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A report of 24 unrecorded bacterial species in Korea belonging to the Phyla *Proteobacteria* and *Bacteroidetes* isolated in 2020

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In 2020, 24 bacterial strains were isolated from algae, kudzu leaf, mud, pine cone, seashore sand, sea water, soil, tidal flat, and wetland from the Republic of Korea. Isolated bacterial strains were identified based on 16S rRNA gene sequences, and those exhibiting at least 98.7% sequence similarity with known bacterial species, but not reported in Korea, were highlighted as unrecorded species. These isolates were allocated to the phyla *Bacteroidetes* and *Proteobacteria* as unrecorded species in Korea. The four *Bacteroidetes* strains were classified into the families *Chitinophagaceae*, *Flavobacteriaceae*, and *Sphingobacteriaceae* (of the orders *Chitinophagales*, *Flavobacteriales*, and *Sphingobacteriales*, respectively). The 20 *Proteobacteria* strains belonged to the *Aeromonadaceae*, *Marinobacter*, *Microbulbiferaceae*, *Enterobacteriaceae*, *Erwiniaceae*, *Morganellaceae*, *Yersiniaceae*, *Lysobacteraceae*, *Halomonadaceae*, *Moraxellaceae*, *Pseudomonadaceae*, *Steroidobacteraceae*, *Xanthomonadaceae*, and *Myxococcaceae* (of the orders *Aeromonadales*, *Alteromonadales*, *Cellvibrionales*, *Enterobacterales*, *Lysobacterales*, *Oceanospirillales*, *Pseudomonadales*, *Steroidobacter*, *Xanthomonadales*, and *Myxococcales*). This study focused on the description of 24 unreported bacterial species in Korea in the phyla *Bacteroidetes* and *Proteobacteria* belonging to six classes.

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

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Introduction

In 2020, 24 unrecorded bacterial species were isolated from environmental samples collected in Korea and identified as members of *Bacteroidetes* and *Proteobacteria*. The *Bacteroidetes* species are all Gram-stain-negative heterotrophs, mainly rod-shaped, and do not form endospores (Krieg *et al*., 2010). They are known to play important roles in the biogeochemical processes such as the decomposition of peptides and polysaccharides (Russell *et al*., 2014; Hahnke *et al*., 2016). The phylum *Proteobacteria* constitutes the largest phylogenetic lineage (Kersters *et al*., 2006) that contains pathogenic bacteria. *Gammaproteobacteria* has the taxonomic rank of class within the phylum *Proteobacteria* (Garrity *et al*., 2005). *Gammaproteobacteria* includes a large and diverse group of bacteria that exhibits wide variation in term of phenotypes, morphologies, metabolic capabilities, and trophism (phototrophs and chemolithotrophs). Members of the class *Gammaproteobacteria* are Gram-staining-negative with different morphologies including rods, cocci, spirilla, and filaments, and isolated from wide range of

environments. The isolated bacteria species belong to the class *Chitinophagia*, *Flavobacteria*, *Sphingobacteria*, *Gammaproteobacteria* and *Deltaproteobacteria*. In this study, we focused on the description of 24 unreported strains.

Materials and Methods

A total of 24 bacterial strains isolated from algae, kudzu leaf, mud, pine cone, seashore sand, sea water, soil, tidal flat, and wetland samples collected in Korea. The samples were serially diluted in distilled water and the aliquot was spread onto R2A and MA medium, incubated at 25−37°C for 2−3 days. The strain IDs, growth media, isolation sources, and incubation conditions are summarized in Table 1. All strains were purified as single strain and stored using 20% glycerol suspension at −80°C as well as freeze-dried ampoules. Morphology of strains was examined by transmission electron microscopy (JEOL, JEM1010) using cells grown for 2−3 days on R2A and MA media. Transmission electron microgram 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 strips according to manufacturer's instruction (bioMérieux). Genomic DNA was extracted and 16S rRNA gene was amplified by PCR with 9F and 1492R universal bacterial primers (Weisburg *et al*., 1991). The 16S rRNA gene sequences of the closely related strains were obtained from EzBioCloud (https://www.ezbiocloud.net) 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 were calculated. Phylogenetic trees were constructed using the neighbor-joining method (Saitou and Nei, 1987) in the MEGA7 program (Kumar *et al*., 2016) with bootstrap values based on 1,000 replications (Felsenstein, 1985).

Results and Discussion

Four strains of *Bacteroidetes* were distributed into three orders: one strains in *Chitinophagales*, one strain in *Flavobacteriales* and two strains in *Sphingobacteriales*. A total of 20 strains were classified into nine orders of *Gammaproteobacteria*: two strains in *Aeromonadales*, one strain in *Alteromonadales*, one strain in *Cellvibrionales*, four strains in *Enterobacterales*, three strains in *Lysobacterales*, one strain in *Oceanospirillales*, five strains in *Pseudomonadales*, one strain in *Steroidobacter*, and one strain in *Xanthomonadales*. Also, one strain was classified into the order *Deltaproteobacteria*: one strain in *Myxococcales* (Table 1). All strains were Gram-staining-negative and one strain was coccus shaped and 23 strains were rod shaped (Fig. 1). In the class of *Bacteroidetes*, one strain was assigned to the genus *Flavihumibacter* of the family *Chitinophagaceae* in the order *Chitinophagaceae* and one strain was assigned to the genus *Aquimarina* of the family *Flavobacteriaceae* in the order *Flavobacteriales*. Two strains in the order *Sphingobacteriales* in the order *Sphingobacteriaceae* belonged to two genera: *Pedobacter* (one strain) *Mucilaginibacter* (one strain) (Fig. 2). In the class of *Proteobacteria*, 20 strains were distributed into 10 orders, *Aeromonadales*, *Alteromonadales*, *Cellvibrionales*, *Enterobacterales*, *Lysobacterales*, *Oceanospirillales*, *Pseudomonadales*, *Steroidobacter*, *Xanthomonadales* and *Myxococcales*. Two strains in *Aeromonadaceae*, one strain in *Marinobacter*, one strain in *Microbulbiferaceae*, four strains in the order *Enterobacterales* were separated into four families: *Enterobacteriaceae* (one strain), *Erwiniaceae* (one strain), *Morganellaceae* (one strain), *Yersiniaceae* (one strain), three strains in the order *Lysobacterales* in the family *Lysobacteraceae*, one strain in *Halomonadaceae*, five strains in the order *Pseudomonadales* were separated into two families: *Moraxellaceae* (one strain), *Pseudomonadaceae* (four strains), one strain in *Steroidobacteraceae*, one strain in *Xanthomonadaceae*, and one strain in *Myxococcaceae*. These strains were Gram-stain-negative and rod-shaped except for the strain L1_34_Aci, which was coccus-shaped (Fig. 1). The identification of the 24 strains based on sequence similarity was supported by the phylogenetic trees. The neighbor-joining trees inferred close relationships of the species and type strains of validly published species. The detailed morphological and physiological characteristics are given in the strain descriptions.

Description of *Flavihumibacter petaseus* SM8

Cells are Gram-stain-negative, non-flagellated, and rod-shaped. Colonies are yellow-colored after 3 days of incubation on R2A at 30°C. In API 20NE test, positive for esculin hydrolysis; but negative for potassium gluconate, 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, and D-maltose were utilized; whereas adipic acid, D-mannitol, *N*-acetyl-D-glucosamine, capric acid, malic acid, trisodium citrate, and phenylacetic acid were not utilized. Strain SM8 (=NIBRBAC000506148) was isolated from a soil sample from Ecological Park in Godeok-dong, Gangdong-gu, Seoul, Korea.

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
Chitinophagales	*Chitinophagaceae*	SM8	NIBRBAC000506148	*Flavihumibacter petaseus*	99.8%	Wetland	R2A at 30°C, 3 days
Flavobacteriales	*Flavobacteriaceae*	KYW2188	NIBRBAC000506233	*Aquimarina aggregatae*	99.9%	Sea water	MA at 25°C, 3 days
Sphingobacteriales	*Sphingobacteriaceae*	HMG1331	NIBRBAC000506261	*Pedobacter aquatilis*	99.9%	Seashore sand	R2A at 25°C, 3days
		HMG2653	NIBRBAC000506268	*Mucilaginibacter ximonensis*	99.3%	Pine cone	R2A at 25°C, 3days
Aeromonadales	*Aeromonadaceae*	JHSTF-R13	NIBRBAC000506395	*Tolumonas osonensis*	99.8%	Tidal flat	R2A at 25°C, 2 days
		HMG1343	NIBRBAC000506262	*Oceanisphaera arctica*	99.3%	Seashore sand	R2A at 25°C, 3days
Alteromonadales	*Marinobacter_f*	CAU 1621	NIBRBAC000506279	*Marinobacter mobilis*	100%	Mud	MA at 30°C, 3−5 days
Cellvibrionales	*Microbulbiferaceae*	BDTF-M8	NIBRBAC000506391	*Microbulbifer elongatus*	99.04%	Tidal flat	MA at 25°C, 3 days
Enterobacterales	*Enterobacteriaceae*	MA20	NIBRBAC000506143	*Citrobacter pasteurii*	99.3%	Wetland	R2A at 30°C, 3 days
	Erwiniaceae	HMG2551	NIBRBAC000506267	*Pantoea wallisii*	99.9%	Kudzu leaf	R2A at 25°C, 3 days
	Morganellaceae	LW_53_Sal	NIBRBAC000506411	*Providencia burhodogranariea*	99.4%	Soil	R2A at 37°C, 3 days
	Yersiniaceae	SO215	NIBRBAC000506239	*Serratia oryzae*	99.9%	Soil	R2A at 25°C, 2 days
Lysobacterales	*Lysobacteraceae*	AsT1	NIBRBAC000506373	*Maritimibacter alkaliphilus*	99.8%	Algae	MA at 30°C, 3 days
		L1_74_Sal	NIBRBAC000506406	*Stenotrophomonas pavanii*	99.0%	Soil	R2A at 37°C, 3 days
		BT648	NIBRBAC000506193	*Lysobacter psychrotolerans*	100%	Soil	R2A at 25°C, 3 days
Oceanospirillales	*Halomonadaceae*	KYW1991	NIBRBAC000506237	*Halomonas axialensis*	100%	Sea water	MA at 25°C, 3 days
Pseudomonadales	*Moraxellaceae*	L1_34_Aci	NIBRBAC000506405	*Acinetobacter seifertii*	99.9%	Soil	R2A at 37°C, 3 days
	Pseudomonadaceae	JHSTF-R6	NIBRBAC000506393	*Pseudomonas composti*	98.9%	Tidal flat	R2A at 25°C, 3 days
		L1_104_Sal	NIBRBAC000506407	*Pseudomonas asiatica*	100%	Soil	R2A at 37°C, 3 days
		LW_92_Aci	NIBRBAC000506410	*Pseudomonas saponiphil*	99.8%	Soil	R2A at 37°C, 3 days
		DM7	NIBRBAC000506145	*Azotobacter bryophylli*	99.8%	Wetland	R2A at 30°C, 3 days
Steroidobacter_o	*Steroidobacteraceae*	HMG1413	NIBRBAC000506264	*Steroidobacter agariperforans*	99.1%	Soil	R2A at 25°C, 3 days
Xanthomonadales	*Xanthomonadaceae*	MA7	NIBRBAC000506142	*Stenotrophomonas bentonitica*	99.9%	Wetland	R2A at 30°C, 3 days
Myxococcales	*Myxococcaceae*	17bor-14	NIBRBAC000501349	*Simulacricoccus ruber*	99.45%	Soil	R2A at 30°C, 3 days

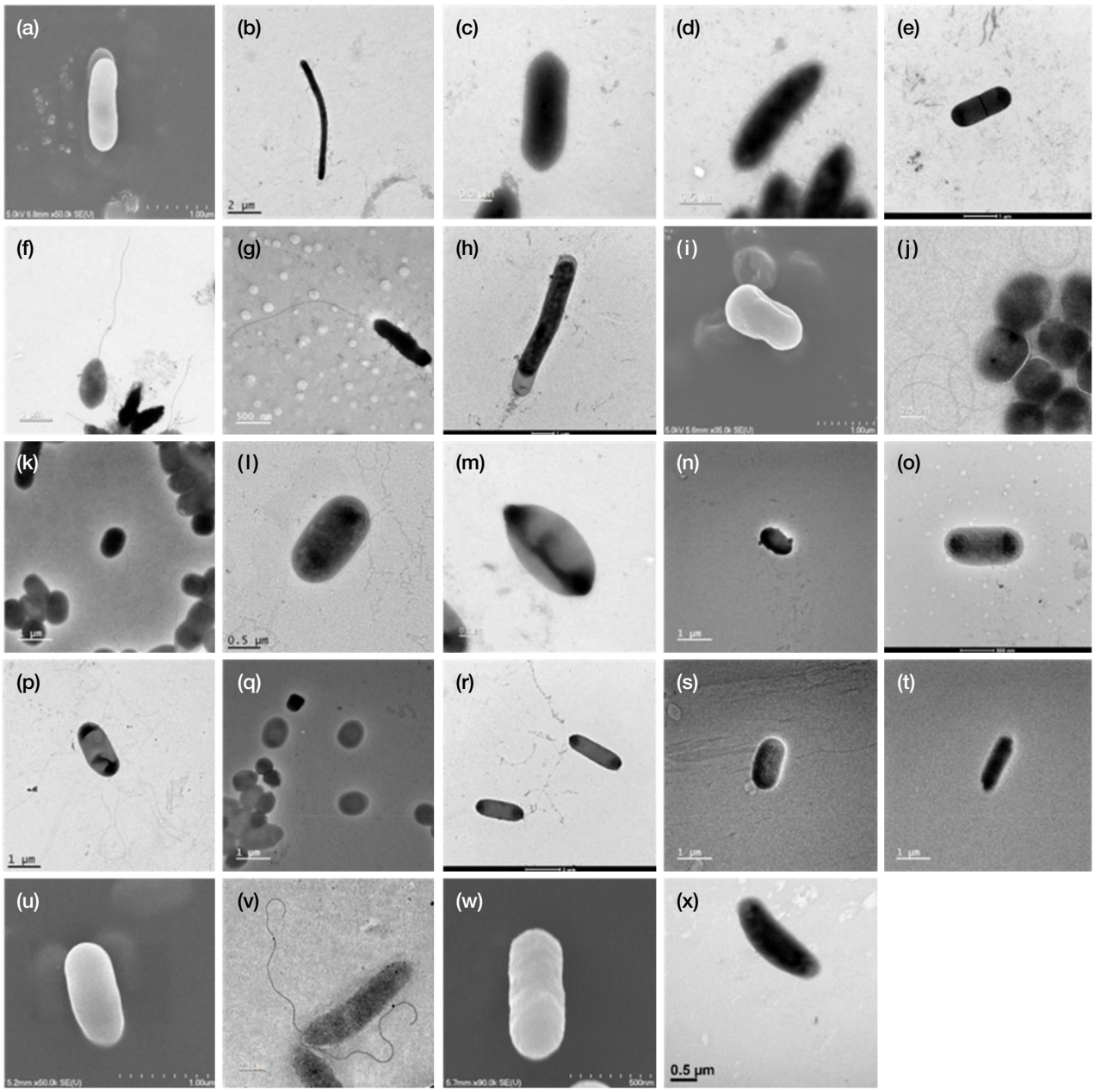

Fig. 1. Transmission electron micrographs of the strains isolated in this study. Strains: a, SM8; b, KYW2188; c, HMG1331; d, HMG2653; e, JHSTF-R13; f, HMG1343; g, CAU 1621; h, BDTF-M8; i, MA20; j, HMG2551; k, LW_53_Sal; l, SO215; m, AsT1; n, L1_74_Sal; o, BT648; p, KYW1991; q, L1_34_Aci; r, JHSTF-R6; s, L1_104_Sal; t, LW_92_Aci; u, DM7; v, HMG1413; w, MA7; x, 17bor-14.

Description of *Aquimarina aggregata* KYW2188

Cells are Gram-stain-negative, non-flagellated, and rod-shaped. Colonies are yellow-colored after 3 days of incubation on MA at 25°C. In API 20NE test, positive for esculin hydrolysis; but negative for potassium gluconate, 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, adipic acid, D-mannitol, capric acid, malic acid, trisodium citrate, and phenylacetic acid were not utilized. Strain KYW2188 (=NIBRBAC000506233) was isolated from a soil sample from Gwangyang Bay, Gwangyang-si, Jeollanam-do, Korea.

Description of *Pedobacter aquatilis* HMG1331

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

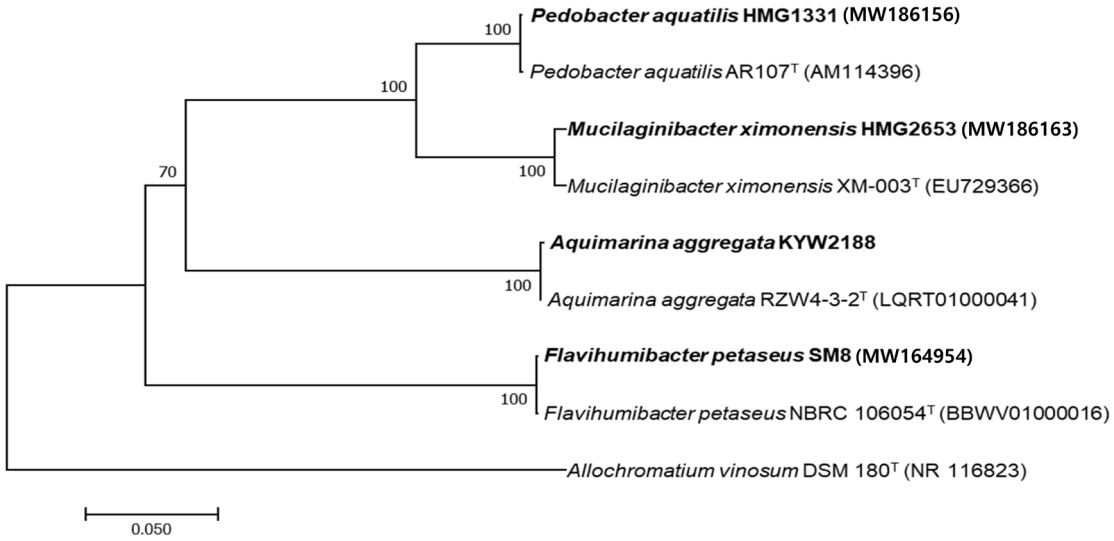

Fig. 2. Neighbor-joining phylogenetic tree based on 16S rRNA gene sequences shows the relationship between the strains isolated in this study and their relatives of the genus *Pedobacter* HMG1331, *Mucilaginibacter* HMG2653, *Aquimarina* KYW2188, and *Flavihumibacter* SM8. Bootstrap values (>70%) are shown above nodes for the neighbor-joining methods. Bar: 0.01 and 0.05 substitutions per nucleotide position, respectively.

shaped. Colonies are pale pink-colored after 3 days of incubation on R2A at 25°C. In API 20NE test, 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, gelatin hydrolysis, urease, and potassium gluconate. D-Glucose, L-arabinose, D-mannose, *N*-acetyl-D-glucosamine, and D-maltose were utilized; whereas adipic acid, malic acid, trisodium citrate, D-mannitol, capric acid, and phenylacetic acid were not utilized. Strain HMG1331 (=NIBRBAC000506261) was isolated from a soil sample from Jumunjin Beach, Jumunjin-eup, Gangneung-si, Gangwon-do, Korea.

Description of *Mucilaginibacter ximonensis* HMF2653

Cells are Gram-stain-negative, non-flagellated, and rod-shaped. Colonies are pale yellow-colored after 3 days of incubation on R2A at 25°C. In API 20NE test, 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, potassium gluconate, and gelatin hydrolysis. D-Glucose was utilized; whereas L-arabinose, D-mannose, D-maltose, adipic acid, malic acid, trisodium citrate, D-mannitol, *N*-acetyl-D-glucosamine, capric acid, and phenylacetic acid were not utilized. Strain HMF2653 (=NIBRBAC000506268) was isolated from a soil sample from Jumunjin Beach, Jumunjin-eup, Gangneung-si, Gangwon-do, Korea.

Description of *Tolumonas osonensis* JHSTF-R13

Cells are Gram-stain-negative, non-flagellated, and rod-shaped. Colonies are white-colored after 2 days of incubation on R2A at 25°C. In API 20NE test, positive for reduction of nitrates (NO_3) to nitrite (NO_2^-), and esculin hydrolysis; but negative for reduction of nitrates (NO_3) to nitrogen (N_2), indole production on tryptophan, glucose fermentation, arginine dihydrolase, urease, potassium gluconate, and gelatin hydrolysis. D-Glucose, L-arabinose, D-mannose, D-maltose, adipic acid, malic acid, trisodium citrate, D-mannitol, *N*-acetyl-D-glucosamine, capric acid, and phenylacetic acid were not utilized. Strain JHSTF-R13 (=NIBRBAC000506395) was isolated from a soil sample from Seocheon-gun, Chungcheongnam-do, Korea.

Description of *Oceanisphaera arctica* HMG1343

Cells are Gram-stain-negative, flagellated, and rod-shaped. Colonies are beige-colored after 3 days of incubation on R2A at 25°C. In API 20NE test, positive for urease and esculin hydrolysis; but negative for potassium gluconate, 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, and gelatin hydrolysis. D-Mannitol, malic acid, trisodium citrate, and phenylacetic acid were utilized; whereas D-glucose, L-arabinose, D-mannose, D-maltose, adipic acid, *N*-acetyl-D-glucosamine, and capric acid were not utilized. Strain HMG1343 (=NIBRBAC000506262) was isolated from a soil sample from Jumunjin Beach, Jumunjin-eup, Gangneung-si, Gangwon-do, Korea.

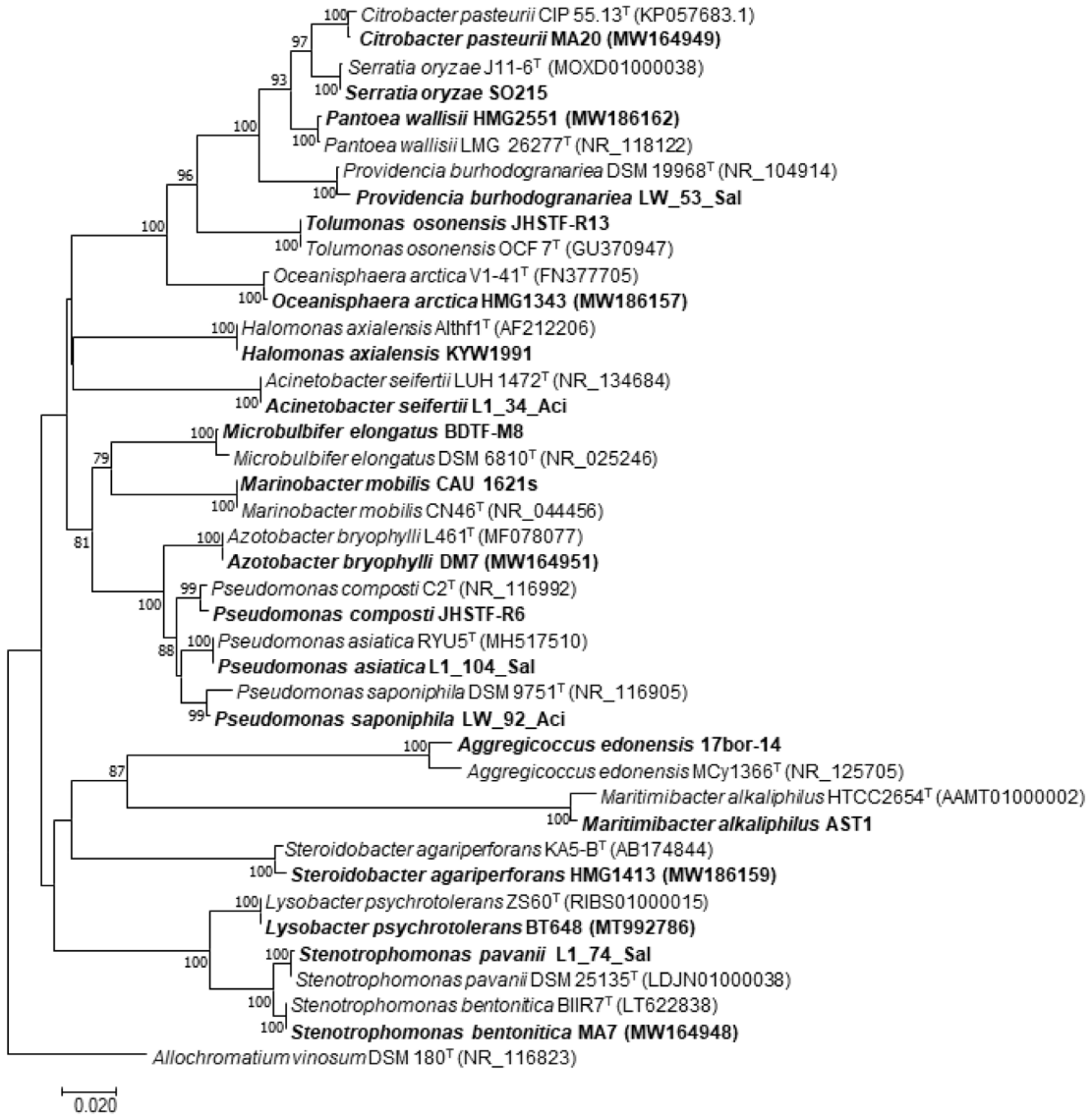

Fig. 3. Neighbor-joining phylogenetic tree based on 16S rRNA gene sequences shows the relationship between the strains isolated in this study and their relatives of the genus *Serratia* SO215, *Citrobacter* MA20, *Pantoea* HMG2551, *Providencia* LW_53_Sal, *Tolumonas* JHSTF-R13, *Oceanisphaera* HMG1343, *Halomonas* KYW1991, *Marinobacter* CAU 1621, *Microbulbifer* BDTF-M8, *Azotobacter* DM7, *Pseudomonas* JHSTF-R6, *Pseudomonas* L1_104_Sal, *Pseudomonas* LW 92 Aci, *Steroidobacter* HMG1413, *Lysobacter* BT648, *Stenotrophomonas* L1_74_Sal, *Stenotrophomonas* MA7, *Maritimibacter* AST1 and *Simulacricoccus* 17bor-14. 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 *Marinobacter mobilis* CAU 1621s

Cells are Gram-stain-negative, flagellated, and rod-shaped. Colonies are creamy white-colored after 3−5 days of incubation on MA at 30°C. In API 20NE test, weekly 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, potassium gluconate, and gelatin hydrolysis. D-Glucose, L-arabinose, D-mannose, D-maltose, adipic acid, malic acid, trisodium citrate, D-mannitol, *N*-acetyl-D-glucosamine, capric acid, and phenylacetic acid were not utilized. Strain CAU 1621s (=NIBRBAC000506279) was isolated from a soil sample from Sindo of Woongjin-gun, Incheon, Korea.

Description of *Microbulbifer elongatus* BDTF-M8

Cells are Gram-stain-negative, non-flagellated, and rod-shaped. Colonies are moderate yellow-colored after 3 days of incubation on MA at 25°C. In API 20NE test, reduction of nitrates (NO_3) to nitrogen (N_2), esculin hydrolysis, gela-

tin hydrolysis, and potassium gluconate; but negative for reduction of nitrates (NO_3) to nitrite (NO_2^-), urease, indole production on tryptophan, glucose fermentation, and arginine dihydrolase. D-Glucose, L-arabinose, D-mannose, D-maltose, adipic acid, malic acid, trisodium citrate, D-mannitol, *N*-acetyl-D-glucosamine, capric acid, and phenylacetic acid were not utilized. Strain BDTF-M8 (=NIBRBAC000506391) was isolated from a soil sample from Bulldo, Ansan-si, Gyeonggi-do, Korea.

Description of *Citrobacter pasteuriis* MA20

Cells are Gram-stain-negative, non-flagellated, and rod-shaped. Colonies are cream-colored after 3 days of incubation on R2A at 30°C. In API 20NE test, positive for reduction of nitrates (NO_3) to nitrogen (N_2), glucose fermentation, esculin hydrolysis, and potassium gluconate; but negative for urease, reduction of nitrates (NO_3) to nitrite (NO_2^-), indole production on tryptophan, arginine dihydrolase, and gelatin hydrolysis. D-Glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-D-glucosamine, D-maltose, capric acid, malic acid, trisodium citrate, and phenylacetic acid were utilized; whereas adipic acid was not utilized. Strain MA20 (=NIBRBAC000506143) was isolated from a soil sample from Ecological Park in Godeok-dong, Gangdong-gu, Seoul, Korea.

Description of *Pantoea wallisii* HMG2551

Cells are Gram-stain-negative, non-flagellated, and short rod shaped-shaped. Colonies are pale yellow-colored after 3 days of incubation on R2A at 25°C. In API 20NE test, positive for reduction of nitrates (NO_3) to nitrogen (N_2), glucose fermentation, esculin hydrolysis, gelatin hydrolysis, and potassium gluconate but negative for urease, reduction of nitrates (NO_3) to nitrite (NO_2^-), indole production on tryptophan, and arginine dihydrolase. D-Glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-D-glucosamine, D-maltose, malic acid, and trisodium citrate were utilized; whereas adipic acid, capric acid, and phenylacetic acid were not utilized. Strain HMG2551 (=NIBRBAC000506267) was isolated from a soil sample from Hankuk University of Foreign Studies, Cheoin-gu, Yongin-si, Gyeonggi-do, Korea.

Description of *Providencia burhodogranariea* LW_53_Sal

Cells are Gram-stain-negative, non-flagellated, and rod-shaped. Colonies are white-colored after 3 days of incubation on R2A at 37°C. In API 20NE test, positive for urease, esculin hydrolysis, reduction of nitrates (NO_3) to nitrite (NO_2^-), reduction of nitrates (NO_3) to nitrogen (N_2), indole production on tryptophan, glucose fermentation, and arginine dihydrolase; but negative for gelatin hydrolysis and potassium gluconate. D-Glucose, D-mannose, D-maltose, malic acid, trisodium citrate, D-mannitol, *N*-acetyl-D-glucosamine, capric acid, and phenylacetic acid were utilized; whereas L-arabinose and adipic acid were not utilized. Strain LW_53_Sal (=NIBRBAC000506411) was isolated from a soil sample from Cheoin-gu, Yongin-si, Gyeonggi-do, Korea.

Description of *Serratia oryzae* SO215

Cells are Gram-stain-negative, non-flagellated, and rod-shaped. Colonies are white-colored after 2 days of incubation on R2A at 25°C. In API 20NE test, positive for potassium gluconate, esculin hydrolysis, reduction of nitrates (NO_3) to nitrite (NO_2^-), reduction of nitrates (NO_3) to nitrogen (N_2), glucose fermentation, and gelatin hydrolysis; but negative for indole production on tryptophan, arginine dihydrolase, and urease. D-Glucose, L-arabinose, D-mannose, D-maltose, malic acid, trisodium citrate, D-mannitol, *N*-acetyl-D-glucosamine, and phenylacetic acid were utilized; whereas capric acid and adipic acid were not utilized. Strain SO215 (=NIBRBAC000506239) was isolated from a soil sample from Sunchon National University, Suncheon-si, Jeollanam-do, Korea.

Description of *Maritimibacter alkaliphilus* AsT1

Cells are Gram-stain-negative, non-flagellated, and short rod-shaped. Colonies are white yellow-colored after 3 days of incubation on MA at 30°C. In API 20NE test, positive for urease, potassium gluconate, esculin hydrolysis, reduction of nitrates (NO_3) to nitrite (NO_2^-), reduction of nitrates (NO_3) to nitrogen (N_2), and arginine dihydrolase; but negative for indole production on tryptophan, glucose fermentation, and gelatin hydrolysis. D-Glucose, L-arabinose, D-mannose, D-maltose, adipic acid, malic acid, trisodium citrate, D-mannitol, *N*-acetyl-D-glucosamine, capric acid, and phenylacetic acid were utilized. Strain AsT1 (=NIBRBAC000506373) was isolated from a soil sample from Taean Coast, Chungcheongbuk-do, Korea.

Description of *Stenotrophomonas pavanii* L1_74_Sal

Cells are Gram-stain-negative, non-flagellated, and short rod-shaped. Colonies are light yellow colored after 3 days of incubation on R2A at 37°C. In API 20NE test, positive for urease, esculin hydrolysis, and gelatin 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, and potassium gluconate. D-Glucose, D-mannose, *N*-acetyl-D-glucosamine, D-maltose, malic acid, and trisodium citrate were utilized; whereas L-arabinose, D-mannitol, capric acid, adipic acid, and phenylacetic acid were not utilized. Strain L1_74_Sal (=NIBR

BAC000506406) was isolated from a soil sample from Cheoin-gu, Yongin-si, Gyeonggi-do, Korea.

Description of *Lysobacter psychrotolerans* BT648

Cells are Gram-stain-negative, non-flagellated, and rod-shaped. Colonies are light yellow-colored after 3 days of incubation on R2A at 25°C. In API 20NE test, positive for reduction of nitrates (NO_3) to nitrite (NO_2^-), reduction of nitrates (NO_3) to nitrogen (N_2), indole production on tryptophan, esculin hydrolysis, and gelatin hydrolysis; but negative for glucose fermentation, arginine dihydrolase, urease, and potassium gluconate. D-Glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-D-glucosamine, D-maltose, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid were not utilized. Strain BT648 (=NIBR BAC000506193) was isolated from a soil sample from Hwam-myeon, Jeongseon-gun, Gangwon-do, Korea.

Description of *Halomonas axialensis* KYW1991

Cells are Gram-stain-negative, flagellated, and rod-shaped. Colonies are cream-colored after 3 days of incubation on MA at 25°C. In API 20NE test, positive for reduction of nitrates (NO_3) to nitrite (NO_2^-), reduction of nitrates (NO_3) to nitrogen (N_2), and esculin hydrolysis; but negative for indole production on tryptophan, glucose fermentation, arginine dihydrolase, urease, gelatin hydrolysis, and potassium gluconate. D-Maltose, adipic acid, and malic acid were utilized; whereas D-glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-D-glucosamine, capric acid, trisodium citrate, and phenylacetic acid were not utilized. Strain KYW1991 (=NIBRBAC000506237) was isolated from a soil sample from Gwangyang Bay, Gwangyang-si, Jeollanam-do, Korea.

Description of *Acinetobacter seifertii* L1_34_Aci

Cells are Gram-stain-negative, non-flagellated, and coccus-shaped. Colonies are white colored after 3 days of incubation on R2A at 37°C. In API 20NE test, positive for glucose fermentation, urease, esculin hydrolysis, and potassium gluconate; 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, arginine dihydrolase, and gelatin hydrolysis. Capric acid, malic acid, trisodium citrate, phenylacetic acid, D-glucose, and *N*-acetyl-D-glucosamine were utilized; whereas L-arabinose, D-mannose, D-mannitol, D-maltose, and adipic acid were not utilized. Strain L1_34_Aci (=NIBRBAC00050 6405) was isolated from a soil sample from Cheoin-gu, Yongin-si, Gyeonggi-do, Korea.

Description of *Pseudomonas composti* JHSTF-R6

Cells are Gram-stain-negative, non-flagellated, and rod-shaped. Colonies are yellowish white colored after 3 days of incubation on R2A at 25°C. In API 20NE test, positive for reduction of nitrates (NO_3) to nitrite (NO_2^-) and reduction of nitrates (NO_3) to nitrogen (N_2); but negative for indole production on tryptophan, glucose fermentation, arginine dihydrolase, urease, esculin hydrolysis, gelatin hydrolysis, and potassium gluconate. D-Glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-D-glucosamine, D-maltose, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid were not utilized. Strain JHSTF-R6 (=NIBRBAC000506393) was isolated from a soil sample from Seocheon-gun, Chungcheongnam-do, Korea.

Description of *Pseudomonas asiatica* L1_104_Sal

Cells are Gram-stain-negative, non-flagellated, and rod-shaped. Colonies are white-colored after 3 days of incubation on R2A at 37°C. In API 20NE test, positive for arginine dihydrolase, urease, esculin hydrolysis, and potassium gluconate; 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, and gelatin hydrolysis. D-Glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-D-glucosamine, D-maltose, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid were utilized. Strain L1_104_Sal (=NIBRBAC000506407) was isolated from a soil sample from Cheoin-gu, Yongin-si, Gyeonggi-do, Korea.

Description of *Pseudomonas saponiphila* LW_92_Aci

Cells are Gram-stain-negative, non-flagellated, and rod-shaped. Colonies are white colored after 3 days of incubation on R2A at 37°C. In API 20NE test, positive for indole production on tryptophan, glucose fermentation, arginine dihydrolase, esculin hydrolysis, and potassium gluconate; but negative for reduction of nitrates (NO_3) to nitrite (NO_2^-), reduction of nitrates (NO_3) to nitrogen (N_2), urease, and gelatin hydrolysis. D-Glucose, D-mannose, D-mannitol, *N*-acetyl-D-glucosamine, capric acid, malic acid, trisodium citrate, and phenylacetic acid were utilized; whereas L-arabinose, D-maltose, and adipic acid were not utilized. Strain LW_92_Aci (=NIBRBAC00050 6410) was isolated from a soil sample from Cheoin-gu, Yongin-si, Gyeonggi-do, Korea.

Description of *Azotobacter bryophylli* DM7

Cells are Gram-stain-negative, non-flagellated, and rod-shaped. Colonies are pale yellow colored after 3 days of incubation on R2A at 30°C. In API 20NE test, positive for reduction of nitrates (NO_3) to nitrite (NO_2^-), reduction of nitrates (NO_3) to nitrogen (N_2), urease, gelatin hydrolysis, and potassium gluconate; but negative for indole produc-

tion on tryptophan, urease, and gelatin hydrolysis. L-Arabinose, D-maltose, adipic acid, D-glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-D-glucosamine, D-maltose, malic acid, trisodium citrate, and phenylacetic acid were utilized; whereas capric acid and adipic acid were not utilized. Strain DM7 (=NIBRBAC000506145) was isolated from a soil sample from Ecological Park in Godeok-dong, Gangdong-gu, Seoul, Korea.

Description of *Steroidobacter agariperforans* HMG1413

Cells are Gram-stain-negative, flagellated, and rod-shaped. Colonies are yellow colored after 3 days of incubation on R2A at 25°C. In API 20NE test, positive for reduction of nitrates (NO_3) to nitrite (NO_2^-), reduction of nitrates (NO_3) to nitrogen (N_2), esculin hydrolysis, gelatin hydrolysis, and potassium gluconate; but negative for indole production on tryptophan, glucose fermentation, arginine dihydrolase, and urease. D-Glucose, L-arabinose, *N*-acetyl-D-glucosamine, D-maltose, malic acid, and trisodium citrate were utilized; whereas D-mannose, D-mannitol, capric acid, adipic acid, and phenylacetic acid were not utilized. Strain HMG1413 (=NIBRBAC000506264) was isolated from a soil sample from Hankuk University of Foreign Studies, Cheoin-gu, Yongin-si, Gyeonggi-do, Korea.

Description of *Stenotrophomonas bentonitica* MA7

Cells are Gram-stain-negative, non-flagellated, and rod-shaped. Colonies are cream-colored after 3 days of incubation on R2A at 30°C. In API 20NE test, positive for esculin hydrolysis and gelatin 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 potassium gluconate. D-Glucose, D-mannose, *N*-acetyl-D-glucosamine, D-maltose, malic acid, and trisodium citrate were utilized; whereas L-arabinose, D-mannitol, capric acid, adipic acid, and phenylacetic acid were not utilized. Strain MA7 (=NIBRBAC000506142) was isolated from a soil sample from Ecological Park in Godeok-dong, Gangdong-gu, Seoul, Korea.

Description of *Simulacricoccus ruber* 17bor-14

Cells are Gram-stain-negative, non-flagellated, and rod-shaped. Colonies are pink-colored after 3 days of incubation on R2A at 30°C. 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), esculin hydrolysis, gelatin hydrolysis, indole production on tryptophan, potassium gluconate, glucose fermentation, and arginine dihydrolase. D-Glucose, L-arabinose, D-mannose, D-maltose, adipic acid, malic acid, and trisodium citrate were utilized; whereas *N*-acetyl-D-glucosamine, D-mannitol, capric acid, and phenylacetic acid were not utilized. Strain 17bor-14 (=NIBRBAC000501349) was isolated from a soil sample from Gongneung-dong, Nowon-gu, Seoul, Korea.

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