

# Taxonomic hierarchy of the phylum *Proteobacteria* and Korean indigenous novel *Proteobacteria* species

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The taxonomic hierarchy of the phylum *Proteobacteria* was assessed, after which the isolation and classification state of *Proteobacteria* species with valid names for Korean indigenous isolates were studied. The hierarchical taxonomic system of the phylum *Proteobacteria* began in 1809 when the genus *Polyangium* was first reported and has been generally adopted from 2001 based on the road map of Bergey's Manual of Systematic Bacteriology. Until February 2018, the phylum *Proteobacteria* consisted of eight classes, 44 orders, 120 families, and more than 1,000 genera. *Proteobacteria* species isolated from various environments in Korea have been reported since 1999, and 644 species have been approved as of February 2018. In this study, all novel *Proteobacteria* species from Korean environments were affiliated with four classes, 25 orders, 65 families, and 261 genera. A total of 304 species belonged to the class *Alphaproteobacteria*, 257 species to the class *Gammaproteobacteria*, 82 species to the class *Betaproteobacteria*, and one species to the class *Epsilonproteobacteria*. The predominant orders were *Rhodobacterales*, *Sphingomonadales*, *Burkholderiales*, *Lysobacterales* and *Alteromonadales*. The most diverse and greatest number of novel *Proteobacteria* species were isolated from marine environments. *Proteobacteria* species were isolated from the whole territory of Korea, with especially large numbers from the regions of Chungnam/Daejeon, Gyeonggi/Seoul/Incheon, and Jeonnam/Gwangju. Most *Halomonadaceae* species isolated from Korean fermented foods and solar salterns were halophilic or halotolerant. Air-borne members of the genera *Microvirga*, *Methylobacterium*, and *Massilia* had common characteristics in terms of G + C content, major respiratory quinones, and major polar lipids.

Keywords: Korean territory, phylum *Proteobacteria*, Taxonomic hierarchy

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Generally, the phylum *Proteobacteria* is known to be comprised of Gram-negative microorganisms, which have an outer membrane mainly composed lipopolysaccharides. Members of this phylum possess diverse characteristics morphologically, physiologically, ecologically, and pathogenically. A variety of cell shapes have been observed such as rods, stalks, buds, and filaments. Many species are motile by means of flagella, whereas some are non-motile or rely on gliding. Moreover, the species have various types of metabolic processes. Most members are facultatively or obligately anaerobic, chemolithoautotrophic, and heterotrophic, whereas some are autotrophic and perform photosynthesis (Imhoff and Hiraishi, 2005; Imhoff *et al.*, 2005; Spieck and Bock, 2005). Members of this phylum are distributed across a wide range of

habitats, including air, freshwater, seawater, soil, plants, animals, and acid mines. Furthermore, members include a wide variety of pathogens as well as nitrogen-fixing and predatory microorganisms. For this reason, the name *Proteobacteria* was chosen due to the group member's diverse properties despite their common ancestry (Stackebrandt *et al.*, 1988; Spain *et al.*, 2009).

For the preservation of prokaryotic resources, a number of new bacterial species have been isolated from various environments in Korea, and the information on the novel species belonging to the phyla *Actinobacteria* (Bae *et al.*, 2016) and *Firmicutes* (Seong *et al.*, 2018) have been compiled.

The present work aimed to elucidate the chronological process of establishing a taxonomic hierarchy for the

phylum *Proteobacteria* as well as the classifications of bacterial species belonging to this phylum isolated from Korean environments. In addition, we report the environmental and regional origins and the properties of the *Proteobacteria* isolates. A hierarchical taxonomic system of the phylum *Proteobacteria* was retrieved from the 'Hierarchical classification of bacteria' in the List of Prokaryotic Names with Standing in Nomenclature (LPSN; <http://www.bacterio.net/>). Then, this system was compared with the 'Taxonomy in NCBI database (<https://www.ncbi.nlm.nih.gov/taxonomy>)'. Finally, all names belonging to this phylum were checked by searching the 'Notification list' and 'Validation list' in the International Journal of Systematic and Evolutionary Microbiology (IJSEM; <http://ijs.microbiologyresearch.org/>). Data mentioned in this paper are limited to the *Proteobacteria* species validated until February 2018.

### History of taxonomic hierarchy of the phylum *Proteobacteria*

The phylum *Proteobacteria* is the largest group in the

domain *Bacteria*. Table 1 shows the periodic history of the phylum *Proteobacteria*, which was first proposed by Garrity *et al.* (2005) and authorized by the International Committee on Systematics of Prokaryotes (ICSP). A systematic history of the phylum *Proteobacteria* was first reported in 1809 by Link, who proposed the genus *Polyangium* with the type species *P. vitellinum* (Skerman *et al.*, 1980). Successively, the genera *Serratia* (type species *S. marcescens*), *Spirillum* (type species *S. volutans*), *Gallionella* (type species *G. ferruginea*), *Chromatium* (type species *C. okenii*), *Vibrio* (type species *V. cholerae*), *Crenothrix* (type species *C. polyspora*), and *Neisseria* (type species *N. gonorrhoeae*) were proposed until 1885 (Skerman *et al.*, 1980). After that, the higher taxa, family and order, were proposed along with the first family *Crenotrichaceae* (by Hansgirg in 1888) and first order *Pseudomonadales* (by Orla-Jensen in 1921) (Skerman *et al.*, 1980). During that time, well-known taxa such as genera *Rhizobium*, *Pseudomonas*, *Rickettsia*, *Escherichia*, and *Shigella* as well as family *Spirillaceae* were created (Skerman *et al.*, 1980).

**Table 1.** Establishment of hierarchical taxonomic system of the phylum *Proteobacteria*.

Year	Taxonomic history	Reference
1809 -1885	Cr. G. <i>Polyangium</i> (1809), <i>Serratia</i> (1823), <i>Spirillum</i> (1832), <i>Gallionella</i> (1838), <i>Chromatium</i> (1852), <i>Vibrio</i> (1854), <i>Crenothrix</i> (1870), <i>Neisseria</i> (1885)	Skerman <i>et al.</i> , 1980
1888 -1920	Cr. F. <i>Crenotrichaceae</i> (1888), <i>Spirillaceae</i> (1894), <i>Nitrobacteraceae</i> (1917)* <sup>1</sup> ; G. <i>Rhizobium</i> (1889), <i>Pseudomonas</i> (1894), <i>Rickettsia</i> (1916), <i>Escherichia</i> , <i>Shigella</i> (1919), <i>Brucella</i> (1920)	Skerman <i>et al.</i> , 1980
1921 -1965	Cr. O. <i>Pseudomonadales</i> (1921), <i>Caulobacterales</i> (1935), <i>Rickettsiales</i> (1939), <i>Spirillales</i> (1940)* <sup>2</sup> , <i>Myxococcales</i> (1945), <i>Hypomicrobiales</i> (1957); F. <i>Archangiaceae</i> , <i>Myxococcaceae</i> , <i>Polyangiaceae</i> , <i>Chromatiaceae</i> , <i>Neisseriaceae</i> (1933), <i>Caulobacteraceae</i> , <i>Gallionellaceae</i> , <i>Nevskiaceae</i> (1935), <i>Pseudomonadaceae</i> , <i>Rickettsiaceae</i> (1936), <i>Enterobacteriaceae</i> (1937), <i>Rhizobiaceae</i> (1938), <i>Brucellaceae</i> (1957), <i>Vibrionaceae</i> (1965)	Skerman <i>et al.</i> , 1980
1968	Cr. K. Prokaryotae	Gibbons & Murray, 1978
1976	Pu. First Draft Approved lists of bacterial names	Ad Hoc, 1976
1978	Cr. Dv. <i>Firmacutes</i> , <i>Gracilicutes</i> , <i>Mollicutes</i> ; O. <i>Lysobacterales</i>	Gibbons & Murray, 1978; Christensen & Cook, 1978
1980	Pu. Approved lists of bacterial names	Skerman <i>et al.</i> , 1980
1988	Cr. C. <i>Proteobacteria</i>	Stakerbrandt <i>et al.</i> , 1988
1989	Pu. Approved lists of bacterial names (Amended)	Skerman <i>et al.</i> , 1989
1990	Cr. Dm. Bacteria higher rank of K. Prokaryotae	Woese <i>et al.</i> , 1990
1994	Ex. K. Prokaryotae	Embley <i>et al.</i> , 1994
1998	Pu. List of Bacterial Names with Standing in Nomenclature (Now LPSN)	<a href="https://www.bacterio.net">https://www.bacterio.net</a>
2001	Cr. O. " <i>Vivriionales</i> "* <sup>3</sup>	Garrity & Holt, 2001
2004	Cr. O. <i>Nautiliales</i>	Miroshnichenko <i>et al.</i> , 2004
2005	Cr. P. <i>Proteobacteria</i> ; C. Alpha-, Beta-, Delta-, Epsilon-, Gammaproteobacteria; O. <i>Kordiimonadales</i> & 27 Os. Pu. Bergey's manual of systematic bacteriology 2 <sup>nd</sup> ed. Vol. 2 (Part B & C)	Garrity <i>et al.</i> , 2005; Kwon <i>et al.</i> , 2005; Brenner <i>et al.</i> , 2005a&b.
2008	Cr. O. <i>Sneathiellales</i>	Kurahashi <i>et al.</i> , 2008
2009	Cr. O. <i>Kiloniellales</i>	Wiese <i>et al.</i> , 2009
2013	Cr. C. <i>Acidithiobacillia</i> * <sup>4</sup> ; O. <i>Magnetococcales</i> , <i>Orbales</i>	Kwong & Moran, 2013
2014	Cr. C. <i>Oligoflexia</i> ; O. <i>Oligoflexales</i>	Nakai <i>et al.</i> , 2014
2015	Cr. O. <i>Acidiferrobacterales</i> , <i>Arenicellales</i> , <i>Cellvibrionales</i> , <i>Nevskiales</i> , <i>Sulfuricellales</i>	Naushad <i>et al.</i> , 2015; Watanabe <i>et al.</i> , 2015
2016	Cr. O. " <i>Enterobacteriales</i> "* <sup>3</sup>	Adeolu <i>et al.</i> , 2016
2017	Cr. C. " <i>Zetaproteobacteria</i> "* <sup>5</sup> , <i>Hydrogenophilalia</i> ; O. " <i>Mariprofundales</i> "* <sup>5</sup> Ex. O. <i>Methylophilales</i> , <i>Sulfuricellales</i>	Makita <i>et al.</i> , 2017; Boden <i>et al.</i> , 2017

\*<sup>1</sup>, Combined to *Bradyrhizobiaceae*; \*<sup>2</sup>, Combined to *Nitrosomonadales*; \*<sup>3</sup>, Shown in "Taxonomic outline", Bergey's manual of systematic bacteriology 2<sup>nd</sup> ed. (Garrity and Holt, 2001); \*<sup>4</sup>, Not listed on "Hierarchical classification of prokaryotes", LPSN; \*<sup>5</sup>, Invalid name.

Abbreviations: Dm., domain; K., kingdom; Dv., division; P., phylum; C., class; O., order; F., family; G. genus; Cr., creation; Ex., exclusion; Pu., publication.

Meanwhile, in 1968, the kingdom *Prokaryotae* was created as the highest level of life and was appropriately at the same level as *Eukaryotae* (Gibbons and Murray, 1978). Its lower rank, the division *Gracilicutes* was created (Gibbons and Murray, 1978). The division name *Gracilicutes* represents thinner cell walls, implying a Gram-negative type of cell wall (Gibbons and Murray, 1978), and this division was further separated into the classes *Photobacteria* (containing subclasses *Oxyphotobacteriae* and *Anoxyphotobacteriae*) and *Scotobacteria* (for non-photosynthetic bacteria). Two other divisions, *Firmicutes* and *Mollicutes*, were also proposed to encompass Gram-positive bacteria and cell wall-lacking bacteria, respectively (Gibbons and Murray, 1978). Around this same time, Murray (1984) proposed that three classes, *Scotobacteria* (for non-photosynthetic bacteria), *Anoxyphotobacteria* (for photosynthetic bacteria having photosystem I alone), and *Oxyphotobacteria* (for bacteria having both photosynthetic systems I and II), be placed under the division *Gracilicutes* in Bergey's Manual of Systematic Bacteriology (BSMB) 1<sup>st</sup> ed. In other words, the class *Photobacteria* was rearranged and divided into the two classes *Anoxyphotobacteria* and *Oxyphotobacteria* which is now classified as the phylum *Cyanobacteria*. Thus, members belonging to photosynthetic and other Gram-negative bacteria had been affiliated within the division *Gracilicutes* (Skerman et al., 1980) until 1988. The taxon name "division" was changed to "phylum" after the phylogenetic relationships were applied to the bacterial taxonomy (Woese, 1987).

With a higher rank than order, the class *Proteobacteria* was created under the division *Gracilicutes* in 1988 by Stackebrandt et al. (1988) in order to encompass the purple bacteria and their relatives. Moreover, the authors suggested to divide the class *Proteobacteria* into Alpha, Beta, Gamma, and Delta groups at the subclass level. In 1990, the domain *Bacteria* was created as a higher rank of the kingdom *Prokaryotae*, which was excluded in 1994 (Woese et al., 1990; Embley et al., 1994). Members of the classes *Scotobacteria* and *Proteobacteria* were reclassified and moved to the new classes *Acidobacteria* and *Chlamydiae* or phyla such as *Cyanobacteria*, *Chloroflexi*, *Plantobacteria*, and *Spirochaetae* (Garrity and Holt, 2001; Cavalier-Smith, 2002). Finally, the phylum *Proteobacteria* was created with its lower rank, classes *Alpha-*, *Beta-*, *Delta-*, *Epsilon-*, and *Gammaproteobacteria*, which was listed in Bergey's Manual of Systematic Bacteriology (Garrity et al., 2005). At that time, 28 orders were proposed: 27 orders in BSMB 2<sup>nd</sup> ed. and order *Kordiimonadales* by Kwon et al. (2005). Members of *Cytophaga*, *Flavobacteria*, and *Sphingobacteria*, previously affiliated within the class *Scotobacteria*, were moved to the phylum *Bacteroidetes* which was created in 2011 (Krieg et al., 2011). Consequently, a hierarchical classification

system of the phylum *Proteobacteria* was generally adopted starting in 2011. Recently, four new classes, *Acidithiobacillia* (from *Gammaproteobacteria*; Williams and Kelly, 2013), *Oligoflexia* (Nakai et al., 2014), "*Zetaproteobacteria*" (Makita et al., 2017), and *Hydrogenophilalia* (from *Betaproteobacteria*; Boden et al., 2017), and 13 new orders were proposed: *Emcibacteriales*, *Iodidimonadales* (Iino et al., 2016), *Magnetococcales* (*Alphaproteobacteria*; Bazylini et al., 2013), *Bradymonadales* (*Deltaproteobacteria*; Wang et al., 2015c), *Enterobacteriales* (Adeolu et al., 2016), *Acidiferrobacteriales* (Kojima et al., 2015), *Arenicellales* (Teramoto et al., 2015), *Cellvibrionales* (Spring et al., 2015), *Nevskiales* (Naushad et al., 2015), *Orbales* (*Gammaproteobacteria*; Kwong and Moran, 2013), *Oligoflexales* (Nakai et al., 2014), *Bacteriovoracales* (Hahn et al., 2017), and *Silvanigrellales* (*Oligoflexia*; Hahn et al., 2017).

As of February 2018, the phylum *Proteobacteria* consisted of nine classes comprising 56 orders, 155 families, and 1,084 genera. In this work, the following taxa were included categorized in one of the following statuses: 1) validated but not shown in the 'Hierarchical classification of prokaryotes (LPSN)' and 2) listed in the 'Taxonomy (NCBI) database' but listed in quotes on the 'Hierarchical classification of prokaryotes (LPSN)'. These taxa are as follows: three classes, *Acidithiobacillia*, *Hydrogenophilalia*, and "*Zetaproteobacteria*", the orders *Enterobacteriales* (Adeolu et al., 2016), *Immundisolibacteriales* (Corteselli et al., 2017), *Emcibacteriales*, *Iodidimonadales* (Iino et al., 2016), *Micropepsales* (Harbison et al., 2017), *Rhodothalassiales* (Venkata Ramana et al., 2013), "*Mari profundales*", "*Parvularculales*", "*Procabacteriales*", and "*Vibrionales*", and the families *Erwiniaceae*, *Pectobacteriaceae*, *Yersiniaceae*, *Hafniaceae*, *Morganellaceae*, *Budviciaceae* (Adeolu et al., 2016), *Thorselliaceae* (Kämpfer et al., 2015), *Micropepsaceae* (Harbison et al., 2017), *Chelatococcaceae* (Dedysh et al., 2016), *Mabikibacteraceae* (Choi et al., 2017), *Notoacmeibacteraceae* (Huang et al., 2017), *Rhodothalassiaceae*, *Vulgatibacteraceae*, *Labilitrichaceae*, *Anaeromyxobacteraceae* (Yamamoto et al., 2014), *Wenzhouxiangellaceae* (Wang et al., 2015b), *Immundisolibacteraceae* (Corteselli et al., 2017), *Kangiellaceae* (Wang et al., 2015a), *Ventosimonadaceae* (Lin et al., 2016), *Fastidiosibacteraceae* (Xiao et al., 2018), "*Salinisphaeraceae*" (Naushad et al., 2015), "*Mari profundaceae*", "*Parvularculaceae*", "*Kordiimonadaceae*", "*Aurantimonadaceae*", "*Procabacteriaceae*", "*Hydrogenimonaceae*", and "*Saccharospirillaceae*".

On the other hand, the orders *Holosporales*, *Kopriimonadales*, *Pelagibacterales*, *Ferritrophicales*, *Ferrovales*, and *Salinisphaerales* and the families *Pelagibacteraceae*, *Geminicoccaceae*, *Ferritrophicaceae*, and *Ferrovaceae* which appeared in the NCBI database were not included due to the lack of validation. Moreover, the orders

*Methylophilales* and *Sulfuricellales* were not included since these orders were combined into the order *Nitroso-monadales* (Boden *et al.*, 2017). The order *Xanthomonadales* and its family *Xanthomonadaceae* were excluded since the names *Lysobacterales* and *Lysobacteraceae* have priority over those names, respectively. The families *Haliangiaceae* and *Sinobacteraceae* were also excluded since families *Kofleriaceae* and *Nevskiaceae* have priority over those names, respectively (Tindal, 2014).

### Novel species belonging to the phylum *Proteobacteria* originating from Korea

Efforts to name the *Proteobacteria* isolates from Korea began in 1999 using the species *Erwinia pyrifoliae* for plant-pathogenic isolates obtained from Asian pear tree (Kim *et al.*, 1999). Since then, many new *Proteobacteria* species have been recorded with valid names. In February 2018, 644 *Proteobacteria* species originating from Korea were approved (Table 2).

All *Proteobacteria* species are affiliated within four classes (*Alpha-*, *Beta-*, *Epsilon-*, and *Gamma-proteobacteria*), 25 orders, 65 families, and 261 genera (including 10 genera of which families were unassigned). A total of 304 species belong to the class *Alphaproteobacteria*, 257 species to the class *Gammaproteobacteria*, 82 species to the class *Betaproteobacteria*, and one species to the class *Epsilonproteobacteria*.

**Composition of novel species belonging to the class *Alphaproteobacteria*:** Novel Korean isolates belonging to the class *Alphaproteobacteria* were affiliated with 129 genera and 23 families within eight orders. A total of 129 species were affiliated with the order *Rhodobacterales*, 77 species with *Sphingomonadales*, 42 species with *Rhizobiales*, 25 species each with *Rhodospirillales* and *Caulobacterales*, and the remaining six species were affiliated with the orders *Kiloniellales*, *Kordiimonadales*, and *Sneathiellales* or with an order unassigned. In the order *Rhodobacterales*, all species were included in 64 genera belonging to the single family *Rhodobacteraceae*. The genera *Paracoccus* (11 species), *Loktanella* (10 species), *Roseovarius* (10 species), *Jannaschia* (seven species), *Sulfitobacter* (six species), *Litoreibacter* (five species), and *Ruegeria* (five species) encompassed five or more Korean novel species. Fifty-six species belonging to 10 genera were affiliated with the family *Sphingomonadaceae*, and 21 species belonging to three genera were with the family *Erythrobacteraceae* of the order *Sphingomonadales*. A number of isolates were affiliated with the *Sphingomonadaceae* genera *Sphingomonas* (29 species) and *Sphingopyxis* (10 species) as well as the two *Erythrobacteraceae* genera *Altererythrobacter* and *Erythrobacter* (nine species each). Forty-two species belong to 24 genera within 13

families in the order *Rhizobiales*. The family *Rhizobiaceae* contained 11 species while one of its genera, *Kaistia*, contained six species. The genera *Devosia* and *Methylobacterium* within the families *Hyphomicrobiaceae* and *Methylobacteriaceae*, respectively, contained five species each. Twenty six *Rhodospirillales* species were distributed within two families, *Acetobacteraceae* (12 species within four genera) and *Rhodospirillaceae* (nine species within eight genera), with four species (one genus) of which the family unassigned. The genus *Roseomonas* of the family *Acetobacteraceae* contained nine novel Korean species.

In the order *Caulobacterales*, 25 novel Korean isolates were affiliated with two families *Caulobacteraceae* (15 species within four genera) and *Hyphomonadaceae* (10 species within eight genera).

**Composition of novel species belonging to the class *Betaproteobacteria*:** *Betaproteobacteria* isolates were affiliated with only three orders, *Burkholderiales* (73 species), *Neisseriales* (seven species), and *Rhodocyclales* (two species). Seventy-three *Burkholderiales* isolates consisted of 23 *Comamonadaceae* species (11 genera), 17 *Burkholderiaceae* species (four genera), 15 *Oxalobacteraceae* species (four genera), 13 *Alcaligenaceae* species, and five species (five genera) of which the family was unassigned. All seven *Neisseriales* species were affiliated with seven different genera of the family *Chromobacteriaceae*. Only two species (two genera) belonged to the family *Zoogloeaceae* within the order *Rhodocyclales*. The genera *Burkholderia* (11 species) and *Massilia* (10 species) within the families *Burkholderiaceae* and *Oxalobacteraceae* of the order *Burkholderiales*, respectively, were dominant.

**Composition of novel species belonging to the class *Gammaproteobacteria*:** Ten orders were detected in the class *Gammaproteobacteria*; *Lysobacterales* (73 species), *Alteromonadales* (65 species), *Oceanospirillales* (39 species), *Pseudomonadales* (23 species), *Cellvibrionales* (20 species), *Chromatiales* (seven species), *Nevskiales* (six species), *Legionellales*, *Orbales*, *Thiotrichales* (one species each), and an order unassigned (four species). Forty-five species (eight genera) and 28 species (eight genera) belonged to two *Lysobacterales* families, *Lysobacteraceae* and *Rhodanobacteraceae*, respectively. Twenty-three, eight, and five novel species were affiliated with the genera *Lysobacter*, *Pseudoxanthomonas*, and *Arenimonas* of the family *Lysobacteraceae*, respectively. Moreover, 12 and eight species belonged to *Rhodanobacter* and *Dyella* of the family *Rhodanobacteraceae*, respectively. Sixty-five *Alteromonadales* species were distributed into 20 genera within nine families. Among them, a larger number of isolates belonged to the families *Alteromonadaceae* (31 species within 11 genera) and *Shewanellaceae*

(13 species within one genus). The genera *Shewanella* (13 species; *Shewanellaceae*), *Marinobacter* (seven species), *Marinobacterium* (six species; *Alteromonadaceae*), and *Idiomarina* (five species; *Idiomarinaceae*) were the most abundant groups. *Oceanospirillales* isolates were composed of seven families (18 genera), including the abundant family *Halomonadaceae* (14 species within four genera). Eleven *Halomonas* (*Halomonadaceae*) species were isolated from Korean environments. The two families *Moraxellaceae* (15 species within four genera) and *Pseudomonadaceae* (eight species within the single genus *Pseudomonas*) were found in the order *Pseudomonadales*. Seven species were affiliated with the genus *Psychrobacter* of the family *Moraxellaceae*. Twenty *Cellvibrionales* species were distributed into five families, including the abundant family *Cellvibrionaceae* (10 species within six genera). Six species were placed in the genus *Microbulbifer* of the family *Microbulbiferaceae*. In addition, remaining *Gammaproteobacteria* isolates were affiliated with the orders “*Vibrionales*” (11 species, three genera, single family), *Chromatiales* (seven species, three genera, three families), *Nevskiales* (six species, four genera, two families), *Aeromonadales* (four species, two genera, single family), ‘*Enterobacteriales*’ (two species, two genera, two families), *Legionellales*, *Orbales*, *Thiotrichales* (one species each), and an order unassigned (four species, three genera). Among them, the genera *Photobacterium* (six species; *Vibrionaceae*) and *Rheinheimera* (five species; *Chromatiaceae*) were dominant.

**Composition of the novel species belonging to the class *Epsilonproteobacteria*:** Only one *Arcobacter* species was affiliated with the family *Campylobacteraceae*, the order *Campylobacterales* within the class *Epsilonproteobacteria*.

**New genera or higher taxa:** The order *Kordiimonadales* within the class *Alphaproteobacteria* (Kwon *et al.*, 2005) and three families, *Cohaesibacteraceae* (Hwang and Cho, 2008) and *Mabikibacteraceae* (Choi *et al.*, 2017) of the order *Rhizobiales* and *Litoricolaceae* (Kim *et al.*, 2007) of the order *Oceanospirillales*, were first created using isolates from the Korean environment as a type genus and species. Unfortunately, the family name “*Kordiimonadaceae*” was not validly published. In addition, 86 genera were first created using isolates from the Korean environment as the type species. Among them, 42 genera consisted of only a single type species (Table 2).

#### Researcher, isolation source, regional origin, and properties of species

**Researchers:** Eighty-one corresponding authors were involved in the proposal of novel species from the Korean

indigenous *Proteobacteria* isolates. Among them, 15 corresponding authors proposed 488 novel species; Yoon, J. H. (172 species; Sungkyunkwan University), Kwon, S. W. (60 species; Rural Development Administration), Jeon, C. O. (42 species; Chung-Ang University), Bae, J. W. (33 species; Kyung Hee University), Lee, S. T. (30 species; KAIST), Seong, C. N. (19 species; Sunchon National University), Lee, T. H. (18 species; Kyung Hee University), Cho, B. C. (17 species; Seoul National University), Chun, J. (16 species; Seoul National University), Im, W. T. (16 species; Hankyong National University), Kim, J. (15 species; Kyeonggi University), Yang, D. C. (14 species; Kyung Hee University), Cho, J. C. (14 species; Inha University), Chung Y. R. (12 species; Gyeongsang National University), and Lee, S. D. (10 species; Jeju National University).

**Isolation sources:** *Proteobacteria* species from Korea were isolated from natural environments such as soil, freshwater, seawater, tidal flat sediments, air, and solar salterns, and a number of species were also isolated from artificial sources such as fermented foods, wastewater, compost, air conditioning systems, and water purifying systems. Several species were associated with animals and plants. Isolation sources of the species are described in detail. A total of 171 species were isolated from soil, including cultivated fields, forest soil, rhizosphere, natural caves, and reclaimed soil. Moreover, seawater (130 species) and tidal flat sediments (118 species) were the main isolation sources for *Proteobacteria*. Other major isolation sources were as follows: marine animals (32 species), wastewater (31 species), seashore sand (30 species), freshwater (27 species), air and air conditioning systems (22 species), solar salterns (19 species), and freshwater sediments (16 species). In addition, there were many other isolation sources for *Proteobacteria* species: Korean traditional fermented foods (jeotgal and kimchi; eight species), terrestrial plants (eight species), marine seaweed (seven species), laboratory cultures (seven species), compost (six species), insect gut (five species), water cooling or purifying systems (four species), freshwater algae (two species), and deep sea sediments (one species). Compared to the isolation sources of novel *Actinobacteria* and *Firmicutes* species, *Proteobacteria* species were isolated more frequently from marine environments such as seawater, tidal flat sediments, marine animals, seashore sand, and air/air conditioning systems but less frequently from Korean traditional fermented foods and clinical specimens (Bae *et al.*, 2016; Seong *et al.*, 2018).

**Regional origin of the isolates:** Novel *Proteobacteria* species were isolated from the whole territory of Korea. Predominant isolation regions of validly named *Proteobacteria* species were as follows (Table 2): 129 species

Table 2. List of novel *Proteobacteria* species with valid name originated from Korea.

Family	Genus	Species (source, region, function)
<b>Class Alphaproteobacteria (304)</b>		
<b>Order Caulobacterales (25)</b>		
Caulobacteraceae (15)	<i>Asticcacaulis</i> (1)	<i>A. solisilvae</i> (sv, GSI)
	<i>Brevundimonas</i> (6)	<i>B. aveniformis</i> (ww, AR), <i>B. basaltis</i> (ss, JJ), <i>B. kwangchunensis</i> (sr, CD), <i>B. lenta</i> (sv, UD), <i>B. naejangsanensis</i> (sv, JB, J(e)), <i>B. terrae</i> (sr, CD)
	<i>Caulobacter</i> (3)	<i>C. daechungensis</i> (fw, CD), <i>C. hibisci</i> (sv, GSI), <i>C. profunda</i> (fs, CD)
	<i>Phenyllobacterium</i> (5)	<i>P. aquaticum</i> (fw, CD), <i>P. composti</i> (co, GSI), <i>P. hankyongense</i> (sv, GSI), <i>P. koreense</i> (ww, CD), <i>P. muchangponense</i> (ss, CD)
	<i>Asprobacter</i> (1)	<i>A. aquaticus</i> (fw, CD)†
	<i>Fretibacter</i> (1)	<i>F. rubidus</i> (sw, JJ)†
	<i>Henriciella</i> (2)	<i>H. litoralis</i> (tf, CD), <i>H. marina</i> (sw, GD)†
	<i>Hirschia</i> (2)	<i>H. litorea</i> (tf, GBU), <i>H. maritima</i> (sw, JJ)
	<i>Litorimonas</i> (1)	<i>L. taeanensis</i> (ss, CD)†
	<i>Marinicauda</i> (1)	<i>M. algicola</i> (mp, CD)
	<i>Maritalea</i> (1)	<i>M. myrionectae</i> (cu, AR)†
	<i>Ponticaulis</i> (1)	<i>P. koreensis</i> (sw, JJ)†
	<i>Kiloniella</i> (1)	<i>K. spongiae</i> (ma, GD)
<b>Order Kiloniellales (1)</b>		
Kiloniellaceae (1)	<i>Kiloniella</i> (1)	<i>K. spongiae</i> (ma, GD)
<b>Order Kordiimonadales (3)†</b>		
Kordiimonadaceae (3)	<i>Kordiimonas</i> (3)	<i>K. aestuarii</i> (tf, CD), <i>K. aquimaris</i> (sw, GW), <i>K. gwangyangensis</i> (tf, JG)†
<b>Order Rhizobiales (42)</b>		
Aurantimonadaceae (2)	<i>Aureimonas</i> (2)	<i>A. frigidaquae</i> (wc, JG), <i>A. ureilytica</i> (ai, GSI)
Bradyrhizobiaceae (1)	<i>Varitibacter</i> (1)	<i>V. gogjawalensis</i> (sv, JJ)†
Brucellaceae (2)	<i>Daeguia</i> (1)	<i>D. caeni</i> (ww, GD)†
	<i>Ochrobactrum</i> (1)	<i>O. daejeonense</i> (ww, CD, J(k))
	<i>Chelatococcus</i> (1)	<i>C. daejeonensis</i> (ww, GD)
	<i>Cohaesibacter</i> (1)	<i>C. gelatinilyticus</i> (tf, UN, J(e)†
	<i>Cucumilbacter</i> (1)	<i>C. marinus</i> (sw, UN)†
	<i>Devosia</i> (5)	<i>D. geojensis</i> (sr, GBU), <i>D. humi</i> (sv, GSI), <i>D. insulae</i> (sv, UD), <i>D. soli</i> (sv, CD), <i>D. subaequoris</i> (tf, JJ)
	<i>Methyloterrigena</i> (1)	<i>M. soli</i> (sr, JB)†
	<i>Mabikibacter</i> (1)	<i>M. ruber</i> (tf, JJ)†
	<i>Methylobacterium</i> (5)	<i>M. aerolatum</i> (ai, GSI), <i>M. dankookense</i> (wc, CD), <i>M. frigidaeris</i> (ai, AR), <i>M. iners</i> (ai, GSI), <i>M. platani</i> (py, GSI)
	<i>Microvirga</i> (2)	<i>M. aerilata</i> (ai, GSI), <i>M. aerophila</i> (ai, GSI)
	<i>Pleomorphomonas</i> (1)	<i>P. koreensis</i> (cu, CD, J(j))
	<i>Hoeflea</i> (1)	<i>H. halophila</i> (tf, GW)
	<i>Leptilioribacter</i> (1)	<i>L. donghaensis</i> (sw, GW)†
	<i>Nitratireductor</i> (3)	<i>N. aquimarinus</i> (cu, AR), <i>N. basaltis</i> (ss, JJ), <i>N. kimnyeongensis</i> (mp, JJ)
	<i>Pseudahrensia</i> (1)	<i>P. aquimaris</i> (mp, CD)†
	<i>Ciceribacter</i> (1)	<i>C. azoifigens</i> (ww, GSI, J(j))
	<i>Kaistia</i> (6)	<i>K. adipata</i> (fw, CB)†, <i>K. dalseonensis</i> (fw, GBU), <i>K. defluvii</i> (fs, GD), <i>K. geumhonensis</i> (fs, GD), <i>K. soli</i> (sv, GW), <i>K. terrae</i> (sv, GW)
	<i>Rhizobium</i> (2)	<i>R. halophytocola</i> (py, GBU), <i>R. soli</i> (sv, UD)
	<i>Shinella</i> (2)	<i>S. daejeonensis</i> (ww, CD, J(k)), <i>S. granuli</i> (ww, AR)†
	<i>Amorphus</i> (1)	<i>A. sudae</i> (mp, GBU)
	<i>Xanthobacteraceae</i> (1)	<i>S. koreensis</i> (py, CD)
<b>Rhizobiaceae (11)</b>		
	<i>Rhizobium</i> (2)	<i>R. halophytocola</i> (py, GBU), <i>R. soli</i> (sv, UD)
	<i>Shinella</i> (2)	<i>S. daejeonensis</i> (ww, CD, J(k)), <i>S. granuli</i> (ww, AR)†
	<i>Amorphus</i> (1)	<i>A. sudae</i> (mp, GBU)
	<i>Xanthobacteraceae</i> (1)	<i>S. koreensis</i> (py, CD)

Table 2. Continued.

Family	Genus	Species (source, region, function)
<b>Order Rhodobacterales (129)</b> Rhodobacteraceae(129)	<i>Aestuariicoccus</i> (1)	<i>A. marinus</i> (tf, CD)†
	<i>Aestuarihabitans</i> (1)	<i>A. beolgyonensis</i> (tf, JG)†
	<i>Aestuariespira</i> (1)	<i>A. insulae</i> (tf, JG, ♯a)†
	<i>Aestuariesvita</i> (1)	<i>A. boseongensis</i> (tf, JG)†
	<i>Albimonas</i> (1)	<i>A. donghaensis</i> (sw, UN)†
	<i>Albirhodobacter</i> (1)	<i>A. confluentis</i> (tf, CD)
	<i>Altiroeoarius</i> (1)	<i>A. pelagivivens</i> (sw, JJ)†
	<i>Aquicoccus</i> (1)	<i>A. porphyridii</i> (mp, CD)†
	<i>Aquimixicola</i> (1)	<i>A. soesokkakensis</i> (sw, JJ, ♯a)†
	<i>Asciaceihabitans</i> (1)	<i>A. donghaensis</i> (ma, GW)†
	<i>Boseongicola</i> (1)	<i>B. aestuarii</i> (tf, JG)†
	<i>Celeribacter</i> (3)	<i>C. baekdonensis</i> (sw, GW), <i>C. marinus</i> (sw, GSI), <i>C. naphthalenivorans</i> (tf, JG, ♯b)
	<i>Citricella</i> (1)	<i>C. aestuarii</i> (tf, CD)
	<i>Citrimonas</i> (1)	<i>C. salinaria</i> (sl, GSI)†
	<i>Confluentimicrobium</i> (1)	<i>C. lipolyticum</i> (sw, JJ, ♯a)†
	<i>Defluviomonas</i> (1)	<i>D. aquaemixtae</i> (sw, JJ)
	<i>Donghicola</i> (1)	<i>D. eburneus</i> (sw, GW)†
	<i>Gemmobacter</i> (1)	<i>G. stramineiformis</i> (wc, JB)
	<i>Halocynthibacter</i> (1)	<i>H. namhaensis</i> (ma, GBU)†
	<i>Haslibacter</i> (1)	<i>H. halocynthiae</i> (ma, GW, ♯h)†
	<i>Hwanghaetcola</i> (1)	<i>H. aestuarii</i> (tf, CD)†
	<i>Jannaschia</i> (7)	<i>J. aquimarina</i> (sw, GBU), <i>J. confluentis</i> (sw, JJ), <i>J. donghaensis</i> (sw, UD), <i>J. faecimaris</i> (tf, CD), <i>J. pohangensis</i> (ss, GD), <i>J. seohaensis</i> (tf, JB), <i>J. seosinensis</i> (sl, GSI)
	<i>Labrenzia</i> (2)	<i>L. marina</i> (tf, CD), <i>L. suaedae</i> (py, GBU)
	<i>Limibaculum</i> (1)	<i>L. halophilum</i> (st, GSI)†
	<i>Litoretibacter</i> (5)	<i>L. arenae</i> (tf, GD), <i>L. ascidiaceicola</i> (ma, GW), <i>L. halocynthiae</i> (ma, UN), <i>L. meonggei</i> (ma, UN), <i>L. ponti</i> (sw, GBU)
	<i>Litorimicrobium</i> (1)	<i>L. taeanense</i> (ss, CD)†
	<i>Litorisedimnicola</i> (1)	<i>L. beolgyonensis</i> (tf, JG)†
	<i>Loktanella</i> (10)	<i>L. acticola</i> (sw, GSI), <i>L. aestuariicola</i> (tf, JG), <i>L. koreensis</i> (ss, GD), <i>L. litorea</i> (sw, GBU), <i>L. maricola</i> (sw, UD), <i>L. ponticola</i> (sw, JG), <i>L. pyoseonensis</i> (ss, JJ), <i>L. soesokkakensis</i> (sw, JJ), <i>L. tamlensis</i> (sw, JJ), <i>L. variabilis</i> (tf, JG)
	<i>Lutimaribacter</i> (1)	<i>L. saemankumensis</i> (tf, JB)†
	<i>Maribius</i> (2)	<i>M. pontitimi</i> (tf, GSI), <i>M. salinus</i> (sl, CD)†
	<i>Marivita</i> (5)	<i>M. byunsanensis</i> (tf, JB), <i>M. cryptomonadis</i> (cu, AR)†, <i>M. geojedonensis</i> (sw, GBU), <i>M. hallyeonensis</i> (sw, GBU), <i>M. litorea</i> (sw, UN)
	<i>Nioella</i> (1)	<i>N. aestuarii</i> (tf, GSI)
	<i>Oceanicola</i> (1)	<i>O. litoreus</i> (tf, GBU)
	<i>Octadecabacter</i> (2)	<i>O. ascidiaceicola</i> (ma, GBU), <i>O. jejudonensis</i> (sw, JJ)
	<i>Palleronia</i> (1)	<i>P. soli</i> (sv, GSI)
	<i>Paracoccus</i> (11)	<i>P. aestuarii</i> (tf, JG), <i>P. caeni</i> (ww, CD), <i>P. fistulariae</i> (ma, UN, ♯a), <i>P. haeundaensis</i> (sw, GBU), <i>P. hibisci</i> (sv, GSI), <i>P. hibiscisoli</i> (sv, GSI), <i>P. homiensis</i> (ss, GD), <i>P. koreensis</i> (ww, CB), <i>P. limosus</i> (ww, GSI), <i>P. litorisedimnis</i> (tf, GSI), <i>P. lutimaris</i> (tf, CD)
	<i>Pelagicola</i> (1)	<i>P. litorisedimnis</i> (tf, JG)
	<i>Phaeobacter</i> (2)	<i>P. aquaemixtae</i> (sw, JJ), <i>P. daeponensis</i> (tf, JG)
	<i>Pontibaca</i> (1)	<i>P. methylaminiivorans</i> (tf, UN)†

Table 2. Continued.

Family	Genus	Species (source, region, function)	
<i>Rhodobacteraceae</i> (129)	<i>Ponticoccus</i> (1)	<i>P. litoralis</i> (sw, UN) <sup>†</sup>	
	<i>Pontivivens</i> (1)	<i>P. insulae</i> (sw, JJ) <sup>†</sup>	
	<i>Pseudohalocynthiibacter</i> (1)	<i>P. aestuariivivens</i> (tf, JG) <sup>†</sup>	
	<i>Pseudopelagicola</i> (1)	<i>P. gjangensis</i> (ma, JG) <sup>†</sup>	
	<i>Pseudorhodobacter</i> (3)	<i>P. aquimaris</i> (sw, CD), <i>P. ponti</i> (sw, CD), <i>P. wandonensis</i> (ss, JG)	
	<i>Pseudoruegeria</i> (3)	<i>P. aquimaris</i> (sw, GW) <sup>†</sup> , <i>P. lutimaris</i> (tf, CB), <i>P. sabulilitoris</i> (ss, GBU)	
	<i>Pseudooseohaetica</i> (1)	<i>P. caenipelagi</i> (tf, JG) <sup>†</sup>	
	<i>Puniceibacterium</i> (1)	<i>P. confluentis</i> (sw, JJ)	
	<i>Roseovivax</i> (3)	<i>R. jejudonensis</i> (sw, JJ), <i>R. lentus</i> (tf, JB), <i>R. roseus</i> (sl, JG)	
	<i>Roseobacter</i> (1)	<i>R. ponti</i> (sw, CD)	
	<i>Roseovarius</i> (10)	<i>R. aestuarii</i> (tf, JB), <i>R. aquimarinus</i> (sw, JJ), <i>R. gaetbuli</i> (tf, JG), <i>R. halocynthiae</i> (ma, UN), <i>R. halotolerans</i> (sw, UN), <i>R. litoreus</i> (sw, GBU), <i>R. lutimaris</i> (tf, CD), <i>R. marinus</i> (sw, CD), <i>R. scapharcae</i> (ma, JG), <i>R. sediminilitoris</i> (tf, GBU)	
	<i>Rubellimicrobium</i> (2)	<i>R. aerolatum</i> (ai, GSI), <i>R. mesophilum</i> (sv, JG)	
	<i>Ruegeria</i> (5)	<i>R. arenilitoris</i> (ss, GBU), <i>R. conchae</i> (ma, JG), <i>R. faecimaris</i> (tf, CD), <i>R. halocynthiae</i> (ma, UN), <i>R. meonggei</i> (ma, UN)	
	<i>Sagittula</i> (1)	<i>S. marina</i> (sw, GD)	
	<i>Salinhabitans</i> (1)	<i>S. flavidus</i> (sl, UN) <sup>†</sup>	
	<i>Seohaetica</i> (1)	<i>S. saemankumensis</i> (tf, JB) <sup>†</sup>	
	<i>Shimia</i> (1)	<i>S. marina</i> (sw, GBU) <sup>†</sup>	
	<i>Sulfitobacter</i> (6)	<i>S. donghicola</i> (sw, UD), <i>S. geojensis</i> (sw, GBU), <i>S. litoralis</i> (sw, UN), <i>S. marinus</i> (sw, GW), <i>S. noctilucae</i> (sw, GBU), <i>S. noctilucicola</i> (sw, GBU)	
	<i>Thalassobius</i> (3)	<i>T. aestuarii</i> (tf, GSI), <i>T. aquaeponi</i> (sw, GBU), <i>T. maritimus</i> (sw, GBU)	
	<i>Thalassococcus</i> (1)	<i>T. lentus</i> (sw, GBU)	
	<i>Thioclava</i> (1)	<i>T. arenosa</i> (ss, GSI)	
	<i>Tropicomonas</i> (2)	<i>T. aquimaris</i> (sw, GBU), <i>T. sediminicola</i> (tf, JG)	
	<i>Wenxinia</i> (1)	<i>W. saemankumensis</i> (tf, JB)	
	<i>Order Rhodospirillales</i> (25)	<i>Belnapia</i> (1)	<i>B. soli</i> (sv, CD)
		<i>Bombella</i> (1)	<i>B. apis</i> (ta, UN)
		<i>Dankookia</i> (1)	<i>D. rubra</i> (fs, CD) <sup>†</sup>
		<i>Roseomonas</i> (9)	<i>R. aeritata</i> (ai, GSI), <i>R. aerofrigidensis</i> (ai, AR), <i>R. aerophila</i> (ai, CD), <i>R. frigidiquae</i> (sw, JG), <i>R. hibiscisoli</i> (sv, GSI), <i>R. riguloci</i> (fw, GBU), <i>R. soli</i> (sv, GSI), <i>R. terrae</i> (sv, UD), <i>R. terricola</i> (sv, CD)
		<i>Caenispirillum</i> (1)	<i>C. bisanense</i> (ww, GD) <sup>†</sup>
		<i>Dongia</i> (2)	<i>D. rigui</i> (fw, GBU), <i>D. soli</i> (sv, UD)
		<i>Inquilinus</i> (1)	<i>I. ginsengisoli</i> (sv, GSI)
		<i>Limibacillus</i> (1)	<i>L. halophilus</i> (sv, GSI) <sup>†</sup>
		<i>Nitrosipirillum</i> (1)	<i>N. iridis</i> (sv, GBU, Jj)
	<i>Pelagibius</i> (1)	<i>P. litoralis</i> (sw, UN) <sup>†</sup>	
<i>Skermanella</i> (1)	<i>S. aerolata</i> (ai, CD)		
<i>Thalassobaculum</i> (1)	<i>T. litoreum</i> (sw, GBU) <sup>†</sup>		
<i>Reyanella</i> (4)	<i>R. aquatilis</i> (fw, GSI), <i>R. graminifolii</i> (sv, JG), <i>R. soli</i> (sv, WS), <i>R. terrae</i> (sv, GSI)		
Unassigned (4)	<i>S. chungangensis</i> (ss, JJ)		
<b>Order Sneathiellales</b> (1)	<i>Sneathiella</i> (1)		
<i>Sneathiellaceae</i> (1)			
<b>Order Spingomonadales</b> (77)	<i>Altererythrobacter</i> (9)		
<i>Erythrobacteraceae</i> (21)	<i>A. aestiquae</i> (sw, CD), <i>A. aestuarii</i> (sw, JG), <i>A. aquaemixtae</i> (sw, JJ), <i>A. aquiaggeris</i> (sw, CD), <i>A. deserti</i> (sr, WS), <i>A. gangjinensis</i> (tf, JG), <i>A. luteolus</i> (tf, UN), <i>A. marensis</i> (sw, JJ), <i>A. namhicola</i> (sw, JG)		



Table 2. Continued.

Family	Genus	Species (source, region, function)
<i>Erythrobacteraceae</i> (21)	<i>Erythrobacter</i> (9)	<i>E. aquimaris</i> (sw, UN), <i>E. aquimixicola</i> (sw, JJ), <i>E. flavus</i> (sw, GW), <i>E. gaebuli</i> (tf, JB), <i>E. gangjinensis</i> (sw, JG), <i>E. jejuensis</i> (sw, JJ), <i>E. lutimaris</i> (tf, JB), <i>E. marinus</i> (sw, JB), <i>E. seohaensis</i> (tf, JB)
<i>Sphingomonadaceae</i> (56)	<i>Porphrobacter</i> (3)	<i>P. algicida</i> (sw, GBU, Jd), <i>P. dokdonensis</i> (sw, UD), <i>P. donghaensis</i> (sw, UN)
	<i>Blastomonas</i> (1)	<i>B. fulva</i> (cu, AR)
	<i>Novosphingobium</i> (3)	<i>N. aquiterrae</i> (fw, CD), <i>N. humi</i> (sr, JG), <i>N. pentaromativorans</i> (tf, GBU, Jb)
	<i>Parasphingopyxis</i> (1)	<i>P. algicola</i> (mp, CD)
	<i>Sphingobium</i> (4)	<i>S. algicola</i> (fa, CD), <i>S. chungbukense</i> (sr, CD, Jb), <i>S. paulinellae</i> (fa, CD), <i>S. vulgare</i> (fs, CD)
	<i>Sphingomicrobium</i> (1)	<i>S. aestuariivivum</i> (tf, JG)
	<i>Sphingomonas</i> (29)	<i>S. aerophila</i> (ai, JJ), <i>S. aestuarii</i> (tf, JG), <i>S. agri</i> (sv, GSI), <i>S. aquatilis</i> (fw, CD), <i>S. carri</i> (ai, AR), <i>S. daechungensis</i> (fs, CD), <i>S. dokdonensis</i> (sv, UD), <i>S. frigidaeris</i> (ai, AR), <i>S. ginsengisoli</i> (sv, GSI), <i>S. ginsenosidimutans</i> (sv, GSI), <i>S. gofjawalisoli</i> (sv, JJ), <i>S. hankookensis</i> (ww, CD), <i>S. insulae</i> (sv, UD), <i>S. jejuensis</i> (ma, JJ), <i>S. jinjuensis</i> (sv, GBU), <i>S. kaisensis</i> (sv, CD), <i>S. koreensis</i> (fw, CD), <i>S. kyungheensis</i> (sv, GSI), <i>S. lacus</i> (sv, CD), <i>S. limnosediminicola</i> (fs, JG), <i>S. natasensis</i> (sv, WS), <i>S. oligoaromativorans</i> (sv, CD), <i>S. oryctiterrae</i> (sv, GBU), <i>S. palustris</i> (fw, GBU), <i>S. rhizophila</i> (sv, GSI), <i>S. sediminicola</i> (fs, CD), <i>S. silvisoli</i> (sv, JG), <i>S. soli</i> (sv, CD), <i>S. vulcanisoli</i> (sv, JJ)
	<i>Sphingopyxis</i> (10)	<i>S. baekryungensis</i> (sw, WS), <i>S. ginsengisoli</i> (sv, GSI), <i>S. granuli</i> (ww, GSI), <i>S. litoris</i> (sw, JJ), <i>S. marina</i> (sw, JJ), <i>S. panaciterrae</i> (sv, GSI), <i>S. panaciterrulae</i> (sv, CD), <i>S. soli</i> (sr, GD), <i>S. solistibvae</i> (sv, GSI), <i>S. taejonensis</i> (fw, CD)
	<i>Sphingorhabdus</i> (4)	<i>S. arenilitoris</i> (ss, GBU), <i>S. flavimaris</i> (sw, WS), <i>S. rigui</i> (fw, GBU), <i>S. wooponensis</i> (fw, GBU)
	<i>Sphingosinicella</i> (2)	<i>S. soli</i> (sr, CD), <i>S. vermicomposti</i> (co, GBU)
<i>Stakelama</i> (1)	<i>S. sediminis</i> (tf, UN)	
<b>Order Unassigned</b> (1)		
Unassigned (1)	<i>Phreatobacter</i> (1)	<i>P. stygius</i> (sr, JJ)
<b>Class Betaproteobacteria</b> (82)		
<b>Order Burkholderiales</b> (73)		
<i>Alcaligenaceae</i> (13)	<i>Azohydromonas</i> (2)	<i>A. riparia</i> (sv, CD), <i>A. ureilytica</i> (sv, CD)
	<i>Castellaniella</i> (2)	<i>C. daejeonensis</i> (sv, CD), <i>C. ginsengisoli</i> (sv, CD)
	<i>Paenacaligenes</i> (1)	<i>P. sawonensis</i> (co, GSI)
	<i>Paracaligenes</i> (2)	<i>P. ginsengisoli</i> (sv, GSI), <i>P. ureilyticus</i> (sv, CB)†
	<i>Parapsyllimonas</i> (1)	<i>P. granuli</i> (ww, CD)†
	<i>Pigmentiphaga</i> (2)	<i>P. daeguensis</i> (ww, GD), <i>P. soli</i> (sv, UN)
	<i>Pusillimonas</i> (3)	<i>P. caeni</i> (ww, AR), <i>P. ginsengisoli</i> (sv, CD), <i>P. harenae</i> (ss, CD)
	<i>Burkholderia</i> (11)	<i>B. denitrificans</i> (sv, UD), <i>B. ginsengisoli</i> (sv, CD), <i>B. humisilvae</i> (sv, CD), <i>B. megalochromosomata</i> (sv, GSI), <i>B. monticola</i> (sv, GSI), <i>B. rhizosphaerae</i> (sv, CD), <i>B. sediminicola</i> (fs, CD), <i>B. soli</i> (sv, CB), <i>B. solistibvae</i> (sv, CD), <i>B. sordidicola</i> (py, GSI), <i>B. terrae</i> (sv, CD)
<i>Burkholderiaceae</i> (17)	<i>Chitinimonas</i> (4)	<i>C. koreensis</i> (sv, GD), <i>C. lacunae</i> (fw, GSI), <i>C. naidadis</i> (fw, JG), <i>C. viridis</i> (fw, GSI)
	<i>Cupriavidus</i> (1)	<i>C. yeoncheonense</i> (sv, GSI)
	<i>Paraburkholderia</i> (1)	<i>P. azotifigens</i> (sv, GSI, Jf)
	<i>Acidovorax</i> (2)	<i>A. lacteus</i> (cu, AR), <i>A. soli</i> (sr, GD)
<i>Comamonadaceae</i> (23)	<i>Caenimonas</i> (2)	<i>C. koreensis</i> (ww, AR)†, <i>C. terrae</i> (sv, GSI)
	<i>Comamonas</i> (2)	<i>C. granuli</i> (ww, CD), <i>C. koreensis</i> (fw, GBU)
	<i>Diaphorobacter</i> (1)	<i>D. aerolatus</i> (ai, GSI)
	<i>Hydrogenophaga</i> (4)	<i>H. bisanensis</i> (ww, GD), <i>H. caeni</i> (fs, AR), <i>H. crassostreae</i> (ma, GSI), <i>H. soli</i> (sv, GSI)
	<i>Melaminivora</i> (1)	<i>M. jejuensis</i> (ww, JJ)
	<i>Polaromonas</i> (1)	<i>P. jejuensis</i> (sv, JJ)

Table 2. Continued.

Family	Genus	Species (source, region, function)	
Comamonadaceae (23)	<i>Ranlibacter</i> (3)	<i>R. alkalicolerans</i> (sv, GSI), <i>R. monticola</i> (sv, GSI), <i>R. rhizophilus</i> (sv, GSI)	
	<i>Simplicispira</i> (2)	<i>S. limi</i> (ww, AR), <i>S. piscis</i> (ma, UN)	
	<i>Variovorax</i> (4)	<i>V. defluvi</i> (ww, GD), <i>V. dokdonensis</i> (sv, UD), <i>V. ginsengisoli</i> (sv, GSI, JI), <i>V. soli</i> (sv, JB)	
	<i>Xenophilus</i> (1)	<i>X. aerolatus</i> (ai, GSI)	
	<i>Herbaspirillum</i> (2)	<i>H. chlorophenolicum</i> (fw, CB, JI), <i>H. rhizosphaerae</i> (sv, UD)	
Oxalobacteraceae (15)	<i>Massilia</i> (10)	<i>M. aerilata</i> (ai, GSI), <i>M. agilis</i> (sv, GSI), <i>M. chloroacetimidivorans</i> (sv, CD, JI), <i>M. jejuensis</i> (ai, JI), <i>M. kyonggiensis</i> (sv, GSI), <i>M. niabensis</i> (ai, GSI), <i>M. niastensis</i> (ai, GSI), <i>M. solisilvae</i> (sv, GSI), <i>M. suwonensis</i> (ai, GSI), <i>M. terrae</i> (sv, GSI)	
	<i>Noviherbaspirillum</i> (1)	<i>N. suwonense</i> (ai, GSI)	
	<i>Undibacterium</i> (2)	<i>U. jejuense</i> (sv, JI), <i>U. seohonense</i> (fw, GSI)	
	<i>Aquabacterium</i> (1)	<i>A. olei</i> (sr, GSI, JIa)	
	<i>Inhella</i> (1)	<i>I. inkyongensis</i> (fw, GSI)†	
	<i>Paucibacter</i> (1)	<i>P. oligotrophus</i> (fw, CD)	
	<i>Piscinibacter</i> (1)	<i>P. aquaticus</i> (fw, GSI)	
	<i>Rhizobacter</i> (1)	<i>R. fulvus</i> (sv, GSI)	
	<i>Andreprevotia</i> (1)	<i>A. chitinihytica</i> (sv, JI, JId)†	
	<i>Aquitalea</i> (1)	<i>A. denitrificans</i> (fs, GW, JI)	
Unassigned (5)	<i>Jeongeupia</i> (1)	<i>J. naejangsanensis</i> (sv, JB, JId)†	
	<i>Leeia</i> (1)	<i>L. oryzae</i> (sv, GBU)†	
	<i>Paludibacterium</i> (1)	<i>P. yongneupense</i> (fs, GW)†	
	<i>Pseudogulbenkiania</i> (1)	<i>P. gefcensis</i> (sv, GSI)	
	<i>Silvimonas</i> (1)	<i>S. terrae</i> (sv, CD, JId)†	
	<i>Uliginosibacterium</i> (1)	<i>U. gangwonense</i> (fs, GW)†	
	<i>Zoogloea</i> (1)	<i>Z. caeni</i> (ww, GD)	
	<i>Arcobacter</i> (1)	<i>A. marinus</i> (sw, UD)	
	<i>Oceanisphaera</i> (3)	<i>O. donghaensis</i> (tf, GW), <i>O. ostreae</i> (sw, UN), <i>O. sediminis</i> (tf, JG)	
	<i>Zobellella</i> (1)	<i>Z. aerophila</i> (ss, UD)	
Class Epsilonproteobacteria (1)	<i>Aestuariatibacter</i> (2)	<i>A. halophilus</i> (tf, GSI), <i>A. salexigens</i> (tf, GSI)†	
	<i>Aestuariatibacteria</i> (1)	<i>A. hydrocarbonica</i> (tf, CD, JIa)†	
	<i>Agarivorans</i> (2)	<i>A. aestuarii</i> (tf, CD, JId), <i>A. litoreus</i> (sw, GBU)	
	<i>Alishewanella</i> (3)	<i>A. aestuarii</i> (tf, JG), <i>A. agri</i> (sr, GD), <i>A. jeotgali</i> (ff, AR)	
	<i>Alteromonas</i> (3)	<i>A. aestuariivivens</i> (tf, JG), <i>A. litorea</i> (tf, CD), <i>A. marina</i> (sw, GW)	
	<i>Bowmanella</i> (1)	<i>B. dokdonensis</i> (sw, UD)	
	<i>Glaciecola</i> (1)	<i>G. nitratireducens</i> (sw, JI)	
	<i>Marinobacter</i> (7)	<i>M. confluens</i> (sw, GW, JIa), <i>M. daepoensis</i> (sw, CD), <i>M. flavinaris</i> (sw, CD), <i>M. goseongensis</i> (sw, GW), <i>M. koreensis</i> (ss, GD), <i>M. litoralis</i> (sw, GW), <i>M. salicampi</i> (sl, JB)	
	Order Rhodocyclales (2)	<i>Uliginosibacterium</i> (1)	<i>U. gangwonense</i> (fs, GW)†
		<i>Zoogloea</i> (1)	<i>Z. caeni</i> (ww, GD)
Class Epsilonproteobacteria (1)	<i>Arcobacter</i> (1)	<i>A. marinus</i> (sw, UD)	
	Order Campylobacteriales (1)	<i>Arcobacter</i> (1)	<i>A. marinus</i> (sw, UD)
Class Gammaproteobacteria (257)		<i>Oceanisphaera</i> (3)	<i>O. donghaensis</i> (tf, GW), <i>O. ostreae</i> (sw, UN), <i>O. sediminis</i> (tf, JG)
	Order Aeromonadales (4)	<i>Zobellella</i> (1)	<i>Z. aerophila</i> (ss, UD)
Order Alteromonadales (65)	<i>Aestuariatibacter</i> (2)	<i>A. halophilus</i> (tf, GSI), <i>A. salexigens</i> (tf, GSI)†	
	Alteromonadaceae (31)	<i>A. aestuarii</i> (tf, CD, JId), <i>A. litoreus</i> (sw, GBU)	
Order Alteromonadales (65)	<i>Agarivorans</i> (2)	<i>A. aestuarii</i> (tf, JG), <i>A. agri</i> (sr, GD), <i>A. jeotgali</i> (ff, AR)	
	<i>Alishewanella</i> (3)	<i>A. aestuarii</i> (tf, JG), <i>A. agri</i> (sr, GD), <i>A. jeotgali</i> (ff, AR)	
Order Alteromonadales (65)	<i>Alteromonas</i> (3)	<i>A. aestuariivivens</i> (tf, JG), <i>A. litorea</i> (tf, CD), <i>A. marina</i> (sw, GW)	
	<i>Bowmanella</i> (1)	<i>B. dokdonensis</i> (sw, UD)	
Order Alteromonadales (65)	<i>Glaciecola</i> (1)	<i>G. nitratireducens</i> (sw, JI)	
	<i>Marinobacter</i> (7)	<i>M. confluens</i> (sw, GW, JIa), <i>M. daepoensis</i> (sw, CD), <i>M. flavinaris</i> (sw, CD), <i>M. goseongensis</i> (sw, GW), <i>M. koreensis</i> (ss, GD), <i>M. litoralis</i> (sw, GW), <i>M. salicampi</i> (sl, JB)	

Table 2. Continued.

Family	Genus	Species (source, region, function)
Alteromonadaceae (31)	<i>Marinobacterium</i> (6)	<i>M. aestuarii</i> (tf, GBU, ♀b), <i>M. halophilum</i> (tf, CD), <i>M. litorale</i> (sw, GSI), <i>M. lutimaris</i> (tf, CD), <i>M. marisflavi</i> (sw, GSI), <i>M. rhizophilum</i> (tf, GSI)
	<i>Paragluticola</i> (3)	<i>P. aestuariivivens</i> (tf, JG), <i>P. agariyitica</i> (tf, GW, ♀d), <i>P. aquimarina</i> (sw, GBU)
	<i>Salinimonas</i> (2)	<i>S. chungwhensis</i> (sl, CD)†, <i>S. lutimaris</i> (tf, GBU, ♀d)
	<i>Cobwellia</i> (3)	<i>C. aestuarii</i> (tf, JB), <i>C. asteriadiis</i> (ma, GW), <i>C. meongget</i> (ma, UN)
	<i>Thalassomonas</i> (2)	<i>T. agariiperforans</i> (tf, GBU, ♀d), <i>T. ganghwensis</i> (tf, GSI)
	<i>Thalassotalea</i> (3)	<i>T. crassostreae</i> (ma, GSI), <i>T. litorea</i> (ss, JJ), <i>T. ponticola</i> (sw, GBU)
	<i>Ferrimonas</i> (1)	<i>F. pelagia</i> (sw, JJ)
	<i>Idiomarina</i> (5)	<i>I. aestuarii</i> (sw, JG), <i>I. halophile</i> (sl, JB), <i>I. homiensis</i> (ss, GD), <i>I. salinarum</i> (sl, UN), <i>I. seosinensis</i> (sl, GSI)
	<i>Paramoritella</i> (1)	<i>P. sediminis</i> (tf, GSI)
	<i>Pseudoalteromonas</i> (3)	<i>P. byunsanensis</i> (tf, JB), <i>P. donghaensis</i> (sw, GW), <i>P. marina</i> (tf, CD)
	<i>Psychrosphaera</i> (3)	<i>P. aestuarii</i> (sw, JG), <i>P. aquimarina</i> (sw, CD), <i>P. haliotis</i> (ma, JG)
	<i>Shewanella</i> (13)	<i>S. aestuarii</i> (tf, JG), <i>S. aquimarina</i> (sw, UN), <i>S. basaltis</i> (ss, JJ), <i>S. dokdonensis</i> (sw, UD), <i>S. donghaensis</i> (ds, GW, ♀g), <i>S. gaetbuli</i> (tf, JG), <i>S. haliotis</i> (ma, JG), <i>S. litorisedimentis</i> (tf, JB), <i>S. marina</i> (sw, JG), <i>S. marisflavi</i> (sw, UN), <i>S. seohaensis</i> (tf, JB), <i>S. spongiae</i> (ma, UN), <i>S. upenei</i> (ma, UN)
	<b>Order Cellvibrionales (20)</b>	
<i>Cellvibrionaceae</i> (10)	<i>Eionea</i> (1)	<i>E. flava</i> (sw, GSI)
	<i>Gilvimirinus</i> (1)	<i>G. agariyiticus</i> (ss, JJ, ♀d)
	<i>Marinimicrobium</i> (3)	<i>M. agariyiticum</i> (tf, JG, ♀d), <i>M. koreense</i> (tf, JG)†, <i>M. locisalis</i> (sl, UN)
	<i>Pseudomarcicurvus</i> (1)	<i>P. alcaniphilus</i> (tf, CD)
	<i>Simiduita</i> (3)	<i>S. aestuariiviva</i> (tf, JG), <i>S. areninigræ</i> (ss, JJ, ♀d), <i>S. curdlanivorans</i> (sw, JJ, ♀d)
	<i>Umbonibacter</i> (1)	<i>U. caenipe lagi</i> (tf, CD)
	<i>Marinimicrobium</i> (1)	<i>M. arenosum</i> (ss, GSI)†
<i>Haliceae</i> (2)	<i>Parahalica</i> (1)	<i>P. aestuarii</i> (sw, CD)
<i>Microbulbiferaceae</i> (6)	<i>Microbulbifer</i> (6)	<i>M. aestuariivivens</i> (tf, JG), <i>M. celer</i> (sl, UN), <i>M. gwangyangensis</i> (tf, JG), <i>M. maritimus</i> (tf, UN), <i>M. pacificus</i> (tf, JG), <i>M. salipaludis</i> (tf, JG)
<i>Porticococcaeae</i> (1)	<i>Porticoccus</i> (1)	<i>P. litoralis</i> (sw, GSI)†
<i>Spongibacteraceae</i> (1)	<i>Zhongshania</i> (1)	<i>Z. aliphaticivorans</i> (tf, CD, ♀a)
<b>Order Chromatiales (7)</b>		
<i>Chromatiaceae</i> (5)	<i>Rheinheimera</i> (5)	<i>R. aestuarii</i> (tf, JJ), <i>R. aquimaris</i> (sw, GW), <i>R. arenilitoris</i> (ss, JG), <i>R. gaetbuli</i> (tf, JJ), <i>R. soli</i> (sr, GBU)
<i>Ectothiorhodospiraceae</i> (1)	<i>Thioalbus</i> (1)	<i>T. denitrificans</i> (tf, GW)†
<i>Granulosicoccaceae</i> (1)	<i>Granulosicoccus</i> (1)	<i>G. undariae</i> (mp, JG)
<b>Order Enterobacteriales (2)</b>		
<i>Enterobacteriaceae</i> (1)	<i>Gibbsiella</i> (1)	<i>G. papilionis</i> (ta, GSI)
<i>Erwinaceae</i> (1)	<i>Erwinia</i> (1)	<i>E. pyrifoliae</i> (py, UN)
<b>Order Legionellales (1)</b>		
<i>Legionellaceae</i> (1)	<i>Legionella</i> (1)	<i>L. busanensis</i> (we, GBU)
<b>Order Lysobacteriales (73)</b>		
<i>Lysobacteraceae</i> (45)	<i>Arenimonas</i> (5)	<i>A. compositi</i> (sv, GBU), <i>A. daechungensis</i> (fs, CB), <i>A. daejeonensis</i> (co, CD)†, <i>A. donghaensis</i> (ss, GD), <i>A. oryziterræ</i> (sv, GBU)

Table 2. Continued.

Family	Genus	Species (source, region, function)
Lysobacteraceae (45)	<i>Chujaibacter</i> (1)	<i>C. soli</i> (sv, JJ)†
	<i>Luteimonas</i> (3)	<i>L. aestuarii</i> (tf, JG), <i>L. lutimaris</i> (tf, CD), <i>L. marina</i> (sw, GSI)
	<i>Lysobacter</i> (23)	<i>L. agri</i> (sv, GSI), <i>L. capsici</i> (sv, GBU, Jf), <i>L. concretiois</i> (ww, AR), <i>L. daejeonensis</i> (sv, CD), <i>L. dokdonensis</i> (sv, UD), <i>L. fragariae</i> (sv, CD), <i>L. ginsengisoli</i> (sv, GSI), <i>L. hanhyongensis</i> (ww, CD), <i>L. koreensis</i> (sv, CD), <i>L. maris</i> (sw, GBU), <i>L. niabensis</i> (sv, GSI), <i>L. niastensis</i> (sv, GD), <i>L. novalis</i> (sv, GSI), <i>L. olei</i> (sr, JB), <i>L. oryzae</i> (sv, GBU), <i>L. panacisoli</i> (sv, GSI), <i>L. panaciterrae</i> (sv, GSI), <i>L. rhizospherae</i> (sv, CD), <i>L. sediminiticola</i> (fs, CD), <i>L. solanacearum</i> (sv, GD), <i>L. soli</i> (sv, CD), <i>L. terrae</i> (sv, GSI), <i>L. yangpyeongensis</i> (sv, GSI)
		<i>Pseudoxanthomonas</i> (8)
	<i>Silanimonas</i> (1)	<i>S. algicola</i> (cu, AR)
	<i>Stenotrophomonas</i> (3)	<i>S. daejeonensis</i> (ww, CD), <i>S. ginsengisoli</i> (sv, CD), <i>S. koreensis</i> (co, CD)
	<i>Thermomonas</i> (1)	<i>T. koreensis</i> (sv, CD)
	<i>Dokdonella</i> (3)	<i>D. ginsengisoli</i> (sv, GSI), <i>D. koreensis</i> (sv, UD)†, <i>D. soli</i> (sv, UD)
	<i>Dyella</i> (8)	<i>D. agri</i> (sv, GSI), <i>D. ginsengisoli</i> (sv, GSI), <i>D. jejuensis</i> (sv, JJ), <i>D. koreensis</i> (sv, CD), <i>D. kyungheensis</i> (sv, GW), <i>D. marensis</i> (sr, JJ), <i>D. soli</i> (sv, JJ), <i>D. terrae</i> (sv, JJ)
		<i>Fluviococcus</i> (1)
	<i>Fulvimonas</i> (1)	<i>F. yonginensis</i> (sv, GSI)
	<i>Luteibacter</i> (1)	<i>L. yeojuensis</i> (sv, GSI)
	<i>Oleigrimonas</i> (1)	<i>O. citrea</i> (tf, JG)
<i>Rhodanobacter</i> (12)	<i>R. aciditrophus</i> (ww, CB), <i>R. caeni</i> (ww, CD), <i>R. fulvus</i> (sv, CD), <i>R. ginsengisoli</i> (sv, GD), <i>R. ginsenosidimitans</i> (sv, GSI), <i>R. lumi</i> (sv, GSI), <i>R. koreensis</i> (sv, GSI), <i>R. rhizospherae</i> (sv, CD), <i>R. soli</i> (sv, GSI), <i>R. terrae</i> (sv, GSI), <i>R. thiooxydans</i> (ww, AR), <i>R. umsongensis</i> (sv, CB)	
	<i>Rudaea</i> (1)	<i>R. cellulolytica</i> (sv, WS, Jd)†
<b>Order Nevskiales</b> (6)	<i>Nevskia</i> (1)	<i>N. terrae</i> (sv, WS)
	<i>Panacagrimonas</i> (1)	<i>P. perspica</i> (sv, GSI)†
<i>Neviskiaceae</i> (4)	<i>Solimonas</i> (2)	<i>S. soli</i> (sv, CD)†, <i>S. terrae</i> (sv, CD)
	<i>Salinisphaera</i> (2)	<i>S. dokdonensis</i> (sw, UD), <i>S. orenii</i> (sl, JB)
<b>Order Oceanospirillales</b> (39)	<i>Alcanivorax</i> (1)	<i>A. gelatiniphagus</i> (tf, CD, Jf)
	<i>Endozoicomonas</i> (1)	<i>E. atrinae</i> (ma, JG)
<i>Hahellaceae</i> (5)	<i>Hahella</i> (2)	<i>H. chejuensis</i> (sw, JJ)†, <i>H. ganghwensis</i> (tf, GSI)
	<i>Kistimonas</i> (2)	<i>K. assterae</i> (ma, GW)†, <i>K. scapharcae</i> (ma, JG)
<i>Halomonadaceae</i> (14)	<i>Cobetia</i> (1)	<i>C. crustatorum</i> (ff, AR)
	<i>Halomonas</i> (11)	<i>H. aestuarii</i> (tf, JB), <i>H. alimentaria</i> (ff, AR), <i>H. cibimaris</i> (ff, AR), <i>H. denitrificans</i> (sw, CD), <i>H. gomseomensis</i> (sl, CD), <i>H. janggokensis</i> (sl, CD), <i>H. jeotgali</i> (ff, AR), <i>H. koreensis</i> (sl, CD), <i>H. kribbensis</i> (sl, UN), <i>H. salticampi</i> (sl, JB), <i>H. taeanensis</i> (sl, CD)
<i>Kushneria</i> (1)		<i>K. marisflavi</i> (sw, CD)
<i>Halomonadaceae</i> (14)	<i>Salinicola</i> (1)	<i>S. salaries</i> (sw, CD)
	<i>Kangiella</i> (4)	<i>K. aquimaria</i> (tf, CD), <i>K. geojedonensis</i> (sw, GBU), <i>K. koreensis</i> (tf, CD)†, <i>K. sediminitioris</i> (tf, JG)
<i>Kangiellaceae</i> (4)	<i>Litoricola</i> (2)	<i>L. lipolytica</i> (sw, GW)†, <i>L. marina</i> (sw, GSI)
	<i>Oceanospirillaceae</i> (9)	<i>Amphritea</i> (1)
<i>Marinomonas</i> (4)		<i>M. algicola</i> (sw, GBU, Jd), <i>M. basaltis</i> (ss, JJ), <i>M. dokdonensis</i> (sw, UD), <i>M. hwangdonensis</i> (sw, CD)
<i>Litoricolaceae</i> (2)†	<i>Neptunomonas</i> (2)	<i>N. acidivorans</i> (tf, GSI), <i>N. concharum</i> (ma, JG)
	<i>Pontibacterium</i> (1)	<i>P. granulatum</i> (tf, CD)†
<i>Oceanospirillales</i> (1)	<i>T. marinus</i> (sw, GSI)	

Table 2. Continued.

Family	Genus	Species (source, region, function)
<i>Saccharospirillaceae</i> (4)	<i>Gyvuella</i> (1) <i>Reinekea</i> (2) <i>Saccharospirillum</i> (1)	<i>G. sunshinyii</i> (py, GBU, ♯f)† <i>R. aestuarii</i> (tf, GSI), <i>R. marina</i> (sw, JB) <i>S. aestuarii</i> (tf, GSI)
<b>Order Orbales</b> (1) <i>Orbaceae</i> (1)	<i>Orbus</i> (1)	<i>O. sasakiae</i> (ta, UN)
<b>Order Pseudomonadales</b> (23) <i>Moraxellaceae</i> (15)	<i>Acinetobacter</i> (4) <i>Paraperlucidibacca</i> (2) <i>Perlucidibacca</i> (2) <i>Psychrobacter</i> (7) <i>Pseudomonas</i> (8)	<i>A. apis</i> (ta, UN), <i>A. brisouii</i> (fs, GW), <i>A. halotolerans</i> (sv, GSI, ♯a), <i>A. soli</i> (sv, JG) <i>P. baekdonensis</i> (sw, GW)†, <i>P. wandonensis</i> (sw, JG) <i>P. aquatic</i> (fw, GW), <i>P. piscinae</i> (fw, GSI)† <i>P. aestuarii</i> (tf, JG), <i>P. alimentarius</i> (ff, AR), <i>P. aquimaris</i> (sw, UN), <i>P. celer</i> (sw, UN), <i>P. cibarius</i> (ff, AR), <i>P. jeotgali</i> (ff, AR), <i>P. namhaensis</i> (sw, UN) <i>P. jinjuensis</i> (sv, GBU), <i>P. koreensis</i> (sv, GSI), <i>P. panacis</i> (py, UN), <i>P. pohangensis</i> (ss, GD), <i>P. sabulinigri</i> (ss, JJ), <i>P. segetis</i> (sv, UD), <i>P. taeanensis</i> (sr, CD), <i>P. umsongensis</i> (sv, CB)
<b>Order Thiotrichales</b> (1) <i>Piscirickettsiaceae</i> (1)	<i>Methylolphaga</i> (1)	<i>M. aminisulfidivorans</i> (sw, JG)
<b>Order Unassigned</b> (4) Unassigned (4)	<i>Litorivivens</i> (2) <i>Pseudohongiella</i> (1) <i>Wohlfahrtiimonas</i> (1)	<i>L. aequoris</i> (sw, GD), <i>L. lipolytica</i> (tf, JG, ♯a)† <i>P. acicola</i> (sw, GW) <i>W. larvae</i> (ta, UN)
<b>Order Vibrionales</b> (11) <i>Vibrionaceae</i> (11)	<i>Grimontia</i> (1) <i>Photobacterium</i> (6) <i>Vibrio</i> (4)	<i>G. marina</i> (sw, JG) <i>P. aestuarii</i> (tf, JG), <i>P. aphysiae</i> (ma, JG), <i>P. gaethulicola</i> (tf, JB), <i>P. ganghwense</i> (sw, GSI), <i>P. lipolyticum</i> (tf, JB, ♯a), <i>P. lutimaris</i> (tf, JB) <i>V. areninigrae</i> (ss, JJ), <i>V. hemi-centroti</i> (ma, JG, ♯d), <i>V. littoralis</i> (tf, CD), <i>V. oceanisediminis</i> (tf, CD, ♯j)

\*Numerals in the parentheses are the number of species. †Denotes the creation of the genus, family, and order. Abbreviations of the source: ai, air and air-conditioning system; co, compost; cu, culture in lab.; ds, deep sea sediment; fa, freshwater algae; ff, fermented food; fs, freshwater sediment; fw, freshwater; ma, marine animal; mp, marine plant or seaweed; py, terrestrial plant, sl, solar saltern and salt lake; sr, soil without vegetation or contaminated soil; ss, seashore sand; sv, soil with vegetation (agricultural and forest); sw, seawater; ta, terrestrial animal; tf, tidal flat sediment; ww, wastewater. Abbreviations of the region: AR, artificial environment; CB, Chungbuk; CD, Chungnam/Deajeon; UD, Ulsang and Dokdo islands; GBU, Gyeongnam/Busan/Ulsan; GD, Gyeongbuk/Daegu; GSI, Gyeonggi/Seoul/Incheon; GW, Gangwon; JB, Jeonbuk; JG, Jeonnam/Gwangju; JJ, Jeju; UN, site unspecified; WS, 5 West sea islands. Abbreviations of the function: ♯a, Aliphatic hydrocarbon degradation; ♯b, Aromatic hydrocarbon degradation; ♯c, Herbicide degradation; ♯d, Polysaccharide degradation; ♯e, Protein degradation; ♯f, Antibiotic production; ♯g, High-pressure cold-adapted substance production; ♯h, Steroid acid production; ♯i, Denitrification; ♯j, Nitrogen fixation; ♯k, Nitrate reduction.

from Chungnam/Daejeon (80 genera, 33 families, 15 orders, and three classes), 120 species from Gyeonggi/Seoul/Incheon (75 genera, 32 families, 15 orders, and three classes), 72 species from Jeonnam/Gwangju (54 genera, 24 families, 14 orders, and three classes), 60 species from Gyeongnam/Busan/Ulsan (47 genera, 19 families, 13 orders, and three classes), 58 species from Jeju (43 genera, 25 families, 14 orders, and three classes), 34 species from Gwangwon (31 genera, 17 families, 11 orders, and three classes), 30 species from Gyeongbuk/Daegu (26 genera, 17 families, 11 orders, and three classes), 30 species from Jeonbuk (23 genera, 16 families, 10 orders, and three classes), and 25 species from Ulreung-/Dok-do Islands (23 genera, 19 families, 12 orders, and four classes). Since 26 species (20 genera, 15 families, 10 orders, and three classes) were isolated from artificial environments such as fermented foods, wastewater treatment systems, and air conditioning systems, their regional origins were not exactly specified. Moreover, regarding the 42 species (33 genera, 20 families, 11 orders, and three classes) from natural environments, their isolation regions could not be obtained.

**Properties of the novel species:** Isolates from soil, freshwater, seawater, and tidal flat sediments of Korea were affiliated with many genera. However, several taxa had co-relationships with isolation sources. In particular, some species were mainly isolated from marine-related environments such as seawater, tidal flat sediments, marine animals, and solar salterns: families *Erythrobacteraceae*, *Kordiimonadaceae*, and *Rhodobacteraceae* of the class *Alphaproteobacteria* as well as *Vibrionaceae*, *Aeromonadaceae*, *Alteromonadaceae*, *Colwelliaceae*, *Idiomarinaceae*, *Pseudoalteromonadaceae*, *Shewanellaceae*, *Cellvibrionaceae*, *Microbulbiferaceae*, *Chromatiaceae*, “*Saccharospirillaceae*”, *Hahellaceae*, *Halomonadaceae*, *Kangiellaceae*, and *Oceanospirillaceae* of the class *Gammaproteobacteria*. In particular, 10 out of 14 *Halomonadaceae* species were isolated from solar salterns and fermented foods. Moreover, these *Halomonadaceae* species were halophilic or halotolerant; in particular, *Halomonas taeanensis* (Lee *et al.*, 2005) and *Halomonas jeotgali* (Kim *et al.*, 2010) could grow at 25% NaCl (w/v). Compared to Korean novel bacterial species of other phyla, these *Halomonas* species were less halophilic than the *Firmicutes* species such as *Lentibacillus kimchii* (Oh *et al.*, 2016) and *Virgibacillus alimentarius* (Kim *et al.*, 2011) but more halophilic than the *Actinobacteria* species such as *No-cardiopsis kunsanensis* (Chun *et al.*, 2000) and *Kocuria koreensis* (Park *et al.*, 2010) as well as the *Bacteroidetes* species such as *Salegentibacter salinarum* (Yoon *et al.*, 2008) and *Psychroflexus salinarum* (Yoon *et al.*, 2009).

Members of the families *Caulobacteraceae*, *Rhizobiaceae*, *Alcaligenaceae*, *Burkholderiaceae*, *Chromobacte-*

*riaceae*, and *Rhodanobacteraceae* were mainly isolated from the terrestrial environment such as cultivated soil, freshwater, and wastewater.

Moreover, both *Microvirga* species and three out of five *Methylobacterium* species of the family *Methylobacteriaceae*, order *Rhizobiales* and five out of 10 *Massilia* species of the family *Oxalobacteraceae*, order *Burkholderiales* were isolated from air samples. The members of the genera *Methylobacterium*, *Microvirga*, and *Massilia* had common characteristics; high G+C content over 60 mol%, ubiquinone -8 or -10 as a major respiratory quinone, and phosphatidylethanolamine, phosphatidylglycerol, and diphosphatidylglycerol as major polar lipids.

Several novel *Proteobacteria* species from Korean environments showed specific functions such as degradation of polysaccharide, protein, lipid or hydrocarbon, and pesticide, and production of bile acid, high-pressure cold-adapted molecule, and antibiotics. Also, some species were involved in the nitrogen cycle with nitrogen fixation, denitrification or nitrate-reduction (Table 2).

Finally, a large number of novel *Proteobacteria* species are being isolated since researchers are aiming to find novel strains from extreme or untapped environments and by using new cultivating methods (Yang *et al.*, 2007; Altankhuu and Kim, 2017).

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