentation, arginine dihydrolase, urease, and gelatin hydrolysis. Does not utilize D-glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, D-maltose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid as sole carbon sources. Strain LS2-11 (=NNIBR2018141BA4) was isolated from sediment of the Hyang-Lake, Gangneung-si, Gangwon-do, Korea. The GenBank accession number of 16S rRNA gene sequence is MK396576.

#### **Description of *Arenimonas maotaiensis* SS7-26**

Cells are Gram-stain-negative, non-flagellated, and rod-shaped. Colonies grown on Reasoner's 2A agar (R2A) are circular, convex, translucent, smooth, and white colored after incubation 2–3 days at 37°C. Positive for oxidase, esculin hydrolysis, and gelatin hydrolysis, but negative for reduction of nitrates, indole production, glucose fermentation, arginine dihydrolase, urease, and  $\beta$ -galactosidase. Does not utilize D-glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, D-maltose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid as sole carbon sources. Strain SS7-26 (=NNIBR2018141BA7) was isolated from sediment of the Nakdonggang River, Sangju-si, Gyeongsangbuk-do, Korea. The GenBank accession number of 16S rRNA gene sequence is MK396579.

#### **Description of *Arenimonas taoyuanensis* SS7-18**

Cells are Gram-stain-negative, non-flagellated, and rod-shaped. Colonies grown on trypticase soy agar (TSA) are circular with margins, convex, opaque, and ivory colored after incubation 2–3 days at 30°C. Positive for oxidase, and gelatin hydrolysis, but negative for reduction of nitrates, indole production, glucose fermentation, arginine dihydrolase, urease, esculin hydrolysis, and  $\beta$ -galactosidase. Does not utilize D-glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, D-maltose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid as sole carbon sources. Strain SS7-18 (=NNIBR2018141BA6) was isolated from sediment of the Nakdonggang River, Sangju-si, Gyeongsangbuk-do, Korea. The GenBank accession number of 16S rRNA gene sequence is MK396578.

#### **Description of *Lysobacter caeni* SS12-55**

Cells are Gram-stain-negative, non-flagellated, and rod-shaped. Colonies grown on Reasoner's 2A agar (R2A) are circular, convex, smooth, and ivory to brown colored after incubation 2–3 days at 30°C. Positive for oxidase, reduction of nitrates to nitrogen, esculin hydrolysis, and gelatin hydrolysis, but negative for indole production, glucose

fermentation, arginine dihydrolase, urease, and  $\beta$ -galactosidase. D-Glucose and D-maltose are utilized as sole carbon sources, but not L-arabinose, D-mannose, D-mannitol, N-acetyl-glucosamine, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid. Strain SS12-55 (= NNIBR2017301BA42) was isolated from sediment of the Nakdonggang River, Sangju-si, Gyeongsangbuk-do, Korea. The GenBank accession number of 16S rRNA gene sequence is MG780338.

### Phylum *Verrucomicrobia*

#### Description of *Roseimicrobium gellanilyticum* GS1-01

Cells are Gram-stain-negative, non-flagellated, and rod-shaped. Colonies grown on Reasoner's 2A agar (R2A) are circular, convex, smooth, and pink to brown colored after incubation 2–3 days at 25°C. Positive for oxidase, urease, esculin hydrolysis, and  $\beta$ -galactosidase, but negative for reduction of nitrates, indole production, glucose fermentation, arginine dihydrolase, and gelatin hydrolysis. D-Glucose and D-mannose are utilized as sole carbon sources, but not L-arabinose, D-mannitol, N-acetyl-glucosamine, D-maltose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid. Strain GS1-01 (= NNIBR2015296BA35) was isolated from sediment of the Nakdonggang River, Gumi-si, Gyeongsangbuk-do, Korea. The GenBank accession number of 16S rRNA gene sequence is KU984672.

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