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

Ahyoung Choi1, Jin-Woo Bae2, Chang-Jun Cha3, Jongsik Chun4, Wan-Taek Im5, Kwang Yeop Jahng6, Che Ok Jeon7, Kiseong Joh8, Seung Bum Kim9, Chi Nam Seong10, Jung-Hoon Yoon11, and Jang-Cheon Cho1,*

1Department of Biological Sciences, Inha University, Incheon 402-751, Korea
2Department of Biology, Kyung Hee University, Seoul 130-701, Korea
3Department of Biotechnology, Chung-Ang University, Anseong 456-756, Korea
4School of Biological Sciences, Seoul National University, Seoul 151-742, Korea
5Department of Biotechnology, Hankyong National University, Anseong 456-749, Korea
6Department of Life Sciences, Chonbuk National University, Jeonju 561-756, Korea
7Department of Life Science, Chung-Ang University, Seoul 156-756, Korea
8Department of Bioscience and Biotechnology, Hankuk University of Foreign Studies, Gyeonggi 449-791, Korea
9Department of Microbiology, Chungnam National University, Daejeon 305-764, Korea
10Department of Biology, Sunchon National University, Suncheon 540-950, Korea
11Department of Food Science and Biotechnology, Sungkyunkwan University, Suwon 440-746, Korea

*Correspondent: chojc@inha.ac.kr

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 Gammaproteobacteria 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

© 2015 National Institute of Biological Resources
DOI:10.12651/JSR.2015.4.2.109

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 Pedroso-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 at −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.

<table>
<thead>
<tr>
<th>Class</th>
<th>Family</th>
<th>Genus</th>
<th>Strain ID</th>
<th>NIBR ID</th>
<th>Most closely related species (Type strain of species)</th>
<th>Similarity to type strain (%)</th>
<th>Isolation source</th>
<th>Medium</th>
<th>Incubation conditions</th>
</tr>
</thead>
<tbody>
<tr>
<td>Betaproteobacteria</td>
<td>Burkholderiaceae</td>
<td>Burkholderia</td>
<td>VNT1</td>
<td>NIBRA0000113976</td>
<td>B. stabilis (LMG 14294 T)</td>
<td>99.6</td>
<td>Soil</td>
<td>VXG</td>
<td>25°C, 3d</td>
</tr>
<tr>
<td></td>
<td>Capriovivadus</td>
<td>RMH2-4</td>
<td>NIBRA0000113939</td>
<td></td>
<td>C. necator (N-1 T)</td>
<td>99.5</td>
<td>Tidal flat</td>
<td>R2A</td>
<td>30°C, 2d</td>
</tr>
<tr>
<td></td>
<td>Oxlalobacteraceae</td>
<td>Collimonas</td>
<td>mNT30</td>
<td>NIBRA0000113979</td>
<td>C. pratensis (Ter91 T)</td>
<td>99.5</td>
<td>Soil</td>
<td>MM</td>
<td>25°C, 3d</td>
</tr>
<tr>
<td></td>
<td>Comamonadaceae</td>
<td>Acidovorax</td>
<td>HME8439</td>
<td>NIBRA0000114079</td>
<td>A. oryzae (FC-143 T)</td>
<td>99.5</td>
<td>Freshwater</td>
<td>R2A</td>
<td>30°C, 2d</td>
</tr>
<tr>
<td></td>
<td>Neisseriaceae</td>
<td>Chromobacterium</td>
<td>HME8586</td>
<td>NIBRA0000114080</td>
<td>C. aquaticum (CC-SEYA-1 T)</td>
<td>99.6</td>
<td>Freshwater</td>
<td>R2A</td>
<td>30°C, 2d</td>
</tr>
<tr>
<td></td>
<td>Colwelliaceae</td>
<td>Colwellia</td>
<td>J6</td>
<td>NIBRA0000114101</td>
<td>C. aestuarii (SMK-10 T)</td>
<td>99.8</td>
<td>Seawater</td>
<td>MA</td>
<td>25°C, 3d</td>
</tr>
<tr>
<td></td>
<td>Alteromonadaceae</td>
<td>Marinobacter</td>
<td>HD47</td>
<td>NIBRA0000113991</td>
<td>M. psychrophilus (20041 T)</td>
<td>99.1</td>
<td>Tidal flat</td>
<td>MA</td>
<td>25°C, 3d</td>
</tr>
<tr>
<td></td>
<td>Shewanellaceae</td>
<td>Shewanella</td>
<td>J4</td>
<td>NIBRA0000114100</td>
<td>S. colwelliana (ATCC 39565 T)</td>
<td>100.0</td>
<td>Seawater</td>
<td>MA</td>
<td>25°C, 3d</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Shewanella</td>
<td>J7</td>
<td>NIBRA0000114102</td>
<td>S. poaehti (TF-27 T)</td>
<td>99.9</td>
<td>Seawater</td>
<td>MA</td>
<td>25°C, 3d</td>
</tr>
<tr>
<td></td>
<td>Pseudoalteromonadaceae</td>
<td>Pseudoalteromonas</td>
<td>KYW799</td>
<td>NIBRA0000114111</td>
<td>P. marina (Mano4 T)</td>
<td>99.8</td>
<td>Seawater</td>
<td>MA</td>
<td>25°C, 2d</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Pseudoalteromonas</td>
<td>WS-MG1</td>
<td>NIBRA0000114003</td>
<td>P. elyakovii (KMM 16 T)</td>
<td>99.9</td>
<td>Seaweed</td>
<td>MA</td>
<td>25°C, 3d</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Pseudoalteromonas</td>
<td>ES05-9M-7-MA</td>
<td>NIBRA0000113915</td>
<td>P. undina (NCIMB 2128 T)</td>
<td>100.0</td>
<td>Seawater</td>
<td>MA</td>
<td>25°C, 2d</td>
</tr>
<tr>
<td></td>
<td>Glaciecola</td>
<td>KA23</td>
<td>NIBRA0000114108</td>
<td></td>
<td>G. mesophilus (KMM 241 T)</td>
<td>99.7</td>
<td>Seawater</td>
<td>MA</td>
<td>25°C, 2d</td>
</tr>
<tr>
<td></td>
<td>Idiomarina</td>
<td>HME8844</td>
<td>NIBRA0000114095</td>
<td></td>
<td>I. fontislavii (I23 T)</td>
<td>99.9</td>
<td>Tidal flat</td>
<td>R2A</td>
<td>37°C, 2d</td>
</tr>
<tr>
<td></td>
<td></td>
<td>IMCC1088</td>
<td>NIBRA0000113912</td>
<td></td>
<td>I. lothii (L2T R)</td>
<td>99.9</td>
<td>Seawater</td>
<td>MA</td>
<td>25°C, 4d</td>
</tr>
<tr>
<td></td>
<td>Pseudomonadaceae</td>
<td>Pseudomonas</td>
<td>WR-R8Y</td>
<td>NIBRA0000114002</td>
<td>P. guineae (MS T)</td>
<td>99.8</td>
<td>Soil</td>
<td>R2A</td>
<td>25°C, 3d</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Pseudomonas</td>
<td>MA16</td>
<td>NIBRA0000113968</td>
<td>P. peli (RI-20 T)</td>
<td>100.0</td>
<td>Soil</td>
<td>MA</td>
<td>25°C, 2d</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Pseudomonas</td>
<td>SB11</td>
<td>NIBRA0000114060</td>
<td>P. marina (KMM 304 T)</td>
<td>99.7</td>
<td>Tidal flat</td>
<td>MA</td>
<td>25°C, 2d</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Pseudomonas</td>
<td>WR-M4W</td>
<td>NIBRA0000114000</td>
<td>P. rhodesiae (CIP 104664 T)</td>
<td>99.9</td>
<td>Soil</td>
<td>R2A</td>
<td>25°C, 3d</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Pseudomonas</td>
<td>MUG3-2</td>
<td>NIBRA0000113937</td>
<td>P. mendocina (LMG 123 T)</td>
<td>99.4</td>
<td>Wetland</td>
<td>MA</td>
<td>30°C, 2d</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Pseudomonas</td>
<td>CR2-4</td>
<td>NIBRA0000113866</td>
<td>P. nitroreducens (DSM 14399 T)</td>
<td>99.4</td>
<td>Plant root</td>
<td>R2A</td>
<td>30°C, 5d</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Pseudomonas</td>
<td>CR5-1</td>
<td>NIBRA0000113952</td>
<td>P. psychrotolerans (C36 T)</td>
<td>99.7</td>
<td>Soil</td>
<td>R2A</td>
<td>30°C, 2d</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Pseudomonas</td>
<td>HWDM10</td>
<td>NIBRA0000113994</td>
<td>P. caeni (HY-14 T)</td>
<td>99.7</td>
<td>Seawater</td>
<td>R2A</td>
<td>25°C, 3d</td>
</tr>
<tr>
<td></td>
<td>Moraxellaceae</td>
<td>Psychrobacter</td>
<td>WS-MW4</td>
<td>NIBRA0000114005</td>
<td>P. foetii (NF2 T)</td>
<td>100.0</td>
<td>Seaweed</td>
<td>MA</td>
<td>25°C, 3d</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Psychrobacter</td>
<td>WS-MW1</td>
<td>NIBRA0000114004</td>
<td>P. nivinartis (88-2 T)</td>
<td>99.9</td>
<td>Seaweed</td>
<td>MA</td>
<td>25°C, 3d</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Acinetobacter</td>
<td>CT3-6</td>
<td>NIBRA0000113859</td>
<td>A. calcoaceticus (DSM 30006 T)</td>
<td>99.9</td>
<td>Plant root</td>
<td>TSA</td>
<td>30°C, 2d</td>
</tr>
</tbody>
</table>
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 14294T (AF148554; 99.6% 16S rRNA gene sequence similarity), *Cupriavidus necator* N-1T (CP002878; 99.5%), *Collimonas pratenisi* Ter91T (AY 281137; 99.5%), *Acidovorax oryzae* FC-143T (DQ 360414; 99.5%), and *Chromobacterium aquaticum* CCSEYA-1T (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 pratenisi* (Höppner-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 pratenisi* 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 *Enterobacterales*, 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 *Chromati-ales* (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. J4; 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. Gsoli549; 39. WSW-MW5.
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 gaeubuli (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 lothiensis (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 (Palenroni 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, Vibrio, 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 Gibbisia 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.

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 Granulosicoccaceae.
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 \( \beta \)-galactosidase. Potassium glucuronate, 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 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 white-beige colored after 3 days on MA at 25°C. Negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, urease, esculin hydrolysis, gelatinase, and \( \beta \)-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. Positive for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, urease, esculin hydrolysis, gelatinase, and \( \beta \)-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 sample, Taean, 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 (= NIBRBA0000114003) 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 IMCC1088 (= 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 wetland 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-
drolisis, 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, 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 (= NIBRBA0000114005) has been isolated from a seawater 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, glucose fermentation, 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 (= NIBRBA0000114004) has been isolated from a seawater 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, Chiaik Mountain, Wonju, Korea.

Description of Cedecea davisa 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, Chiaik 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 phenylactic acid. Strain HY_N_1_1 (= NIBRBA0000114036) has been isolated from a gut of insect sample collected from Seoul, Korea.

Description of Gibbsiella quercineans 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 (= NIBRBA0000114070) 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, adipic 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 kimchi, 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, esculin hydrolysis, 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 (= NIBRBA0000114115) 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, 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 cocoides WSS-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 L-arabinose, D-mannose, D-mannitol, 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.

Acknowledgements

This study was supported by the research grant “The Survey of Korean Indigenous Species” from the National Institute of Biological Resources of the Ministry of Environment in Korea.

References


Submitted: May 15, 2015
Revised: July 10, 2015
Accepted: July 27, 2015