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A report of 39 unrecorded bacterial species in Korea, belonging to the *Betaproteobacteria* and *Gammaproteobacteria*

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As a subset study to discover indigenous prokaryotic species in Korea, a total of 39 bacterial strains assigned to the classes *Betaproteobacteria* and *Gammaproteobacteria* were isolated from diverse environmental samples collected from soil, tidal flat, freshwater, seawater, seaweed, wetland, plant roots, guts of insects, and fermented foods. From the high 16S rRNA gene sequence similarity (>99.1%) and formation of a robust phylogenetic clade with the closest species, it was determined that each strain belonged to each independent and predefined bacterial species. There is no official report that these 39 species have been described in Korea; therefore 4 species of 4 genera in the order *Burkholderiales* and 1 species in the order *Neisseriales* within the class *Betaproteobacteria*, and 10 species of 6 genera in the order *Alteromonadales*, 11 species of 3 genera in the order *Pseudomonadales*, 4 species of 4 genera in the order *Enterobacteriales*, 2 species of 2 genera in the order *Vibrionales*, 1 species in the order *Aeromonadales*, 3 species of 3 genera in the order *Oceanospirillales*, 2 species of 2 genera in the order *Xanthomonadales*, and 1 species in the order *Chromatiales* within the *Gammaproteobacteia* are reported for proteobacterial species found in Korea. Gram reaction, colony and cell morphology, basic biochemical characteristics, isolation source, and strain IDs are also described in the species description section.

Keywords: 16S rRNA, bacterial diversity, *Betaproteobacteria*, *Gammaproteobacteria*, unrecorded species

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Introduction

Approximately 4-6×10^{30} prokaryotic cells reside in our planet, the Earth, and they are considered to be key players for climate control, material transformation, nutrient cycling, and energy conservation (Whitman *et al*., 1998). Most of these cells are thought to be uncultured, because the current cultivation methods can deliver only small fraction (<0.1%) of total microbial cells (Delong *et al*., 1989; Giovannoni *et al*., 1990). Owing to successful innovative methods for cultivating the uncultured, most of which have mimicked natural environmental conditions (Connon and Giovannoni, 2002; Cho and Giovannoni, 2004; Watanabe *et al*., 2009; Sipkema *et al*., 2011), and the polyphasic taxonomic approaches, 600-800 new names of prokaryotic species have been validly published annually since 2006 (Oren and Garr-

ity, 2014). At a time of writing, approximately 11,500 prokaryotic species have been validly published (Parte, 2014). This number of described prokaryotic species in total, however, is overwhelmingly small when we consider the number of insect species (>950,000) that scientists have identified. According to Pedros-Alio (2006), the Earth contains at least 10^7 prokaryotic species to be described. This indicates that microbial taxonomists have uncovered only the tip of the iceberg of microbial diversity and therefore should accelerate the isolation and description of hidden prokaryotic species.

Since the first valid publication of 2 novel bacterial species in 1997 (Chun *et al*., 1997; Yoon *et al*., 1997), Korea has become one of the leading countries in describing new prokaryotic species. During 2005-2008, Korea was the top country in the numbers of newly described microbial species and became the first country to report more than 100 novel prokaryotic species in a year. A recent study (Oren and Garrity, 2014) shows that 66.8% of new taxa proposal to International Journal of Systematic and Evolutionary Microbiology (IJSEM) was submitted from Asian countries, led by China (25.9%) and Korea (16.4%). The successful story of microbial taxonomy in Korea must be owing to strengthened manpower in the systematics, increased government funds for taxonomy and genomics, and foundation of government-guided research institutes such as National Institute of Biological Resources (NIBR). Since 2006, NIBR has supported Korean microbial taxonomists to describe new prokaryotic species or unrecorded prokaryotic species in Korea, in the research program of 'The Survey of Korean Indigenous Species'. The present study is also a part of this research program.

In 2012, we collected diverse environmental samples and isolated myriads of novel bacterial species and unrecorded bacterial species in Korea. The identified bacterial species belonged to the classes/phyla *Alphaproteobacteria*, *Betaproteobacteria*, *Gammaproteobacteria*, *Deltaproteobacteria*, *Bacteroidetes*, *Firmicutes*, *Actinobacteria*, *Deinococci*, and *Verrucomicrobia*. As a subset of this study, the present report focuses on the description of unrecorded species belonging to the *Betaproteobacteria* and *Gammaproteobacteria*. The class *Betaproteobacteria* is comprised of 7 orders, which are mainly found in terrestrial environments except for a group of marine *Methylophilaceae* called the OM43 clade (Giovannoni *et al*., 2008). The class *Gammaproteobacteria* is the largest class in the phylum *Proteobacteria* and currently composed of 16 orders. Here we report 39 unrecorded bacterial species in Korea belonging to 4 families of 2 orders in the *Betaproteobacteria* and 14 families of 8 orders in the *Gammaproteobacteria*.

Materials and Methods

A total of 39 bacterial strains assigned to the classes *Betaproteobacteria* and *Gammaproteobacteria* were isolated from diverse environmental samples collected from soil, tidal flat, freshwater, seawater, seaweed, wetland, plant roots, ginseng field, guts of insects, and fermented food *kimchii* and *jeotgal* (Table 1). Each environmental sample was processed separately, spread onto diverse culture media including R2A, Marine Agar 2216, Tryptic Soy Agar and Nutrient Agar (all media from BD Difco), and incubated at 25-30°C for 2-5 days (Table 1). The designated strain IDs, sources, culture media, and incubation conditions are summarized in Table 1. All strains were purified as single colonies and stored as 10-20% glycerol suspension −80°C as well as lyophilized ampoules.

Colony morphology of the strains was observed on agar plates with a magnifying glass after cells grew up to stationary phase. Cellular morphology and cell size were examined by either transmission electron microscopy or scanning electron microscopy. Gram staining was performed using a Gram-staining kit or the standard procedures. Biochemical characteristics were tested by using API 20NE galleries (bioMérieux) according to the manufacturer's instructions.

Bacterial DNA extraction, PCR amplification and 16S rRNA gene sequencing were performed using the standard procedures described elsewhere. The 16S rRNA gene sequences of the strains assigned to the *Betaproteobacteria* and *Gammaproteobacteria* were compared with the sequences held in GenBank by BLASTN and also analyzed using the EzTaxon-e server (Kim *et al*., 2012). For phylogenetic analyses, the 16S rRNA gene sequences were aligned using the SILVA Incremental Aligner (SINA v.1.2.11) (Pruesse *et al*., 2012) and imported in the ARB software package (Ludwig *et al*., 2004). Phylogenetic trees were generated by using neighbor-joining (Saitou and Nei, 1987) and maximum-likelihood (Felsenstein, 1981) algorithms that are programmed in MEGA 6.0 (Tamura *et al*., 2013). 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, 5 strains, designated VNT1, RMH2-4, mNT30, HME8439, and HME8586, were assigned to the *Betaproteobacteria*. They were all Gram-

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

Class	Family	Genus	Strain ID	NIBR ID	Most closely related species (Type strain of species)	Similarity to type strain (%)	Isolation source	Medium	Incubation conditions
Betaproteobacteria	*Burkholderiaceae*	*Burkholderia*	VNT1	NIBRBA0000113976	*B. stabilis* (LMG 14294^T)	99.6	Soil	VXG	25°C, 3d
		Cupriavidus	RMH2-4	NIBRBA0000113939	*C. necator* (N-1^T)	99.5	Tidal flat	R2A	30°C, 2d
	Oxalobacteraceae	*Collimonas*	mNT30	NIBRBA0000113979	*C. pratensis* (Ter91^T)	99.5	Soil	MM	25°C, 3d
	Comamonadaceae	*Acidovorax*	HME8439	NIBRBA0000114079	*A. oryzae* (FC-143^T)	99.5	Freshwater	R2A	30°C, 2d
	Neisseriaceae	*Chromobacterium*	HME8586	NIBRBA0000114080	*C. aquaticum* (CC-SEYA-1^T)	99.6	Freshwater	R2A	30°C, 2d
Gammaproteobacteria	*Colwelliaceae*	*Colwellia*	J6	NIBRBA0000114101	*C. aestuarii* (SMK-10^T)	99.8	Seawater	MA	25°C, 3d
	Alteromonadaceae	*Marinobacter*	HD47	NIBRBA0000113991	*M. psychrophilus* (20041^T)	99.1	Tidal flat	MA	25°C, 3d
	Shewanellaceae	*Shewanella*	J4	NIBRBA0000114100	*S. colwelliana* (ATCC 39565^T)	100.0	Seawater	MA	25°C, 3d
		Shewanella	J7	NIBRBA0000114102	*S. gaetbuli* (TF-27^T)	99.9	Seawater	MA	25°C, 3d
	Pseudoalteromonadaceae	*Pseudoalteromonas*	KYW799	NIBRBA0000114111	*P. marina* (Mano4^T)	99.8	Seawater	MA	25°C, 2d
		Pseudoalteromonas	WS-MG1	NIBRBA0000114003	*P. elyakovii* (KMM 162^T)	99.9	Seaweed	MA	25°C, 3d
		Pseudoalteromonas	ES05-9M-7-MA	NIBRBA0000113915	*P. undina* (NCIMB 2128^T)	100.0	Seawater	MA	25°C, 2d
	Alteromonadaceae	*Glaciecola*	KA23	NIBRBA0000114108	*G. mesophila* (KMM 241^T)	99.7	Seawater	MA	25°C, 2d
		Idiomarina	HME8844	NIBRBA0000114095	*I. fontislapidosi* (F23^T)	99.9	Tidal flat	R2A	37°C, 2d
		Idiomarina	IMCC1088	NIBRBA0000113912	*I. loihiensis* (L2TR^T)	99.9	Seawater	MA	25°C, 4d
	Pseudomonadaceae	*Pseudomonas*	WR-R8Y	NIBRBA0000114002	*P. guineae* (M8^T)	99.8	Soil	R2A	25°C, 3d
		Pseudomonas	MA16	NIBRBA0000113968	*P. peli* (R-20805^T)	100.0	Soil	MA	25°C, 2d
		Pseudomonas	SB11	NIBRBA0000114060	*P. marincola* (KMM 3042^T)	99.7	Tidal flat	MA	25°C, 2d
		Pseudomonas	WR-M4W	NIBRBA0000114000	*P. rhodesiae* (CIP 104664^T)	99.9	Soil	R2A	25°C, 3d
		Pseudomonas	MUG3-2	NIBRBA0000113937	*P. mendocina* (LMG 1223^T)	99.4	Wetland	MA	30°C, 2d
		Pseudomonas	CR2-4	NIBRBA0000113866	*P. nitroreducens* (DSM 14399^T)	99.4	Plant root	R2A	30°C, 5d
		Pseudomonas	CRS5-1	NIBRBA0000113952	*P. psychrotolerans* (C36^T)	99.7	Soil	R2A	30°C, 2d
		Pseudomonas	HWDM10	NIBRBA0000113994	*P. caeni* (HY-14^T)	99.7	Seawater	R2A	25°C, 3d
	Moraxellaceae	*Psychrobacter*	WS-MW4	NIBRBA0000114005	*P. fozii* (NF23^T)	100.0	Seaweed	MA	25°C, 3d
		Psychrobacter	WS-MW1	NIBRBA0000114004	*P. nivimaris* (88/2-7^T)	99.9	Seaweed	MA	25°C, 3d
		Acinetobacter	CT3-6	NIBRBA0000113859	*A. calcoaceticus* (DSM 30006^T)	99.9	Plant root	TSA	30°C, 2d

Table 1. Continued.

Class	Family	Genus	Strain ID	NIBR ID	Most closely related species (Type strain of species)	Similarity to type strain (%)	Isolation source	Medium	Incubation conditions
Gammaproteobacteria	*Enterobacteriaceae*	*Cedecea*	HME8588	NIBRBA0000114081	*C. davisae* (DSM 4568^T)	99.6	Lake water	R2A	30°C, 2d
		Enterobacter	CR6-3	NIBRBA0000113862	*E. ludwigii* (DSM 16688^T)	99.2	Plant root	R2A	30°C, 3d
		Pantoea	HY_N_1_1	NIBRBA0000114036	*P. vagans* (LMG 24199^T)	99.6	Gut of insect	NA	25°C, 2d
		Gibbsiella	LE_C_1_2	NIBRBA0000114015	*G. quercinecans* (FRB 97^T)	99.9	Gut of insect	CA	25°C, 2d
	Vibrionaceae	*Vibrio*	ES05-27M-7	NIBRBA0000113914	*V. tapetis* (HH6087^T)	100.0	Seawater	MA	25°C, 4d
		Enterovibrio	J19	NIBRBA0000114103	*E. norvegicus* (LMG 19839^T)	99.4	Seawater	MA	25°C, 3d
	Aeromonadaceae	*Aeromonas*	HME8508	NIBRBA0000114070	*A. veronii* (ATCC 35624^T)	100.0	River water	R2A	30°C, 1d
	Halomonadaceae	*Chromohalobacter*	M8	NIBRBA0000114055	*C. canadensis* (ATCC43984^T)	99.9	*Kimchi*	MA	25°C, 2d
		Kushneria	PM3	NIBRBA0000114057	*K. indalinina* (CG2.1^T)	99.2	*Jeotgal*	MA	25°C, 2d
	Oceanospirillaceae	*Neptunomonas*	KYW889	NIBRBA0000114115	*N. concharum* (LHW37^T)	99.9	Seawater	MA	25°C, 2d
	Xanthomonadaceae	*Lysobacter*	CT5-2	NIBRBA0000113858	*L. enzymogenes* (DSM 2043^T)	99.5	Plant root	TSA	30°C, 2d
		Rhodanobacter	Gsoil549	NIBRBA0000113891	*R. lindaniclasticus* (RP5557^T)	99.9	Soil	R2A	25°C, 2d
	Granulosicoccaceae	*Granulosicoccus*	WSW-MW5	NIBRBA0000114008	*G. coccoides* (Z 271^T)	100.0	Seawater	MA	25°C, 5d

staining-negative, chemoheterotrophic, and rod-shaped bacteria (Fig. 1). Colony size, morphology, and physiological characteristics are shown in the species description section.

Strains VNT1, RMH2-4, mNT30, HME8439, and HME8586 were most closely related to *Burkholderia stabilis* LMG 14294^T (AF148554; 99.6% 16S rRNA gene sequence similarity), *Cupriavidus necator* N-1^T (CP002878; 99.5%), *Collimonas pratensis* Ter91^T (AY 281137; 99.5%), *Acidovorax oryzae* FC-143^T (DQ 360414; 99.5%), and *Chromobacterium aquaticum* CC-SEYA-1^T (EU109734; 99.6%), respectively (Table 1). As expected from high 16S rRNA gene sequence similarities of the 5 strains with their closest relatives, each strain formed a robust phylogenetic clade with the most closely related species (Fig. 2). From the high 16S rRNA gene sequence similarity and robust formation of phylogenetic clade, it is concluded that strains VNT1, RMH2-4, mNT30, HME8439, and HME8586 are members of the species *Burkholderia stabilis* (Vandamme *et al*., 2000), *Cupriavidus necator* (Makkar and Casida, 1987), *Collimonas pratensis* (Höppener-Ogawa *et al*., 2008), *Acidovorax oryzae* (Schaad *et al*., 2008), and *Chromobacterium aquaticum* (Young *et al*., 2008), respectively. There has been no official report that these species have been isolated in Korea; therefore *Burkholderia stabilis* and *Cupriavidus necator* of the family *Burkholderiaceae*, *Collimonas pratensis* of the *Oxalobacteraceae*, *Acidovorax oryzae* of the *Comamonadaceae*, and *Chromobacterium aquaticum* of the *Neisseriaceae* are reported for 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 34 strains were assigned to the class *Gammaproteobacteria*. The 34 strains were distributed in 8 orders of the *Gammaproteobacteria*; 10 strains for the order *Alteromonadales*, 11 strains for the *Pseudomonadales*, 4 strains for the *Enterobacteriales*, 2 strains for the *Vibrionales*, 1 strain for the *Aeromonadales*, 3 strains for the *Oceanospirillales*, 2 strains for the *Xanthomonadales*, and 1 strain for the *Chromatiales* (Table 1). These strains were Gram-staining-negative, chemoheterotrophic, and rod-shaped bacteria except for strain WSW-MW5 showing coccoid-shaped (Fig. 1). Colony size, morphology, and physiological characteristics are also shown in the species description section.

The strains in the order *Alteromonadales* (Fig. 3) isolated from this study were composed of strains exclusively retrieved from marine environments (Table 1). Based on the phylogenetic analyses showing robust clades (Fig. 3) and comparative sequence analyses representing high

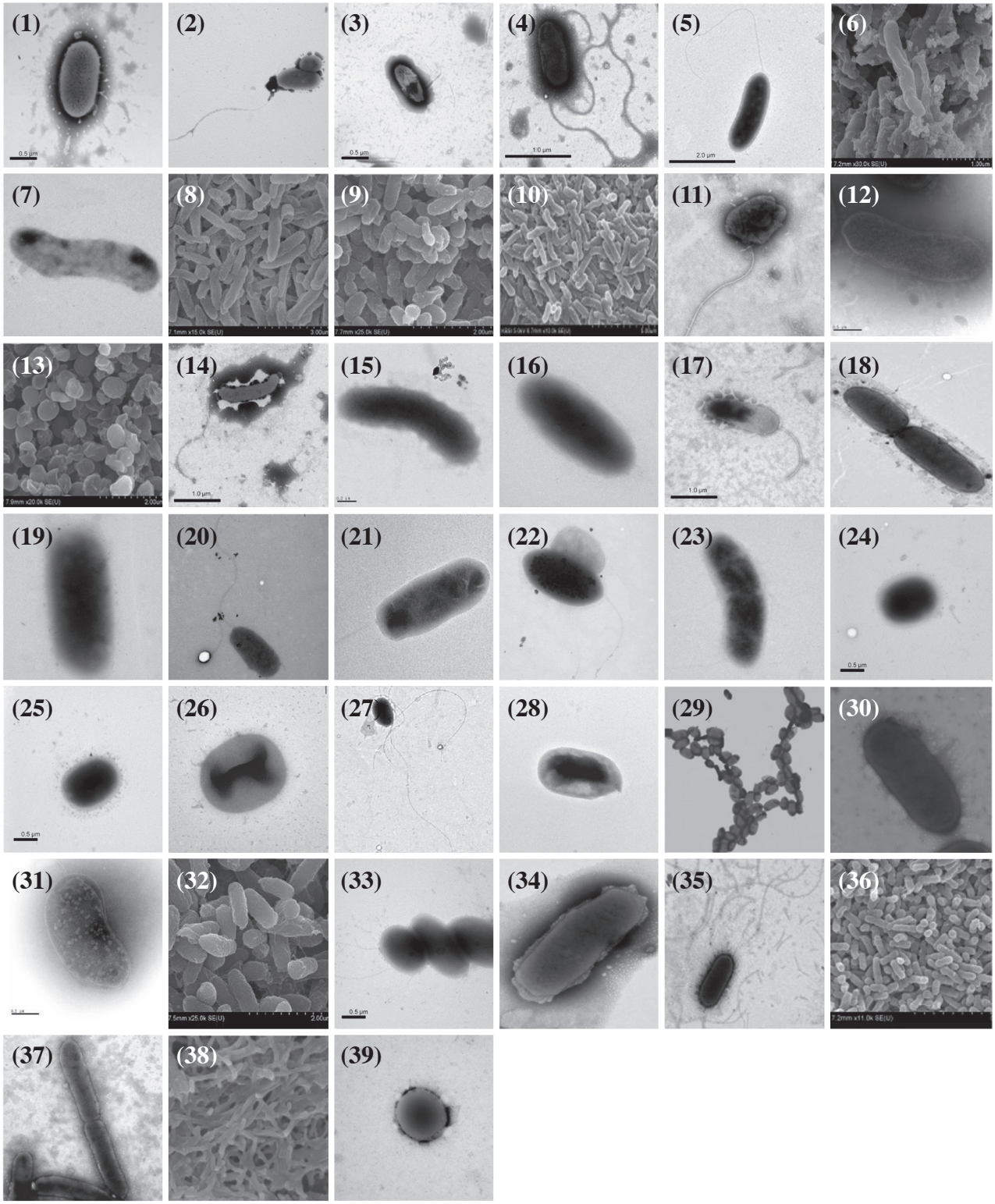

Fig. 1. Transmission electron micrographs or scanning electron micrographs of cells of the strains isolated in this study. Strains: 1. VNT1; 2. RMH2-4; 3. mNT30; 4. HME8439; 5. HME8586; 6. J6; 7. HD47; 8. J4; 9. J7; 10. KYW799; 11. WS-MG1; 12. ES05-9M-7-MA; 13. KA23; 14. HME8844; 15. IMCC1088; 16. WR-R8Y; 17. MA16; 18. SB11; 19. WR-M4W; 20. MUG3-2; 21. CR2-4; 22. CRS5-1; 23. HWDM10; 24. WS-MW4; 25. WS-MW1; 26. CT3-6; 27. HME8588; 28. CR6-3; 29. HY_N_1_1; 30. LE_C_1_2; 31. ES05-27M-7; 32. J19; 33. HME8508; 34. M8; 35. PM3; 36. KYW889; 37. CT5-2; 38. Gsoil549; 39. WSW-MW5.

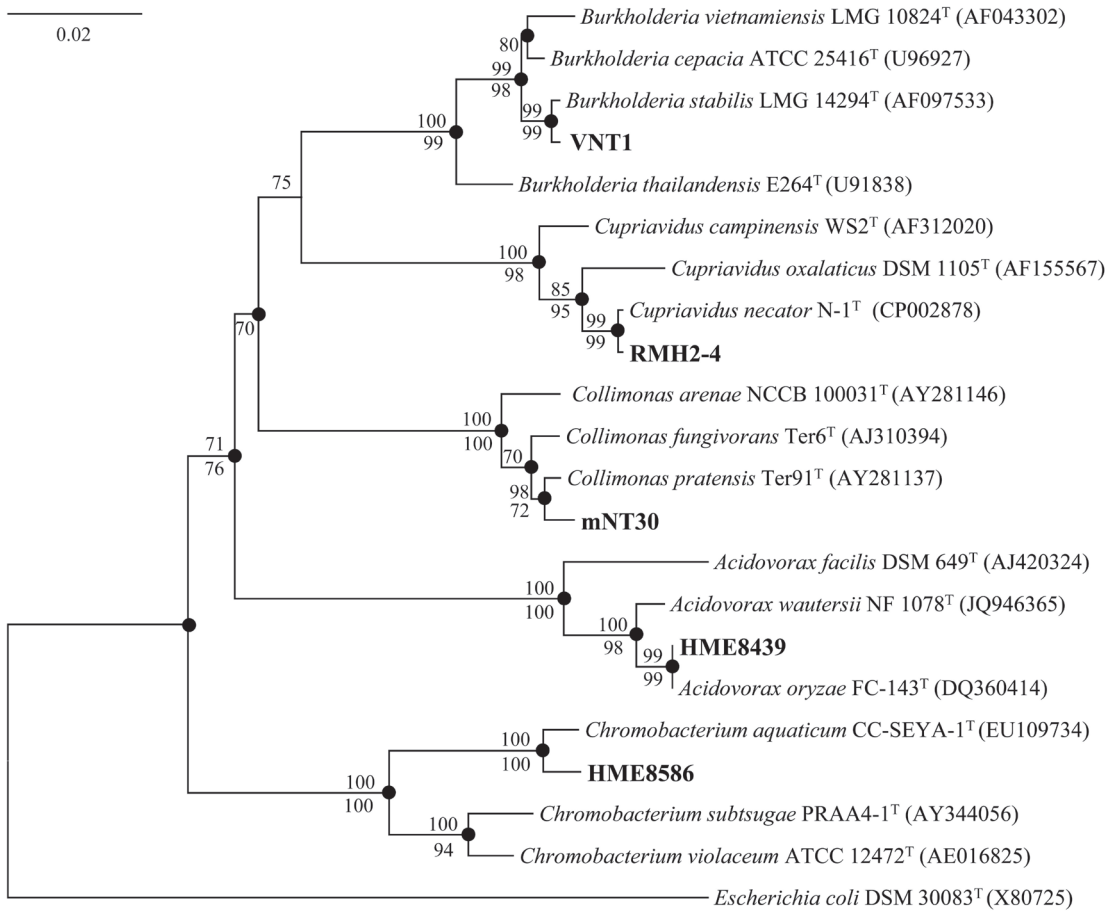

Fig. 2. Neighbor-joining phylogenetic tree, based on 16S rRNA gene sequences, showing the relationship between the strains isolated in this study and their relatives of the class *Betaproteobacteria*. Bootstrap values (>70%) are shown above nodes for the neighbor-joining and below nodes for the maximum-likelihood methods. Filled circles indicate the nodes recovered by the two treeing methods. Bar, 0.02 substitutions per nucleotide position.

16S rRNA gene sequence similarities with the closest relatives (Table 1), it was found that the strains in the order *Alteromonadales* belonged to 10 separate species: *Colwellia aestuarii* (Jung *et al*., 2006), *Marinobacter psychrophilus* (Zhang *et al*., 2008), *Shewanella colwelliana* (Coyne *et al*., 1989), *Shewanella gaetbuli* (Yoon *et al*., 2004), *Pseudoalteromonas marina* (Nam *et al*., 2007), *Pseudoalteromonas elyakovii* (Sawabe *et al*., 2000), *Pseudoalteromonas undina* (Gauthier *et al*., 1995), *Glaciecola mesophila* (Romanenko *et al*., 2003), *Idiomarina fontislapidosi* (Martínez-Cánovas *et al*., 2004), and *Idiomarina loihiensis* (Donachie *et al*., 2003).

A total of 11 strains were assigned to the order *Pseudomonadales*: 8 strains for the family *Pseudomonadaceae* and 3 strains for the *Moraxellaceae* (Fig. 4, Table 1). All strains assigned to the family *Pseudomonadaceae* belonged to the genus *Pseudomonas* and were isolated mainly from terrestrial ecosystem. Phylogenetic analyses based on 16S rRNA gene sequences showed that 8 strains are members of the following species of the genus *Pseudomonas*: *P. guineae* (Bozal *et al*., 2007), *P. peli* (Vanparys *et al*., 2006), *P. marincola* (Romanenko *et al*., 2008), *P. rhodesiae* (Coroler *et al*., 1996), *P. mendocina* (Palleroni *et al*., 1970), *P. nitroreducens* (Lang *et al*., 2007), *P. psychrotolerans* (Hauser *et al*., 2004), and *P. caeni* (Xiao *et al*., 2009). Three strains of the family *Moraxellaceae* belonged to *Psychrobacter fozii* (Bozal *et al*., 2003), *Psychrobacter nivimaris* (Heuchert *et al*., 2004), and *Acinetobacter calcoaceticus* (Bouvet and Grimont, 1986).

Fig. 5 shows phylogenetic assignment of 13 strains into 13 species of the orders *Enterobacteriales*, *Vibrionales*, *Aeromonadales*, *Oceanospirillales*, *Xanthomonadales*, and *Chromatiales*. These strains belonged to *Cedecea davisae* (Bouvet and Grimont, 1986), *Enterobacter ludwigii* (Hoffmann *et al*., 2005), *Pantoea vagans* (Brady *et al*., 2009), and *Gibbsiella quercinecans* (Brady *et al*., 2010) of the family *Enterobacteriaceae*, *Vibrio tapetis* (Borrego *et al*., 1996) and *Enterovibrio norvegi-*

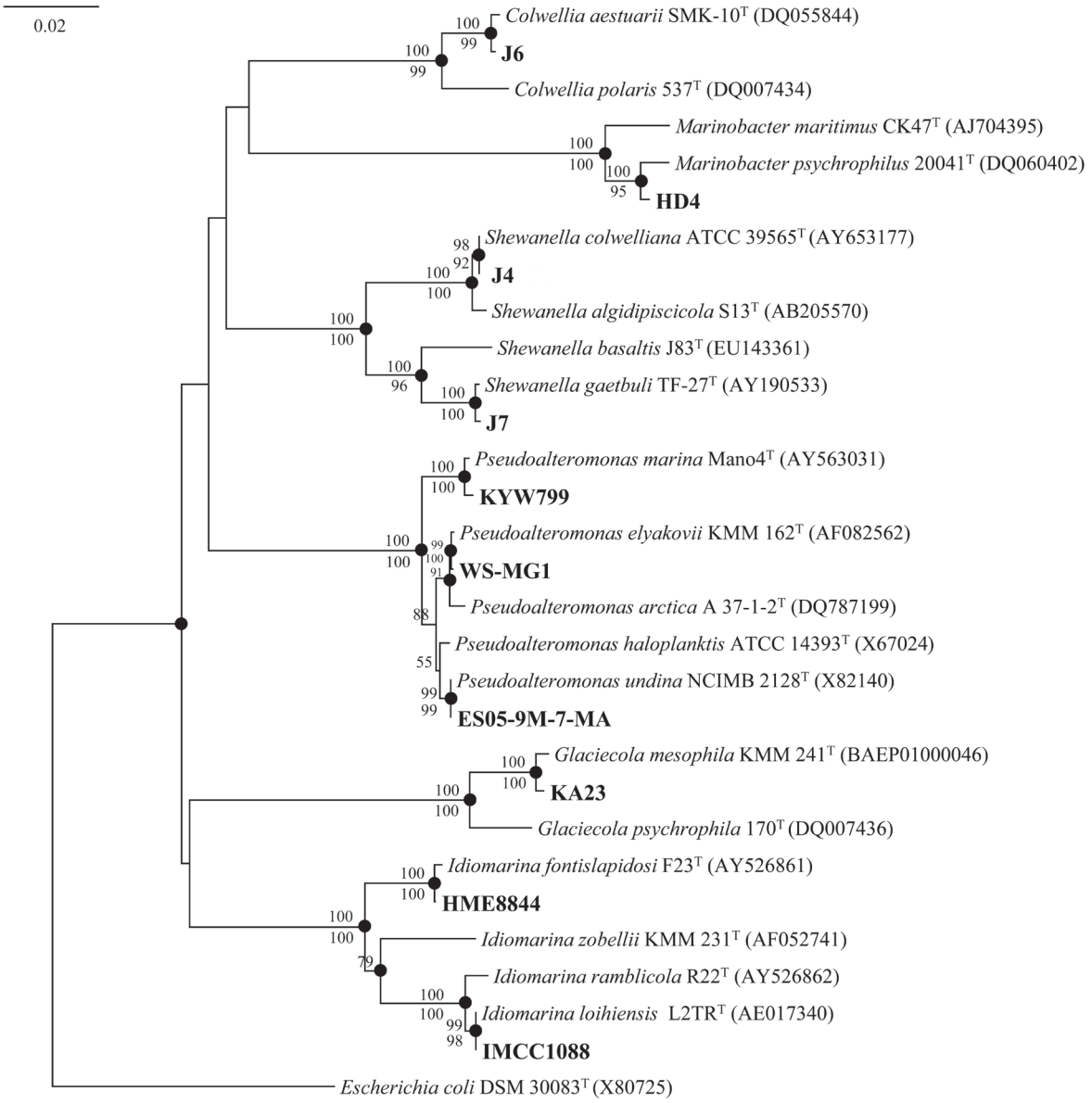

Fig. 3. Neighbor-joining phylogenetic tree, based on 16S rRNA gene sequences, showing the relationship between the strains isolated in this study and their relatives of the order *Alteromonadales* in the class *Gammaproteobacteria*. Bootstrap values (>70%) are shown above nodes for the neighbor-joining and below nodes for the maximum-likelihood methods. Filled circles indicate the nodes recovered by the two treeing methods. Bar, 0.02 substitutions per nucleotide position.

cus (Thompson *et al*., 2002) of the family *Vibrionaceae*, *Aeromonas veronii* (Hickman-Brenner *et al*., 1987) of the family *Aeromonadaceae*, *Chromohalobacter canadensis* (Arahal *et al*., 2001) and *Kushneria indalinina* (Sánchez-Porro *et al*., 2009) of the family *Halomonadaceae*, *Neptunomonas concharum* (Lee *et al*., 2012) of the family *Oceanospirillaceae*, *Lysobacter enzymogenes* (Christensen and Cook, 1978) and *Rhodanobacter lindaniclasticus* (Nalin *et al*., 1999) of the family *Xanthomonadaceae*, and *Granulosicoccus coccoides* (Kurilenko *et al*., 2010) of the family *Granulosicoccaceae*.

There is no official report that these 34 species have been isolated in Korea; therefore 10 species in 6 genera of 5 families in the order *Alteromonadales*, 11 species in 3 genera of 2 families in the order *Pseudomonadales*, 4 species in 4 genera in the order *Enterobacteriales*, 2 species in 2 genera in the order *Vibrionales*, 1 species in the order *Aeromonadales*, 3 species in 3 genera of 2 families in the order *Oceanospirillales*, 2 species in 2 genera in the order *Xanthomonadales*, and 1 species in the order

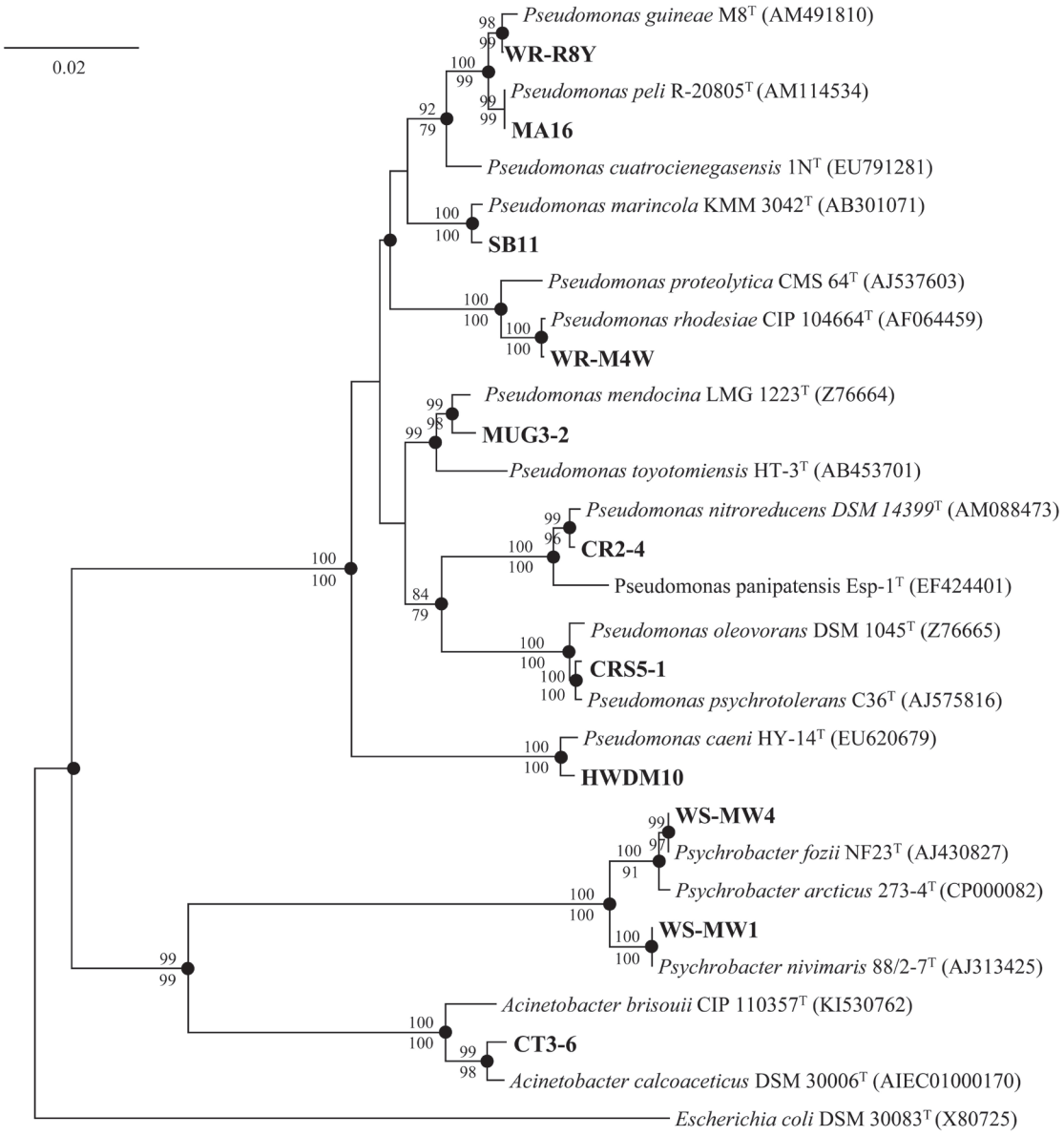

Fig. 4. Neighbor-joining phylogenetic tree, based on 16S rRNA gene sequences, showing the relationship between the strains isolated in this study and their relatives of the order *Pseudomonadales* in the class *Gammaproteobacteria*. Bootstrap values (>70%) are shown above nodes for the neighbor-joining and below nodes for the maximum-likelihood methods. Filled circles indicate the nodes recovered by the two treeing methods. Bar, 0.02 substitutions per nucleotide position.

Chromatiales are reported for gammaproteobacterial species found in Korea.

Description of *Burkholderia stabilis* VNT1

Cells are Gram-staining-negative, non-flagellated, non-pigmented, and rod-shaped. Colonies are circular, convex, and yellow-colored after 3 days of incubation on VXG at 25°C. Positive for glucose fermentation, esculin hydrolysis, gelatinase, and β-galactosidase in API 20NE, but negative for nitrate reduction, indole production, arginine dihydrolase, and urease. D-Glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, D-maltose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid are utilized. Strain VNT1 (=NIBRBA0000113976) has been isolated from a soil sample, Gwanak Mountain, Seoul, Korea.

Description of *Cupriavidus necator* RMH2-4

Cells are Gram-staining-negative, flagellated, non-pigmented, and short rod-shaped. Colonies are circular,

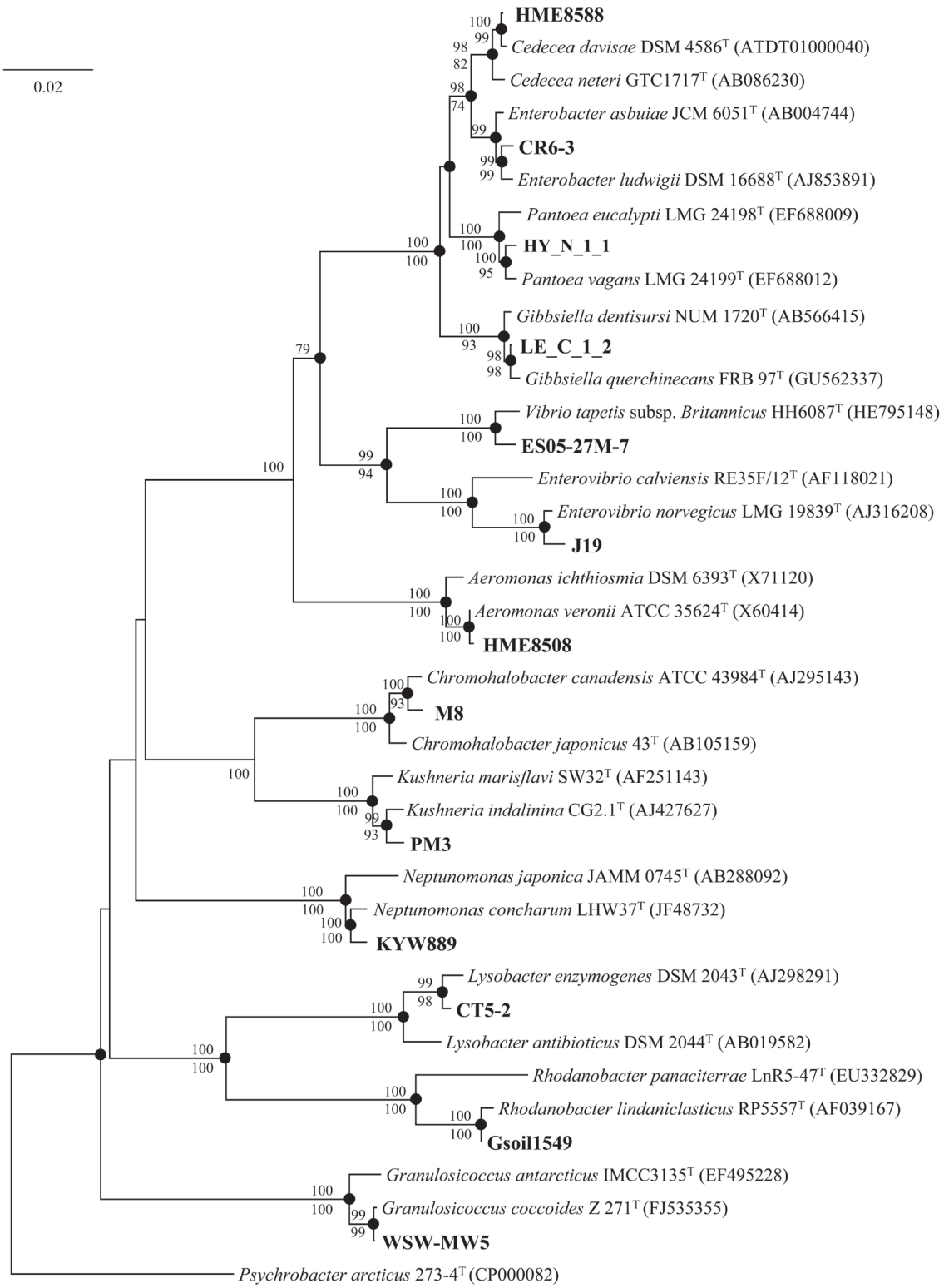

Fig. 5. Neighbor-joining phylogenetic tree, based on 16S rRNA gene sequences, showing the relationship between the strains isolated in this study and their relatives of the class *Gammaproteobacteria*. Bootstrap values (>70%) are shown above nodes for the neighbor-joining and below nodes for the maximum-likelihood methods. Filled circles indicate the nodes recovered by the two treeing methods. Bar, 0.02 substitutions per nucleotide position.

entire, smooth, and white colored after 2 days of incubation on R2A at 30°C. Positive for nitrate reduction in API 20NE, but negative for indole production, glucose fermentation, arginine dihydrolase, urease, esculin hydrolysis, gelatinase and β-galactosidase. Potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid are utilized. Does not utilize D-glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, and D-maltose. Strain RMH2-4 (=NIBRBA0000113939) has been isolated from a tidal flat sample, Taean, Korea.

Description of *Collimonas pratensis* mNT30

Cells are Gram-staining-negative, non-flagellated, non-pigmented, and rod-shaped. Colonies are circular and white-beige colored after 3 days of incubation on minimal medium at 25°C. Positive for gelatinase and β-galactosidase in API 20NE, but negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, urease, and esculin hydrolysis. D-Glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, potassium gluconate, malic acid, and trisodium citrate are utilized. Does not utilize D-maltose, capric acid, adipic acid, and phenylacetic acid. Strain mNT30 (=NIBRBA0000113979) has been isolated from a forest soil sample, Gwanak Mountain, Seoul, Korea.

Description of *Acidovorax oryzae* HME8439

Cells are Gram-staining-negative, flagellated, and rod-shaped. Colonies are circular, convex, entire, and yellow colored after 2 days of incubation on R2A at 30°C. Positive for nitrate reduction, urease, and β-galactosidase in API 20NE, but negative for indole production, glucose fermentation, arginine dihydrolase, esculin hydrolysis, and gelatinase. D-Glucose, L-arabinose, D-mannitol, potassium gluconate, capric acid, adipic acid, and malic acid are utilized. Does not utilize D-mannose, *N*-acetyl-glucosamine, D-maltose, trisodium citrate, and phenylacetic acid. Strain HME8439 (=NIBRBA0000114079) has been isolated from a freshwater sample, Yongin, Korea.

Description of *Chromobacterium aquaticum* HME8586

Cells are Gram-staining-negative, flagellated, and rod-shaped. Colonies are circular, raised, entire, and white colored after 2 days of incubation on R2A at 30°C. Positive for nitrate reduction, arginine dihydrolase, and gelatinase in API 20NE, but negative for indole production, glucose fermentation, urease, esculin hydrolysis, and β-galactosidase. D-Glucose, D-mannitol, *N*-acetyl-glucosamine, potassium gluconate, capric acid, malic acid, trisodium citrate, and phenylacetic acid are utilized. Does not utilize L-arabinose, D-mannose, D-maltose, and adipic acid. Strain HME8586 (=NIBRBA0000114080) has been isolated from a freshwater sample, Juam Reservoir, Korea.

Description of *Colwellia aestuarii* J6

Cells are Gram-staining-negative, non-flagellated, non-pigmented, and rod-shaped. Colonies are opaque, round, smooth, convex, and cream colored after 3 days on MA at 25°C. Negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, urease, esculin hydrolysis, gelatinase, and β-galactosidase in API 20NE. Does not utilize D-glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, D-maltose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid. Strain J6 (=NIBRBA0000114101) has been isolated from a seawater sample, Gwangyang Bay, Korea.

Description of *Marinobacter psychrophilus* HD47

Cells are Gram-staining-negative, non-flagellated, non-pigmented, and rod-shaped. Colonies are circular, convex, smooth, and cream colored after 3 days on MA at 25°C. Negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, urease, esculin hydrolysis, gelatinase, and β-galactosidase in API 20NE. Does not utilize D-glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, D-maltose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid. Strain HD47 (=NIBRBA0000113991) has been isolated from a tidal flat, Taean, Korea.

Description of *Shewanella colwelliana* J4

Cells are Gram-staining-negative, non-flagellated, non-pigmented, and rod-shaped. Colonies are opaque, round, smooth, convex, and cream colored after 3 days on MA at 25°C. Positive for nitrate reduction and esculin hydrolysis in API 20NE, but negative for indole production, glucose fermentation, arginine dihydrolase, urease, gelatinase, and β-galactosidase. *N*-Acetyl-glucosamine and malic acid are utilized. Does not utilize D-glucose, L-arabinose, D-mannose, D-mannitol, D-maltose, potassium gluconate, capric acid, adipic acid, trisodium citrate, and phenylacetic acid. Strain J4 (=NIBRBA 0000114100) has been isolated from a seawater sample, Gwangyang Bay, Korea.

Description of *Shewanella gaetbuli* J7

Cells are Gram-staining-negative, non-flagellated, non-pigmented, and rod-shaped. Colonies are opaque, round,

smooth, convex, and beige colored after 3 days on MA at 25°C. Positive for nitrate reduction and esculin hydrolysis in API 20NE, but negative for indole production, glucose fermentation, arginine dihydrolase, urease, gelatinase, and β-galactosidase. *N*-Acetyl-glucosamine is utilized. Does not utilize D-glucose, L-arabinose, D-mannose, D-mannitol, D-maltose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid. Strain J7 (=NIBRBA0000114102) has been isolated from a seawater sample, Gwangyang Bay, Korea.

Description of *Pseudoalteromonas marina* KYW799

Cells are Gram-staining-negative, non-flagellated, non-pigmented, and rod-shaped. Colonies are opaque, round, smooth, convex, and cream colored after 2 days on MA at 25°C. Positive for esculin hydrolysis and β-galactosidase in API 20NE, but negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, urease, and gelatinase. Does not utilize D-glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, D-maltose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid. Strain KYW799 (=NIBRBA0000114111) has been isolated from a seawater sample, Gwangyang Bay, Korea.

Description of *Pseudoalteromonas elyakovii* WS-MG1

Cells are Gram-staining-negative, flagellated, non-pigmented, and irregular-shaped. Colonies are circular, smooth, glistening, and dark-grey colored after 3 days on MA at 25°C. Positive for nitrate reduction, esculin hydrolysis, gelatinase, and β-galactosidase in API 20NE, but negative for indole production, glucose fermentation, arginine dihydrolase, and urease. D-Mannitol is utilized. Does not utilize D-glucose, L-arabinose, D-mannose, *N*-acetyl-glucosamine, D-maltose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid. Strain WS-MG1 (=NIBRBA 0000114003) has been isolated from a seaweed sample, Wando, Korea.

Description of *Pseudoalteromonas undina* ES05-9M-7-MA

Cells are Gram-staining-negative, non-flagellated, and rod-shaped. Colonies are circular, smooth, and pale yellow colored after 2 days on MA at 25°C. Positive for esculin hydrolysis and gelatinase in API 20NE, but negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, urease, and β-galactosidase. Does not utilize D-glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, D-maltose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid. Strain ES05-9M-7-MA (=NIBRBA0000113915) has been isolated from a seawater sample, Pohang, the East Sea, Korea.

Description of *Glaciecola mesophila* KA23

Cells are Gram-staining-negative, non-flagellated, non-pigmented, and short rod-shaped. Colonies are opaque, round, with raised margin, smooth, convex, and white colored after 3 days on MA at 25°C. Negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, urease, esculin hydrolysis, gelatinase, and β-galactosidase in API 20NE. Does not utilize D-glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, D-maltose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid. Strain KA23 (=NIBRBA0000114108) has been isolated from a seawater sample, Gwangyang Bay, Korea.

Description of *Idiomarina fontislapidosi* HME8844

Cells are Gram-staining-negative, flagellated, non-pigmented, and rod-shaped. Colonies are circular, raised, entire, and white colored after 2 days on R2A at 37°C. Positive for esculin hydrolysis in API 20NE, but negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, urease, gelatinase, and β-galactosidase. Does not utilize D-glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, D-maltose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid. Strain HME8844 (=NIBRBA0000114095) has been isolated from a tidal flat sample, Sinan, Korea.

Description of *Idiomarina loihiensis* IMCC1088

Cells are Gram-staining-negative, non-flagellated, and rod-shaped. Colonies are circular, convex, smooth, and beige colored after 4 days on MA at 25°C. Positive for gelatinase in API 20NE, but negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, urease, esculin hydrolysis, and β-galactosidase. Does not utilize D-glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, D-maltose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid. Strain IMCC 1088 (=NIBRBA0000113912) has been isolated from a seawater sample, Kosung, the East Sea, Korea.

Description of *Pseudomonas guineae* WR-R8Y

Cells are Gram-staining-negative, non-flagellated, non-pigmented, and rod-shaped. Colonies are irregular, smooth, glistening, and pale yellow colored after 3 days

on R2A at 25°C. Positive for nitrate reduction, arginine dihydrolase, urease, and gelatinase in API 20NE, but negative for indole production, glucose fermentation, esculin hydrolysis, and β-galactosidase. L-Arabinose, capric acid, malic acid, and trisodium citrate are utilized. Does not utilize D-glucose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, D-maltose, potassium gluconate, adipic acid, and phenylacetic acid. Strain WR-R8Y (=NIBRBA 0000114002) has been isolated from a soil sample of a field of reeds, Wando, Korea.

Description of *Pseudomonas peli* MA16

Cells are Gram-staining-negative, flagellated, non-pigmented, and rod-shaped. Colonies are round and yellow-colored after 2 days on MA at 25°C. Positive for glucose fermentation and arginine dihydrolase in API 20NE, but negative for nitrate reduction, indole production, urease, esculin hydrolysis, gelatinase, and β-galactosidase. Capric acid, malic acid, and trisodium citrate are utilized. Does not utilize D-glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, D-maltose, potassium gluconate, adipic acid, and phenylacetic acid. Strain MA16 (=NIBRBA0000113968) has been isolated from a forest soil sample, Gwanak Mountain, Korea.

Description of *Pseudomonas marincola* SB11

Cells are Gram-staining-negative, non-flagellated, non-pigmented, and rod-shaped. Colonies are circular, raised, entire, and yellow colored after 2 days on MA at 25°C. Positive for nitrate reduction, arginine dihydrolase, esculin hydrolysis, and β-galactosidase in API 20NE, but negative for indole production, glucose fermentation, urease, and gelatinase. D-Glucose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, potassium gluconate, capric acid, malic acid and trisodium citrate are utilized. Does not utilize L-arabinose, D-maltose, adipic acid, and phenylacetic acid. Strain SB11 (=NIBRBA0000114060) has been isolated from a tidal flat sample, Taean, Korea.

Description of *Pseudomonas rhodesiae* WR-M4W

Cells are Gram-staining-negative, non-flagellated, non-pigmented, and rod-shaped. Colonies are irregular, smooth, glistening, and pale yellow colored after 3 days on R2A at 25°C. Positive for nitrate reduction, glucose fermentation, arginine dihydrolase, urease, esculin hydrolysis, and gelatinase in API 20NE, but negative for indole production and β-galactosidase. D-Glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, D-maltose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid are utilized. Strain WR-M4W (=NIBRBA0000114000) has been isolated from a soil sample of a field of reeds, Wando, Korea.

Description of *Pseudomonas mendocina* MUG3-2

Cells are Gram-staining-negative, flagellated, and rod-shaped. Colonies are irregular, undulate, smooth, and white colored after 2 days on MA at 30°C. Positive for nitrate reduction in API 20NE, but negative for indole production, glucose fermentation, arginine dihydrolase, urease, esculin hydrolysis, gelatinase, and β-galactosidase. D-Glucose, capric acid, malic acid and trisodium citrate are utilized. Does not utilize L-arabinose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, D-maltose, potassium gluconate, adipic acid, and phenylacetic acid. Strain MUG3-2 (=NIBRBA0000113937) has been isolated from a wet land sample, Taean, Korea.

Description of *Pseudomonas nitroreducens* CR2-4

Cells are Gram-staining-negative, flagellated, non-pigmented and rod-shaped. Colonies are complex, smooth, and pale white colored after 5 days on R2A at 30°C. Positive for nitrate reduction, arginine dihydrolase, and urease in API 20NE, but negative for indole production, glucose fermentation, esculin hydrolysis, gelatinase, and β-galactosidase. D-Glucose, *N*-acetyl-glucosamine, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid are utilized. Does not utilize L-arabinose, D-mannose, D-mannitol, and D-maltose. Strain CR2-4 (=NIBRBA0000113866) has been isolated from a plant root sample, Chiak Mountain, Wonju, Korea.

Description of *Pseudomonas psychrotolerans* CRS5-1

Cells are Gram-staining-negative, flagellated, and rod-shaped. Colonies are circular, entire, smooth, and yellow colored after 2 days on R2A at 30°C. Negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, urease, esculin hydrolysis, gelatinase, and β-galactosidase in API 20NE. D-Glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, D-maltose, potassium gluconate, capric acid, adipic acid, malic acid, and trisodium citrate are utilized. Does not utilize phenylacetic acid. Strain CRS5-1 (=NIBRBA0000113952) has been isolated from a soil sample of Ginseng field, Ansung, Korea.

Description of *Pseudomonas caeni* HWDM10

Cells are Gram-staining-negative, non-flagellated, non-pigmented, and rod-shaped. Colonies are circular, smooth, glistening, and yellowish-white colored after 3 days on R2A at 25°C. Positive for nitrate reduction in API 20NE, but negative for indole production, glucose fermentation, arginine dihydrolase, urease, esculin hy-

drolysis, gelatinase, and β-galactosidase. Capric acid is utilized. Does not utilize D-glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, D-maltose, potassium gluconate, adipic acid, malic acid, trisodium citrate, and phenylacetic acid. Strain HWDM10 (=NIBRBA0000113994) has been isolated from a seawater sample, Taean, Korea.

Description of *Psychrobacter fozii* WS-MW4

Cells are Gram-staining-negative, non-flagellated, non-pigmented, and oval-shaped. Colonies are circular, smooth, glistening, and cream colored after 3 days on MA at 25°C. Positive for nitrate reduction and urease in API 20NE, but negative for indole production, glucose fermentation, arginine dihydrolase, esculin hydrolysis, gelatinase, and β-galactosidase. Malic acid is utilized. Does not utilize D-glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, D-maltose, potassium gluconate, capric acid, adipic acid, trisodium citrate, and phenylacetic acid. Strain WS-MW4 (=NIBRBA 0000114005) has been isolated from a seaweed sample, Wando, Korea.

Description of *Psychrobacter nivimaris* WS-MW1

Cells are Gram-staining-negative, non-flagellated, non-pigmented, and oval-shaped. Colonies are circular, smooth, glistening, and cream colored after 3 days on MA at 25°C. Positive for nitrate reduction, glucose fermentation, and urease in API 20NE, but negative for indole production, arginine dihydrolase, esculin hydrolysis, gelatinase, and β-galactosidase. Capric acid, malic acid, and phenylacetic acid are utilized. Does not utilize D-glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, D-maltose, potassium gluconate, adipic acid, and trisodium citrate. Strain WS-MW1 (=NIBRBA 0000114004) has been isolated from a seaweed sample, Wando, Korea.

Description of *Acinetobacter calcoaceticus* CT3-6

Cells are Gram-staining-negative, non-flagellated, non-pigmented, and cocci-shaped. Colonies are round and ivory colored after 2 days on TSA at 30°C. Positive for urease in API 20NE, but negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, esculin hydrolysis, gelatinase, and β-galactosidase. Capric acid, malic acid, trisodium citrate, and phenylacetic acid are utilized. Does not utilize D-glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, D-maltose, potassium gluconate, and adipic acid. Strain CT3-6 (=NIBRBA0000113859) has been isolated from a plant root sample, Chiak Mountain, Wonju, Korea.

Description of *Cedecea davisae* HME8588

Cells are Gram-staining-negative, flagellated, non-pigmented, and rod-shaped. Colonies are circular, convex, entire, and white colored after 2 days on R2A at 30°C. Positive for nitrate reduction, glucose fermentation, arginine dihydrolase, esculin hydrolysis, and β-galactosidase in API 20NE, but negative for indole production, urease and gelatinase. D-Glucose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, D-maltose, potassium gluconate, malic acid, trisodium citrate, and phenylacetic acid are utilized. Does not utilize L-arabinose, capric acid, and adipic acid. Strain HME8588 (=NIBRBA0000114081) has been isolated from a freshwater sample, Juam Reservoir, Korea.

Description of *Enterobacter ludwigii* CR6-3

Cells are Gram-staining-negative, non-flagellated, non-pigmented, and rod-shaped. Colonies are round, smooth, convex, and white colored after 3 days on R2A at 30°C. Positive for nitrate reduction, glucose fermentation, arginine dihydrolase, esculin hydrolysis, and β-galactosidase in API 20NE, but negative for indole production, urease, and gelatinase. D-Glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, D-maltose, potassium gluconate, malic acid, trisodium citrate, and phenylacetic acid are utilized. Does not utilize capric acid and adipic acid. Strain CR6-3 (=NIBRBA0000113862) has been isolated from a plant root sample, Chiak Mountain, Wonju, Korea.

Description of *Pantoea vagans* HY_N_1_1

Cells are Gram-staining-negative, non-flagellated, and rod-shaped. Colonies are irregular and yellow colored after 2 days on NA at 25°C. Positive for nitrate reduction, glucose fermentation, gelatinase, and β-galactosidase in API 20NE, but negative for indole production, arginine dihydrolase, urease, and esculin hydrolysis. Does not utilize D-glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, D-maltose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid. Strain HY_N_1_1 (=NIBRBA0000114036) has been isolated from a gut of insect sample collected from Seoul, Korea.

Description of *Gibbsiella quercinecans* LE_C_1_2

Cells are Gram-staining-negative, non-flagellated, and rod-shaped. Colonies are circle, raised, entire, and white colored after 2 days on CA at 25°C. Positive for nitrate reduction, glucose fermentation, urease, esculin hydrolysis, and β-galactosidase in API 20NE, but negative for indole production, arginine dihydrolase, and gelatinase. Does not utilize D-glucose, L-arabinose, D-mannose,

D-mannitol, *N*-acetyl-glucosamine, D-maltose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid. Strain LE_C_1_2 (=NIBRBA0000114015) has been isolated from a gut of insect sample collected from Seoul, Korea.

Description of *Vibrio tapetis* ES05-27M-7

Cells are Gram-staining-negative, non-flagellated, and rod-shaped. Colonies are circular, undulate, and beige-colored after 4 days on MA at 25°C. Positive for nitrate reduction, indole production, glucose fermentation, esculin hydrolysis, gelatinase, and β-galactosidase in API 20NE, but negative for arginine dihydrolase and urease. Malic acid is utilized. Does not utilize D-glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, D-maltose, potassium gluconate, capric acid, adipic acid, trisodium citrate, and phenylacetic acid. Strain ES05-27M-7 (=NIBRBA0000113914) has been isolated from a seawater sample, Pohang, the East Sea, Korea.

Description of *Enterovibrio norvegicus* J19

Cells are Gram-staining-negative, non-flagellated, non-pigmented, and rod-shaped. Colonies are opaque, round, smooth, convex, and cream colored after 3 days on MA at 25°C. Positive for nitrate reduction, indole production, and β-galactosidase in API 20NE, but negative for glucose fermentation, arginine dihydrolase, urease, esculin hydrolysis, and gelatinase. Does not utilize D-glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, D-maltose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid. Strain J19 (=NIBRBA0000114103) has been isolated from a seawater sample, Gwangyang Bay, Korea.

Description of *Aeromonas veronii* HME8508

Cells are Gram-staining-negative, non-flagellated, non-pigmented, and rod-shaped. Colonies are circular, convex, entire, and white colored after 1 day on R2A at 30°C. Positive for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, gelatinase, and β-galactosidase in API 20NE, but negative for urease and esculin hydrolysis. D-Glucose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, D-maltose, potassium gluconate, capric acid, malic acid, and trisodium citrate are utilized. Does not utilize L-arabinose, adipic acid, and phenylacetic acid. Strain HME8508 (=NIBRBA0000114070) has been isolated from a freshwater sample, Geongan Stream, Yongin, Korea.

Description of *Chromohalobacter canadensis* M8

Cells are Gram-staining-negative, non-flagellated, non-pigmented, and rod-shaped. Colonies are circular, raised, entire, and yellow colored after 2 days on MA at 25°C. Positive for nitrate reduction, esculin hydrolysis, gelatinase, and β-galactosidase in API 20NE, but negative for indole production, glucose fermentation, arginine dihydrolase, and urease. D-Glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, potassium gluconate, malic acid, and phenylacetic acid are utilized. Does not utilize D-maltose, capric acid, adipic acid, and phenylacetic acid. Strain M8 (=NIBRBA0000114055) has been isolated from *kimchii*, Korean fermented food.

Description of *Kushneria indalinina* PM3

Cells are Gram-staining-negative, flagellated, non-pigmented, and rod-shaped. Colonies are circular, raised, entire, and yellow colored after 2 days on MA at 25°C. Positive for esculin hydrolysis in API 20NE, but negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, urease, gelatinase, and β-galactosidase. D-Glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, D-maltose, potassium gluconate, malic acid, trisodium citrate, and phenylacetic acid are utilized. Does not utilize capric acid and adipic acid. Strain PM3 (=NIBRBA0000114057) has been isolated from *jeotgal*, Korean fermented food, collected at Pohang, Korea.

Description of *Neptunomonas concharum* KYW889

Cells are Gram-staining-negative, non-flagellated, non-pigmented, and rod-shaped. Colonies are opaque, round, smooth, convex, and cream colored after 2 days on MA at 25°C. Positive for nitrate reduction in API 20NE, but negative for indole production, glucose fermentation, arginine dihydrolase, urease, esculin hydrolysis, gelatinase, and β-galactosidase. Does not utilize D-glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, D-maltose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid. Strain KYW889 (=NIBRBA 0000114115) has been isolated from a seawater sample, Gwangyang Bay, Korea.

Description of *Lysobacter enzymogenes* CT5-2

Cells are Gram-staining-negative, non-flagellated, non-pigmented, and rod-shaped. Colonies are round and pale yellow colored after 2 days on TSA at 30°C. Positive for esculin hydrolysis, gelatinase, and β-galactosidase in API 20NE, but negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, and urease. Does not utilize D-glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, D-maltose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid. Strain

CT5-2 (=NIBRBA0000113858) has been isolated from a plant root sample, Chiak Mountain, Wonju, Korea.

Description of *Rhodanobacter lindaniclasticus* Gsoil549

Cells are Gram-staining-negative, non-flagellated, non-pigmented, and rod-shaped. Colonies are circular, raised, entire, and yellow colored after 2 days on R2A at 25°C. Positive for esculin hydrolysis in API 20NE, but negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, urease, gelatinase, and β-galactosidase. D-Glucose, *N*-acetyl-glucosamine, and D-maltose are utilized. Does not utilize L-arabinose, D-mannose, D-mannitol, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid. Strain GSoil549 (=NIBRBA0000113891) has been isolated from a soil sample of Ginseng field, Pochun, Korea.

Description of *Granulosicoccus coccoides* WSW-MW5

Cells are Gram-staining-negative, non-flagellated, non-pigmented, and coccus-shaped. Colonies are circular, convex, glistening, and cream colored after 5 days on MA at 25°C. Positive for esculin hydrolysis and β-galactosidase in API 20NE, but negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, urease, and gelatinase. Does not utilize D-glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, D-maltose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid. Strain WSS-MW5 (=NIBRBA0000114008) has been isolated from a seawater sample, Wando, Korea.

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