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ORIGINAL ARTICLE

Polyphasic analysis in the description of *Sulfitobacter salinus* sp. nov., a marine alphaproteobacterium isolated from seawater

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Abstract

Purpose A polyphasic analysis was performed on a novel bacterium, designated strain KMU-143^T, which was isolated from seawater collected in the Republic of Korea.

Methods A novel marine bacterium KMU-143^T was analyzed and described using a polyphasic taxonomic method including 16S rRNA gene sequence analysis, DNA–DNA hybridization, and physiological, biochemical, and chemotaxonomic analyses.

Results Strain KMU-143^T was Gram-stain-negative, strictly aerobic, oval-shaped, non-motile, and chemoorganoheterotrophic. Phylogenetic analysis based on the 16S rRNA gene sequence demonstrated that the novel marine bacterium belongs to the family *Rhodobacteraceae*, of the class *Alphaproteobacteria*, and that it possessed the highest (97.1%) sequence similarity with *Sulfitobacter pontiacus* ChLG 10^T and *Sulfitobacter undariae* W-BA2^T. DNA–DNA relatedness values between strains KMU-143^T, *S. pontiacus* JCM 21789^T, and *S. undariae* KCTC 42200^T were less than 70%. The major isoprenoid quinone of the novel isolate was ubiquinone-10 (Q-10) and the major (> 10%) cellular fatty acids were C16:0 and C18:1 ω7*c*. The genomic DNA G+C content of strain KMU-143^T was 56.1 mol%. The polar lipid profile of the strain KMU-143^T was found to consist of phosphatidylglycerol, diphosphatidylglycerol, phosphatidylcholine, an unidentified aminolipid, and two unidentified lipids.

Conclusion Based on the discriminative phylogenetic position and combination of genotypic and phenotypic properties, the strain is considered to represent a new species of the genus *Sulfitobacter* for which the name *Sulfitobacter salinus* sp. nov. is proposed. The type strain of *S. salinus* sp. nov. is KMU-143^T (= KCCM 90322^T = NBRC 113459^T).

Keywords *Alphaproteobacteria* · *Sulfitobacter salinus* sp. nov. · Seawater · 16S rRNA gene · Polyphasic taxonomy

Introduction

The class *Alphaproteobacteria* (Stackebrandt et al. 1988; Garrity et al. 2005) is one of the main phylogenetic lineages among the marine bacterioplankton, along with species of the class *Gammaproteobacteria* and the phylum *Bacteroidetes* (Giovannoni and Rappé 2000). In particular, this class comprises heterogeneous and various phylogenetic groups with diverse microbial properties and thought to carry out significant environmental roles (Giovannoni and Rappé 2000). The genus *Sulfitobacter*, a member of the family *Rhodobacteraceae* within the class *Alphaproteobacteria*, was first formally established by Sorokin (1995) to describe a sulfur-oxidizing chemoheterotrophic type species isolated from the Black Sea with *Sulfitobacter pontiacus* ChLG 10^T. An emended description of the genus was later presented by Yoon et al. (2007). At the time of writing, the genus *Sulfitobacter* includes nineteen validly named species (http://www.bacterio.net/sulfitobacter.html), which were isolated from a variety of marine ecosystems such as Antarctic lake (Labrenz et al. 2000), seawater (Park et al. 2007; Sorokin 1995; Kwak et al. 2014), tidal flat sediment (Park et al. 2018), and marine organisms (Fukui et al. 2015; Hong et al. 2015; Kumari et al. 2016). In 2018, in the course of screening the culturable marine microorganisms from diverse marine environments, a bacterium designated KMU-143^T was

The digital protologue database (DPD) number for the strain KMU-143^T is TA00838. The GenBank/EMBL/DDBJ accession number of the 16S rRNA gene sequence of strain KMU-143^T is LC464517.

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isolated from the seawater collected at Hamdeok Beach in Jeju Island. In the present study, a novel marine bacterium KMU-143^T was analyzed and described using a polyphasic taxonomic method (Colwell 1970) including 16S rRNA gene sequence analysis, DNA–DNA hybridization, and physiological, biochemical, and chemotaxonomic analyses. On the basis of data from this polyphasic taxonomic approach, the novel isolate is suggested to represent a new species of the genus *Sulfitobacter* within the class *Alphaproteobacteria*.

Materials and methods

Isolation of the bacterial strain and culture condition

The seawater sample was collected at Hamdeok Beach, Jeju Island, Republic of Korea (GPS data, 33° 32′ 36.6″ N 126° 40′ 10.5″ E), in April 2018 by use of a 500 mL sterile polyethylene bottle. A 50-μL aliquot of the sample was plated onto the surface of marine agar 2216 (Difco). Several colonies that developed at 25 °C were then picked and re-streaked onto new marine agar 2216 plates, and the procedure was repeated twice. A beige-colored colony was picked as a representative of morphologically similar colonies, named KMU-143^T, and was used for further analysis. For comparative purpose, *Sulfitobacter pontiacus* JCM 21789^T and *Sulfitobacter undariae* KCTC 42200^T were used as reference strains. KMU-143^T and the reference strains were routinely subcultured on marine agar 2216 at 25 °C and maintained in marine broth 2216 (Difco) supplemented with 40% (v/v) glycerol at – 80 °C.

Morphological, physiological, and biochemical analysis

The bacterial cell shape was observed via transmission electron microscopy (TEM) and scanning electron microscopy (SEM). Cell motility was investigated by phase-contrast microscopy (Primo Star, Zeiss). For TEM analysis, cells were grown on marine agar 2216 at 25 °C for 3 days, loaded onto glow-discharged EM grids covered with a continuous carbon film, and negatively stained with 1% (w/v) uranyl acetate. The grids were observed using a Tecnai G2 Spirit (FEI) transmission electron microscope (Korea Basic Science Institute) at 120 kV with a magnification of × 21,000; SEM analysis was performed by previously established methods (Schädler et al. 2008; Wang et al. 2015). The temperature range (4, 10, 15, 20, 25, 30, 37, 40, and 45 °C) and pH range (5.5–9.5 at increments of 0.5 pH) for growth were tested by incubating the isolate for 1 week on marine agar 2216. The pH tests were performed with the buffers prepared by previously reported method (Yoon et al. 2016). The NaCl concentration for growth was examined on TY agar medium [1% tryptone, 0.3% yeast extract, 0.9% $MgCl_2 \cdot 6H_2O$, 0.9% $MgSO_4 \cdot 7H_2O$, 0.2% $CaCl_2 \cdot 2H_2O$, 0.06% KCl, and 1.5% agar (w/v) with 0–10% (w/v) NaCl (at increments of 1%)], and the cells were grown at 25 °C. Gram-staining assay was performed using the BD Gram-Staining Kit (Becton, Dickinson and Company, USA). Anaerobic growth was assessed for up to 2 weeks on marine agar 2216 in a jar containing the AnaeroPack-Anaero (Mitsubishi Gas Chemical), which can act as an O_2 absorber and CO_2 generator. Catalase activity was tested by bubble formation in 3% (v/v) H_2O_2 solution. An oxidase activity was tested using a commercialized dropper oxidase reagent (Becton Dickinson and Company, Sparks, MD, USA). DNase activity was examined using marine agar 2216 containing 0.2% DNA and 0.005% methyl green (Hansen and Sørheim 1991). Casein hydrolysis was evaluated on marine agar 2216 containing 0.1% skim milk (Power and Johnson 2009). A tyrosine degradation was tested according to the previously described method (Lewin and Lounsbery 1969). The ability to hydrolyze Tween 20 and 80 was tested based on Hansen and Sørheim's method (1991). API 20E, API 50CH, and API ZYM strips (bioMérieux) were utilized to evaluate physiological and biochemical properties. All the media for the API test strips were supplemented with NaCl solution (final concentration 0.85%, w/v). The API 20E, API 50CH, and API ZYM strips were incubated at 25 °C for 3 days, 9 days, and 3 h, respectively, and the results were interpreted according to the manufacturer's instructions. The hydrolysis of gelatin and urea as well as nitrate reduction was assessed using the API 20E strip. The hydrolysis of agar and starch was tested using marine agar 2216 and the API 50CH strip, respectively. Utilization of organic substrates as sole carbon and energy sources was evaluated using Biolog GEN III MicroPlate systems (Biolog) according to the manufacturers' instructions.

Determination of DNA G+C content, 16S rRNA gene sequencing, and phylogenetic analysis

Extraction of the genomic DNA was performed using the Wizard® Genomic DNA Purification Kit (Promega) according to the manufacturer's instructions, and cells were harvested from marine agar 2216 plates after 3 days of incubation at 25 °C. The DNA base composition was determined using the HPLC method of Mesbah et al. (1989). The genomic DNA G+C content was calculated in triplicate. The 16S rRNA gene was PCR-amplified from the extracted DNA using a bacterial universal primer set specific to the 16S rRNA gene: 27F and 1492R (Lane 1991). The amplified PCR product was purified using a PCR purification kit (BIOFACT) and sequenced directly by the fluorescent dye-terminator method using an ABI 3730XL Capillary DNA Analyzer (Applied Biosystems) at BIOFACT Co., Ltd (Daejeon, Korea). The almost full-length 16S rRNA gene sequence was compiled using the SeqMan software (DNASTAR). Sequence similarities of the 16S

rRNA gene were determined using the EzBioCloud database (https://www.ezbiocloud.net/) (Yoon et al. 2017). To elucidate the phylogenetic position of the novel bacterium, the 16S rRNA gene sequence of strain KMU-143^T was compared with the sequences obtained from GenBank/EMBL/DDBJ database. Multiple alignments of the sequences were performed using CLUSTAL_X (version 1.83) (Thompson et al. 1997). Phylogenetic distances (distance options according to Kimura's two-parameter model; Kimura 1980) were calculated, and clustering was performed with the neighbor-joining (Saitou and Nei 1987), maximum-parsimony (Fitch 1971), and maximum-likelihood (Felsenstein 1985) algorithms using the MEGA5 software (Tamura et al. 2011). The topology of the evolutionary tree was calculated by the bootstrap resampling method of Felsenstein (1985) with 1000 replicates.

DNA–DNA hybridization test

Chromosomal DNA was extracted using the Wizard® Genomic DNA Purification Kit (Promega) following the manufacturer's instructions. DNA–DNA hybridization was performed by the membrane filter method (Suzuki et al. 1981). Each mixture of labeled and unlabeled DNAs was incubated at 37 °C for 12 h. Reciprocal hybridization tests were performed in triplicate.

Chemotaxonomic analysis

Gas chromatographic analysis of the cellular fatty acid methyl esters (FAMEs) was performed using the MIDI TSBA database (version 6.1) (Sasser 1990). Strain KMU-143^T and the reference strains were cultured on marine agar 2216 at 25 °C for 3 days for the FAMEs analysis. Polar lipids were extracted according to the procedures described by Minnikin et al. (1984). They were identified by two-dimensional thin-layer chromatography followed by spraying with the appropriate detection reagents (Minnikin et al. 1984; Komagata and Suzuki 1987). Whole lipids were detected by spraying with 5% molybdatophosphoric acid (5 g molybdatophosphoric acid hydrate in 100 mL ethanol) followed by heating at 150 °C (Worliczek et al. 2007). Phospholipids were detected by spraying with 1.4% molybdenum blue. Glycolipids were detected by spraying with 2.5% α-naphthol followed by heating at 180 °C. Aminolipids were detected by spraying with 0.2% ninhydrin followed by heating at 180 °C. Quinones were extracted from freeze-dried cells with chloroform/methanol (2:1, v/v). Samples were eluted with methanol/isopropyl ether (4:1, v/v) at a flow rate of 1 mL min^{-1}. Analysis of the respiratory quinone system was performed as described previously (Collins and Jones 1981).

Results and discussion

Morphological, physiological, and biochemical properties

The discriminative phenotypic properties of strain KMU-143^T are shown in Table 1 and in the species description. Cells of strain KMU-143^T grown on marine agar 2216 were mostly oval-shaped with 0.9–1.0 μm in width and 1.0–1.2 μm in length (Fig. 1a, b). The bacterial cells did not have flagella or appendages (Fig. 1a, b) and produced a beige pigment. Observation of a SEM image indicated that the novel strain reproduces by binary fission (Fig. 1b). Strain KMU-143^T was distinguished from the most closely related species by observing main characteristics such as motility (negative), acid production (positive for 5-keto-gluconate), enzyme activity [positive for esterase (C4) and negative for acid phosphatase, arginine dihydrolase, α-galactosidase, lysine decarboxylase, ornithine decarboxylase, and valine arylamidase], and utilization of organic substrates (positive for citric acid and negative for *N*-acetylneuraminic acid, *N*-acetyl-D-galactosamine, *N*-acetyl-β-D-mannosamine, γ-aminobutyric acid, L-arginine, L-aspartic acid, dextrin, D-gluconic acid, D-glucuronic acid, L-glutamic acid, α-hydroxybutyric acid, inosine, D-malic acid, and pectin) (Table 1).

Determination of DNA G+C content, phylogenetic analysis, and DNA–DNA hybridization

The G+C content of the genomic DNA of the type strain KMU-143^T was 56.1 mol%. Furthermore, the almost complete 16S rRNA gene sequence (1404 bp) was determined for the novel strain. An evolutionary tree on the basis of the neighbor-joining algorithm was generated for a visual comparison of 16S rRNA gene sequences and revealed that strain KMU-143^T was phylogenetically affiliated with *Sulfitobacter*, a genus belonging to the family *Rhodobacteraceae*, of the class *Alphaproteobacteria* (Fig. 2). A comparative phylogenetic investigation based on the 16S rRNA gene sequences revealed that strain KMU-143^T had a similarity of 97.1% to *S. pontiacus* ChLG 10^T and *S. undariae* W-BA2^T, 96.9% to *Sulfitobacter donghicola* DSW-25^T, and 96.8% to *Sulfitobacter guttiformis* EL-38^T. 16S rRNA gene sequence similarities to all other species of the family *Rhodobacteraceae* with validly published names were less than 96.5%. The overall phylogenetic tree topologies calculated using the maximum-parsimony and maximum-likelihood methods also supported the neighbor-joining tree (Fig. 2). DNA–DNA hybridization values between strain KMU-143^T and strains *S. pontiacus* JCM 21789^T and *S. undariae* KCTC 42200^T were 9.9 ± 1.0% and 10.5 ± 2.0%, respectively. These values are sufficient to classify strain KMU-143^T as a novel species that is distinct from the

Table 1 Discriminative properties of strain KMU-143^T and closely related species

Characteristic	1	2	3
Isolation source	Seawater	Seawater[a]	Brown algae reservoir[b]
Cell morphology	Oval-shaped	Rod-shaped[a]	Coccoid, ovoid, or rod-shaped[b]
Motility	−	+[a]	−[b]
Growth conditions for			
Temperature (°C)	10–37 (25)	4–35 (22–25)[a]	4–30 (25)[b]
pH	6.5–9.5 (7.5)	6.5–8.5 (7.3–7.5)[a]	5.5–8.0 (7.0–8.0)[b]
NaCl (%, w/v)	1.0–6.0 (2.0)	0.5–8.0 (2.0–2.5)[a]	0–10.0 (2.0–3.0)[b]
Reaction of			
Voges-Proskauer	−	+	+
Hydrolysis of:			
o-Nitrophenyl-β-D-galactopyranoside (ONPG)	+	+	−
Acid production from			
5-Keto-gluconate	+	+	−
Enzyme activity of:			
Acid phosphatase	−	+	+
Arginine dihydrolase	−	+	−
Esterase (C4)	+	−	−
α-Galactosidase	−	+	−
Lysine decarboxylase	−	+	−
Ornithine decarboxylase	−	+	−
Valine arylamidase	−	−	+
Utilization of			
N-Acetylneuraminic acid	−	+	+
N-Acetyl-D-galactosamine	−	+	+
N-Acetyl-β-D-mannosamine	−	+	+
γ-Aminobutyric acid	−	+	+
L-Arginine	−	+	+
L-Aspartic acid	−	+	+
Citric acid	+	−	−
Dextrin	−	+	+
D-Gluconic acid	−	+	+
D-Glucuronic acid	−	+	+
L-Glutamic acid	−	+	+
α-Hydroxybutyric acid	−	+	+
Inosine	−	+	+
D-Malic acid	−	+	+
Pectin	−	+	+
Polar lipids	PG, DPG, PC, AL, 2L	PE, PG, DPG, PC, AL, 3L	PE, PG, DPG, PC, AL, 2L
DNA G+C content (mol%)	56.1	62.1[a]	55.0[b]

Strains: 1 KMU-143^T (*Sulfitobacter salinus* sp. nov.; present study), 2 *Sulfitobacter pontiacus* JCM 21789^T, 3 *Sulfitobacter undariae* KCTC 42200^T

All data are from this study except where indicated otherwise. Numbers in parentheses are optimal growth conditions

PE phosphatidylethanolamine, *PG* phosphatidylglycerol, *DPG* diphosphatidylglycerol, *PC* phosphatidylcholine, *AL* unidentified aminolipid, *L* unidentified lipid

+, positive; −, negative

[a] Data from Sorokin 1995

[b] Data from Park et al. 2015

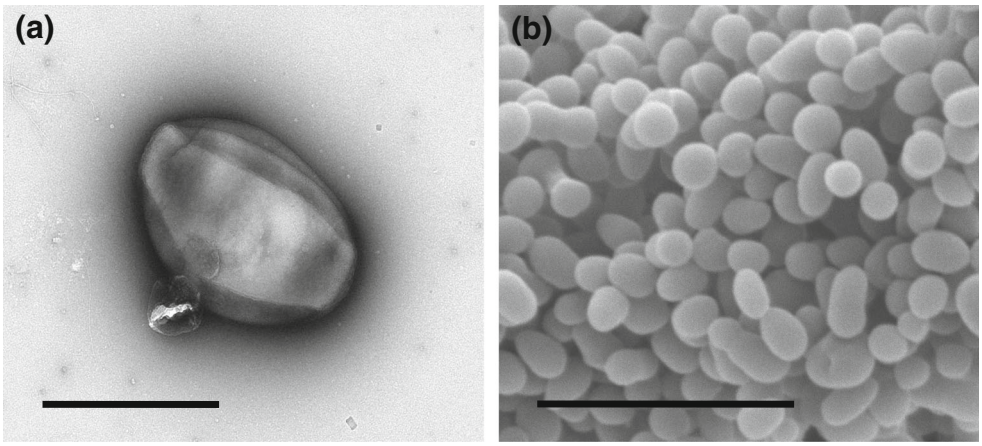

Fig. 1 Transmission electron micrograph of a negatively stained cell of strain KMU-143^T (**a**). Scanning electron micrograph of strain KMU-143^T (**b**). Bars, 1 μm (**a**) and 3 μm (**b**)

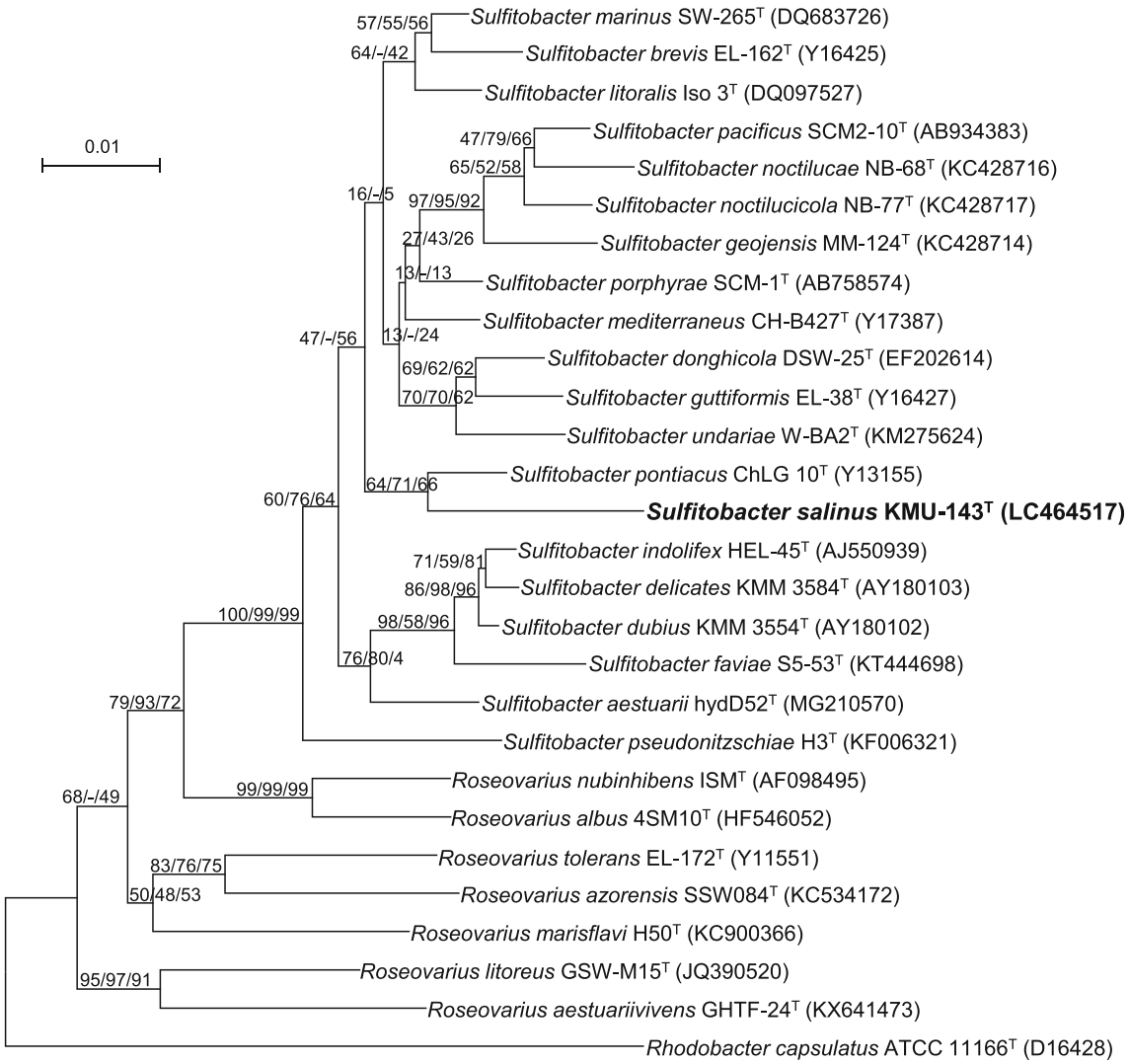

Fig. 2 Neighbor-joining tree of 16S rRNA gene sequence similarity. The phylogenetic positions of the strain KMU-143^T and representatives of closely related and other more distantly related species in the genus *Sulfitobacter* are shown. The tree was rooted using *Rhodobacter capsulatus* ATCC 11166^T (D16428) as an outgroup. The numbers at the nodes indicate the percentages of the occurrence of the strain in 1000 bootstrapped trees. The sequence determined in this study is shown in bold. Bootstrap values from neighbor-joining, maximum-parsimony, and maximum-likelihood analyses are shown (NJ/MP/ML). Bar, 1% sequence divergence

validly recognized *Sulfitobacter* members (Stackebrandt and Goebel 1994).

Chemotaxonomic properties

The major (> 10%) cellular fatty acids of strain KMU-143^T were identified as C16:0 and C18:1 *ω7c* (Table 2). Based on the cellular fatty acid composition, strain KMU-143^T could be differentiated from the most closely related phylogenetic taxa *S. pontiacus* JCM 21789^T and *S. undariae* KCTC 42200^T through the differing proportions of iso-C18:0, C18:1 *ω7c*, and 11-methyl C18:1 *ω7c* (Table 2) indicating that strain KMU-143^T probably represents a separate species of the genus *Sulfitobacter*. The polar lipids present in strain KMU-143^T were composed of phosphatidylglycerol (PG), diphosphatidylglycerol (DPG), phosphatidylcholine (PC), an unidentified aminolipid (AL), and two unidentified lipids (L1–2) (Table 1 and Supplementary Fig. 1). The polar lipid profile of strain KMU-143^T was similar to that of *S. pontiacus* JCM 21789^T and *S. undariae* KCTC 42200^T in that the strain had PG, DPG, PC, AL, and L1–2. However, phosphatidylethanolamine (PE) was only found in *S. pontiacus* JCM 21789^T and *S. undariae* KCTC 42200^T, and a L3 was only detected in *S. pontiacus* JCM 21789^T (Table 1 and Supplementary Fig. 1). The sole isoprenoid quinone of the novel strain was ubiquinone-10 (Q-10), which is in accordance with the description of genus *Sulfitobacter*.

Table 2 Comparison of cellular fatty acids for strain KMU-143^T and closely related species

Fatty acid	1	2	3
C10:0 3-OH	5.1	4.7	3.3
C12:0 3-OH	tr	1.6	–
C14:0	tr	–	tr
anteiso-C15:0	–	tr	tr
C16:0	10	8.3	8.9
C17:1 *ω8c*	–	tr	–
iso-C18:0	–	–	4.4
C18:1 *ω7c*	74.2	81.4	79.9
C18:0	2.9	1.3	1.1
11-methyl C18:1 *ω7c*	5.1	–	–
C19:0 cyclo *ω8c*	tr	–	–
Summed feature 2[a]	tr	tr	–
Summed feature 3[b]	tr	tr	1.2
Summed feature 5[c]	–	–	tr
Summed feature 7[d]	tr	tr	–

Strains: 1 KMU-143^T (*Sulfitobacter salinus* sp. nov.; present study), 2 *Sulfitobacter pontiacus* JCM 21789^T, 3 *Sulfitobacter undariae* KCTC 42200^T

All data are from this study. The data were typically obtained by GLC using the MIDI system

tr trace (less than 1.0%), – not detected

[a] Summed feature 2 comprised C12:0 aldehyde ?

[b] Summed feature 3 comprised C16:1 *ω7c* and/or C16:1 *ω6c*

[c] Summed feature 5 comprised ante-C18:0 and/or C18:2 *ω6,9c*

[d] Summed feature 7 comprised C19:1 *ω7c* and/or C19:1 *ω6c*

Polyphasic taxonomic conclusion

On the basis of the distinct phylogenetic position and combination of genotypic and phenotypic characteristics, strain KMU-143^T cannot be assigned to any previously recognized bacterial species and thus can be described as representing a novel species within a genus *Sulfitobacter*, *Sulfitobacter salinus* sp. nov.

Description of *Sulfitobacter salinus* sp. nov.

Sulfitobacter salinus (sa.li'nus. N.L. masc. adj. *salinus* salty)

Cells are Gram-stain-negative, strictly aerobic, oval-shaped that are mostly 0.9–1.0 μm in width and 1.0–1.2 μm in length. Cells lack flagella and are non-motile. Colonies grown on marine agar 2216 are circular and beige-pigmented after 3 days of incubation at 25 °C. Growth occurs at 10–37 °C (optimum 25 °C), at pH 6.5–9.5 (optimum pH 7.5), and with 1.0–6.0% (w/v) NaCl (optimum 2.0%). Positive for catalase and oxidase, but negative for reduction of nitrate. Tween 20 and Tween 80 are hydrolyzed, but agar, casein, DNA, gelatin, tyrosine, and urea are not. The reaction for *o*-nitrophenyl-β-D-galactopyranoside (ONPG) is positive, but Voges-Proskauer test, arginine dihydrolase, lysine decarboxylase, ornithine decarboxylase, tryptophan deaminase, citrate utilization, hydrogen sulfide production, and indole production tests are negative (API 20E). Acids are produced from esculin ferric citrate and 5-keto-gluconate, but not from amygdalin, arbutin, gentiobiose, melezitose, ribose, D-arabinose, D-turanose, D-lyxose, D-xylose, L-xylose, D-tagatose, D-fucose, L-fucose, D-arabitol, L-arabitol, gluconate, fructose, salicin, cellobiose, maltose, raffinose, methyl-β-D-xylopyranoside, glucose, lactose, galactose, mannose, melibiose, sucrose, trehalose, starch, glycogen, sorbose, rhamnose, sorbitol, methyl-α-D-mannopyranoside, L-arabinose, methyl-α-D-glucopyranoside, *N*-acetyl-glucosamine, inulin, glycerol, erythritol, adonitol, dulcitol, inositol, mannitol, xylitol, and 2-keto-gluconate (API 50CH). Alkaline phosphatase, esterase (C4), leucine arylamidase, and naphthol-AS-BI-phosphohydrolase are present, but valine arylamidase, trypsin, acid phosphatase, β-glucosidase, α-glucosidase, β-galactosidase, *N*-acetyl-β-glucosaminidase, esterase lipase (C8), α-galactosidase, lipase (C4), cystine arylamidase, α-chymotrypsin, β-glucuronidase, α-mannosidase, and α-fucosidase are absent (API ZYM). Uses the organic substrate α-D-glucose, L-alanine, L-serine, citric acid, L-malic acid, Tween 40, β-hydroxy-D,L-butyric acid, acetoacetic acid, and acetic acid, but not dextrin, gelatin, pectin, glycyl-L-proline, D-galacturonic

acid, D-melibiose, D-fructose, D-arabitol, D-lactic acid methyl ester, β-methyl-D-glucoside, *myo*-inositol, L-arginine, D-gluconic acid, L-lactic acid, D-cellobiose, glycerol, L-aspartic acid, D-glucuronic acid, D-fucose, D-glucose-6-phosphate, L-glutamic acid, glucuronamide, α-ketoglutaric acid, sucrose, *N*-acetyl-β-D-mannosamine, L-fucose, D-fructose-6-phosphate, L-histidine, mucic acid, D-turanose, *N*-acetyl-D-galactosamine, L-rhamnose, L-pyroglutamic acid, quinic acid, stachyose, *N*-acetylneuraminic acid, D-saccharic acid, D-raffinose, D-sorbitol, *p*-hydroxyphenylacetic acid, α-D-lactose, D-mannose, D-mannitol, methyl pyruvate, γ-aminobutyric acid, D-maltose, *N*-acetyl-D-glucosamine, L-galactonic acid lactone, α-hydroxybutyric acid, D-trehalose, D-galactose, D-salicin, 3-methyl glucose, α-ketobutyric acid, gentiobiose, D-malic acid, propionic acid, D-aspartic acid, inosine, D-serine, bromosuccinic acid, and formic acid (Biolog GEN III MicroPlate). The predominant (> 10%) cellular fatty acids are C16:0 and C18:1 *ω7c*. The sole respiratory isoprenoid quinone is ubiquinone-10. The major polar lipids are phosphatidylglycerol, diphosphatidylglycerol, phosphatidylcholine, an unidentified aminolipid, and two unidentified lipids. The G+C content within the genomic DNA of the type strain is 56.1 mol%.

The type strain is KMU-143^T (= KCCM 90322^T = NBRC 113459^T), which was isolated from seawater collected at Hamdeok Beach, Jeju Island, Republic of Korea.

Compliance with ethical standards

Conflict of interest The author declares that he has no conflicts of interest.

Research involving human participants and/or animals This article does not contain any studies with human participants or animals performed by any of the author.

Informed consent N/A

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