A report of 12 unrecorded prokaryotic species isolated from gastrointestinal tracts and feces of various endangered animals in Korea

Pil Soo Kim¹,§, Ki-Eun Lee²,§, Euon Jung Tak¹, Myung-Suk Kang³ and Jin-Woo Bae¹,*

¹Department of Biology and Department of Life and Nanopharmaceutical Sciences, Kyung Hee University, Seoul 02447, Republic of Korea
²Microorganism Resources Division, National Institute of Biological Resources, Incheon 22689, Republic of Korea
³Biological Resources Utilization Department, National Institute of Biological Resources, Incheon 22689, Republic of Korea

*Correspondent: baejw@khu.ac.kr
§These authors contributed equally to this work.

In 2016 and 2017, as part of a comprehensive investigation to identify the prokaryotic species in Korea, a total of 12 bacterial strains were isolated from the gastrointestinal tract and/or fecal samples of four endangered species, including reptile, bird, and marine and terrestrial mammals. Phylogenetic analysis with the 16S rRNA gene sequence was used to assign these strains to the phyla, Firmicutes, Actinobacteria or Proteobacteria. Furthermore, most of the strains Firmicutes belonged to the order Lactobacillales. Interestingly, 12 of the isolated strains have not been previously reported from the Korean Peninsula. Also, based on their high 16S rRNA gene sequence similarities ( > 98.7%) and formation of strong monophyletic clades with the closest type species, each isolated strain of isolates was assigned to an independent, predefined bacterial species. Gram-stain reaction, colony and cell morphology, biochemical characteristics, isolation source, and NIBR IDs are described in the species description section.

Keywords: 16S rRNA sequence, endangered animals, gut microbiota, Korean Peninsula, unrecorded species

INTRODUCTION

At present, it is estimated that there are more than 1.5 million animal species on Earth. However, since the beginning of the Industrial Revolution, the natural habitats of wild animals have come under threat from environmental disruption and climate change (Baillie et al., 2004), and currently approximately 20,000 species of animal are threatened with extinction. In South Korea, the Ministry of Environment has designated 246 animal species as endangered, and considerable effort and resources are being spent on conservation programs.

Symbiotic microbiota helps animals adapt to different habitats and niches by providing metabolic benefits and promoting homeostasis (Bäckhed et al., 2005; Turnbaugh et al., 2006). For example, the gut microbiota aids digestive functioning by promoting intestinal epithelial proliferation, nutrient absorption and energy conversion, and also affords protection against entero-pathogenic bacteria (Bäckhed et al., 2004; Stecher et al., 2007; Hoffmann et al., 2009; Round and Mazmanian, 2009).

In 2016–2017, we investigated the gut microbiota of various endangered animals living on the Korean Peninsula. Hundreds of bacterial species were isolated and among these species, several unreported bacterial species in South Korea were identified. We characterized the isolates with various phenotypic and genotypic identification, and phylogenetic analysis. From the gut microbiota of the endangered animal species that were included in our study, we report 12 bacterial species that have not been recorded from the Korean Peninsula.

MATERIALS AND METHODS

Strain isolation and characterization

Twelve unreported bacterial strains were isolated from the gastrointestinal tract (GIT) and/or feces of various endangered species (green sea turtle, finless porpoise, Siberian musk deer, and Andean condor) found on the Korean
Peninsula, which were collected by National Institute of Biological Resources and Seoul Grand Zoo. These isolates were assigned to the phyla Firmicutes, Bacteroidetes, or Proteobacteria, and of the Firmicutes, most belong to the order Lactobacillales (Table 1). Samples were collected under aseptic conditions. Homogenized GIT tissue and fecal samples were serially diluted with sterile phosphate buffered saline (PBS) and spread onto different culture media (Reasoner’s 2A Agar [R2A], Marine Agar 2216 [MA], Tryptic Soy Agar [TSA], and Brain heart infusion [BHI] agar), supplemented with 5% sheep blood, and incubated for at 25–30°C for 1 week. Isolated, single bacterial colonies were prepared using the streak-plating method. The colony morphology and cell size were recorded after incubation on the appropriate growth media (R2A, TSA or MA) at 25–30°C for 2 days. Transmission electron micrographs (obtained using the LIBRA 120, transmission electron microscope, Carl Zeiss) of the isolated strains are shown in Figure 1. Biochemical analysis and gram-staining were performed using API kits (API 20NE, API ZYM and API ID 32GN; bioMerieux), GEN III microplates (Biolog) and a Gram-stain kit according to manufacturer’s instructions. The results are shown in Table 1 and in the strain description (below).

Analysis of 16S ribosomal RNA gene sequence

For selected pure isolate colonies, genomic DNA was extracted using the AccuPrep Genomic DNA Extraction kit (Bioneer, Korea) or UltraClean Microbial DNA Isolation Kit (MoBio, USA). Amplification of the 16S ribosomal RNA (16S rRNA) gene sequences was performed using the PCR Premix (iNtron Biotechnology, Korea) and bacterial, universal forward and reverse primers (forward primer 27F, 5′-AGAGTTTGTATCCTGGCTCAG-3′; reverse primer 1088R 5′-GCTCGTTGCGGGACTTAACC-3′ or 1492R 5′-GYTACTCTTACGACTT-3′) (Lane, 1991). The 16S rRNA gene amplicons were sequenced by a certified service provider (MACrogen, Korea) using an automated DNA analyzer (Applied Biosystems 3730xl DNA Analyzer). DNA sequences were assembled using SeqMan (DNASTAR) and near full-length 16S rRNA gene sequences were aligned with the 16S rRNA gene sequences of bacterial reference strains using the EzBioCloud database (Yoon et al., 2017).

Phylogenetic analysis

The 16S rRNA gene sequences of the bacterial isolates were aligned with the corresponding sequences of bacterial reference strains using the BioEdit software with the multiple alignment algorithm [CLUSTAL W; (Thompson et al., 1994; Hall, 1999)]. Phylogenetic trees, using the 16S rRNA gene sequences of the isolates and the closely related bacterial species were constructed using the MEGA 7 software (Kumar et al., 2016). Neighbor-joining (NJ), maximum parsimony (MP), and maximum likelihood (ML) methods with 1000 bootstrap replicates were used to ascertain phylogenetic correlations (Kluge and Farris, 1969; Felsenstein, 1981; 1985; Saitou and Nei, 1987).

RESULTS AND DISCUSSION

Based on the phylogenetic analysis of the 16S rRNA gene sequences, the 12 isolated strains (AE4-1, B3, M3, M3R204, M3R205, M1T305, M1T307, VT2414, VT2418, VT2504, VM2501, and VM3408) were assigned to the phyla Firmicutes, Bacteroidetes or Proteobacteria. The isolated strains were confirmed as chemoheterotrophic and rod or coccolid-shaped bacteria (Fig. 1). The morphological, physiological, and biochemical characteristics of isolated strains are described in detail below.

Based on the 16S rRNA gene sequences, the 12 strains isolated in our study (strains AE4-1, B3, M3, M3R204, M3R205, M1T305, M1T307, VT2414, VT2418, VT2504, VM2501, and VM3408) were most closely related to Enterococcus thailandicus DSM 21767T (JXLE01000039; 100% sequence identity); Vogococcus fessus M2661/98/1T (AJ243326; 100% sequence identity); Lactobacillus sakei subsp. carnosus DSM 15831T (AZFG01000015; 100% sequence identity); Microbacterium oxydans DSM 20578T (Y17227; 99.85% sequence similarity); Ochrobactrum pituiosum CCUG 50899T (AM490609; 99.62% sequence similarity); Lysinibacillus mangiferihumi M-GX18T (JF731238; 99.19%), Streptococcus galolyticus subsp. macedonicus ACA-DC 206T (Z94012; 99.70% sequence similarity); Rhodococcus phenolicus DSM 44812T (LRRH01000094; 98.85% sequence similarity); Brevibacterium siliguriense DSM 23676T (LT629766; 99.35% sequence similarity); Glutamicibacter mysores LMG 16219T (AJ639831; 99.35% sequence similarity); Arthrobacter rhombi F98.3HR.69T (Y15885; 99.35%); and Escherichia marmotae HT073016T (JNBP01000188; 99.26% sequence similarity), respectively. A phylogenetic analysis of the isolated bacterial strains was performed based on 16S rRNA gene sequences. In the consensus phylogenetic tree, isolated strains formed robust phylogenetic clades with the most closely related species in the phyla Firmicutes, Bacteroidetes, and Proteobacteria and order Lactobacillales, as expected from high 16S rRNA gene sequence similarities (Fig. 2).

Description of Enterococcus thailandicus AE4-1

Cells are Gram-staining positive, non-flagellated, and coccolid. Colonies are circular, raised, entire, and white colored after 2 days of incubation on MRS agar at 30°C. Positive for adipate, malate in API 20NE, but negative
Table 1. Summary of the isolated strains from the gastrointestinal tract of the endangered species in Korea and their taxonomic affiliations.

<table>
<thead>
<tr>
<th>Phylum</th>
<th>Class</th>
<th>Order</th>
<th>Family</th>
<th>Genus</th>
<th>Strain ID</th>
<th>NIBR ID</th>
<th>Accession number</th>
<th>Most closely related species</th>
<th>Similarity (%)</th>
<th>Isolation source</th>
</tr>
</thead>
<tbody>
<tr>
<td>Firmicutes</td>
<td>Bacilli</td>
<td>Lactobacillales</td>
<td>Enterococcae</td>
<td>Enterococcus</td>
<td>AE4-1</td>
<td>NIBRBAC000503069</td>
<td>MN524154</td>
<td>Enterococcus thailandicus</td>
<td>100</td>
<td>Green sea turtle (Chelonia mydas)</td>
</tr>
<tr>
<td>Firmicutes</td>
<td>Bacilli</td>
<td>Lactobacillales</td>
<td>Enterococcae</td>
<td>Vagococcus</td>
<td>B3</td>
<td>NIBRBAC000503068</td>
<td>MN524155</td>
<td>Vagococcus fessus</td>
<td>100</td>
<td>Finless porpoise (Neophocaena phocoenoides)</td>
</tr>
<tr>
<td>Firmicutes</td>
<td>Bacilli</td>
<td>Lactobacillales</td>
<td>Lactobacillae</td>
<td>Lactobacillus</td>
<td>M3</td>
<td>NIBRBAC000503070</td>
<td>MN524156</td>
<td>Lactobacillus sakei subsp. camosae</td>
<td>100</td>
<td>Finless porpoise (Neophocaena phocoenoides)</td>
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<tr>
<td>Actinobacteria</td>
<td>Actinobacteria</td>
<td>Micrococcales</td>
<td>Microbacteriae</td>
<td>Microbacterium</td>
<td>M3R204</td>
<td>NIBRBAC000499672</td>
<td>KX881415</td>
<td>Ochrobactrum nitratophilum</td>
<td>99.65</td>
<td>Siberian musk deer (Moschus moschiferus)</td>
</tr>
<tr>
<td>Proteobacteria</td>
<td>Alphaproteobacteria</td>
<td>Rhizobiales</td>
<td>Brucellae</td>
<td>Ochrobacter</td>
<td>M3R205</td>
<td>NIBRBAC000499689</td>
<td>KX881416</td>
<td>Ochrobactrum nitratophilum</td>
<td>99.62</td>
<td>Siberian musk deer (Moschus moschiferus)</td>
</tr>
<tr>
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<td>Bacillales</td>
<td>Planococcae</td>
<td>Lysinibacillus</td>
<td>M1T305</td>
<td>NIBRBAC000499685</td>
<td>KX881417</td>
<td>Lysinibacillus mungoferi</td>
<td>99.2</td>
<td>Siberian musk deer (Moschus moschiferus)</td>
</tr>
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<td>Streptococcus</td>
<td>M1T307</td>
<td>NIBRBAC000499688</td>
<td>KX881418</td>
<td>Streptococcus gallolyticus subsp. macedonicus</td>
<td>99.70</td>
<td>Siberian musk deer (Moschus moschiferus)</td>
</tr>
<tr>
<td>Actinobacteria</td>
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<td>Myxobacteriales</td>
<td>Nocardiae</td>
<td>Rhodococcus</td>
<td>VT2414</td>
<td>NIBRBAC000499827</td>
<td>MF-80439</td>
<td>Rhodococcus phoenicicola</td>
<td>98.85</td>
<td>Andean condor (Vultur gryphus)</td>
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<tr>
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<td>Actinobacteria</td>
<td>Micrococcales</td>
<td>Brevibacteriaceae</td>
<td>Brevibacterium</td>
<td>VT2418</td>
<td>NIBRBAC000499828</td>
<td>MF-80440</td>
<td>Brevibacterium siligense</td>
<td>99.35</td>
<td>Andean condor (Vultur gryphus)</td>
</tr>
<tr>
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<td>Actinobacteria</td>
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<td>Micrococcaceae</td>
<td>Gluconobacter</td>
<td>VT2504</td>
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<td>MF-80441</td>
<td>Gluconobacter mucroakens</td>
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<tr>
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<td>Actinobacteria</td>
<td>Micrococcales</td>
<td>Micrococcaceae</td>
<td>Arthrobacter</td>
<td>VM2501</td>
<td>NIBRBAC000499830</td>
<td>MF-80442</td>
<td>Arthrobacter rhombi</td>
<td>99.35</td>
<td>Andean condor (Vultur gryphus)</td>
</tr>
<tr>
<td>Proteobacteria</td>
<td>Gammaproteobacteria</td>
<td>Enterobacteriales</td>
<td>Enterobacteriaceae</td>
<td>Escherichia</td>
<td>VM3408</td>
<td>NIBRBAC000499831</td>
<td>MF-80443</td>
<td>Escherichia marmotae</td>
<td>99.26</td>
<td>Andean condor (Vultur gryphus)</td>
</tr>
</tbody>
</table>
for nitrate reduction, reduction of nitrates to nitrogen, indole production, glucose acidification, arginine dihydrolase, urease, β-glucosidase, protease, β-galactosidase, d-glucose, l-arabinose, d-mannose, d-mannitol, N-acetyl-glucosamine, d-maltose, gluconate, caprate, citrate, and phenyl-acetate. d-sorbitol, l-histidine, 4-hydroxy-benzoate, d-sucrose, and acetate are utilized. Does not utilize d-mannitol, d-glucose, salicin, l-fucose, l-arabinose, propionate, caprate, valerate, l-histidine, 4-hydroxy-benzoate, d-ribose, d-sucrose, malonate, acetate, d, l-lactate, l-alanine, 5-ketogluconate, glycogen, 3-hydroxy-benzoate, and l-serine.

Strain AE4-1 (= NIBRBAC000503069) was isolated from the feces of a green sea turtle (Chelonia mydas), Chungcheongnam Province, Korea.

Description of \textit{Vagococcus fessus} B3

Cells are Gram-staining positive, non-flagellated, and coccus. Colonies are circular, raised, entire, and white colored after 2 days of incubation on MRS agar at 30°C. Positive for nitrate reduction, β-glucosidase, l-arabinose, d-mannose, N-acetyl-glucosamine, d-maltose, gluconate, malate, and citrate in API 20NE, but negative for indole production, glucose acidification, arginine dihydrolase, urease, protease, β-galactosidase, d-mannitol, caprate, adipate, phenyl-acetate. d-glucose, salicin, d-melibiose, l-arabinose, citrate, 2-ketoglucconate, 3-hydroxy-butyrate, l-proline, l-rhamnose, N-acetyl-glucosamine, inositol, d-maltose, itaconate, and suberate are utilized. Does not utilize d-mannitol, l-fucose, d-sorbitol, propionate, caprate, valerate, l-histidine, 4-hydroxy-benzoate, d-ribose, d-sucrose, malonate, acetate, d, l-lactate, l-alanine, 5-ketogluconate, glycogen, 3-hydroxy-benzoate, and l-serine.

Strain B3 (= NIBRBAC000503068) was isolated from the intestinal tract of a finless porpoise (\textit{Neophocaena phocaenoides}), Chungcheongnam Province, Korea.

Description of \textit{Lactobacillus sakei} subsp. \textit{carnosus} M3

Cells are Gram-staining positive, non-flagellated, and rod. Colonies are circular, raised, entire, and white colored after 2 days of incubation on MRS agar at 30°C. Positive for β-glucosidase, l-arabinose in API 20NE, but negative for nitrate reduction, reduction of nitrates to nitrogen, indole production, glucose acidification, arginine dihydrolase, urease, protease, β-galactosidase, d-glucose, d-mannose, d-mannitol, N-acetyl-glucosamine, d-maltose, gluconate, caprate, adipate, malate, citrate, phenyl-acetate, d-melibiose and l-arabinose are utilized. Does not utilize d-mannitol, d-glucose, salicin, l-fucose, d-sorbitol, propionate, caprate, valerate, l-histidine, 2-ketogluconate, 3-hydroxy-butyrate, 4-hydroxy-benzoate, l-proline, l-rhamnose, N-acetyl-glucosamine, d-ribose, inositol, d-sucrose, d-maltose, itaconate, suberate, malonate, acetate, d, l-lactate, l-alanine, 5-ketogluconate, glycogen, 3-hydroxy-benzoate, and l-serine.

Strain M3 (= NIBRBAC000503070) was isolated from the intestinal tract of a finless porpoise (\textit{Neophocaena phocaenoides}), Chungcheongnam Province, Korea.
Fig. 2. Phylogenetic tree based on 16S rRNA gene sequence comparisons, showing the relationship between the isolated strains in this study and the notable species from phylum Firmicutes (a) order Lactobacillales (In particular Enterococcus, Lactobacillus and Vagococcus), phylum Actinobacteria (c) and phylum Proteobacteria (d) and. The trees were mainly reconstructed using the neighbor-joining algorithm (NJ), Maximum parsimony (MP) and maximum likelihood (ML) algorithms were applied for additional comparison. Filled diamonds indicate branches present in the phylogenetic trees generated using the three different methods. Numbers on the nodes (> 70%) represent bootstrap values as percentages of 1000 replicates (NJ/MP/ML). Clostridium butyricum DSM 10702T (AAQQ01000149), Bifidobacterium bifidum DSM 2266T (HE171023) and Spirochaeta aurantia subsp. aurantia DSM 1902T (FR749896) were used as outgroups, respectively. Bar, 0.02 (a, c, d) and 0.01 (b) accumulated changes per nucleotide.
**Description of Microbacterium oxydans M3R204**

Cells are Gram-staining positive. Colonies are circular, raised, entire, and white colored after 2 days of incubation on R2A agar at 20°C. Dextrin, D-maltose, D-trehalose, D-cellobiose, gentiobiose, sucrose, D-turanose, D-salicin, D-mannose, D-fructose, N-acetyl-D-glucosamine, N-acetyl-D-galactosamine, α-D-glucose, D-galactose, L-rhamnose, inosine, 1% sodium lactate, myo-inositol, glycerol, rifamycin SV, L-alanine, L-histidine, guanidine chloride, pectin, tetrazolium blue, methyl pyruvate, nalidixic acid, lithium chloride, L-keto-butyric acid, acetocetic acid, acetic acid, sodium butyrate, D-mannitol, glycy1-L-proline, L-aspartic acid, L-glutamic acid, L-serine, D-gluconic acid, 4-hydroxyphenylacetetic acid, L-lactic acid, D-malic acid, L-malic acid, bromosuccinic acid, Tween 40, α-hydroxybutyric acid, propionic acid, aztreonam, and sodium bromate are utilized as the sole source of carbon. α-D-lactose, β-methyl-D-glucoside, N-acetyl-β-D-mannosamine, 3-methyl glucose, D-fucose, L-fucose, fusidic acid, D-serine, D-glucose-6-phosphate, D-fructose-6-phosphate, troleandomycin, minocycline, lincomycin, D-galacturonic acid, L-galactonic acid lactone, D-glucuronic acid, glucuronamidase, vancomycin, tetrazolium violet, potassium tellurite, stachyose, D-raffinose, D-melibiose, N-acetyl neuraminic acid, D-sorbitol, D-arabitol, D-aspartic acid, D-serine, gelatin, L-arginine, L-pyroglutamic acid, niaproof 4, mucic acid, quinic acid, D-saccharic acid, D-lactic acid methyl ester, citric acid, α-keto-glutaric acid, γ-aminobutyric acid, β-hydroxy-D, L-butyric acid, and formic acid are not utilized as the sole source of carbon (Biolog GEN III).

Strain M3R204 (=NIBRBAC000499672) was isolated from the feces of a Siberian musk deer (*Moschus phocaenoides*), Chungcheongnam Province, Korea.
Description of *Ochrobactrum pituitosum* M3R205

Cells are Gram-staining positive. Colonies are circular, smooth, convex, and yellowish-white colored after 2 days of incubation on R2A agar at 20°C. Dextrin, N-acetyl-d-glucosamine, N-acetyl-d-galactosamine, α-d-glucose, d-mannose, d-fructose, d-galactose, l-rhamnose, inosine, 1% sodium lactate, myo-inositol, rifamycin SV, l-alanine, l-histidine, guanidinium chloride, tetrazolium blue, methyl pyruvate, lithium chloride, acetoacetic acid, acetic acid, glycyl-l-proline, l-aspartic acid, l-glutamic acid, l-serine, l-lactic acid, d-malic acid, d-malic acid, bromosuccinic acid, propionic acid, aztreonam, d-fucose, d-mannose, d-fructose, a-glucose, d-mannose, d-fructose, d-galactose, l-rhamnose, inosine, 1% sodium lactate, myo-inositol, rifamycin SV, l-alanine, l-histidine, guanidinium chloride, tetrazolium blue, methyl pyruvate, lithium chloride, acetoacetic acid, acetic acid, glycyl-l-proline, l-aspartic acid, l-glutamic acid, l-serine, l-lactic acid, d-malic acid, d-malic acid, bromosuccinic acid, propionic acid, aztreonam, d-fucose,
l-fucose, troleandomycin, lincomycin, d-galacturonic acid, l-galactonic acid lactone, d-glucuronic acid, vancomycin, tetrazolium violet, potassium tellurite, d-sorbitol, d-arabitol, niaprotein 4, citric acid, and γ-aminobutyric acid are utilized as the sole source of carbon. However, d-maltose, d-trehalose, d-cellobiose, gentiobiose, sucrose, d-turanose, d-salicin, glycerol, pectin, nalidixic acid, α-keto-butyric acid, sodium butyrate, d-mannitol, d-glucuronic acid, 4-hydroxyphenylacetic acid, Tween 40, α-hydroxybutyric acid, sodium bromate, α-d-lactose, β-methyl-d-glucoside, N-acetyl-β-d-mannosamine, 3-methyl glucose, fusidic acid, d-serine, d-glucose-6-phosphate, d-fructose-6-phosphate, minocycline, glucuronamide, stachyose, d-raffinose, d-melibiose, N-acetyl neuraminic acid, d-aspartic acid, d-serine, d-glucuronic acid, d-saccharic acid, d-lactic acid methyl ester, α-keto-glutaric acid, β-hydroxy-d-l-butyril acid, and formic acid are not utilized as the sole source of carbon (Biolog GEN III).

Strain M3R205 (= NIBRBAC000499689) was isolated from the feces of a Siberian musk deer (*Moschus moschiferus*), Hwacheon, Gangwon Province, Korea. The DNA G+C content of the type strain is 55.0 mol%.

**Description of Lysinibacillus mangiferihumi M1T305**

Cells are Gram-staining positive. Colonies are circular, smooth, convex, and yellowish-white colored after 2 days of incubation on R2A agar at 37°C. Dextrin, N-acetyl-d-glucosamine, N-acetyl-d-galactosamine, d-fructose, d-galactose, l-rhamnose, inosine, 1% sodium lactate, *myo*-inositol, l-alanine, l-histidine, methyl pyruvate, lithium chloride, acetobutyric acid, propionic acid, aztreonam, d-serine, d-fructose, d-galacturonic acid, l-galactonic acid lactone, d-glucuronic acid, potassium tellurite, d-arabitol, citric acid, γ-aminobutyric acid, d-trehalose, d-cellobiose, gentiobiose, sucrose, d-turanose, d-salicin, glycerol, α-keto-butyric acid, sodium butyrate, d-mannitol, d-glucuronic acid, Tween 40, α-hydroxybutyric acid, d-glucoside, N-acetyl-β-d-mannosamine, 3-methyl glucose, fusidic acid, d-serine, d-glucuronic acid, d-saccharic acid, d-lactic acid methyl ester, α-keto-glutaric acid, β-hydroxy-d-l-butyril acid, and formic acid are utilized as the sole source of carbon (Biolog GEN III).

Strain M3R205 (= NIBRBAC000499689) was isolated from the feces of a Siberian musk deer (*Moschus moschiferus*), Hwacheon, Gangwon Province, Korea. The DNA G+C content of the type strain is 55.0 mol%.
er, α-d-glucose, d-mannose, rifamycin SV, guanidinium chloride, tetravalent blue, troleandomycin, lincomycin, vancomycin, tetravalent violet, d-sorbitol, niaprof 4, d-maltose, pectin, naldixic acid, 4-hydroxphenylacetic acid, sodium bromate, α-d-lactose, fusidic acid, minocycline, and d-raffinose are not utilized as the sole source of carbon (Biolog GEN III).

Strain M1T305 (= NIBRBAC000499685) was isolated from the feces of a Siberian musk deer (Moschus moschiferus), Hwacheon, Gangwon Province, Korea. The DNA G+C content of the type strain is 35.9 mol%.

Description of Streptococcus galloxy-richus subsp. macedonicus M1T307

Cells are Gram-staining positive. Colonies are circular, smooth, convex, and yellowish-white colored after 2 days of incubation on Tryptic soy agar (TSA) at 37°C. Dextrin, N-acetyl-d-glucosamine, d-fructose, d-galactose, l-rhamnose, 1% sodium lactate, acetoclastic acid, aztreonam, d-fucose, potassium tellurite, d-trehalose, d-cellobiose, gentiobiose, sucrose, d-turanose, d-salicin, sodium butyrate, d-mannitol, β-methyl-d-glucoside, N-acetyl-β-d-mannosamine, d-serine, glucuronamide, stachyose, d-melibiose, α-d-glucose, d-mannose, tetravalent blue, vancomycin, tetravalent violet, d-maltose, pectin, naldixic acid, α-d-lactose, fusidic acid, and d-raffinose are utilized as the sole source of carbon. N-acetyl-d-galactosamine, inosine, myo-inositol, l-alanine, l-histidine, methyl pyruvate, lithium chloride, acetic acid, glycy1-l-proline, l-aspartic acid, l-glutamic acid, l-serine, l-lactic acid, d-malic acid, l-malic acid, bromosuccinic acid, propionic acid, l-fucose, d-galacturonic acid, l-galactonic acid lactone, d-glucuronic acid, d-arabitol, citric acid, γ-amino-butyric acid, glycerol, α-keto-butyric acid, d-gluconic acid, Tween 40, α-hydroxybutyric acid, 3-methyl glucose, d-glucose-6-phosphate, d-fructose-6-phosphate, N-acetyl neuraminic acid, d-aspartic acid, d-serine, gelatin, l-arginine, l-pyroglutamic acid, mucic acid, quinic acid, sodium lactate, and sodium butyrate are utilized as the sole source of carbon (Biolog GEN III).

Strain M1T307 (= NIBRBAC000499688) was isolated from the feces of an Andean condor (Vultur gryphus), Gwacheon, Gyeonggi Province, Korea. The DNA G+C content of the type strain is 65.77 mol%.

Description of Brevibacterium siligunense VT2418

Cells are Gram-staining positive, non-flagellated, and rod-shaped. Colonies are circular, smooth, convex, and ivory colored after 2 days of incubation on TSA at 20°C. N-glucosamin, N-galactosamin, α-d-glucose, d-fructose, d-galactose, d-fucose, l-fucose, l-fucose, l-fucose, l-fucose, l-fucose, l-glucosamine, l-mannitol, d-arabitol, glycerol, d-glyceraldehyde, d-fructose, d-asparatic acid, glycerol-1-l-proline, l-alanine, l-serine, l-glutamic acid, l-histidine, pyrogallol, α-glutamic acid, d-glutamic acid, d-glutamic acid, d-glutamic acid, d-glutamic acid, d-glutamic acid, d-glutamic acid, d-glutamic acid, d-glutamic acid, d-glutamic acid, d-glutamic acid, d-glutamic acid, d-glutamic acid, d-glutamic acid, d-glutamic acid, d-glutamic acid, d-glutamic acid, d-glutamic acid, d-glutamic acid, d-glutamic acid, d-glutamic acid, d-glutamic acid, d-glutamic acid, d-glutamic acid, d-glutamic acid, d-glutaminase, cystine arylamidase, trypsin and naphthol-AS-BI-phosphohydrolase (API ZYM and API 20NE). Positive for the utilization of following substrates: valerate, 3-hydroxy-butyrate, suberate, acetate, d-lactate, and 3-hydroxy-benzozate (API ID 32 GN).

Strain VT2412 (= NIBRBAC000499827) was isolated from the feces of an Andean condor (Vultur gryphus), Gwacheon, Gyeonggi Province, Korea. The DNA G+C content of the type strain is 65.77 mol%.

Description of Glutamicibacter myoresens VT2504

Cells are Gram-staining positive, non-flagellated, and rod-shaped. Colonies are circular, smooth, convex, and ivory colored after 2 days of incubation on TSA at 20°C.
Dextrin, d-maltose, d-trehalose, d-cellobiose, gentiobiose, sucrose, d-turanose, \( \beta \)-d-glucoside, d-salicin, \( \alpha \)-d-glucose, d-mannose, d-fructose, d-galactose, inosine, sodium lactate, d-sorbitol, d-arabitol, glycerol, d-aspartic acid, gelatin, glyceryl-\( l \)-proline, l-alanine, l-arginine, l-aspartic acid, l-glutamic acid, l-histidine, pyroglyutamic acid, l-serine, d-gluconic acid, quinic acid, phylalactic acid, l-lactic acid, citric acid, \( \alpha \)-glutaric acid, l-malic acid, succinic acid, nalidixic acid, lithium chloride, potassium tellurite, Tween 40, \( \beta \)-butyric acid, acetoacetic acid, propionic acid, acetic acid, aztreonam, sodium butyrate, and sodium bromate are utilized as the sole source of carbon (Biolog GEN III). Positive for following enzyme activities: nitrate reduction, \( \beta \)-glucosidase, esterase (C4), esterase lipase (C8), lipase (C14), leucine arylamidase, valine arylamidase, cystine arylamidase, trypsin, naphthol-AS-Bl-phosphohydrolase, \( \alpha \)-glucosidase, \( \beta \)-glucosidase, and \( \alpha \)-mannosidase (API ZYM and API 20NE). Positive for the utilization of following substrates: d-mannitol, d-glucose, d-sorbitol, l-arabinose, propionate, valerate, 3-hydroxy-butyrate, 4-hydroxy-benzoate, l-proline, l-rhamnose, d-ribose, d-sucrose, d-maltose, suberate, acetate, \( l \)-lactate, l-alanine, 5-ketogluconate, glycollgen, 3-hydroxy-benzoate, and l-serine (API ID 32 GN).

Strain VT2504 (= NIBRBAC000499829) was isolated from the feces of an Andean condor (Vultur gryphus), Gwacheon, Gyeonggi Province, Korea. The DNA G+C content of the type strain is 60.35 mol%.

**Description of Arthrobacter rhombi VM2501**

Cells are Gram-staining positive, non-flagellated, and rod-shaped. Colonies are circular, smooth, convex, and pale yellow colored after 2 days of incubation on MA at 20°C. d-maltose, d-trehalose, d-cellobiose, gentiobiose, sucrose, d-turanose, neumarinc acid, \( \alpha \)-d-glucose, sodium lactate, d-gluconic acid, nalidixic acid, sodium butyrate, and sodium bromate are utilized as the sole source of carbon (Biolog GEN III). Positive for following enzyme activities: nitrate reduction, glucose acidification, \( \beta \)-galactosidase, alkaline phosphatase, esterase (C4), esterase lipase (C8), leucine arylamidase, valine arylamidase, cystine arylamidase, trypsin, acid phosphatase, naphthol-AS-BI-phosphohydrolase, \( \alpha \)-glucosidase, and \( \beta \)-glucosidase (API ZYM and API 20NE). Positive for the utilization of following substrates: d-mannitol, d-glucose, d-melibiose, l-fucose, d-sorbitol, l-arabinose, propionate, l-proline, l-rhamnose, \( N \)-acetyl-glucosamine, d-ribose, d-maltose, acetate, \( d \), l-lactate, l-alanine, and l-serine (API ID 32 GN).

Strain VM2501 (= NIBRBAC000499830) was isolated from the feces of an Andean condor (Vultur gryphus), Gwacheon, Gyeonggi Province, Korea. The DNA G+C content of the type strain is 67.90 mol%.

**Description of Escherichia marmotae VM3408**

Cells are Gram-staining positive, non-flagellated, and rod-shaped. Colonies are circular, smooth, convex, and ivory colored after 2 days of incubation on MA at 37°C. d-trehalose, d-melibiose, \( \beta \)-d-glucoside, \( N \)-glucosamine, \( \beta \)-mannosamin, \( N \)-galactosamin, neumarinc acid, d-mannose, d-fructose, d-galactose, l-fucose, l-rhamnose, inosine, sodium lactate, fusidic acid, d-sorbitol, glycerol, d-glucose, d-fructose, d-serine, troleandomycin, rifampycin SV, glycoll-\( l \)-proline, l-alanine, l-aspartic acid, \( l \)-glutamic acid, l-serine, lincomycin, guanidinium chloride, niaproph 4, galacturonic acid, l-galactonic lactone, d-gluconic acid, d-glucuronic acid, glucuronamide, mucic acid, d-saccharic acid, vancomycin, tetraultuziol violet, tetraultuziol blue, methyl pyruvate, l-lactic acid, \( \alpha \)-glutaric acid, d-malic acid, l-malic acid, succinic acid, nalidixic acid, \( \alpha \)-butyric acid, \( \beta \)-butyric acid, propionic acid, acetic acid, and sodium butyrate are utilized as the sole source of carbon (Biolog GEN III). Positive for following enzyme activities: nitrate reduction, indole production, glucose acidification, \( \beta \)-galactosidase, alkaline phosphatase, esterase (C4), leucine arylamidase, valine arylamidase, cystine arylamidase, trypsin, acid phosphatase, naphthol-AS-BI-phosphohydrolase, \( \beta \)-galactosidase, and \( \alpha \)-glucosidase (API ZYM and API 20NE). Positive for the utilization of following substrates: d-mannitol, d-glucose, d-melibiose, l-fucose, d-sorbitol, l-arabinose, propionate, l-proline, l-rhamnose, \( N \)-acetyl-glucosamine, d-ribose, d-maltose, acetate, \( d \), l-lactate, \( l \)-alanine, and l-serine (API ID 32 GN).

Strain VM3408 (= NIBRBAC000499831) was isolated from the feces of an Andean condor (Vultur gryphus), Gwacheon, Gyeonggi Province, Korea. The DNA G+C content of the type strain is 48.49 mol%.

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**References**