Journal of Species Research 8(4):319-336, 2019

A report on 53 unrecorded bacteria species in Korea in the class *Gammaproteobacteria*

Rungravee Kanjanasuntree[1], Chang-Jun Cha[2], Jang-Cheon Cho[3], Wan-Taek Im[4], Myung Kyum Kim[5], Che-Ok Jeon[6], Kiseong Joh[7], Seung-Bum Kim[8], Chi-Nam Seong[9], Hana Yi[10], Soon Dong Lee[11], Jin-Woo Bae[12] and Wonyong Kim[1,*]

[1]*Department of Microbiology, Chung-Ang University College of Medicine, Seoul 06974, Republic of Korea*
[2]*Department of Biotechnology, Chung-Ang University, Anseong 17546, Republic of Korea*
[3]*Department of Biological Science, Inha University, Incheon 22212, Republic of Korea*
[4]*Department of Biotechnology, Hankyong National University, Anseong 17579, Republic of Korea*
[5]*Division of Chemistry and Bio-Environmental Sciences, Seoul Women's University College of Natural Sciences, Seoul 01797, Republic of Korea*
[6]*Department of Life Sciences, Chung-Ang University, Seoul 06974, Republic of Korea*
[7]*Department of Bioscience and Biotechnology, Hankuk University of Foreign Studies, Geonggi 17035, Republic of Korea*
[8]*Department of Microbiology, Chungnam National University, Daejeon 34134, Republic of Korea*
[9]*Department of Biology, Sunchon Narional University, Suncheon 57922, Republic of Korea*
[10]*School of Biosystem and Biomedical Science, Department of Public Health Science, Korea University, Seoul 02841, Republic of Korea*
[11]*Department of Science Education, Jeju National University, Jeju 63243, Republic of Korea*
[12]*Department of Biology, Kyung Hee University, Seoul 02447, Republic of Korea*

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

During an investigation of unrecorded prokaryotic species in Republic of Korea, a total of 53 bacterial strains belonging to the class *Gammaproteobacteria* were isolated from soil, seawater, tidal flats, rhizosphere, salt ponds, beach sand, urine, manure, sediment, and animal intestine (Russian grayling butterfly [*Hipparchia autonoe*], mouse [*Mus musculus*], and sea bass [*Lateolabrax japonicus*]). Strains were identified to species using the 16S rRNA gene sequence, showing high similarity (>98.7%) with the closest bacterial species and forming a robust clade in the neighbor-joining phylogenetic tree. The 53 strains of *Gammaproteobacteria* in this study have not been report previously in Korea. Therefore, we describe 27 genera of 16 families in 7 orders: 13 strains in the order *Alteromonadales*, 1 strain in the order *Chromatiales*, 11 strains in the order *Enterobacterales*, 7 strains in the order *Oceanospirillales*, 10 strains in the order *Pseudomonadales*, 8 strains in the order *Vibrionales*, and 3 strains in the order *Xanthomonadales*. Gram reaction, strain ID, isolation source, and morphological and basic biochemical characteristics are described for each species.

Keywords: 16S rRNA, *Gammaproteobacteria*, unrecorded species

© 2019 National Institute of Biological Resources
DOI:10.12651/JSR.2019.8.4.319

Introduction

The understanding of the bacterial phylogeny has rapidly transformed over past decades. The introduction of small subunit ribosomal RNA gene (Woese and Fox, 1977), followed by the development of next-generation sequencing techniques and bioinformatics expanded to large-scale, cost-effective multiplex analyses, producing new data to study the taxonomy 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) that contains many of pathogenic bacteria. *Gammaproteobacteria* has the taxonomic rank of class within the phylum *Proteobacteria* that was first proposed by Garrity *et al*. (2005a) and ammended by Williams and Kelly (2013). *Gammaproteobacteria* contains 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. At the time of this writing, 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, 2005), *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), *Methylococcales* (Bowman, 2005), *Nevskiales* (Naushad *et al*., 2015), *Oceanospirillales* (Garrity *et al*., 2005e), *Orbales* (Kwong and Moran, 2013), *Pasteurellales* (Garrity *et al*., 2005f), *Pseudomonadales* (Orla-Jensen, 1921), *Salinisphaerales* (Skerman *et al*., 1980), *Thiotrichales* (Garrity *et al*., 2005c), *Vibrionales* (Skerman *et al*., 1980), and *Xanthomonadales* (Saddler and Bradbury, 2005).

In 2017, we collected diverse environmental samples from habitats in Korea and isolated novel and unrecorded bacteria species in Korea. The isolated bacteria species belong to the class *Actinobacteria*, *Alphaproteobacteria*, *Bacteroidetes*, *Deinococci*, *Deltaproteobacteria*, *Epsilonproteobacteria*, *Firmicutes*, *Fusobacteria*, and *Gammaproteobacteria*. In this study, we focused on the description of 53 unreported strains belonging to 16 families of 7 orders in the class *Gammaproteobacteria*.

Materials and Methods

The strains were isolated from samples collected from soil, seawater, tidal flats, rhizosphere, salt ponds, beach sand, urine, manure, sediment, and animal intestine (Russian grayling butterfly [*H. autonoe*], mouse [*M. musculus*], and sea bass [*Lateolabrax japonicus*]). Each sample was separately homogenized and suspended in the appropriate solution based on its source. The suspensions were serially diluted and an aliquot (100 μL) of each sample was placed on various culture media including marine agar 2216 (MA), trypticase soy agar (TSA), Luria-Bertani (LB), MacConkey (MAC), nutrient agar (NA), brain heart infusion (BHI), yeast malt agar (ISP medium No.2), R2A, R5A, R8A, R10A, R12A, R15A, and R17A. The plates were incubated at 25−37°C for 2−5 days (Table 1). All 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.

Extraction of genomic DNA of each strain was carried out using a genomic DNA extraction kit (Intron). The 16S rRNA gene was amplified by PCR as described previously using two universal primers, 8F (5′-AGAGTTTGATCCTTGGCTCAG-3′) and 1525R (5′-AAGGAGGTGWTCCARCC-3′) (Lane, 1991). The BigDye Terminator Cycle Sequencing Kit (Applied Biosystems) and the 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 calculations of gene sequence similarity between each strain and most closely related strains were performed by using EzTaxon-e – EzBioCloud.net (http://www.ezbiocloud.net/eztaxon) (Kim *et al*., 2012). A phylogenetic tree was constructed using neighbor-joining (Saitou and Nei, 1987), maximum-likelihood (Felsenstein, 1981), and maximum-parsimony (Fitch and Margoliash, 1967), algorithms in MEGA7 program (Kumar *et al*., 2016). Evolutionary distance matrices were generated by the neighbor-joining described by Jukes and Cantor (1969). Branch support in the neighbor-joining tree was estimated by the bootstrap resampling method (Felsenstein, 1985) with 1000 replicates.

Colony morphology was observed for morphological features such as appearance, pigmentation, size, shape, and texture on agar plates incubated at optimal conditions. Cell morphology was examined under JEM 1010 transmission electron microscope (JEOL) using cells grown in the exponential phase. Gram staining was performed using Gram staining kit (bioMérieux) according to the manufacturer's instructions. Biochemical properties and enzyme activities were determined for each strain using API 20NE (except for one strain that was determined by using API 20A) according to the manufacturer's instructions (bioMérieux) and read after incubation for 48 hours.

Results and Discussion

On the basis of 16S rRNA sequence comparison and phylogenetic analysis, a total of 53 strains were assigned to the class *Gammaproteobacteria* and were classified into 16 families of 7 orders: 13 species in 6 genera of 6 families within the order *Alteromonadales*, 1 species in genus *Wenzhouxiangella* of family *Wenzhouxiangellaceae* within the order *Chromatiales*, 11 species in 7 genera of 3 families within the order *Enterobacterales*, 7 species in 5 genera of 2 families within the order *Oceanospirillales*, 10 species in 2 genera of 2 families within the order *Pseudomonadales*, 8 species in 3 genera of family *Vibrionaceae* within the order *Vibrionales*, and 3 species in 3 genera of family *Xanthomonadaceae* within the order *Xanthomonadales*. All strains were Gram-staining-negative, chemoheterotrophic, and rod-shaped, except for 10 strains that were coccoid or ovoid-shaped (Figs. 1 and 2). Details of

Table 1. Lists of isolated strain 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
Alteromonadales	*Agarivorans*	*Agarivorans*	IMCC34138	NIBRBAC000501087	*A. gilvus* WH0801^T	99	Tidal flat	R5A	25°C, 3d
	Colwelliaceae	*Thalassotalea*	KYW1359	NIBRBAC000501128	*T. loyana* CBMAI 722^T	99.5	Seawater	MA	25°C, 3d
	Idiomarinaceae	*Idiomarina*	HMF8561	NIBRBAC000501173	*I. baltica* OS145^T	98.9	Salt-pond	MA	30°C, 3d
		Idiomarina	LPB0188	NIBRBAC000501016	*I. donghaiensis* 908033^T	99.72	Seawater	MA	25°C, 3d
	Marinobacter	*Marinobacter*	LPB0300	NIBRBAC000501021	*M. szutsaonensis* NTU-104^T	99.72	Seawater	MA	25°C, 3d
	Pseudoalteromonadaceae	*Pseudoalteromonas*	LPB0182	NIBRBAC000501198	*P. lipolytica* CGMCC 1.8499^T	100	Seawater	MA	25°C, 3d
		Pseudoalteromonas	IMCC34178	NIBRBAC000501097	*P. phenolica* KCTC 12086^T	99.3	Tidal flat	R12A	25°C, 3d
		Pseudoalteromonas	KYW1326	NIBRBAC000501126	*P. ruthenica* KMM 300^T	99.7	Seawater	MA	25°C, 3d
		Pseudoalteromonas	IMCC34174	NIBRBAC000501098	*P. spongiae* UST010723-006^T	99.7	Tidal flat	R10A	25°C, 3d
	Shewanellaceae	*Shewanella*	LPB0308	NIBRBAC000501023	*S. corallii* fav-2-10-05^T	98.9	Seawater	MA	25°C, 3d
		Shewanella	LPB0180	NIBRBAC000501009	*S. fidelis* KMM 3582^T	99.79	Seawater	MA	25°C, 3d
		Shewanella	LPB0184	NIBRBAC000501012	*S. halifaxensis* HAW-EB4^T	99.93	Seawater	MA	25°C, 3d
		Shewanella	LPB0186	NIBRBAC000501014	*S. schlegeliana* HRKA1^T	99.71	Seawater	MA	25°C, 3d
Chromatiales	*Wenzhouxiangellaceae*	*Wenzhouxiangella*	HMF8517	NIBRBAC000501172	*W. sediminis* XDB06^T	98.8	Salt-pond	MA	30°C, 3d
Enterobacterales	*Enterobacteriaceae*	*Citrobacter*	BT3507	NIBRBAC000501139	*C. europaeus* 97/99^T	99.92	Russian grayling butterfly	TSA	37°C, 2d
		Citrobacter	BT3301	NIBRBAC000501140	*C. farmeri* CDC 2991-81^T	99.15	Russian grayling butterfly	TSA	37°C, 2d
		Enterobacter	BR3501	NIBRBAC000501141	*E. aerogenes* KCTC 2190^T	99.79	Russian grayling butterfly	R2A	37°C, 2d
		Enterobacter	BC3307	NIBRBAC000501142	*E. asburiae* JCM 605^T	99.3	Russian grayling butterfly	MacConkey	37°C, 2d
		Escherichia	LPB0191	NIBRBAC000501300	*E. coli* ATCC 11775^T	99.93	Mouse	LB	25°C, 3d
		Escherichia	BC3202	NIBRBAC000501143	*E. marmotae* HT073016^T	99.28	Russian grayling butterfly	MacConkey	37°C, 2d
		Klebsiella	BT2501	NIBRBAC000501144	*K. pneumoniae* subsp. *pneumoniae* DSM 30104^T	99.72 99.72	Russian grayling butterfly	TSA	20°C, 2d 37°C, 2d
		Klebsiella	BT3409	NIBRBAC000501145	*K. variicola* DSM 15968^T		Russian grayling butterfly	TSA	
	Erwiniaceae	*Pantoea*	KYW1346	NIBRBAC000501127	*P. septica* LMG 5345^T	99.6	Seawater	MA	25°C, 3d
	Yersiniaceae	*Rahnella*	MMS17-GJ020	NIBRBAC000501193	*R. variigena* CIP 105588^T	98.9	Soil	ISP 2, pH5	30°C, 5d
		Serratia	CAU 1471	NIBRBAC000501234	*S. marcescens* subsp. *marcescens* ATCC 1388^T	99.9	Urine	BHI	37°C, 2d
Oceanospirillales	*Halomonadaceae*	*Halomonas*	KYW1415	NIBRBAC000501130	*H. sulfidaeris* ATCC BAA-803^T	100	Seawater	MA	25°C, 3d
		Larsenimonas	GH3-6	NIBRBAC000501043	*L. salina* M1-18^T	99.9	Rhizosphere	MA	30°C, 3d
	Oceanospirillaceae	*Amphritea*	HMF9021	NIBRBAC000501174	*A. atlantica* DSM 18887^T	99.7	Sea sand	MA	30°C, 3d
		Amphritea	LPB0189	NIBRBAC000501017	*A. balenae* JAMM 1525^T	100	Seawater	MA	25°C, 3d
		Amphritea	LPB0185	NIBRBAC000501013	*A. japonica* JAMM 1866^T	99.42	Seawater	MA	25°C, 3d
		Marinobacterium	LPB0208	NIBRBAC000501019	*M. stanieri* DSM 7027^T	98.85	Seawater	MA	25°C, 3d
		Marinomonas	KYW1404	NIBRBAC000501129	*M. communis* LMG 2864^T	98.9	Seawater	MA	25°C, 3d
Pseudomonadales	*Moraxellaceae*	*Acinetobacter*	16_S3_M11	NIBRBAC000501074	*A. beijerinckii* CIP 110307^T	99.9	Soil	R2A	30°C, 2d
		Acinetobacter	16_H2_V4	NIBRBAC000501072	*A. guillouiae* CIP 63.46^T	99.9	Manure	R2A	30°C, 2d
		Acinetobacter	LPB0181	NIBRBAC000501010	*A. indicus* CIP 110367^T	99.78	Seawater	MA	25°C, 3d
		Acinetobacter	16_H3_M12	NIBRBAC000501071	*A. johnsonii* CIP 64.6^T	99.6	Soil	R2A	30°C, 3d
		Acinetobacter	16_H2_M14	NIBRBAC000501073	*A. tjernbergiae* DSM 14971^T	99.3	Manure	R2A	30°C, 3d
		Acinetobacter	16_H6_M1	NIBRBAC000501076	*A. towneri* DSM 14962^T	99.6	Soil	R2A	30°C, 3d
		Acinetobacter	16_H5_M7	NIBRBAC000501075	*A. ursingii* DSM 16037^T	99.6	Soil	R2A	30°C, 3d
		Acinetobacter	BC3402	NIBRBAC000501137	*A. vivianii* NIPH 2168^T	99.93	Russian grayling butterfly	MacConkey	37°C, 2d

Table 1. Continued.

Order	Family	Genus	Strain ID	NIBR ID	Most closely related species	Similarity (%)	Isolation source	Medium	Incubation condition
Pseudomonadales	*Pseudomonadaceae*	*Pseudomonas*	Gsoil 1532	NIBRBAC000500996	*P. mohnii* DSM 18327^T	99.4	Soil	R2A	30°C, 2d
		Pseudomonas	BC3406	NIBRBAC000501147	*P. nitritireducens* WZBFD3-5A2^T	99.65	Russian grayling butterfly	MacConkey	37°C, 2d
Vibrionales	*Vibrionaceae*	*Aliivibrio*	IMCC34228	NIBRBAC000501090	*A. fischeri* JCM 18803^T	100	Seawater	R2A	25°C, 5d
		Photobacterium	LPB0174	NIBRBAC000501008	*P. damselae* subsp. *piscicida* NCIMB 2058^T	99.92 99.33	Sea bass	MA	30°C, 3d 25°C, 3d
		Vibrio	LPB0190	NIBRBAC000501301	*V. comitans* GHG21^T	99.5	Seawater	MA	25°C, 3d
		Vibrio	IMCC34186	NIBRBAC000501102	*V. hispanicus* LMG 13240^T	99.71	Tidal flat	R15A	25°C, 3d
		Vibrio	LPB0202	NIBRBAC000501018	*V. nereis* DSM 19584^T	99.3	Seawater	MA	25°C, 3d
		Vibrio	IMCC34213	NIBRBAC000501103	*V. penaeicida* DSM 14398^T	99.9	Beach sand	R17A	25°C, 5d
		Vibrio	IMCC34225	NIBRBAC000501104	*V. scophthalmi* LMG 19158^T	99.1	Seawater	R2A	25°C, 5d
		Vibrio	IMCC34148	NIBRBAC000501105	*V. tritonius* JCM 16456^T		Tidal flat	R8A	
Xanthomonadales	*Xanthomonadaceae*	*Lysobacter*	17J9-2	NIBRBAC000501324	*L. ximonensis* XM415^T	100	Soil	R2A	25°C, 4d
		Pseudoxanthomonas	MMS17-SY254	NIBRBAC000501210	*P. kaohsiungensis* J36^T	99.1	Soil	NA	30°C, 3d
		Stenotrophomonas	16H1E7	NIBRBAC000501080	*S. acidaminiphila* JCM 13310^T	100	Sediment	R2A	30°C, 1d

colony morphology and physiology are reported in the species description section.

Comparison of 16S rRNA gene sequences showed high similarities (>98.6%) with the closest related strains. Thirteen strains of the order *Alteromonadales* (IMCC34138, KYW1359, HMF8561, LPB0188, LPB0300, LPB0182, IMCC34178, KYW1326, IMCC34174, LPB0308, LPB0180, LPB0184 and LPB0186), one strain of the order *Chromatiales* (HMF8517), and eleven strains of the order *Enterobacterales* (BT3507, BT3301, BR3501, BC3307, LPB0191, BC3202, BT2501, BT3409, KYW1346, MMS17-GJ020, and CAU 1471) had the highest similarities to *Agarivorans gilvus* WH0801^T (CP013021; 99.00%), *Thalassotalea loyana* CBMAI 722^T (AY643537; 99.50%), *Idiomarina baltica* OS145^T (AJ440214; 98.90%), *Idiomarina donghaiensis* 908033^T (EU600204; 99.72%), *Marinobacter szutsaonensis* NTU-104^T (EU164778; 99.772%), *Pseudoalteromonas lipolytica* CGMCC 1.8499^T (FJ40472; 100%), *Pseudoalteromonas phenolica* KCTC 12086^T (CP013187; 99.30%) *Pseudoalteromonas ruthenica* KMM 300^T (AF316891; 99.70%), *Pseudoalteromonas spongiae* UST010723-006^T (AHCE02000026; 99.70%), *Shewanella corallii* fav-2-10-05^T (FJ041083; 98.90%), *Shewanella fidelis* KMM 3582^T (AF420312; 99.79%), *Shewanella halifaxensis* HAW-EB4^T (CP000931; 99.93%), *Shewanella schlegeliana* HR-KA1^T (AB081760; 99.71%), *Wenzhouxiangella sediminis* XDB06^T (KU645983; 98.80%), *Citrobacter europaeus* 97/99^T (FLYB01000015; 99.92%), *Citrobacter farmeri* CDC 2991-81^T (AF025371; 99.15%), *Enterobacter aerogenes* KCTC 2190^T (CP002824; 99.79%), *Enterobacter asburiae* JCM 6051^T (BBED01000197; 99.30%), *Escherichia coli* ATCC 11775^T (X80725; 99.93%), *Escherichia marmotae* HT073016^T (JNBP01000188; 99.28%), *Klebsiella pneumoniae* subsp. *pneumoniae* DSM 30104^T (AJJI01000018; 99.72), *Klebsiella variicola* DSM 15968^T (CP010523; 99.72), *Pantoea septica* LMG 5345^T (MLJJ01000077; 99.60%), *Rahnella variigena* CIP 105588^T (GQ148969; 98.90%), *Serratia marcescens* subsp. *marcescens* ATCC 13880^T (JMPQ01000005; 99.90%). Eight strains of the order *Oceanospirillales* (KYW1415, GH3-6, HMF9021, LPB0189, LPB0185, LPB0208, and KYW1404), 10 strains of the order *Pseudomonadales* (16_S3_M11, 16_H2_V4, LPB0181, 16_H3_M12, 16_H2_M14, 16_H6_M1, 16_H5_M7, BC3402, Gsoil 1532, and BC3406), 8 strains of the order *Vibrionales* (IMCC34228, LPB0174, LPB0190, IMCC34186, LPB0202, IMCC34213, IMCC34225, and IMCC34148), and 3 strains of the order *Xanthomonadales* (17J9-2, MMS17-SY254, and 16H1E7), had the highest similarities to *Halomonas sulfidaeris* ATCC BAA-803^T (AF212204; 100%), *Larsenimonas salina* M1-18^T (HF678441; 99.90%), *Amphritea atlantica* DSM 18887^T (FOGB01000032; 99.70%), *Amphritea balenae*

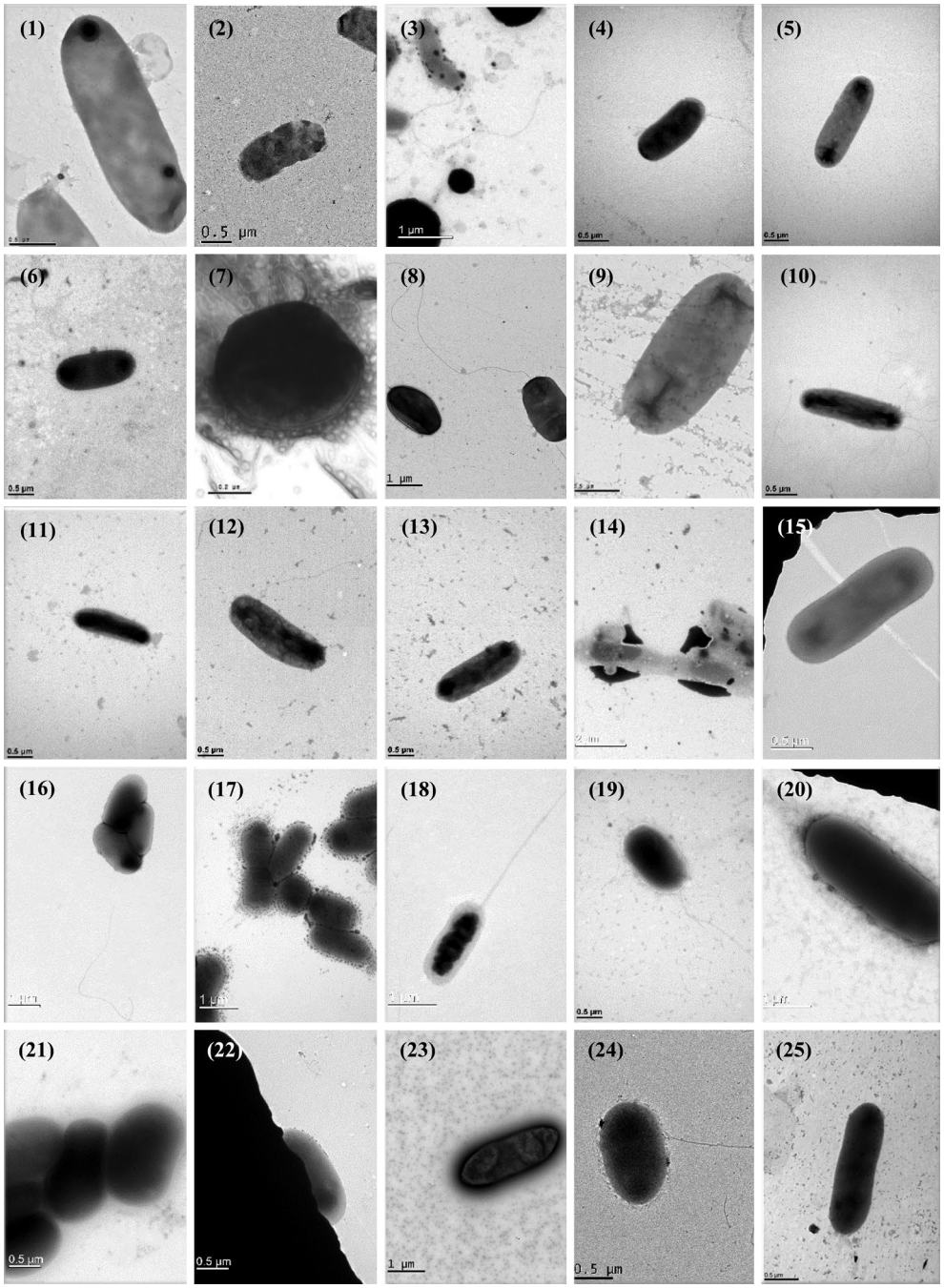

Fig. 1. Transmission electron micrographs of cells of the species in the order *Alteromonadales*, *Chromatiales* and *Enterobacterales* belonging to the class *Gammaproteobacteria* in this study. Strain: 1, IMCC34138; 2, KYW1359; 3, HMF8561; 4, LPB0188; 5, LPB0300; 6, LPB0182; 7, IMCC34178; 8, KYW1326; 9, IMCC34174; 10, LPB0308; 11, LPB0180; 12, LPB0184; 13, LPB0186; 14, HMF8517; 15, BT3507; 16, BT3301; 17, BR3501; 18, BC3307; 19, LPB0191; 20, BC3202; 21, BT2501; 22, BT3409; 23, KYW1346; 24, MMS17-GJ020; 25, CAU 1471.

JAMM 1525^{T} (AB330883; 100%), *Amphritea japonica* JAMM 1866^{T} (AB330881; 99.42%), *Marinobacterium stanieri* DSM 7027^{T} (AB021367; 98.85%), *Marinomonas communis* LMG 2864^{T} (DQ011528; 98.90%), *Acinetobacter beijerinckii* CIP 110307^{T} (APQL01000005; 99.90%), *Acinetobacter guillouiae* CIP 63.46^{T} (APOS 01000028; 99.90%), *Acinetobacter indicus* CIP 110367^{T} (KI530754; 99.78%), *Acinetobacter johnsonii* CIP 64.6^{T} (APON01000005; 99.60%), *Acinetobacter tjernbergiae* DSM 14971^{T} (ARFU01000016; 99.30%), *Acinetobacter towneri* DSM 14962^{T} (APPY01000064; 99.60%), *Acinetobacter ursingii* DSM 16037^{T} (AIEA01000080; 99.60%),

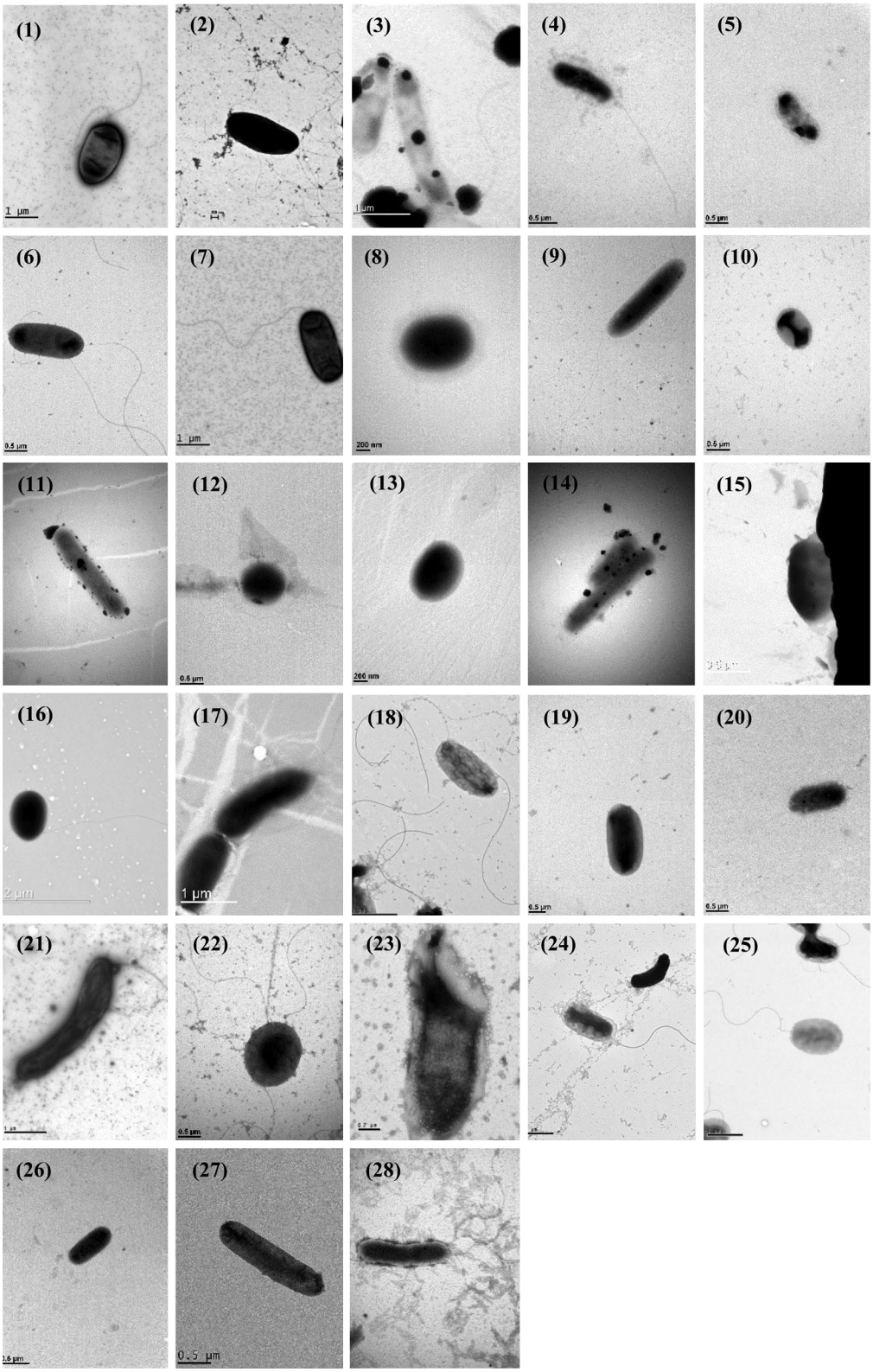

Fig. 2. Transmission electron micrographs of cells of the species in the order *Oceanospirillales*, *Pseudomonadales*, *Vibrionales* and *Xanthomonadales* belonging to the class *Gammaproteobacteria* in this study. Strain: 1, KYW1415; 2, GH3-6; 3, HMF9021; 4, LPB0189; 5, LPB0185; 6, LPB0208; 7, KYW1404; 8, 16_S3_M11; 9, 16_H2_V4; 10, LPB0181; 11, 16_H3_M12; 12, 16_H2_M14; 13, 16_H6_M1; 14, 16_H5_M7; 15, BC3402; 16, Gsoli 1532; 17, BC3406; 18, IMCC34228; 19, LPB0174; 20, LPB0190; 21, IMCC34186; 22, LPB0202; 23, IMCC34213; 24, IMCC34225; 25, IMCC34148; 26, 17J9-2; 27, MMS17-SY254; 28, 16H1E7.

Acinetobacter vivianii NIPH 2168^T (KB850133; 99.93%), *Pseudomonas mohnii* DSM 18327^T (FNRV01000001; 99.40%), *Pseudomonas nitritireducens* WZBFD3-5A2^T (HM246143; 99.65%), *Aliivibrio fischeri* JCM 18803^T (BBEE01000115; 100%), *Photobacterium damselae* subsp. *piscicida* NCIMB 2058^T (X78105; 99.92%), *Vibrio comitans* GHG21^T (DQ922915; 99.33%), *Vibrio hispanicus* LMG 13240^T (AY254039; 99.50%), *Vibrio nereis* DSM 19584^T (LHPJ01000025; 99.71%), *Vibrio penaeicida* DSM 14398^T (AJ421444; 99.30%), *Vibrio scophthalmi* LMG 19158^T (AFWE01000105; 99.90%), *Vibrio tritonius* JCM 16456^T (AP014635; 99.10%), *Lysobacter ximonensis* XM415^T (EU237492; 100%), *Pseudoxanthomonas kaohsiungensis* J36^T (AY650027; 99.10%) and *Stenotrophomonas acidaminiphila* JCM 13310^T (LDJO01000053; 100%).

Phylogenetic analyses showed that isolated strains formed a robust clade with the most closely related species in the orders *Alteromonadales*, *Chromatiales*, *Enterobacterales* (Fig. 3), *Oceanospirillales*, *Pseudomonadales*, *Vibrionales*, and *Xanthomonadales* (Fig. 4). There are no official report of these 53 strains in Korea. Therefore, these 53 strains in the class *Gammaproteobacteria* are new records to Korea: 13 species in the order *Alteromonadales*, 1 species in the order *Chromatiales*, 11 species in the order *Enterobacterales*, 7 species in the order *Oceanospirillales*, 10 species in the order *Pseudomonadales*, 8 species in the order *Vibrionales*, and 3 species in the order *Xanthomonadales*.

Species Descriptions

Agarivorans gilvus IMCC34138

Cells are Gram-staining-negative, non-flagellated, and rod shaped. Colonies are cream to yellow color, circular, convex, and entire margin after incubation on R2A at 25°C for 3 days under aerobic conditions. Strain is positive for esculin hydrolysis, gelatinase, cytochrome oxidase, and utilization of glucose, mannitol, maltose, malic acid, and trisodium citrate; but negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, urease, β-galactosidase, and utilization of arabinose, mannose, *N*-acetyl-glucosamine, adipic acid, potassium gluconate, capric acid, and phenylacetic acid in API 20NE. Strain IMCC34138 (=NIBRBAC000501087) was isolated from tidal flat from Jangbong-do, Incheon, Republic of Korea.

Thalassotalea loyana KYW1359

Cells are Gram-staining-negative, non-flagellated, and rod shaped. Colonies are cream color, circular, convex, and smooth after incubation on MA at 25°C for 3 days. Strain is positive for esculin hydrolysis, β-galactosidase, and cytochrome oxidase; but negative for nitrate reduction, glucose fermentation, indole production, arginine dihydrolase, urease, gelatinase, and utilization of glucose, arabinose, mannose, mannitol, *N*-acetyl-glucosamine, maltose, potassium gluconate, malic acid, capric acid, adipic acid, trisodium citrate, and phenylacetic acid. Strain KYW1359 (=NIBRBAC000501128) was isolated from seawater from Gwangyang, Jeollanam-do, Republic of Korea.

Idiomarina baltica HMF8561

Cells are Gram-staining-negative, flagellated, and rod shaped. Colonies are beige color, circular, convex, and smooth after incubation on MA at 30°C for 3 days. Strain is positive for esculin hydrolysis and cytochrome oxidase; but negative for nitrate reduction, indole production, arginine dihydrolase, urease, gelatinase, β-galactosidase, glucose fermentation, and utilization of glucose, arabinose, mannose, mannitol, *N*-acetyl-glucosamine, maltose, potassium gluconate, malic acid, trisodium citrate, capric acid, adipic acid, and phenylacetic acid. Strain HMF8561 (=NIBRBAC000501173) was isolated from a salt pond from Sinan-gun, Jeollanam-do, Republic of Korea.

Idiomarina donghaiensis LPB0188

Cells are Gram-staining-negative, flagellated, and rod shaped. Colonies are cream color, circular, convex, and smooth after incubation on MA at 25°C for 3 days under aerobic conditions. Strain is positive for gelatinase (weak) and cytochrome oxidase; but negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, esculin hydrolysis, β-galactosidase, urease, and utilization of glucose, arabinose, mannose, mannitol, *N*-acetyl-glucosamine, maltose, potassium gluconate, adipic acid, malic acid, capric acid, trisodium citrate, and phenylacetic acid in API 20NE. Strain LPB0188 (=NIBRBAC000501016) was isolated from seawater from Munseom, Jeju-do, Republic of Korea.

Marinobacter szutsaonensis LPB0300

Cells are Gram-staining-negative, non-flagellated, and rod shaped. Colonies are cream color, circular, convex, and smooth after incubation on MA at 25°C for 3 days under aerobic conditions. Strain is positive for nitrate reduction; but negative for indole production, glucose fermentation, arginine dihydrolase, esculin hydrolysis, β-galactosidase, gelatinase, urease, cytochrome oxidase, and utilization of glucose, arabinose, mannose, mannitol, *N*-acetyl-glucosamine, maltose, potassium gluconate, adipic acid, malic acid, capric acid, trisodium citrate, and phenylacetic acid in API 20NE. Strain LPB0300 (=NI-

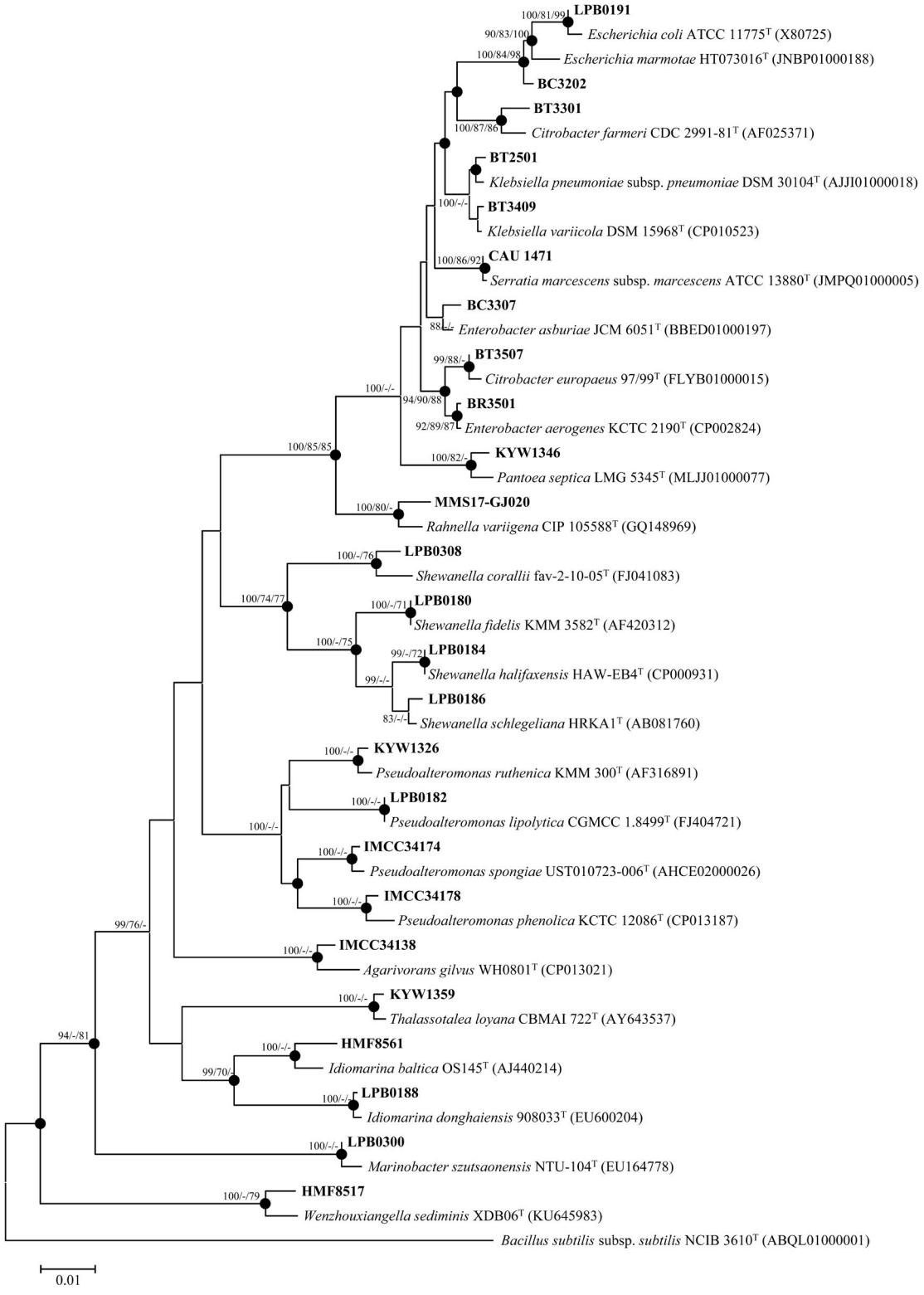

Fig. 3. Neighbor-joining phylogenetic tree (NJ) based on nearly complete 16S rRNA gene sequences showing the relationships between 25 isolated strains and their most closely related from the order *Alteromonadales*, *Chromatiales* and *Enterobacterales* of the class *Gammaproteobacteria*. Dots indicate that the corresponding nodes that were also recovered in the trees created with the maximum likelihood (ML) and maximum parsimony (MP) algorithms. Bootstrap values are indicated as percentages of 1000 resampled datasets, when greater than 70% (NJ/ML/MP). Bar, 0.01 substitutions per nucleotide position. *Bacillus subtilis* subsp. *subtilis* NCIB 3610^T (ABQL01000001) was used as the outgroup.

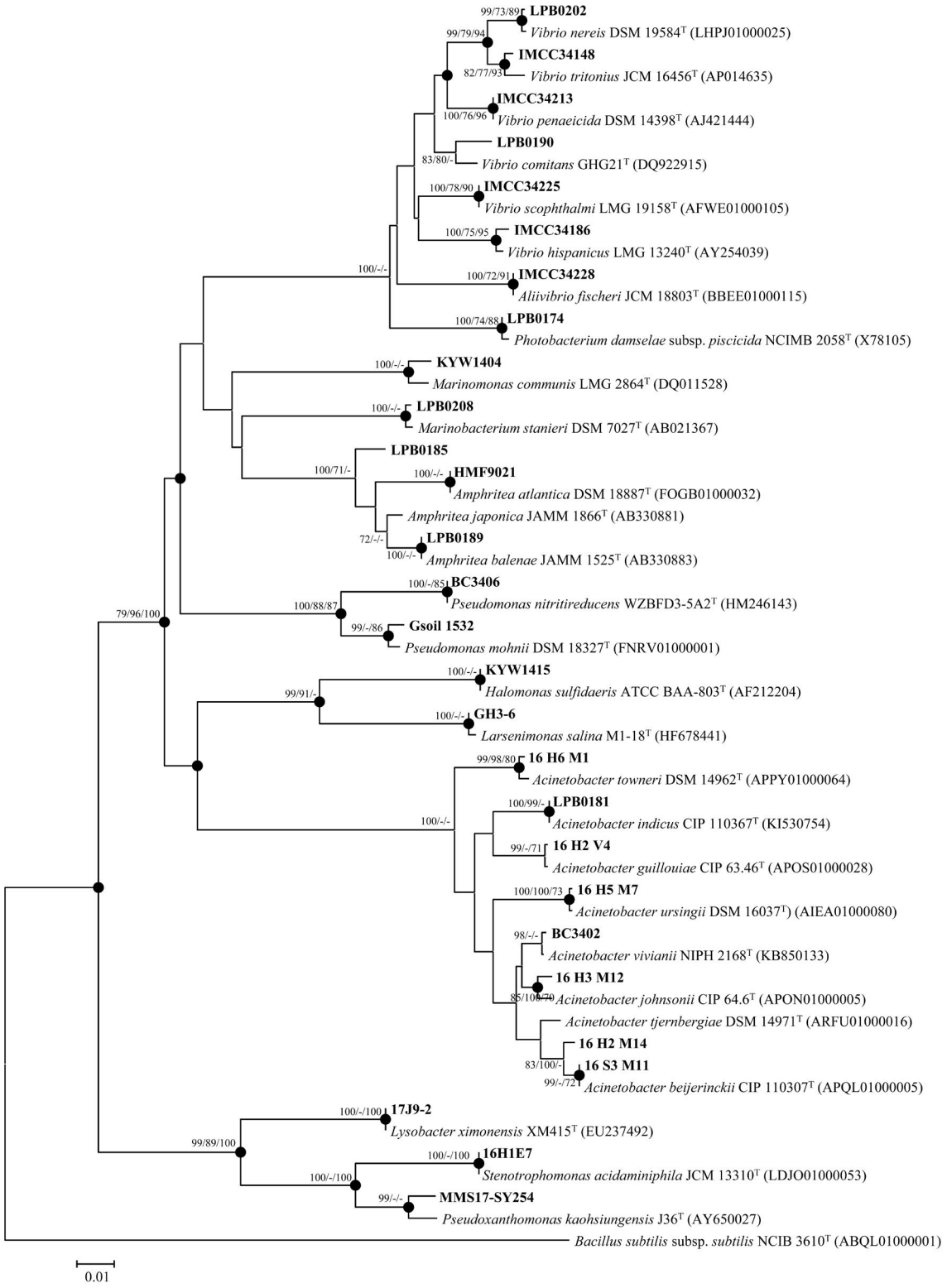

Fig. 4. Neighbor-joining phylogenetic tree (NJ) based on nearly complete 16S rRNA gene sequences showing the relationships between 28 isolated strains and their most closely related from the order *Oceanospirillales*, *Pseudomonadales*, *Vibrionales* and *Xanthomonadales* of the class *Gammaproteobacteria*. Dots indicate that the corresponding nodes that were also recovered in the trees created with the maximum likelihood (ML) and maximum parsimony (MP) algorithms. Bootstrap values are indicated as percentages of 1000 resampled datasets, when greater than 70% (NJ/ML/MP). Bar, 0.01 substitutions per nucleotide position. *Bacillus subtilis* subsp. *subtilis* NCIB 3610^T (ABQL01000001) was used as the outgroup.

BRBAC000501021) was isolated from seawater from Incheon, Ganghwa-do, Republic of Korea.

***Pseudoalteromonas lipolytica* LPB0182**

Cells are Gram-staining-negative, non-flagellated, and rod shaped. Colonies are cream color, circular, convex, and smooth after incubation on MA at 25°C for 3 days under aerobic conditions. Strain is positive for nitrate reduction, indole production, glucose fermentation, esculin hydrolysis, gelatinase, β-galactosidase, cytochrome oxidase, and utilization of arabinose and maltose; but negative for arginine dihydrolase, urease, and utilization of glucose, mannose, mannitol, *N*-acetyl-glucosamine, potassium gluconate, adipic acid, malic acid, capric acid, trisodium citrate, and phenylacetic acid in API 20NE. Strain LPB0182 (=NIBRBAC000501198) was isolated from seawater from Munseom, Jeju-do, Republic of Korea.

***Pseudoalteromonas phenolica* IMCC34178**

Cells are Gram-staining-negative, flagellated, and cocci shaped. Colonies are beige to brown color, circular, convex, and entire margin after incubation on R2A at 25°C for 3 days under aerobic conditions. Strain 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, adipic acid, capric acid, malic acid, trisodium citrate, and phenylacetic acid in API 20NE. Strain IMCC34178 (=NIBRBAC000501097) was isolated from tidal flat from Jangbong-do, Incheon, Republic of Korea.

***Pseudoalteromonas ruthenica* KYW1326**

Cells are Gram-staining-negative, flagellated, and rod shaped. Colonies are cream color, circular, flat, and smooth after incubation on MA at 25°C for 3 days. Strain is positive for nitrate reduction, glucose fermentation, esculin hydrolysis, gelatinase, β-galactosidase, cytochrome oxidase, and utilization of glucose, arabinose, mannose, *N*-acetyl-glucosamine, maltose, potassium gluconate, and malic acid; but negative for indole production, arginine dihydrolase, urease, and utilization of mannitol, capric acid, adipic acid, trisodium citrate, and phenylacetic acid. Strain KYW1326 (=NIBRBAC000501126) was isolated from seawater from Gwangyang, Jeollanam-do, Republic of Korea.

***Pseudoalteromonas spongiae* IMCC34174**

Cells are Gram-staining-negative, non-flagellated, and rod shaped. Colonies are slightly orange color, circular, raised, and entire margin after incubation on R2A at 25°C for 3 days under aerobic conditions. Strain 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, adipic acid, capric acid, malic acid, trisodium citrate, and phenylacetic acid in API 20NE. Strain IMCC34174 (=NIBRBAC000501098) was isolated from tidal flat from Jangbong-do, Incheon, Republic of Korea.

***Shewanella corallii* LPB0308**

Cells are Gram-staining-negative, flagellated, and rod shaped. Colonies are orange color, circular, convex, and smooth after incubation on MA at 25°C for 3 days under aerobic conditions. Strain is positive for nitrate reduction, arginine dihydrolase (weak), esculin hydrolysis (weak), and utilization of *N*-acetyl-glucosamine and maltose; but negative for indole production, glucose fermentation, β-galactosidase, gelatinase, urease, cytochrome oxidase, and utilization of glucose, arabinose, mannose, mannitol, potassium gluconate, adipic acid, malic acid, capric acid, trisodium citrate, and phenylacetic acid in API 20NE. Strain LPB0308 (=NIBRBAC000501023) was isolated from seawater from Incheon, Ganghwa-do, Republic of Korea.

***Shewanella fidelis* LPB0180**

Cells are Gram-staining-negative, non-flagellated, and rod shaped. Colonies are ivory color, circular, convex, and smooth after incubation on MA at 25°C for 3 days under aerobic conditions. Strain is positive for nitrate reduction, esculin hydrolysis (weak), gelatinase, and cytochrome oxidase; but negative for glucose fermentation, indole production, arginine dihydrolase, urease, β-galactosidase, and utilization of glucose, arabinose, mannose, mannitol, *N*-acetyl-glucosamine, maltose, potassium gluconate, malic acid, capric acid, adipic acid, trisodium citrate, and phenylacetic acid in API 20NE. Strain LPB0180 (=NIBRBAC000501009) was isolated from seawater from Munseom, Jeju-do, Republic of Korea.

***Shewanella halifaxensis* LPB0184**

Cells are Gram-staining-negative, flagellated, and rod shaped. Colonies are cream color, circular, convex, and smooth after incubation on MA at 25°C for 3 days under aerobic conditions. Strain 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, adipic acid, malic acid, capric acid, trisodium citrate, and phenylacetic acid in API 20NE. Strain LPB0184 (=NIBRBAC000501012) was isolated from seawater from Munseom, Jeju-do, Republic of Korea.

***Shewanella schlegeliana* LPB0186**

Cells are Gram-staining-negative, non-flagellated, and rod shaped. Colonies are cream color, circular, convex, and smooth after incubation on MA at 25°C for 3 days under aerobic conditions. Strain is positive for nitrate reduction, esculin hydrolysis (weak), gelatinase, and cytochrome oxidase; but negative for indole production, glucose fermentation, arginine dihydrolase, β-galactosidase, urease, and utilization of glucose, arabinose, mannose, mannitol, *N*-acetyl-glucosamine, maltose, potassium gluconate, adipic acid, malic acid, capric acid, trisodium citrate, and phenylacetic acid in API 20NE. Strain LPB0186 (=NIBRBAC000501014) was isolated from seawater from Munseom, Jeju-do, Republic of Korea.

***Wenzhouxiangella sediminis* HMF8517**

Cells are Gram-staining-negative, non-flagellated, and rod shaped. Colonies are yellow color, circular, convex, and smooth after incubation on MA at 30°C for 3 days. Strain is positive for esculin hydrolysis, gelatinase, and cytochrome oxidase; but negative for nitrate reduction, indole production, arginine dihydrolase, urease, β-galactosidase, glucose fermentation, and utilization of glucose, arabinose, mannose, mannitol, *N*-acetyl-glucosamine, maltose, potassium gluconate, malic acid, trisodium citrate, capric acid, adipic acid, and phenylacetic acid. Strain HMF8517 (=NIBRBAC000501172) was isolated from a salt pond from Sinan-gun, Jeollanam-do, Republic of Korea.

***Citrobacter europaeus* BT3507**

Cells are Gram-staining-negative, flagellated, and rod shaped. Colonies are white color, circular, and convex after incubation on TSA at 37°C for 2 days. Strain is positive for nitrate reduction, glucose fermentation, arginine dihydrolase, β-galactosidase, and utilization of glucose, arabinose, mannose, mannitol, *N*-acetyl-glucosamine, maltose, potassium gluconate, malic acid and trisodium citrate; but negative for indole production, esculin hydrolysis, gelatinase, urease, cytochrome oxidase, and utilization of capric acid, adipic acid, and phenylacetic acid. Strain BC3507 (=NIBRBAC000501139) was isolated from intestines of Russian grayling butterfly (*H. autonoe*) from Jeju, Jeju-do, Republic of Korea.

***Citrobacter farmeri* BT3301**

Cells are Gram-staining-negative, flagellated, and short-rod shaped. Colonies are beige color, circular, and convex after incubation on TSA at 37°C for 2 days. Strain is positive for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, 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, urease, cytochrome oxidase, and utilization of capric acid, adipic acid, and phenylacetic acid. Strain BC3301 (=NIBRBAC000501140) was isolated from intestines of Russian grayling butterfly (*H. autonoe*) from Jeju, Jeju-do, Republic of Korea.

***Enterobacter aerogenes* BR3501**

Cells are Gram-staining-negative, flagellated, and cocci or ovoid shaped. Colonies are white color, circular, and convex after incubation on R2A at 37°C for 2 days. Strain is positive for nitrate reduction, glucose fermentation, esculin hydrolysis, β-galactosidase, and utilization of glucose, arabinose, mannose, mannitol, *N*-acetyl-glucosamine, maltose, potassium gluconate, malic acid, trisodium citrate, capric acid, adipic acid, and phenylacetic acid; but negative for indole production, arginine dihydrolase, gelatinase, urease, and cytochrome oxidase. Strain BC3501 (=NIBRBAC000501141) was isolated from intestines of Russian grayling butterfly (*H. autonoe*) from Jeju, Jeju-do, Republic of Korea.

***Enterobacter asburiae* BC3307**

Cells are Gram-staining-negative, flagellated, and rod shaped. Colonies are pink color, circular and convex after incubation on MacConkey at 37°C for 2 days. Strain is positive for nitrate reduction, indole production, arginine dihydrolase, glucose fermentation, esculin hydrolysis, gelatinase, β-galactosidase, and utilization of glucose, arabinose, mannose, mannitol, *N*-acetyl-glucosamine, maltose, potassium gluconate, adipic acid, malic acid, trisodium citrate, and phenylacetic acid; but negative for cytochrome oxidase, and utilization of capric acid in API 20NE. Strain BC3307 (=NIBRBAC000501142) was isolated from intestine of Russian grayling butterfly (*H. autonoe*) from Jeju, Jeju-do, Republic of Korea.

***Escherichia coli* LPB0191**

Cells are Gram-staining-negative, flagellated, and rod shaped. Colonies are cream color, circular, convex, and smooth after incubation on LB at 25°C for 3 days under aerobic condition. Strain is positive for nitrate reduction, indole production, glucose fermentation, β-galactosidase, and utilization of glucose, arabinose, mannose, mannitol,

N-acetyl-glucosamine, potassium gluconate, and maltose; but negative for arginine dihydrolase, esculin hydrolysis, gelatinase, urease, cytochrome oxidase, and utilization of adipic acid, malic acid, capric acid, trisodium citrate, and phenylacetic acid in API 20NE. Strain LPB0191 (=NIBRBAC000501300) was isolated from intestine of mouse (*M. musculus*) from Seongbuk-gu, Seoul, Republic of Korea.

***Escherichia marmotae* BC3202**

Cells are Gram-staining-negative, non-flagellated, and rod shaped. Colonies are magenta color, circular, and convex after incubation on MacConkey at 37°C for 2 days. Strain is positive for nitrate reduction, indole production, arginine dihydrolase, glucose fermentation, esculin hydrolysis, β-galactosidase, and utilization of glucose, arabinose, mannose, mannitol, *N*-acetyl-glucosamine, maltose, potassium gluconate, malic acid, and phenylacetic acid; but negative for gelatinase, urease, cytochrome oxidase, and utilization of capric acid, adipic acid, and trisodium citrate. Strain BC3202 (=NIBRBAC000501143) was isolated from intestines of Russian grayling butterfly (*H. autonoe*) from Jeju, Jeju-do, Republic of Korea.

***Klebsiella pneumoniae* subsp. *pneumoniae* BT2501**

Cells are Gram-staining-negative, non-flagellated, and cocci or ovoid shaped. Colonies are white color, circular, and convex after incubation on TSA at 20°C for 2 days. Strain is positive for nitrate reduction, glucose fermentation, esculin hydrolysis, urease, β-galactosidase, and utilization of glucose, arabinose, mannose, mannitol, *N*-acetyl-glucosamine, maltose, potassium gluconate, malic acid, trisodium citrate, capric acid, adipic acid, and phenylacetic acid; but negative for indole production, arginine dihydrolase, gelatinase and cytochrome oxidase. Strain BT2501 (=NIBRBAC000501144) was isolated from intestines of Russian grayling butterfly (*H. autonoe*) from Jeju, Jeju-do, Republic of Korea.

***Klebsiella variicola* BT3409**

Cells are Gram-staining-negative, non-flagellated, and rod shaped. Colonies are white color, circular, convex, and massive after incubation on TSA at 37°C for 2 days. Strain is positive for nitrate reduction, glucose fermentation, esculin hydrolysis, urease, β-galactosidase, and utilization of glucose, arabinose, mannose, mannitol, *N*-acetyl-glucosamine, maltose, potassium gluconate, malic acid, trisodium citrate, capric acid, adipic acid, and phenylacetic acid; but negative for indole production, arginine dihydrolase, gelatinase and cytochrome oxidase. Strain BT3409 (=NIBRBAC000501145) was isolated from intestines of Russian grayling butterfly (*H. autonoe*) from Jeju, Jeju-do, Republic of Korea.

***Pantoea septica* KYW1346**

Cells are Gram-staining-negative, non-flagellated, and rod shaped. Colonies are yellow color, circular, convex, and smooth after incubation on MA at 25°C for 3 days. Strain is positive for nitrate reduction, glucose fermentation, 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 indole production, arginine dihydrolase, urease, gelatinase, cytochrome oxidase, and utilization of capric acid, adipic acid, and phenylacetic acid. Strain KYW1346 (=NIBRBAC000501127) was isolated from seawater from Gwangyang, Jeollanam-do, Republic of Korea.

***Rahnella variigena* MMS17-GJ020**

Cells are Gram-staining-negative, flagellated, and rod shaped. Colonies are pale yellow color, circular, convex, smooth, and glistening after incubation on ISP2 at pH5 at 30°C for 5 days under aerobic conditions. Strain is positive for nitrate reduction, glucose fermentation, esculin hydrolysis, β-galactosidase, and utilization of glucose, mannose, mannitol, *N*-acetyl-glucosamine, maltose, potassium gluconate, malic acid, and trisodium citrate; but negative for indole production, arginine dihydrolase, urease, gelatinase, cytochrome oxidase, and utilization of arabinose, capric acid, adipic acid, and phenylacetic acid in API 20NE. Strain MMS17-GJ020 (=NIBRBAC000501193) was isolated from soil from Daejeon, Republic of Korea.

***Serratia marcescens* subsp. *marcescens* CAU 1471**

Cells are Gram-staining-negative, flagellated, and rod shaped. Colonies are cream color, circular, convex, opaque, and shiny after incubation on BHI at 30°C for 2 days under aerobic conditions. Strain is positive for esculin hydrolysis, and utilization of glucose, mannose, mannitol, and maltose; but negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, urease, gelatinase, β-galactosidase, cytochrome oxidase, and utilization of arabinose, *N*-acetyl-glucosamine, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid in API 20NE. Strain CAU 1471 (=NIBRBAC000501234) was isolated from urine from Kyunghee University Hospital, Dongdaemun-gu, Seoul, Republic of Korea.

***Halomonas sulfidaeris* KYW1415**

Cells are Gram-staining-negative, flagellated, and short rod shaped. Colonies are pale yellow color, circular, en-

tire margin, opaque, and smooth after incubation on MA at 25°C for 3 days. Strain is positive for cytochrome oxidase; but negative for nitrate reduction, glucose fermentation, indole production, arginine dihydrolase, urease, gelatinase, esculin hydrolysis, β-galactosidase, and utilization of glucose, arabinose, mannose, mannitol, *N*-acetyl-glucosamine, maltose, potassium gluconate, malic acid, capric acid, adipic acid, trisodium citrate, and phenylacetic acid. Strain KYW1415 (=NIBRBAC000501130) was isolated from seawater from Gwangyang, Jeollanam-do, Republic of Korea.

***Larsenimonas salina* GH3-6**

Cells are Gram-staining-negative, flagellated, and rod shaped. Colonies are light yellow color, irregular, and convex with entire margin after incubation on MA at 30°C for 5 days under aerobic conditions. Strain is positive for esculin hydrolysis; but negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, urease, gelatinase, β-galactosidase, cytochrome oxidase, and utilization of glucose, arabinose, mannose, mannitol, *N*-acetyl-glucosamine, maltose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid in API 20NE. Strain GH3-6 (=NIBRBAC000501043) was isolated from rhizosphere from Ganghwa-gun, Incheon, Republic of Korea.

***Amphritea atlantica* HMF9021**

Cells are Gram-staining-negative, flagellated, and rod shaped. Colonies are white color, circular, convex, and smooth after incubation on MA at 30°C for 3 days. Strain is positive for utilization of malic acid and cytochrome oxidase; but negative for nitrate reduction, indole production, arginine dihydrolase, esculin hydrolysis, urease, gelatinase, β-galactosidase, glucose fermentation, and utilization of glucose, arabinose, mannose, mannitol, *N*-acetyl-glucosamine, maltose, potassium gluconate, malic acid, trisodium citrate, capric acid, adipic acid, and phenylacetic acid. Strain HMF9021 (=NIBRBAC000501174) was isolated from sea sand from Boseong-gun, Jeollanam-do, Republic of Korea.

***Amphritea balenae* LPB0189**

Cells are Gram-staining-negative, flagellated, and rod shaped. Colonies are cream color, circular, convex, and smooth after incubation on MA at 25°C for 3 days under aerobic conditions. Strain is positive for cytochrome oxidase; but negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, esculin hydrolysis, β-galactosidase, gelatinase, urease, and utilization of glucose, arabinose, mannose, mannitol, *N*-acetyl-glucosamine, maltose, potassium gluconate, adipic acid, malic acid, capric acid, trisodium citrate, and phenylacetic acid in API 20NE. Strain LPB0189 (=NIBRBAC000501017) was isolated from seawater from Munseom, Jeju-do, Republic of Korea.

***Amphritea japonica* LPB0185**

Cells are Gram-staining-negative, non-flagellated, and rod shaped. Colonies are cream color, circular, convex, and smooth after incubation on MA at 25°C for 3 days under aerobic conditions. Strain is positive for nitrate reduction and cytochrome oxidase; but negative for indole production, glucose fermentation, arginine dihydrolase, esculin hydrolysis, gelatinase, β-galactosidase, urease, and utilization of glucose, arabinose, mannose, mannitol, *N*-acetyl-glucosamine, maltose, potassium gluconate, adipic acid, malic acid, capric acid, trisodium citrate, and phenylacetic acid in API 20NE. Strain LPB0185 (=NIBRBAC000501013) was isolated from seawater from Munseom, Jeju-do, Republic of Korea.

***Marinobacterium stanieri* LPB0208**

Cells are Gram-staining-negative, flagellated, and rod shaped. Colonies are cream color, circular, convex, and smooth after incubation on MA at 25°C for 3 days under aerobic conditions. Strain is negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, esculin hydrolysis, β-galactosidase, gelatinase, urease, cytochrome oxidase, and utilization of glucose, arabinose, mannose, mannitol, *N*-acetyl-glucosamine, maltose, potassium gluconate, adipic acid, malic acid, capric acid, trisodium citrate, and phenylacetic acid in API 20NE. Strain LPB0208 (=NIBRBAC000501019) was isolated from seawater from Incheon, Ganghwa-do, Republic of Korea.

***Marinomonas communis* KYW1404**

Cells are Gram-staining-negative, flagellated, and rod shaped. Colonies are ivory color, circular, flat, opaque, and smooth after incubation on MA at 25°C for 3 days. Strain is positive for esculin hydrolysis, β-galactosidase, and cytochrome oxidase; but negative for nitrate reduction, glucose fermentation, indole production, arginine dihydrolase, urease, gelatinase, and utilization of glucose, arabinose, mannose, mannitol, *N*-acetyl-glucosamine, maltose, potassium gluconate, malic acid, capric acid, adipic acid, trisodium citrate, and phenylacetic acid. Strain KYW1404 (=NIBRBAC000501129) was isolated from seawater from Gwangyang, Jeollanam-do, Republic of Korea.

***Acinetobacter beijerinckii* 16_S3_M11**

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

rod shaped. Colonies are cream color, circular, and convex after incubation on R2A at 30°C for 2 days under aerobic conditions. Strain is positive for utilization of capric acid, malic acid, and trisodium citrate; but negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, urease, esculin hydrolysis, gelatinase, β-galactosidase, cytochrome oxidase, and utilization of glucose, arabinose, mannose, mannitol, *N*-acetyl-glucosamine, maltose, potassium gluconate, adipic acid, and phenylacetic acid in API 20NE. Strain 16_S3_M11 (=NIBRBAC000501074) was isolated from soil from Yeosu, Gyeonggi-do, Republic of Korea.

***Acinetobacter guillouiae* 16_H2_V4**

Cells are Gram-staining-negative, non-flagellated, and rod shaped. Colonies are pale white color, circular, convex, and glistening after incubation on R2A at 30°C for 2 days under aerobic conditions. Strain is positive for nitrate reduction, and utilization of glucose, mannose, *N*-acetyl-glucosamine, and potassium gluconate; but negative for indole production, glucose fermentation, arginine dihydrolase, urease, esculin hydrolysis, gelatinase, β-galactosidase, cytochrome oxidase, and utilization of arabinose, mannitol, maltose, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid in API 20NE. However, utilization pf maltose showed both positive and negative activity. Strain 16_H2_V4 (=NIBRBAC000501072) was isolated from manure from Guri, Gyeonggi-do, Republic of Korea.

***Acinetobacter indicus* LPB0181**

Cells are Gram-staining-negative, non-flagellated, and cocci shaped. Colonies are cream color, circular, convex, and smooth after incubation on MA at 25°C for 3 days under aerobic conditions. Strain is positive for utilization of adipic acid; but negative for nitrate reduction, esculin hydrolysis, gelatinase, glucose fermentation, indole production, arginine dihydrolase, urease, β-galactosidase, cytochrome oxidase, and utilization of glucose, arabinose, mannose, mannitol, *N*-acetyl-glucosamine, maltose, potassium gluconate, malic acid, capric acid, trisodium citrate. and phenylacetic acid in API 20NE. Strain LPB0181 (=NIBRBAC000501010) was isolated from seawater from Incheon, Ganghwa-do, Republic of Korea.

***Acinetobacter johnsonii* 16_H3_M12**

Cells are Gram-staining-negative, non-flagellated, and rod shaped. Colonies are white color, circular, raised, and entire margin after incubation on R2A at 30°C for 3 days under aerobic conditions. Strain is positive for urease, and utilization of capric acid, malic acid, and trisodium citrate (waek); but negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, esculin hydrolysis, gelatinase, β-galactosidase, cytochrome oxidase, and utilization of glucose, arabinose, mannose, mannitol, *N*-acetyl-glucosamine, maltose, adipic acid, potassium gluconate, and phenylacetic acid in API 20NE. Strain 16_H3_M12 (=NIBRBAC000501071) was isolated from soil from Seongdong-gu, Seoul, Republic of Korea.

***Acinetobacter tjernbergiae* 16_H2_M14**

Cells are Gram-staining-negative, non-flagellated, and cocci shaped. Colonies are cream color, circular, and convex after incubation on R2A at 30°C for 3 days under aerobic conditions. Strain is positive for nitrate reduction, arginine dihydrolase, gelatinase, and utilization of glucose, arabinose, mannose, mannitol, *N*-acetyl-glucosamine, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid; but negative for indole production, glucose fermentation, urease, esculin hydrolysis, β-galactosidase, and cytochrome oxidase in API 20NE. However, utilization of maltose showed both positive and negative activity. Strain 16_H2_M14 (=NIBRBAC000501073) was isolated from manure from Guri, Gyeonggi-do, Republic of Korea.

***Acinetobacter towneri* 16_H6_M1**

Cells are Gram-staining-negative, non-flagellated, and cocci shaped. Colonies are white color, circular, and convex after incubation on R2A at 30°C for 3 days under aerobic condition. Strain is positive for nitrate reduction, esculin hydrolysis, gelatinase, β-galactosidase, and utilization of glucose, mannose, *N*-acetyl-glucosamine, maltose, capric acid, malic acid, and trisodium citrate; but negative for indole production, glucose fermentation, arginine dihydrolase, urease, cytochrome oxidase, and utilization of arabinose, mannitol, potassium gluconate, adipic acid, and phenylacetic acid in API 20NE. Strain 16_H6_M1 (NIBRBAC000501076) was isolated from soil from Mapo-gu, Seoul, Republic of Korea.

***Acinetobacter ursingii* 16_H5_M7**

Cells are Gram-staining-negative, non-flagellated, and rod shaped. Colonies are white color, circular, and flat after incubation on R2A at 30°C for 3 days under aerobic conditions. Strain is positive for urease, and utilization of capric acid, adipic acid, malic acid, and trisodium citrate; but negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, esculin hydrolysis, gelatinase, β-galactosidase, cytochrome oxidase, and utilization of glucose, arabinose, mannose, mannitol, *N*-acetyl-glucosamine, maltose, potassium gluconate, and phenylacetic acid in API 20NE. Strain 16_H5_M7 (=NI-

BRBAC000501075) was isolated from soil from Mapo-gu, Seoul, Republic of Korea.

***Acinetobacter vivianii* BC3402**

Cells are Gram-staining-negative, non-flagellated, and cocci or ovoid shaped. Colonies are pink color, circular, and convex after incubation on MacConkey at 37°C for 2 days. Strain is positive for esculin hydrolysis, gelatinase, and utilization of capric acid, adipic acid, malic acid, trisodium citrate and phenylacetic acid; but negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, urease, β-galactosidase, cytochrome oxidase, and utilization of glucose, arabinose, mannose, mannitol, *N*-acetyl-glucosamine, maltose and potassium gluconate. Strain BC3402 (=NIBRBAC000501137) was isolated from intestines of Russian grayling butterfly (*H. autonoe*) from Jeju, Jeju-do, Republic of Korea.

***Pseudomonas mohnii* KA-176**

Cells are Gram-staining-negative, flagellated, and oval shaped. Colonies are cream color, circular, and convex after incubation on R2A at 30°C for 2 days under aerobic conditions. Strain is positive for nitrate reduction, arginine dihydrolase, gelatinase, cytochrome oxidase, and utilization of glucose, arabinose, mannose, *N*-acetyl-glucosamine, potassium gluconate, capric acid, malic acid, trisodium citrate, and phenylacetic acid; but negative for indole production, glucose fermentation, urease, esculin hydrolysis, β-galactosidase, and utilization of mannitol, maltose, and adipic acid in API 20NE. Strain KA-176 (=NIBRBAC000500996) was isolated from soil from Pocheon, Gyeonggi-do, Republic of Korea.

***Pseudomonas nitritireducens* BC3406**

Cells are Gram-staining-negative, flagellated, and rod shaped. Colonies are pink color, circular, and convex after incubation on MacConkey at 37°C for 2 days. Strain is positive for nitrate reduction, arginine dihydrolase, esculin hydrolysis, and utilization of glucose, arabinose, mannose, mannitol, *N*-acetyl-glucosamine, maltose, potassium gluconate, malic acid, trisodium citrate, capric acid, adipic acid, and phenylacetic acid; but negative for indole production, glucose fermentation, urease, gelatinase, β-galactosidase, and cytochrome oxidase. Strain BC3406 (=NIBRBAC000501147) was isolated from intestines of Russian grayling butterfly (*H. autonoe*) from Jeju, Jeju-do, Republic of Korea.

***Aliivibrio fischeri* IMCC34228**

Cells are Gram-staining-negative, flagellated, and rod shaped. Colonies are cream to yellow color, circular, convex, and entire margin after incubation on R2A at 25°C for 5 days under aerobic conditions. Strain is positive for nitrate reduction, indole production, glucose fermentation, esculin hydrolysis, cytochrome oxidase, and utilization of glucose, mannitol, potassium gluconate, and malic acid; but negative for arginine dihydrolase, gelatinase, urease, β-galactosidase, and utilization of arabinose, mannose, *N*-acetyl-glucosamine, maltose, adipic acid, capric acid, trisodium citrate, and phenylacetic acid in API 20NE. Strain IMCC34228 (=NIBRBAC000501090) was isolated from seawater from Jeju, Jeju-do, Republic of Korea.

***Photobacterium damselae* subsp. *piscicida* LPB0174**

Cells are Gram-staining-negative, flagellated, and rod shaped. Colonies are translucent, circular, convex, and smooth after incubation on MA at 30°C for 3 days under facultatively anaerobic conditions. Strain is positive for urease and acid production from glucose (weak) and mannose (weak); but negative for indole production, hydrolysis of esculin and gelatin, and acid production from mannitol, lactose, saccharose, maltose, salicin, xylose, arabinose, glycerol, cellobiose, mannose, melezitose, raffinose, sorbitol, rhamnose, and trehalose in API 20A. Strain LPB0174 (=NIBRBAC000501008) was isolated from intestine of sea bass (*L. japonicus*) from Incheon, Ganghwa-do, Republic of Korea.

***Vibrio comitans* LPB0190**

Cells are Gram-staining-negative, flagellated, and rod shaped. Colonies are cream color, circular, convex, and smooth after incubation on MA at 25°C for 3 days under aerobic conditions. Strain is positive for esculin hydrolysis and β-galactosidase; but negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, gelatinase, urease, cytochrome oxidase, and utilization of glucose, arabinose, mannose, mannitol, *N*-acetyl-glucosamine, maltose, potassium gluconate, adipic acid, malic acid, capric acid, trisodium citrate, and phenylacetic acid in API 20NE. Strain LPB0190 (=NIBRBAC000501301) was isolated from seawater from Munseom, Jeju-do, Republic of Korea.

***Vibrio hispanicus* IMCC34186**

Cells are Gram-staining-negative, flagellated, and rod shaped. Colonies are white color, circular, convex, and entire margin after incubation on R15A at 25°C for 3 days under aerobic conditions. Strain is positive for nitrate reduction, arginine dihydrolase, esculin hydrolysis, β-galactosidase, cytochrome oxidase, and utilization of potassium gluconate; but negative for indole production, glucose fermentation, urease, gelatinase, and utilization of glucose, arabinose, mannose, mannitol, *N*-acetyl-glucosamine, maltose, adipic acid, capric acid, malic acid, triso-

dium citrate, and phenylacetic acid in API 20NE. Strain IMCC34186 (=NIBRBAC000501102) was isolated from tidal flat from Jangbong-do, Incheon, Republic of Korea.

***Vibrio neresis* LPB0202**

Cells are Gram-staining-negative, flagellated, and cocci shaped. Colonies are cream color, circular, convex, and smooth after incubation on MA at 25°C for 3 days under aerobic conditions. Strain is negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, esculin hydrolysis, β-galactosidase, gelatinase, urease, cytochrome oxidase, and utilization of glucose, arabinose, mannose, mannitol, *N*-acetyl-glucosamine, maltose, potassium gluconate, adipic acid, malic acid, capric acid, trisodium citrate, and phenylacetic acid in API 20NE. Strain LPB0202 (=NIBRBAC000501018) was isolated from seawater from Incheon, Ganghwa-do, Republic of Korea.

***Vibrio penaeicida* IMCC34213**

Cells are Gram-staining-negative, flagellated, and rod shaped. Colonies are white color, circular, raised, and entire margin after incubation on R17A at 25°C for 3 days under aerobic conditions. Strain is positive for nitrate reduction, indole production, glucose fermentation, gelatinase, β-galactosidase, cytochrome oxidase, and utilization of malic acid; but negative for arginine dihydrolase, esculin hydrolysis, urease, and utilization of glucose, arabinose, mannose, mannitol, *N*-acetyl-glucosamine, maltose, adipic acid, potassium gluconate, capric acid, trisodium citrate, and phenylacetic acid in API 20NE. Strain IMCC34213 (=NIBRBAC000501103) was isolated from beach sand from Wando, Jeollanam-do, Republic of Korea.

***Vibrio scophthalmi* IMCC34225**

Cells are Gram-staining-negative, flagellated, and rod shaped. Colonies are white color, circular, raised, and entire margin after incubation on R2A at 25°C for 5 days under aerobic conditions. Strain is positive for nitrate reduction, indole production, glucose fermentation, esculin hydrolysis, cytochrome oxidase, and utilization of glucose, mannose, *N*-acetyl-glucosamine, maltose, potassium gluconate, and malic acid; but negative for arginine dihydrolase, gelatinase, urease, β-galactosidase, and utilization of arabinose, mannitol, adipic acid, capric acid, trisodium citrate, and phenylacetic acid in API 20NE. Strain IMCC34225 (=NIBRBAC000501104) was isolated from seawater from Gimnyeong, Jeju-do, Republic of Korea.

***Vibrio tritonius* IMCC34148**

Cells are Gram-staining-negative, flagellated, and rod shaped. Colonies are cream color, circular, convex, and entire margin after incubation on R8A at 25°C for 5 days under aerobic conditions. Strain is positive for nitrate reduction, glucose fermentation, esculin hydrolysis, β-galactosidase, and cytochrome oxidase; but negative for indole production, arginine dihydrolase, urease, gelatinase, and utilization of glucose, arabinose, mannose, mannitol, *N*-acetyl-glucosamine, maltose, potassium gluconate, adipic acid, capric acid, malic acid, trisodium citrate, and phenylacetic acid in API 20NE. Strain IMCC34148 (=NIBRBAC000501105) was isolated from tidal flat from Jangbong-do, Incheon, Republic of Korea.

***Lysobacter ximonensis* 17J9-2**

Cells are Gram-staining-negative, flagellated, and rod shaped. Colonies are yellow color, circular, convex, and smooth after incubation on R2A at 25°C for 4 days under aerobic conditions. Strain is positive for arginine dihydrolase, urease, esculin hydrolysis, gelatinase, β-galactosidase, and utilization of glucose, mannose, mannitol, *N*-acetyl-glucosamine, maltose, adipic acid, malic acid, and trisodium citrate; but negative for nitrate reduction, indole production, glucose fermentation, cytochrome oxidase, and utilization of arabinose, capric acid, potassium gluconate, and phenylacetic acid in API 20NE. Strain 17J9-2 (=NIBRBAC000501324) was isolated from soil from Jeju-do, Republic of Korea.

***Pseudoxanthomonas kaohsiungensis* MMS17-SY254**

Cells are Gram-staining-negative, non-flagellated, and rod shaped. Colonies are light yellow color, circular, convex, and smooth with entire margin after incubation on NA at 30°C for 3 days under aerobic conditions. Strain is positive for esculin hydrolysis, β-galactosidase, cytochrome oxidase, and utilization of glucose, arabinose, *N*-acetyl-glucosamine, and maltose; but negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, urease, gelatinase, and utilization of mannose, mannitol, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid in API 20NE. Strain MMS17-SY254 (=NIBRBAC000501210) was isolated from soil from Okdo-myeon, Gunsan, Jeollabuk-do, Republic of Korea.

***Stenotrophomonas acidaminiphila* 16_H1_E7**

Cells are Gram-staining-negative, flagellated, and rod shaped. Colonies are yellow color, circular, and convex after incubation on R2A at 30°C for 1 days under aerobic conditions. Strain is positive for nitrate reduction, esculin hydrolysis, gelatinase, β-galactosidase, cytochrome oxidase, and utilization of glucose, mannose, *N*-acetyl-glucosamine, maltose, and malic acid; but negative for indole

production, glucose fermentation, arginine dihydrolase, urease, and utilization of arabinose, mannitol, potassium gluconate, capric acid, adipic acid, trisodium citrate, and phenylacetic acid in API 20NE. Strain 16_H1_E7 (=NIBRBAC000501080) was isolated from sediment from Namyangju, Gyeonggi-do, Republic of Korea.

Acknowledgements

This work was supported by the project on 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 Evolution 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. 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(3):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(6):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(4):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 natural 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(1):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(2):353-358.

Thompson, J.D., T.J. Gibson, F. Plewniak, F. Jeanmougin and 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(8):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: July 31, 2018
Revised: October 18, 2019
Accepted: October 21, 2019