Halobacillus andaensis sp. nov., a moderately halophilic bacterium isolated from saline and alkaline soil

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A Gram-stain-positive, endospore-forming, moderately halophilic bacterial strain, NEAU-ST10-40T, was isolated from a saline and alkaline soil in Anda City, China. It was strictly aerobic, rod-shaped and motile by peritrichous flagella. It formed light yellow colonies and grew at NaCl concentrations of 3–15 % (w/v) (optimum, 8 %, w/v), at pH 7.0–9.0 (optimum, pH 8.0) and at 4–60 °C (optimum, 30 °C). It contained meso-diaminopimelic acid in the cell-wall peptidoglycan. Phylogenetic analysis based on 16S rRNA gene sequences indicated that it belonged to the genus Halobacillus. Levels of 16S rRNA gene sequence similarity between strain NEAU-ST10-40T and the type strains of related species of the genus Halobacillus ranged from 98.8 % (Halobacillus alkaliphilus FP5T) to 97.1 % (Halobacillus kuroshimensis IS-Hb7T). DNA–DNA hybridization relatedness values between strain NEAU-ST10-40T and H. alkaliphilus DSM 18525T, Halobacillus campisalis KCTC 13144T, Halobacillus yeomjeoni DSM 17110T, Halobacillus halophilus DSM 2266T, Halobacillus litoralis DSM 10405T, Halobacillus dabanensis DSM 18199T, Halobacillus salinus DSM 18897T, Halobacillus naozhouensis DSM 21183T, Halobacillus trueperi DSM 10404T and Halobacillus salsuginis DSM 21185T were from 43 ± 1 to 19 ± 1 % (mean ± sd). The DNA G + C content was 39.3 mol%. The major fatty acids (>10 %) were anteiso-C15:0, anteiso-C17:0 and iso-C16:0, the only respiratory quinone detected was MK-7, and polar lipids consisted of diphosphatidylglycerol, phosphatidylethanolamine, phosphatidylglycerol, two unknown phospholipids and three unknown lipids. On the basis of the data presented, strain NEAU-ST10-40T is considered to represent a novel species, for which the name Halobacillus andaensis sp. nov. is proposed. The type strain is NEAU-ST10-40T (=CGMCC 1.12153T=DSM 25866T).

The genus Halobacillus was created by Spring et al. (1996) with the description of two novel species, Halobacillus litoralis and Halobacillus trueperi, and the reclassification of Sporosarcina halophila (Claus et al., 1983) to Halobacillus as the type species of the genus, Halobacillus halophilus. The genus Halobacillus belongs to the family Bacillaceae within the phylum Firmicutes. At the time of writing (September 2014), this genus comprised 18 recognized species (Parte, 2014), with the addition of H. salinus (Yoon et al., 2003), H. karajensis (Amoozegar et al., 2003), H. locisalis (Yoon et al., 2004), H. yeomjeoni (Yoon et al., 2005), H. dabanensis and H. aidingensis (Liu et al., 2005), H. profundi and H. kuroshimensis (Hua et al., 2007), H. campisalis (Yoon et al., 2007), H. faecis (An et al., 2007), H. alkaliphilus (Romano et al., 2008), H. seohaensis (Yoon et al., 2008), H. mangrovi (Soto-Ramírez et al., 2008), H. naozhouensis (Chen et al., 2009a) and H. salsuginis (Chen et al., 2009b). Due to their ability to grow at high salt concentrations, members of the genus Halobacillus have been predominantly isolated from saline environments such as saline soils (Claus et al., 1983; Amoozegar et al., 2003), salt lakes (Spring et al., 1996; Yoon et al., 2003; Liu et al., 2005; Romano et al., 2008), marine solar salterns (Yoon et al., 2004, 2005, 2007, 2008), deep-sea carbonate rock (Hua et al., 2007), mangrove-growing soil (An et al., 2007), surface of black mangrove leaves (Soto-Ramírez et al., 2008), sea anemone (Chen et al., 2009a) and subterranean brine (Chen et al., 2009b). All members are aerobic,

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Abbreviations: meso-DAP, meso-diaminopimelic acid.

The GenBank/EMBL/DDBJ accession number for the 16S rRNA gene sequence of strain NEAU-ST10-40T is JQ762290.

One supplementary table and two supplementary figures are available with the online Supplementary Material.
endospore-forming, Gram-stain-positive, and contain MK-7 as the predominant menaquinone, and one or more of anteiso-C\textsubscript{15:0}, iso-C\textsubscript{15:0}, iso-C\textsubscript{16:0} and anteiso-C\textsubscript{17:0} as major fatty acids (Soto-Ramírez et al., 2008; Yoon et al., 2008; Chen et al., 2009a). Members of the genus contain cell-wall peptidoglycan of the L-Orn–D-Asp type (Soto-Ramírez et al., 2008; Yoon et al., 2008; Chen et al., 2009a), with the exception of H. campisalis (Yoon et al., 2007) and H. seohaensis (Yoon et al., 2008) containing cell-wall peptidoglycan of the meso-diaminopimelic acid (meso-DAP) type. During our study on the microbial diversity and taxonomy of the halotolerant and halophilic bacteria from saline and alkaline soils in Songnen Plain (Pan et al., 2012), a moderately halophilic bacterium, designated strain NEAU-ST-10-40\textsuperscript{T}, was shown to share 16S rRNA gene sequence similarity of 98.8 % with \textit{H. alkalophilus} FP\textsuperscript{5}\textsuperscript{T}, suggesting that it might represent a novel species or share the same taxon with \textit{H. alkalophilus} FP\textsuperscript{5}\textsuperscript{T}. The present study provides a detailed characterization of strain NEAU-ST10-40\textsuperscript{T} in order to determine its exact taxonomic position. On the basis of the polyphasic taxonomic data, we propose that it represents a novel species of the genus \textit{Halobacillus}.

Strain NEAU-ST10-40\textsuperscript{T} was isolated from the 5–10 cm deep saline, alkaline soil in Anda City, Heilongjiang Province, China (46° 05‘ 08.83” N 125° 51‘ 58.37” E). In this area, the soils contain sodium carbonate and sodium bicarbonate as the predominant salts, followed by lesser amounts of sodium sulfate and sodium chloride, with pH values in the range 8.0–11.0, and total organic carbon of 13.8–39.0 g per kg soil, and the atmospheric temperature changes dramatically from −30 to 30 °C with an average annual temperature of 2–6 °C. For isolation, the soil sample was suspended in 5 % (w/v) NaCl modified S-G liquid medium (Sehgal & Gibbons, 1960) with the following composition (per litre: 10 g tryptone, 5 g yeast extract, 5 g casein, 2 g KCl, 3 g sodium citrate, 20 g MgSO\textsubscript{4}.7H\textsubscript{2}O and 50 g NaCl (pH 7.2–7.4)). After 2–3 days of incubation at 28 °C on a shaker incubator, the bacterial suspension was serially diluted and spread on 5, 10, 15 and 20 % (w/v) NaCl modified S-G agar medium containing 1.5 % (w/v) agar. Plates continued to be incubated at 28 °C for 7 days. Representative colonies were then transferred to the same medium as above. A pure culture was obtained by repeated streaking, confirmed based on the uniformity of cell morphology, and then stored in 20 % glycerol at −80 °C for further use.

\textit{H. alkalophilus} DSM 18525\textsuperscript{T}, \textit{H. yeomjeoni} DSM 17110\textsuperscript{T}, \textit{H. halophilus} DSM 2266\textsuperscript{T}, \textit{H. litoralis} DSM 10405\textsuperscript{T}, \textit{H. dabanensis} DSM 18199\textsuperscript{T}, \textit{H. salinus} DSM 18897\textsuperscript{T}, \textit{H. naozhouensis} DSM 21185\textsuperscript{T}, \textit{H. trueperi} DSM 10404\textsuperscript{T} and \textit{H. salsuginis} DSM 21185\textsuperscript{T} were obtained from German Collection of Microorganisms and Cell Cultures (DSMZ), and \textit{H. campisalis} KCTC 13144\textsuperscript{T} was obtained from Korean Collection for type Cultures (KCTC), and then stored in 20 % glycerol at −80 °C.

Cell size, morphology and motility were observed by light microscopy (CX21; Olympus) and transmission electron microscopy (H7650; Hitachi). Gram staining was carried out by using the standard Gram reaction. Colony morphology was examined after 3 days of incubation on solid S-G medium at 30 °C. The NaCl, pH and temperature ranges and optima for growth were determined in modified Luria–Bertani (LB) liquid medium consisting of 10 g tryptone l\textsuperscript{−1} and 5 g yeast extract l\textsuperscript{−1}. For determination of the NaCl range and optimum, growth was observed at NaCl concentrations of 0.5, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 15, 22 and 25 % (w/v). For tests of pH range and optimum, pH values were adjusted to 3–11 at increments of 1.0 pH units by adding different buffers (0.1 M acetate buffer for pH 3–6, 0.1 M Tris/HCl for pH 7–9 and 0.05 M potassium bicarbonate buffer for pH 10–11). For determination of the temperature range and optimum, growth was tested at 0, 4, 10, 28, 30, 32, 35, 37, 40, 42, 50, 55, 60 and 65 °C. Antimicrobial susceptibility tests were performed in modified S-G liquid medium with different antibiotic concentrations (0, 10, 20, 40, 50 and 100 µg ml\textsuperscript{−1}). Cell growth was determined after 2 days of incubation and monitored by measuring the increase in optical density at 600 nm (OD\textsubscript{600}) of the culture using a spectrophotometer. Routine cultivation of strain NEAU-ST10-40\textsuperscript{T} was performed in 8 % (w/v) NaCl modified S-G liquid medium, at pH 8.0 and at 30 °C (the optimum growth conditions) for 2 days, if not otherwise indicated. Phenotypic tests were performed according to the proposed minimal standards for describing new taxa of aerobic, endospore-forming bacteria by Logan et al. (2009). Endospores were observed by light microscopy (Eclipse E100; Nikon) and imaged after 60 h of incubation in modified seawater agar (Spring et al., 1996) supplemented with 8 % (w/v) NaCl at pH 8.0 and at 30 °C (the optimum growth conditions) according to the methods of Schaeffer-Fulton (Smibert & Krieg, 1994). Tests for methyl red and Voges–Proskauer reactions, \textit{H}_2\textit{S} production from \textit{l}-cysteine, indole production, and nitrate and nitrite reduction were done as recommended by Smibert & Krieg (1994). Catalase activity was determined by observing bubble production in a 3 % (v/v) hydrogen peroxide solution. Oxidase activity was determined using 1 % (w/v) \textit{N}_2\textit{N},\textit{N}’\textit{N}’-tetramethyl-1,4-phenylenediamine dihydrochloride. Other enzyme activities, including ONPG, arginine dihydrolase and phenylalanine deaminase, were assayed using the API ZYM system (bioMérieux) according to the manufacturer’s instructions, after the inoculum was prepared with 0.85 % sterilized NaCl solution. The utilization of substrates as single carbon sources was determined as described by Zhou et al. (2007), using modified ammonia salt-sugar medium \{0.2 % (NH\textsubscript{4})\textsubscript{2}SO\textsubscript{4}, 0.05 % Na\textsubscript{2}HPO\textsubscript{4}.2H\textsubscript{2}O, 0.02 % MgSO\textsubscript{4}.7H\textsubscript{2}O, 0.01 % CaCl\textsubscript{2}.2H\textsubscript{2}O and 0.05 % K\textsubscript{2}HPO\textsubscript{4} w/v\} containing 1 % of each tested carbon source. Hydrolysis of casein, gelatin, starch and Tweens 20 and 80 was determined as described by Cowan & Steel (1965).
The phylogenetic position of strain NEAU-ST10-40T was determined by analysing its 16S rRNA gene sequence. The 16S rRNA gene was amplified by PCR using primers 27F and 1492R (Xu et al., 2007) and sequenced by Beijing Genomics Institute (Beijing, China), and pairwise 16S rRNA gene sequence similarities were then calculated using the web-based EzTaxon-e program (http://eztaxon-e.ezbiocloud.net; Kim et al., 2012). Phylogenetic analysis was performed by using the software MEGA version 5.0 (Tamura et al., 2011) after multiple alignment of the sequence data by CLUSTAL X (Thompson et al., 1997). A distance matrix was generated using Kimura's two-parameter model (Kimura, 1980) and clustering was performed using the neighbour-joining (Saitou & Nei, 1987), maximum-likelihood (Felsenstein, 1981) and maximum-parsimony (Kluge & Farris, 1969) methods. The stability of clusters was ascertained by performing a bootstrap analysis with 1000 replicates (Felsenstein, 1985).

Genomic DNA was prepared according to the method of Marmur (1961) and the purity was checked spectrophotometrically. The DNA G+C content was determined by thermal denaturation ($T_m$) (Marmur & Doty, 1962) by using the genomic DNA of Escherichia coli K-12 as the standard for calibration. DNA–DNA hybridization assays were performed in triplicate using the thermal denaturation and renaturation method of De Ley et al. (1970), as modified by Huss et al. (1983), using a Beckman DU 800 spectrophotometer. Values are presented as mean ± SD.

The 16S rRNA gene sequence of strain NEAU-ST10-40T was 1437 bp in length. It shared 98.8, 98.8, 98.5, 98.4, 98.3, 98.1, 98.1, 98.1, 98.0, 97.9, 97.9, 97.8, 97.8, 97.8, 97.8, 97.6, 97.4, 97.1 and 97.1% similarity with the corresponding genes from H. campisalis ASL-17T, H. yeomjeonii MSS-402T, H. halophilus DSM 2266T, H. litoralis SL-4T, H. dabanensis D-8T, H. salinus HSL-3T, H. nazohouensis JSM 071068T, H. trueperi DSM 10404T, H. faecis KCTC 13121T, H. profundi IS- HB4T, H. mangrovi MS10T, H. loyalis MSS-155T, H. hunanensis JSM 071077, H. soohwaensis ISL-50T, H. salsuginis JSM 078133T, H. karajensis DSM 14948T, H. aidingensis AD-6T, H. kuroshimensis DSM 18393T and Thalassobacillus devorans G-19.1T, respectively. Phylogenetic analysis based on the neighbour-joining (Fig. 1), maximum-likelihood (data not shown) and maximum-parsimony (data not shown) algorithms revealed that strain NEAU-ST10-40T was included in the cluster of species of the genus Halobacillus. However, the three phylogenetic trees showed that strain NEAU-ST10-40T and H. salsuginis DSM 21185T formed a separate clade, although the two strains shared 16S rRNA gene sequence similarity of 97.8%.

The DNA G+C content of strain NEAU-ST10-40T was 39.3 mol%. The type strains of the most closely related species showing 16S rRNA gene sequence similarities higher than 98.0% plus H. salsuginis DSM 21185T were chosen for DNA–DNA hybridization assays. Levels of DNA–DNA relatedness between strain NEAU-ST10-40T and H. alkaliophilus DSM 18525T, H. campisalis KCTC 13144T, H. yeomjeonii DSM 17110T, H. halophilus DSM 2266T, H. litoralis DSM 10405T, H. dabanensis DSM 18199T, H. salinus DSM 18897T, H. naohouensis DSM 21183T, H. trueperi DSM 10404T and H. salsuginis DSM 21185T were 43 ± 1, 40 ± 1, 37 ± 2, 32 ± 3, 30 ± 2, 27 ± 2, 24 ± 2, 22 ± 1, 20 ± 1 and 19 ± 1%, respectively, which are significantly below the threshold value of 70% recommended by Wayne et al. (1987) for assigning strains to the same species.

The amino acids of whole-cell hydrolysates were analysed as described by Hasegawa et al. (1983), using H. alkaliophilus DSM 18525T and H. campisalis KCTC 13144T as the respective reference strains for the presence of L-Orn–D-Asp and meso-DAP. For fatty acid analyses, strain NEAU-ST10-40T and the reference strains were grown in modified marine agar 2216 (Difco) supplemented with 8% (w/v) NaCl at pH 8.0 and at 30 °C (the optimum growth conditions) for 3 days, which corresponded to the exponential phase of strain NEAU-ST10-40T. Fatty acids were analysed by GC/MS (Kuykendall et al., 1988). The respiratory quinone of the strain was isolated, purified and analysed as described by Lee et al. (2001). Polar lipids were analysed following the polar lipid extraction procedure and tested by two-dimensional TLC according to the methods of Minnikin et al. (1984).

The major fatty acids (>10%) detected in strain NEAU-ST10-40T were anteiso-C15:0 (48.5%), anteiso-C17:0 (13.4%) and iso-C16:0 (11.0%). The detailed fatty acid profiles of strain NEAU-ST10-40T and the type strains of nine closely related species plus the most phylogenetically closely related species of the genus Halobacillus are shown in Table S1 (available in the online Supplementary Material). All the strains were tested under the same growth conditions in this study in order to compare types and percentages of fatty acids between strain NEAU-ST10-40T and the above-mentioned ten reference type strains. As shown in Table S1, strain NEAU-ST10-40T contained a combination of fatty acids found in other species of the genus Halobacillus, indicating that strain NEAU-ST10-40T is a member of the genus Halobacillus. However, regarding the major fatty acids (>10%), although the most abundant major fatty acid was anteiso-C15:0, there were quantitative differences in the other two most abundant major fatty acids between strain NEAU-ST10-40T and the above-mentioned ten reference type strains (Table S1). Also, there were quantitative differences in the other fatty acids between strain NEAU-ST10-40T and each of the above-mentioned ten reference type strains (Table S1). Based on comparison of the fatty acids, strain NEAU-ST10-40T can be easily differentiated from the most closely related and the most phylogenetically closely related species. Analysis of the quinones showed that strain NEAU-ST10-40T contained MK-7 as the only respiratory quinone, consistent with data for the type strain of the most closely related species, H. alkaliophilus DSM 18525T (Romano et al., 2008), but contrasting with
data for the type strain of the most phylogenetically closely related species, *H. salsuginis* DSM 21185T, containing MK-7 (98.5%) as the predominant respiratory quinone plus a small quantity (1.5%) of MK-8 (Chen et al., 2009b). Analysis of the polar lipids showed that strain NEAU-S10-40T contained diphosphatidylglycerol, phosphatidylethanolamine, phosphatidylglycerol, two unknown phospholipids and three unknown lipids (Fig. S1), in contrast to the type strain of the most closely related species, *H. alkaliphilus* DSM 18525T, which contained phosphatidylglycerol, diphosphatidylglycerol and one unidentified glycolipid (Romano et al., 2008). Strain NEAU-ST10-40T contained meso-DAP in the cell-wall peptidoglycan as the diagnostic diamino acid (Table 1), which is different from that of *H. alkaliphilus* DSM 18525T (Romano et al., 2008) but consistent with that of *H. salsuginis* DSM 21185T (Chen et al., 2009b).

Cells of strain NEAU-ST10-40T were strictly aerobic, Gram-stain-positive, endospore-forming, rod-shaped, motile by peritrichous flagella and approximately 0.6–0.8 μm × 1.5–2.2 μm (Fig. S2). Physiological and biochemical characteristics are presented in Table 1 and the novel species description. The strain was susceptible to ampicillin (10 μg ml⁻¹), chloramphenicol (10 μg ml⁻¹),

**Fig. 1.** Phylogenetic tree based on 16S rRNA gene sequence analysis and reconstructed using the neighbour-joining method showing the phylogenetic positions of strain NEAU-ST10-40T, species of the genus Halobacillus and some other related taxa. Closed circles indicate branches that were also obtained using the maximum-likelihood and maximum-parsimony methods. Numbers at nodes indicate bootstrap values (>50%) based on a neighbour-joining analysis of 1000 resampled datasets. Bar, 1 substitution per 100 nt positions.
Table 1. Characteristics used to distinguish strain NEAU-ST10-40<sup>T</sup> from closely related species of the genus *Halobacillus*

<table>
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<td>Rods or long rods</td>
<td>Cocci or oval</td>
<td>Rods</td>
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<td>–</td>
<td>+</td>
</tr>
<tr>
<td>Trehalose</td>
<td>+</td>
<td>+</td>
<td>+</td>
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<td>+</td>
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<td>+</td>
<td>+</td>
</tr>
<tr>
<td>Cell-wall type</td>
<td>meso-DAP</td>
<td>L-Orn → – D-Asp</td>
<td>meso-DAP</td>
<td>L-Orn → D-Asp</td>
<td>L-Orn → D-Asp</td>
<td>L-Orn → D-Asp</td>
<td>L-Orn → D-Asp</td>
<td>L-Orn → D-Asp</td>
<td>L-Orn → D-Asp</td>
<td>L-Orn → D-Asp</td>
<td>L-Orn → D-Asp</td>
</tr>
<tr>
<td>DNA G + C content (mol%)</td>
<td>39.3</td>
<td>43.5</td>
<td>42.2</td>
<td>42.1</td>
<td>42.9</td>
<td>40.1–40.9</td>
<td>42.0</td>
<td>45.0</td>
<td>42.8</td>
<td>41.4</td>
<td>43.0</td>
</tr>
</tbody>
</table>

*E, ellipsoidal; S, spherical.
†Data were from this study.
‡D-Asp, D-asparagine; meso-DAP, meso-diaminopimelic acid; L-Orn, L-ornithine.

Strains: 1, NEAU-ST10-40<sup>T</sup>; 2, *H. alkaliphilus* DSM 18525<sup>T</sup>; 3, *H. salsuginis* DSM 21185<sup>T</sup> (data for 1–3 from this study); 4, *H. campisalis* ASL-17<sup>T</sup> (data from Yoon et al., 2007); 5, *H. yeomjeoni* MSS-402<sup>T</sup> (Yoon et al., 2005); 6, *H. halophilus* DSM 2266<sup>T</sup> (Claus et al., 1983; Spring et al., 1996; Romano et al., 2008); 7, *H. litoralis* SL-4<sup>T</sup> (Spring et al., 1996); 8, *H. salinus* HSL-3<sup>T</sup> (Yoon et al., 2005); 9, *H. naozhouensis* JSM 071068<sup>T</sup> (Chen et al., 2009a); 10, *H. dabanensis* (Liu et al., 2005); 11, *H. trueperi* DSM 10404<sup>T</sup> (Spring et al., 1996). +, Positive; (, negative; w, weakly positive; v, variable.
and gentamicin (10 μg ml⁻¹), but resistant to kanamycin (10 μg ml⁻¹), tetracycline (20 μg ml⁻¹), streptomycin (20 μg ml⁻¹) and spectinomycin (100 μg ml⁻¹). As can be seen from Table 1, strain NEAU-ST10-40T could be differentiated from the type strain of the most closely related species, H. alkaliphilus FP5⁷, or that of the most phylogenetically closely related species, H. salsuginis JS7 07813³, based on several characteristics, such as cell morphology, endospore production and position, colony pigmentation, motility, NaCl, pH and temperature range and optima for growth, hydrolysis of Tween 80, utilization of several carbon sources, production of acids from several sugars, and DNA G+C content.

In conclusion, on the basis of its morphological, physiological, biochemical, chemotaxonomic and phylogenetic characteristics, we suggest that strain NEAU-ST10-40T represents a novel species of the genus Halobacillus, for which the name Halobacillus andaensis sp. nov. is proposed.

Description of Halobacillus andaensis sp. nov.

Halobacillus andaensis (an.da.en’sis. N.L. masc. adj. andaensis pertaining to Anda City, Heilongjiang Province, China, where the type strain was isolated).

Cells are Gram-stain-positive, strictly aerobic rods (0.6–0.8 × 1.5–2.2 μm), occurring singly, in pairs or in short chains. Motile by means of peritrichous flagella. Central or subterminal ellipsoidal endospores are produced in swollen sporangia after 60 h of incubation in modified sea-water agar supplemented with 8% (w/v) NaCl at pH 8.0 and at 30 °C (Fig. S2). Colonies are light yellow, circular and opaque, of low convexity, are smooth and approximately 2.0–3.5 mm in diameter after incubation on 8% (w/v) NaCl modified S-G agar at 30 °C for 3 days. Growth occurs in 3–15% (w/v) NaCl with 8% optimal for growth. The temperature range for growth is 4–60 °C (optimum, 30 °C). The pH range for growth is pH 7.0–9.0 (optimum, pH 8.0). Chemo-organotrophic. Under aerobic conditions, nitrate is not reduced. Oxidase- and catalase-positive. Acid is produced from cellobiose, D-fructose, D-mannose, ribose, trehalose, D-xylene and glycerol but not from D-galactose, lactose, maltose, adonitol, ethanol, D-glucose, L-arabinose, sucrose, L-rhamnose, D-mannitol, sorbitol, myo-inositol or amygdalin. Indole production and ONPG tests are positive. Voges–Proskauer, methyl red and oxidation/fermentation of D-glucose tests are negative. H₂S is not produced from L-cysteine. Tweens (20 and 80) are hydrolysed, but starch, gelatin and casein are not. Does not produce tryptophan deaminase, arginine dihydrolase, phenylalanine deaminase, lysine decarboxylase, ornithine decarboxylase or urease. The following compounds are used as sole carbon and energy sources: cellobiose, raffinose, L-rhamnose, sucrose, adonitol, acetate, citrate and succinate, but L-arabinose, D-fructose, D-galactose, D-glucose, lactose, maltose, D-mannose, ribose, trehalose, D-xylene, ethanol, glucol, D-mannitol, sorbitol, fumarate and malonate are not. The following compounds are used as sole carbon, nitrogen and energy sources: L-alanine, L-histidine, L-serine and L-valine, but L-arginine, L-lysine and L-methionine are not. The cell-wall peptidoglycan is of meso-DAP type. The only respiratory quinone is MK-7 and polar lipids consist of diphosphatidylglycerol, phosphatidylethanolamine, phosphatidyglycerol, two unknown phospholipids and three unknown lipids. The major fatty acids (>10%) are anteiso-C₁₅:₀, anteiso-C₁₇:₀ and iso-C₁₆:₀.

The type strain, NEAU-ST10-40T (=CGMCC 1.12153² = DSM 25866³), was isolated from the saline and alkaline soil in Anda City, Heilongjiang Province, China. The DNA G+C content of the type strain is 39.3 mol% (Tₘ method).

Acknowledgements

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References


