Algoriphagus locisalis sp. nov., isolated from a marine solar saltern

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Two Gram-negative, rod-shaped, non-motile bacterial strains, MSS-170^T and MSS-171, were isolated from sea water of a marine solar saltern of the Yellow Sea, Korea, and characterized by using a polyphasic taxonomic approach. The two isolates grew optimally at 30 °C and in the presence of 2 % (w/v) NaCl. They were characterized chemotaxonomically as having MK-7 as the predominant menaquinone and major amounts of fatty acids iso-C_{15:0} and C_{16:1}ω7c and/or iso-C_{15:0} 2-OH. The DNA G + C content of each of the two strains was 42 mol%. Phylogenetic analyses based on 16S rRNA gene sequences showed that the two strains fall within the evolutionary radiation enclosed by the genus *Algoriphagus*. Strains MSS-170^T and MSS-171 had identical 16S rRNA gene sequences and exhibited a mean DNA–DNA relatedness level of 93 %. The two strains exhibited 16S rRNA gene sequence similarity levels of 96.4–98.9 % with respect to the type strains of recognized *Algoriphagus* species. DNA–DNA relatedness levels between the two strains and the type strains of six *Algoriphagus* species were less than 35 %. On the basis of phenotypic data and phylogenetic and genetic distinctiveness, strains MSS-170^T and MSS-171 were classified in the genus *Algoriphagus* as members of a novel species, for which the name *Algoriphagus locisalis* sp. nov. is proposed. The type strain is MSS-170^T (=KCTC 12310^T = JCM 12597^T).

The genus *Algoriphagus* was first described by Bowman *et al.* (2003). At present, the genus comprises seven species with validly published names: *Algoriphagus ratkowskyi* (Bowman *et al.*, 2003), *A. aquimarinus*, *A. chordae* and *A. winogradskyi* (Nedashkovskaya *et al.*, 2004), *A. halophilus* (Yi & Chun, 2004; Nedashkovskaya *et al.*, 2004), *A. antarcticus* (Van Trappen *et al.*, 2004) and *A. yeomjeoni* (Yoon *et al.*, 2005). In the study, we report on the taxonomic characterization of two slightly halophilic, orange-pigmented, *Algoriphagus*-like bacterial strains, MSS-170^T and MSS-171, which were isolated from sea water of a marine solar saltern of the Yellow Sea in Korea.

Sea water collected from a marine solar saltern of the Yellow Sea, Korea, was used as the source for the isolation of bacterial strains. Strains MSS-170^T and MSS-171 were isolated by using the standard dilution-plating technique on marine agar 2216 (MA; Difco) at 25 °C. *A. ratkowskyi* CIP 107452^T was obtained from the Collection de l'Institut Pasteur (Paris, France). *A. aquimarinus* LMG 21971^T, *A. chordae* LMG 21970^T, *A. winogradskyi* LMG 21969^T and *A. antarcticus* LMG 21980^T were obtained from the Laboratorium voor Microbiologie, Universiteit Gent

(Ghent, Belgium). *A. yeomjeoni* MSS-160^T was obtained from the study of Yoon *et al.* (2005). The morphological and physiological characteristics of strains MSS-170^T and MSS-171 were investigated on MA at 30 °C. Cell morphology was examined by using light microscopy (E600; Nikon) and transmission electron microscopy. The presence of flagella was investigated by using transmission electron microscopy with cells from exponentially growing cultures. Gliding motility was determined as described by Bowman (2000). The Gram-reaction was determined by using the bioMérieux Gram Stain kit according to the manufacturer's instructions. Growth at various temperatures (4–40 °C) was measured on MA. The pH range for growth was determined in marine broth 2216 (Difco) that had been adjusted to various pH values (initial pH 4.5, rising to pH 10.5 at intervals of 0.5 pH units). The pH was adjusted prior to sterilization to various levels by the addition of Na₂CO₃. Growth under anaerobic conditions was determined after incubation in a Forma anaerobic chamber on MA and MA supplemented with nitrate, both of which had been prepared anaerobically using nitrogen. Catalase and oxidase activities and hydrolysis of casein and starch were determined as described by Cowan & Steel (1965). Hydrolysis of hypoxanthine, tyrosine and xanthine was tested on MA using the substrate concentrations described by Cowan & Steel (1965). Hydrolysis of aesculin, gelatin, urea and Tweens 20, 40, 60 and 80 and nitrate reduction

The GenBank/EMBL/DDBJ accession numbers for the 16S rRNA gene sequences of strains MSS-170^T and MSS-171 are AY835922 and AY835923, respectively.

were studied as described previously (Lanyi, 1987) but with the modification that artificial sea water was used for preparation of the media. The artificial sea water contained the following (per litre distilled water): 23.6 g NaCl, 0.64 g KCl, 4.53 g $\text{MgCl}_2 \cdot 6\text{H}_2\text{O}$, 5.94 g $\text{MgSO}_4 \cdot 7\text{H}_2\text{O}$ and 1.3 g $\text{CaCl}_2 \cdot 2\text{H}_2\text{O}$ (Bruns *et al.*, 2001). H_2S production was tested as described by Bruns *et al.* (2001). The presence of flexirubin pigment was investigated as described by Reichenbach (1992). Susceptibility to antibiotics was tested on MA plates by using discs containing the following

antibiotics: ampicillin (10 µg), benzylpenicillin (10 µg), carbenicillin (100 µg), gentamicin (10 µg), kanamycin (30 µg), lincomycin (15 µg), neomycin (30 µg), oleandomycin (15 µg), polymyxin B (300 U), streptomycin (10 µg), chloramphenicol (100 µg) or tetracycline (30 µg). Acid production from carbohydrates was determined as described by Leifson (1963). Utilization of various substrates for growth was determined as described by Yurkov *et al.* (1994). The morphological, cultural, physiological and biochemical characteristics of strains MSS-170^T and

Table 1. Differential phenotypic characteristics of *Algoriphagus* species

Species: 1, *A. locisalis* sp. nov.; 2, *A. winogradskyi*; 3, *A. yeomjeoni*; 4, *A. aquimarinus*; 5, *A. ratkowskyi*; 6, *A. chordae*; 7, *A. antarcticus*; 8, *A. halophilus*. Data are from Bowman *et al.* (2003), Yi & Chun (2004), Nedashkovskaya *et al.* (2004), Van Trappen *et al.* (2004) and Yoon *et al.* (2005). Symbols: +, positive; −, negative; w, weakly positive; v, variable; ND, not determined. Data in parentheses are for the type strain. All species are Gram-negative and rod-shaped and positive for catalase and oxidase. All species are negative for gliding motility, flexirubin pigment production, H_2S and indole production, utilization of citrate, and susceptibility to ampicillin, benzylpenicillin, gentamicin, kanamycin, neomycin, polymyxin B and streptomycin.

Characteristic	1	2	3	4	5	6	7	8
Nitrate reduction	−	+	−	−	−	−	−	−
NaCl requirement for growth	+	−	+	−	+	+	ND	−
Optimal temp. for growth (°C)	30	25–28	25–30	23–25	16–19	23–25	20	35
Growth in/at:								
10 % NaCl	−	−	−	+	−	+	−	−
37 °C	−	+	−	−	−	−	−	+
Hydrolysis of:								
Agar	−	+	−	+	−	+	−	−
Casein	−	−	+	+	v	−	−	−
Gelatin	−	+	v (+)	+	−	−	−	+
Starch	−	+	−	−	v	−	−	+
Tween 80	+	−	+	+	−	−	ND	+
Acid production from:								
L-Arabinose	+	−	−	−	+	−	−	−
D-Cellobiose	+	+	+	+	+	+	ND	−
D-Galactose	+	+	+	−	+	+	ND	−
D-Glucose	+	+	+	+	+	+	−	+
Lactose	+	+	+	+	−	+	ND	−
Maltose	+	+	+	−	+	+	ND	+
D-Melibiose	+	+	+	+	+	+	−	−
L-Rhamnose	+	+	+	+	+	+	−	−
Sucrose	+	+	+	+	−	+	−	+
D-Xylose	+	+	+	+	+	+	ND	+
Utilization of:								
L-Arabinose	−	+	−	+	+	+	−	+
D-Glucose	+	+	+	+	+	+	−	+
D-Mannose	+	+	+	+	+	+	−	+
Malate	−	−	−	−	v	−	−	−
Susceptibility to:								
Carbenicillin	−	v	+	+	+	−	ND	+
Lincomycin	+	v	+	+	+	+	ND	+
Oleandomycin	+	+	+	+	+	−	ND	+
Tetracycline	−	v	−	+	+	−	ND	+
DNA G + C content (mol%)	42	39–42	41	41	35–37	37–40	40–41	37

MSS-171 are shown in Table 1 or are given in the species description (see below). The two strains were similar in most phenotypic characteristics, except for the utilization of D-trehalose and acid production from D-trehalose.

Cell biomass for isoprenoid quinone analysis and for DNA extraction was obtained from cultivation for 2 days in marine broth 2216 at 30 °C. Chromosomal DNA was isolated and purified as described previously (Yoon *et al.*, 1996), with the exception that RNase T1 was applied in combination with RNase A to minimize the contamination with RNA. The 16S rRNA gene was amplified by a PCR using two universal primers as described previously (Yoon *et al.*, 1998). Sequencing of the 16S rRNA gene and phylogenetic analysis were performed as described previously (Yoon *et al.*, 2003). Isoprenoid quinones were analysed as described by Komagata & Suzuki (1987), using reversed-phase HPLC. For fatty acid methyl ester analysis, cell mass of each of the two isolates was harvested from agar plates after incubation for 3 days on MA at 30 °C. The fatty acid methyl esters were extracted and prepared according to the standard protocol of the MIDI/Hewlett Packard Microbial Identification System (Sasser, 1990). The DNA G + C content was determined by the method of Tamaoka & Komagata (1984), with the modification that DNA was hydrolysed and the resultant nucleotides were analysed by reversed-phase HPLC. DNA–DNA hybridization was performed fluorometrically by the method of Ezaki *et al.* (1989), using photobiotin-labelled DNA probes and micro-dilution wells. Hybridization was performed with five replications for each sample. The highest and lowest values obtained in each sample were excluded; the means of the remaining three values are quoted as DNA–DNA relatedness values.

The almost-complete 16S rRNA gene sequences of strains MSS-170^T and MSS-171 determined in this study each comprised 1477 nucleotides, representing approximately 96 % of the *Escherichia coli* 16S rRNA gene sequence. The 16S rRNA gene sequences of strains MSS-170^T and MSS-171 were identical. Comparative 16S rRNA gene sequence analyses showed that strains MSS-170^T and MSS-171 are phylogenetically most related to *Algoriphagus* species (Fig. 1). In the phylogenetic tree based on the neighbour-joining algorithm, strains MSS-170^T and MSS-171 fell within the radiation of the cluster comprising *Algoriphagus* species (Fig. 1). Similar tree topologies were found in the trees generated with the maximum-likelihood and maximum-parsimony algorithms (data not shown). Similarity values between the 16S rRNA gene sequences of the two isolates and those of recognized *Algoriphagus* species ranged from 96.4 % (*A. halophilus* IMSNU 14013^T) to 98.9 % (*A. winogradskyi* KMM 3956^T). Sequence similarities to other species included in the phylogenetic analysis were below 94.6 % (Fig. 1).

The chemotaxonomic properties, i.e. predominant menaquinone, fatty acid profiles and DNA G + C content, support the result of the monothetic phylogenetic classification,

Fig. 1. Neighbour-joining phylogenetic tree, based on 16S rRNA gene sequences, showing the positions of strains MSS-170^T and MSS-171 and some other related taxa. Bootstrap values (1000 replications) are shown as percentages at each node only if they are 50 % or greater. Bar, 0.01 substitutions per nucleotide position. *Flavobacterium aquatile* IAM 12316^T was used as the outgroup (not shown).

namely that the two isolates might be members of the genus *Algoriphagus* (Bowman *et al.*, 2003; Nedashkovskaya *et al.*, 2004; Yoon *et al.*, 2005). The predominant isoprenoid quinone detected in strains MSS-170^T and MSS-171 was MK-7, at a peak area ratio of approximately 96 %. The fatty acid profiles of the two isolates were characterized as sharing straight-chain, branched, unsaturated and hydroxy fatty acids in similar amounts; the major fatty acids were iso-C_{15:0} and C_{16:1}ω7c and/or iso-C_{15:0} 2-OH (Table 2). These fatty acid profiles were similar to those of *Algoriphagus* species (Table 2). The DNA G + C contents of strains MSS-170^T and MSS-171 were the same, both being 42 mol%.

Strains MSS-170^T and MSS-171 exhibited a mean level of DNA–DNA relatedness of 93 % when their DNAs were used individually as labelled DNA probes for cross-hybridization, indicating that the two strains are members of the same genomic species. The two strains exhibited DNA–DNA relatedness levels of 9–35 % with respect to the type strains of the six *Algoriphagus* species that showed 16S rRNA gene sequence similarity values of more than 97.0 % with respect to the two strains (the exception being *A. halophilus*; see above). In view of the combined phenotypic, phylogenetic and genetic similarity, strains MSS-170^T and MSS-171 were considered as members of the same species. There were some differences between the two strains and recognized *Algoriphagus* species in terms of phenotypic characteristics (Table 1). The phylogenetic and genetic distinctiveness was sufficient to separate strains MSS-170^T and MSS-171 from other *Algoriphagus* species with validly published names (Wayne *et al.*, 1987; Stackebrandt & Goebel, 1994). Therefore, on the basis of the data presented, strains MSS-170^T and MSS-171 should be placed in the genus *Algoriphagus* as members of a novel species, for which the name *Algoriphagus locisalis* sp. nov. is proposed.

Table 2. Cellular fatty acid compositions (%) of *Algoriphagus* species

Strains: 1, *A. locisalis* sp. nov. MSS-170^T; 2, *A. locisalis* sp. nov. MSS-171; 3, *A. winogradskyi* KMM 3956^T; 4, *A. yeomjeoni* MSS-160^T; 5, *A. aquimarinus* KMM 3958^T; 6, *A. ratkowskyi* LMG 21435^T; 7, *A. chordae* KMM 3957^T; 8, *A. halophilus* LMG 22067^T. Data for reference strains were taken from Nedashkovskaya *et al.* (2004) and Yoon *et al.* (2005). Fatty acids that represented less than 0.5% in all strains are omitted. ND, Not detected.

Fatty acid	1	2	3	4	5	6	7	8
Straight-chain fatty acids								
C _{15:0}	1.5	1.3	1.2	0.6	1.6	1.6	2.5	1.0
C _{16:0}	0.7	0.6	1.0	0.8	1.7	2.9	1.4	ND
Branched fatty acids								
iso-C _{11:0}	0.7	0.8	ND	ND	ND	ND	ND	ND
anteiso-C _{11:0}	1.6	1.6	1.2	ND	0.6	2.1	1.0	1.5
iso-C _{14:0}	0.3	0.3	0.3	1.6	0.7	1.4	0.3	0.6
iso-C _{15:0}	31.2	30.6	36.6	28.6	38.9	30.5	38.1	28.4
iso-C _{15:1} G	0.8	0.8	2.9	ND	0.3	1.1	ND	ND
anteiso-C _{15:0}	0.8	0.7	1.6	1.2	3.2	3.6	1.9	2.8
iso-C _{16:0}	3.5	3.5	3.9	4.8	2.4	3.4	5.8	7.7
iso-C _{16:1} H	1.6	1.4	2.1	1.9	2.4	1.7	1.5	3.5
iso-C _{17:1} ω9c	2.8	2.7	4.0	2.3	5.3	1.5	4.4	9.0
Unsaturated fatty acids								
C _{15:1} ω6c	1.6	1.5	1.3	0.8	2.3	2.1	1.0	1.8
C _{16:1} ω5c	3.7	3.6	3.6	3.3	5.2	5.8	3.6	3.5
C _{17:1} ω6c	1.7	2.0	0.8	1.0	0.7	0.5	1.2	3.4
Hydroxy fatty acids								
iso-C _{15:0} 3-OH	2.7	2.6	2.0	3.0	1.8	2.9	1.6	2.5
C _{16:0} 2-OH	0.8	0.9	ND	1.3	ND	ND	ND	ND
C _{16:0} 3-OH	1.9	1.8	0.8	1.1	0.5	1.9	1.9	0.7
iso-C _{16:0} 3-OH	1.7	1.8	1.9	3.3	1.0	2.8	0.9	3.1
iso-C _{17:0} 3-OH	7.5	8.0	6.4	7.8	5.9	9.2	6.4	5.9
Summed features*								
3	29.0	29.5	24.6	33.7	20.4	22.3	22.2	19.0
4	1.5	1.6	1.6	1.3	1.8	0.9	1.7	2.7

*Summed features represent groups of two or three fatty acids which could not be separated by GLC with the MIDI system. Summed feature 3 contained C_{16:1} ω7c and/or iso-C_{15:0} 2-OH; summed feature 4 contained iso-C_{17:1} I and/or anteiso-C_{17:1} B.

Description of *Algoriphagus locisalis* sp. nov.

Algoriphagus locisalis (lo.ci.sa'lis. L. n. locus place, locality; L. gen. n. salis of salt; N.L. gen. n. locisalis from a place of salt).

Cells are Gram-negative, non-flagellated rods that are 0.4–0.7 × 1.5–3.0 µm in size. Non-motile. Colonies are circular, convex, smooth, glistening, orange-coloured and 1.0–1.8 mm in diameter after 3 days incubation on MA at 30 °C. Optimum growth temperature is 30 °C; growth occurs at 4 and 35 °C, but not at 36 °C. The optimal pH for growth is between pH 7.0 and 8.0; growth is observed at pH 5.5, but not at pH 5.0. Optimal growth occurs in the presence of 2% (w/v) NaCl; growth does not occur in

the presence of >9% (w/v) NaCl. Growth does not occur under anaerobic conditions on MA or MA supplemented with nitrate. Aesculin and Tweens 20, 40 and 60 are hydrolysed. Hypoxanthine, xanthine, tyrosine and urea are not hydrolysed. Susceptible to chloramphenicol. D-Cellobiose, D-fructose, maltose, sucrose and salicin are utilized as carbon and energy sources, but D-galactose, D-xylose, acetate, benzoate, pyruvate, succinate, formate and L-glutamate are not. Utilization of D-trehalose is variable (positive for type strain). Acid is produced from D-mannose and weakly produced from D-fructose and D-raffinose. No acid is produced from D-melezitose, D-ribose, *myo*-inositol, D-mannitol or D-sorbitol. Acid production from D-trehalose is variable (positive for type strain). The predominant menaquinone is MK-7. The major fatty acids are iso-C_{15:0} and C_{16:1} ω7c and/or iso-C_{15:0} 2-OH. The DNA G+C content is 42 mol%. Other phenotypic properties are given in Table 1.

The type strain, MSS-170^T (=KCTC 12310^T=JCM 12597^T), was isolated from sea water from a marine solar saltern of the Yellow Sea in Korea.

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