Ohtaekwangia koreensis gen. nov., sp. nov. and *Ohtaekwangia kribbensis* sp. nov., isolated from marine sand, deep-branching members of the phylum *Bacteroidetes*

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Two Gram-stain-negative, non-motile, non-spore-forming, rod-shaped bacterial strains, designated 3B-2^T and 10AO^T, were isolated from a sand sample collected from the west coast of the Korean peninsula by using low-nutrient media, and their taxonomic positions were investigated in a polyphasic study. The strains did not grow on marine agar. They grew optimally at 30 °C and pH 6.5–7.5. Strains 3B-2^T and 10AO^T shared 97.5 % 16S rRNA gene sequence similarity and mean level of DNA–DNA relatedness of 12 %. In phylogenetic trees based on 16S rRNA gene sequences, strains 3B-2^T and 10AO^T, together with several uncultured bacterial clones, formed independent lineages within the evolutionary radiation encompassed by the phylum *Bacteroidetes*. Strains 3B-2^T and 10AO^T contained MK-7 as the predominant menaquinone and iso-C_{15:0} and C_{16:1ω5c} as the major fatty acids. The DNA G + C contents of strains 3B-2^T and 10AO^T were 42.8 and 44.6 mol%, respectively. Strains 3B-2^T and 10AO^T exhibited very low levels of 16S rRNA gene sequence similarity (<85.0 %) to the type strains of recognized bacterial species. These data were sufficient to support the proposal that the novel strains should be differentiated from previously known genera of the phylum *Bacteroidetes*. On the basis of the data presented, we suggest that strains 3B-2^T and 10AO^T represent two distinct novel species of a new genus, for which the names *Ohtaekwangia koreensis* gen. nov., sp. nov. (the type species; type strain 3B-2^T = KCTC 23018^T = CCUG 58939^T) and *Ohtaekwangia kribbensis* sp. nov. (type strain 10AO^T = KCTC 23019^T = CCUG 58938^T) are proposed.

The majority of prokaryotes present in nature cannot be cultured by using routine laboratory methods (Staley & Konopka, 1985; Amann *et al.*, 1995; Torsvik *et al.*, 2002; Keller & Zengler, 2004). Culture-independent methods have shown that these uncultivated organisms are distributed in a variety of environments (Amann *et al.*, 1995; Rappé & Giovannoni, 2003; Handelsman, 2004). Several useful methods to improve the culturability of micro-organisms from environmental samples have been developed over the last 10 years (Bruns *et al.*, 2002; Kaerberlein *et al.*, 2002; Zengler *et al.*, 2002; Bae *et al.*, 2005; Bollmann *et al.*, 2007). One of these methods is to use low-nutrient media, with which many novel bacterial strains have been isolated (Connon & Giovannoni, 2002; Janssen *et al.*, 2002; Joseph *et al.*, 2003; Stevenson *et al.*, 2004), but the culturability of marine bacteria (<0.1 % of the total) remains lower than that of bacteria present in other environments (Amann *et al.*,

1995). A diverse range of novel marine bacteria, including members of the alphaproteobacterial clade SAR11, have been cultivated by high-throughput techniques combined with dilution to extinction by using low-nutrient media (Connon & Giovannoni, 2002; Morris *et al.*, 2002).

During the screening of uncultivated micro-organisms from the west coast of the Korean peninsula by using low-nutrient media, several novel bacterial strains have been isolated and analysed phylogenetically. Two of these isolates (designated 3B-2^T and 10AO^T), which were not able to grow on marine agar (MA; Difco), the medium routinely used for isolation and cultivation of marine bacteria, were shown to share very low levels of 16S rRNA gene similarity with recognized bacterial taxa. The aim of the present study was to investigate the taxonomic status of the two novel bacterial strains by using a polyphasic approach that included detailed phylogenetic analysis based on 16S rRNA gene sequences and determination of phenotypic and chemotaxonomic properties.

The GenBank/EMBL/DDBJ accession numbers for the 16S rRNA gene sequences of strains 3B-2^T and 10AO^T are GU117702 and GU117703, respectively.

A sand sample collected from the coast at Saemankum, Korea, was used as the source for the isolation of bacterial strains. A solid medium containing 0.1 % (w/v) $\text{CaCl}_2 \cdot 2\text{H}_2\text{O}$ and 1.0 % (w/v) agar was prepared, and cells of cultured *Escherichia coli* were spread on the surface of the medium after washing with sterilized distilled water. A sand sample (1 g) was scattered onto the solid medium on which cells of *E. coli* were spread. In a second isolation strategy, another sample (1 g) was diluted serially by using sterilized distilled water, and the suspension was spread onto 10-fold-diluted MA. The agar plates were incubated at 25 °C, and colonies were restreaked on several different solid media, including R2A agar (Difco), MA, and 5- and 10-fold-diluted MA, to obtain pure cultures. Bacterial isolates were preserved in liquid nitrogen after being suspended in 20 % (w/v) glycerol mixed in distilled water. Strains 10AO^T and 3B-2^T were isolated by using the former and the latter methods, respectively, and selected for further study. For short-term preservation, strains 3B-2^T and 10AO^T were maintained on R2A agar at 4 °C. Growth was investigated on MA, 5-, 10-, 50- and 100-fold-diluted MA, R2A agar, nutrient agar (Difco) and trypticase soy agar (Difco). The morphological, physiological and biochemical characteristics of strains 10AO^T and 3B-2^T were investigated by routine cultivation on R2A agar at 30 °C. Cell morphology was examined by light microscopy (E600; Nikon) and transmission electron microscopy (CM-20; Philips). The presence of flagella was assessed by using transmission electron microscopy on cells from an exponentially growing culture. For this, cells were negatively stained with 1 % (w/v) phosphotungstic acid and the grids were examined after being air-dried. The Gram reaction was determined by using the bioMérieux Gram stain kit according to the manufacturer's instructions. Optimal temperature for growth and growth at 4, 10, 20, 25, 28, 30, 35, 37, 39 and 40 °C were assessed on R2A agar. Growth in the presence of 0, 0.5, 1.0, 2.0 and 3.0 % (w/v) NaCl was investigated in R2A broth prepared according to the formula of the Difco medium except that agar was excluded. The optimal pH and pH range for growth were determined in R2A broth adjusted to pH 4.5–10.5 (in increments of 0.5 pH units) by the addition of HCl or Na_2CO_3 . Growth under anaerobic conditions was determined after incubation in an anaerobic chamber on R2A agar and on R2A agar supplemented with potassium nitrate (0.1 %, w/v), both of which had been prepared anaerobically under a nitrogen atmosphere. Catalase and oxidase activities and hydrolysis of aesculin, casein, gelatin, hypoxanthine, xanthine, starch, Tween 80, L-tyrosine and urea were investigated as described by Cowan & Steel (1965) and Lányi (1987). The presence of flexirubin-type pigments was investigated as described by Reichenbach (1992). Assimilation of various substrates was determined by using the GN2 MicroPlate assay (Biolog) as recommended by the manufacturer. Susceptibility to antibiotics was investigated on R2A agar plates by using discs (Advantec) containing the following antibiotics: polymyxin B (100 U), streptomycin (50 µg), penicillin G (20 U),

chloramphenicol (100 µg), ampicillin (10 µg), cephalothin (30 µg), gentamicin (30 µg), novobiocin (5 µg), tetracycline (30 µg), kanamycin (30 µg), lincomycin (15 µg), oleandomycin (15 µg), neomycin (30 µg) and carbenicillin (100 µg). Other physiological and biochemical tests were performed with the API 20E and API ZYM systems (bioMérieux).

Cell biomass of strains 3B-2^T and 10AO^T for DNA extraction and for isoprenoid quinone and polar lipid analyses was obtained from cultures grown for 5 days in R2A broth at 30 °C. Chromosomal DNA was isolated and purified according to the method described previously (Yoon *et al.*, 1996), except that RNase T1 was used together with RNase A. The 16S rRNA gene was amplified by PCR by using universal forward (5'-GAGTTTGATCCTGGC-TCAG-3') and reverse (5'-AGAAAGGAGGTGATCCAG-CC-3') primers, as described previously (Yoon *et al.*, 1998). Sequencing of the amplified 16S rRNA gene and phylogenetic analysis were performed as described by Yoon *et al.* (2003). The DNA G+C content was determined by the method of Tamaoka & Komagata (1984) with the modification that DNA was hydrolysed by using nuclease P1 (Sigma) and the resultant nucleotides were analysed by reversed-phase HPLC. DNA–DNA hybridization was performed fluorometrically by the method of Ezaki *et al.* (1989) by using photobiotin-labelled DNA probes and microdilution wells. Hybridization was performed at 45 °C with five replications for each sample. The highest and lowest values obtained in each sample were excluded, and the means of the remaining three values are quoted as DNA–DNA relatedness values. Isoprenoid quinones were extracted according to the method of Komagata & Suzuki (1987) and were analysed by reversed-phase HPLC with a YMC ODS-A (250 × 4.6 mm) column. For fatty acid methyl ester analysis, cell mass of strains 3B-2^T and 10AO^T was harvested from R2A agar plates after incubation for 5 days at 30 °C. The fatty acids were extracted, and fatty acid methyl esters were prepared according to the standard protocol of the MIDI/Hewlett Packard Microbial Identification System (Sasser, 1990). Polar lipids were extracted according to the procedures described by Minnikin *et al.* (1984) and were identified by two-dimensional TLC followed by spraying with appropriate detection reagents (Minnikin *et al.*, 1984; Komagata & Suzuki, 1987).

Strains 3B-2^T and 10AO^T were aerobic, Gram-stain-negative, non-spore-forming, non-motile and rod-shaped. Best growth was achieved on R2A agar and 10-fold-diluted MA and weak growth occurred on nutrient agar. The two strains also grew on 5-, 10-, 50- and 100-fold-diluted MA, but not on MA or trypticase soy agar. Tween 80 was hydrolysed weakly only by strain 3B-2^T and L-tyrosine was hydrolysed only by strain 10AO^T. In the API ZYM system, the two strains showed activities for most enzymes; valine arylamidase activity was found only for strain 10AO^T. Morphological, cultural, physiological and biochemical characteristics of strains 3B-2^T and 10AO^T are given in the genus and species descriptions and in Table 1.

Table 1. Differential characteristics between strains 3B-2^T and 10AO^T

The two strains are positive for assimilation of dextrin, D-glucose, methyl pyruvate, α -ketoglutaric acid and L-proline and negative for assimilation of Tweens 40 and 80, N-acetyl-D-galactosamine, N-acetyl-D-glucosamine, adonitol, L-arabinose, D-arabitol, i-erythritol, D-fructose, L-fucose, *myo*-inositol, maltose, D-mannitol, D-psicose, D-sorbitol, xylitol, monomethyl succinate, acetic acid, *cis*-aconitic acid, citric acid, formic acid, D-galactonic acid lactone, D-galacturonic acid, D-glucosaminic acid, D-glucuronic acid, α -hydroxybutyric acid, β -hydroxybutyric acid, *p*-hydroxyphenylacetic acid, itaconic acid, α -ketobutyric acid, α -ketovaleric acid, DL-lactic acid, malonic acid, propionic acid, quinic acid, D-saccharic acid, sebacic acid, bromo-succinic acid, glucuronamide, alaninamide, D- and L-alanine, L-alanyl glycine, L-asparagine, L-aspartic acid, glycyl L-aspartic acid, glycyl L-glutamic acid, L-histidine, hydroxy-L-proline, L-leucine, L-ornithine, L-phenylalanine, L-pyroglyutamic acid, D- and L-serine, L-threonine, DL-carnitine, γ -aminobutyric acid, urocanic acid, inosine, uridine, thymidine, phenylethylamine, putrescine, 2-aminoethanol, 2, 3-butanediol, DL- α -glycerol phosphate, glucose 1-phosphate and glucose 6-phosphate. +, Positive; –, negative; w, weakly positive.

Characteristic	3B-2 ^T	10AO ^T
Hydrolysis of:		
Gelatin	–	+
L-Tyrosine	–	+
Assimilation of (Biolog GN2):		
α -Cyclodextrin	–	+
Glycogen	–	+
Cellobiose	–	+
D-Galactose	–	w
Gentiobiose	–	+
Lactose	–	+
Lactulose	–	+
D-Mannose	–	+
Melibiose	–	+
Methyl β -D-glucoside	–	+
Raffinose	–	+
L-Rhamnose	–	+
Sucrose	–	+
Trehalose	–	+
Turanose	–	+
D-Gluconic acid	–	w
γ -Hydroxybutyric acid	–	+
Succinic acid	+	–
Succinamic acid	–	+
L-Glutamic acid	–	w
Glycerol	–	+
Valine arylamidase (API ZYM)	–	+
Susceptibility to:		
Gentamicin (30 μ g)	+	–
Lincomycin (15 μ g)	+	–
Neomycin (30 μ g)	+	–
DNA G + C content (mol%)	42.8	44.6

The almost-complete 16S rRNA gene sequences of strains 3B-2^T and 10AO^T determined in this study each comprised 1444 nt, representing approximately 96 % of the *E. coli* 16S

rRNA gene sequence. The level of 16S rRNA gene sequence similarity between the two strains was 97.5 %. Comparative 16S rRNA gene sequence analyses showed that strains 3B-2^T and 10AO^T were most closely affiliated to members of the phylum *Bacteroidetes* (Fig. 1). In the phylogenetic tree based on the neighbour-joining algorithm, strains 3B-2^T and 10AO^T and several uncultured bacterial clones formed a distinct cluster within the evolutionary radiation encompassed by the phylum *Bacteroidetes* and their closest relatives were members of the genera *Flexibacter*, *Cytophaga* and *Sporocytophaga*, classified in the family *Cytophagaceae* (Ludwig *et al.*, 2008) (Fig. 1). The cluster comprising the two novel strains and uncultured bacterial clones joined the phylogenetic lineage of *Flexibacter flexilis* ATCC 23079^T at a bootstrap resampling value of 65.7 %, but strains 3B-2^T and 10AO^T exhibited very low levels of 16S rRNA gene sequence similarity (83.9 and 84.8 %, respectively) to *F. flexilis* ATCC 23079^T. The relationships between strains 3B-2^T and 10AO^T, the uncultured bacterial clones and *F. flexilis* ATCC 23079^T were also maintained in trees constructed by using the maximum-likelihood and maximum-parsimony algorithms (Fig. 1). Strains 3B-2^T and 10AO^T shared 93.4–97.3 % 16S rRNA gene sequence similarity with the uncultured bacterial clones and 76.8–85.0 % with the type strains of recognized bacterial species used in this phylogenetic analysis. The mean level of DNA–DNA relatedness between strains 3B-2^T and 10AO^T was 12 % when their DNAs were used individually as labelled DNA probes for cross-hybridization, indicating that the two strains are members of different genomic species (Wayne *et al.*, 1987). The DNA G + C contents of strains 3B-2^T and 10AO^T were 42.8 and 44.6 mol%, respectively.

Strains 3B-2^T and 10AO^T contained menaquinone-7 (MK-7) as the predominant isoprenoid quinone, with peak area ratios of approximately 93–95 %. The cellular fatty acid profiles of strains 3B-2^T and 10AO^T contained large amounts of branched, unsaturated, hydroxy and straight-chain components (Table 2). The major fatty acids detected in the two strains (>10 % of the total) were iso-C_{15:0} and C_{16:1} ω 5c (Table 2). Strains 3B-2^T and 10AO^T shared identical polar lipid profiles, with phosphatidylethanolamine, an unidentified aminolipid and two unidentified lipids as the major components.

In this study, many uncultured bacterial clones, including those that are not shown in the phylogenetic tree, were found to form a phylogenetic cluster that is independent of all other phylogenetic clusters and lineages within the phylum *Bacteroidetes* (Fig. 1). However, to the best of our knowledge, no bacterial strains belonging to this phylogenetic cluster have been isolated previously. The two novel bacterial strains 3B-2^T and 10AO^T were isolated from marine sand by using low-nutrient media, and they were found to fall within this phylogenetic cluster.

The predominant menaquinone (MK-7) detected in strains 3B-2^T and 10AO^T is the same as found in all members of the phylum *Bacteroidetes* used in the phylogenetic analysis

Fig. 1. Neighbour-joining phylogenetic tree based on 16S rRNA gene sequences showing the positions of strains 3B-2^T and 10AO^T, several uncultured bacterial clones and representatives of other related taxa in the phylum *Bacteroidetes*. Bootstrap values (1000 replications) are shown as percentages at nodes; only values $\geq 70\%$ are shown. Closed circles indicate that the corresponding nodes were also recovered in trees generated with the maximum-likelihood and maximum-parsimony algorithms. *Flavobacterium aquatile* DSM 1132^T was used as an outgroup. Bar, 0.05 substitutions per nucleotide position.

(Nakagawa *et al.*, 1997; Nedashkovskaya *et al.*, 2004, 2005, 2006, 2007; Vancanneyt *et al.*, 2006; Weon *et al.*, 2006; Vaz-Moreira *et al.*, 2007; Finster *et al.*, 2009; Srisukchayakul *et al.*, 2007; Tang *et al.*, 2009). Strains 3B-2^T and 10AO^T could not be differentiated clearly from other members of the phylum *Bacteroidetes* based on their fatty acid profiles, but their fatty acid profiles showed differences in the nature and proportion of the major fatty acid(s) compared with several genera used in the phylogenetic analysis (Bowman *et al.*, 2003; Brettar *et al.*, 2004; Nedashkovskaya *et al.*, 2005, 2006, 2007; Schmidt *et al.*, 2006; Ying *et al.*, 2006; Arun *et al.*, 2009; Liu *et al.*, 2009). The levels of 16S rRNA gene sequence similarity between strains 3B-2^T and 10AO^T and other bacterial taxa were sufficient to differentiate these novel strains from previously known genera of the phylum *Bacteroidetes*. Accordingly, the phylogenetic and chemotaxonomic data suggest that strains 3B-2^T and 10AO^T should be classified in a new genus within the phylum *Bacteroidetes*. Because of the very low levels of 16S rRNA gene sequence similarity between the novel strains and the type strains of their closest phylogenetic neighbours, we did not use the latter as reference strains for other tests performed in this study. The two novel strains are considered to belong to different species based on the result of DNA–DNA hybridization and differences in their phenotypic properties, including assimilation of several substrates.

On the basis of the data presented, we suggest that strains 3B-2^T and 10AO^T represent two novel species of a new genus, for which the names *Ohtaekwangia koreensis* gen.

nov., sp. nov. and *Ohtaekwangia kribbensis* sp. nov., respectively, are proposed.

Description of *Ohtaekwangia* gen. nov.

Ohtaekwangia (Oh.tae.kwan'gi.a. N.L. fem. n. *Ohtaekwangia* named after Dr Oh Tae-Kwang, a Korean microbiologist who has contributed significantly to microbiology and bacterial systematics).

Cells are strictly aerobic, Gram-stain-negative, non-spore-forming, non-flagellated and rod-shaped. Catalase- and oxidase-positive. The predominant menaquinone is MK-7. The major fatty acids ($>10\%$ of the total) are iso-C_{15:0} and C_{16:1 ω 5c}. The major polar lipids are phosphatidylethanolamine, an unidentified aminolipid and two unidentified lipids. The DNA G + C content is 42.8–44.6 mol% (HPLC). The type species is *Ohtaekwangia koreensis*.

Description of *Ohtaekwangia koreensis* sp. nov.

Ohtaekwangia koreensis (ko.re.en'sis. N.L. fem. adj. *koreensis* pertaining to Korea, where the type strain was isolated).

Exhibits the following properties in addition to those given in the genus description. Cells are 0.3–0.6 μ m in diameter and 1.0–5.0 μ m long. Colonies on R2A agar are irregular and yellow. Optimal growth at 30 °C; grows at 10 and 39 °C, but not at 4 or 40 °C. Optimal growth at pH 6.5–7.5; grows at pH 5.5 and 9.0, but not at pH 5.0 or 9.5. Optimal growth occurs in the absence of NaCl, but growth

Table 2. Cellular fatty acid compositions of strains 3B-2^T and 10AO^T

Values are percentages of total fatty acids. Fatty acids that represented <0.5% in both strains were omitted. —, Not detected; ECL, equivalent chain-length.

Fatty acid	3B-2 ^T	10AO ^T
Straight-chain		
C _{14:0}	0.9	1.4
C _{15:0}	1.2	2.3
C _{16:0}	6.2	6.8
C _{18:0}	1.2	3.0
Branched		
iso-C _{13:0}	3.7	4.0
iso-C _{14:0}	1.8	3.0
iso-C _{15:0}	37.2	29.8
anteiso-C _{15:0}	0.7	0.9
iso-C _{16:0}	5.2	6.1
Unsaturated		
C _{16:1} ω5c	19.9	15.4
C _{17:1} ω6c	—	1.0
C _{18:1} ω7c	—	1.4
Hydroxy		
C _{15:0} 3-OH	—	0.6
iso-C _{15:0} 3-OH	3.8	4.2
C _{16:0} 3-OH	1.9	2.7
iso-C _{16:0} 3-OH	1.1	1.5
iso-C _{17:0} 3-OH	7.3	6.2
Summed feature 3*	5.4	7.0
Unknown		
ECL 14.959	0.7	1.3
ECL 16.582	0.9	0.7

*Summed features represent groups of two or three fatty acids that could not be separated by GLC with the MIDI system. Summed feature 3 comprised C_{16:1}ω7c and/or iso-C_{15:0} 2-OH.

occurs in the presence of up to 0.2% (w/v) NaCl. Growth does not occur under anaerobic conditions on R2A agar or on R2A agar supplemented with nitrate. Flexirubin-type pigments are produced. Nitrate is not reduced to nitrite. Hydrolyses aesculin, casein and Tween 80, but not gelatin, hypoxanthine, xanthine, starch, L-tyrosine or urea. Assimilation data of substrates in the GN2 microplate system are given in Table 1. Susceptible to chloramphenicol, gentamicin, lincomycin, neomycin, novobiocin, streptomycin and tetracycline, and weakly susceptible to polymyxin B, but resistant to ampicillin, carbenicillin, cephalothin, kanamycin, oleandomycin and penicillin G. In assays with the API ZYM system, positive for activities of alkaline phosphatase, esterase (C4), esterase lipase (C8), leucine arylamidase, cystine arylamidase, α-chymotrypsin, acid phosphatase, naphthol-AS-BI-phosphohydrolase, α-galactosidase, β-galactosidase, α-glucosidase, β-glucosidase, N-acetyl-β-glucosaminidase and α-fucosidase, but negative for activities of lipase (C14), valine arylamidase, trypsin, β-glucuronidase and α-mannosidase. The DNA G+C content of the type strain is 42.8 mol% (HPLC).

The type strain, 3B-2^T (=KCTC 23018^T =CCUG 58939^T), was isolated from a sand sample collected from the coast at Saemankum, Korea.

Description of *Ohtaekwangia kribbensis* sp. nov.

Ohtaekwangia kribbensis (kri.bben'sis. N.L. fem. adj. *kribbensis* pertaining to KRIBB, an arbitrary adjective formed from the acronym of the Korea Research Institute of Bioscience and Biotechnology, KRIBB, where taxonomic studies on this species were performed).

Exhibits the following properties in addition to those given in the genus description. Cells are 0.2–0.5 µm in diameter and 1.5–7.5 µm long. Colonies on R2A agar are irregular and yellow. Optimal growth at 30 °C; grows at 10 and 39 °C, but not at 4 or 40 °C. Optimal growth at pH 6.5–7.5; grows at pH 5.0 and 8.5, but not at pH 4.5 or 9.0. Optimal growth occurs in the presence of NaCl, but growth occurs in the presence of up to 0.2% (w/v) NaCl. Growth does not occur under anaerobic conditions on R2A agar or on R2A agar supplemented with nitrate. Flexirubin-type pigments are produced. Nitrate is not reduced to nitrite. Hydrolyses aesculin, casein, gelatin, Tween 80 and L-tyrosine, but not hypoxanthine, xanthine, starch or urea. Assimilation data of substrates in the GN2 microplate system are given in Table 1. Susceptible to chloramphenicol, novobiocin, streptomycin and tetracycline, and weakly susceptible to polymyxin B, but resistant to ampicillin, carbenicillin, cephalothin, gentamicin, kanamycin, lincomycin, neomycin, oleandomycin and penicillin G. In assays with the API ZYM system, positive for activities of alkaline phosphatase, esterase (C4), esterase lipase (C8), leucine arylamidase, valine arylamidase, cystine arylamidase, α-chymotrypsin, acid phosphatase, naphthol-AS-BI-phosphohydrolase, α-galactosidase, β-galactosidase, α-glucosidase, β-glucosidase, N-acetyl-β-glucosaminidase and β-fucosidase, but negative for activities of lipase (C14), trypsin, β-glucuronidase and α-mannosidase. The DNA G+C content is 44.6 mol% (HPLC).

The type strain, 10AO^T (=KCTC 23019^T =CCUG 58938^T), was isolated from a sand sample collected from the coast at Saemankum, Korea.

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