Oceanobacillus halophilus sp. nov.,
a novel moderately halophilic bacterium from a hypersaline lake

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A moderately halophilic bacterium was isolated from a brine sample of a hypersaline lake, Aran-Bidgol, in Iran. The strain, designated J8B T, was Gram-stain-positive, endospore-forming, rod-shaped, strictly aerobic, motile and produced cream colonies. Strain J8B T grew in NaCl at between 3.0–15.0 % (w/v) (optimally at 7.5 % NaCl, w/v), between pH 6.5–9.0 (optimally at pH 8.0) and between 20–45 °C (optimally at 35 °C). Phylogenetic analysis, based on 16S rRNA gene sequences, revealed that strain J8B T is a member of the genus Oceanobacillus and most closely related to Oceanobacillus profundus CL-MP28 T, Oceanobacillus polygoni SA9 T and Oceanobacillus oncorhynchi R-2 T (96.9 %, 96.3 % and 96.2 % similarities, respectively). The level of DNA–DNA relatedness between the novel isolate and O. profundus IBRC-M 10567 T was 10 %. The major cellular fatty acids of the isolate were anteiso-C 15 : 0, iso-C15 : 0 and anteiso-C 17 : 0. The polar lipid pattern of strain J8B T consisted of phosphatidylglycerol, diphosphatidylglycerol, five phospholipids, two aminolipids and two glycoaminolipids. It contained MK-7 as the predominant menaquinone and meso-diaminopimelic acid in the cell-wall peptidoglycan. The G+C content of the genomic DNA of this strain was 39.2 mol%. Phenotypic characteristics, phylogenetic analysis and DNA–DNA relatedness data suggest that this strain represents a novel species of the genus Oceanobacillus, for which the name Oceanobacillus halophilus sp. nov. is proposed. The type strain is strain J8B T (ICP 1; =IBRC-M 10444 T=DSM 23996 T).

The genus Oceanobacillus was firstly described by Lu et al. (2001) to accommodate the species Oceanobacillus iheyensis, which is an extremely halotolerant and alkaliophilic species isolated from deep sea. Members of the genus Oceanobacillus are aerobic, rod-shaped, endospore-forming, halophilic bacteria widely distributed in various environments such as marine environments (Lu et al., 2001; Kim et al., 2007; Yu et al., 2014; Kim et al., 2015), wastewater treatment systems (Nam et al., 2008), soil (Lee et al., 2013; Wu et al., 2014), fermented foods (Namwong et al., 2009; Tominga et al., 2009; Whon et al., 2010), saline environments (Lee et al., 2010; Amoozegar et al., 2014) and activated sludge (Yang et al., 2010). At the time of writing, the genus comprises 18 species with validly published names (www.bacterio.net/m/marinobacter.html; Euzéby, 1997; Parte, 2014). These species are characterized chemotaxonomically by the presence of menaquinone-7 as the major isoprenoid
quinone and anteiso-C\textsubscript{15} : 0 as the predominant cellular fatty acid (Lee et al., 2006). The aim of the present work was to describe the isolation and polyphasic characterization of a novel, moderately halophilic, micro-organism derived from a hypersaline lake in Iran and to propose this strain as a representative of a novel species of the genus Oceanobacillus.

Strain J8B\textsuperscript{T} was isolated by diluting-plating techniques from a water sample (pH 7.2, salinity 30 %) of Aran-Bidgol salt lake [in the centre of Iran (34° 26’ N 51° 48’ E)]. The 7.5 % (w/v) HM medium used for its isolation contained (g l\textsuperscript{-1}): NaCl, 60.75; MgCl\textsubscript{2} \cdot 6H\textsubscript{2}O, 5.25; MgSO\textsubscript{4} \cdot 7H\textsubscript{2}O, 7.2; CaCl\textsubscript{2} \cdot 2H\textsubscript{2}O, 0.27; KCl, 1.5; NaHCO\textsubscript{3}, 0.045; NaBr, 0.0195; proteose-peptone no. 3, 5.0; yeast extract, 10.0, w/v and glucose, 1.0 [solidified with 1.5 % (w/v) agar (Ventosa et al., 1982)]. The pH of this medium was adjusted to pH 7.5. After successive cultivation, a pure isolate, designated strain J8B\textsuperscript{T}, was obtained and routinely grown on 7.5 % HM solid medium at 35 °C. In order to characterize phenotypically the novel strain, standard phenotypic tests were selected according to the recommendations of the minimal standards for describing aerobic, endospore-forming bacteria (Logan et al., 2009) and the notes on the characterization of prokaryote strains for taxonomic purposes (Tindall et al., 2010). Ornithinibacillus contaminans IBRC-M 10626\textsuperscript{T}, Oceanobacillus kapialis IBRC-M 10565\textsuperscript{T}, Oceanobacillus profundus IBRC-M 10567\textsuperscript{T} and Oceanobacillus polygoni JCM 17252\textsuperscript{T} were used as reference strains for comparison in our study.

The genomic DNA of the isolate was extracted with a DNA extraction kit (High Pure PCR Template Preparation kit; Roche) according to the manufacturer’s protocol and the 16S rRNA gene was amplified using the bacterial universal primers 27F and 1492R (Lane et al., 1985). Direct sequence determination of the PCR-amplified DNA was conducted on an ABI 3730XL DNA sequencer at Macrogen (Seoul, South Korea). Phylogenetic analysis was performed with the ARB software package (Ludwig et al., 2004). The 16S rRNA gene sequence was aligned with published sequences of closely related bacteria and the alignment was confirmed and checked against both primary and secondary structures of the 16S rRNA molecule using the alignment tool of the ARB software package (Ludwig et al., 2004).

The identification of phylogenetic neighbours and calculation of pairwise 16S rRNA gene sequence similarity were achieved using the EzTaxon-e database (Kim et al., 2012). Phylogenetic trees were reconstructed using three different methods: maximum-parsimony (Fitch, 1971), maximum-likelihood (Felsenstein, 1981) and neighbour-joining (Saitou & Nei, 1987), with algorithms integrated in ARB software for phylogenetic inference.

An almost complete 16S rRNA gene sequence of strain J8B\textsuperscript{T} (1445 nt) was obtained. The gene sequence of the novel strain showed that strain J8B\textsuperscript{T} is a member of the genus Oceanobacillus. The closest relative of strain J8B\textsuperscript{T} was O. profundus CL-MP28\textsuperscript{T}, with a sequence similarity of 96.9 %. The sequence similarities of the novel strain to other related species, including Oceanobacillus polygoni SAG\textsuperscript{T}, Oceanobacillus kapialis SSK2-2\textsuperscript{T} and Oceanobacillus oncorhyhini R-2\textsuperscript{T} were 96.3 %, 96.2 % and 96.1 %, respectively. Phylogenetic analysis, using the maximum-likelihood algorithm, revealed that the novel strain clustered with members of the genus Oceanobacillus, although in a separate clade (Fig. 1). These data clearly support the novel isolate not being phylogenetically related to the Ornithinibacillus cluster. The chemotaxonomic data also supported strain J8B\textsuperscript{T} belonging to the genus Oceanobacillus (see below). This phylogenetic position was also confirmed in trees generated using the neighbour-joining and maximum-parsimony algorithms (Fig. 1).

Cell morphology was examined by light microscopy (Olympus; model BX41) of exponentially growing cultures. Gram-staining was performed by the Burke method (Murray et al., 1994). Physiological tests were conducted using HM broth or agar, unless stated otherwise. Broth cultures were incubated at 35 °C in an orbital incubator at 150 r.p.m. Growth was monitored from the turbidity at OD\textsubscript{600} using a spectrophotometric method (Shimadzu; model UV-160 A). To determine the optimal temperature and pH for growth, broth cultures of the strain were incubated at temperatures of 10–50 °C at intervals of 5 °C, and at pH 5.5–10.0 at intervals of 0.5 pH units. pH values below 6, pH 6–9 and pH values above 9 were obtained using 50 mM sodium acetate/acetate acid, Tris/HCl and glycine/sodium hydroxide buffers, respectively. Growth at different NaCl concentrations (1.0, 3.0, 5.0, 7.5, 10, 12.5, 15 % and 20 %, w/v) was tested on HM medium at pH 7.5.

The presence of endospores was investigated by using the Schaeffer-Fulton staining method (Murray et al., 1994). Motility was analysed by the wet-mount method (Murray et al., 1994). Catalase, oxidase and urease activities, nitrate and nitrite reduction, hydrolysis of aesculine, DNA, gelatin and starch, production of indole and H\textsubscript{2}S, the methyl red and Voges-Proskauer reaction and citrate utilization tests were carried out as recommended by Smith & Krieg (1994). Hydrolysis of Tween was examined as described by Harrigan & McCance (1976). Determination of acid production from carbohydrates, as well as the utilization of different compounds as a single source of carbon, nitrogen and energy, was performed as recommended by Ventosa et al. (1982). Antibiotic susceptibility tests were performed on Mueller-Hinton agar [plus 7.5 % (w/v) sea salts (Ventosa et al., 1982)] seeded with a bacterial suspension containing 1.5 × 10\textsuperscript{6} c.f.u. ml\textsuperscript{-1} using discs (HiMedia) impregnated with various antimicrobial compounds. The plates were incubated at 35 °C for 48 h and the inhibition zone was interpreted according to the manufacturer’s manual. Other physiological and biochemical tests were performed as described previously (Mata et al., 2002; Quesada et al., 1984; Ventosa et al., 1982).

Strain J8B\textsuperscript{T} was Gram-stain-positive, motile and strictly aerobic. It was catalase- and oxidase-positive and produced

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Oceanobacillus halophilus sp. nov.

Fig. 1. Maximum-likelihood phylogenetic tree, based on 16S rRNA gene sequences, showing the relationship of strain J8BT with other species of the genus Oceanobacillus and related genera. Accession numbers of the sequences are given in parentheses. The sequence of Salinicribium flavidum ISL-25T (FJ357160) was used as an outgroup. Bootstrap values (%) are based on 1000 replicates. Only values higher than 70 % are shown. Bar, 0.01 substitutions per nucleotide position. Dark circles indicate that branches were also recovered using the neighbour-joining and maximum-parsimony algorithms.

Oval subterminal endospores in swollen sporangia. Cells were rod-shaped with a width of 0.8–0.9 μm and a length of 1.5–2.0 μm (Fig. S1, available in the online Supplementary Material). When grown for 2 days at 35 °C on 7.5 % HM medium, the colonies were circular, convex, entire, smooth and cream with a diameter of 3.2 mm. This isolate was moderately halophilic, growing in media containing from 3.0 to 15.0 % (w/v) NaCl and optimally in media containing 7.5 % (w/v) NaCl. No growth was observed in the absence of NaCl. The pH range for growth was 6.5–9.0 (optimum growth was at pH 8.0) and the isolate grew at 20–45 °C (optimum growth was at 35 °C). Strain J8BT was sensitive to ampicillin (10 μg per disc), bacitracin (10 U), carbenicillin (100 μg), cephalolin (30 μg), chloramphenicol (30 μg), nitrofurantoin (300 μg), penicillin G (10 U), streptomycin (10 μg), tetracycline (30 μg) and tobramycin (10 μg), but resistant to amikacin (30 μg), amoxicillin (25 μg), erythromycin (5 μg), kanamycin (5 μg), gentamicin (10 μg), nalidixic acid (30 μg), polymixin B (100 U) and rifampicin (5 μg). Other phenotypic features are included in Table 1 and the species description.

For determination of the DNA base composition and DNA–DNA hybridization, cells were disrupted by using a Constant Systems TS 0.75 kW (IUL Instruments) and the DNA in the crude lysate was purified by chromatography on hydroxyapatite, as described by Cashion et al. (1977). The DNA G+C content was determined by reversed-phase HPLC of nucleosides according to Mesbah et al. (1989). The G+C content of the DNA of strain J8BT was 39.2 mol%. This value is in the range described for species of the genus Oceanobacillus (Table 1). DNA–DNA hybridization was carried out as described by De Ley et al. (1970) with the modifications described by Huss et al. (1983), using a Cary 100 Bio UV/VIS spectrophotometer equipped with a Peltier thermostatted 6 × 6 multichannel changer and a temperature controller with an in situ temperature probe (Varian). DNA–DNA hybridization relatedness values between strain J8BT and its closest relative, Oceanobacillus profundus IBRC-M 10567T, was 10 %. Hence, according to the 70 % threshold proposed by Wayne et al. (1987) for the discrimination of prokaryotic species using DNA–DNA relatedness this result confirmed that the novel isolate constitutes a novel genospecies.

Cell biomass for fatty acid, isoprenoid quinone, polar lipid and cell-wall peptidoglycan analyses was obtained by cultivation in 7.5 % HM broth at 150 r.p.m. and 35 °C. Cells were harvested in the mid-exponential growth phase. The whole-cell fatty acid composition of strain J8BT and related taxa were determined according to the standard protocol of the Microbial Identification System (MIDI, Version 6.1; Identification Library TSBA40 4.1; Microbial ID). Extracts were analysed using a Hewlett Packard model HP6890A gas chromatograph equipped with a flame-ignition detector as described by Kämpfer & Kroppenstedt (1996). Fatty acid peaks were identified using the TSBA40 database. The fatty acid profile of strain J8BT was characterized by including the fatty acids anteiso-C15:0 (46.4 %), iso-C15:0 (24.4 %) and anteiso-C17:0 (12.6 %) as the major fatty acids.
The major isoprenoid quinone was MK-7. For analysis of the peptidoglycan the whole-cell hydrolysate (4 M HCl, 100 °C, 16 h) was analysed by chromatography on a cellulose thin-layer plate using the solvent system described in Table 1.

### Table 1. Differential characteristics between strain J8BT and phylogenetically related species of the genus Oceanobacillus

<table>
<thead>
<tr>
<th>Characteristic</th>
<th>1</th>
<th>2</th>
<th>3</th>
<th>4</th>
</tr>
</thead>
<tbody>
<tr>
<td>Endospore position</td>
<td>Subterminal</td>
<td>Terminal</td>
<td>Central</td>
<td>Terminal</td>
</tr>
<tr>
<td>Temperature for growth (°C)</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Range</td>
<td>20–45</td>
<td>15–40</td>
<td>5–48</td>
<td>8–43</td>
</tr>
<tr>
<td>Optimum</td>
<td>35</td>
<td>35</td>
<td>35</td>
<td>37</td>
</tr>
<tr>
<td>pH for growth</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Range</td>
<td>6.5–9.0</td>
<td>6.5–9.5</td>
<td>7.0–12</td>
<td>6.0–9.0</td>
</tr>
<tr>
<td>Optimum</td>
<td>8.0</td>
<td>7.5–8.5</td>
<td>9.0</td>
<td>8.0</td>
</tr>
<tr>
<td>NaCl concentration for growth (%)</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Range</td>
<td>3–15</td>
<td>0–14</td>
<td>3–12</td>
<td>0.5–24</td>
</tr>
<tr>
<td>Optimum</td>
<td>7.5</td>
<td>3</td>
<td>3</td>
<td>6–14</td>
</tr>
<tr>
<td>NaCl requirement</td>
<td>+</td>
<td>–</td>
<td>+</td>
<td>+</td>
</tr>
<tr>
<td>Nitrate reduction</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>–</td>
</tr>
<tr>
<td>Voges–Proskauer test</td>
<td>–</td>
<td>–</td>
<td>+</td>
<td>–</td>
</tr>
<tr>
<td>Hydrolysis of:</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Aesculin</td>
<td>–</td>
<td>+</td>
<td>+</td>
<td>–</td>
</tr>
<tr>
<td>Gelatin</td>
<td>–</td>
<td>+</td>
<td>–</td>
<td>+</td>
</tr>
<tr>
<td>Tween 20</td>
<td>+</td>
<td>–</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>Acid production from:</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Fructose</td>
<td>–</td>
<td>+</td>
<td>+</td>
<td>+</td>
</tr>
<tr>
<td>Galactose</td>
<td>+</td>
<td>–</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>Mannose</td>
<td>–</td>
<td>+</td>
<td>+</td>
<td>+</td>
</tr>
<tr>
<td>Mannitol</td>
<td>–</td>
<td>+</td>
<td>–</td>
<td>+</td>
</tr>
<tr>
<td>DNA G+C content (mol%)</td>
<td>39.2</td>
<td>40.2&lt;sup&gt;a&lt;/sup&gt;</td>
<td>40.6&lt;sup&gt;b&lt;/sup&gt;</td>
<td>39.7&lt;sup&gt;c&lt;/sup&gt;</td>
</tr>
</tbody>
</table>

Data taken from: a Kim et al. (2007); b Hirota et al. (2013); c Namwong et al. (2009).

The cellular fatty acid composition of strain J8BT and the type strains of phylogenetically related species of the genus Oceanobacillus are shown in Table 2. The fatty acid profile of strain J8BT was similar to those of other species of the genus Oceanobacillus in that anteiso-C<sub>15</sub>:<sub>0</sub> is the predominant fatty acid, however there were some differences in the proportions of some fatty acids, particularly iso-C<sub>14</sub>:<sub>0</sub>, iso-C<sub>15</sub>:<sub>0</sub> and anteiso-C<sub>15</sub>:<sub>0</sub> (Table 2). The polar lipids and respiratory quinones of strain J8BT were analysed as described by Groth et al. (1996). The polar lipids detected in strains J8BT were phosphatidylglycerol, diphosphatidylglycerol, five phospholipids, two aminolipids and two glycoaminolipids (Fig. S2). The polar lipid pattern is also in line with those of other species of the genus Oceanobacillus in that phosphatidylglycerol and diphosphatidylglycerol are the two dominant compounds. However, the novel isolate contained some amino(glyco)lipids as the minor phospholipids, which were not detected in other phylogenetically related species (Kim et al., 2007; Namwong et al., 2009; Hirota et al., 2013).

### Table 2. Cellular fatty acid composition of strain J8BT and the type strains of phylogenetically related species of the genus Oceanobacillus

<table>
<thead>
<tr>
<th>Fatty acid</th>
<th>1</th>
<th>2</th>
<th>3</th>
</tr>
</thead>
<tbody>
<tr>
<td>Straight-chain</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>C&lt;sub&gt;12&lt;/sub&gt;:0</td>
<td>0.7</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>C&lt;sub&gt;14&lt;/sub&gt;:0</td>
<td>0.6</td>
<td>0.8</td>
<td>2.0</td>
</tr>
<tr>
<td>C&lt;sub&gt;16&lt;/sub&gt;:0</td>
<td>4.0</td>
<td>2.5</td>
<td>9.0</td>
</tr>
<tr>
<td>C&lt;sub&gt;18&lt;/sub&gt;:0</td>
<td>TR</td>
<td>–</td>
<td>TR</td>
</tr>
<tr>
<td>Unsaturated</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>C&lt;sub&gt;16&lt;/sub&gt;:10&lt;sup&gt;c&lt;/sup&gt;O alcohol</td>
<td>–</td>
<td>2.4</td>
<td>0.5</td>
</tr>
<tr>
<td>C&lt;sub&gt;18&lt;/sub&gt;:10&lt;sup&gt;c&lt;/sup&gt;O</td>
<td>–</td>
<td>–</td>
<td>1.5</td>
</tr>
<tr>
<td>Branched chain</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>iso-C&lt;sub&gt;13&lt;/sub&gt;:0</td>
<td>0.6</td>
<td>–</td>
<td>TR</td>
</tr>
<tr>
<td>anteiso-C&lt;sub&gt;13&lt;/sub&gt;:0</td>
<td>0.7</td>
<td>–</td>
<td>0.5</td>
</tr>
<tr>
<td>iso-C&lt;sub&gt;14&lt;/sub&gt;:0</td>
<td>2.4</td>
<td>13.4</td>
<td>3.5</td>
</tr>
<tr>
<td>iso-C&lt;sub&gt;15&lt;/sub&gt;:0</td>
<td>24.4</td>
<td>4.1</td>
<td>8.5</td>
</tr>
<tr>
<td>anteiso-C&lt;sub&gt;15&lt;/sub&gt;:0</td>
<td>46.4</td>
<td>48.9</td>
<td>60.0</td>
</tr>
<tr>
<td>iso-C&lt;sub&gt;16&lt;/sub&gt;:0</td>
<td>4.0</td>
<td>16.6</td>
<td>3.6</td>
</tr>
<tr>
<td>iso-C&lt;sub&gt;17&lt;/sub&gt;:0</td>
<td>3.0</td>
<td>0.5</td>
<td>1.3</td>
</tr>
<tr>
<td>anteiso-C&lt;sub&gt;17&lt;/sub&gt;:0</td>
<td>12.6</td>
<td>10.7</td>
<td>8.6</td>
</tr>
</tbody>
</table>

Strains: 1, J8BT; 2, Oceanobacillus profundus IBRC-M 10567<sup>T</sup>; 3, Oceanobacillus polygoni JCM 17252<sup>T</sup>; 4, Oceanobacillus kapialis IBRC-M 10565<sup>T</sup>. Data are from this study unless otherwise indicated. +, Positive; –, negative.

Acids, followed by C<sub>16</sub>:0 (4.0 %), iso-C<sub>16</sub>:0 (4.0 %), iso-C<sub>17</sub>:0 (3.2 %). The cellular fatty acids profiles of the novel strain and two related species of the genus Oceanobacillus are shown in Table 2. The fatty acid profile of strain J8BT was similar to those of other species of the genus Oceanobacillus in that anteiso-C<sub>15</sub>:0 is the predominant fatty acid, however there were some differences in the proportions of some fatty acids, particularly iso-C<sub>14</sub>:0, iso-C<sub>15</sub>:0 and anteiso-C<sub>15</sub>:0 (Table 2). The polar lipids and respiratory quinones of strain J8BT were analysed as described by Groth et al. (1996). The polar lipids detected in strains J8BT were phosphatidylglycerol, diphosphatidylglycerol, five phospholipids, two aminolipids and two glycoaminolipids (Fig. S2). The polar lipid pattern is also in line with those of other species of the genus Oceanobacillus in that phosphatidylglycerol and diphosphatidylglycerol are the two dominant compounds. However, the novel isolate contained some amino(glyco)lipids as the minor phospholipids, which were not detected in other phylogenetically related species (Kim et al., 2007; Namwong et al., 2009; Hirota et al., 2013).

The major isoprenoid quinone was MK-7. For analysis of the peptidoglycan the whole-cell hydrolysate (4 M HCl, 100 °C, 16 h) was analysed by chromatography on a cellulose thin-layer plate using the solvent system described

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by RhuIand et al. (1955). The strain contained meso-
diaminopimelic acid as the diagnostic diamino acid in the
cell-wall peptidoglycan and this distinguished the
novel isolate from members of the genus Ornithinibacillus,
which contain l-ornithine in their cell-wall peptidoglycan
(Mayr et al., 2006).

In conclusion, some chemotaxonomic characteristics such
as the fatty acid and polar lipid compositions, cell-wall
peptidoglycan, as well as the phylogenetic analysis indicate
that the novel strain belongs to the genus Oceanobacillus.
However, strain J8B\(^T\) could be distinguished due to several
features such as the NaCl concentration range and the
temperature range for growth, acid production from
carbohydrates (Table 1), 16S rRNA gene sequence analysis
as well as DNA–DNA hybridization with other species of
this genus Oceanobacillus. Accordingly, the results obtained
from this polyphasic study indicate that strain J8B\(^T\)
represents a novel species of the genus Oceanobacillus,
for which the name Oceanobacillus halophilus sp. nov. is
proposed.

**Description of Oceanobacillus halophilus sp. nov.**

Oceanobacillus halophilus (ha.lo'phi.lus. Gr. n. /0 salt; Gr.

Cells of the single isolate are Gram-stain-positive, motile rods. 0.8–0.9 × 1.5–2.0 \(\mu\)m in size. Oval subterminal endo-
spores are observed in swollen sporangia. Colonies are
 circular, convex, entire, smooth, cream and 3.2 mm in
diameter after incubation for 48 h at 35 \(^\circ\)C on 7.5 % HM
agar. Strictly aerobic. Moderately halophilic, growing at NaCl concentrations from 3.0 to 15 % (w/v), with optimal
growth at 7.5 % (w/v) NaCl. No growth occurs in the absence of NaCl. Grows at 20–45 \(^\circ\)C (optimally at 35 \(^\circ\)C) and
pH 6.5–9.0 (optimally at pH 8.0). Catalase- and
oxidase-positive. Tween 20 is hydrolysed, while aesculin,
casein, DNA, gelatin, starch, Tween 40, 60 and 80, and
urea are not. Nitrate is reduced, but nitrite is not reduced.

Neither indole nor H\(_2\)S are produced. The methyl red,
Voges–Proskauer, citrate utilization, lysine and ornithine
decarboxylase and arginine dihydrolase tests are negative.

Produces acid from D-glucose, D-galactose lactose, maltose,
D-ribose, sucrose and D-xylene, but not from D-fructose
and D-mannitol. The following compounds are utilized as
the sole source of carbon and energy: cellobiose, D-fructose,
D-galactose, D-glucose, D-ribose, sucrose and D-xylene. The
following compounds are not utilized as the sole source
of carbon and energy: L-arabinose, glycerol, D-mannitol,
D-mannose, melibiose, raffinose, trehalose, L-alanine,
L-arginine, L-asparagine, L-aspartic acid, L-cysteine,
L-glutamic acid, L-hisidine, L-methionine, L-phenylalanine,
L-proline, L-tyrosine and l-valine. The major isoprenoid
quinone is MK-7. Meso-diaminopimelic acid is the diag-
nostic diamino acid. Polar lipids are phosphatidylglycerol,
diphosphatidylglycerol, five phospholipids, two aminoli-
pids and two glycolipidolipids. The predominant fatty
acids are anteiso-C\(_{15:0}\) iso-C\(_{15:0}\) and anteiso-C\(_{17:0}\).

The type strain is J8B\(^T\) (=IBRC-M 10444\(^T\)=DSM 23966\(^T\))
isolated from Aran-Bidgol hypersaline lake, Iran. The DNA
G+C content of the type strain is 39.2 mol% (HPLC).

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