Halomonas lutea sp. nov., a moderately halophilic bacterium isolated from a salt lake

Yun Wang,1† Shu-Kun Tang,2† Kai Lou,1 Pei-Hong Mao,3 Xiang Jin,3 Cheng-Lin Jiang,2 Li-Hua Xu2 and Wen-Jun Li2,4

1 Xinjiang Institute of Microbiology, Xinjiang Academy of Agricultural Science, Urumqi, Xinjiang 830091, PR China
2 The Key Laboratory for Microbial Resources of Ministry of Education, PR China, and Laboratory for Conservation and Utilization of Bio-resources, Yunnan Institute of Microbiology, Yunnan University, Kunming 650091, PR China
3 The Center of Ion Beam Biotechnology, Xinjiang University, Urumqi, Xinjiang 830008, PR China
4 Guangdong Key Laboratory of Marine Materia Medica, South China Sea Institute of Oceanology, Chinese Academy of Sciences, Guangzhou 510301, PR China

A Gram-negative, moderately halophilic bacterium, designated YIM 91125T, was isolated from a salt lake in Xinjiang province, north-west China. The isolate grew at salinities in the range 1–20% (w/v) and at 4–45 °C. Optimal growth occurred at 37 °C, pH 7.5 and 5–10% (w/v) NaCl. Cells were short rods motile by means of single polar flagella. The major fatty acids were C18:1ω7c, C16:0, C18:0 cyclo ω8c and C12:0 3-OH. The DNA G+C content was 60.8 mol%. The predominant respiratory quinone was Q-9. A comparison of 16S rRNA gene sequences revealed its relationship to Halomonas species, its closest neighbours being Halomonas pantelleriensis (95.9% similarity to the type strain) and Halomonas muralis (95.4% similarity). On the basis of chemotaxonomic, phylogenetic and phenotypic evidence, strain YIM 91125T represents a novel member of the genus Halomonas, for which the name Halomonas lutea sp. nov. is proposed. The type strain is YIM 91125T (=KCTC 12847T =CCTCC AB 206093T).

The family Halomonadaceae of the class Gammaproteobacteria currently comprises seven genera, Carnimonas, Chromohalobacter, Cobetia, Halomonas, Halotalea, Medisalibacter and Zymobacter, and more than half of the taxa in the family have been reclassified according to their heterogeneous features (Franzmann et al., 1988; Mellado et al., 1995; Dobson & Franzmann, 1996; Arahal et al., 2002a, b). At the time of writing, Halomonas is the largest genus in the family Halomonadaceae and comprises 52 species with validly published names; most of these species were isolated from saline environments (Dobson & Franzmann, 1996; Mata et al., 2002; Ventosa et al., 1998; Cabrera et al., 2007; Kim et al., 2007; Soto-Ramírez et al., 2007; Wang et al., 2007a, b). Halomonas was described as comprising Gram-negative, aerobic, moderately halophilic bacteria. Some members of this genus have been recognized for their potential use in biotechnology, such as fermented food production, enzyme production (amylases, DNases, lipases, proteases and pullulanases) and the degradation of toxic compounds (Margesin & Schinner, 2001; Ventosa & Neito, 1995; Ventosa et al., 1998; Sánchez-Porro et al., 2003).

In the course of a programme of screening for halophilic bacteria, a moderately halophilic bacterium belonging to the genus Halomonas was isolated from Ebinur Lake (82°35′–83°16′ E 44°05′–45°08′ N), in Xinjiang, north-west China, a highly saline lake that has been a long-term target for the study of element cycling and microbial biota under extremely high-salinity conditions (Cui et al., 2006). The results of a polyphasic characterization of this Halomonas strain, designated YIM 91125T, are described here. On the basis of the data presented below, a novel species of the genus Halomonas is proposed to accommodate this isolate.

Strain YIM 91125T was isolated using the dilution plating method on modified ISP 5 medium at 37 °C. This medium contained the following [l distilled water]−1: 1 g 1- asparagine, 10 g glycerol, 5 g yeast extract, 1 g K2HPO4, 5 g KNO3, 100 g NaCl and 15 g agar. NaCl was sterilized separately before being added to the medium. The medium was adjusted to pH 7.5. Strain YIM 91125T was maintained on modified ISP 5 agar slants (5% NaCl, w/v; pH 7.5) at 4 °C and as 20% (w/v) glycerol suspensions at –20 °C. Biomass for chemical and molecular studies was obtained

†These authors contributed equally to this work.
The GenBank/EMBL/DDBJ accession number for the 16S rRNA gene sequence of strain YIM 91125T is EF674852.
from cultivation in shaken flasks (about 150 r.p.m.) in modified ISP 5 medium (5% NaCl, w/v; pH 7.5) at 37 °C for about 1 week.

Gram staining was carried out using the standard Gram reaction and was confirmed using the KOH lysis test (Cerny, 1978). Cell motility was confirmed by the presence of turbidity throughout a tube containing semisolid medium (Leifson, 1960). Morphology was examined using transmission electron microscopy (H-800 microscope; Hitachi) with cells from exponentially growing cultures. Poly-β-hydroxybutyrate inclusions in cells were stained with Sudan black B (Drews, 1983) and viewed with phase-contrast microscopy. Colony morphology was observed on modified ISP 5 medium containing 5% NaCl (pH 7.5) after incubation at 37 °C for 3 days. Growth was tested at various temperatures (0, 4, 10, 20, 28, 37, 45 and 55 °C) on modified ISP 5 medium containing 5% NaCl. The pH range for growth was investigated between pH 4.0 and 10.0 (in increments of 1 pH unit) with the buffer system described by Xu et al. (2005). Liquid cultures were grown in tubes at 37 °C for 2–3 weeks, using modified ISP 5 as the basal medium. Tolerance of chlorides of sodium, potassium, magnesium and calcium at concentrations between 0 and 30% (in increments of 1%) were tested using the same basal medium. Catalase activity was determined by assessing bubble production after the addition of a drop of 3% H2O2. Oxidase activity was determined by assessing the oxidation of tetramethyl-p-phenylenediamine. The methyl red and Voges–Prokauer tests were performed as described by Lánya (1987). Production of DNase and hydrolysis of casein, starch and Tween 40 and 80 were tested as described by Smibert & Krieg (1994). The API 20E system (bioMérieux) was used to determine the following: hydrolysis of gelatin and ONPG, activity of lysine and ornithine decarboxylases, urease and arginine dihydrolase and production of acetoin, H2S and indole. Nitrate reduction and aesculin hydrolysis were tested using the API 20NE system (bioMérieux). The utilization of different compounds as sole carbon, nitrogen and energy sources was determined using GN2 microplates with the Microlog system (Biolog; 95 substrates). Acid production from carbohydrates was determined by using the API 50 CH system (bioMérieux) and enzyme activities were determined by means of the API ZYM system (bioMérieux). Antibiotic susceptibility was determined using the disc diffusion method on agar (Reva et al., 1995).

Strain YIM 91125T comprised Gram-negative, short rods, approximately 0.4–0.7 μm wide and 0.6–1.0 μm long after cultivation for 3 days at 37 °C on modified ISP 5 agar containing 5% NaCl (w/v). Cells were motile by means of single polar flagella. On modified ISP 5 agar containing 5% NaCl (w/v), colonies were orange, flat, opaque and mucoid with slightly irregular edges. Cells were oxidase- and catalase-positive. The other physiological and biochemical properties determined for strain YIM 91125T are given in Table 1 and in the species description.

For the analysis of fatty acids, strain YIM 91125T was cultivated at 37 °C for 48 h on tryptic soy agar (Difco) containing 5% NaCl and investigated as described by Sasser (1990), using the Microbial Identification System (MIDI). Isoprenoid quinones were extracted and purified as described by Komagata & Suzuki (1987). The purified ubiquinones were dissolved in acetone and separated by reversed-phase HPLC. The predominant respiratory quinone found in strain YIM 91125T was Q-9, similar to members of the genus Halomonas. The fatty acids (>1%)

<table>
<thead>
<tr>
<th>Characteristic</th>
<th>1</th>
<th>2</th>
<th>3</th>
<th>4</th>
<th>5</th>
</tr>
</thead>
<tbody>
<tr>
<td>Cell morphology</td>
<td>Short rods</td>
<td>Rods</td>
<td>Rods</td>
<td>Rods</td>
<td>Cocci or short rods</td>
</tr>
<tr>
<td>Pigmentation</td>
<td>Orange</td>
<td>Cream</td>
<td>Cream</td>
<td>NA</td>
<td>Yellow-cream</td>
</tr>
<tr>
<td>Flagellation</td>
<td>Single flagellum</td>
<td>Peritrichous</td>
<td>Peritrichous</td>
<td>Peritrichous</td>
<td>Single flagellum</td>
</tr>
<tr>
<td>NaCl range (% w/v)</td>
<td>1–20</td>
<td>0–15</td>
<td>1–15</td>
<td>0–18</td>
<td>1–14</td>
</tr>
<tr>
<td>pH range</td>
<td>5.0–9.0</td>
<td>5.5–10.0</td>
<td>6.0–11.0</td>
<td>7.0–11.0</td>
<td>5.5–9.5</td>
</tr>
<tr>
<td>Temperature range (°C)</td>
<td>4–45</td>
<td>10–35</td>
<td>10–45</td>
<td>10–48</td>
<td>10–40</td>
</tr>
<tr>
<td>Oxidase</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>–</td>
</tr>
<tr>
<td>Hydrolysis of:</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Aesculin</td>
<td>–</td>
<td>+</td>
<td>+</td>
<td>NA</td>
<td>+</td>
</tr>
<tr>
<td>Gelatin</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>+</td>
</tr>
<tr>
<td>Urea</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>Major fatty acids</td>
<td>C18:1ω7c, C16:0, C18:0</td>
<td>C18:1ω7c, C16:0, C16:1ω7c and/or iso-C15:0 2-OH</td>
<td>C16:0, C18:1ω7c</td>
<td>C18:0, C19:0 cyclo</td>
<td>C16:0, C18:0 cyclo</td>
</tr>
<tr>
<td>DNA G + C content (mol%)</td>
<td>60.8</td>
<td>62.4</td>
<td>65.0</td>
<td>66.0</td>
<td>66.0</td>
</tr>
</tbody>
</table>

Table 1. Differential characteristics of strain YIM 91125T and its closest neighbours in the genus Halomonas

Strains: 1, YIM 91125T; 2, H. muraNis DM 20969T; 3, H. pantelleriensis DSM 9661T; 4, H. desiderata DSM 9502T; 5, H. kribbensis KCTC 12584T. Data for reference strains are from Heyrman et al. (2002), Romano et al. (1997), Berendes et al. (1996) and Jeon et al. (2007), respectively. +, Positive; −, negative; NA, data not available.
were C16:1ω7c (25.1 %), C16:0 (17.0 %), C19:0 cyclo ω8c (13.6 %), C12:0 3-OH (10.7 %), C12:0 (7.9 %), C10:0 (6.0 %) and C17:0 cyclo (4.6 %). The profile of major fatty acids in strain YIM 91125T was also similar to those of members of the genus Halomonas (Heyrman et al., 2002; Romano et al., 1997; Berendes et al., 1996; Jeon et al., 2007).

To determine the G+C content of strain YIM 91125T, genomic DNA was prepared according to the method of Marmur (1961). The G+C content of the DNA was determined by reversed-phase HPLC (Mesbah et al., 1989) as 60.8 mol%.

Extraction of genomic DNA and PCR amplification of 16S rRNA gene were done as described by Li et al. (2007). The sequence obtained was compared with reference 16S rRNA gene sequences retrieved from GenBank/EMBL by means of a BLAST search. Multiple alignments and calculations of evolutionary distances were carried out using CLUSTAL_X software (Thompson et al., 1997). Gaps at the 5′ and 3′ ends of the alignment were omitted for further analysis.

Phylogenetic analyses were performed using three tree-making algorithms: neighbour joining (Saitou & Nei, 1987; Fitch, 1971). A neighbour-joining phylogenetic tree was constructed from \( K_{\text{nuc}} \) values (Kimura, 1980) using MEGA, version 3.0 (Kumar et al., 2004). The topology of the phylogenetic tree was evaluated using the bootstrap resampling method, with 1000 replicates (Felsenstein, 1985).

An almost-complete 16S rRNA gene sequence was determined for strain YIM 91125T. Alignment data showed that strain YIM 91125T had the highest levels of 16S rRNA gene sequence similarity with respect to members of the Gammaproteobacteria, in particular with respect to the genus Halomonas. In the phylogenetic tree based on the neighbour-joining algorithm, strain YIM 91125T clustered together with the type strains of Halomonas kribbensis, Halomonas desiderata, Halomonas muralis and Halomonas pantelleriensis (Fig. 1); this relationship was supported by all of the tree-making methods used in this study. The results of the 16S rRNA gene sequence comparisons clearly demonstrated that strain YIM 91125T was a member of the genus Halomonas. The similarities between the 16S rRNA gene sequence of strain YIM 91125T and those of the type strains of 52 Halomonas species with validly published names ranged from 92.0 to 95.9 %. The closest relatives of strain YIM 91125T were the type strains of H. pantelleriensis (95.9 % sequence similarity) and H. muralis (95.4 %).

On the basis of chemotaxonomic and phylogenetic data and some phenotypic features that distinguish the novel isolate from its closest neighbours in the genus Halomonas (Table 1), strain YIM 91125T represents a novel species of the genus Halomonas, for which the name Halomonas lutea sp. nov. is proposed.
L-serine, inosine, uridine, 2,3-butanediol, glycerol and glucose 6-phosphate. The remaining substrates of the Biolog GN2 system are not utilized. In the API 50 CH system, acid is produced from glycerol, D-arabinose, L-arabinose, D-ribose, D-xylose, L-xylose, D-galactose, D-glucose, D-fructose, L-sorbitose, L-rhamnose, D-mannose, D-mannitol, D-sorbitol, aesculin, cellobiose, maltose, D-lactose, melibiose, starch, trehalose, gentiobiose, D-lyxose, D-tagatose, D-fucose, L-fucose, D-arabitol, potassium 2-ketoglutarate and potassium 5-ketoglucurate, but not from erythritol, inositol, D-adenitol, methyl β-D-xylpyranoside, arbutin, dulcitol, methyl α-D-mannopyranoside, methyl α-D-glucopyranoside, N-acetylglucosamine, amygdalin, salicin, sucrose, inulin, melezitose, raffinose, glycogen, xylitol, turanose, potassium glucuronate or L-arabitol. In the API ZYM system, alkaline phosphatase, esterase (C4), esterase lipase (C8), cysteine arylamidase, acid phosphatase, lipase (C14), leucine arylamidase, valine arylamidase, trypsin, α-galactosidase, β-galactosidase, β-glucuronidase, α-glucosidase, N-acetyl-β-glucosaminidase, β-glucosidase, α-mannosidase and α-fucosidase are negative. The type strain is sensitive to the following antibiotics (μg per disc, unless indicated otherwise): amoxicillin (10), ampicillin (10), chloramphenicol (30), ciprofloxacin (5), erythromycin (15), gentamicin (10), neomycin (30), netilmicin sulfate (30), norfloxacin (10), novobiocin (30), penicillin G (10), rifampicin (5), streptomycin sulfate (10), tetracycline (30), tobramycin (10), trimethoprim/sulfonamides (23.7/1.25) and vancomycin (30). Resistance is exhibited only to amikacin (30 μg) and lincomycin (2 μg). Q-9 is the predominant ubiquinone. The major cellular fatty acids are C₁₈:1ω7c, C₁₆:0, C₁₉:0 Cyclo ω8c and C₁₂:0 3-OL. The DNA G+C content of the type strain is 60.8 mol%.

The type strain, YIM 91125T (=KCTC 12847T =CCTCC AB 206093T), was isolated from a salt lake in Xinjiang Province, north-west China.

Acknowledgements

We are grateful to Dr Jean Euzéby for his help with nomenclature. This research was supported by the National Basic Research Program of China (no. 2004CB719601), the Key Project of the Chinese Ministry of Education (no. 206139), the National Natural Science Foundation of China (no. 30600001), the Yunnan Provincial International Cooperative Program (no. 2005G621), the Open Project Program of the Extremophiles Laboratory of Xinjiang (no. XJYS0203-2005-01) and the Youth Technological Innovation Foundation of Xinjiang Academy of Agricultural Science (no. 2007Q007). W.-J. L. was supported by the Program for New Century Excellent Talents in University.

References


