Maritimibacter lacisalsi sp. nov., isolated from a salt lake, and emended description of the genus Maritimibacter Lee et al. 2007

Zhi-Ping Zhong,1,2 Ying Liu,1 Yu-Guang Zhou,3 Hong-Can Liu,3 Fang Wang4 and Zhi-Pei Liu1

Correspondence
Zhi-Pei Liu
liuzhp@sun.im.ac.cn

1State Key Laboratory of Microbial Resources, Institute of Microbiology, Chinese Academy of Sciences, Beijing 100101, PR China
2University of Chinese Academy of Sciences, Beijing 100049, PR China
3China General Microbiological Culture Collection Center, Institute of Microbiology, Chinese Academy of Sciences, Beijing 100101, PR China
4State Key Laboratory of Simulation and Regulation of Water Cycle in River Basin, China Institute of Water Resources and Hydropower Research, Beijing 100089, PR China

A Gram-staining-negative, non-motile, strictly aerobic bacterium, strain X12M-4T, was isolated from Xiaochaidan Lake, a salt lake (salinity 9.9 %, w/w) in Qaidam basin, Qinghai Province, China. Its taxonomic position was determined by using a polyphasic approach. Strain X12M-4T was catalase- and oxidase-positive. Cells were rod-shaped, 0.5–0.8 μm wide and 1.1–1.6 μm long. Growth was observed in the presence of 0–11.0 % (w/v) NaCl (optimum, 5.0–6.0 %) and at 15–40 °C (optimum, 25 °C) and pH 6.5–9.5 (optimum, pH 7.0). No growth occurred at 10 °C or 45 °C. Strain X12M-4T contained C18 : 1ω7c, C19 : 0 cyclo ω8c and C16 : 0 as the major fatty acids (>10.0 %). The predominant respiratory quinone was Q-10. The major polar lipids were phosphatidylcholine, phosphatidylglycerol, diphosphatidylglycerol, an unknown aminolipid and an unidentified lipid. The DNA G+C content was 65.7 mol% (determined using Tm). Strain X12M-4T showed highest 16S rRNA gene sequence similarities to Maritimibacter alkaliphilus HTCC2654T (96.7 %), Roseibacterium elongatum DSM 19469T (96.4 %), Tropicimonas aquimaris DPG-21T (95.6 %), 'Roseibacterium beibuensis' JLT1202r (95.6 %) and Tropicimonas sediminicola M97T (95.5 %) to others. Phylogenetic trees based on 16S rRNA gene sequences indicated that strain X12M-4T formed a robust cluster with M. alkaliphilus. On the basis of the data, it is concluded that strain X12M-4T represents a novel species of the genus Maritimibacter, for which the name Maritimibacter lacisalsi sp. nov. is proposed. The type strain is X12M-4T (=CGMCC 1.12922T =JCM 30555T). To accommodate the novel species, the description of the genus Maritimibacter was emended.

Members of the family Rhodobacteraceae belonging to the class Alphaproteobacteria (Garrity et al., 2005, 2006) are widely found in aquatic environments (Buchan et al., 2005). In recent years, the number of genera within the family Rhodobacteraceae has increased steadily through descriptions of novel genera, such as Sinorhodobacter (Yang et al., 2013), Paenirhodobacter (Wang et al., 2014), Cribrirhabitans (Chen et al., 2014) and Youngimonas (Hameed et al., 2014). The genus Maritimibacter of the family Rhodobacteraceae was established by Lee et al. (2007) with Maritimibacter alkaliphilus as the type species, which was isolated from the western Sargasso Sea and characterized as being non-motile, rod-shaped and aerobic, containing C16 : 0 2-OH, C18 : 1ω7c 11-methyl and C18 : 0ω7c as the major fatty acids and phosphatidylcholine, phosphatidylethanolamine and phosphatidylglycerol as the major polar lipids. At the time of writing, M. alkaliphilus was the only species in this genus. During a study on the microbial diversity of Xiaochaidan Lake in Qinghai Province, China, strain X12M-4T was isolated from Xiaochaidan Lake, a salt lake (salinity 9.9 %, w/w) in Qaidam basin, Qinghai Province, China. Its taxonomic position was determined by using a polyphasic approach. Strain X12M-4T was catalase- and oxidase-positive. Cells were rod-shaped, 0.5–0.8 μm wide and 1.1–1.6 μm long. Growth was observed in the presence of 0–11.0 % (w/v) NaCl (optimum, 5.0–6.0 %) and at 15–40 °C (optimum, 25 °C) and pH 6.5–9.5 (optimum, pH 7.0). No growth occurred at 10 °C or 45 °C. Strain X12M-4T contained C18 : 1ω7c, C19 : 0 cyclo ω8c and C16 : 0 as the major fatty acids (>10.0 %). The predominant respiratory quinone was Q-10. The major polar lipids were phosphatidylcholine, phosphatidylglycerol, diphosphatidylglycerol, an unknown aminolipid and an unidentified lipid. The DNA G+C content was 65.7 mol% (determined using Tm). Strain X12M-4T showed highest 16S rRNA gene sequence similarities to Maritimibacter alkaliphilus HTCC2654T (96.7 %), Roseibacterium elongatum DSM 19469T (96.4 %), Tropicimonas aquimaris DPG-21T (95.6 %), 'Roseibacterium beibuensis' JLT1202r (95.6 %) and Tropicimonas sediminicola M97T (95.5 %) to others. Phylogenetic trees based on 16S rRNA gene sequences indicated that strain X12M-4T formed a robust cluster with M. alkaliphilus. On the basis of the data, it is concluded that strain X12M-4T represents a novel species of the genus Maritimibacter, for which the name Maritimibacter lacisalsi sp. nov. is proposed. The type strain is X12M-4T (=CGMCC 1.12922T =JCM 30555T). To accommodate the novel species, the description of the genus Maritimibacter was emended.

Abbreviations: DPG, diphosphatidylglycerol; PC, phosphatidylcholine; PG, phosphatidylglycerol.

The GenBank/EMBL/DDBJ accession number for the 16S rRNA gene sequence of strain X12M-4T is KJ782425.

Three supplementary figures are available with the online Supplementary Material.
affiliated with the genus *Maritimibacter* was obtained. In this study, its taxonomic position was investigated through a polyphasic approach.

A water sample was collected from Xiaochaidan Lake [GPS location 37° 28’ 53” N 95° 30’ 19” E; depth 9.1 m, salinity 9.9 % (w/v), dissolved oxygen (DO) 3.1 mg L⁻¹, pH 8.2 and temperature 12.2 °C] at 1.0 m beneath the surface. Strain X12M-4ᵀ was isolated by a standard dilution plating technique on marine agar 2216 (MA; Difco) at 30 °C. Strain X12M-4ᵀ could also grow well in marine broth 2216 (MB; Difco); but not in trypticase soy broth (TSB; Bacto) or Luria–Bertani (LB) broth. The strain was preserved in MB supplemented with 20 % (v/v) glycerol at −80 °C. All the experiments were performed in triplicate and parallel on *M. alkaliphilus* CGMCC 1.7698ᵀ, except for the morphological studies, growth tests and DNA G+C content analyses. Cells for all analyses were obtained after cultivation on MA at 30 °C for 3 days unless otherwise stated.

Cell morphology and flagellation were observed using an optical microscope (BH-2, Olympus) and a transmission electron microscope (H-600, Hitachi) after negative staining with 1 % (w/v) phosphotungstic acid. The Gram reaction was performed according to the protocol of Dong & Cai (2001). Growth at 5, 10, 15, 20, 25, 30, 35, 40 and 45 °C was measured in MB. Growth at pH 6.0–10.0 (at intervals of 0.5 pH units) was determined in MB at 30 °C using two different buffers (final concentration, 50 mM): sodium phosphate buffer (for pH 6.0–8.0) and Tris/HCl buffer (for pH 8.0–10.0). Tolerance to NaCl was examined in modified marine broth 2216 with final NaCl concentration of 0–12.0 % (w/v, at intervals of 0.5 %), as described previously (Zhong et al., 2014).

The requirement for oxygen was tested in an anaerobic system (Anaero-Gen). Production of hydrogen sulphide was assessed with lead acetate paper. Catalase and oxidase activities, nitrate reduction, D-glucose fermentation and hydrolysis of casein, starch and Tweens 20, 40, 60 and 80 were determined according to the protocol of Dong & Cai (2001). Utilization of carbon substrates (0.5 %, w/v) was tested according to the method of Dong & Cai (2001) with artificial seawater instead of distilled water; 0.01 % (w/v) yeast extract was added as a supplement. The artificial seawater contained (per litre distilled water): 24.0 g NaCl, 5.1 g MgCl₂, 4 g Na₂SO₄, 1.1 g CaCl₂, 0.7 g KCl, 0.2 g NaHCO₃, 0.1 g KBr, 0.027 g H₂BO₃, 0.024 g SrCl₂ and 0.003 g NaF. Susceptibility to antibiotics was determined by the disc diffusion method using filter-paper discs (Beijing Pharmaceutical Company) which contained various antibiotics as specified in Table 1. Growth-inhibition effects were observed and estimated according to the protocol of Okhah & Schlegel (1983) after incubation on MA for 4 days at 30 °C. Additionally, API ZYM strips (bioMérieux) were used for tests of enzyme activities according to the manufacturer’s instructions.

### Table 1. Characteristics of strain X12M-4ᵀ and *M. alkaliphilus* CGMCC 1.7698ᵀ

<table>
<thead>
<tr>
<th>Characteristic</th>
<th>1</th>
<th>2</th>
<th>3</th>
</tr>
</thead>
<tbody>
<tr>
<td>Growth in NaCl (%, w/v)</td>
<td>0–11.0</td>
<td>0.5–7.5*</td>
<td>10.0</td>
</tr>
<tr>
<td>Optimum</td>
<td>5.0–6.0</td>
<td>2.5–3.0*</td>
<td>12.0</td>
</tr>
<tr>
<td>Growth pH</td>
<td>6.5–9.5</td>
<td>4.0–12.0*</td>
<td></td>
</tr>
<tr>
<td>Optimum</td>
<td>7.0</td>
<td>10.0</td>
<td></td>
</tr>
<tr>
<td>Growth at:</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>15 °C</td>
<td>+</td>
<td>−</td>
<td>+</td>
</tr>
<tr>
<td>40 °C</td>
<td>+</td>
<td>−</td>
<td>+</td>
</tr>
<tr>
<td>Temperature for optimal growth (°C)</td>
<td>25</td>
<td>30*</td>
<td></td>
</tr>
<tr>
<td>Nitrate reduction</td>
<td>+</td>
<td>−</td>
<td>+</td>
</tr>
<tr>
<td>Hydrolysis of:</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Urea, Tweens 40, 80</td>
<td>−</td>
<td>+</td>
<td></td>
</tr>
<tr>
<td>Enzyme activities (API ZYM)</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>α-Glucosidase, β-glucosidase</td>
<td>+</td>
<td>−</td>
<td></td>
</tr>
<tr>
<td>Assimilation of:</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>α-D-Fructose, glycogen, D-tagatose</td>
<td>−</td>
<td>+</td>
<td></td>
</tr>
<tr>
<td>α-D-Mannose, L-rhamnose</td>
<td>−</td>
<td>+ (−)*</td>
<td></td>
</tr>
<tr>
<td>Cellobiose, L-fucose</td>
<td>+</td>
<td>−</td>
<td></td>
</tr>
<tr>
<td>Resistance to antibiotics (µg per disc):</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Erythromycin (15), streptomycin (10)</td>
<td>+</td>
<td>−</td>
<td></td>
</tr>
<tr>
<td>DNA G+C content (mol%)</td>
<td>65.7</td>
<td>64.1</td>
<td></td>
</tr>
</tbody>
</table>

*Data from Lee et al. (2007).*

Colonies of strain X12M-4ᵀ were 0.4–0.8 mm in diameter, circular, smooth and slightly beige after cultivation on MA (pH 7.5) at 30 °C for 4 days. Cells of strain X12M-4ᵀ were Gram-staining-negative, non-motile, rod-shaped,
0.5–0.8 μm wide and 1.1–1.6 μm long (Fig. S1 available in the online Supplementary Material). The enzyme activities, detected using API ZYM strips, and utilization of carbon sources by strain X12M-4T and M. alkaliphilus CGMCC 1.7698T are specified in Table 1. More morphological, physiological and biochemical characteristics of strain X12M-4T are given in Table 1 as well as in the species description. Almost all the results obtained in this study for M. alkaliphilus CGMCC 1.7698T were consistent with those described by Lee et al. (2007), except for the assimilation of D-mannose and L-rhamnose, indicating that these properties may be variable for M. alkaliphilus.

Biomass for chemotaxonomic analyses was obtained by cultivating the strains on MA at 30 °C for 3 days to late exponential phase. Genomic DNA was extracted by using a bacterial genomic kit (D3350-1, Omega Bio-Tek). The DNA base composition was determined by the thermal denaturation method (Marmur & Doty, 1962), with genomic DNA of Escherichia coli K-12 as a reference. Isoprenoid quinones were extracted from freeze-dried biomass and purified according to the protocol of Collins (1985) and analysed by HPLC (Wu et al., 1989), with the extracts from M. alkaliphilus CGMCC 1.7698T as references. Cellular fatty acids were analysed using the standard MIDI Sherlock Microbial Identification System (version 6.0) and peaks were identified on an Agilent 6890N Network GC system using the MBA6 peak-naming table. Polar lipids of strain X12M-4T and M. alkaliphilus CGMCC 1.7698T were extracted using a chloroform/methanol system and identified using two-dimensional TLC, as described by Kates (1986). Merck silica gel 60 F254 aluminium-backed thin-layer plates were used in TLC analysis.

The DNA G+C content of strain X12M-4T was 65.7 mol% (determined from Tm). The major respiratory quinone was Q-10, consistent with the description of the genus Maritimibacter (Lee et al., 2007). The fatty acid profiles of strain X12M-4T and M. alkaliphilus CGMCC 1.7698T are shown in Table 2. The cellular fatty acid profile obtained in this study for M. alkaliphilus CGMCC 1.7698T was similar to that in the original description (Lee et al., 2007) and reported in other publications (Kim et al., 2010; Lee et al., 2007; Yoon et al., 2009) in terms of major fatty acids, although there were differences in proportions, which might be due to the different culture conditions. Strain X12M-4T had a fatty acid profile similar to that of M. alkaliphilus CGMCC 1.7698T under the same cultivation conditions (Table 2). The major fatty acids (>10.0 %) of strain X12M-4T were C18:1 (56.9 %), C19:0 cyclo (10.5 %) and C16:0 (10.2 %). Strain X12M-4T could be differentiated from M. alkaliphilus CGMCC 1.7698T as it contained a large amount of C18:2 (4.5 %), C19:0 cyclo (10.5 %) and C17:1ω8c (3.5 %), which were detected as minor components or not detected in M. alkaliphilus CGMCC 1.7698T. C16:1ω2-OH is a major fatty acid of M. alkaliphilus CGMCC 1.7698T, but a minor fatty acid of strain X12M-4T. In addition, strain X12M-4T could be further distinguished from M. alkaliphilus CGMCC 1.7698T by presence and absence of some minor fatty acids (Table 2). The polar lipid profiles obtained in this study for strain X12M-4T and M. alkaliphilus CGMCC 1.7698T are shown in Fig. S2. Strain X12M-4T exhibited a complex polar lipid profile consisting of phosphatidylcholine (PC), phosphatidylglycerol (PG), diphosphatidylglycerol (DPG), an unknown aminolipid, an unidentified phospholipid and five uncharacterized lipids. The polar lipid profile obtained in this study for M. alkaliphilus CGMCC 1.7698T was similar to that described by Lee et al. (2007), except that a small amount of DPG and an unknown aminolipid were detected. Strain X12M-4T could be distinguished from M. alkaliphilus CGMCC 1.7698T by the absence of phosphatidylethanolamine and an unknown phospholipid (PL2) and the presence of an unidentified lipid (L5). Furthermore, an uncharacterized lipid (L1) was detected in M. alkaliphilus CGMCC 1.7698T as a significant component, but only a small amount of L1 was found in strain X12M-4T. This also made these two strains definitely different.

The 16S rRNA gene was amplified with primers 27F and 1492R (Weisburg et al., 1991) and cloned into the pEASY-T1 vector and sequenced by Sinogenomax (Beijing, China) with primers M13f and M13r. The 16S rRNA gene sequence from this study for M. alkaliphilus CGMCC 1.7698T is specified in Table 1. More morphological, physiological and biochemical characteristics of strain X12M-4T are given in Table 1 as well as in the species description. Almost all the results obtained in this study for M. alkaliphilus CGMCC 1.7698T were consistent with those described by Lee et al. (2007), except for the assimilation of D-mannose and L-rhamnose, indicating that these properties may be variable for M. alkaliphilus.

### Table 2. Cellular fatty acid contents (percentages) of strain X12M-4T and M. alkaliphilus CGMCC 1.7698T

<table>
<thead>
<tr>
<th>Fatty acid</th>
<th>1</th>
<th>2</th>
</tr>
</thead>
<tbody>
<tr>
<td>C10:0</td>
<td>–</td>
<td>TR</td>
</tr>
<tr>
<td>C12:0, C14:0</td>
<td>TR</td>
<td>TR</td>
</tr>
<tr>
<td>C16:0</td>
<td>10.2</td>
<td>11.5</td>
</tr>
<tr>
<td>C17:0</td>
<td>TR</td>
<td>1.4</td>
</tr>
<tr>
<td>C18:0</td>
<td>4.5</td>
<td>TR</td>
</tr>
<tr>
<td>C10:0 3-OH, C15:0 2-OH</td>
<td>–</td>
<td>TR</td>
</tr>
<tr>
<td>C16:0 2-OH</td>
<td>TR</td>
<td>10.9</td>
</tr>
<tr>
<td>C16:1 2-OH, C17:0 2-OH</td>
<td>–</td>
<td>TR</td>
</tr>
<tr>
<td>C18:1 2-OH</td>
<td>1.0</td>
<td>4.1</td>
</tr>
<tr>
<td>C18:1 3-OH</td>
<td>–</td>
<td>TR</td>
</tr>
<tr>
<td>C19:0 cyclo 8c</td>
<td>10.5</td>
<td>TR</td>
</tr>
<tr>
<td>C19:0 11-methyl</td>
<td>–</td>
<td>TR</td>
</tr>
<tr>
<td>C18:1 0:07c 11-methyl</td>
<td>7.9</td>
<td>13.1</td>
</tr>
<tr>
<td>C17:1 0:08c</td>
<td>3.5</td>
<td>–</td>
</tr>
<tr>
<td>C18:1 0:07c</td>
<td>56.9</td>
<td>53.7</td>
</tr>
<tr>
<td>C20:1 0:07c</td>
<td>1.5</td>
<td>–</td>
</tr>
<tr>
<td>C20:1 0:06,9c</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>Summed feature 3*</td>
<td>1.7</td>
<td>1.5</td>
</tr>
</tbody>
</table>

*Summed features represent groups of two or three fatty acids that could not be separated by GLC with the MIDI system (version 6.0). Summed feature 3 contains C16:1ω7c and/or C16:1ω6c.
Maritimibacter lacisalsi sp. nov.

In addition to phylogenetic and biochemical data, strain X12M-4T also showed some important properties, which are consistent with those reported for members of the genus Maritimibacter, including being strictly aerobic, oxidase- and catalase-positive, beige in colour, unable to produce indole and unable to hydrolyse L-arginine and gelatin, and also with respect to some enzyme activities detected by API ZYM. Nevertheless, strain X12M-4T could be differentiated from M. alkaliphilus by the following traits: reduction of nitrate, non-requirement of NaCl for growth, inability to hydrolyse urea, Tweens 40 and 80, possessing x-glucosidase and β-glucosidase activities, assimilation of some carbon substrates and DNA G+C content (Table 1). Combining the above phenotypic, chemotaxonomic and genotypic results, it is concluded that strain X12M-4T represents a novel species of the genus Maritimibacter, for which the name Maritimibacter lacisalsi sp. nov. is proposed.

Strain X12M-4T showed some characteristics different from the description of the genus Maritimibacter (Lee et al., 2007). To accommodate the novel species described in this study, the description of the genus Maritimibacter should be emended.

Emended description of the genus Maritimibacter

Lee et al. 2007

The description given by Lee et al. (2007) is altered with respect to the following properties: NaCl is not absolutely necessary for growth. C16:0 and C18:1ω7c are the major fatty acids. C16:0 2-OH, C19:0 cyclo ω8c and C18:1ω7c 11-methyl may also be detected as major fatty acids in some strains. The predominant respiratory quinone is Q-10. The major polar lipid profile consists of PC, PG, DPG, an unknown aminolipid, an unidentified phospholipid and an uncharacterized lipid. A small amount of phosphatidylethanolamine might be detected. The DNA G+C content is 64.1–65.7 %.

Description of Maritimibacter lacisalsi sp. nov.

Maritimibacter lacisalsi (la.ci.sal’si. L. n. lacus lake; L. adj. salsus salted, salt; N.L. gen. n. lacisalsi of a salt lake, the habitat from which the type strain was isolated).

Strictly aerobic, oxidase- and catalase-positive. Cells are Gram-staining-negative, rod-shaped, non-motile, 0.5–0.8 μm wide and 1.1–1.6 μm long. Colonies are 0.4–0.8 mm in diameter, circular, smooth, and slightly beige after cultivation on MA (pH 7.5) at 30 °C for 4 days. Positive for nitrate reduction and hydrolysis of aesculin; negative for D-glucose fermentation, production of H2S and indole, and hydrolysis of urea, L-tyrosine, casein, L-arginine, gelatin, starch and Tweens 20, 40, 60 and 80. Growth occurs at 15–40 °C (optimum, 25 °C) and pH 6.5–9.5 (optimum, pH 7.0) and in the presence of 0–11.0 % (w/v) NaCl (optimum, 5.0–6.0 %). No growth occurs at 10 °C or 45 °C, pH 6.0 or pH 10.0, or in the

Downloaded from www.microbiologyresearch.org by IP: 54.70.40.11 On: Fri, 07 Dec 2018 04:07:25
Fig. 1. Neighbour-joining tree based on 16S rRNA gene sequences showing the phylogenetic position of strain X12M-4T and closely related species. Bootstrap values (expressed as percentages of 1000 replications) >50 % are shown at the branch points. Filled circles indicate branches that were also recovered in both maximum likelihood (ML) and maximum parsimony (MP) trees; open circles indicate branches that were recovered in either the ML or MP tree. *Rhodocyclus purpureus* 6770T was used as an outgroup. Bar, evolutionary distance (K_{nu} of 0.01.

---

**Maritimibacter lacisalsi** X12M-4T (KJ782425)  
**Maritimibacter alkaliphilus** HTCC2654T (AAMT01000002)  
**Roseibacterium elongatum** DSM 19469T (CP004372)  
**'Roseibacterium beibuensis'** JLT1202r (JN247667)  
**Tropicimonas isoalkanivorans** BS1T (AB302379)  
**Tropicimonas aquamaris** DPG-21T (HQ340608)  
**Tropicimonas sediminicola** M97T (JF748735)  
**Boseongicola aestuarii** BS-W15T (KF977837)  
**Celeribacter neptunius** H 14T (FJ535354)  
**Celeribacter baekdonensis** L6T (HM997022)  
**Celeribacter marinus** IMCC12053T (KF146343)  
**Actibacterium atlanticum** 22II-S11-z10 (KJ159064)  
**Actibacterium mucosum** KCTC 23349T (JFKE01000018)  
**Roseovarius tolerans** EL-172T (Y11551)  
**Roseovarius indicus** B108T (EU742628)  
**Roseovarius litoreus** GSW-M15T (UQ390520)  
**Roseovarius halotolerans** HJ50T (EU431217)  
**Roseovarius pacificus** 81-2T (DQ120726)  
**Cribrihabitans marinus** CZ-AM5T (JX306766)  
**Cribrihabitans neustonicus** CC-AMHB-3T (KF582605)  
**Lutimaribacter litoralis** KU5D5T (AB627076)  
**Lutimaribacter pacificus** W11-2B (DQ659449)  
**Lutimaribacter saemankumensis** SMK-117T (EU336981)  
**Oceanicola marinus** AZO-C (DQ822569)  
**Oceanicola antarcticus** Ar-45T (JX844452)  
**Oceanicola nanhaiensis** DSM 18065T (JHZF01000008)  
**Oceanicola batsensis** HTCC2597T (AAMO01000005)  
**Oceanicola nitratireducens** JLT1210T (EU581832)  
**Oceanicola flagellatus** DY470T (KF434118)  
**Oceanicola granulosus** HTCC2512T (AAOT01000056)  
**Loktanella cinnabarina** LL-001T (BATB010000114)  
**Loktanella soesokkakensis** DSSK1-5T (KC987356)  
**Loktanella vestfoldensis** DSM 16212T (ARNL01000008)  
**Loktanella maricola** DSW-18T (EPF02613)  
**Rhodocyclus purpureus** 6770T (M34132)
presence of 11.5 % (w/v) NaCl. Utilizes adipic acid, D-glucose, D-mannitol, D-sorbitol, ascorcin ferric citrate, cello-biose, maltose, sucrose, trehalose, L-fucose and D-arabitol; does not utilize capric acid, malic acid, trisodium citrate, phenylacetic acid, glycerol, erythritol, D-arabinose, L-arabinose, D-ribose, D-xylene, L-xylene, D-adonitol, methyl β-D-xylopyranoside, D-galactose, D-fructose, D-mannose, L-sorbose, L-rhamnose, dulcitol, inositol, methyl α-D-mannopyranoside, methyl α-D-glucopyranoside, N-acetylglucosamine, amygdalin, arbutin, salicin, lactose, melibiose, inulin, melezitose, raffinose, starch, glycogen, xyitol, gentiobiose, turanose, D-lyxose, D-tagatose, D-fucose, L-arabitol, potassium gluconate, potassium 2-ketogluconate and potassium 5-ketogluconate. According to the API ZYM system, positive for alkaline phosphatase, esterase (C4), esterase lipase (C8), leucine arylamidase, α-glucosidase and β-glucosidase; negative for lipase (C14), valine arylamidase, cystine arylamidase, trypsin, α-chymotrypsin, acid phosphatase, naphthol-AS-BI-phosphohydrolase, α-galactosidase, β-galactosidase, β-glucuronidase, N-acetyl-β-glucosaminidase, α-mannosidase and α-fucosidase. The major fatty acids are C16:0, C19:0 cyclo-7c and C18:1 ω7c. The major respiratory quinone is Q-10. The polar lipid profile consists of PC, PG, DPG, an unknown aminolipid and an unidentified lipid as the major polar lipids. Resistant to norfloxacin, sulfamethoxazole, erythromycin and streptomycin; susceptible to nalidixic acid, tetracycline, ampicillin, gentamicin, kanamycin and vancomycin.

The type strain is X12M-4T (=CGMCC 1.12922T = JCM 30555T), isolated from a surface water sample of a salt lake, Xiaoachaidan Lake in Qaidam basin, Qinghai province, China. The DNA G+C content is 65.7 mol% (Tm).

Acknowledgements

This study was supported by grants of the Agriculture-Transfer Foundation of China (no. SQ2011EC3320022) and the Project of China State Key Laboratory of Simulation and Regulation of Water Cycle in River Basin (no. 2013ZY06). We thank Dr Lei Song and Mr Qing Liu [China General Microbiological Culture Collection Center, (CGMCC)] for preserving strains and Ms Jing-Nan Liang for taking transmission electronic micrographs.

References


