Altererythrobacter namhicola sp. nov. and *Altererythrobacter aestuarii* sp. nov., isolated from seawater

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Two non-motile, orange- or yellow-pigmented bacteria, designated strains KYW48^T and KYW147^T, were isolated from seawater collected from the South Sea, Republic of Korea. Cells of both strains were Gram-reaction-negative, aerobic and catalase- and oxidase-positive. The major fatty acids of strain KYW48^T were C_{18:1}ω7c (35.3%), summed feature 3 (iso-C_{15:0} 2-OH and/or C_{16:1}ω7c) (22.7%), C_{17:1}ω6c (19.8%), C_{14:0} 2-OH (7.4%) and C_{16:0} (5.9%), and those of strain KYW147^T were C_{18:1}ω7c (36.0%), summed feature 3 (18.3%), C_{16:0} (14.7%), 11-methyl C_{18:1}ω7c (10.7%), C_{16:0} 2-OH (9.1%) and C_{18:1}ω9c (8.0%). The predominant isoprenoid quinone of both strains was ubiquinone 10 (Q-10). The DNA G+C contents of strains KYW48^T and KYW147^T were 63.8 and 67.2 mol%, respectively. A phylogenetic tree based on 16S rRNA gene sequences showed that strains KYW48^T and KYW147^T were grouped with the members of the family *Erythrobacteraceae* and formed a distinct clade with the members of the genus *Altererythrobacter* (<95.7% sequence similarity). On the basis of the evidence presented in this study, the novel species *Altererythrobacter namhicola* sp. nov. (type strain KYW48^T = KCTC 22736^T = JCM 16345^T) and *Altererythrobacter aestuarii* sp. nov. (type strain KYW147^T = KCTC 22735^T = JCM 16339^T) are proposed.

The genus *Altererythrobacter* was proposed by Kwon *et al.* (2007) and belongs to the family *Erythrobacteraceae* (Lee *et al.*, 2005). At the time of writing, the genus included five species, *Altererythrobacter epoxidivorans* (type species; Kwon *et al.*, 2007), *A. luteolus* (Yoon *et al.*, 2005; Kwon *et al.*, 2007), *A. indicus* (Ramesh Kumar *et al.*, 2008), *A. marinus* (Lai *et al.*, 2009) and *A. marensis* (Seo & Lee, 2010). Members of the genus have been isolated from marine environments such as the mangrove rhizosphere, cold-seep sediments and seawater of tidal flats. *Altererythrobacter* species are Gram-reaction-negative, aerobic, chemo-organotrophic, non-motile, yellow-pigmented and lacking in bacteriochlorophyll (BChl) *a* (Kwon *et al.*, 2007). In the course of our study on the

microbial diversity of seawater, two bacterial strains, designated KYW48^T and KYW147^T, were isolated and were the subject of a taxonomic investigation.

Gwangyang Bay (34° 51' N 127° 47' E) is located on the southern coast of Korea. Strains KYW48^T and KYW147^T were isolated from seawater samples collected from Gwangyang Bay in July 2008, using the standard dilution plating technique. Seawater samples were collected from a shallow coastal region (2 m depth; KYW147^T) and from the mouth (30 m depth; KYW48^T) of the bay in the morning at high tide. The physico-chemical properties of the seawater samples were as follows: at 2 m depth, pH 8.2, temperature 28.0 °C, salinity 26.4‰; at 30 m, pH 8.2, temperature 26.2 °C, salinity 29.0‰. Isolation was achieved on marine agar 2216 (MA; Becton Dickinson) (Yang *et al.*, 2006) at 25 °C for 7 days. The isolates were routinely cultured on MA and maintained at –80 °C as suspensions in marine broth (MB; Becton Dickinson) containing glycerol (20%, w/v). Reference strains *A. epoxidivorans* JCM 13815^T, *A. indicus* KACC 13863^T and *A. luteolus* KCTC 12311^T were obtained from culture collections. *A. marensis* MSW-14^T and *A. marinus* H32^T were gifts from Professor S. D. Lee (Jeju University, Korea) and Director Z. Shao (State Oceanic Administration, China).

Abbreviations: BChl, bacteriochlorophyll; DPG, diphosphatidylglycerol; GL, unknown glycolipid; PC, phosphatidylcholine; PE, phosphatidylethanolamine; PG, phosphatidylglycerol; PL, unknown phospholipid; SGL, sphingoglycolipid.

The GenBank/EMBL/DDBJ accession numbers for the 16S rRNA gene sequence of strains KYW48^T and KYW147^T are FJ935793 and FJ997597, respectively.

Two supplementary figures and a supplementary table are available with the online version of this paper.

Bacterial DNA preparation and PCR amplification and sequencing of the 16S rRNA gene were carried out as described previously (Chun & Goodfellow, 1995). Identification of phylogenetic neighbours and calculation of pairwise 16S rRNA gene sequence similarities were achieved using the EzTaxon server (<http://www.eztaxon.org/>; Chun *et al.*, 2007). Related sequences and the novel sequences were aligned by using CLUSTAL_X (Thompson *et al.*, 1997) and the alignment was refined using PHYDIT version 3.1 (<http://plaza.snu.ac.kr/~jchun/phydit/>). Phylogenetic analysis was performed by using the computer packages PHYLIP (Felsenstein, 1993) and PAUP* 4.0 (Swofford, 1998). Phylogenetic trees were inferred using the maximum-likelihood (Felsenstein, 1993), maximum-parsimony (Fitch, 1971) and neighbour-joining (Saitou & Nei, 1987) algorithms. The distance matrix for the neighbour-joining method was generated according to the model of Jukes & Cantor (1969). The robustness of the topology of the phylogenetic trees was evaluated by bootstrap analyses (Felsenstein, 1985) of the neighbour-joining method based on 1000 resamplings.

Preliminary sequence comparison with 16S rRNA gene sequences held in GenBank indicated that the two isolates were related to the family *Erythrobacteraceae*. Strains KYW48^T and KYW147^T showed the highest 16S rRNA gene sequence similarity to each other (96.2%) followed by type strains of other *Altererythrobacter* species (<95.9%). To elucidate the phylogenetic relationship between the novel isolates and other species of the family *Erythrobacteraceae*, phylogenetic trees were constructed using three different tree-making algorithms. The neighbour-joining tree (Fig. 1) showed that strains KYW48^T and KYW147^T were grouped with the members of the genus

Altererythrobacter and formed a distinct phyletic line distinguishable from other *Altererythrobacter* species, as in the maximum-parsimony and maximum-likelihood trees.

Physiological tests were carried out on strains KYW48^T and KYW147^T and the reference strains under the same conditions. Cells grown on MA for 2 days or to exponential phase in MB at 30 °C were used as the inoculum for physiological tests. Growth on various standard bacteriological media, nutrient agar (NA; Becton Dickinson), tryptic soy agar (TSA; Becton Dickinson), R2A agar (Becton Dickinson) and glucose-yeast extract agar (GYEA; Gordon & Mihm, 1962), was tested according to the manufacturer's instructions. The morphology of cells grown at 30 °C for 2 days in MB was observed with a phase-contrast microscope (TMS-F; Nikon) and a scanning electron microscope (S-4800; Hitachi). For scanning electron microscopy, a subsample was soaked for several hours in 0.1 M sodium phosphate buffer (pH 7.4), fixed in 0.5% glutaraldehyde and 0.5% paraformaldehyde in 0.1 M sodium phosphate buffer (pH 7.4) and dehydrated through an ethanol/isoamyl alcohol series. The sample was subsequently critical-point-dried in an SPI dry (JSM 5310; SPI Supplies) apparatus and osmium coater (Hollow Cathode Plasma CVD; Vacuum Device). Gliding motility was investigated by examining the edge of a hanging drop of a fresh MB culture, as recommended by Bernardet *et al.* (2002). The requirement for NaCl (final concentration 0–12%, in increments of 1%) for growth was tested using synthetic ZoBell liquid and agar medium (ZoBell, 1941; 5 g Bacto peptone, 1 g yeast extract, 0.1 g ferric citrate and 15 g Bacto agar in 1 l distilled water) for up to 7 days. All media used in physiological tests were supplemented with 2%

Fig. 1. Neighbour-joining tree based on 16S rRNA gene sequences showing the phylogenetic position of strains KYW48^T and KYW147^T within the family *Erythrobacteraceae*. Evolutionary distances, generated using the Jukes–Cantor model, were based on 1319 unambiguously aligned nucleotides. Bootstrap support percentages (>50%) are shown at nodes. Asterisks indicate that the corresponding branch was found in both the maximum-parsimony and maximum-likelihood trees. Bar, 0.01 substitutions per nucleotide position.

NaCl unless MA or MB was used. The pH range for growth was determined in ZoBell's liquid medium supplemented with 2 % (w/v) NaCl; the medium was adjusted to pH 4–11 (in increments of 1 pH unit) by the addition of HCl and NaOH and sterilized by filtration. Growth temperature (4–50 °C) and growth in an anaerobic chamber (CO₂/H₂/N₂, 10 : 10 : 80; Sheldon Manufacturing) were examined on MA after incubation for up to 1 week. Catalase and oxidase activities were determined using 3 % (v/v) hydrogen peroxide and Kovács' reagent (Kovács, 1956), respectively. Acid production from glucose was tested as described by Yamaguchi & Yokoe (2000). Nitrate reduction was tested in MB containing 0.2 % KNO₃ (Skerman, 1967). Indole production was determined with Kovács' indole reagent on SIM agar (Becton Dickinson). H₂S production was determined on Kligler iron agar (Becton Dickinson). Hydrolysis of CM-cellulose (1 %, w/v), casein (2 %, w/v, skimmed milk), egg yolk (10 %, w/v), starch (0.2 %, w/v) and Tweens 20 and 80 (both 1 %, w/v) was tested as described by Smibert & Krieg (1994) using MA as the basal medium. Hydrolysis of L-tyrosine (0.5 %, w/v) and xylan (1 %, w/v) were tested using MA as the basal medium (Barrow & Feltham, 1993). DNase activity was determined with DNase test agar (Becton Dickinson) supplemented with 2 % (w/v) NaCl. Other biochemical characters and enzyme activities were tested using the API 20NE and API ZYM kits (bioMérieux) and the GN2 MicroPlate (Biolog), prepared according to the manufacturers' instructions except that bacterial strains were suspended in distilled water supplemented with 2 % (w/v) NaCl. Antibiotic resistance was determined by the disc diffusion method using commercial antibiotic-impregnated discs (BBL Becton Dickinson). After 5 days of incubation at 25 °C on MA, the results were interpreted according to the guidelines set forth by the CLSI (2003). Cellular pigments were extracted with methanol from a culture grown on MA and absorption spectra were measured with a spectrophotometer (UV-2100Pro; Amersham).

The two isolates formed circular, convex, smooth and opaque colonies with entire margins, approximately 1.0–2.0 mm in diameter after 7 days at 30 °C (pH 7). They produced orange (KYW48^T) or yellow (KYW147^T) pigments. Physiological, morphological and biochemical characteristics are described in Table 1 and in the species descriptions. The absence of pleomorphism, motility and BChl *a* in strains KYW48^T and KYW147^T indicated that the two strains could not be affiliated to the genus *Erythrobacter* or *Porphyrobacter* (Yoon *et al.*, 2006; Yurkov *et al.*, 1994). No shared intragenomic characters were found that discriminate the genus *Altererythrobacter*, including strains KYW48^T and KYW147^T, from the genus *Erythrobacter*. However, a number of phenotypic characteristics clearly distinguished strains KYW48^T and KYW147^T from other species in the genus *Altererythrobacter* (Ivanova *et al.*, 2005; Kwon *et al.*, 2007; Yoon *et al.*, 2005).

Cells of the isolates and reference strains grown on MA for 2 days at 28 °C were prepared in duplicate and analysed for

fatty acids by GLC according to the instructions of the Microbial Identification System (MIDI, 1999). Polar lipids were isolated by using standard procedures (Komagata & Suzuki, 1987) and separated by TLC according to the method of Minnikin *et al.* (1975). Isoprenoid quinones were isolated by using the method of Minnikin *et al.* (1984) and were analysed by HPLC (Varian) as described by Collins (1985). For G+C content calculations, the DNA sample was prepared in triplicate and the G+C content was determined by the thermal denaturation method (Marmur & Doty, 1962).

The fatty acid profiles of strains KYW48^T and KYW147^T are given in Table 2. The predominant fatty acid of strains KYW48^T and KYW147^T was the monounsaturated fatty acid C_{18:1}ω7c, as in *Altererythrobacter* species. However, significant differences were found between the strains in the composition and content of major fatty acids. The DNA G+C contents of strains KYW48^T and KYW147^T were 63.8 and 67.2 mol%, respectively. Both strains had ubiquinone 10 (Q-10) as a predominant isoprenoid quinone, as for all members of the family *Erythrobacteraceae* (Ramesh Kumar *et al.*, 2008; Kwon *et al.*, 2007).

The polar lipid profile of strain KYW48^T consisted of the major compounds diphosphatidylglycerol (DPG), phosphatidylethanolamine (PE), sphingoglycolipid (SGL) and unknown phospholipid (PL3) and minor amounts of phosphatidylcholine (PC), phosphatidylglycerol (PG), an unknown glycolipid (GL2) and an unknown phospholipid (PL1) (Supplementary Fig. S1, available in IJSEM Online), whereas that of strain KYW147^T consisted of the major compounds DPG, PE, PG, SGL and PC and minor amounts of unknown glycolipid GL1 and unknown phospholipids PL1 and PL2 (Supplementary Fig. S1). *A. epoxidivorans* and *A. indicus* contained an unknown aminolipid as a minor polar lipid (Ramesh Kumar *et al.*, 2008). The absence of this unknown aminolipid in strains KYW147^T and KYW48^T is a striking characteristic that may be useful for differentiation at the species level.

On the basis of the data from this polyphasic study, strains KYW48^T and KYW147^T represent novel species of the genus *Altererythrobacter*, for which the names *Altererythrobacter namhicola* sp. nov. and *Altererythrobacter aestuarii* sp. nov., respectively, are proposed.

Description of *Altererythrobacter namhicola* sp. nov.

Altererythrobacter namhicola (nam.hi'co.la. N.L. n. *namhae* Namhae, the Korean name of the South Sea; L. suff. -cola from L. n. *incola* a dweller, inhabitant; N.L. masc. n. *namhicola* a dweller of the South Sea, referring to the isolation of the type strain).

Cells are non-motile, ovoid rods, 1 µm wide and 1.4 µm long (Supplementary Fig. S2a). Colonies on MA are orange-pigmented, circular, smooth and convex with

Table 1. Characteristics that differentiate strains KYW48^T and KYW147^T from type strains of *Altererythrobacter* species

Strains: 1, KYW48^T; 2, KYW147^T; 3, *A. epoxidivorans* JCM 13815^T; 4, *A. indicus* KACC 13863^T; 5, *A. marensis* MSW-14^T; 6, *A. marinus* H32^T; 7, *A. luteolus* KCTC 12311^T. Data are from this study unless indicated. All strains are rod-shaped, show optimum growth at 30 °C and are positive for hydrolysis of aesculin and Tweens 20 and 80 and activity of catalase, alkaline phosphatase and leucine arylamidase. All strains are negative for nitrate reduction, presence of BChl *a*, production of H₂S and indole, assimilation of *N*-acetylglucosamine, adipate, arabinose, caprate, citrate, gluconate, glucose, mannitol, mannose and phenylacetate, hydrolysis of casein, CM-cellulose, egg yolk and xylan and activity of *N*-acetyl- β -glucosaminidase, arginine dihydrolase, β -glucuronidase, lipase (C14) and α -mannosidase.

Characteristic	1	2	3	4	5	6	7
Colony colour	Orange	Yellow	Yellow	Yellow	Yellow	Yellow	Yellow
Oxidase	+	+	+	–	+	+	+
NaCl concentration for growth (% w/v)							
Range	1–2	0–6	0–6	0–13	0–8	0–8	1–6
Optimum	1	1	2	2	2	2	2
Temperature range for growth (°C)	15–37	10–40	10–42	4–42	10–42	10–42	10–42
Hydrolysis of:							
DNA	–	–	–	+	–	–	–
Gelatin	–	–	+	–	–	–	+
Starch	+	–	–	+	–	–	–
Tyrosine	+	–	+	+	–	–	–
Urea	–	–	+	–	–	–	–
Assimilation of:							
Malate	–	–	–	–	–	+	–
Maltose	–	–	–	–	+	–	–
Enzyme activity (API ZYM)							
Acid phosphatase	+	–	+	+	+	+	+
α -Chymotrypsin	+	–	+	–	+	+	+
Cystine arylamidase	–	–	+	–	–	–	–
Esterase (C4)	–	–	+	+	–	+	+
Esterase lipase (C8)	–	–	+	–	+	+	+
α -Galactosidase	–	–	–	+	–	–	+
β -Galactosidase	–	–	–	+	–	–	+
α -Glucosidase	–	–	–	–	+	–	+
β -Glucosidase	–	+	–	+	–	–	–
Naphthol-AS-BI-phosphohydrolase	+	–	+	+	–	+	+
Trypsin	+	+	+	–	+	+	+
Valine arylamidase	+	–	+	+	+	+	–
DNA G + C content (mol%)	63.8	67.2	54.5 ^{a*}	66.8 ^b	63.1 ^c	66.5 ^d	60.3 ^e

*Data from: *a*, Kwon *et al.* (2007); *b*, Ramesh Kumar *et al.* (2008); *c*, Seo & Lee (2010); *d*, Lai *et al.* (2009); *e*, Yoon *et al.* (2005).

entire margins, approximately 1.0–2.0 mm in diameter after 7 days at 30 °C (pH 7). Growth occurs at 15–37 °C (optimum, 30 °C) and at pH 5–11 (optimum, pH 6–7). Growth occurs in 1–2% (w/v) NaCl. Does not contain BChl *a* as a photosynthetic pigment. Methanol-soluble pigment is characterized by an absorption maximum at 460 nm. Oxidase- and catalase-positive. Negative for acid production from D-glucose and maltose, production of indole and H₂S, nitrate reduction and assimilation of *N*-acetylglucosamine, adipate, arabinose, caprate, citrate, gluconate, glucose, malate, maltose, mannitol, mannose and phenylacetate. Aesculin, starch, L-tyrosine and Tweens 20 and 80 are degraded, but casein, CM-cellulose, DNA, egg yolk, gelatin, urea and xylan are not. In the API ZYM gallery, acid and alkaline phosphatase, α -chymotrypsin, leucine arylamidase, naphthol-AS-BI-phosphohydrolase,

trypsin and valine arylamidase activities are present, but *N*-acetyl- β -glucosaminidase, esterase (C4), esterase lipase (C8), cystine arylamidase, α -fucosidase, α - and β -galactosidase, α - and β -glucosidase, β -glucuronidase, lipase (C14) and α -mannosidase activities are absent. In the GN2 microplate (Biolog), acetic acid, γ -aminobutyric acid, DL-carnitine, α -cyclodextrin, dextrin, glycyl L-aspartic acid, glucose 1-phosphate, glucose 6-phosphate, DL- α -glycerol phosphate, glycyl L-glutamic acid, β -hydroxybutyric acid, succinic acid, succinamic acid, L-phenylalanine, L-alanine (weak), L-alaninamide (weak), L-alanyl glycine (weak), α -ketoglutaric acid (weak), phenylethylamine (weak), L-proline (weak), L-pyroglutamic acid (weak) and D-serine (weak) are utilized. The remaining substrates of the Biolog GN2 system are not utilized (Supplementary Table S1). Cells are sensitive to (μ g per disc, unless indicated)

Table 2. Cellular fatty acid contents of strains KYW48^T and KYW147^T and type strains of *Altererythrobacter* species

Strains: 1, KYW48^T; 2, KYW147^T; 3, *A. epoxidivorans* JCM 13815^T; 4, *A. indicus* KACC 13863^T; 5, *A. marensis* MSW-14^T; 6, *A. marinus* H32^T; 7, *A. luteolus* KCTC 12311^T. Data were obtained in this study using cells grown on MA for 3 days at 30 °C. Values are percentages of total fatty acids; –, not present.

Fatty acid	1	2	3	4	5	6	7
Straight-chain							
C _{15:0}	3.2	—	—	—	0.8	—	—
C _{16:0}	5.8	14.6	4.9	7.0	9.0	5.3	4.7
C _{18:0}	—	—	—	0.5	—	—	—
Unsaturated							
C _{16:1} ω5c	—	—	3.2	—	1.9	1.1	3.1
C _{17:1} ω6c	19.9	2.9	2.1	5.4	3.8	5.0	1.8
C _{17:1} ω8c	2.1	—	—	1.2	—	0.7	—
C _{18:1} ω5c	—	—	1.2	1.0	—	1.9	1.1
C _{18:1} ω7c	35.2	36.1	42.6	63.6	40.4	48.8	41.7
C _{18:1} ω9c	—	7.9	—	—	—	—	—
11-Methyl C _{18:1} ω7c	—	11.0	6.0	—	18.1	23.7	5.0
Cyclopropane acids							
C _{19:0} cyclo ω8c	—	—	—	—	—	0.7	—
Hydroxy							
C _{14:0} 2-OH	7.5	—	3.7	13.8	5.7	3.2	3.9
C _{15:0} 2-OH	3.5	—	—	1.2	—	—	—
C _{16:0} 2-OH	—	9.0	2.1	0.8	3.0	1.8	2.1
C _{17:0} 3-OH	—	—	3.2	4.5	5.4	2.7	5.3
C _{16:1} 2-OH	—	—	1.2	—	—	—	1.2
Summed feature 3*	22.7	18.4	29.8	1.1	12.7	4.6	29.1

*Summed features are groups of two or three fatty acids that cannot be separated by GLC with the Microbial Identification System. Summed feature 3 consists of C_{16:1}ω7c and/or iso-C_{15:0} 2-OH.

ampicillin (10), chloramphenicol (30), erythromycin (15), penicillin (10 IU), tetracycline (30) and vancomycin (30), but resistant to amikacin (30), gentamicin (10), kanamycin (30), nalidixic acid (30), polymyxin B (300 IU) and streptomycin (10). DPG, PE, SGL and unknown phospholipid PL3 are the major polar lipids (Supplementary Fig. S1). The predominant whole-cell fatty acids (>5%) are C_{18:1}ω7c, summed feature 3 (iso-C_{15:0} 2-OH and/or C_{16:1}ω7c), C_{17:1}ω6c, C_{14:0} 2-OH and C_{16:0}. The predominant isoprenoid quinone is Q-10. The DNA G+C content of the type strain is 63.8 mol%.

The type strain, KYW48^T (=KCTC 22736^T =JCM 16345^T), was isolated from a seawater sample collected from the South Sea, Republic of Korea.

Description of *Altererythrobacter aestuarii* sp. nov.

Altererythrobacter aestuarii (aes.tu.a'i.i. L. gen. n. *aestuarii* of a tidal flat, from where the type strain was isolated).

Cells are non-motile rods, 1 µm wide and 3.5–5.7 µm long (Supplementary Fig. S2b). Colonies on MA are yellow-pigmented, circular, smooth and convex with entire margins, approximately 1.0–2.0 mm in diameter after 7 days at 30 °C (pH 7). Growth occurs at 10–40 °C

(optimum, 30 °C) and at pH 5–11 (optimum, pH 6–8). Growth occurs in 0–6% (w/v) NaCl (optimum 1–2%). Does not contain BChl *a* as a photosynthetic pigment. Methanol-soluble pigment is characterized by absorption maxima at 447 and 475 nm. Oxidase- and catalase-positive. Negative for acid production from D-glucose and maltose, production of indole and H₂S, nitrate reduction and assimilation of N-acetylglucosamine, adipate, arabinose, caprate, citrate, gluconate, glucose, malate, maltose, mannitol, mannose and phenylacetate. Aesculin and Tweens 20 and 80 are degraded, but casein, CM-cellulose, DNA, egg yolk, gelatin, starch, L-tyrosine, urea and xylan are not. In the API ZYM gallery, alkaline phosphatase, β-glucosidase, leucine arylamidase and trypsin activities are present, but N-acetyl-β-glucosaminidase, acid phosphatase, α-chymotrypsin, cystine arylamidase, esterase (C4), esterase lipase (C8), α-fucosidase, α- and β-galactosidase, α-glucosidase, β-glucuronidase, α-mannosidase, naphthol-AS-BI-phosphohydrolase and valine arylamidase activities are absent. In the GN2 microplate (Biolog), dextrin, formic acid, pyruvic acid methyl ester, β-hydroxybutyric acid (weak), α-D-glucose (weak), DL-lactic acid (weak) and succinic acid monomethyl ester (weak) are utilized. The remaining substrates of the Biolog GN2 system are not utilized (Supplementary Table S1). Cells are sensitive to (µg per disc, unless indicated) amikacin (30), ampicillin

(10), chloramphenicol (30), erythromycin (15), gentamicin (10), kanamycin (30), penicillin (10 IU), streptomycin (10) and vancomycin (30), but resistant to nalidixic acid (30), polymyxin B (300 IU) and tetracycline (30). DPG, PE, PG, SGL and PC are the major polar lipids (Supplementary Fig. S1). The predominant whole-cell fatty acids (>5%) are C_{18:1}ω7c, summed feature 3 (iso-C_{15:0} 2-OH and/or C_{16:1}ω7c), C_{16:0}, 11-methyl C_{18:1}ω7c, C_{16:0} 2-OH and C_{18:1}ω9c. The predominant isoprenoid quinone is Q-10. The DNA G+C content of the type strain is 67.2 mol%.

The type strain, KYW147^T (=KCTC 22735^T =JCM 16339^T), was isolated from a seawater sample collected from the South Sea, Republic of Korea.

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