**Sediminibacillus albus** sp. nov., a moderately halophilic, Gram-positive bacterium isolated from a hypersaline lake, and emended description of the genus *Sediminibacillus* Carrasco *et al.* 2008

Xiaowei Wang,¹,² Yanfen Xue¹ and Yanhe Ma¹

¹State Key Laboratory of Microbial Resources, Institute of Microbiology, Chinese Academy of Sciences, 100101 Beijing, PR China
²Graduate University of the Chinese Academy of Sciences, 100049 Beijing, PR China

A moderately halophilic, Gram-positive-staining, endospore-forming, rod-shaped and strictly aerobic bacterium, designated strain NHBX5⁵, was isolated from Lake Nanhuobuxun in China. Strain NHBX5⁵ was able to grow at NaCl concentrations of 0–22 % (w/v) (optimally at 7 %, w/v), at pH 6.0–9.0 (optimally at pH 7.5) and at temperatures of 10–45 °C (optimally at 37 °C). The cell-wall peptidoglycan of strain NHBX5⁵ contained meso-diaminopimelic acid as the diagnostic diamino acid. The predominant isoprenoid quinone was MK-7. The major cellular fatty acids were anteiso-C₁₅:₀ and anteiso-C₁₇:₀. The polar lipids were phosphatidylglycerol, diphasphatidylglycerol and a glycolipid. The genomic DNA G+C content of strain NHBX5⁵ was 44.9 mol%. Phylogenetic analysis based on 16S rRNA gene sequence comparisons revealed that strain NHBX5⁵ was most closely related to *Sediminibacillus halophilus* EN8dT (98.6 % gene sequence similarity). The level of DNA–DNA relatedness between strain NHBX5⁵ and *S. halophilus* CGMCC 1.6199⁵ was 34.6 %. Based on the data presented, strain NHBX5⁵ represents a novel species of the genus *Sediminibacillus*, for which the name *Sediminibacillus albus* sp. nov. is proposed. The type strain is NHBX5⁵ (=DSM 19340T = CGMCC 1.6502T). In addition, an emended description of the genus *Sediminibacillus* is presented.

Moderately halophilic bacteria that can grow optimally in media containing salt concentrations of 3–15 % (w/v) make up an extremely heterogeneous group of microorganisms that are distributed widely in diverse saline habitats such as salt lakes, brines, saline soils, soda lakes, salted foods and some other hypersaline environments (Kushner, 1985; Ventosa et al., 1998). The genus *Sediminibacillus*, which belongs to this moderately halophilic group of bacteria, was first proposed by Carrasco *et al.* (2008) to accommodate moderately halophilic, facultatively anaerobic, Gram-positive, rod-shaped bacteria related phylogenetically to members of the genera *Thalassobacillus* and *Halobacillus* within the family *Bacillaceae*. The genus *Sediminibacillus* comprises the single species *Sediminibacillus halophilus*, the type strain of which was isolated from sediment of Lake Eriannor in Inner Mongolia, China. During the course of an investigation of the diversity of halophilic microorganisms in Nanhuobuxun salt lake (36° 43’ 14.7” N 95° 42’ 41” E), a spore-forming, Gram-positive, moderately halophilic strain (NHBX5⁵) was isolated that appeared to represent a novel species of the genus *Sediminibacillus*. In this study, the phenotypic, chemotaxonomic and genotypic characteristics of this moderately halophilic strain are presented.

Nanhuobuxun salt lake is located at 2700 m above sea level in the south-east Bieletan region of Qaidam basin of Qinghai province, China. It is a very typical chloride saline lake, with a high salinity of 31.8 % and a near-neutral pH of 6.7. Strain NHBX5⁵ was isolated from a sediment sample of Nanhuobuxun salt lake by enrichment in liquid SG medium (Sehgal & Gibbons, 1960) at 37 °C followed by serial dilution plating of enrichment cultures on SG agar medium (pH adjusted to 7.0–7.2 with 1 M NaOH before autoclaving at 121 °C for 20 min) containing the following (g l⁻¹): Casamino acids (Difco), 7.5; yeast extract (Difco), 10.0; sodium glutamate, 1.0; trisodium citrate, 3.0; MgSO₄·7H₂O, 20.0; KCl, 2.0; NaCl, 200; FeSO₄·7H₂O, 0.036; and MnCl₂·4H₂O, 0.00036. Strain NHBX5⁵ was cultured routinely on growth medium (GM; pH 7.0–7.5) containing the following (g l⁻¹): Casamino acids (Difco), 7.5; yeast extract (Difco), 10.0; sodium glutamate, 1.0; trisodium citrate, 3.0; MgSO₄·7H₂O, 20.0; KCl, 2.0; NaCl, 200; FeSO₄·7H₂O, 0.036; and MnCl₂·4H₂O, 0.00036.

The GenBank/EMBL/DDBJ accession number for the 16S rRNA gene sequence of strain NHBX5⁵ is DQ989634.

A scanning electron micrograph of cells of strain NHBX5⁵ and the cellular fatty acid profiles of strain NHBX5⁵ and *S. halophilus* EN8dT are available as supplementary material with the online version of this paper.
Strain NHBX5T was maintained in this medium supplemented with 30 % (v/v) glycerol at ~80 °C for long-term preservation. S. halophilus CGMCC 1.6199T was obtained from the Chinese General Microbiological Culture Collection and used as a reference strain for comparative phenotypic studies and DNA–DNA hybridization tests. The recommended medium and culture conditions for growth of this bacterium were used.

The morphology, pigmentation and size of colonies were observed on GM agar after 48 h incubation at 37 °C. Cell morphology and motility were examined using light and scanning electron microscopes. Gram-type was determined by the staining method (Doetsch, 1981) and the KOH lysis method (Gregersen, 1978). The range of NaCl concentration for growth was determined in modified GM medium with different NaCl concentrations (0, 1, 3, 5, 7, 9, 12, 16, 20, 22 and 25 %, w/v). The pH range for growth was tested at intervals of 0.5 pH unit in liquid GM medium buffered with 20 mM MES (pH 5.0–6.5), PIPES (pH 6.5–7.5), HEPES (pH 7.0–8.0), Tricine (pH 7.5–9.0) and CHES (pH 9.0–10.0). Growth at different temperatures (4, 10, 15, 20, 25, 30, 37, 40, 45 and 50 °C) was determined in GM medium. General biochemical tests (including the presence of oxidase and catalase, urease activity, H2S production, nitrate reduction, NH₃ production, citrate utilization, indole production, Voges–Proskauer reaction, methyl red test and hydrolysis of Tweenes 20, 40, 60 and 80, gelatin, aesculin, starch and casein) were performed according to previously described methods (Smibert & Krieg, 1981; Ventosa et al., 1982). Anaerobic growth in the presence of nitrate was tested as described previously (Mancinelli & Hochstein, 1986). The utilization of glucose by oxidation or fermentation and of various substrates as sole carbon and energy sources were determined as described previously (Ventosa et al., 1982). Unless otherwise indicated, all tests were carried out in triplicate in media containing 7 % (w/v) NaCl at 37 °C. Growth was monitored by turbidity at OD₆₀₀. API 50CH test strips (Analytab Products; bioMérieux) were also used to examine assimilation of carbohydrates and the production of acid as recommended by the manufacturer, but with a modification that the suspension medium supplied by bioMérieux and used to resuspend cells of strain NHBX5T was supplemented with 7 % (w/v) NaCl. Susceptibility to antimicrobial agents was tested by spreading exponential-phase cultures on GM agar medium plates with absorbent paper discs impregnated with antimicrobial agents. Zones of inhibition were determined after incubation at 37 °C for 3 days.

Cells of strain NHBX5T were aerobic rods and formed terminal ellipsoidal or spherical endospores after 48 h incubation at 37 °C on GM agar supplemented with 5 mg MnSO₄.1-1 (see Supplementary Fig. S1, available in IJSEM Online). Anaerobic growth of strain NHBX5T was not detected in the presence of glucose or nitrate. Nitrate reduction by strain NHBX5T under aerobic conditions was not observed. Strain NHBX5T utilized glucose by oxidation. It was moderately halophilic, growing in modified GM medium with 0–22 % (w/v) NaCl (optimally at 7 %). Other phenotypic features are presented in the species description.

Preparation of the cell wall and determination of peptidoglycan structure were performed by the methods described by Schleifer & Kandler (1972) with the modification that the TLC on cellulose sheets was used instead of paper chromatography. The amino acid composition of the cell wall hydrolysate was determined using one-dimensional descending film chromatography on cellulose sheets. Respiratory quinones were extracted according to the method of Collins et al. (1977) and analysed by reversed-phase HPLC (Groth et al., 1996). Polar lipids were extracted and identified by one-dimensional TLC followed by spraying with the appropriate detection reagent (Kates, 1986). Fatty acids were extracted, methylated and analysed by GC using the standard Sherlock MIDI (Microbial Identification) system (Sasser, 1990; Kämpfer & Kroppenstedt, 1996). Genomic DNA of strain NHBX5T was extracted using the method described by Marmur (1961). Cell mass used for procedures mentioned above was obtained by cultivating the strain at 37 °C on GM agar. The genomic DNA G+C content was determined by the thermal denaturation method according to Marmur & Doty (1962).

Strain NHBX5T possessed peptidoglycan type A1γ with meso-diaminopimelic acid as the diagnostic diamino acid. The isoprenoid quinones detected in strain NHBX5T were MK-7 (96.9 %) and MK-6 (3.1 %). The cellular polar lipids were dihydroxybutyrylglycerol, phosphatidylglycerol and a glycolipid. The major fatty acids (>1 %) in cells of strain NHBX5T were branched anteiso-C₁₅:₀ (45.1 %), anteiso-C₁₇:₀ (30.7 %), iso-C₁₅:₀ (9.0 %), iso-C₁₆:₀ (4.8 %) and iso-C₁₇:₀ (1.4 %) and straight-chain C₁₆:₀ (3.5 %). The genomic DNA G+C content of strain NHBX5T was 44.9 mol%. These chemotaxonomic data are in accordance with those described for the genus Sediminibacillus.

The 16S rRNA gene was amplified by PCR using universal bacterial primers (8F and 1495R) as described previously (Duckworth et al., 1996). The almost-complete nucleotide sequence (1468 bp) was determined by direct sequencing and compared with available 16S rRNA gene sequences in GenBank by using the BLAST program. Multiple alignment with sequences from closely related species was performed by using the program CLUSTAL_X (Thompson et al., 1997). Ambiguous and unalignable bases were manually omitted and then the phylogenetic tree was constructed from the evolutionary distance matrix calculated by using the neighbour-joining, minimum-evolution and maximum-parsimony methods in the program MEGA version 3.1 (Kumar et al., 2004). The robustness of the resultant tree topology was evaluated by bootstrap resampling analysis with 1000 replicates (Felsenstein, 1985). A comparative analysis using 16S rRNA gene sequences available in the database revealed that strain NHBX5T was most closely
related to *S. halophilus* EN8dT, with a sequence similarity of 98.6 %, and had less than 96.7 % gene sequence similarity to other known species of the closely related genera, such as 94.4–96.7 % to members of the genus *Virgibacillus*, 95.2–96.3 % to members of the genus *Halobacillus*, 95.2 % to the type strain of *Thalassobacillus devorans* (the sole species of the genus *Thalassobacillus*), 94.4–95.3 % to members of the genus *Gracilibacillus* and 93.9–95.2 % to members of the genus *Amphibacillus*. The phylogenetic tree (Fig. 1) based on the neighbour-joining method showed that strain NHBX5T clustered with *S. halophilus* EN8dT with significant bootstrap support (100 %). Topologies of phylogenetic trees constructed using the minimum-evolution and maximum-parsimony algorithms were similar to that of the tree constructed using neighbour-joining analysis (data not shown). DNA–DNA hybridization was performed by the spectrophotometric renaturation rate method (Huß et al., 1983; De Ley et al., 1970) to determine the level of genomic DNA relatedness between strain NHBX5T and *S. halophilus* CGMCC 1.6199T. The level of DNA–DNA relatedness between strain NHBX5T and *S. halophilus* CGMCC 1.6199T was 34.6 % (mean of three independent experiments, which did not differ by more than 4 %). This low value indicates that strain NHBX5T is not related genotypically to *S. halophilus* CGMCC 1.6199T.

Several phenotypic features that also distinguish strain NHBX5T from *S. halophilus* EN8dT are shown in Table 1. Strain NHBX5T was strictly aerobic, whereas *S. halophilus* EN8dT was able to grow under anaerobic conditions. Cells of *S. halophilus* EN8dT did not display endospores, whereas strain NHBX5T easily formed ellipsoidal or spherical endospores, causing swelling of sporangia. Differences in other features such as pigmentation, range of temperature for growth, nitrate reduction and H2S production and the genomic DNA G+C content enable strain NHBX5T to be distinguished from *S. halophilus* EN8dT.

Therefore, on the basis of the polyphasic evidence above, strain NHBX5T represents a novel species of the genus *Sediminibacillus*. The name *Sediminibacillus halophilus* sp. nov. is proposed for this species. Based on differential phenotypic characteristics of strain NHBX5T not reported in the description of the genus *Sediminibacillus* by Carrasco et al. (2008), an emended description of the genus is presented.

**Emended description of the genus *Sediminibacillus* Carrasco et al. 2008**

The description of the genus *Sediminibacillus* is as given by Carrasco et al. (2008) with the following amendments. Endospores may be formed terminally in swollen sporangia or not be observed. Cells are aerobic or facultatively anaerobic. Nitrate may or may not be reduced. The genomic DNA G+C content ranges from 44.9 to 47.5 mol%. The type species is *Sediminibacillus halophilus*.

**Description of *Sediminibacillus albus* sp. nov.**

*Sediminibacillus albus* (al’bus. L. masc. adj. albus white).

Cells are Gram-positive-staining rods (0.4–0.6 × 2.0–4.0 μm), strictly aerobic, spore-forming and motile by means of peritrichous flagella. Ellipsoidal or spherical endospores are formed terminally in swollen sporangia. Cells occur singly, in pairs or in short chains. After cultivation on GM agar at 37 °C for 2 days, colonies are circular, white, opaque and slightly convex, 1.5–2.0 mm in diameter. Grows at 10–45 °C (optimum 37 °C) and at pH 5.5–9.0 (optimum pH 7.5). Can grow at NaCl concentrations between 0 and 22 % (w/v) with optimum growth at 7 % (w/v) NaCl. Positive for oxidase, catalase, methyl red reaction, H2S production from thiosulfate, NH3 production from peptone, indole production, citrate utilization and hydrolysis of gelatin, aesculin and Tween 20, 40, 60 and 80, but is negative for the Voges–Proskauer reaction, nitrate reduction, urease production and casein hydrolysis. Produces acids from D-glucose by oxidation. Produces acid in the API 50CH gallery from glycerol, L-arabinose, D-xylose, D-glucose, D-galactose, D-fructose, D-mannose, L-sorbose, L-rhamnose, mannotol, amygdalin, arbutin, salicin, starch, cellobiose, maltose, lactose, melibiose, trehalose, gentiobiose and N-acetylglucosamine, but not from D-sorbitol, sucrose, erythritol, D-ribose, turanose, D-arabinose, D-adonitol, methyl β-D-xylopyranoside, dulcitol, inositol, methyl-α-D-glucopyranoside, inulin, melezi-

![Fig. 1. Phylogenetic tree showing the relationship between strain NHBX5T and related strains based on 16S rRNA gene sequences. Numbers at nodes represent the levels of bootstrap support (%) based on a neighbour-joining analysis of 1000 resampled datasets. Accession numbers of nucleotide sequences are given in parentheses. Bar, 1% sequence divergence.](image-url)
Table 1. Characteristics that distinguish strain NHBX5<sup>T</sup> from <i>S. halophilus</i> EN8d<sup>T</sup>

Data for <i>S. halophilus</i> EN8d<sup>T</sup> were taken from Carrasco et al. (2008). Both strains are rod-shaped, motile and positive for Gram-staining reaction, oxidase, catalase and the Voges–Proskauer reaction. Both strains hydrolyse aesculin, gelatin and Tween 80, but not casein or starch. Both strains produce acid from D-glucose, D-galactose, D-mannose, trehalose, D-fructose and glycerol. The following compounds are utilized as sole carbon and energy sources: D-arabinose, cellobiose, D-galactose and D-lactose. The following compounds are not utilized as sole carbon and energy sources: D-mannose and D-sorbitol. The following compounds are not used as sole carbon, nitrogen and energy sources: L-arginine, aspartic acid, L-cysteine, glutamic acid, L-methionine and phenylalanine. +, Positive; −, negative; ND, not observed.

<table>
<thead>
<tr>
<th>Characteristic</th>
<th>Strain NHBX5&lt;sup&gt;T&lt;/sup&gt;</th>
<th>S. halophilus EN8d&lt;sup&gt;T&lt;/sup&gt;</th>
</tr>
</thead>
<tbody>
<tr>
<td>Colony pigmentation</td>
<td>White</td>
<td>Cream</td>
</tr>
<tr>
<td>Size of cells (μm)</td>
<td>0.4–0.6 x 2.0–4.0</td>
<td>0.9 x 1.5–7.0</td>
</tr>
<tr>
<td>Spore formation</td>
<td>+</td>
<td>ND</td>
</tr>
<tr>
<td>Anaerobic growth</td>
<td>−</td>
<td>+</td>
</tr>
<tr>
<td>pH range for growth</td>
<td>5.5–9.0</td>
<td>5.0–9.5</td>
</tr>
<tr>
<td>Temperature range for growth (°C)</td>
<td>10–45</td>
<td>20–55</td>
</tr>
<tr>
<td>NaCl concentration for growth (% w/v)</td>
<td>Range</td>
<td>Optimum</td>
</tr>
<tr>
<td></td>
<td>0–22</td>
<td>7.0</td>
</tr>
<tr>
<td></td>
<td></td>
<td>5.0–7.5</td>
</tr>
<tr>
<td>Indole test</td>
<td>+</td>
<td>−</td>
</tr>
<tr>
<td>Nitrate reduction</td>
<td>−</td>
<td>+</td>
</tr>
<tr>
<td>H&lt;sub&gt;2&lt;/sub&gt;S production</td>
<td>+</td>
<td>−</td>
</tr>
<tr>
<td>Utilization of maltose, melibiose and D-xylene as sole carbon and energy sources</td>
<td>+</td>
<td>−</td>
</tr>
<tr>
<td>Utilization of L-alanine and L-serine as sole carbon and energy sources</td>
<td>−</td>
<td>+</td>
</tr>
<tr>
<td>DNA G + C content (mol%)</td>
<td>44.9</td>
<td>47.5</td>
</tr>
</tbody>
</table>

Acknowledgements

This work was supported by grants from the Ministry of Science and Technology of China (973 programs 2003CB716001 and 2004CB719605; 863 programs 2006AA020201 and 2007AA021306) and the Chinese Academy of Sciences (Knowledge Innovation program, KSCX2-YW-G-011).

References


