A novel Gram-positive-staining, aerobic, spore-forming, rod-shaped bacterium, designated strain YIM 91119\(^T\), was isolated from Ebinur Lake in Xinjiang Province, north-west China. Cells were motile, produced terminal endospores and grew at pH 6.0–8.0 (optimally at pH 7.0), 4–45 °C (optimally at 28–37 °C) and 1–22 % (w/v) NaCl, (optimally at 10–15 %, w/v). Comparative 16S rRNA gene sequence analysis showed that strain YIM 91119\(^T\) belongs to the genus *Gracilibacillus*, exhibiting the highest sequence similarity with respect to the type strain of *Gracilibacillus orientalis* (97.8 %); the next most similar 16S rRNA gene sequences were those of the type strains of *Gracilibacillus boraciitolerans* (96.8 %), *Gracilibacillus dipsosauri* (96.5 %) and *Gracilibacillus halotolerans* (95.8 %). DNA–DNA hybridization with G. *orientalis* AS 1.4250\(^T\) showed a relatedness of 55 %. The major fatty acids of strain YIM 91119\(^T\) were anteiso-C\(_{15:0}\), iso-C\(_{15:0}\) and anteiso-C\(_{17:0}\). The peptidoglycan type was A1\(\_\_\)L (directly cross-linked meso-diaminopimelate). The genomic DNA G+C content was 40.1 mol% and the predominant respiratory quinone was MK-7. The major polar lipids were diphosphatidylglycerol, phosphatidylglycerol and phosphatidylyethanolamine. On the basis of the evidence from this polyphasic study, strain YIM 91119\(^T\) represents a novel species of the genus *Gracilibacillus*, for which the name *Gracilibacillus saliphilus* sp. nov. is proposed, with YIM 91119\(^T\) (=DSM 19802\(^T\) =CCTCC AA 208015\(^T\)) as the type strain.
the pH was 7.2 and the major ions were Na\(^+\) (4.2 %), Mg\(^{2+}\) (0.2 %), Ca\(^{2+}\) (0.4 %), Cl\(^-\) (2.1 %) and SO\(_4^{2-}\) (3.0 %). For isolation, serial dilutions of the sample were spread on modified ISP5 medium (containing 1 g L-asparagine, 10 g glycerol, 5 g yeast extract, 1 g K\(_2\)HPO\(_4\), 5 g KNO\(_3\), 100 g NaCl and 15 g agar, per litre distilled water). Colonies were picked and repeatedly restreaked onto modified ISP5 medium, until purity was confirmed. After the strain had grown to late-exponential phase on modified ISP5 medium, its cell morphology and flagellation were investigated using a transmission electron microscope (H-800; Hitachi). The Gram reaction was determined using the KOH lysis method (Cerny, 1978). Cell motility was confirmed by the presence of turbidity throughout a tube containing semisolid medium (Leifson, 1960). Methyl red and Voges–Proskauer tests were performed as described previously (Smibert & Krieg, 1981). The temperature range for growth was determined by incubating cells for 1 week on modified ISP5 medium at the following temperatures: 0, 4, 10, 15, 20, 28, 37, 45 and 55 °C. The pH growth range was investigated between pH 4.0 and pH 10.0 (in increments of 1 pH unit), using the buffer system described by Xu et al. (2005). NaCl concentrations between 0 and 30 % (w/v) were tested, using modified ISP5 as the basal medium. Catalase activity was determined by assessing bubble production after the addition of a drop of 3 % \(\text{H}_2\text{O}_2\). Oxidase activity was determined by assessing the oxidation of tetramethyl-\(p\)-phenylenediamine. Hydrolysis of casein, starch and Tweens 40 and 80 were determined as described by Cowan & Steel (1965). Metabolic properties and enzyme activities were determined by means of the API 20E, API 50 CHB and API ZYM systems (bioMérieux) according to the manufacturer’s instructions. The utilization of different compounds as sole carbon or nitrogen and energy sources was tested as described by Carrasco et al. (2006). The sensitivity of strain YIM 91119\(^T\) to antibiotics was tested using Sensi-Discs after incubation for 72 h on modified ISP5 medium. \(G.\) \(orientalis\) AS 1.4250\(^T\) (obtained from the China General Microbiological Culture Collection Center, Academia Sinica, Beijing) was used as a reference strain for phenotypic and DNA–DNA hybridization studies. The morphological, cultural and physiological properties of strain YIM 91119\(^T\) are given in Table 1 and in the species description.

Peptidoglycan was purified and the cell-wall amino acids and peptides in cell-wall hydrolysates were analysed by means of two-dimensional ascending TLC on cellulose plates with the solvent systems of Schleifer & Kandler.

### Table 1. Characteristics that serve to differentiate strain YIM 91119\(^T\) and closely related previously described species

<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>Pigmentation</td>
<td>Creamy white</td>
<td>Cream</td>
<td>Light pink to red</td>
<td>White</td>
<td>Creamy white</td>
</tr>
<tr>
<td>Spore shape*</td>
<td>S</td>
<td>S</td>
<td>S/E</td>
<td>S</td>
<td>E</td>
</tr>
<tr>
<td>NaCl concentration for growth</td>
<td>(%, w/v)</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Range</td>
<td>1–22</td>
<td>1–20</td>
<td>0–11</td>
<td>0–15</td>
<td>0–20</td>
</tr>
<tr>
<td>Optimum</td>
<td>10–15</td>
<td>10</td>
<td>0.5–3.0</td>
<td>3</td>
<td>0</td>
</tr>
<tr>
<td>pH range</td>
<td>6.0–8.0</td>
<td>5.0–9.0</td>
<td>6.0–9.7</td>
<td>ND</td>
<td>5.0–10.0</td>
</tr>
<tr>
<td>Temperature range (°C)</td>
<td>4–45</td>
<td>4–45</td>
<td>16–37</td>
<td>28–50</td>
<td>6–50</td>
</tr>
<tr>
<td>Nitrate reduction</td>
<td>+</td>
<td>–</td>
<td>–</td>
<td>+</td>
<td>+</td>
</tr>
<tr>
<td>Oxidase activity</td>
<td>+</td>
<td>–</td>
<td>+</td>
<td>+</td>
<td>+</td>
</tr>
<tr>
<td>H(_2)S production</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>+</td>
</tr>
<tr>
<td>Voges–Proskauer</td>
<td>+</td>
<td>ND</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>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>Tween 80</td>
<td>–</td>
<td>–</td>
<td>ND</td>
<td>ND</td>
<td>+</td>
</tr>
<tr>
<td>Polar lipids†</td>
<td>DPG, PG, PE, APL, PGL, GL</td>
<td>DPG, PG, PE, PL, APL</td>
<td>DPG, PE, PL</td>
<td>DPG, PG, PL</td>
<td>DPG, PG, PL</td>
</tr>
<tr>
<td>Major fatty acid(s) (&gt;10 %)</td>
<td>i-C(<em>{15}), ai-C(</em>{15}), ai-C(_{17})</td>
<td>i-C(<em>{15}), ai-C(</em>{15}), ai-C(_{17})</td>
<td>i-C(<em>{15}), ai-C(</em>{15}), ai-C(_{17})</td>
<td>i-C(<em>{15}), ai-C(</em>{15}), ai-C(_{17})</td>
<td>ai-C(_{15})</td>
</tr>
<tr>
<td>DNA G + C content (mol%)</td>
<td>40.1</td>
<td>37.1</td>
<td>35.8</td>
<td>39.4</td>
<td>38</td>
</tr>
</tbody>
</table>

*E, Ellipsoidal; S, spherical.
†APL, Aminophospholipid; DPG, diphasatidylglycerol; GL, unknown glycolipid; PE, phosphatidylethanolamine; PG, phosphatidylglycerol; PGL, phosphoglycolipid; PI, phosphatidylinositol; PL, phospholipid.

http://ijs.sgmjournals.org
(1972). For fatty acid analysis, cells of strain YIM 91119<T> were cultured on tryptic soy agar (Difco) containing 10 % NaCl at 37 °C for 48 h. Analysis of the cellular fatty acid pattern was performed as described by Sasser (1990), using the Microbial Identification System (MIDI). Menaquiones were isolated using the methods of Minnikin et al. (1984) and were separated using HPLC (Kroppenstedt, 1982). Polar lipids were extracted, examined by two-dimensional TLC and identified using published procedures (Minnikin et al., 1984). The peptido glyc can contained directly cross-linked meso-diaminopimelic acid, type A3 (peptidoglycan type A1γ; http://www.dsmz.de/microorganisms/main.php?content_id=35), which is characteristic of the genus Gracilibacillus. The cellular fatty acid composition of strain YIM 91119<T> was anteiso-C<sub>15:0</sub> (32.9%), iso-C<sub>15:0</sub> (22.2%), anteiso-C<sub>17:0</sub> (16.5%), C<sub>16:0</sub> (7.2%), iso-C<sub>17:0</sub> (6.1%), C<sub>15:0</sub> (3.6%) and C<sub>17:0</sub> (3.0%). The predominant menaquinone was menaquinone-7 (MK-7). The major polar lipids were diphosphatidylglycerol, phosphatidylglycerol and phosphatidylethanolamine (Supplementary Fig. S1, available in IJSEM Online). All of these features are consistent with the chemotaxonomic description of the genus Gracilibacillus (Wainø et al., 1999).

Genomic DNA was extracted and purified according to the method described by Li et al. (2007). The 16S rRNA gene was amplified by means of a PCR with primers Eubac 27F and 1492R (DeLong, 1992) and the PCR products were purified using a Sangon PCR purification kit. The purified PCR product was sequenced using the ABI PRISM BigDye Terminator cycle sequencing kit (Applied Biosystems) and an automatic DNA sequencer (model 310; Applied Biosystems). The resulting sequence data were analysed with the GenBank programs BLASTN and BLASTX. Sequences were aligned using CLUSTAL X (Thompson et al., 1997) and the alignment was corrected manually. Gaps at the 5’ and 3’ ends of the alignment were omitted from further analyses. Phylogenetic analyses were performed using three tree-making algorithms, the neighbour-joining (Saitou & Nei, 1987), maximum-likelihood (Felsenstein, 1981) and maximum-parsimony (Fitch, 1971) methods. A neighbour-joining phylogenetic tree was constructed from K<sub>max</sub> values (Kimura, 1980) by 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 (1501 bp) was obtained for strain YIM 91119<T>. Fig. 1 shows the relationship between the novel strain and its closest phylogenetic relatives. The levels of 16S rRNA gene sequence similarity between strain YIM 91119<T> and the type strains of species from the genus Gracilibacillus were as follows: 97.8 % (G. orientalis), 96.8 % (G. boraciitolerans), 96.5 % (G. dipsosauri) and 95.8 % (G. halotolerans). In the neighbour-joining phylogenetic tree, strain YIM 91119<T> clustered with G. orientalis XH-63<T> (Fig. 1). The results of the 16S rRNA gene sequence comparisons clearly demonstrated that strain YIM 91119<T> was a member of the genus Gracilibacillus. The topologies of the phylogenetic trees constructed using the maximum-likelihood and maximum-parsimony algorithms were similar to that of the neighbour-joining tree (data not shown).

The genomic G+C content of the DNA of strain YIM 91119<T> was determined according to the method of Mesbah et al. (1989), using DNA from Escherichia coli K-12 as a control. DNA–DNA hybridization was performed fluorometrically using the method of Ezaki et al. (1989), with photobiotin-labelled DNA probes and microdilution wells. The genomic G+C content of the DNA of strain YIM 91119<T> was 40.1 mol%. The genomic relatedness between strain YIM 91119<T> and G. orientalis AS 1.4250<T> was 55 %, which is lower than the cut-off point (70 %) recommended by Wayne et al. (1987) for assigning strains to the same species.

On the basis of the phenotypic (Table 1), chemotaxonomic (Table 1 and Supplementary Table S1), phylogenetic (Fig. 1) and DNA–DNA hybridization data indicating differences between the strain isolated from Lake Ebinur and previously described Gracilibacillus species, YIM 91119<T> represents a novel species of the genus, for which we propose the name Gracilibacillus saliphilus sp. nov.

![Fig. 1.](image-url)
**Description of Gracilibacillus saliphilus sp. nov.**

*Gracilibacillus saliphilus* (sa.li’ phi.lus. L. n. sal, salis salt; Gr. adj. philos loving; N.L. masc. adj. saliphilus salt-loving).

Cells are Gram-positive-staining, aerobic, thin rods, 0.7–0.9 × 2.0–10.0 μm (Fig. 2). Cells are motile and spherical endospores are produced in a terminal position. Colonies are circular, creamy white, convex, opaque and 0.5–1 mm in diameter on modified ISP5 medium. Moderately halophilic, growing over a wide range (1–22 %, w/v) of NaCl concentrations (optimally at 10–15 %, w/v). No growth occurs in the absence of NaCl. Growth occurs at 4–45 °C and pH 6.0–8.0; optimal growth occurs at 28–37 °C and pH 7.0. Positive for oxidase and catalase and in the methyl red and Voges–Proskauer tests. Indole and H2S are not produced. Negative (in API 20E tests) for ONPG, lysine and ornithine decarboxylases, arginine dihydrolase and tryptophan deaminase. Nitrate is reduced. Aesculin, gelatin, starch and urea are hydrolysed, but casein, gelatin and Tweens 40 and 80 are not hydrolysed. Acids are produced (in API 50 CHB tests) from N-acetylgalactosamine, aesculin, amygdalin, D- and L-arabinose, arbutin, cellubiose, D-fructose, L-fucose, D-galactose, gentiobiose, methyl α-D-glucopyranoside, D-glucose, glycerol, glycosgen, lactose, D-lyxose, maltose, D-mannose, D-mannitol, melibiose, potassium gluconate, potassium 2-ketogluconate, potassium 5-ketogluconate, raffinose, L-rhamnose, D-ribose, sucrose, salicin, L-sorbose, starch, D-tagatose, trehalose, turanose, methyl β-D-xylpyranoside and D-xylene. In the API ZYM system, results are positive for alkaline phosphatase, esterase lipase (C8), naphthol-AS-BI-phosphohydrolase, β-galactosidase and β-glucosidase, but negative for α-chymotrypsin, cystine arylamidase, esterase (C4), α-galactosidase, α-glucosidase, β-glucuronidase, acetyl-β-glucosaminidase, α-fucosidase, leucine arylamidase, lipase (C14), α-mannosidase, acid phosphatase, trypsin and valine arylamidase. L-Arginine, cellubiose, glycine and L-lysine are utilized as sole carbon, nitrogen and energy sources, but the following substrates are not: acetate, adenine, aspartic acid, citrate, dulcitol, L-histidine, hypoxanthine, inositol, propionate, L-proline, L-serine, L-threonine, L-tyrosine, xanthine and xylitol. Resistant to the following antibiotics: amikacin (30 μg), ampicillin (10 μg), ciprofloxacin (5 μg), erythromycin (15 μg), gentamicin (10 μg), novobiocin (30 μg), streptomycin (10 μg), tobramycin (10 μg) and vancomycin (30 μg). Susceptible to amoxicillin (10 μg), chloramphenicol (30 μg), lincomycin (2 μg), neomycin (10 μg), netilmicin sulfate (30 μg), norfloxacin (10 μg), penicillin (10 U), rifampicin (5 μg), trimethoprim sulfonamides (1.25 mg) and tetracycline (30 μg). The predominant isoprenoid quinone is MK-7. The polar lipids consist of diphosphatidylglycerol, phosphatidylglycerol, phosphatidylethanolamine, phosphatidylinositol, four unknown phosphoglycolipids, an unknown aminophospholipid and unknown glycolipids (Supplementary Fig. S1). The cellular fatty acid composition includes (in decreasing abundance) anteiso-C15:0, iso-C15:0, anteiso-C17:0, C16:0, iso-C17:0, C15:0 and C17:0. The DNA G+C content of the type strain is 40.1 mol%.

The type strain, YIM 91119T (=DSM 19802T =CCTCC AA 208015T), was isolated from a saline soil collected from Ebinur Lake in Xinjiang Province, north-west China.

**Acknowledgements**

This research was supported by the National Basic Research Program of China (no. 2004CB719601), the National Natural Science Foundation of China (30600001, 30870005), the Open Project Program of the Extremophiles Lab. of Xinjiang (no. XJYS0203-2003-01) and the Youth Technological Innovation Foundation of Xinjiang Academy of Agricultural Science (no. 2007Q07). W.-J. L. was supported by the Program for New Century Excellent Talents in University.

**References**


Cui, H.-L., Tohty, D., Feng, J., Zhou, P.-J. & Liu, S.-J. (2006a). *Natronorubrum aibiense* sp. nov., an extremely halophilic archaeon isolated from Aibi salt lake in Xin-Jiang, China, and emended...


