Journal of Species Research 6(2):101-118, 2017

A report on 57 unrecorded bacterial species in Korea in the classes *Betaproteobacteria* and *Gammaproteobacteria*

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In an investigation of indigenous prokaryotic species in Korea, a total of 57 bacterial strains assigned to the classes *Betaproteobacteria* and *Gammaproteobacteria* were isolated from diverse environments. Samples were collected from fresh water, natural caves, soil, paddy fields, lakes, sea water, jeotgal (fermented seafood), salt flats, soil from abandoned mines, plant roots, digestive organs of both Japanese crested ibis (*Nipponia nippon*) and Burmese python (*Python molurus bivittatus*) and tidal flats. From the high 16S rRNA gene sequence similarity (>98.7%) and formation of robust phylogenetic clades with closely related species, it was determined that each strain belonged to an independent and predefined bacterial species within either the *Betaproteobacteria* or *Gammaproteobacteria*. There is no official report or publication that describes these 57 proteobacterial species in Korea. Overall, in the class *Betaproteobacteria* there were 16 species in 12 genera of 4 families in the order *Burkholderiales* and two species in two genera of one family in the order *Neisseriales*. Within the class *Gammaproteobacteia*, there were five species in four genera of four families in the order *Alteromonadales*, 12 species in 11 genera of one family in the order *Enterobacteriales*, four species in four genera of three families in the order *Oceanospirillales*, 11 species in four genera of two families in the order *Pseudomonadales*, two species in the order *Vibrionales* and five species in five genera of one family in the order *Xanthomonadales*. Gram reaction, colony and cell morphology, basic biochemical characteristics, isolation source and strain IDs are described in the species description section.

Keywords: 16S rRNA, Bacterial diversity, *Betaproteobacteria*, *Gammaproteobacteria*, Unrecorded species

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DOI:10.12651/JSR.2017.6.2.101

Introduction

Recent advances in sequencing techniques, particularly the powerful combination of genome sequencing and bioinformatics-driven analysis of sequence data, have been applied to microbial study and transformed our understanding of the interactions between microbial communities and their niches (Lauber *et al*., 2009; Pas-

cault *et al*., 2014; Loman and Pallen, 2015). Sequencing methods have undergone remarkable innovation, and the transition of NGS techniques and bioinformatics into various fields are imminent. However, current culture-independent approaches have limitations, especially with respect to sequencing depth and resolution of the 16S rRNA gene sequence as well as accurate microbial descriptions from diverse environments. In sequence-based techniques, insufficient sequencing depth leads to match irrelevant populations. Moreover, a major short coming of culture-independent approaches is the impossibility of providing specific metabolic function information of the functions of each bacterial species or strain (Shigematsu *et al*., 2009). Therefore, culture-dependent approaches as putative building blocks for applied science remain important preliminary tools in microbial studies. A major advantage of this approach is that a pure culture can be obtained and deposited in a culture collection as biomaterial. Cultivation, isolation and characterization of these organisms will provide a comprehensive understanding of their physiology and their complex biogeochemical characteristics will be better understood.

The phylum *Proteobacteria* is the largest bacterial phylogenetic clade, comprising 116 validated families according to the List of Prokaryotic Names with Standing in Nomenclature (http://www.bacterio.net/) and is highly abundant in various ecological niches such as soil (36.5%), plants (62%), the atmosphere (77.9%), seawater (57.9%) and freshwater (61.3%) (Shin *et al*., 2015). Moreover, despite being represented by only a minor proportion of this phylum, an imbalanced gut microbiota in mammals was recognized as a potential diagnostic signature of dysbiosis and risk of other diseases related to metabolism and inflammation. Therefore, identifying novel bacterial species in the phylum *Proteobacteria*, describing their phylogenetic relationships and investigating their various functions in different ecological niches are of preeminent importance.

In 2015, we collected diverse environmental samples from the Korean Peninsula and isolated myriads of novel bacterial species and unrecorded bacterial species in Korea. We isolated bacterial species in the classes/phyla *Alphaproteobacteria*, *Betaproteobacteria*, *Gammaproteobacteria*, *Deltaproteobacteria*, *Bacteroidetes*, *Firmicutes*, *Actinobacteria*, *Deinococci* and *Verrucomicrobia*. As a subset of this study, we present a report focused on the description of unrecorded species belonging to the *Betaproteobacteria* and *Gammaproteobacteria*.

Materials and Methods

Various environmental samples were used to isolate various bacterial species, which were collected from fresh water, natural caves, soil, paddy fields, lakes, sea water, jeotgal (fermented seafood), salt flats, abandoned mines, plant roots, tidal flats, and digestive organs of both Japanese crested ibis (*Nipponia nippon*) and Burmese python (*Python molurus bivittatus*). Homogenized samples were separately spread onto diverse culture media, including R2A, Tryptic Soy Agar (TSA), Marine Agar 2216 (MA), 0.1% of diluted MA, Nutrient Agar (NA) and International Streptomyces Project yeast malt extract (ISP2), which were incubated at 25-30°C for 1-10 days. To obtain pure cultures, single colonies were transferred repeatedly to fresh media. All strains were preserved at −80°C in optimal media containing 10-20% (v/v) glycerol as well as lyophilized ampoules.

To confirm morphological, physiological and biochemical characterization, Gram-staining, electron microscopy, and API 20NE tests were performed after cells were grown to a stationary phase. A Gram-staining kit (bioMérieux), was used according to the manufacturer's instructions. To observe detailed cellular morphology and surface characteristics, cellular morphology and cell size were examined by either transmission electron microscopy or scanning electron microscopy. Enzyme oxidase activity was determined by examining for a blue colour change upon exposure to 1% (w/v) tetramethyl-*p*-phenylenediamine (bioMérieux). Amino acid hydrolysis and assimilation reactions were tested using API 20NE test strips (bioMérieux) with API AUX medium, according to the manufacturer's instructions.

For the phylogenetic analysis, amplification of the 16S rRNA gene from strains were performed using a standard PCR method with a PCR pre-mix and two universal bacteria-specific primers (Bac 8F (5′-AGAGTTTGATCCT GGCTCAG-3′) and Bac 1492R (5′-GGYTACCTTGT TACGACTT-3′)) (Lane, 1991). The 16S rRNA gene amplicons were sequenced using a BigDye Terminator Cycle Sequencing Ready Reaction kit (Applied Biosystems), according to the manufacturer's instructions. The gene fragments of the 16S rRNA sequences of strains were then assembled. To determine theirs taxonomic position, 16S rRNA gene sequences were compared with those of closely related strains in the EzTaxon-e server (Kim *et al*., 2012), then those sequences were aligned using the multiple alignment program CLUSTAL W (Thompson *et al*., 1997). Phylogenetic consensus trees were obtained using the programme MEGA version 5 (Tamura *et al*., 2011). The neighbour-joining (NJ) algorithm (Saitou and Nei, 1987) was the primary tool for tree construction. The maximum parsimony (MP) (Kluge and Farris, 1969) and maximum likelihood (ML) algorithms were used for additional comparisons. The robustness of the phylogenetic trees was confirmed by bootstrap analyses based on 1000 random replicates.

Results and Discussion

Strains assigned to the *Betaproteobacteria*

Based on the comparative 16S rRNA gene sequence analyses and phylogeny, 18 strains, designated HMF 3907, HMF4008, HMF4075, JD2, JD5, JD24, JD50, IMCC25601, IMCC25614, IMCC25617, C1-1, C1-11, NJ-1-5, GF5, JF-5, 2015-3, NDH-10 and RDH4 were assigned to the *Betaproteobacteria*. They were all Gram-staining-negative, chemoheterotrophic, non-pigmented and rod-shaped bacteria (Fig. 1). Detailed morphology and physiological characteristics are shown in the species description section.

Strains HMF3907, HMF4008, HMF4075, JD2, JD5, JD24, JD50, IMCC25601, IMCC25614, IMCC25617, C1-

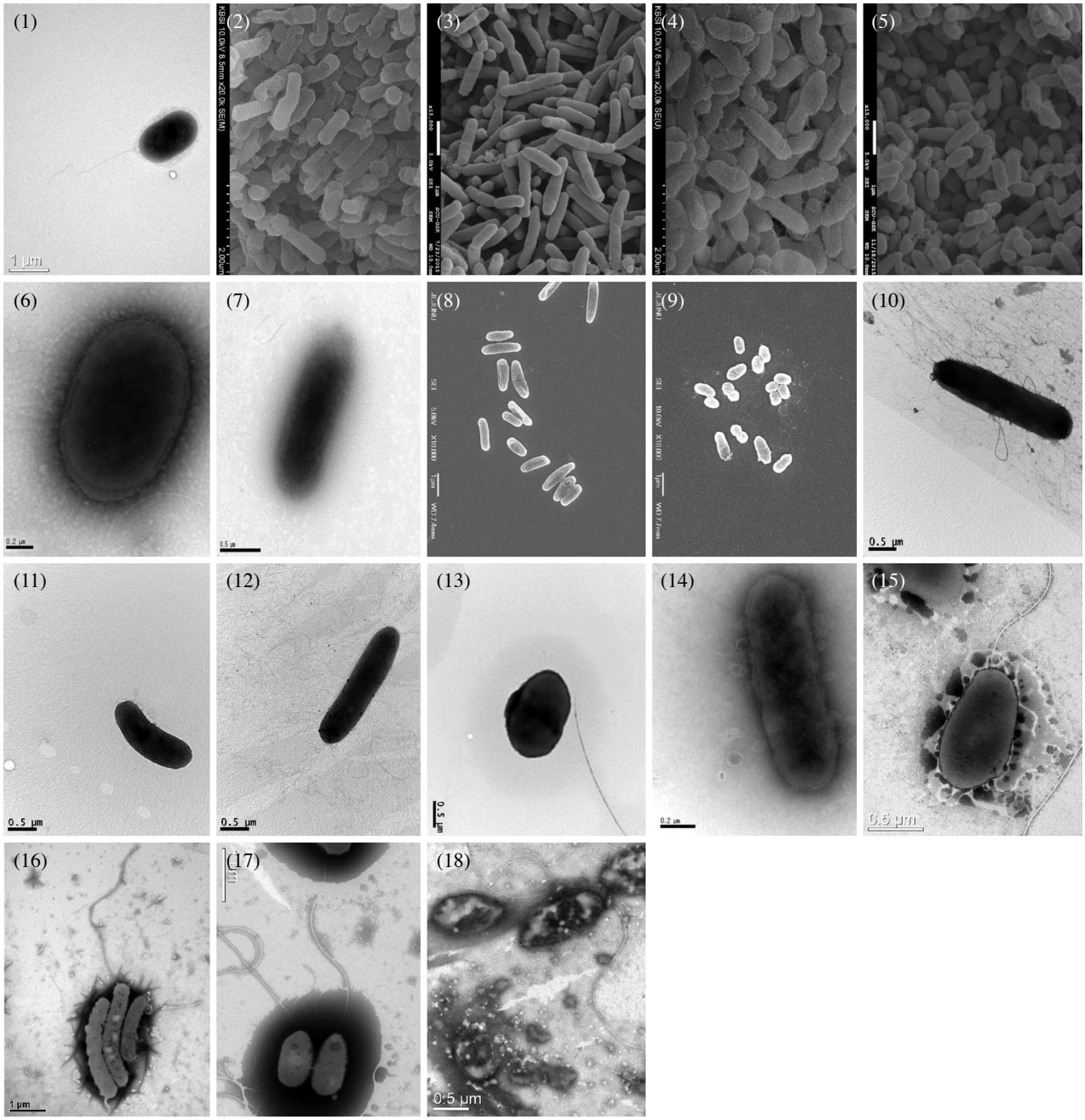

Fig. 1. Transmission electron micrographs or scanning electron micrographs of cells of the species belonging to the *Betaproteobacteria* isolated in this study. Strains: 1, HMF3907; 2, JD2; 3, JD5; 4, JD24; 5, JD50; 6, IMCC25601; 7, IMCC25614; 8, C1-1; 9, C1-11; 10, NJ-1-5; 11, GF5; 12, JF-5; 13, 2015-3; 14, IMCC25617; 15, NDH-10; 16, RDH4; 17, HMF4008; 18, HMF4075.

Table 1. Summary of strains isolated belonging to the *Betaproteobacteria* and *Gammaproteobacteria* and their taxonomic affiliations

Phylum	Family	Genus	Strain ID	NIBR ID	Most closely related species	Similarity (%)	Isolation source	Medium	Incubation conditions
Betaproteobacteria	*Alcaligenaceae*	*Achromobacter*	C1-11	NIBRBAC000498019	*A. xylosoxidans* NBRC 15126^T	99.02	Natural cave	TSA	30°C, 3d
		Candidimonas	C1-1	NIBRBAC000498018	*C. bauzanensis* BZ59^T	98.95	Natural cave	TSA	30°C, 3d
	*Lautropia*_f	*Limnobacter*	NDH-10	NIBRBAC000498058	*L. thiooxidans* CS-K2^T	99.93	Paddy field	R2A	30°C, 2d
	Oxalobacteraceae	*Duganella*	HMF3907	NIBRBAC000497904	*D. zoogloeoides* IAM 12670^T	99.72	Fresh water	R2A	30°C, 3d
		Herbaspirillum	GF5	NIBRBAC000498039	*H. autotrophicum* IAM 14942^T	98.72	Fresh water	R2A	25°C, 2d
		Herbaspirillum	IMCC25601	NIBRBAC000497991	*H. hiltneri* N3^T	99.93	Fresh water	R2A	20°C, 10d
		Janthinobacterium	JD24	NIBRBAC000497938	*J. lividum* DSM 1522^T	99.79	Fresh water	R2A	25°C, 2d
		Janthinobacterium	JD50	NIBRBAC000497939	*J. svalbardensis* JA-1^T	99.50	Fresh water	R2A	25°C, 2d
		Massilia	IMCC25614	NIBRBAC000498004	*M. varians* CCUG 35299^T	99.92	Fresh water	R2A	20°C, 10d
		Noviherbaspirillum	IMCC25617	NIBRBAC000498007	*N. malthae* CC-AFH3^T	99.51	Fresh water	R2A	20°C, 10d
		Noviherbaspirillum	2015-3	NIBRBAC000498055	*N. soli* SUEMI10^T	100.00	Soil	R2A	25°C, 2d
		Pseudoduganella	NJ-1-5	NIBRBAC000498038	*P. violaceinigra* YIM 31327^T	98.92	Fresh water	R2A	25°C, 2d
	*Sphaerotilus*_f	*Rhizobacter*	RDH4	NIBRBAC000498078	*R. gummiphilus* NS21^T	99.01	Lake	R2A	30°C, 2d
		Roseateles	JF-5	NIBRBAC000498046	*R. terrae* CCUG 52222^T	99.86	Fresh water	R2A	25°C, 2d
	Comamonadaceae	*Acidovorax*	JD2	NIBRBAC000497934	*A. temperans* CCUG 11779^T	99.51	Fresh water	R2A	25°C, 4d
		Acidovorax	JD5	NIBRBAC000497935	*A. valerianellae* CFBP 4730^T	98.75	Fresh water	R2A	25°C, 7d
	Neisseriaceae	*Chromobacterium*	HMF4075	NIBRBAC000497911	*C. vaccinii* MWU205^T	99.18	Fresh water	R2A	30°C, 3d
		Vogesella	HMF4008	NIBRBAC000497908	*V. indigofera* ATCC 19706^T	99.59	Fresh water	R2A	30°C, 3d
Gammaproteobacteria	*Alishewanella*_f	*Rheinheimera*	TJB7	NIBRBAC000498051	*R. texasensis* A62-14BT	99.30	Fresh water	R2A	25°C, 2d
		Rheinheimera	JF6	NIBRBAC000498056	*R. tilapiae* Ruye-90^T	99.90	Fresh water	R2A	25°C, 2d
	Alteromonadaceae	*Alteromonas*	KYW1005	NIBRBAC000497923	*A. macleodii* ATCC 27126^T	99.58	Sea water	MA	25°C, 3d
	*Marinobacter*_f	*Marinobacter*	HMF3946	NIBRBAC000497907	*M. maritimus* CK47^T	99.10	Sea water	MA	30°C, 3d
	Psychromonadaceae	*Psychromonas*	LPB0073	NIBRBAC000497973	*P. arctica* DSM 14288^T	99.19	Sea water	MA	26°C, 2d
	Enterobacteraceae	*Raoultella*	KHL6	NIBRBAC000497837	*R. ornithinolytica* JCM 6096^T	98.87	Burmese python	R2A	25°C, 3d
		Kosakonia	KHN5	NIBRBAC000497843	*K. cowanii* CIP 107300^T	99.39	Japanese crested ibis	R2A	25°C, 3d
		Escherichia	KHM5	NIBRBAC000497846	*E. marmotae* HT073016^T	99.27	Japanese crested ibis	R2A	25°C, 3d
		Enterobacter	KHN16	NIBRBAC000497849	*E. xiangfangensis* 10-17^T	99.93	Japanese crested ibis	R2A	25°C, 3d
		Citrobacter	KHL16	NIBRBAC000497850	*C. youngae* CECT 5335^T	99.89	Burmese python	R2A	25°C, 3d
		Erwinia	IMCC25602	NIBRBAC000497992	*E. persicina* ATCC 35998^T	99.72	Fresh water	R2A	20°C, 10d
		Providencia	KM3	NIBRBAC000498041	*P. rettgeri* DSM 4542^T	99.50	Sea water	R2A	25°C, 2d
		Hafnia	DF-5	NIBRBAC000498045	*H. paralvei* ATCC 29927^T	99.60	Fresh water	R2A	25°C, 2d
		Pantoea	TW2C3	NIBRBAC000498083	*P. agglomerans* DSM 3493^T	99.11	Soil of mine	NA	30°C, 2d
		Pantoea	TW2I3	NIBRBAC000498086	*P. eucalypti* LMG 24198^T	99.26	Soil of mine	ISP2	30°C, 2d
		Serratia	GT 8-07	NIBRBAC000498088	*S. plymuthica* DSM 4540^T	99.06	Plant root	R2A	30°C, 2d
		Ewingella	HMF3896	NIBRBAC000497902	*E. americana* ATCC 33852^T	99.90	Soil	R2A	30°C, 3d
	Halomonadaceae	*Cobetia*	KM2	NIBRBAC000498040	*C. amphilecti* KMM 1561^T	99.80	Sea water	R2A	25°C, 2d
		Halomonas	HMF4436	NIBRBAC000497917	*H. fontilapidosi* 5CRT	100.00	Salt	MA	30°C, 3d
	*Kangiella*_f	*Kangiella*	LPB0099	NIBRBAC000497979	*K. japonica* KMM 3899^T	99.66	Sea water	MA	26°C, 2d
	Oceanospirillaceae	*Marinomonas*	LPB0063	NIBRBAC000497972	*M. arenicola* KMM 3893^T	99.19	Sea water	MA	26°C, 2d

Table 1. Continued

Phylum	Family	Genus	Strain ID	NIBR ID	Most closely related species	Similarity (%)	Isolation source	Medium	Incubation conditions
Gammaproteobacteria	*Moraxellaceae*	*Acinetobacter*	KHN15	NIBRBAC000497835	*A. lwoffii* NCTC 5866^T	98.79	Japanese crested ibis	TSA	25°C, 3d
		Psychrobacter	IMCC25605	NIBRBAC000497995	*P. frigidicola* DSM 12411^T	99.45	Fresh water	0.1% MA	20°C, 7d
		Moraxella	YH-5	NIBRBAC000498036	*M. osloensis* NCTC 10465^T	99.60	Fresh water	R2A	25°C, 2d
		Acinetobacter	S6-6	NIBRBAC000497887	*A. junii* CIP 64.5^T	99.47	Tidal flat	MA	30°C, 2d
	Pseudomonadaceae	*Pseudomonas*	LPB0123	NIBRBAC000497989	*P. indoloxydans* IPL-1^T	99.03	Sea water	MA	26°C, 1d
		Pseudomonas	KYW941	NIBRBAC000497924	*P. songnenensis* NEAU-ST5-5^T	99.24	Sea water	MA	25°C, 3d
		Pseudomonas	KYW1051	NIBRBAC000497928	*P. kummingensis* HL22-2^T	99.47	Sea water	MA	25°C, 4d
		Pseudomonas	YF5	NIBRBAC000498042	*P. chlororaphis* subsp. *piscium* JF3835^T	99.10	Fresh water	R2A	25°C, 2d
		Pseudomonas	JD11	NIBRBAC000497936	*P. fragi* ATCC 4973^T	99.51	Fresh water	R2A	25°C, 2d
		Pseudomonas	JD16	NIBRBAC000497937	*P. viridiflava* LMG 2352^T	99.86	Fresh water	R2A	25°C, 3d
		Pseudomonas	JD57	NIBRBAC000497940	*P. graminis* DSM 11363^T	98.87	Fresh water	R2A	25°C, 3d
	Vibrionaceae	*Vibrio*	LPB0083	NIBRBAC000497974	*V. atlanticus* Vb 11.11^T	99.48	Sea water	MA	26°C, 2d
		Vibrio	IMCC25618	NIBRBAC000498008	*V. zhanjiangensis* E414^T	99.93	Fresh water	MA	20°C, 15d
	Xanthomonadaceae	*Stenotrophomonas*	KHC14	NIBRBAC000497840	*S. rhizophila* DSM 14405^T	99.72	Japanese crested ibis	R2A	25°C, 3d
		Rhodanobacter	C2-29	NIBRBAC000498024	*R. soli* DCY45^T	98.91	Natural cave	TSA	30°C, 13d
		Pseudoxanthomonas	NR 4-01	NIBRBAC000498087	*P. indica* P15^T	99.41	Plant root	R2A	30°C, 2d
		Xanthomonas	NR 5-07	NIBRBAC000498090	*X. translucens* DSM 18974^T	99.71	Plant root	R2A	30°C, 2d
		Pseudomonas	HMF4401	NIBRBAC000497913	*P. hibiscicola* ATCC 19867^T	99.50	Jeotgal	MA	30°C, 3d

1, C1-11, NJ-1-5, GF5, JF-5, 2015-3, NDH-10 and RDH4 were most closely related to *Duganella zoogloeoides* IAM 12670^T (D14256; 99.70% 16S rRNA gene sequence similarity), *Vogesella indigofera* ATCC 19706^T (AB 021385; 99.60%), *Chromobacterium vaccinia* MWU205^T (JZJL01000120; 99.10%), *Acidovorax temperans* CCUG 11779^T (AF078766; 99.51%), *Acidovorax valerianellae* CFB 4730^T (AJ431731; 98.75%), *Janthinobacterium lividum* DSM 1522^T (Y08846; 99.8%), *Janthinobacterium svalbardensis* JA-1^T (DQ355146; 99.50%), *Herbaspirillum hiltneri* N3^T (DQ150563; 99.93%), *Massilia varians* CCUG 35299^T (AM774587; 99.85%), *Noviherbaspirillum malthae* CC-AFH3^T (DQ490985; 99.42%), *Candidimonas bauzanensis* BZ59^T (GQ246953; 98.95%), *Achromobacter xylosoxidans* DSM 10346^T (Y14908; 99.09%), *Pseudoduganella violaceinigra* Y9^T (AY376163; 98.90%), *Herbaspirillum autotrophicum* IAM 14942^T (AB074524; 98.7%), *Roseateles terrae* CCUG 52222^T (AB003626; 99.9%), *Noviherbaspirillum soli* SUEM 110^T (HQ830498; 100%), *Limnobacter thiooxidans* CS-K2^T (AJ289885; 99.93%) and *Rhizobacter gummiphilus* NS21^T (AB609313; 99.01%), respectively (Table 1).

From the high 16S rRNA gene sequence similarity and robust formation of phylogenetic clades, it was concluded that strains HMF3907, JD2, JD5, JD24, JD50, IMCC25601, IMCC25614, C1-1, C1-11, NJ-1-5, GF5, JF-5, 2015-3, IMCC25617, NDH-10 and RDH4 were members of the order *Burkholderiales* and strains HMF4008 and HMF4075 were members of the order *Neisseriales*, respectively (Fig. 4). At present, there has been no official report that these 18 species have been isolated in Korea; therefore 16 species in 12 genera of four families in the order *Burkholderiales* and two species in tow genera of one family in the order *Neisseriales* are reported as betaproteobacterial species found in Korea.

Strains assigned to the *Gammaproteobacteria*

On the basis of 16S rRNA gene sequence comparisons and phylogenetic analyses, a total of 39 strains, designated TJB7, JF6, KYW1005, HMF3946, LPB0073, KHL6, KHN5, KHM5, KHN16, KHL16, IMCC25602, KM3, DF-5, TW2C3, TW2I3, GT 8-07, HMF3896, KM2, HMF4436, LPB0099, LPB0063, KHN15, IMCC25605, YH-5, S6-6, LPB0123, KYW941, KYW1051, YF5, JD11, JD16, JD57, LPB0083, IMCC25618, KHC14, C2-29, NR 4-01, NR 5-07 and HMF4401 were assigned to the *Gammaproteobacteria*. The 39 strains were distributed in six orders of the *Gammaproteobacteria*; five strains in the order *Alteromonadales*, 12 strains in the *Enterobacteriales*, four strains in the *Oceanospirillales*, 11 strains for the *Pseudomonadales*, two strain in the *Vibrionales* and five strains in the *Xanthomonadales*

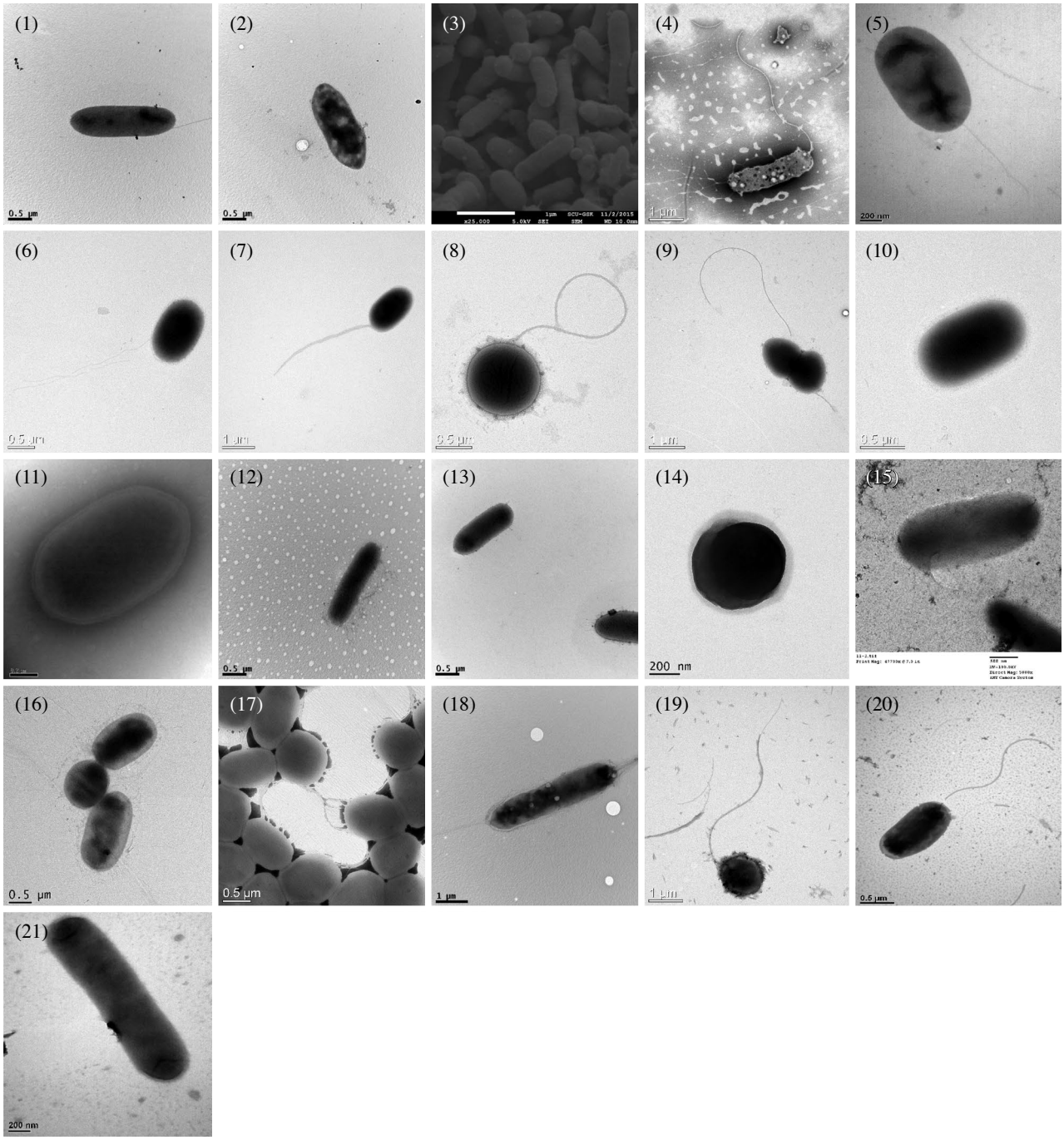

Fig. 2. Transmission electron micrographs or scanning electron micrographs of cells of the species in the order *Alteromonadales*, *Enterobacteriales* and *Oceanospirillales* belonging to the *Gammaproteobacteria* isolated in this study. Strains: 1, TJB7; 2, JF6; 3, KYW1005; 4, HMF3946; 5, LPB0073; 6, KHL6; 7, KHN5; 8, KHM5; 9, KHN16; 10, KHL16; 11, IMCC25602; 12, KM3; 13, DF-5; 14, TW2C3; 15, TW2I3; 16, GT 8-07; 17, HMF3896; 18, KM2; 19, HMF4436; 20, LPB0099; 21, LPB0063.

(Table 1). These strains were Gram-staining-negative, chemoheterotrophic and rod- or coccoid-shaped bacteria (Fig. 2). Colony size, morphology and physiological characteristics are also shown in the species description section. Strains TJB7, JF6, KYW1005, HMF3946, LPB0073, KHL6, KHN5, KHM5, KHN16, KHL16, IMCC25602, KM3, DF-5, TW2C3, TW2I3, GT 8-07, HMF3896, KM2, HMF4436, LPB0099, LPB0063, KHN15, IMCC25605, YH-5, S6-6, LPB0123, KYW941, KYW1051, YF5, JD11, JD16, JD57, LPB0083,

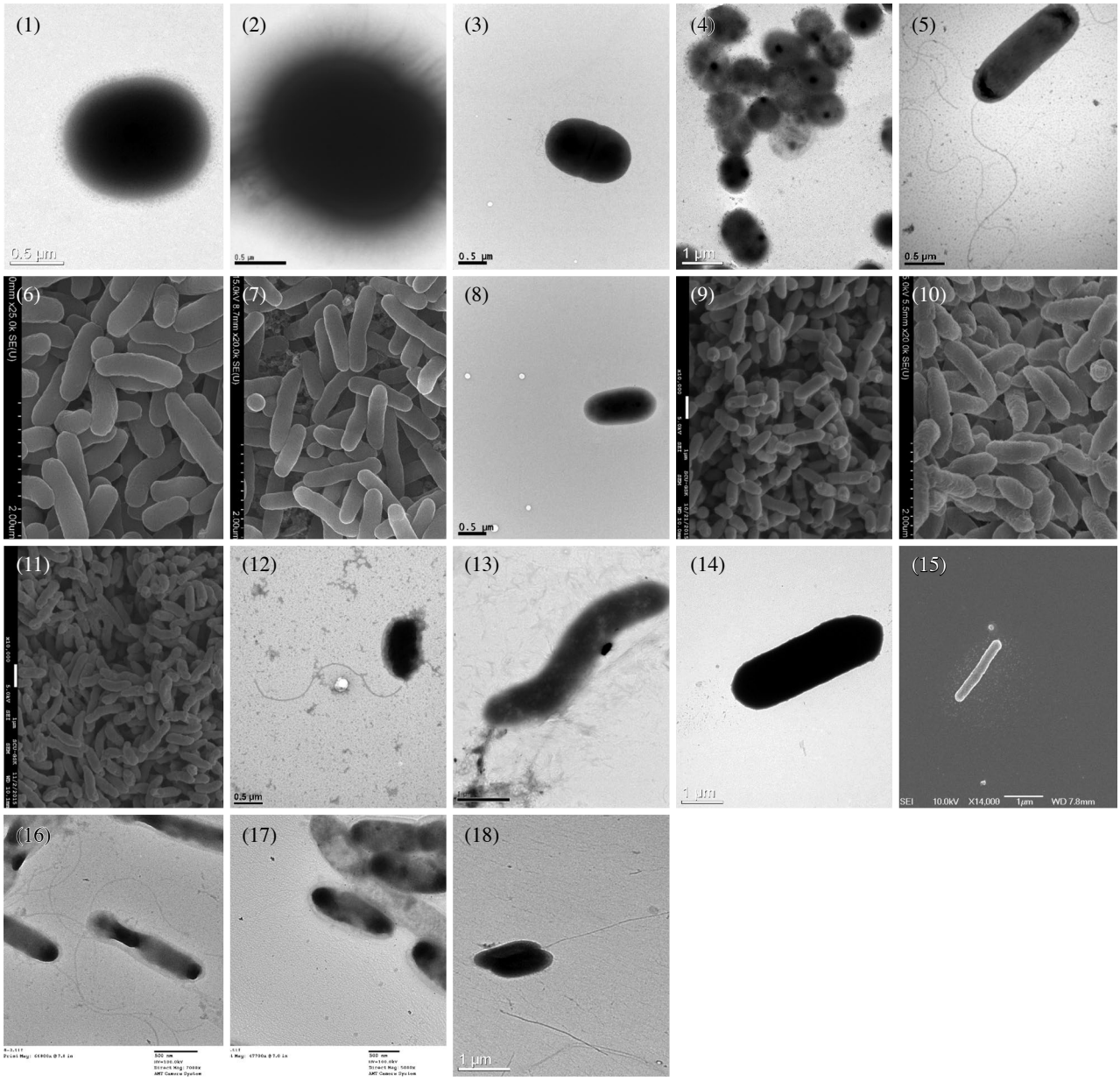

Fig. 3. Transmission electron micrographs or scanning electron micrographs of cells of the species in the order *Pseudomonadales*, *Vibrionales* and *Xanthomonadales* belonging to the *Gammaproteobacteria* isolated in this study. Strains: 1, KHN15; 2, IMCC25605; 3, YH-5; 4, S6-6; 5, LPB0123; 6, KYW941; 7, KYW1051; 8, YF5; 9, JD11; 10, JD16; 11, JD57; 12, LPB0083; 13, IMCC25618; 14, KHC14; 15, C2-29; 16, NR 4-01; 17, NR 5-07; 18, HMF4401.

IMCC25618, KHC14, C2-29, NR 4-01, NR 5-07 and HMF4401 were most closely related to *Rheinheimera texasensis* A62-14B^T (AY701891; 99.30% 16S rRNA gene sequence similarity), *Rheinheimera tilapiae* Ruye-90^T (HQ111524; 99.90%), *Alteromonas macleodii* ATCC 27126^T (CP003841; 99.58%), *Marinobacter maritimus* CK47^T (AJ704395; 99.10%), *Psychromonas arctica* DSM 14288^T (AXWP01000011; 99.19%), *Raoultella ornithinolytica* JCM 6096^T (AJ251467; 98.87%), *Kosakonia cowanii* CIP 107300^T (AJ508303; 99.39%), *Escherichia marmotae* HT073016^T (JNBP01000188; 99.27%), *Enterobacter xiangfangensis* 10-17^T (HF679035; 99.93%), *Citrobacter youngae* CECT 5335^T (AJ564736; 99.89%), *Erwinia persicina* ATCC 35998^T (U80205; 99.72%), *Providencia rettgeri* DSM 4542^T (AM040492; 99.50%), *Hafnia paralvei* ATCC 29927^T (FM179943; 99.60%), *Pantoea agglomerans* DSM 3493^T (AJ233423; 99.11%), *Pantoea eucalypti* LMG 24198^T (EF688009;

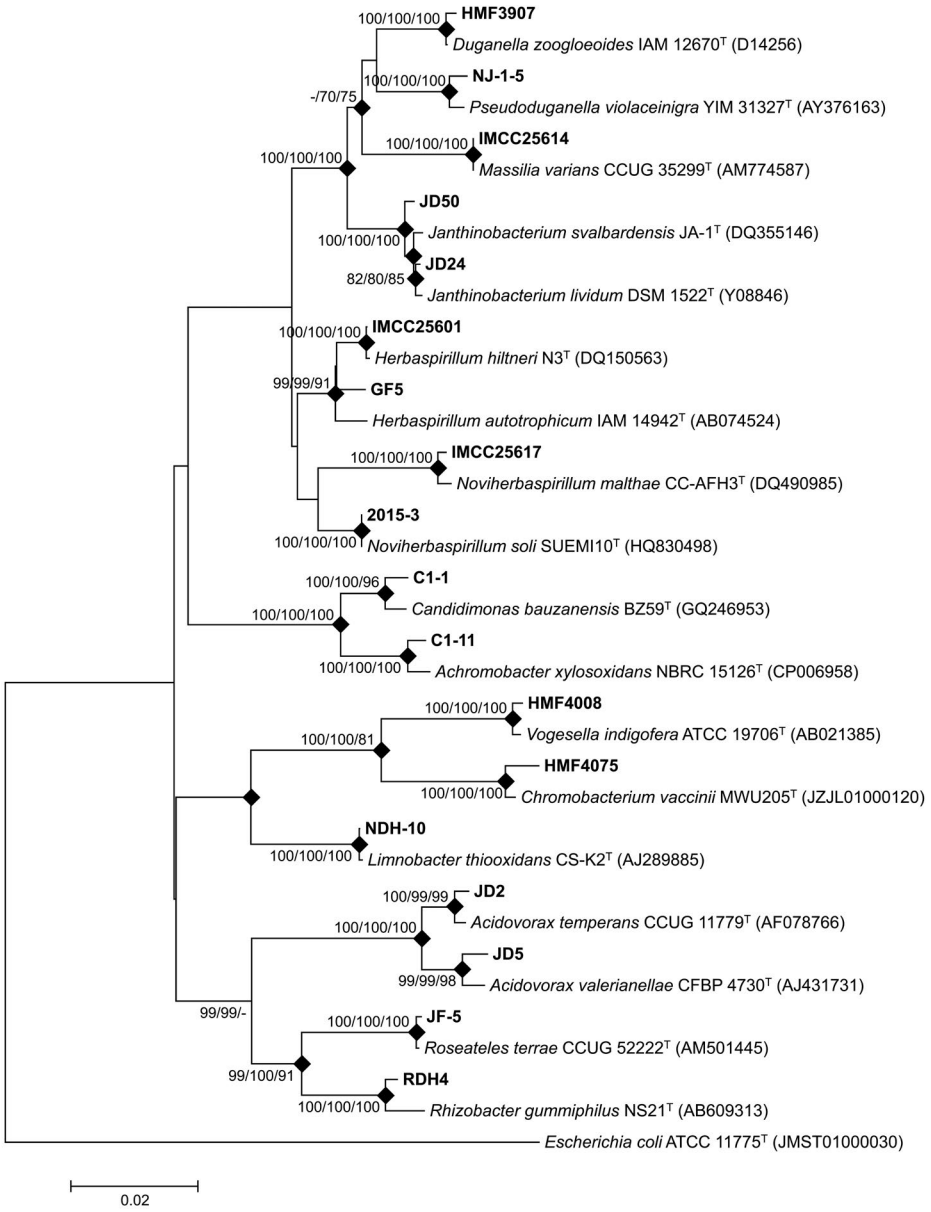

Fig. 4. Neighbour-joining (NJ) tree based on the 16S rRNA gene sequence comparisons, showing the taxonomic position between the 18 strains isolated in this study and the notable type species from the class *Betaproteobacteria*. The tree was primarily reconstructed using a neighbor-joining algorithm (NJ). Maximum parsimony (MP) and maximum likelihood (ML) algorithms were applied for additional comparisons. Corresponding branches are presented as filled diamonds; at the nodes, only bootstrap values of more than 70% are shown, which are expressed as a percentage of 1000 replicates (NJ/MP/ML). *Escherichia coli* ATCC 11775^T (JMST01000030) was established as an outgroup. The bar indicates 0.02 substitutions per nucleotide.

99.26%), *Serratia plymuthica* DSM 4540^T (AJ233433; 99.06%), *Ewingella americana* ATCC 33852^T (JMPJ 01000013; 99.90%), *Cobetia amphilecti* KMM 1561^T (AB646236; 99.80%), *Halomonas fontilapidosi* 5CR^T (EU541349; 100%), *Kangiella japonica* KMM 3899^T (AB505051; 99.66%), *Marinomonas arenicola* KMM 3893^T (AB467281; 99.19%), *Acinetobacter lwoffii* NCTC 5866^T (AIEL01000120; 98.79%), *Psychrobacter frigidicola* DSM 12411^T (AJ609556; 99.45%), *Moraxella osloensis* NCTC 10465^T (X74897; 99.60%), *Acinetobacter junii* CIP 64.5^T (APPX01000010; 99.47%), *Pseudomonas indoloxydans* IPL-1^T (DQ916277; 99.03%), *Pseudomonas songnenensis* NEAU-ST5-5^T (JQ762269; 99.24%), *Pseudomonas kunmingensis* HL22-2^T (JQ246444; 99.47 %), *Pseudomonas chlororaphis* subsp. *piscium* JF3835^T (FJ168539; 99.10%), *Pseudomonas fragi* ATCC 4973^T

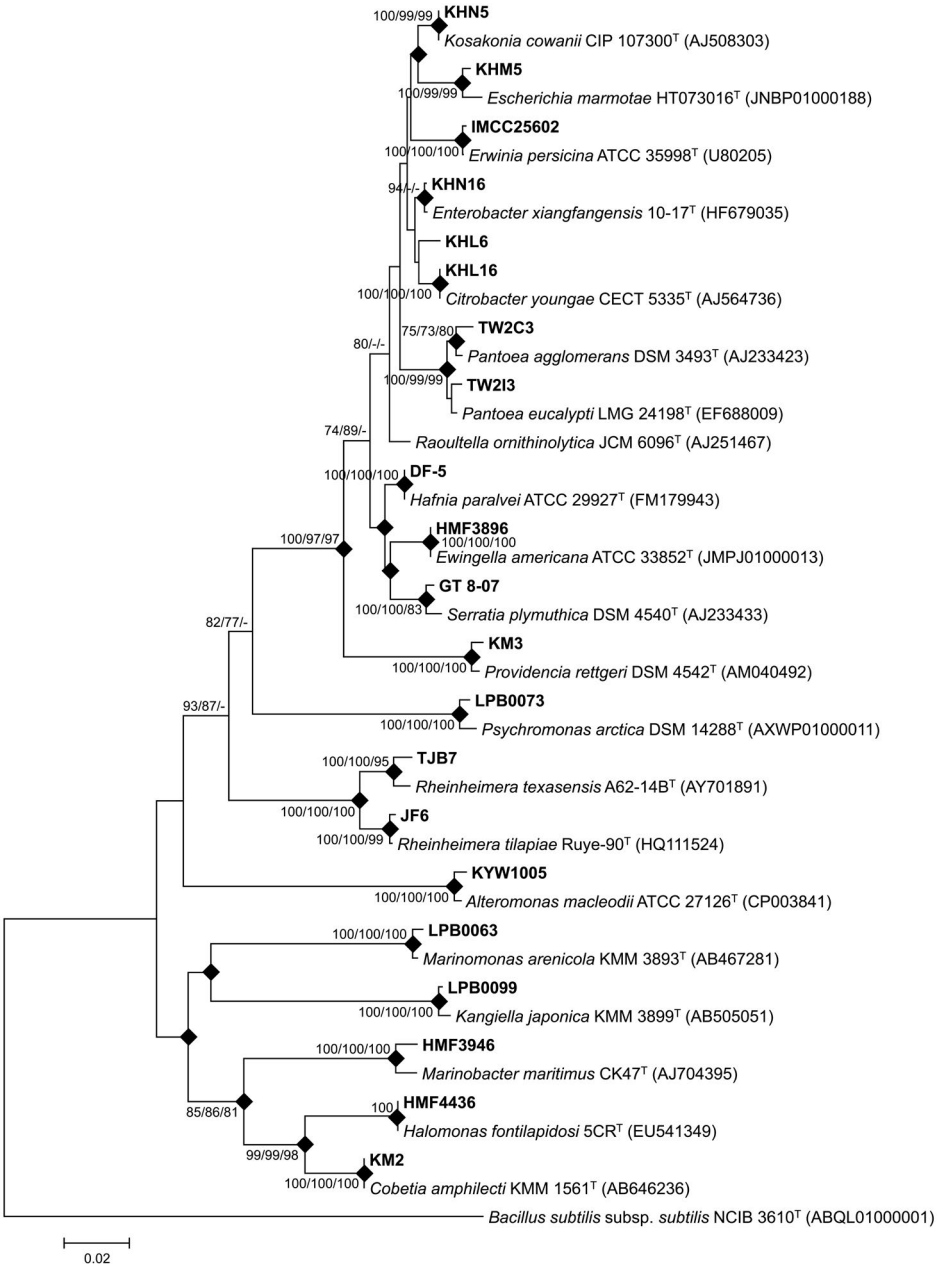

Fig. 5. Neighbour-joining (NJ) tree based on the 16S rRNA gene sequence comparisons, showing the taxonomic position between the 21 strains isolated in this study and the notable type species from the orders *Alteromonadales*, *Enterobacteriales* and *Oceanospirillales* in the class *Gammaproteobacteria*. The tree was primarily reconstructed using a neighbor-joining algorithm (NJ). Maximum parsimony (MP) and maximum likelihood (ML) algorithms were applied for additional comparisons. Corresponding branches are presented as filled diamonds; at the nodes, only bootstrap values of more than 70% are shown, which are expressed as a percentage of 1000 replicates (NJ/MP/ML). *Bacillus subtilis* subsp. *subtilis* NCIB 3610^T (ABQL01000001) was established as an out-group. The bar indicates 0.02 substitutions per nucleotide.

(AF094733; 99.51%), *Pseudomonas viridiflava* LMG 2352^T (Z76671; 99.86%), *Pseudomonas graminis* DSM 11363^T (Y11150; 98.87%), *Vibrio atlanticus* Vb 11.11^T (EF599163; 99.48%), *Vibrio zhanjiangensis* E414^T (JF 931139; 99.93%), *Stenotrophomonas rhizophila* DSM 14405^T (CP007597; 99.72%), *Rhodanobacter soli* DCY 45^T (FJ605268; 98.91%), *Pseudoxanthomonas indica* P15^T (EF424397; 99.41%), *Xanthomonas translucens* DSM 18974^T (CAPJ01000550; 99.71%) and *Pseudomonas hibiscicola* ATCC 19867^T (AB021405; 99.50%), respectively (Table 1). In the conjoined, phylogenetic consensus tree, isolated strains provided a robust phylogenetic clade with the most closely related species in the orders *Alteromonadales*, *Enterobacteriales*,

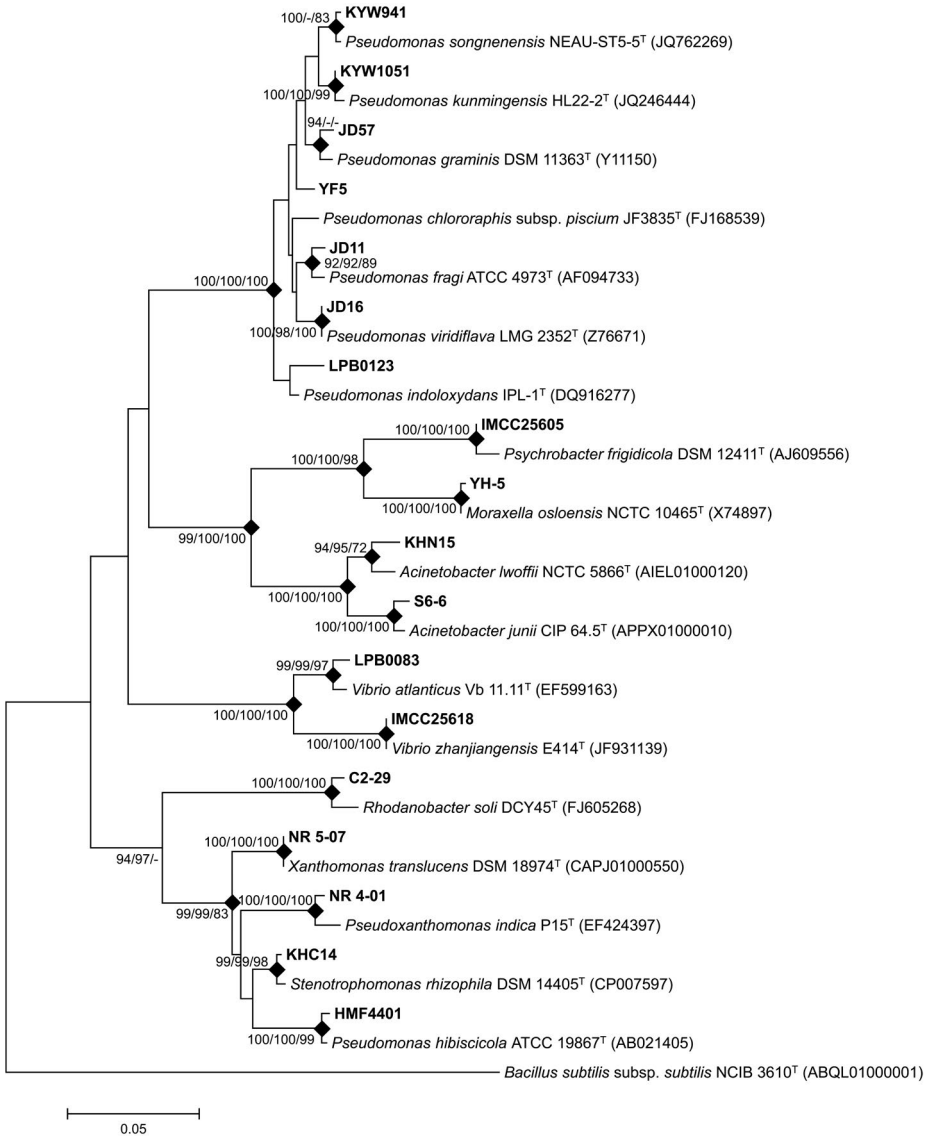

Fig. 6. Neighbour-joining (NJ) tree based on the 16S rRNA gene sequence comparisons, showing the taxonomic position between the isolated 18 strains in this study and the notable type species from the orders *Pseudomonadales*, *Vibrionales* and *Xanthomonadales* in the class *Gammaproteobacteria*. The tree was primarily reconstructed using a neighbor-joining algorithm (NJ). Maximum parsimony (MP) and maximum likelihood (ML) algorithms were applied for additional comparisons. Corresponding branches are presented as filled diamonds; at the nodes, only bootstrap values of more than 70% are shown, which are expressed as a percentage of 1000 replicates (NJ/MP/ML). *Bacillus subtilis* subsp. *subtilis* NCIB 3610^T (ABQL01000001) was established as an out-group. The bar indicates 0.05 substitutions per nucleotide.

Oceanospirillales (Fig. 5), *Pseudomonadales*, *Vibrionales* and *Xanthomonadales* (Fig. 6) within the class *Gammaproteobacteria*, as expected from high 16S rRNA gene sequence similarities. There is no official report that these 39 species have been isolated in Korea; therefore five species in four genera of four families in the order *Alteromonadales*, 12 species in 11 genera of one family in the order *Enterobacteriales*, four species in four genera of three families in the order *Oceanospirillales*, 11 species in four genera of two families in the order *Pseudomonadales*, two species in the order *Vibrionales* and five species in five genera of one family in the order *Xanthomonadales* are reported for gammaproteobacterial species found in Korea.

Description of *Duganella zoogloeoides* HMF3907

Cells are Gram-staining-negative, flagellated, non-pigmented and rod-shaped. Colonies are circular, convex, entire and pale yellow-colored after 3 days of incubation on R2A at 30°C. Positive for cytochrome oxidase, esculin hydrolysis and β-galactosidase, but negative

for arginine dihydrolase, gelatinase, glucose fermentation, indole production, nitrates reduction and urease in API 20NE test. L-Arabinose, D-maltose, malic acid, D-mannose, phenylacetic acid and trisodium citrate are utilized. Strain HMF3907 (=NIBRBAC000497904) has been isolated from fresh water sample, Yongin, Gyeonggi-do, Korea.

Description of *Vogesella indigofera* HMF4008

Cells are Gram-staining-negative, flagellated, non-pigmented and rod-shaped. Colonies are circular, convex, entire and white-colored after 3 days of incubation on R2A at 30°C. Positive for cytochrome oxidase, but negative for arginine dihydrolase, esculin hydrolysis, β-galactosidase, gelatinase, glucose fermentation, indole production, nitrates reduction and urease in API 20NE test. *N*-Acetyl-glucosamine, capric acid, malic acid, D-maltose and potassium gluconate are utilized. Strain HMF4008 (=NIBRBAC000497908) has been isolated from fresh water sample, Gyeongju, Gyeongsangbuk-do, Korea.

Description of *Chromobacterium vaccinia* HMF4075

Cells are Gram-staining-negative, flagellated, non-pigmented and rod-shaped. Colonies are circular, convex, entire and violet-colored after 3 days of incubation on R2A at 30°C. Positive for arginine dihydrolase, cytochrome oxidase, esculin hydrolysis, gelatinase, glucose fermentation, nitrates reduction and urease, but negative for β-galactosidase and indole production in API 20NE test. *N*-Acetyl-glucosamine, capric acid, D-glucose, potassium gluconate and trisodium citrate are utilized. Strain HMF4075 (=NIBRBAC000497911) has been isolated from fresh water sample, Jeju, Jeju-do, Korea.

Description of *Acidovorax temperans* JD2

Cells are Gram-staining-negative, non-flagellated, non-pigmented and rod-shaped. Colonies are convex, smooth and white-colored after 4 days of incubation on R2A at 25°C. Positive for nitrates reduction and urease, but negative for arginine dihydrolase, cytochrome oxidase, esculin hydrolysis, β-galactosidase, gelatinase, glucose fermentation and indole production in API 20NE test. L-Arabinose, D-glucose, malic acid, D-mannitol, D-mannose, potassium gluconate and trisodium citrate are utilized. Strain JD2 (=NIBRBAC000497934) has been isolated from fresh water sample, Changwon, Gyeongsangnam-do, Korea.

Description of *Acidovorax valerianellae* JD5

Cells are Gram-staining-negative, non-flagellated, non-pigmented and rod-shaped. Colonies are circular, raised and white-colored after 7 days of incubation on R2A at 25°C. Positive for urease, but negative for arginine dihydrolase, cytochrome oxidase, esculin hydrolysis, β-galactosidase, gelatinase, glucose fermentation, indole production and nitrates reduction in API 20NE test. L-Arabinose, D-glucose, malic acid, D-mannitol, D-mannose and potassium gluconate are utilized. Strain JD5 (=NIBRBAC000497935) has been isolated from fresh water sample, Changwon, Gyeongsangnam-do, Korea.

Description of *Janthinobacterium lividum* JD24

Cells are Gram-staining-negative, non-flagellated, non-pigmented and rod-shaped. Colonies are circular, convex, smooth and purple-white-colored after 2 days of incubation on R2A at 25°C. Positive for cytochrome oxidase, esculin hydrolysis, gelatinase and nitrates reduction, but negative for arginine dihydrolase, β-galactosidase, glucose fermentation, indole production and urease in API 20NE test. Adipic acid, L-arabinose, capric acid, D-glucose, malic acid, D-maltose, D-mannitol, D-mannose, phenylacetic acid and trisodium citrate are utilized. Strain JD24 (=NIBRBAC000497938) has been isolated from fresh water sample, Changwon, Gyeongsangnam-do, Korea.

Description of *Janthinobacterium svalbardensis* JD50

Cells are Gram-staining-negative, non-flagellated, non-pigmented and rod-shaped. Colonies are circular, convex, smooth and pale yellow-colored after 2 days of incubation on R2A at 25°C. Positive for esculin hydrolysis, β-galactosidase and nitrates reduction, but negative for arginine dihydrolase, cytochrome oxidase, gelatinase, glucose fermentation, indole production and urease in API 20NE test. Adipic acid, L-arabinose, D-glucose, malic acid, D-maltose, D-mannitol, D-mannose, phenylacetic acid and trisodium citrate are utilized. Strain JD50 (=NIBRBAC000497939) has been isolated from fresh water sample, Changwon, Gyeongsangnam-do, Korea.

Description of *Herbaspirillum hiltneri* IMCC25601

Cells are Gram-staining-negative, non-flagellated, non-pigmented and rod-shaped. Colonies are circular, raised, entire and white-colored after 10 days of incubation on R2A at 20°C. Positive for esculin hydrolysis, β-galactosidase and indole production, but negative for arginine dihydrolase, cytochrome oxidase, gelatinase, glucose fermentation, nitrates reduction and urease in API 20NE test. *N*-Acetyl-glucosamine, L-arabinose, D-glucose, malic acid, D-maltose, D-mannitol, D-mannose and potassium gluconate are utilized. Strain IMCC25601 (=NIBRBAC000497991) has been isolat-

ed from fresh water sample, Chuncheon, Gangwon-do, Korea.

Description of *Massilia varians* IMCC25614

Cells are Gram-staining-negative, non-flagellated, non-pigmented and rod-shaped. Colonies are circular, raised, entire and white-colored after 10 days of incubation on R2A at 20°C. Positive for gelatinase and urease, but negative for arginine dihydrolase, cytochrome oxidase, esculin hydrolysis, β-galactosidase, glucose fermentation, indole production and nitrates reduction in API 20NE test. *N*-Acetyl-glucosamine, adipic acid, L-arabinose, capric acid, D-glucose, malic acid, D-maltose, D-mannitol, D-mannose, phenylacetic acid, potassium gluconate and trisodium citrate are utilized. Strain IMCC25614 (=NIBRBAC000498004) has been isolated from fresh water sample, Nam-gu, Incheon, Korea.

Description of *Noviherbaspirillum malthae* IMCC25617

Cells are Gram-staining-negative, non-flagellated, non-pigmented and rod-shaped. Colonies are circular, raised, entire and yellow-colored after 10 days of incubation on R2A at 20°C. Positive for cytochrome oxidase and esculin hydrolysis, but negative for arginine dihydrolase, β-galactosidase, gelatinase, glucose fermentation, indole production, nitrates reduction and urease in API 20NE test. Strain IMCC25617 (=NIBRBAC 000498007) has been isolated from fresh water sample, Nam-gu, Incheon, Korea.

Description of *Candidimonas bauzanensis* C1-1

Cells are Gram-staining-negative, non-flagellated, non-pigmented and rod-shaped. Colonies are circular, convex, entire and cream-colored after 3 days of incubation on TSA at 30°C. Positive for cytochrome oxidase and urease, but negative for arginine dihydrolase, esculin hydrolysis, β-galactosidase, gelatinase, glucose fermentation, indole production and nitrates reduction in API 20NE test. Adipic acid, malic acid, phenylacetic acid and trisodium citrate are utilized. Strain C1-1 (=NIBRBAC000498018) has been isolated from natural cave, Jeju, Jeju-do, Korea.

Description of *Candidimonas bauzanensis* C1-11

Cells are Gram-staining-negative, non-flagellated, non-pigmented and rod-shaped. Colonies are circular, convex, entire and cream-colored after 3 days of incubation on TSA at 30°C. Positive for cytochrome oxidase and urease, but negative for arginine dihydrolase, esculin hydrolysis, β-galactosidase, gelatinase, glucose fermentation, indole production and nitrates reduction in API 20NE test. Adipic acid, malic acid, phenylacetic acid and trisodium are utilized. Strain C1-11 (=NIBRBAC 000498019) has been isolated from natural cave, Jeju, Jeju-do, Korea.

Description of *Pseudoduganella violaceinigra* NJ-1-5

Cells are Gram-staining-negative, flagellated, non-pigmented and rod-shaped. Colonies are circular, convex and purple-colored after 2 days of incubation on R2A at 25°C. Negative for arginine dihydrolase, cytochrome oxidase, esculin hydrolysis, β-galactosidase, gelatinase, glucose fermentation, indole production, nitrates reduction and urease in API 20NE test. D-Glucose is utilized. Strain NJ-1-5 (=NIBRBAC000498038) has been isolated from fresh water sample, Naju, Jeollanam-do, Korea.

Description of *Herbaspirillum autotrophicum* GF5

Cells are Gram-staining-negative, flagellated, non-pigmented and rod-shaped. Colonies are circular, convex and white-colored after 2 days of incubation on R2A at 25°C. Positive for cytochrome oxidase and urease, but negative for arginine dihydrolase, esculin hydrolysis, β-galactosidase, gelatinase, glucose fermentation, indole production and nitrates reduction in API 20NE test. *N*-Acetyl-glucosamine, L-arabinose, D-glucose, malic acid, D-mannose, phenylacetic acid, potassium gluconate and trisodium citrate are utilized. Strain GF5 (=NIBRBAC 000498039) has been isolated from fresh water sample, Jeju, Jeju-do, Korea.

Description of *Roseateles terrae* JF-5

Cells are Gram-staining-negative, flagellated, non-pigmented and rod-shaped. Colonies are circular, flat and white-colored after 2 days of incubation on R2A at 25°C. Positive for cytochrome oxidase, β-galactosidase and gelatinase, but negative for arginine dihydrolase, esculin hydrolysis, glucose fermentation, indole production, nitrates reduction and urease in API 20NE test. D-Glucose, L-arabinose, D-mannose, D-mannitol, D-maltose and potassium gluconate are utilized. Strain JF-5 (=NIBRBAC000498046) has been isolated from fresh water sample, Jeonju, Jeollabuk-do, Korea.

Description of *Noviherbaspirillum soli* 2015-3

Cells are Gram-staining-negative, flagellated, non-pigmented and rod-shaped. Colonies are circular, flat and white-colored after 2 days of incubation on R2A at 25°C. Positive for cytochrome oxidase, but negative for arginine dihydrolase, esculin hydrolysis, β-galactosidase, gelatinase, glucose fermentation, indole production, nitrates reduction and urease in API 20NE test. Potassium gluconate is utilized. Strain 2015-3 (=NIBRBAC

000498055) has been isolated from soil sample, Wanjoo, Jeollabuk-do, Korea.

Description of *Limnobacter thiooxidans* NDH-10

Cells are Gram-staining-negative, flagellated, non-pigmented and rod-shaped. Colonies are circular, entire, smooth, flat and cream-colored after 2 days of incubation on R2A at 30°C. Positive for cytochrome oxidase, esculin hydrolysis, β-galactosidase and nitrates reduction, but negative for arginine dihydrolase, gelatinase, glucose fermentation, indole production and urease in API 20NE test. Strain NDH-10 (=NIBRBAC 000498058) has been isolated from paddy field, Anseong, Gyeonggi-do, Korea.

Description of *Rhizobacter gummiphilus* RDH4

Cells are Gram-staining-negative, flagellated, non-pigmented and rod-shaped. Colonies are smooth, shiny, convex and yellow-colored after 2 days of incubation on R2A at 30°C. Positive for esculin hydrolysis and β-galactosidase and urease, but negative for arginine dihydrolase, cytochrome oxidase, gelatinase, glucose fermentation, indole production and nitrates reduction in API 20NE test. Adipic acid, L-arabinose, D-glucose, D-maltose, D-mannitol, D-mannose and potassium gluconate are utilized. Strain RDH4 (=NIBRBAC000498078) has been isolated from lake sample, Dongjak-gu, Seoul, Korea.

Description of *Ewingella americana* HMF3896

Cells are Gram-staining-negative, non-flagellated, non-pigmented and rod-shaped. Colonies are circular, convex, entire and cream-colored after 3 days of incubation on R2A at 30°C. Positive for esculin hydrolysis, β-galactosidase, glucose fermentation and nitrates reduction, but negative for arginine dihydrolase, cytochrome oxidase, gelatinase, indole production and urease in API 20NE test. *N*-Acetyl-glucosamine, D-glucose, malic acid, D-maltose, D-mannitol, D-mannose, potassium gluconate and trisodium citrate are utilized. Strain HMF3896 (=NIBRBAC000497902) has been isolated from soil sample, Yongin, Gyeonggi-do, Korea.

Description of *Marinobacter maritimus* HMF3946

Cells are Gram-staining-negative, flagellated, non-pigmented and rod-shaped. Colonies are circular, convex, entire and cream-colored after 3 days of incubation on MA at 30°C. Positive for cytochrome oxidase and nitrates reduction, but negative for arginine dihydrolase, esculin hydrolysis, β-galactosidase, gelatinase, glucose fermentation, indole production and urease in API 20NE test. Strain HMF3946 (=NIBRBAC000497907) has been isolated from sea water sample, Pohang, Gyeongsangbuk-do, Korea.

Description of *Pseudomonas hibiscicola* HMF4401

Cells are Gram-staining-negative, flagellated, non-pigmented and rod-shaped. Colonies are circular, convex, entire and beige-colored after 3 days of incubation on MA at 30°C. Positive for cytochrome oxidase, esculin hydrolysis, β-galactosidase and gelatinase, but negative for arginine dihydrolase, glucose fermentation, indole production, nitrates reduction and urease in API 20NE test. *N*-Acetyl-glucosamine, capric acid, D-glucose, malic acid, D-maltose, D-mannose and trisodium citrate are utilized. Strain HMF4401 (=NIBRBAC000497913) has been isolated from jeotgal sample, Buan, Jeollabuk-do, Korea.

Description of *Halomonas fontilapidosi* HMF4436

Cells are Gram-staining-negative, flagellated, non-pigmented and rod-shaped. Colonies are circular, convex, entire and beige-colored after 3 days of incubation on MA at 30°C. Positive for cytochrome oxidase, nitrates reduction, but negative for arginine dihydrolase, esculin hydrolysis, β-galactosidase, gelatinase, glucose fermentation, indole production and urease in API 20NE test. Strain HMF4436 (=NIBRBAC000497917) has been isolated from salt sample, Buan, Jeollabuk-do, Korea.

Description of *Pseudomonas hibiscicola* IMCC25602

Cells are Gram-staining-negative, non-flagellated, non-pigmented and rod-shaped. Colonies are circular, raised, entire and white-colored after 10 days of incubation on R2A at 20°C. Positive for esculin hydrolysis, β-galactosidase and indole production, but negative for arginine dihydrolase, cytochrome oxidase, gelatinase, glucose fermentation, nitrates reduction and urease in API 20NE test. *N*-Acetyl-glucosamine, L-arabinose, D-glucose, malic acid, D-maltose, D-mannitol, D-mannose and potassium gluconate are utilized. Strain IMCC25602 (=NIBRBAC000497992) has been isolated from fresh water sample, Chuncheon, Gangwon-do, Korea.

Description of *Psychrobacter frigidicola* IMCC25605

Cells are Gram-staining-negative, non-flagellated, non-pigmented and rod-shaped. Colonies are circular, raised, entire and white-colored after 7 days of incubation on 0.1% of diluted MA at 20°C. Positive for cytochrome oxidase and urease, but negative for arginine dihydrolase, esculin hydrolysis, β-galactosidase,

gelatinase, glucose fermentation, indole production and nitrates reduction in API 20NE test. Strain IMCC25605 (=NIBRBAC000497995) has been isolated from fresh water sample, Chuncheon, Gangwon-do, Korea.

Description of *Vibrio zhanjiangensis* IMCC25618

Cells are Gram-staining-negative, non-flagellated, non-pigmented and rod-shaped. Colonies are circular, raised, entire and white-colored after 15 days of incubation on MA at 20°C. Positive for cytochrome oxidase and esculin hydrolysis, but negative for arginine dihydrolase, β-galactosidase, gelatinase, glucose fermentation, indole production, nitrates reduction and urease in API 20NE test. Strain IMCC25618 (=NIBRBAC 000498008) has been isolated from fresh water sample, Nam-gu, Incheon, Korea.

Description of *Rhodanobacter soli* C2-29

Cells are Gram-staining-negative, non-flagellated, non-pigmented and rod-shaped. Colonies are circular, convex, entire and light yellow-colored after 13 days of incubation on TSA at 30°C. Positive for nitrates reduction, but negative for arginine dihydrolase, cytochrome oxidase, esculin hydrolysis, β-galactosidase, gelatinase, glucose fermentation, indole production and urease in API 20NE test. *N*-Acetyl-glucosamine and D-maltose are utilized. Strain C2-29 (=NIBRBAC000498024) has been isolated from natural cave, Jeju, Jeju-do, Korea.

Description of *Moraxella osloensis* YH-5

Cells are Gram-staining-negative, non-flagellated, non-pigmented and rod-shaped. Colonies are convex, opaque and white-colored after 2 days of incubation on R2A at 25°C. Positive for cytochrome oxidase and nitrates reduction, but negative for arginine dihydrolase, esculin hydrolysis, β-galactosidase, gelatinase, glucose fermentation, indole production and urease in API 20NE test. *N*-Acetyl-glucosamine, D-glucose, D-mannose and adipic acid are utilized. Strain YH-5 (=NIBRBAC 000498036) has been isolated from fresh water sample, Jeonju, Jeollabuk-do, Korea.

Description of *Cobetia amphilecti* KM2

Cells are Gram-staining-negative, flagellated, non-pigmented and rod-shaped. Colonies are transparent, shiny and white-colored after 2 days of incubation on R2A at 25°C. Positive for β-galactosidase, but negative for arginine dihydrolase, cytochrome oxidase, esculin hydrolysis, gelatinase, glucose fermentation, indole production, nitrates reduction and urease in API 20NE test. Strain KM2 (=NIBRBAC000498040) has been isolated from sea water sample, Jeju, Jeju-do, Korea.

Description of *Providencia rettgeri* KM3

Cells are Gram-staining-negative, non-flagellated, non-pigmented and rod-shaped. Colonies are opaque, flat and white-colored after 2 days of incubation on R2A at 25°C. Positive for arginine dihydrolase, esculin hydrolysis, glucose fermentation, indole production, nitrates reduction and urease, but negative cytochrome oxidase, β-galactosidase and gelatinase in API 20NE test. *N*-Acetyl-glucosamine, capric acid, D-glucose, malic acid, D-mannitol, D-mannose, potassium gluconate and trisodium citrate are utilized. Strain KM3 (=NIBRBAC 000498041) has been isolated from sea water sample, Jeju, Jeju-do, Korea.

Description of *Pseudomonas chlororaphis* subsp. *piscium* YF5

Cells are Gram-staining-negative, non-flagellated, non-pigmented and rod-shaped. Colonies are irregular, transparent and yellow-colored after 2 days of incubation on R2A at 25°C. Positive for arginine dihydrolase, cytochrome oxidase, gelatinase, glucose fermentation and urease, but negative for esculin hydrolysis and β-galactosidase, indole production and nitrates reduction in API 20NE test. *N*-Acetyl-glucosamine, L-arabinose, capric acid, D-glucose, malic acid, D-mannitol, D-mannose, potassium gluconate and trisodium citrate are utilized. Strain YF5 (=NIBRBAC000498042) has been isolated from fresh water sample, Jangsu, Jeollabuk-do, Korea.

Description of *Hafnia paralvei* DF-5

Cells are Gram-staining-negative, non-flagellated, non-pigmented and rod-shaped. Colonies are irregular and white-colored after 2 days of incubation on R2A at 25°C. Positive for β-galactosidase, glucose fermentation and nitrates reduction, but negative for arginine dihydrolase, cytochrome oxidase, esculin hydrolysis, gelatinase, indole production and urease in API 20NE test. *N*-Acetyl-glucosamine, D-glucose, malic acid, D-maltose, D-mannitol, D-mannose and potassium gluconate are utilized. Strain DF-5 (=NIBRBAC000498045) has been isolated from fresh water sample, Jangsu, Jeollabuk-do, Korea.

Description of *Rheinheimera texasensis* TJB7

Cells are Gram-staining-negative, flagellated, non-pigmented and rod-shaped. Colonies are circular, transparent and yellow-colored after 2 days of incubation on R2A at 25°C. Positive for cytochrome oxidase and gelatinase, but negative for arginine dihydrolase, esculin hydrolysis, β-galactosidase, glucose fermentation, indole production, nitrates reduction and urease in API

20NE test. Potassium gluconate is utilized. Strain TJB7 (=NIBRBAC000498051) has been isolated from fresh water sample, Yeonggwang, Jeollanam-do, Korea.

Description of *Rheinheimera tilapiae* JF6

Cells are Gram-staining-negative, flagellated, non-pigmented and rod-shaped. Colonies are circular, raised and yellow-colored after 2 days of incubation on R2A at 25°C. Positive for cytochrome oxidase, esculin hydrolysis, β-galactosidase and nitrates reduction, but negative for arginine dihydrolase, gelatinase, glucose fermentation, indole production and urease in API 20NE test. Strain JF6 (=NIBRBAC000498056) has been isolated from fresh water sample, Jeonju, Jeollabuk-do, Korea.

Description of *Pantoea agglomerans* TW2C3

Cells are Gram-staining-negative, non-flagellated, non-pigmented and coccoid-shaped. Colonies are circular, convex, entire and yellow-colored after 2 days of incubation on NA at 30°C. Positive for gelatinase, but negative for arginine dihydrolase, cytochrome oxidase, esculin hydrolysis, β-galactosidase, glucose fermentation, indole production, nitrates reduction and urease in API 20NE test. D-Glucose, D-maltose and potassium gluconate are utilized. Strain TW2C3 (=NIBRBAC 000498083) has been isolated from soil sample of abandoned mine, Boeun, Chungcheongbuk-do, Korea.

Description of *Pantoea eucalypti* TW2I3

Cells are Gram-staining-negative, non-flagellated, non-pigmented and rod-shaped. Colonies are circular, umbonate, entire and yellow-colored after 2 days of incubation on ISP2 media at 30°C. Positive for gelatinase, but negative for arginine dihydrolase, cytochrome oxidase, esculin hydrolysis, β-galactosidase, glucose fermentation, indole production, nitrates reduction and urease in API 20NE test. D-Glucose, D-maltose, D-mannitol and potassium gluconate are utilized. Strain TW2I3 (=NIBRBAC000498086) has been isolated from soil sample of abandoned mine, Boeun, Chungcheongbuk-do, Korea.

Description of *Pseudoxanthomonas indica* NR 4-01

Cells are Gram-staining-negative, flagellated, non-pigmented and rod-shaped. Colonies are circular, convex, entire and yellow-colored after 2 days of incubation on R2A at 30°C. Positive for cytochrome oxidase, esculin hydrolysis, β-galactosidase and nitrates reduction, but negative for arginine dihydrolase, gelatinase, glucose fermentation, indole production and urease in API 20NE test. *N*-Acetyl-glucosamine, D-glucose, D-maltose and D-mannose and are utilized. Strain NR 4-01 (=NIBRBAC 000498087) has been isolated from plant root sample, Jeongeup, Jeollabuk-do, Korea.

Description of *Serratia plymuthica* GT 8-07

Cells are Gram-staining-negative, flagellated, non-pigmented and short rod-shaped. Colonies are circular, pulvinate, entire and ivory-colored after 2 days of incubation on TSA at 30°C. Positive for cytochrome oxidase, esculin hydrolysis, β-galactosidase, gelatinase, glucose fermentation and nitrates reduction, but negative for arginine dihydrolase, indole production and urease in API 20NE test. *N*-Acetyl-glucosamine, L-arabinose, capric acid, D-glucose, malic acid, D-maltose, D-mannitol, D-mannose, phenylacetic acid, potassium gluconate and trisodium citrate are utilized. Strain GT 8-07 (=NIBRBAC 000498088) has been isolated from plant root sample, Gumi, Gyeongsangbuk-do, Korea.

Description of *Xanthomonas translucens* NR 5-07

Cells are Gram-staining-negative, non-flagellated, non-pigmented and short rod-shaped. Colonies are circular, convex, smooth and yellow-colored after 2 days of incubation on R2A at 30°C. Positive for cytochrome oxidase, esculin hydrolysis, β-galactosidase and nitrates reduction, but negative for arginine dihydrolase, gelatinase, glucose fermentation, indole production and urease in API 20NE test. *N*-Acetyl-glucosamine, D-glucose, D-maltose and D-mannose are utilized. Strain NR 5-07 (=NIBRBAC000498090) has been isolated from plant root sample, Jeongeup, Jeollabuk-do, Korea.

Description of *Alteromonas macleodii* KYW1005

Cells are Gram-staining-negative, non-flagellated, non-pigmented and rod-shaped. Colonies are circular, smooth, raised and cream-colored after 3 days of incubation on MA at 25°C. Positive for cytochrome oxidase, esculin hydrolysis and β-galactosidase, but negative for arginine dihydrolase, gelatinase, glucose fermentation, indole production, nitrates reduction and urease in API 20NE test. Strain KYW1005 (=NIBRBAC000497923) has been isolated from sea water sample, Gwangyang, Jeollanam-do, Korea.

Description of *Pseudomonas songnenensis* KYW941

Cells are Gram-staining-negative, non-flagellated, non-pigmented and rod-shaped. Colonies are radial wrinkled and light yellow-colored after 3 days of incubation on MA at 25°C. Positive for cytochrome oxidase and nitrates reduction, but negative for arginine dihydrolase, esculin hydrolysis, β-galactosidase, gelatinase, glucose

fermentation, indole production and urease in API 20NE test. Adipic acid, capric acid, D-glucose, malic acid, D-maltose, D-mannitol, potassium gluconate and trisodium citrate are utilized. Strain KYW941 (=NIBRBAC 000497924) has been isolated from sea water sample, Gwangyang, Jeollanam-do, Korea.

Description of *Pseudomonas kunmingensis* KYW1051

Cells are Gram-staining-negative, non-flagellated, non-pigmented and rod-shaped. Colonies are circular, opaque and pale yellow-colored after 4 days of incubation on MA at 25°C. Positive for cytochrome oxidase and nitrates reduction, but negative for arginine dihydrolase, esculin hydrolysis, β-galactosidase, gelatinase, glucose fermentation, indole production and urease in API 20NE test. Adipic acid, capric acid, D-glucose, malic acid, D-maltose, D-mannitol, potassium gluconate and trisodium citrate are utilized. Strain KYW1051 (=NIBRBAC 000497928) has been isolated from sea water sample, Gwangyang, Jeollanam-do, Korea.

Description of *Pseudomonas kunmingensis* JD11

Cells are Gram-staining-negative, non-flagellated, non-pigmented and rod-shaped. Colonies are circular, smooth and white-colored after 2 days of incubation on R2A at 25°C. Positive for arginine dihydrolase, cytochrome oxidase and urease, but negative for esculin hydrolysis, β-galactosidase, gelatinase, glucose fermentation, indole production and nitrates reduction in API 20NE test. Capric acid, D-glucose, malic acid, D-mannitol, D-mannose, phenylacetic acid, potassium gluconate and trisodium citrate are utilized. Strain JD11 (=NIBRBAC 000497936) has been isolated from fresh water sample, Changwon, Gyeongsangnam-do, Korea.

Description of *Pseudomonas viridiflava* JD16

Cells are Gram-staining-negative, non-flagellated, pigmented and rod-shaped. Colonies are circular, smooth and pale yellow-colored after 3 days of incubation on R2A at 25°C. Positive for esculin hydrolysis, gelatinase and glucose fermentation, but negative for arginine dihydrolase, cytochrome oxidase, β-galactosidase, indole production, nitrates reduction and urease in API 20NE test. L-Arabinose, capric acid, D-glucose, malic acid, D-mannitol, D-mannose, potassium gluconate and trisodium citrate are utilized. Strain JD16 (=NIBRBAC 000497937) has been isolated from fresh water sample, Changwon, Gyeongsangnam-do, Korea.

Description of *Pseudomonas graminis* JD57

Cells are Gram-staining-negative, non-flagellated, non-pigmented and rod-shaped. Colonies are translucent, convex and cream-colored after 3 days of incubation on R2A at 25°C. Positive for arginine dihydrolase and cytochrome oxidase, but negative for esculin hydrolysis, β-galactosidase, gelatinase, glucose fermentation, indole production, nitrates reduction and urease in API 20NE test. L-Arabinose, capric acid, D-glucose, malic acid, D-mannitol, D-mannose, potassium gluconate and trisodium citrate are utilized. Strain JD57 (=NIBRBAC 000497940) has been isolated from fresh water sample, Changwon, Gyeongsangnam-do, Korea.

Description of *Acinetobacter lwoffii* KHN15

Cells are Gram-staining-negative, non-flagellated, non-pigmented and coccoid-shaped. Colonies are circular and cream-colored after 3 days of incubation on TSA at 25°C. Negative for arginine dihydrolase, cytochrome oxidase, esculin hydrolysis, β-galactosidase, gelatinase, glucose fermentation, indole production, nitrates reduction and urease in API 20NE test. Capric acid, malic acid and phenylacetic acid are utilized. Strain KHN15 (=NIBRBAC000497835) has been isolated from gut of Japanese crested ibis (*Nipponia nippon*), Gwacheon, Gyeonggi-do, Korea.

Description of *Raoultella ornithinolytica* KHL6

Cells are Gram-staining-negative, flagellated, non-pigmented and rod-shaped. Colonies are irregular and cream-colored after 3 days of incubation on R2A at 25°C. Positive for esculin hydrolysis, β-galactosidase, glucose fermentation, indole production and nitrates reduction, but negative for arginine dihydrolase, cytochrome oxidase, gelatinase and urease in API 20NE test. *N*-Acetyl-glucosamine, L-arabinose, D-glucose, malic acid, D-maltose, D-mannitol, D-mannose, phenylacetic acid and potassium gluconate are utilized. Strain KHL6 (=NIBRBAC000497837) has been isolated from gut of burmese python (*Python molurus bivittatus*), Gwacheon, Gyeonggi-do, Korea.

Description of *Stenotrophomonas rhizophila* KHC14

Cells are Gram-staining-negative, non-flagellated, non-pigmented and rod-shaped. Colonies are circular, convex and light yellow-colored after 3 days of incubation on R2A at 25°C. Positive for cytochrome oxidase, esculin hydrolysis, β-galactosidase and gelatinase, but negative for arginine dihydrolase, glucose fermentation, indole production, nitrates reduction and urease in API 20NE test. *N*-Acetyl-glucosamine, D-glucose, malic acid, D-maltose, D-mannose and trisodium citrate are utilized. Strain KHC14 (=NIBRBAC000497840) has been isolated from gut of Japanese crested ibis (*Nipponia nippon*), Gwacheon, Gyeonggi-do, Korea.

Description of *Kosakonia cowanii* KHN5

Cells are Gram-staining-negative, flagellated, non-pigmented and short rod-shaped. Colonies are circular and cream-colored after 3 days of incubation on R2A at 25°C. Positive for esculin hydrolysis, β-galactosidase, glucose fermentation and nitrates reduction, but negative for arginine dihydrolase, cytochrome oxidase, gelatinase, indole production and urease in API 20NE test. *N*-Acetyl-glucosamine, L-arabinose, D-glucose, malic acid, D-maltose, D-mannitol, D-mannose, potassium gluconate and trisodium citrate are utilized. Strain KHN5 (=NIBRBAC000497843) has been isolated from gut of Japanese crested ibis (*Nipponia nippon*), Gwacheon, Gyeonggi-do, Korea.

Description of *Escherichia marmotae* KHM5

Cells are Gram-staining-negative, flagellated, non-pigmented and coccoid-shaped. Colonies are circular and white-colored after 3 days of incubation on R2A at 25°C. Positive for β-galactosidase, glucose fermentation, indole production and nitrates reduction, but negative for arginine dihydrolase, cytochrome oxidase, esculin hydrolysis, gelatinase and urease in API 20NE test. *N*-Acetyl-glucosamine, L-arabinose, D-glucose, malic acid, D-maltose, D-mannitol, D-mannose and potassium gluconate are utilized. Strain KHM5 (=NIBRBAC 000497846) has been isolated from gut of Japanese crested ibis (*Nipponia nippon*), Gwacheon, Gyeonggi-do, Korea.

Description of *Enterobacter xiangfangensis* KHN16

Cells are Gram-staining-negative, non-flagellated, non-pigmented and diplococcirod-shaped. Colonies are circular and cream-colored after 3 days of incubation on R2A at 25°C. Positive for arginine dihydrolase, β-galactosidase, glucose fermentation, nitrates reduction and urease, but negative for cytochrome oxidase, esculin hydrolysis, gelatinase and indole production in API 20NE test. *N*-Acetyl-glucosamine, L-arabinose, malic acid, D-maltose, D-mannitol, D-mannose, phenylacetic acid, potassium gluconate and trisodium citrate are utilized. Strain KHN16 (=NIBRBAC000497849) has been isolated from gut of Japanese crested ibis (*Nipponia nippon*), Gwacheon, Gyeonggi-do, Korea.

Description of *Citrobacter youngae* KHL16

Cells are Gram-staining-negative, non-flagellated, non-pigmented and rod-shaped. Colonies are irregular and cream-colored after 3 days of incubation on R2A at 25°C. Positive for β-galactosidase, glucose fermentation, indole production and nitrates reduction, but negative for arginine dihydrolase, cytochrome oxidase, esculin hydrolysis, gelatinase and urease in API 20NE test. *N*-Acetyl-glucosamine, L-arabinose, D-glucose, malic acid, D-maltose, D-mannitol, D-mannose, potassium gluconate and trisodium citrate are utilized. Strain KHL16 (=NIBRBAC000497850) has been isolated from gut of burmese python (*Python molurus bivittatus*), Gwacheon, Gyeonggi-do, Korea.

Description of *Citrobacter youngae* S6-6

Cells are Gram-staining-negative, non-flagellated, non-pigmented and rod-shaped. Colonies are circular, raised, entire and pale yellow-colored after 2 days of incubation on MA at 30°C. Positive for esculin hydrolysis and nitrates reduction, but negative for arginine dihydrolase, cytochrome oxidase, β-galactosidase, gelatinase, glucose fermentation, indole production and urease in API 20NE test. Strain S6-6 (=NIBRBAC000497887) has been isolated from tidal flat, Taean, Chungcheongnam-do, Korea.

Description of *Marinomonas arenicola* LPB0063

Cells are Gram-staining-negative, flagellated, non-pigmented and rod-shaped. Colonies are circular and white-colored after 2 days of incubation on MA at 26°C. Negative for arginine dihydrolase, cytochrome oxidase, esculin hydrolysis, β-galactosidase, gelatinase, glucose fermentation, indole production, nitrates reduction and urease in API 20NE test. Strain LPB0063 (=NIBRBAC 000497972) has been isolated from sea water sample, Ongjin, Incheon, Korea.

Description of *Psychromonas arctica* LPB0073

Cells are Gram-staining-negative, flagellated, non-pigmented and rod-shaped. Colonies are circular and white-colored after 2 days of incubation on MA at 26°C. Positive for cytochrome oxidase, but negative for arginine dihydrolase, esculin hydrolysis, β-galactosidase, gelatinase, glucose fermentation, indole production, nitrates reduction and urease in API 20NE test. Strain LPB0073 (=NIBRBAC000497973) has been isolated from sea water sample, Ongjin, Incheon, Korea.

Description of *Vibrio atlanticus* LPB0083

Cells are Gram-staining-negative, flagellated, non-pigmented and curved rod-shaped. Colonies are irregular and beige-colored after 2 days of incubation on MA at 26°C. Positive for cytochrome oxidase, but negative for arginine dihydrolase, esculin hydrolysis, β-galactosidase, gelatinase, glucose fermentation, indole production, nitrates reduction and urease in API 20NE test.

Strain LPB0083 (=NIBRBAC000497974) has been isolated from sea water sample, Ongjin, Incheon, Korea.

Description of *Kangiella japonica* LPB0099

Cells are Gram-staining-negative, non-flagellated, non-pigmented and rod-shaped. Colonies are circular, glistening and yellowish-colored after 2 days of incubation on MA at 26°C. Positive for cytochrome oxidase and gelatinase, but negative for arginine dihydrolase, esculin hydrolysis, β-galactosidase, glucose fermentation, indole production, nitrates reduction and urease in API 20NE test. Trisodium citrate is utilized. Strain LPB0099 (=NIBRBAC000497979) has been isolated from sea water sample, Ongjin, Incheon, Korea.

Description of *Kangiella japonica* LPB0123

Cells are Gram-staining-negative, flagellated, non-pigmented and rod-shaped. Colonies are circular and light yellow-colored after 1 days of incubation on MA at 26°C. Positive for cytochrome oxidase, esculin hydrolysis and β-galactosidase, but negative for arginine dihydrolase, gelatinase, glucose fermentation, indole production, nitrates reduction and urease in API 20NE test. Capric acid, D-glucose, malic acid, D-maltose, D-mannitol, D-mannose, potassium gluconate and trisodium citrate are utilized. Strain LPB0123 (=NIBRBAC 000497989) has been isolated from sea water sample, Haeundae, Busan, Korea.

Acknowledgements

This work was supported by the National Research Foundation of Korea, funded by the Ministry of Education of Korea and the National Institute of Biological Resources (NIBR no. 2013-02-001) funded by the Ministry of Environment of Korea.

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Submitted: September 2, 2016
Revised: October 6, 2016
Accepted: June 14, 2017