Halorubrum kocurii sp. nov., an archaeon isolated from a saline lake

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A Gram-negative, non-motile, neutrophilic, rod-shaped, extremely halophilic archaeon, designated strain BG-1T, was isolated from a salt lake, Lake Bagaejinnor, in Inner Mongolia, China. Strain BG-1T was able to grow at 25–55 °C, required at least 2.5 M NaCl for growth (with an optimum at 3.4 M NaCl) and grew at pH 6.0–9.0 (with an optimum at pH 7.5). Hypotonic treatment with less than 2.0 M NaCl caused cell lysis. Phylogenetic analysis of the almost-complete 16S rRNA gene sequence positioned the isolate within the genus Halorubrum in the family Halobacteriaceae. Strain BG-1T was most closely related to Halorubrum aidingense 31-hongT (98.8 % sequence similarity), Halorubrum saccharovorum NCIMB 2081T (98.6 %), Halorubrum lacusprofundi ACAM 34T (98.6 %) and Halorubrum lipolyticum 9-3T (98.4 %). However, values for DNA–DNA hybridization between strain BG-1T and the most closely related members of the genus Halorubrum were below 40 %. Analysis of the polar lipids of strain BG-1T revealed the presence of mannosyl-2-sulfate-(1-4)-glycosyl-archaeol, the main glycolipid found in neutrophilic species of the genus Halorubrum. The G+C content of the genomic DNA was 69.4 mol% (Tm). Comparison of the phenotypic characteristics of the strain with those of Halorubrum species supported the conclusion that BG-1T represents a novel species within this genus, for which the name Halorubrum kocurii sp. nov. is proposed. The type strain is BG-1T (=CECT 7322T =CGMCC 1.7018T =JCM 14978T).

Aerobic, extremely halophilic archaea typically comprise red-pigmented micro-organisms that belong to the family Halobacteriaceae (Grant et al., 2001). They are the most halophilic organisms known and are predominant in hypersaline environments in which the salt concentration exceeds 250 g l−1 (Rodriguez-Valera et al., 1981; Ventosa, 2006). Cell densities may be sufficiently high in hypersaline brines to impart a red colour. Recent studies based on phylogenetic analyses of 16S rRNA genes have revealed a very high taxonomic diversity at both the genus and species level within the family Halobacteriaceae (Grant et al., 2001; Ventosa, 2006). At the time of writing, the family Halobacteriaceae includes 26 genera and 85 species (Oren et al., 2007).

The genus Halorubrum was originally proposed by McGinley & Grant (1995) to accommodate several species previously included in the genus Halobacterium. Currently, the genus Halorubrum comprises 19 species with validly published names: Halorubrum saccharovorum (Tomlinson & Hochstein, 1976), Hrr. trapanicum (Petter, 1931), Hrr. sodomense (Oren, 1983), Hrr. lacusprofundi (Franzmann et al., 1988), Hrr. coriense (Oren & Ventosa, 1996), Hrr. distributum (Oren & Ventosa, 1996), Hrr. vacuolatum...
Strain BG-1\(^T\) was isolated from a sediment and water sample from a saline lake, Lake Bagaejinnor (45° 09’ N 116° 36’ E). At the time of sampling (September 2003), the water of this lake had a temperature of 20.5 \(\pm\) C, a pH of 8.5 and a conductivity of 146.7 mS cm\(^{-1}\). Approximately 0.5 g of the sample was dissolved in the medium and serially diluted; 100 \(\mu\)l of each dilution was plated on plates with solid isolation medium containing the following (1\(^{-1}\)): yeast extract, 10 g; Casamino acids, 7.5 g; NaCl, 130 g; MgCl\(_2\), 7-H\(_2\)O, 71.16 g; Na\(_2\)SO\(_4\), 45.6 g; trisodium citrate, 3 g; KCl, 2.48 g; Na\(_2\)B\(_4\)O\(_7\), 1.62 g; NaBr, 0.84 g; NaHCO\(_3\), 0.62 g; Na\(_2\)CO\(_3\), 0.36 g; the pH was adjusted to 8.0. Strain BG-1\(^T\) was isolated and a pure culture was obtained after several transfers on the same medium.

Table 1. Differentiation of strain BG-1\(^T\) from closely related species of the genus Halorubrum

<table>
<thead>
<tr>
<th>Characteristic</th>
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<th>3</th>
<th>4</th>
<th>5</th>
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<tr>
<td>Motility</td>
<td>–</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
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<td>Mg(^{2+}) required</td>
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<td>+</td>
<td>–</td>
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<td>+</td>
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<tr>
<td>H(_2)S formation</td>
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<td>–</td>
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<tr>
<td>Nitrate reduction</td>
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<td>+</td>
<td>+</td>
<td>–</td>
<td>W</td>
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<tr>
<td>Indole formation</td>
<td>–</td>
<td>–</td>
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<td>–</td>
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<tr>
<td>Starch hydrolysis</td>
<td>–</td>
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<td>+</td>
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<td>Urease</td>
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<td>Gelatin liquefaction</td>
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<td>Utilization of:</td>
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<tr>
<td>– Glucose</td>
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<td>+</td>
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<tr>
<td>– Galactose</td>
<td>–</td>
<td>–</td>
<td>+</td>
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<tr>
<td>– Mannose</td>
<td>–</td>
<td>+</td>
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<td>– Ribose</td>
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<td>– Xylose</td>
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<td>Acetate</td>
<td>–</td>
<td>+</td>
<td>–</td>
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<tr>
<td>DNA G+C content (mol%)</td>
<td>69.4</td>
<td>71.2</td>
<td>64.2</td>
<td>65.3</td>
<td>65.9</td>
</tr>
</tbody>
</table>

To determine the utilization of different organic substrates as carbon and energy sources or as carbon, nitrogen and energy sources, a medium containing yeast extract at 0.05 % (w/v), supplemented with 1 % (w/v) of the tested substrate, was used (Torreblanca et al., 1986). Susceptibility to antibiotics was determined on agar plates by using antibiotic discs with the following amounts: ampicillin (10 \(\mu\)g), bacitracin (10 \(\mu\)U), chloramphenicol (30 \(\mu\)g), erythromycin (15 \(\mu\)g); gentamicin (10 \(\mu\)g), nalidixic acid (30 \(\mu\)g), neomycin (10 \(\mu\)g), novobiocin (30 \(\mu\)g), penicillin G (10 \(\mu\)U), rifampicin (30 \(\mu\)g), streptomycin (10 \(\mu\)g) and tetracycline (30 \(\mu\)g). The results for the utilization of different substrates and for antibiotic susceptibility are included in the species description.

Cell morphology and motility were examined using an Olympus BX41 microscope equipped with phase-contrast optics. Cells were non-motile and rod-shaped (Fig. 1). Colony morphology was observed on solid medium under optimal growth conditions after incubation at 37 °C for 5 days. Colonies of strain BG-1\(^T\) that formed on agar plates were circular, smooth, entire, opaque, red-pigmented and 0.5–1.5 mm in diameter.

Polar lipids were extracted with chloroform/methanol as described previously (Kamekura, 1993). TLC was done using Merck HPTLC silica gel 60 plates (art. 5641) in the solvent system, chloroform/methanol/acetic acid/water (85:22.5:10:4, by vol.). Glycolipids were detected as purple spots by spraying with 0.5 % \(\alpha\)-napthol in
methanol/water (1:1) and then with sulfuric acid/ethanol (1:1), followed by heating at 160 °C. The polar lipids of strain BG-1T are C20C20 derivatives of phosphatidylglycerol, phosphatidylglycerol phosphate methyl ester and a sulfated diglycosyl archaeol [mannosyl-2-sulfate-(1-4)-glycosyl-archaeol] (see Supplementary Fig. S1, available in IJSEM Online). This polar lipid profile has been shown to be a distinctive feature of non-alkaliphilic species of the genus Halorubrum (McGenity & Grant, 2001).

Chromosomal DNA of strain BG-1T was isolated and purified according to the method described by Marmur (1961). The G+C content of genomic DNA was determined from the mid-point (Tm) of the thermal denaturation profile (Marmur & Doty, 1962), using the equation of Owen & Hill (1979). The DNA G+C content of strain BG-1T was 69.4 mol%. The 16S rRNA gene of strain BG-1T was amplified using a PCR with three universal primer sets, as described previously (Lopez-Garcia et al., 2001; Arahal et al., 1996) and the almost-complete nucleotide sequence (1369 bp) was determined. The ARB software package (Ludwig et al., 2004) was used for 16S rRNA gene sequence analysis. Base-frequency filters were applied in the sequence-comparison analysis and the effects on the results were evaluated. In the phylogenetic tree constructed with the maximum-parsimony method (Saitou & Nei, 1987), strain BG-1T clustered with the type strains of species of the genus Halorubrum (Fig. 2). The 16S rRNA gene sequence similarities between strain BG-1T and the most closely related Halorubrum type strains, Hrr. aidingense 31-hongT, Hrr. saccharovorum NCIMB 2081T, Hrr. lacusprofundi ACAM 34T and Hrr. lipolyticum 9-3T, were 98.8, 98.6, 98.6 and 98.4 %, respectively. Similar tree topologies were obtained when other treeing methods (neighbour joining and maximum likelihood) were used.

To verify the species status of strain BG-1T, DNA–DNA hybridization studies were carried out with the type strains of the most closely related species of Halorubrum. These studies were performed using the competition procedure of the membrane method (Johnson, 1994) as described in detail by Ventosa et al. (2004). The levels of DNA–DNA relatedness for strain BG-1T with respect to Hrr. aidingense JCM 13560T, Hrr. saccharovorum NCIMB 2081T, Hrr. lipolyticum JCM 13559T and Hrr. lacusprofundi ACAM 34T were 27, 28, 36 and 39 %, respectively. These data indicate that strain BG-1T represents a novel species of the genus Halorubrum, having DNA–DNA hybridization values <70 % with respect to members of recognized species (Stackebrandt & Goebel, 1994). In addition, several phenotypic differences were observed between strain BG-1T and the most closely related Halorubrum species, including those concerning motility, urease production and the utilization of glucose and other sugars (Table 1).

Therefore, on the basis of the data from this polyphasic study, strain BG-1T represents a novel species of the genus Halorubrum, for which the name Halorubrum kocurii sp. nov. is proposed.

Fig. 1. Phase-contrast micrograph of cells of strain BG-1T grown in liquid medium under optimal conditions. Bar, 15 μm.

Fig. 2. Maximum-parsimony phylogenetic tree, based on 16S rRNA gene sequence comparison, showing the position of strain BG-1T among the species of the genus Halorubrum. EMBL accession numbers are given in parentheses. Bar, 1 % sequence divergence.
Description of *Halorubrum kocurii* sp. nov.

*Halorubrum kocurii* (ko.cu’ri.i. N.L. gen. masc. n. *kocurii* of Kocur, named for the Czech microbiologist M. Kocur, a pioneer in the study of halophilic archaea and bacteria). Cells are non-motile, rod-shaped (2–5 × 0.9–1.1 μm) (Fig. 1) and Gram-negative. Colonies are circular, smooth, entire, opaque, red-pigmented and 0.5–1.5 mm in diameter after 5 days at 37 °C on plates containing 20% (w/v) total salts. Cells are extremely halophilic and lyse in water. At least 2.5 M NaCl is required for growth, the optimum concentration being 3.4 M NaCl. MgCl₂ is not required for growth. The pH and temperature ranges for growth are pH 6.0–9.0 (optimum, pH 7.5) and 25–55 °C (optimum, 37 °C). Chemo-organotrophic, aerobic and oxidase- and catalase-positive. Indole is not produced from tryptophan. Methyl red, Voges–Proskauer and Simmons’ citrate tests produce negative results. Acid is not produced from lactose, glycerol, D-glucose, sucrose, D-fructose, D-arabinose, maltose, D-galactose, trehalose or D-mannose. Does not grow anaerobically in the presence of nitrate or L-arginine. Starch, gelatin, DNA, aesculin and casein are not hydrolysed. Urea is hydrolysed. Does not produce arginine dihydrolase, lysine decarboxylase or ornithine decarboxylase. Nitrate is reduced to nitrite; gas is not produced from nitrite. Utilizes D-xylose. No growth is observed on D-glucose, D-fructose, glycerol, maltose, trehalose, starch, propionate, fumarate, acetate, L-lysine, D-mannitol, D-sorbitol, lactose, D-arabinose, D-galactose, D-mannose, raffinose, D-ribose, malate, succinate, glutamate, isoleucine, L-serine or glycine. Sensitive to bacitracin, novobiocin and rifampicin. Resistant to ampicillin, chloramphenicol, erythromycin, gentamicin, nalidixic acid, neomycin, penicillin G, streptomycin and tetracycline. The polar lipids are phosphatidylglycerol, phosphatidylglycerol phosphate, erythromycin, gentamicin, nalidixic acid, neomycin, penicillin G, streptomycin and tetracycline. The lipid polar lipids are phosphatidylglycerol, phosphatidylglycerol phosphate, and phosphatidylglycerol phosphate. The DNA G+C content is 69.4 mol% (Tm).

The type strain, BG-1 T (=CECT 7322 T =CGMCC 1.7018 T =JCM 14978 T), was isolated from saline Lake Bagaejinnor in Inner Mongolia, China.

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References


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