Journal of Species Research 10(3):201-216, 2021

A report on 38 unrecorded bacterial species in Korea in the class Gammaproteobacteria

Veeraya Weerawongwiwat[1], Myung Kyum Kim[2], Kiseong Joh[3], Seung-Bum Kim[4], Chi-Nam Seong[5], Hana Yi[6], Jung-Hoon Yoon[7] and Wonyong Kim[1,*]

[1]*Department of Microbiology, Chung-Ang University College of Medicine, Seoul 06974, Republic of Korea*
[2]*Division of Chemistry and Bio-Environmental Sciences, Seoul Women's University College of Natural Sciences, Seoul 01797, Republic of Korea*
[3]*Department of Bioscience and Biotechnology, Hankuk University of Foreign Studies, Gyeonggi 17035, Republic of Korea*
[4]*Department of Microbiology, Chungnam National University, Daejeon 34134, Republic of Korea*
[5]*Department of Biology, Sunchon National University, Suncheon 57922, Republic of Korea*
[6]*School of Biosystem and Biomedical Science, Department of Public Health Science, Korea University, Seoul 02841, Republic of Korea*
[7]*Department of Food Science and Biotechnology, Sungkyunkwan University, Seoul 03063, Republic of Korea*

**Correspondent: kimwy@cau.ac.kr*

During an investigation of indigenous prokaryotic species in the Republic of Korea, a total of 38 bacterial strains belonging to the class Gammaproteobacteria were isolated from diverse environments. Samples were collected from soil, seawater, sand, sedimentary soil, rabbit feces, rat intestines, marine wetland, and tidal flats. The strains were identified to the species level using the high 16S rRNA gene sequences and showed high similarity (>98.7%) with the closest bacterial species and formed a robust clade in the neighbor-joining phylogenetic tree; it was determined that each strain belonged to independent, predefined bacteria species within the class Gammaproteobacteria. The 38 strains of Gammaproteobacteria analyzed in this study have not been reported in the Republic of Korea. Therefore, this study describes 20 genera of 13 families in 8 orders: Aeromonadales, Alteromonadales, Cellvibrionales, Enterobacterales, Lysobacterales, Oceanospirillales, Pseudomonadales, and Vibrionales. For each species, we describe Gram reaction, strain ID, isolation source, colony and cell morphology, cultural, physiological, and basic biochemical characteristics.

Keywords: 16S rRNA, Gammaproteobacteria, unrecorded species

DOI:10.12651/JSR.2021.10.3.201

Introduction

The understanding of bacterial phylogeny has rapidly transformed over the past few decades. The introduction of small subunit ribosomal RNA genes (Woese and Fox, 1977), followed by the development of next-generation sequencing techniques and bioinformatics have expanded to large-scale, cost-effective multiplex analyses, producing new data to study the taxonomic and functional diversity of the microbial community (Lauber *et al*., 2009; Whon *et al*., 2012; Pascault *et al*., 2014).

The phylum Proteobacteria constitutes the largest phylogenetic lineage (Kersters *et al*., 2006); it contains many pathogenic bacteria. Gammaproteobacteria is a class within the phylum Proteobacteria; it was first proposed by Garrity *et al*. (2005a) and amended by Williams and Kelly (2013). Gammaproteobacteria contains a large and diverse group of bacteria that exhibit wide variation in terms of phenotype, morphology, metabolic capability, and tropism (phototrophs and chemolithotrophs). Members of the class Gammaproteobacteria are gram-negative bacteria, including rods, cocci, spirilla, and filaments, with different morphological characteristics; they are isolated from a wide range of environments. At the time of writing this article, the class has been divided into 20 orders: Acidithiobacillales (Kojima *et al*., 2015), Aeromonadales (Martin-Carnahan and Joseph, 2005), Alteromonadales (Bowman and McMeekin, 2005), Arenicellales (Teramoto, 2015), Cardiobacteriales (Garrity *et al*., 2005b), Cellvibrionales (Spring *et al*., 2015), Chromatiales (Imhoff, 2005), Enterobacterales (Adeolu *et al*., 2016), Immundisolibacterales (Corteselli *et al*., 2017), Legionellales (Garrity *et al*., 2005d), Methyl-

ococcales (Bowman, 2005), Nevskiales (Naushad *et al*., 2015), Oceanospirillales (Garrity *et al*., 2005e), Orbales (Kwong and Moran, 2013), Pasteurellales (Garrity *et al*., 2005f), Pseudomonadales, Salinisphaerales (Skerman *et al*., 1980), Thiotrichales (Garrity *et al*., 2005c), Vibrionales (Skerman *et al*., 1980), and Xanthomonadales (Saddler and Bradbury, 2005).

In 2019, diverse environmental samples were collected from habitats in Korea, and novel and unrecorded bacterial species were isolated. The isolated bacterial species belong to the following taxa: Actinobacteria, Alphaproteobacteria, Bacteroidetes, Betaproteobacteria, Firmicutes, and Gammaproteobacteria. This study focused on the description of 38 unreported strains belonging to 13 families within 8 orders in the class Gammaproteobacteria.

Materials and Methods

The strains were isolated from samples collected from soil, seawater, sand, sedimentary soil, rabbit feces, rat intestines, marine wetlands, and tidal flats. Each sample was separately homogenized and suspended in appropriate solutions based on its source. The suspensions were serially diluted and aliquots (100 μL) of each sample were plated on various culture media, including ISP7, marine agar 2216 (MA), trypticase soy agar (TSA), nutrient agar (NA), Anaerobe basal medium, 1/10 LB, and R2A. The plates were incubated at 25−37°C for 2−4 days (Table 1). All the strains were purified by subculturing a single colony on fresh media, and pure cultures were stored in optimal media supplemented with 25% glycerol (v/v) at −80°C as lyophilized ampules.

Genomic DNA was extracted from each strain using a genomic DNA extraction kit (Intron). The 16S rRNA gene was amplified using PCR as described previously with two universal primers, 8F (5′-AGAGTTTGATCCTTGGCTCAG-3′) and 1525R (5′-AAGGAGGTGWTCCARCC-3′) (Lane, 1991). The BigDye Terminator Cycle Sequencing Kit (Applied Biosystems) and a 3730 automatic DNA sequencer (Applied Biosystems) were used to sequence the 16S rRNA gene amplicons. Multiple sequence alignments were constructed using CLUSTAL X (Thompson *et al*., 1997), and calculation of gene sequence similarity between each strain and the most closely related strains were performed using EzTaxon-e - EzBioCloud.net (http://www.ezbiocloud.net/eztaxon) (Kim *et al*., 2012). A phylogenetic tree was constructed using the neighbor-joining (Saitou and Nei, 1987), maximum-likelihood (Felsenstein, 1981), and maximum-parsimony (Fitch and Margoliash, 1967) algorithms in the MEGA7 program (Kumar *et al*., 2016). Evolutionary distance matrices were generated using the neighbor-joining method, as described by Jukes and Cantor (1969). Branch support in the neighbor-joining

Table 1. Lists of isolated strains belonging to the class Gammaproteobacteria and their taxonomic affiliations.

Order	Family	Genus	Strain ID	NIBR ID	Most closely related species	Similarity (%)	Isolation source	Medium	Incubation condition
Aeromonadales	*Aeromonadaceae*	*Aeromonas*	F-7	NIBRBAC000503374	*A. sanarellii* LMG 24682^{T}	99.23	Soil	ISP7	30°C, 3d
Alteromonadales	*Alteromonadaceae*	*Marinobacter*	HMF6821	NIBRBAC000503114	*M. adhaerens* HP 15^{T}	99.86	Sedimentary soil	MA	30°C, 3d
		Alteromonas	CAU 1518	NIBRBAC000503225	*A. gracilis* 9a2^{T}	99.09	Sand	MA	30°C, 2d
	Pseudoalteromonadaceae	*Pseudoalteromonas*	HMF6852	NIBRBAC000503115	*P. fenneropenaei* rzy34^{T}	99.86	Sedimentary soil	MA	30°C, 3d
	Shewanellaceae	*Shewanella*	HMF6915	NIBRBAC000503116	*S. inventionis* KX27^{T}	100.00	Seawater	MA	30°C, 3d
		Shewanella	HMF9426	NIBRBAC000503119	*S. electrodiphila* MAR441^{T}	99.39	Seawater	MA	25°C, 3d
Cellvibrionales	*Microbulbiferaceae*	*Microbulbifer*	LPB0320	NIBRBAC000503353	*M. variabilis* Ni-2088^{T}	98.71	Seawater	MA	25°C, 3d
Enterobacterales	*Enterobacteriaceae*	*Enterobacter*	LPB0291	NIBRBAC000503337	*E. hormaechei* subsp. *xiangfangensis* LMG 27195^{T}	99.86	Rabbit feces	Anaerobe basal medium	30°C, 3d
		Rosenbergiella	LPB0301	NIBRBAC000503362	*R. epipactidis* 2.1A^{T}	98.71	Sand	R2A	25°C, 3d
		Lelliottia	R-6	NIBRBAC000503386	*L. amnigena* NBRC 105700^{T}	99.93	Soil	R2A	37°C, 3d
	Erwiniaceae	*Pantoea*	BT361	NIBRBAC000503001	*P. brenneri* LMG 5343^{T}	99.64	Soil	R2A	25°C, 3d
	Morganellaceae	*Morganella*	LPB0234	NIBRBAC000503357	*M. morganii* subsp. *morganii* ATCC 25830^{T}	99.41	Rat intestinal	Anaerobe basal medium	30°C, 3d

Table 1. Continued.

Order	Family	Genus	Strain ID	NIBR ID	Most closely related species	Similarity (%)	Isolation source	Medium	Incubation condition
Lysobacterales	*Lysobacteraceae*	*Pseudomonas*	BSSL-CR1	NIBRBAC000503331	*P. geniculata* ATCC 19374^T	99.78	Tidal flat	R2A	25°C, 2d
		Luteimonas	HMF6088	NIBRBAC000503108	*L. terrae* THG-MD21^T	99.38	Seawater	R2A	30°C, 3d
		Pseudoxanthomonas	HMF6713	NIBRBAC000503113	*P. composti* GSS15^T	99.73	Sedimentary soil	MA	30°C, 3d
		Pseudoxanthomonas	HMF9812	NIBRBAC000503120	*P. spadix* DSM 18855^T	98.98	Marine wetland	MA	30°C, 3d
		Stenotrophomonas	jr18	NIBRBAC000503383	*S. lactitubi* M15^T	99.93	Soil	R2A	30°C, 3d
Oceanospirillales	*Halomonadaceae*	*Halomonas*	KYW1820	NIBRBAC000503288	*H. shengliensis* SL014B-85^T	99.86	Seawater	MA	25°C, 3d
		Halomonas	KYW1809	NIBRBAC000503291	*H. titanicae* BH1^T	99.31	Seawater	MA	25°C, 3d
		Halomonas	KYW1985	NIBRBAC000503308	*H. xianhensis* A-1^T	99.73	Seawater	MA	25°C, 2d
Pseudomonadales	*Moraxellaceae*	*Acinetobacter*	LPB0278	NIBRBAC000503343	*A. dispersus* ANC 4105^T	99.79	Soil	MA	25°C, 3d
		Psychrobacter	LPB0279	NIBRBAC000503342	*P. pacificensis* IFO 16279^T	99.30	Soil	R2A	25°C, 3d
	Pseudomonadaceae	*Pseudomonas*	SCBP1	NIBRBAC000503281	*P. luteola* NBRC 103146^T	99.86	Soil	MA	25°C, 3d
		Pseudomonas	KYW1748	NIBRBAC000503302	*P. zhaodongensis* NEAU-ST5-21^T	99.86	Seawater	MA	25°C, 4d
		Pseudomonas	CAU 1519	NIBRBAC000503226	*P. benzenivorans* DSM 8628^T	99.04	Sand	R2A	30°C, 2d
		Pseudomonas	CAU 1560	NIBRBAC000503232	*P. soli* F-279,208^T	99.93	Sand	MA	37°C, 2d
		Pseudomonas	BT58	NIBRBAC000502990	*P. caspiana* FBF102^T	99.38	Soil	R2A	25°C, 3d
		Pseudomonas	BT76	NIBRBAC000502994	*P. silesiensis* A3^T	99.52	Soil	R2A	25°C, 3d
		Pseudomonas	BT345	NIBRBAC000503000	*P. parafulva* NBRC 16636^T	98.70	Soil	R2A	25°C, 3d
		Pseudomonas	LPB0305	NIBRBAC000503345	*P. oleovorans* subsp. *oleovorans* DSM 1045^T	98.71	Sand	R2A	25°C, 3d
		Pseudomonas	MMS19-T15	NIBRBAC000503370	*P. cremoricolorata* IAM 1541^T	99.25	Soil	R2A	30°C, 3d
		Pseudomonas	F-130	NIBRBAC000503379	*P. citronellolis* NBRC 103043^T	99.72	Soil	R2A	30°C, 3d
		Pseudomonas	BG108	NIBRBAC000503381	*P. laurylsulfativorans* AP3_22^T	99.79	Soil	TSA	30°C, 3d
		Pseudomonas	BG24	NIBRBAC000503375	*P. flavescens* LMG 18387^T	98.69	Soil	TSA	30°C, 3d
		Pseudomonas	BT59	NIBRBAC000502991	*P. chlororaphis* subsp. *aurantiaca* DSM 19603^T	99.86	Soil	1/10 LB	25°C, 3d
Vibrionales	*Vibrionaceae*	*Grimontia*	LPB0317	NIBRBAC000503352	*G. indica* AK16^T	98.92	Seawater	MA	25°C, 3d
		Vibrio	LPB0315	NIBRBAC000503351	*V. hangzhouensis* CN83^T	99.50	Seawater	MA	25°C, 3d
		Vibrio	LPB0326	NIBRBAC000503356	*V. hyugaensis* 090810a^T	99.78	Sand	MA	25°C, 3d

tree was estimated using the bootstrap resampling method (Felsenstein, 1985) with 1,000 replicates.

The morphological features of the colonies, such as appearance, pigmentation, size, shape, and texture, were observed following their growth on agar plates incubated under optimal conditions. Cell morphology was examined under a JEM 1010 transmission electron microscope (JEOL) using cells in the exponential phase of growth. Gram staining was performed using a Gram staining kit (bioMérieux) according to the manufacturer's instructions. Biochemical properties and enzyme activities were determined for each strain using the API 20NE kit (except for two strains, for which the biochemical properties and enzyme activities were determined using the API 20A kit), according to the manufacturer's instructions (bioMérieux); read after incubation for 48 h of the strains.

Results and Discussion

On the basis of the 16S rRNA sequence comparison and phylogenetic analysis, a total of 38 strains were assigned to the class Gammaproteobacteria and were classified into 13 families of 8 orders: one species in the genus *Aeromonas* of the family *Aeromonadaceae* within the order Aeromonadales, five species in five genera of three families within the order Alteromonadales, one species in the genus *Microbulbifer* of the family *Microbulbiferaceae* within the order Cellvibrionales, five species in five genera of three families within the order Enterobacterales, five species in four genera of the family *Lysobacteraceae* within the order Lysobacterales, three species in the genus *Halomonas* of the family *Halomonadaceae* within the order Oceanospirillales, 15 species in three genera of two families within the order Pseudomonadales, and three species in two genera of the family *Vibrionaceae* within the order Vibrionales. All the strains were gram-negative and chemoheterotrophic, with rod-shaped cells, except for three strains, the cells of which were coccoid-shaped (Fig. 1 and Fig. 2). Details of the colony morphology and physiology of the strains are reported in the species description section.

Comparison of 16S rRNA gene sequences showed high similarities (>98.6%) with the closest related strains. One strain of the order Aeromonadales (F-7), five strains of the order Alteromonadales (HMF6821, CAU1518, HMF6852, HMF6915, and HMF9426), one strain of the order Cellvibrionales (LPB0320), five strains of the order Enterobacterales (LPB0291, LPB0301, R-6, BT361, and LPB 0234), and five strains of the order Alteromonadales (HMF6821, CAU1518, HMF6852, HMF6915 and HMF 9426) had the highest similarities to *Aeromonas sanarellii* LMG24682^T (CDBN01000061; 99.23%), *Marinobacter adhaerens* HP15^T (CP001978; 99.86%), *Alteromonas gracilis* 9a2^T (AB920393; 99.09%), *Pseudoalteromonas fenneropenaei* rzy34^T (KR709258; 99.86%), *Shewanella inventionis* KX27^T (KT781407; 100.00%), *Shewanella electrodiphila* MAR441^T (FR744784; 99.39%), *Microbulbifer variabilis* Ni-2088^T (AB167354; 98.71%), *Enterobacter hormaechei* subsp. *xiangfangensis* LMG 27195^T (FYBF01000083; 99.86%), *Rosenbergiella epipactidis* 2.1A^T (KF876184; 99.85%), *Lelliottia amnigena* NBRC 105700^T (BCNN01000001; 99.93%), *Pantoea brenneri* LMG 5343^T (MIEI01000169; 99.64%), *Morganella morganii* subsp. *morganii* ATCC 25830^T (AJ301681; 99.41 %), *Pseudomonas geniculata* ATCC 19374^T (AB021404; 99.78%), *Luteimonas terrae* THG-MD21^T (KJ769177; 99.38%), *Pseudoxanthomonas composti* GSS15^T (SAWZ 01000021; 99.73%), *Pseudoxanthomonas spadix* DSM 18855^T (RDQN01000022; 98.98%), and *Stenotrophomonas lactitubi* M15^T (LT222224; 99.93%). Three strains of the order Oceanospirillales (KYW1820, KYW1809, and KYW1985), 15 strains of the order Pseudomonadales (LPB 0278, LPB0279, SCBP1, KYW1748, CAU 1519, CAU 1560, BT58, BT76, BT345, LPB0305, MMS19-T15, F-130, BG108, BG24 and BT59), and tree strains of the order Vibrionales (LPB0317, LPB0315, and LPB0326) had the highest similarities to *Halomonas shengliensis* SL014B-85^T (EF121853; 99.86%), *Halomonas titanicae* BH1^T (AOPO01000038; 99.31%), *Halomonas xianhensis* A-1^T (EF421176; 99.73%), *Acinetobacter dispersus* ANC 4105^T (KB850049; 99.79%), *Psychrobacter pacificensis* IFO 16279^T (AB016057; 99.30%), *Pseudomonas luteola* NBRC 103146^T (BDAE01000066; 99.86%), *Pseudomonas zhaodongensis* NEAU-ST5-21^T (RFFM01000015; 99.86%), *Pseudomonas benzenivorans* DSM 8628^T (FNCT01000040; 99.04%), *Pseudomonas soli* F-279,208^T (HF930598; 99.93%), *Pseudomonas caspiana* FBF102^T (LOHF01000033; 99.38%), *Pseudomonas silesiensis* A3T (KX276592; 99.52%), *Pseudomonas parafulva* NBRC 16636^T (BBIU01000051; 98.70%), *Pseudomonas oleovorans* subsp. *oleovorans* DSM 1045^T (NIUB01000072; 98.71%), *Pseudomonas cremoricolorata* IAM 1541^T (AB060137; 99.25%), *Pseudomonas citronellolis* NBRC 103043^T (BCZY01000096; 99.72%), *Pseudomonas laurylsulfativorans* AP3_22^T (MF554631; 99.79%), *Pseudomonas flavescens* LMG 18387^T (FNDG01000047; 98.69 %), *Pseudomonas chlororaphis* subsp. *aurantiaca* DSM 19603^T (CP027746; 99.86%), *Grimontia indica* AK16^T (ANFM02000053; 98.99%), *Vibrio hangzhouensis* CN83^T (EU082035; 99.50%), and *Vibrio hyugaensis* 090810a^T (LC004912; 99.78%).

Phylogenetic analyses showed that the isolated strains formed a robust clade with the most closely related species in the orders Aeromonadales, Alteromonadales, Cellvibrionales, Enterobacterales, and Lysobacterales (Fig. 3), and Oceanospirillales, Pseudomonadales, and Vibrionales (Fig. 4). There are no official reports of these 38 strains

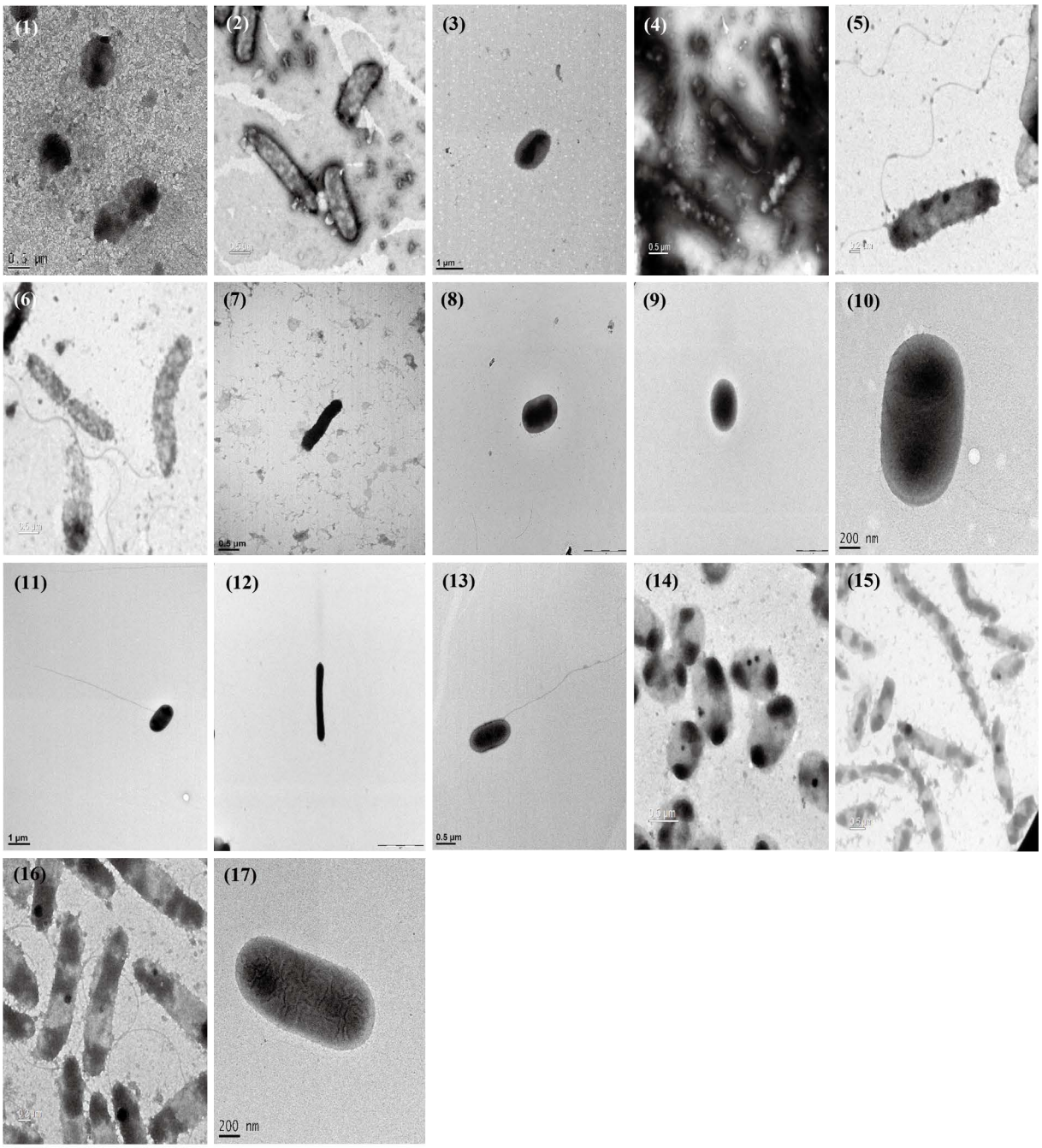

Fig. 1. Transmission electron micrographs of cells of the species in the orders Aeromonadales, Alteromonadales, Cellvibrionales, Enterobacterales and Lysobacterales belonging to the class Gammaproteobacteria in this study. Strain: 1, F-7; 2, HMF6821; 3, CAU 1518; 4, HMF6852; 5, HMF6915; 6, HMF9426; 7, LPB0320; 8, LPB0291; 9, LPB0301; 10, R-6; 11, BT361; 12, LPB0234; 13, BSSL-CR1; 14, HMF6088; 15, HMF6713; 16, HMF9812; 17, jr18.

in Korea. Therefore, these 38 strains in the class Gammaproteobacteria are newly reported strains in Korea: one species in the order Aeromonadales, five species in the order Alteromonadales, one species in the order Cellvibrionales, five species in the order Enterobacterales, five species in the order Lysobacterales, three species in the order Oceanospirillales, 15 species in the order Pseudomonadales, and three species in the order Vibrionales.

Description of *Aeromonas sanarellii* F-7

The cells are gram-negative, non-flagellated, and cocci shaped. The colonies are light yellow in color, circular,

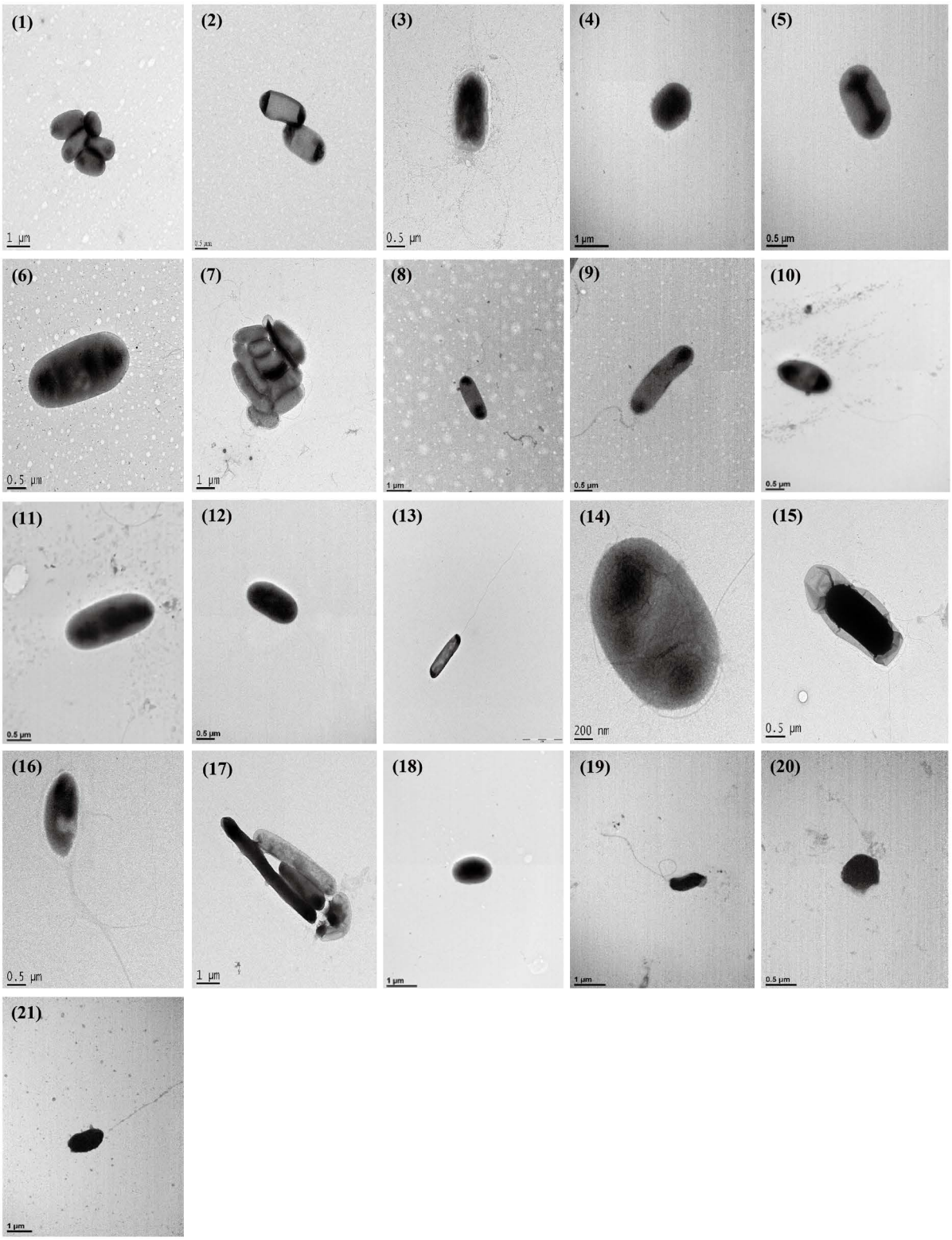

Fig. 2. Transmission electron micrographs of cells of the species in the orders Oceanospirillales, Pseudomonadales, and Vibrionales belonging to the class Gammaproteobacteria in this study. Strain: 1, KYW1820; 2, KYW1809; 3, KYW1985; 4, LPB0278; 5, LPB0279; 6, SCBP1; 7, KYW1748; 8, CAU 1519; 9, CAU 1560; 10, BT58; 11, BT76; 12, BT345; 13, LPB0305; 14, MMS19-T15; 15, F-130; 16, BG108; 17, BG24; 18, BT59; 19, LPB0317; 20, LPB0315; 21, LPB0326.

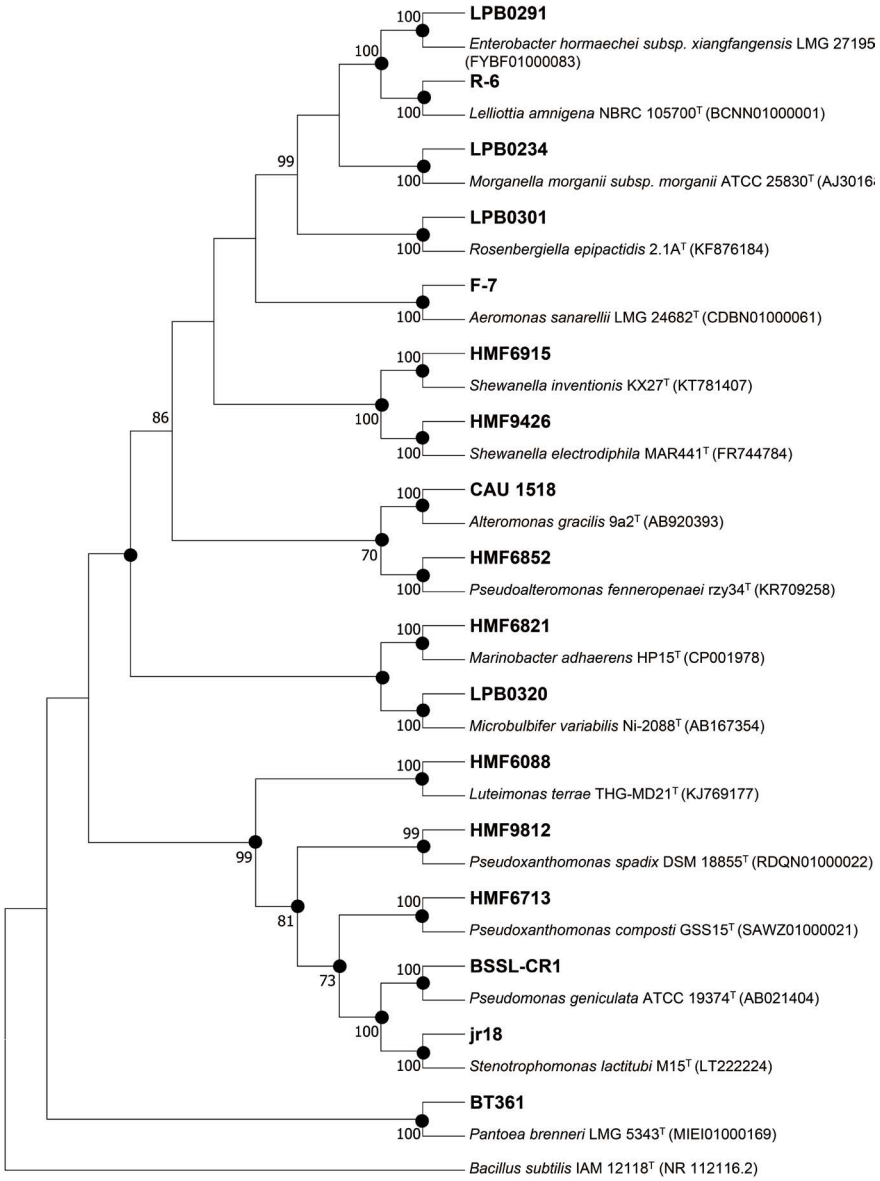

Fig. 3. Neighbor-joining (NJ) phylogenetic tree constructed based on nearly complete 16S rRNA gene sequences showing the relationships between 17 isolated strains and their most closely related species from the orders Aeromonadales, Alteromonadales, Cellvibrionales, Enterobacterales, and Lysobacterales of the class Gammaproteobacteria. The dots indicate that the corresponding nodes were also recovered in the trees created using the maximum-likelihood (ML) and maximum-parsimony (MP) algorithms. Bootstrap values are indicated as percentages of 1,000 resampled datasets, when greater than 70% (NJ/ML/MP). Bar, 0.01 substitutions per nucleotide position. *Bacillus subtilis* IAM 12118^{T} (NR_112116.2) is used as an outgroup organism.

convex, and undulate after incubation on ISP7 at 30°C for 3 days under aerobic conditions. The strains are positive for nitrate reduction, arginine dihydrolase, urease, esculin hydrolysis, gelatinase, β-galactosidase, and utilization of glucose, mannose, mannitol, *N*-acetyl-glucosamine, maltose, capric acid, malic acid, and phenylacetic acid; but negative for indole production, glucose fermentation, and utilization of arabinose, potassium gluconate, adipic acid, trisodium citrate, and cytochrome oxidase, per the analysis using the API 20NE kit. Strain F-7 (=NIBRBAC 000503374) was isolated from soil in Gung-dong, Yuseong-gu, Daejeon, Republic of Korea.

Description of *Marinobacter adhaerens* HMF6821

The cells are gram-negative, non-flagellated, and rod-shaped. The colonies are light yellow in color, circular, convex, and smooth after incubation on MA at 30°C for 3 days under aerobic conditions. The strains are positive

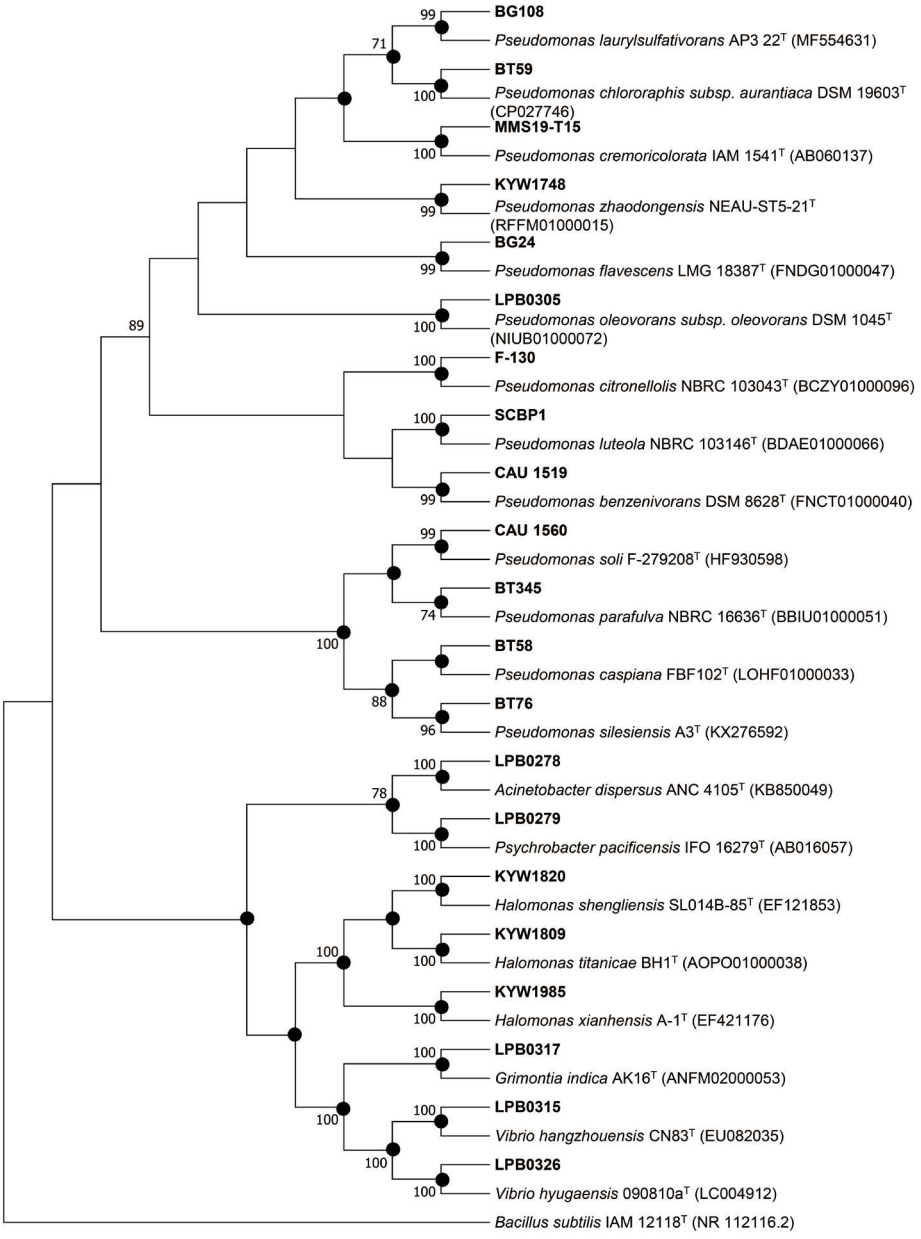

Fig. 4. Neighbor-joining (NJ) phylogenetic tree constructed based on nearly complete 16S rRNA gene sequences showing the relationships between 21 isolated strains and their most closely related species from the orders Oceanospirillales, Pseudomonadales, and Vibrionales of the class Gammaproteobacteria. The dots indicate that the corresponding nodes were also recovered in the trees created using the maximum-likelihood (ML) and maximum-parsimony (MP) algorithms. Bootstrap values are indicated as percentages of 1,000 resampled datasets, when greater than 70% (NJ/ML/MP). Bar, 0.01 substitutions per nucleotide position. *Bacillus subtilis* IAM 12118^T (NR_112116.2) is used as an outgroup organism.

for nitrate reduction, utilization of malic acid, and cytochrome oxidase; but negative for indole production, glucose fermentation, arginine dihydrolase, urease, esculin hydrolysis, gelatinase, β-galactosidase, and utilization of glucose, arabinose, mannose, mannitol, *N*-acetyl-glucosamine, maltose, potassium gluconate, capric acid, adipic acid, trisodium citrate, and phenylacetic acid, per the analysis using the API 20NE kit. Strain HMF6821 (=NIBR BAC000503114) was isolated from sedimentary soil in Wando-gun, Jeollanam-do, Republic of Korea.

Description of *Alteromonas gracilis* CAU 1518

The cells are gram-negative, non-flagellated, and short rod-shaped. The colonies are cream-colored, circular, convex, mucoid, and smooth after incubation on MA at

30°C for 2 days under aerobic conditions. It is positive for esculin hydrolysis, gelatinase, and β-galactosidase; but negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, urease, and utilization of glucose, arabinose, mannose, mannitol, *N*-acetyl-glucosamine, maltose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid, per the analysis using the API 20NE kit. However, the result for the presence of cytochrome oxidase is not available. Strain CAU 1518 (=NIBRBAC000503225) was isolated from sand in Jung-dong, Haeundae-gu, Busan, Republic of Korea.

Description of *Pseudoalteromonas fenneropenaei* HMF6852

The cells are gram-negative, non-flagellated, and rod-shaped. The colonies are white-colored, circular, convex, and smooth after incubation on MA at 30°C for 3 days under aerobic conditions. It is positive for esculin hydrolysis, gelatinase, and cytochrome oxidase; but negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, urease, β-galactosidase, and utilization of glucose, arabinose, mannose, mannitol, *N*-acetyl-glucosamine, maltose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid, per the analysis using the API 20NE kit. Strain HMF 6852 (=NIBRBAC000503115) was isolated from sedimentary soil in Wando-gun, Jeollanam-do, Republic of Korea.

Description of *Shewanella inventionis* HMF6915

The cells are gram-negative, non-flagellated, and rod-shaped. The colonies are pale pink in color, circular, convex, and smooth after incubation on MA at 30°C for 3 days under aerobic conditions. It is positive for nitrate reduction, esculin hydrolysis, gelatinase, β-galactosidase, and cytochrome oxidase; but negative for indole production, glucose fermentation, arginine dihydrolase, urease, and utilization of glucose, arabinose, mannose, mannitol, *N*-acetyl-glucosamine, maltose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid, per the analysis using the API 20NE kit. Strain HMF6915 (=NIBRBAC000503116) was isolated from seawater in Sinan-gun, Jeollanam-do, Republic of Korea.

Description of *Shewanella electrodiphila* HMF9426

The cells are gram-negative, non-flagellated, and rod-shaped. The colonies are pale pink in color, circular, convex, and smooth after incubation on MA at 25°C for 3 days under aerobic conditions. It is positive for glucose fermentation, esculin hydrolysis, gelatinase, and cytochrome oxidase; but negative for nitrate reduction, indole production, arginine dihydrolase, urease, β-galactosidase, utilization of glucose, arabinose, mannose, mannitol, *N*-acetyl-glucosamine, maltose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid, per the analysis using the API 20NE kit. Strain HMF9426 (=NIBRBAC000503119) was isolated from seawater in Gangneung-si, Gangwon-do Republic of Korea.

Description of *Microbulbifer variabilis* LPB0320

The cells are gram-negative, non-flagellated, and rod-shaped. The colonies are cream-colored, circular, convex, and entire after incubation on MA at 25°C for 3 days under aerobic conditions. It is positive for nitrate reduction, esculin hydrolysis, gelatinase, and cytochrome oxidase; but negative for indole production, glucose fermentation, arginine dihydrolase, urease, β-galactosidase, and utilization of glucose, arabinose, mannose, mannitol, *N*-acetyl-glucosamine, maltose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid, per the analysis using the API 20NE kit. Strain LPB0320 (=NIBRBAC000503353) was isolated from seawater in Anmyeon-eup, Taean-gun, Chungcheongnam-do, Republic of Korea.

Description of *Enterobacter hormaechei* subsp. *xiangfangensis* LPB0291

The cells are gram-negative, non-flagellated, and rod-shaped. The colonies are cream-colored, circular, entire, and convex after incubation on Anaerobe basal medium at 30°C for 3 days under anaerobic conditions. It is positive for urease (weak) and acidification of glucose, mannitol, saccharose, maltose, xylose, arabinose, cellobiose, mannose, raffinose, sorbitol, rhamnose, and trehalose; but negative for indole formation, acidification of lactose, salicin, glycerol, and melezitose, gelatinase, esculin hydrolysis, and cytochrome oxidase, per the analysis using the API 20A kit. Strain LPB0291 (=NIBRBAC000503337) was isolated from rabbit feces in Hasidong-ri, Gangdong-myeon, Gangneung-si, Gangwon-do, Republic of Korea.

Description of *Rosenbergiella epipactidis* LPB0301

The cells are gram-negative, non-flagellated, and cocci-shaped. The colonies are yellow in color, circular, convex, and entire after incubation on R2A plates at 25°C for 3 days under aerobic conditions. It is positive for glucose fermentation, arginine dihydrolase, esculin hydrolysis, β-galactosidase, and utilization of glucose, arabinose, mannitol, *N*-acetyl-glucosamine (weak), potassium gluconate, trisodium citrate (weak), and phenylacetic acid; but negative for nitrate reduction, indole production, urease, gelatinase, utilization of mannose, maltose, capric acid, adipic acid, and malic acid, and cytochrome oxidase, per the anal-

ysis using the API 20NE kit. Strain LPB0301 (=NIBR BAC000503362) was isolated from sand in Hasidong-ri, Gangdong-myeon, Gangneung-si, Gangwon-do, Republic of Korea.

Description of *Lelliottia amnigena* R-6

The cells are gram-negative, non-flagellated, and rod-shaped. The colonies are cream-colored, opaque, raised, and punctiform after incubation on R2A plates at 37°C for 3 days under aerobic conditions. It is positive for nitrate reduction, indole production (weak), glucose fermentation, arginine dihydrolase, urease, esculin hydrolysis, β-galactosidase, and utilization of glucose, arabinose, mannose, mannitol, *N*-acetyl-glucosamine, maltose potassium gluconate, malic acid, and trisodium citrate; but negative for gelatinase and utilization of capric acid, adipic acid, and phenylacetic acid, per the analysis using the API 20NE kit. However, the result for the presence of cytochrome oxidase is not available. Strain R-6 (=NIBRBAC000503386) was isolated from soil in Yangcheon-ri, Ganjeon-myeon, Gurye-gun, Jeollanam-do, Republic of Korea.

Description of *Pantoea brenneri* BT361

The cells are gram-negative, flagellated, and rod-shaped. The colonies are yellow in color, circular, and smooth after incubation on R2A plates at 25°C for 3 days under aerobic conditions. It is positive for glucose fermentation, esculin hydrolysis, β-galactosidase, and utilization of glucose, arabinose, mannose, mannitol, *N*-acetyl-glucosamine (weak), maltose, potassium gluconate, and malic acid; but negative for nitrate reduction, indole production, arginine dihydrolase, urease, gelatinase, utilization of capric acid, adipic acid, trisodium citrate, and phenylacetic acid, and cytochrome oxidase in API 20NE. Strain BT361 (=NIBR BAC000503001) was isolated from soil in Jeju-do, Republic of Korea.

Description of *Morganella morganii* subsp. *morganii* LPB0234

The cells are gram-negative, non-flagellated, and rod-shaped. The colonies are cream-colored, circular, convex, and entire after incubation on Anaerobe basal medium at 30°C for 3 days under anaerobic conditions. It is positive for acidification of glucose, mannitol, lactose, saccharose (weak), maltose (weak), salicin, xylose (weak), glycerol (weak), cellobiose, mannose, melezitose, raffinose (weak), sorbitol, rhamnose, and trehalose; but negative for indole formation, urease, acidification of arabinose, gelatinase, esculin hydrolysis, and cytochrome oxidase, per the analysis using the API 20A kit. Strain LPB0234 (=NIBRBAC 000503357) was isolated from rat intestines in Jeonmin-dong, Yuseong-gu, Daejeon, Republic of Korea.

Description of *Pseudomonas geniculata* BSSL-CR1

The cells are gram-negative, non-flagellated, and rod-shaped. The colonies are yellowish-white in color, circular, slightly convex, and glistening after incubation on R2A plates at 25°C for 2 days under aerobic conditions. It is positive for nitrate reduction, arginine dihydrolase, urease, esculin hydrolysis, gelatinase, β-galactosidase, and utilization of glucose, arabinose, mannose, *N*-acetyl-glucosamine, maltose, malic acid, and trisodium citrate; but negative for indole production, glucose fermentation, utilization of mannitol, potassium gluconate, capric acid, adipic acid, and phenylacetic acid, and cytochrome oxidase, per the analysis using the API 20NE kit. Strain BSSL-CR1 (=NIBRBAC000503331) was isolated from a tidal flat in Sohwang-ri, Ungcheon-eup, Boryeong-si, Chungcheongnam-do, Republic of Korea.

Description of *Luteimonas terrae* HMF6088

The cells are gram-negative, non-flagellated, and rod-shaped. The colonies are yellow in color, circular, convex, and smooth after incubation on R2A plates at 30°C for 3 days under aerobic conditions. It is positive for esculin hydrolysis, gelatinase, utilization of malic acid, and cytochrome oxidase; but negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, urease, β-galactosidase, and utilization of glucose, arabinose, mannose, mannitol, *N*-acetyl-glucosamine, maltose, potassium gluconate, capric acid, adipic acid, trisodium citrate, and phenylacetic acid, per the analysis using the API 20NE kit. Strain HMF6088 (=NIBRBAC000503 108) was isolated from seawater in Jeju-si, Jeju-do, Republic of Korea.

Description of *Pseudoxanthomonas composti* HMF6713

The cells are gram-negative, flagellated, and rod-shaped. The colonies are yellow in color, circular, convex, and smooth after incubation on MA at 30°C for 3 days under aerobic conditions. It is positive for urease, esculin hydrolysis, gelatinase, β-galactosidase, utilization of glucose, mannose, mannitol, *N*-acetyl-glucosamine, maltose, potassium gluconate, malic acid, and trisodium citrate, and cytochrome oxidase; but negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, and utilization of arabinose, capric acid, adipic acid, and phenylacetic acid in API 20NE. Strain HMF6713 (=NIBRBAC000503113) was isolated from sedimentary soil in Wando-gun, Jeollanam-do, Republic of Korea.

Description of *Pseudoxanthomonas spadix* HMF9812

The cells are gram-negative, non-flagellated, and rod-shaped. The colonies are yellow in color, circular, convex,

and smooth after incubation on MA plates at 30°C for 3 days under facultative anaerobic conditions. It is positive for arginine dihydrolase, urease, esculin hydrolysis, gelatinase, β-galactosidase, utilization of glucose, mannose, mannitol, *N*-acetyl-glucosamine, maltose, malic acid, and trisodium citrate, and cytochrome oxidase; but negative for nitrate reduction, indole production, glucose fermentation, and utilization of arabinose, potassium gluconate, capric acid, adipic acid, and phenylacetic acid, per the analysis using the API 20NE. Strain HMF9812 (=NIBR BAC000503120) was isolated from a marine wetland in Gangneung-si, Gangwon-do, Republic of Korea.

Description of *Stenotrophomonas lactitubi* jr18

The cells are gram-negative, non-flagellated, and rod-shaped. The colonies are light green in color, circular, convex, and entire after incubation on R2A plates at 30°C for 3 days under aerobic conditions. It is positive for nitrate reduction, arginine dihydrolase, urease, esculin hydrolysis, gelatinase, β-galactosidase, and utilization of glucose, mannose, *N*-acetyl-glucosamine, maltose, malic acid, and trisodium citrate; but negative for indole production, glucose fermentation, and utilization of arabinose, mannitol, potassium gluconate, capric acid, adipic acid, and phenylacetic acid, per the analysis using the API 20NE kit. However, the result for the presence of cytochrome oxidase is not available. Strain jr18 (=NIBRBAC000503383) was isolated from soil in Yangcheon-ri, Ganjeon-myeon, Gurye-gun, Jeollanam-do, Republic of Korea.

Description of *Halomonas shengliensis* KYW1820

The cells are gram-negative, non-flagellated, and short rod-shaped. The colonies are cream-colored, circular, smooth, opaque, and convex after incubation on MA plates at 25°C for 3 days under aerobic conditions. It is positive for cytochrome oxidase; but negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, urease, esculin hydrolysis, gelatinase, β-galactosidase, and utilization of glucose, arabinose, mannose, mannitol, *N*-acetyl-glucosamine, maltose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid, per the analysis using the API 20NE kit. Strain KYW1820 (=NIBRBAC000503288) was isolated from seawater in Gwangyang-si, Jeollanam-do, Republic of Korea.

Description of *Halomonas titanicae* KYW1809

The cells are gram-negative, non-flagellated, and rod-shaped. The colonies are cream-colored, circular, convex, opaque, and smooth after incubation on MA plates at 25°C for 3 days under aerobic conditions. It is positive for nitrate reduction, indole production, glucose fermentation, esculin hydrolysis, β-galactosidase, and utilization of glucose, arabinose, mannitol, *N*-acetyl-glucosamine, maltose, potassium gluconate, malic acid, trisodium citrate, and phenylacetic acid, and cytochrome oxidase; but negative for arginine dihydrolase, urease, gelatinase, and utilization of mannose, capric acid, and adipic acid, per the analysis using the API 20NE kit. Strain KYW1809 (=NIBRBAC 000503291) was isolated from seawater from Gwangyang-si, Jeollanam-do, Republic of Korea.

Description of *Halomonas xianhensis* KYW1985

The cells are gram-negative, non-flagellated, and short rod-shaped. The colonies are pale yellow in color, circular, smooth, translucent, and convex after incubation on MA plates at 25°C for 2 days under aerobic conditions. It is positive for glucose fermentation and esculin hydrolysis; but negative for nitrate reduction, indole production, arginine dihydrolase, urease, gelatinase, β-galactosidase, utilization of glucose, arabinose, mannose, mannitol, *N*-acetyl-glucosamine, maltose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid, and cytochrome oxidase, per the analysis using the API 20NE kit. Strain KYW1985 (=NIBRBAC000503 308) was isolated from seawater in Gwangyang-si, Jeollanam-do, Republic of Korea.

Description of *Acinetobacter dispersus* LPB0278

The cells are gram-positive, non-flagellated, and rod-shaped. The colonies are cream-colored, circular, entire, and convex after incubation on MA plates at 25°C for 3 days under aerobic conditions. It is positive for esculin hydrolysis (weak), gelatinase (weak), and utilization of capric acid, malic acid, trisodium citrate, and phenylacetic acid; but negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, urease, β-galactosidase, utilization of glucose, arabinose, mannose, mannitol, *N*-acetyl-glucosamine, maltose, potassium gluconate, and adipic acid, and cytochrome oxidase, per the analysis using the API 20NE kit. Strain LPB0278 (=NIBR BAC000503343) was isolated from soil in Anam-dong 5-ga, Seongbuk-gu, Seoul, Republic of Korea.

Description of *Psychrobacter pacificensis* LPB0279

The cells are gram-negative, non-flagellated, and rod-shaped. The colonies are cream-colored, circular, convex, and entire after incubation on R2A plates at 25°C for 3 days under aerobic conditions. It is positive for esculin hydrolysis (weak), utilization of malic acid, and cytochrome oxidase; but negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, urease, gelatinase, β-galactosidase, and utilization of glucose, arabinose, mannose, mannitol, *N*-acetyl-glucosamine,

maltose, potassium gluconate, capric acid, adipic acid, trisodium citrate, and phenylacetic acid, per the analysis using the API 20NE kit. Strain LPB0279 (=NIBRBAC 000503342) was isolated from soil in Anam-dong 5-ga, Seongbuk-gu, Seoul, Republic of Korea.

Description of *Pseudomonas luteola* SCBP1

The cells are gram-negative, non-flagellated, and rod-shaped. The colonies are pale yellow in color, wrinkled, erose, drop-like, and opaque after incubation on MA plates at 25°C for 3 days under aerobic conditions. It is positive for nitrate reduction, urease, esculin hydrolysis, gelatinase, β-galactosidase, and utilization of glucose, arabinose, mannose, mannitol, maltose, potassium gluconate, capric acid, malic acid, and trisodium citrate; but negative for indole production, glucose fermentation, arginine dihydrolase, utilization of *N*-acetyl-glucosamine, adipic acid, and phenylacetic acid, and cytochrome oxidase, per the analysis using the API 20NE kit. Strain SCBP1 (=NIBRBAC 000503281) was isolated from soil in Suncheon-si, Jeollanam-do, Republic of Korea.

Description of *Pseudomonas zhaodongensis* KYW1748

The cells are gram-negative, non-flagellated, and rod-shaped. The colonies are beige in color, circular, raised, smooth, and translucent after incubation on MA plates 25°C for 4 days under aerobic conditions. It is positive for nitrate reduction, esculin hydrolysis, utilization of glucose, arabinose, mannitol, maltose, potassium gluconate, malic acid, and trisodium citrate, and cytochrome oxidase; but negative for indole production, glucose fermentation, arginine dihydrolase, urease, gelatinase, β-galactosidase, and utilization of mannose, *N*-acetyl-glucosamine, capric acid, adipic acid, and phenylacetic acid, per the analysis using the API 20NE kit. Strain KYW1748 (=NIBRBAC 000503302) was isolated from seawater in Gwangyang-si, Jeollanam-do, Republic of Korea.

Description of *Pseudomonas benzenivorans* CAU 1519

The cells are gram-negative, non-flagellated, and rod-shaped. The colonies are cream-colored, convex, smooth, and irregular after incubation on R2A plates at 30°C for 2 days under aerobic conditions. It is positive for esculin hydrolysis (weak), gelatinase, and utilization of glucose, mannitol, maltose, potassium gluconate, malic acid, and trisodium citrate (weak); but negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, urease, β-galactosidase, and utilization of arabinose, mannose, *N*-acetyl-glucosamine, capric acid, adipic acid, and phenylacetic acid, per the analysis using the API 20NE kit. However, the result for the presence of cytochrome oxidase is not available. Strain CAU 1519 (=NIBRBAC 000503226) was isolated from sand in Jung-dong, Haeundae-gu, Busan, Republic of Korea.

Description of *Pseudomonas soli* CAU 1560

The cells are gram-negative, non-flagellated, and rod-shaped. The colonies are cream-colored, circular, convex, and shiny after incubation on NA plates at 37°C for 2 days under anaerobic conditions. It is positive for glucose fermentation, gelatinase, and utilization of glucose, arabinose, mannose, mannitol, *N*-acetyl-glucosamine, maltose, and potassium gluconate; but negative for nitrate reduction, indole production, arginine dihydrolase, urease, esculin hydrolysis, β-galactosidase, and utilization of capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid, per the analysis using the API 20NE kit. However, the result for the presence of cytochrome oxidase is not available. Strain CAU 1560 (=NIBRBAC000503232) was isolated from sand in Hupyeong-dong, Chuncheon-si, Gangwon-do, Republic of Korea.

Description of *Pseudomonas caspiana* BT58

The cells are gram-negative, flagellated, and rod-shaped. The colonies are white in color, circular, convex, and smooth after incubation on R2A plates at 25°C for 3 days under aerobic conditions. It is positive for arginine dihydrolase, esculin hydrolysis (weak), gelatinase (weak), utilization of glucose, arabinose, mannose, mannitol (weak), *N*-acetyl-glucosamine, potassium gluconate (weak), capric acid (weak), malic acid (weak), and trisodium citrate (weak), and cytochrome oxidase; but negative for nitrate reduction, indole production, glucose fermentation, urease, β-galactosidase, and utilization of maltose, adipic acid, and phenylacetic acid, per the analysis using the API 20NE kit. Strain BT58 (=NIBRBAC000502990) was isolated from soil in Hoenggye-ri, Daegwallyeong-myeon, Pyeongchang-gun, Gangwon-do, Republic of Korea.

Description of *Pseudomonas silesiensis* BT76

The cells are gram-negative, non-flagellated, and rod-shaped. The colonies are white in color, circular, and smooth after incubation on R2A plates at 25°C for 3 days under aerobic conditions. It is positive for nitrate reduction, arginine dihydrolase (weak), urease, gelatinase, utilization of potassium gluconate and capric acid, and cytochrome oxidase; but negative for indole production, glucose fermentation, esculin hydrolysis, β-galactosidase, and utilization of glucose, arabinose, mannose, mannitol, *N*-acetyl-glucosamine, maltose, adipic acid, malic acid, trisodium citrate, and phenylacetic acid, per the analysis using the API 20NE kit. Strain BT76 (=NIBRBAC00050 2994) was isolated from soil in Hoenggye-ri, Daegwal-

lyeong-myeon, Pyeongchang-gun, Gangwon-do, Republic of Korea.

Description of *Pseudomonas parafulva* BT345

The cells are gram-positive, non-flagellated, and rod-shaped. The colonies are white in color, circular, convex, and smooth after incubation on R2A plates at 25°C for 3 days under aerobic conditions. It is positive for nitrate reduction, esculin hydrolysis, gelatinase (weak), utilization of glucose, arabinose, mannose, mannitol, potassium gluconate, capric acid (weak), malic acid (weak), and trisodium citrate (weak), and cytochrome oxidase; but negative for indole production, glucose fermentation, arginine dihydrolase, urease, β-galactosidase, and utilization of *N*-acetyl-glucosamine, maltose, adipic acid, and phenylacetic acid, per the analysis using the API 20NE kit. Strain BT345 (=NIBRBAC000503000) was isolated from soil in Jeju-do, Republic of Korea.

Description of *Pseudomonas oleovorans* subsp. *oleovorans* LPB0305

The cells are gram-negative, non-flagellated, and rod-shaped. The colonies are yellow in color, circular, convex, and entire after incubation on R2A plates at 25°C for 3 days under aerobic conditions. It is positive for esculin hydrolysis (weak), utilization of glucose, mannose, mannitol, potassium gluconate, capric acid, malic acid, and trisodium citrate, and cytochrome oxidase; but negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, urease, gelatinase, β-galactosidase, and utilization of arabinose, *N*-acetyl-glucosamine, maltose, adipic acid, and phenylacetic acid, per the analysis using the API 20NE kit. Strain LPB0305 (=NIBRBAC 000503345) was isolated from sand in Hasidong-ri, Gangdong-myeon, Gangneung-si, Gangwon-do, Republic of Korea.

Description of *Pseudomonas cremoricolorata* MMS19-T15

The cells are gram-negative, non-flagellated, and rod-shaped. The colonies are yellow in color, circular, convex, and entire after incubation on R2A plates at 30°C for 3 days under aerobic conditions. It is positive for esculin hydrolysis (weak), utilization of glucose, *N*-acetyl-glucosamine, potassium gluconate, capric acid, malic acid, trisodium citrate, and phenylacetic acid, and cytochrome oxidase; but negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, urease, gelatinase, β-galactosidase, and utilization of arabinose, mannose, mannitol, maltose, and adipic acid, per the analysis using the API 20NE kit. Strain MMS19-T15 (=NIBR BAC000503370) was isolated from soil in Banggwang-ri, Gwangui-myeon, Gurye-gun, Jeollanam-do, Republic of Korea.

Description of *Pseudomonas citronellolis* F-130

The cells are gram-negative, non-flagellated, and rod-shaped. The colonies are cream-colored, circular, convex, and entire after incubation on R2A plates at 30°C for 3 days under aerobic conditions. It is positive for nitrate reduction, esculin hydrolysis, gelatinase, utilization of glucose, arabinose, *N*-acetyl-glucosamine, maltose, potassium gluconate, malic acid, and trisodium citrate, and cytochrome oxidase; but negative for indole production, glucose fermentation, arginine dihydrolase, urease, β-galactosidase, and utilization of mannose, mannitol, capric acid, adipic acid, and phenylacetic acid, per the analysis using the API 20NE kit. Strain F-130 (=NIBRBAC000503379) was isolated from soil in Gung-dong, Yuseong-gu, Daejon, Republic of Korea.

Description of *Pseudomonas laurylsulfativorans* BG108

The cells are gram-negative, non-flagellated, and rod-shaped. The colonies are cream-colored, circular, convex, and entire after incubation on TSA plates at 30°C for 3 days under aerobic conditions. It is positive for nitrate reduction, glucose fermentation, arginine dihydrolase, urease (weak), esculin hydrolysis (weak), utilization of glucose, arabinose (weak), mannose, mannitol, *N*-acetyl-glucosamine, potassium gluconate, capric acid, malic acid, trisodium citrate, and phenylacetic acid, and cytochrome oxidase; but negative for indole production, gelatinase, β-galactosidase, and utilization of maltose and adipic acid, per the analysis using the API 20NE kit. Strain BG108 (=NIBRBAC000503381) was isolated from a forest in Banggwang-ri, Gwangui-myeon, Gurye-gun, Jeollanam-do, Republic of Korea.

Description of *Pseudomonas flavescens* BG24

The cells are gram-negative, non-flagellated, and rod-shaped. The colonies are yellow in color, circular, convex, and entire after incubation on TSA plates at 30°C for 3 days under aerobic conditions. It is positive for nitrate reduction, glucose fermentation, esculin hydrolysis, gelatinase, β-galactosidase, and utilization of glucose, *N*-acetyl-glucosamine, maltose, potassium gluconate, and malic acid; but negative for indole production, arginine dihydrolase, urease, utilization of arabinose, mannose, mannitol, capric acid, adipic acid, trisodium citrate, and phenylacetic acid, and cytochrome oxidase, per the analysis using the API 20NE kit. Strain BG24 (=NIBRBAC000503375) was isolated from soil in Banggwang-ri, Gwangui-myeon, Gurye-gun, Jeollanam-do, Republic of Korea.

Description of *Pseudomonas chlororaphis* subsp. *aurantiaca* BT59

The cells are gram-negative, non-flagellated, and cocci-shaped. The colonies are yellow in color, circular, and smooth after incubation on 1/10 LB plates at 25°C for 3 days under aerobic conditions. It is positive for nitrate reduction, arginine dihydrolase, gelatinase, utilization of glucose, arabinose (weak), mannose (weak), mannitol, *N*-acetyl-glucosamine (weak), potassium gluconate, capric acid (weak), malic acid (weak), trisodium citrate (weak), and phenylacetic acid, and cytochrome oxidase; but negative for indole production, glucose fermentation, urease, esculin hydrolysis, β-galactosidase, and utilization of maltose and adipic acid, per the analysis using the API 20NE kit. Strain BT59 (=NIBRBAC000502991) was isolated from soil in Hoenggye-ri, Daegwallyeong, Pyeongchang-gun, Gangwon-do, Republic of Korea.

Description of *Grimontia indica* LPB0317

The cells are gram-negative, single polar flagellated, and rod-shaped. The colonies are cream-colored, circular, entire, and convex after incubation on MA plates at 25°C for 3 days under aerobic conditions. It is positive for nitrate reduction, indole production, glucose fermentation, esculin hydrolysis (weak), gelatinase, β-galactosidase, and cytochrome oxidase; but negative for arginine dihydrolase, urease, and utilization of glucose, arabinose, mannose, mannitol, *N*-acetyl-glucosamine, maltose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid, per the analysis using the API 20NE kit. Strain LPB0317 (=NIBRBAC000503352) was isolated from seawater in Anmyeon-eup, Taean-gun, Chungcheongnam-do, Republic of Korea.

Description of *Vibrio hangzhouensis* LPB0315

The cells are gram-negative, non-flagellated, and rod-shaped. The colonies are cream-colored, circular, entire, and convex after incubation on MA plates at 25°C for 3 days under aerobic conditions. It is positive for nitrate reduction, indole production, glucose fermentation, β-galactosidase, utilization of mannitol, and cytochrome oxidase; but negative for arginine dihydrolase, urease, esculin hydrolysis, gelatinase, and utilization of glucose, arabinose, mannose, *N*-acetyl-glucosamine, maltose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid, per the analysis using the API 20NE kit. Strain LPB0315 (=NIBRBAC000503351) was isolated from seawater in Anmyeon-eup, Taean-gun, Chungcheongnam-do, Republic of Korea.

Description of *Vibrio hyugaensis* LPB0326

The cells are gram-negative, non-flagellated, and rod-shaped. The colonies are cream-colored, circular, entire, and convex after incubation on TSA plates at 25°C for 3 days under aerobic conditions. It is positive for nitrate reduction, indole production, glucose fermentation, esculin hydrolysis, gelatinase, β-galactosidase activity, and cytochrome oxidase; but negative for arginine dihydrolase, urease, and utilization of glucose, arabinose, mannose, mannitol, *N*-acetyl-glucosamine, maltose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid, per the analysis using the API 20NE kit. Strain LPB0326 (=NIBRBAC000503356) was isolated from sand in Anmyeon-eup, Taean-gun, Chungcheongnam-do, Republic of Korea.

Acknowledgements

This work was supported by the project on the survey of indigenous species of Korea of the National Institute of Biological Resources (NIBR) under the Ministry of Environment (MOE).

References

Adeolu, M., S. Alnajar, S. Naushad and R.S. Gupta. 2016. Genome-based phylogeny and taxonomy of the '*Enterobacteriales*': proposal for *Enterobacterales* ord. nov. divided into the families *Enterobacteriaceae*, *Erwiniaceae* fam. nov., *Pectobacteriaceae* fam. nov., *Yersiniaceae* fam. nov., *Hafniaceae* fam. nov., *Morganellaceae* fam. nov., and *Budviciaceae* fam. nov. International Journal of Systematic and Evolutionary Microbiology 66(12):5575-5599.

Bowman, J.P. 2005. Order VII. *Methylococcales* ord. nov. In: D.J. Brenner, N.R. Krieg, J.T. Staley and G.M. Garrity (eds.), Bergey's Manual of Systematic Bacteriology, second edition, vol. 2 (The *Proteobacteria*), Part B, (The *Gammaproteobacteria*), Springer, New York, pp. 248-252.

Bowman, J.P. and T.A. McMeekin. 2005. Order *X. Alteromonadales* ord. nov. In: D.J. Brenner, N.R. Krieg, J.T. Staley and G.M. Garrity (eds.), Bergey's Manual of Systematic Bacteriology, second edition, vol. 2 (The *Proteobacteria*), Part B, (The *Gammaproteobacteria*), Springer, New York, p. 443.

Corteselli, E.M., M.D. Aitken and D.R. Singleton. 2017. Description of *Immundisolibacter cernigliae* gen. nov., sp. nov., a high-molecular-weight polycyclic aromatic hydrocarbon-degrading bacterium within the class *Gammaproteobacteria*, and proposal of *Immundisolibacterales* ord. nov. and *Immundisolibacteraceae* fam. nov. International Journal of Systematic and Evolutionary Microbiology 67(4):925-931.

Felsenstein, J. 1981. Evolutionary trees from DNA sequences: a maximum likelihood approach. Journal Molecular Evo-

lution 17(6):368-376.
Felsenstein, J. 1985. Confidence limits on phylogenies: an approach using the bootstrap. Evolution 39(4):783-791.
Fitch, W.M. and E. Margoliash. 1967. Construction of phylogenetic trees. Science 155(3760):279-284.
Garrity, G.M., J.A. Bell and T. Lilburn. 2005a. Class III. *Gammaproteobacteria* class. nov. In: D.J. Brenner, N.R. Krieg, J.T. Staley and G.M. Garrity (eds.), Bergey's Manual of Systematic Bacteriology, second edition, vol. 2 (The *Proteobacteria*), Part B, (The *Gammaproteobacteria*), Springer, New York, p. 1.
Garrity, G.M., J.A. Bell and T. Lilburn. 2005b. Order IV. *Cardiobacteriales* ord. nov. In: D.J. Brenner, N.R. Krieg, J.T. Staley and G.M. Garrity (eds.), Bergey's Manual of Systematic Bacteriology, second edition, vol. 2 (The *Proteobacteria*), Part B, (The *Gammaproteobacteria*), Springer, New York, p. 123.
Garrity, G.M., J.A. Bell and T. Lilburn. 2005c. Order V. *Thiotrichales* ord. nov. In: D.J. Brenner, N.R. Krieg, J.T. Staley and G.M. Garrity (eds.), Bergey's Manual of Systematic Bacteriology, second edition, vol. 2 (The *Proteobacteria*), Part B, (The *Gammaproteobacteria*), Springer, New York, p. 131.
Garrity, G.M., J.A. Bell and T. Lilburn. 2005d. Order VI. *Legionellales* ord. nov. In: D.J. Brenner, N.R. Krieg, J.T. Staley and G.M. Garrity (eds.), Bergey's Manual of Systematic Bacteriology, second edition, vol. 2 (The *Proteobacteria*), Part B, (The *Gammaproteobacteria*), Springer, New York, p. 210.
Garrity, G.M., J.A. Bell and T. Lilburn. 2005e. Order VIII. *Oceanospirillales* ord. nov. In: D.J. Brenner, N.R. Krieg, J.T. Staley and G.M. Garrity (eds.), Bergey's Manual of Systematic Bacteriology, second edition, vol. 2 (The *Proteobacteria*), Part B, (The *Gammaproteobacteria*), Springer, New York, p. 270.
Garrity, G.M., J.A. Bell and T. Lilburn. 2005f. Order XIV. *Pasteurellales* ord. nov. In: D.J. Brenner, N.R. Krieg, J.T. Staley and G.M. Garrity (eds.), Bergey's Manual of Systematic Bacteriology, second edition, vol. 2 (The *Proteobacteria*), Part B, (The *Gammaproteobacteria*), Springer, New York, p. 850.
Imhoff, J.F. 2005. Order I. *Chromatiales* ord. nov. In: D.J. Brenner, N.R. Krieg, J.T. Staley and G.M. Garrity (eds.), Bergey's Manual of Systematic Bacteriology, second edition, vol. 2 (The *Proteobacteria*), Part B, (The *Gammaproteobacteria*), Springer, New York, pp. 1-3.
Jukes, T.H. and C.R. Cantor. 1969. Evolution of protein molecules. In: H.N. Munro (ed.), Mammalian Protein Metabolism. Academic Press, New York, pp. 21-132.
Kersters, K., P. de Vos, M. Gillis, J. Swings, P. Vandamme, and E. Stackebrandt. 2006. Introduction to the proteobacteria. The Prokaryotes, Springer, New York, pp. 3-37.
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(Pt3):716-721.
Kojima, H., A. Shinohara and M. Fukui. 2015. *Sulfurifustis variabilis* gen. nov., sp. nov., a sulfur oxidizer isolated from a lake, and proposal of *Acidiferrobacteraceae* fam. nov. and *Acidiferrobacterales* ord. nov. International Journal of Systematic and Evolutionary Microbiology 65(10):3709-3713.
Kumar, S., G. Stecher and K. Tamura. 2016. MEGA7: molecular evolutionary genetics analysis version 7.0 for bigger datasets. Molecular Biology Evolution 33(7):1870-1874.
Kwong, W.K. and N.A. Moran. 2013. Cultivation and characterization of the gut symbionts of honey bees and bumble bees: description of *Snodgrassella alvi* gen. nov., sp. nov., a member of the family *Neisseriaceae* of the *Betaproteobacteria*, and *Gilliamella apicola* gen. nov., sp. nov., a member of *Orbaceae* fam. nov., *Orbales* ord. nov., a sister taxon to the order '*Enterobacteriales*' of the *Gammaproteobacteria*. International Journal of Systematic and Evolutionary Microbiology 63(Pt6):2008-2018.
Lane, D.J. 1991. 16S/23S RNA sequencing. In: E. Stackebrandt and M. Goodfellow (eds.), Nucleic Acid Techniques in Bacterial Systematics. John Wiley & Sons Ltd., London, pp. 115-175.
Lau, S.C.K., M.M.Y. Tsoi, X. Li, S. Dobretsov, Y. Plakhotnikova, P.K. Wong and P.Y. Qian. 2005. *Pseudoalteromonas spongiae* sp. nov., a novel member of the γ-*Proteobacteria* isolated from the sponge *Mycale adhaerens* in Hong Kong waters. International Journal of Systematic and Evolutionary Microbiology 55(Pt4):1593-1596.
Lauber, C.L., M. Hamady, R. Knight and N. Fierer. 2009. Pyrosequencing-based assessment of soil pH as a predictor of soil bacterial community structure at the continental scale. Applied and Environmental Microbiology 75(15):5111-5120.
Martin-Carnahan, A. and S.W. Joseph. 2005. Order XII. *Aeromonadales* ord. nov. In: D.J. Brenner, N.R. Krieg, J.T. Staley and G.M. Garrity (eds.), Bergey's Manual of Systematic Bacteriology, second edition, vol. 2 (The *Proteobacteria*), Part B, (The *Gammaproteobacteria*), Springer, New York, p. 556.
Naushad, S., M. Adeolu, S. Wong, M. Sohail, H.E. Schellhorn and R. Gupta. 2015. A phylogenomic and molecular marker based taxonomic framework for the order *Xanthomonadales*: proposal to transfer the families *Algiphilaceae* and *Solimonadaceae* to the order *Nevskiales* ord. nov. and to create a new family within the order *Xanthomonadales*, the family *Rhodanobacteraceae* fam. nov., containing the genus *Rhodanobacter* and its closest relatives. Antonie van Leeuwenhoek 107(2):467-485.
Orla-Jensen, S. 1921. The main lines of the nature bacterial system. Journal of Bacteriology 6(3):263-273.
Pascault, N., S. Roux, J. Artigas, S. Pesce, J. Leloup, R.D. Tadonleke, D. Debroas A. Bouchez and J.F. Humbert.

2014. A high-throughput sequencing ecotoxicology study of freshwater bacterial communities and their responses to tebuconazole. FEMS Microbiology Ecology 90(3):563-574.

Saddler, G.S. and J.F. Bradbury. 2005. Order III. *Xanthomonadales* ord. nov. In: D.J. Brenner, N.R. Krieg, J.T. Staley and G.M. Garrity (eds.), Bergey's Manual of Systematic Bacteriology, second edition, vol. 2 (The *Proteobacteria*), Part B, (The *Gammaproteobacteria*), Springer, New York, p. 63.

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

Skerman, V.B.D., V. McGowan and P.H.A. Sneath. 1980. Approved Lists of Bacterial Names. International Journal of Systematic and Evolutionary Microbiology 30:225-420.

Spring, S., C. Scheuner, M. Göker and H.P. Klenk. 2015. A taxonomic framework for emerging groups of ecologically important marine gammaproteobacteria based on the reconstruction of evolutionary relationships using genome-scale data. Frontiers in Microbiology 6:281.

Teramoto, M., K.I. Yagyu and M. Nishijima. 2015. *Perspicuibacter marinus* gen. nov., sp. nov., a semi-transparent bacterium isolated from surface seawater, and description of *Arenicellaceae* fam. nov. and *Arenicellales* ord. nov. International Journal of Systematic and Evolutionary Microbiology 65(Pt2):353-358.

Thompson, J.D., T.J. Gibson, F. Plewniak, F. Jeanmougin, D.G. Higgins. 1997. The CLUSTAL_X Windows interface: flexible strategies for multiple sequence alignment aided by quality analysis tools. Nucleic Acids Research 25(24):4876-4882.

Whon, T.W., M.S. Kim, S.W. Roh, N.R. Shin, H.W. Lee and J.W. Bae. 2012. Metagenomic characterization of airborne viral DNA diversity in the near-surface atmosphere. Journal of Virology 86(15):8221-8231.

Williams, K.P. and D.P. Kelly. 2013. Proposal for a new class within the phylum *Proteobacteria*, *Acidithiobacillia* classis nov., with the type order *Acidithiobacillales*, and emended description of the class *Gammaproteobacteria*. International Journal of Systematic and Evolutionary Microbiology 63(Pt8):2901-2906.

Woese, C.R. and G.E. Fox. 1977. Phylogenetic structure of the prokaryotic domain: the primary kingdoms. Proceeding of the National Academy of Sciences of the United States of America 74(11):5088-5090.

Submitted: November 12, 2020
Revised: November 18, 2020
Accepted: November 18, 2020