**Vibrio salilacus** sp. nov., a new member of the Anguillarum clade with six alleles of the 16S rRNA gene from a saline lake

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A Gram-stain-negative, catalase- and oxidase-positive, facultatively aerobic bacterium, strain DSG-S6T, was isolated from Dasugan Lake (salinity 3.1 %, w/w), China. Its taxonomic position was determined by using a polyphasic approach. Cells of strain DSG-S6T were non-spore-forming, slightly bent rods, and motile by means of a single polar flagellum. Growth occurred in the presence of 0–7.0 % (w/v) NaCl (optimum, 2.0 %), at 4–35 °C (optimum, 30 °C) and at pH 6.0–10.5 (optimum, pH 8.0–8.5). C16 : 0, C18 : 1 \( \omega_7 \) c and C16 : 1 \( \omega_7 \) c and/or C16 : 1 \( \omega_6 \) c were the major fatty acids. Six alleles of the 16S rRNA gene sharing 98.9–99.9 % similarity were detected in strain DSG-S6T, which showed highest 16S rRNA gene sequence similarity to *Vibrio aestuarianus* ATCC 35048T (97.7 %), then to *Vibrio pacinii* LMG 19999T (97.6 %) and *Vibrio metschnikovii* CIP 69.14T (96.8 %). Multilocus sequence analysis of four housekeeping genes and 16S rRNA genes clearly clustered it as a member of the Anguillarum clade. Mean DNA–DNA relatedness between strain DSG-S6T and *V. aestuarianus* NBRC 15629T, *V. pacinii* CGMCC 1.12557T and *V. metschnikovii* JCM 21189T was 20.6 ± 2.3, 38.1 ± 3.5 and 24.2 ± 2.8 %, respectively. The DNA G+C content was 46.8 mol% (Tm). Based on the data, it is concluded that strain DSG-S6T represents a novel species of the genus *Vibrio*, for which the name *Vibrio salilacus* sp. nov. is proposed. The type strain is DSG-S6T (=CGMCC 1.12427T =JCM 19265T).

The genus *Vibrio* was first described with the type species *Vibrio cholerae*, the causative agent of cholera, by the Italian physician Filippo Pacini in 1854. However, the pure culture of *V. cholerae* was not obtained until 1883 by Robert Koch (Thompson et al., 2004). *Vibrios* are quite abundant in aquatic environments, including estuary water (Kirchberger et al., 2014), seawater (Yoshizawa et al., 2010) and sediment (Xu et al., 2009), and also in some eukaryotic organisms such as clams (Lasa et al., 2013), sponge (Hoffmann et al., 2012) and fish (Birkbeck & Treasurer, 2014). At the time of writing, the genus *Vibrio* consists of about 100 validly named species. Members of the genus *Vibrio* have been classified into 16 monophyletic clades (Cholerae, Anguillarum, Vulnificus, Harveyi, Haliotici, Fischeri, Splendidus, Nereis, Orientalis, Coralliilyticus, Scophthalmi, Diazotrophicus, Mediterranei, Pectenicida, Porteresiae and Rumoiensis) by multilocus sequence analysis (MLSA) based on eight housekeeping genes and 16S rRNA genes (Sawabe et al., 2007, 2013). The Anguillarum clade consists of three members: *Vibrio anguillarum*, *Vibrio aestuarianus* and *Vibrio ordalii* (Sawabe et al., 2007). During a survey of bacterial diversity in Dasugan Lake, Qinghai Province, China, a new Anguillarum-like strain, designated DSG-S6T, was isolated from a saline water sample. Its taxonomic position was investigated through a polyphasic approach in this study.
The saline water sample was collected from Dasugan Lake at GPS site 38° 52’ 30” N 93° 54’ 26” E (depth 4.8 m, salinity 3.1 %, dissolved oxygen 6.1 mg l⁻¹, pH 9.2 and temperature 18.2 °C), 0.3 m beneath the surface. Strain DSG-S6ᵀ was isolated by the standard dilution plating technique on marine agar 2216 (MA; Difco) at 30 °C. Strain DSG-S6ᵀ was also able to grow well in Luria–Bertani (LB; 3 % NaCl, w/v) broth and marine broth 2216 (MB; Difco). The strain was preserved in MB supplemented with 20 % (v/v) glycerol at −80 °C. The experiments reported here were performed in triplicate and in parallel with V. aestuarianus NBRC 15629ᵀ, V. pacinii CGMCC 1.12557ᵀ and V. metschnikovii JCM 21189ᵀ, except for the morphological studies, growth tests and DNA G+C content analyses. Biomass for all analyses was obtained after cultivation on MA at 30 °C for 24 h unless otherwise stated.

Cell morphology and flagellation were observed by optical microscopy (BH-2; Olympus) and transmission electron microscopy (H-600; Hitachi) after negative staining with 1 % (w/v) phosphotungstic acid. The Gram reaction was performed according to Dong & Cai (2001). Growth at 0, 4, 10, 15, 20, 25, 30, 35 and 40 °C was measured in LB. Growth at pH 5.0–11.0 (at intervals of 0.5 pH units) was determined in LB broth supplemented with 3 % (w/v) NaCl at 30 °C using three different buffers (final concentration, 50 mM): sodium acetate buffer (for pH 5.0–5.5), sodium phosphate buffer (for pH 6.0–8.0) and Tris/HCl buffer (for pH 8.0–11.0). Tolerance to NaCl was examined in LB broth with final NaCl concentrations of 0–80 % (w/v, at intervals of 0.5 %).

The requirement for oxygen was tested in an anaerobic system (Anaero-Gen). Production of H₂S was assessed with lead acetate paper. Catalase and oxidase activities and hydrolysis of casein, tyrosine, starch and Tweens 20, 40, 60 and 80 were determined according to Dong & Cai (2001). Susceptibility to antibiotics was determined by the disc diffusion method using filter-paper discs (Beijing Pharmaceutical Company) containing various antibiotics as specified in Table 1 and in the species description. Growth inhibition effects were estimated according to Nokhal & Schlegel (1983) after incubation on MA (pH 7.5) for 48 h at 30 °C. The inhibition zones were measured from the edges of susceptibility discs to the edges of the clear zones: <2, 2–5 and ≥5 mm of the inhibition zones represent resistance, weak resistance and susceptibility, respectively (Nokhal & Schlegel, 1983). Additionally, API ZYM, API 50CH and API 20NE systems (bioMérieux) were used for tests of enzyme activities, utilization of carbon substrates and other physiological and biochemical traits according to the manufacturer’s instructions.

Colonies of strain DSG-S6ᵀ were 1.0–2.0 mm in diameter, smooth, non-pigmented, transparent and glistening after cultivation on MA at 30 °C for 24 h. Cells of strain DSG-S6ᵀ were Gram-stain-negative, non-spore-forming slightly bent rods, 0.6–0.9 μm wide, 1.5–2.0 μm long and motile by means of a single polar flagellum (Fig. S1, available in the online Supplementary Material). Strain DSG-S6ᵀ was facultatively aerobic, and catalase- and oxidase-positive. It was able to grow in the presence of 0–7.0 % (w/v) NaCl (optimum, 2.0 %), and at 4–35 °C (optimum, 30 °C) and pH 6.0–10.5 (optimum, pH 8.0–8.5). No growth occurred at 0 or 40 °C, at pH 5.5 or 11.0, or in the presence of 7.5 % (w/v) NaCl. H₂S was produced. Strain DSG-S6ᵀ hydrolysed L-tyrosine, but not starch, casein, urea, L-arginine or Tweens 20, 40, 60 and 80, and was negative for nitrate reduction, indole production and β-galactosidase activity. Differential characteristics between strain DSG-S6ᵀ and the three reference type strains are listed in Table 1. All the results obtained in this study for the reference type strains were consistent with those originally presented (Gomez-Gil et al., 2003; Lee et al., 1978; Tison & Seidler, 1983) and other description (Beaz-Hidalgo et al., 2010). In addition, strain DSG-S6ᵀ and the three reference type strains shared many common characteristics. They were all motile, Gram-stain-negative and catalase-positive, positive for D-glucose fermentation, hydrolysis of aesculin and gelatin and negative for hydrolysis of urea. They were able to assimilate malic acid, glycerol, D-ribose, D-mannitol, trehalose and potassium gluconate, but not capric acid, adipic acid, phenylacetic acid, erthritol, D-arabinose, L-arabinose, D-xylose, L-xylose, D-adonitol, methyl β-D-xlyopyranoside, L-sorbose, L-rhamnose, dulcitol, D-sorbitol, methyl α-D-mannopyranoside, methyl α-D-glucopyranoside, inulin, melezitose, raffinose, xylitol, D-lyxose, D-tagatose, D-fucose, L-fucose, D-arabitol, L-arabitol or potassium 5-ketogluconate. All were resistant to (μg per disc) erythromycin (15), clindamycin (2), vancomycin (30) and sulfamethoxazole (300), but sensitive to chloramphenicol (30), streptomycin (10), ampicillin (10) and norfloxacin (10). All were positive for alkaline phosphatase and leucine arylamidase, but negative for esterase (C4), lipase (C14), valine arylamidase, cystine arylamidase, trypsin, α-chymotrypsin, α-galactosidase, β-glucuronidase, β-glucosidase, α-mannosidase and α-fucosidase. Additional morphological, physiological and biochemical characteristics of strain DSG-S6ᵀ are given in the species description.

Biomass for chemotaxonomic analyses was cultivated on MA at 30 °C for 24 h to late exponential phase. Genomic DNA was extracted by using a bacterial genomic kit (D3350-1; Omega Bio-Tek). The DNA base composition was determined by thermal denaturation method (Marmur & Doty, 1962), with DNA of Escherichia coli K-12 as a reference. Cellular fatty acids were analysed using the standard MIDI Sherlock Microbial Identification System (version 6.0), and peaks were identified on an Agilent 6890N Network GC system using the TSBA6 peak-naming table. Polar lipids were extracted using a chloroform/methanol system and identified using two-dimensional TLC. Merck silica gel 60 F₂₅₄ aluminium-backed thin-layer plates were used in TLC analysis.

The DNA G+C content of strain DSG-S6ᵀ was 46.8 mol% (Tₘ), within the range (38–51 mol%) reported for the
genus *Vibrio* (Farmer et al., 2005). The fatty acid profiles of strain DSG-S6<sup>T</sup> and the three reference type strains are shown in Table 2. The cellular fatty acid profile obtained in this study for *V. pacinii* CGMCC 1.12557<sup>T</sup> was similar to that described originally by Gomez-Gil et al. (2003). However, the amounts of iso-C<sub>16 : 0</sub>, iso-C<sub>17 : 0</sub>, iso-C<sub>14 : 0</sub> 3-OH and C<sub>18 : 1</sub><sup>v7c</sup> detected were much less in this study than that by Gomez-Gil et al. (2003), which might be attributed to different culture conditions. In terms of major fatty acids, similar profiles were also detected for the other two reference type strains compared with those reported before (Gomez-Gil et al., 2003; Prado et al., 2014). All these strains contained C<sub>16 : 0</sub> and summed feature 3 as major fatty acids, although in different study.
proportions, which might be due to the different culture conditions. Strain DSG-S6T had a fatty acid profile similar to those of the type strains of closely related species under the same cultivation conditions (Table 2). The major fatty acids of strain DSG-S6T were C16:0, C18:1ω7c and summed feature 3, the same as closely related species. However, strain DSG-S6T could be differentiated from the reference type strains in the proportions of the major fatty acids. Furthermore, C18:1ω7c was the major fatty acid for strain DSG-S6T but not for V. pacinii CGMCC 1.12557T, a significant differential characteristic between the two. A significant amount of iso-C16:0 was present in strain DSG-S6T but absent in V. metschnikovii JCM 21189T, which could also be used to differentiate strain DSG-S6T from V. metschnikovii JCM 21189T (Table 2).

Strain DSG-S6T exhibited a polar lipid profile consisting of phosphatidylethanolamine (PE) and phosphatidylglycerol (PG) as major lipids, which was consistent with that for the type strain of Vibrio xiamenensis (Gao et al., 2012) and species of the family Vibrionaceae (Wilkinson, 1988); two unknown aminophospholipids and an uncharacterized phospholipid were found as minor lipids in strain DSG-S6T (Fig. S2).

The 16S rRNA genes were amplified with primers 27F and 1492R (Weisburg et al., 1991). Purified PCR products were ligated into a pEASY-T1 cloning vector (TransGen Biotech). Transformation was performed by heat shock at 42°C for 30 s with Escherichia coli Trans1-T1 (TransGen Biotech) as the competent cells. Cells were incubated with shaking (200 r.p.m.) at 37°C in 250 ml LB medium for 1 h, and then plated onto LB plates containing ampicillin (100 μg ml⁻¹) and incubated at 37°C for 16 h. Plasmid extraction was performed by using a Plasmid Mini kit (D6943-01; Omega Bio-Tek) according to the manufacturer's instructions. Positive clones were identified by PCR amplification with primers M13f (5’-CAGGAAACAGCTATGAC-3’).

**Table 2.** Cellular fatty acids (%) of strain DSG-S6T and closely related species

<table>
<thead>
<tr>
<th>Fatty acid</th>
<th>1</th>
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<th>3</th>
<th>4</th>
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<td>C11:0</td>
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<td></td>
</tr>
<tr>
<td>C12:0</td>
<td>4.2</td>
<td>3.3</td>
<td>4.7</td>
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<tr>
<td>C13:0</td>
<td>TR</td>
<td>TR</td>
<td>TR</td>
<td></td>
</tr>
<tr>
<td>C14:0</td>
<td>5.1</td>
<td>7.3</td>
<td>7.4</td>
<td>8.7</td>
</tr>
<tr>
<td>C16:0</td>
<td>19.5</td>
<td>24.9</td>
<td>19.8</td>
<td>26.0</td>
</tr>
<tr>
<td>iso-C13:0 anteiso-C13:0</td>
<td>TR</td>
<td>TR</td>
<td></td>
<td></td>
</tr>
<tr>
<td>iso-C14:0</td>
<td>TR</td>
<td>TR</td>
<td>TR</td>
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</tr>
<tr>
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<td>TR</td>
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<tr>
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<td>1.3</td>
<td>4.6</td>
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<td>TR</td>
<td></td>
<td></td>
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<tr>
<td>iso-C18:0</td>
<td>TR</td>
<td>TR</td>
<td></td>
<td></td>
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<tr>
<td>C16:0 N alcohol</td>
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<td></td>
<td>TR</td>
<td>TR</td>
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<tr>
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<td>TR</td>
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<tr>
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<tr>
<td>iso-C12:0 3-OH, iso-C13:0 3-OH, iso-C14:0 3-OH</td>
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<tr>
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<tr>
<td>C12:0 3-OH</td>
<td>2.4</td>
<td>3.1</td>
<td>2.1</td>
<td>3.8</td>
</tr>
<tr>
<td>C16:0 3-OH</td>
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<td>TR</td>
</tr>
<tr>
<td>C19:0 10-methyl</td>
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<tr>
<td>C18:1ω7c 11-methyl</td>
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<td></td>
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</tr>
<tr>
<td>C15:1ω6c, C15:1ω8c</td>
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<tr>
<td>C17:1ω6c, C17:1ω8c, C18:1ω5c</td>
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<td></td>
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<tr>
<td>C18:1ω7c</td>
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<td>6.1</td>
<td>14.7</td>
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<td>Summed feature 1*</td>
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<td>TR</td>
<td></td>
<td></td>
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<tr>
<td>Summed feature 2*</td>
<td>2.4</td>
<td>3.2</td>
<td>2.5</td>
<td>5.3</td>
</tr>
<tr>
<td>Summed feature 3*</td>
<td>38.1</td>
<td>44.3</td>
<td>39.0</td>
<td>30.4</td>
</tr>
</tbody>
</table>

*Summed features represent groups of two or three fatty acids that could not be separated by GLC with the MIDI system (version 6.0). Summed feature 1 contains iso-C15:1 H and/or C13:0 3-OH; summed feature 2 contains one or more of C12:0 aldehyde, C14:0 3-OH and iso-C16:1 I; summed feature 3 contains C16:1ω7c and/or C16:1ω6c.
and M13r (5′-GTAAAACGACGGCCAGT-3′) and gel electrophoresis. Positive PCR products were sequenced by Sinogenmax with primers M13f and M13r is (5′-CAGGAAA CAGCTATGAC-3′) and (5′-GTTAAAGCAGGCGCAT-3′), respectively. The 16S rRNA gene sequences were obtained and compared with available sequences in the GenBank database using the BLAST program (Altschul et al., 1990) at NCBI (http://www.ncbi.nlm.nih.gov). The gene sequences of strain DSG-S6T and closely related taxa were aligned with CLUSTAL X version 2.0 (Larkin et al., 2007). Neighbour-joining (Saitou & Nei, 1987), maximum-parsimony (Fitch, 1971) and maximum-likelihood (Felsenstein, 1981) trees were reconstructed using MEGA version 5 (Tamura et al., 2011). Evolutionary distances were calculated by Kimura’s two-parameter model (Kimura, 1983) and the gaps/missing data treatment option chosen was pairwise-deletion.

Six different sequences (1521 nt for each) of the 16S rRNA gene were obtained for strain DSG-S6T, which suggested this strain contains several different alleles of the 16S rRNA gene. Diversity of 16S rRNA genes is commonly found in members of the genus Vibrio (Gomez-Gil et al., 2004; Harth et al., 2007; Sun et al., 2013). The RNAmer method has shown an accurate and rapid ability to predict SS, 16S and 23S rRNA genes for prokaryotic organisms (Lagesen et al., 2007). Predicted by RNAmer, a comprehensive summary of the copy numbers and divergence of 16S rRNA genes for 34 strains of the genus Vibrio, the genomes of which have been completely sequenced, is provided in Table S1. The results indicated that all these species of the genus Vibrio contained diverse 16S rRNA genes. López-López et al. (2007) studied the intragenomic 16S rRNA gene divergence in Halocarcula marismortui, and found that divergence of 16S rRNA genes was an adaptation to different temperatures. The presence of divergent 16S rRNA genes in strain DSG-S6T and other members of the genus Vibrio might contribute to their adaptation to the variable environmental conditions in natural habitats. Therefore, the diversity of members of the genus Vibrio might be seriously underestimated when using 16S rRNA gene sequencing to determine a sample’s microbial diversity.

The neighbour-joining phylogenetic tree based on 16S rRNA gene sequences is shown in Fig. 1. The six 16S rRNA gene sequences of strain DSG-S6T formed a distinct, stable cluster, and shared 98.9–99.9 % similarity. Strain DSG-S6T was closely related to species of the genus Vibrio, and exhibited highest 16S rRNA gene sequence similarity to V. aestuarianus ATCC 35048T (97.7 %), then to V. pacinii LMG 19999T (97.6 %) and V. metschnikovi CIP 69.14T (96.8 %), and <96.8 % to the type strains of other species of the genus Vibrio. However, separate from V. aestuarianus ATCC 35048T, strain DSG-S6T formed a distinct lineage with Vibrio cincinnatiensis ATCC 35912T, V. pacinii LMG 19999T and V. metschnikovi CIP 69.14T, which was also recovered in the maximum-likelihood tree, although with low bootstrap support. In addition, two different topologies of the maximum-parsimony and maximum-likelihood trees (data not shown) were reconstructed, indicating that the phylogenetic trees based on 16S rRNA gene sequences were not robust for members of the genus Vibrio, in agreement with those by other studies (Lasa et al., 2014; Sawabe et al., 2013).

Species of vibrios are defined as clusters of strains with high phenotypic and genotypic similarities. On the basis of 16S rRNA gene sequence phylogeny, there is no robust monophyletic lineage formed within the genus Vibrio (Sawabe et al., 2013). MLSA with partial sequences of nine genes (gapA, mreB, topA, gyrB, ftsZ, pyrH, recA, rpoA and 16S rRNA genes) will establish a more robust inference of the evolutionary history of vibrios and has been considered to be a reliable and straightforward method for determining the phylogenetic relationships among vibrios (Sawabe et al., 2007; Thompson et al., 2005, 2007). The clades classified by these nine genes were always retained in the analysis even when the number of genes was reduced to five loci, i.e. gapA (glyceraldehyde-3-phosphate dehydrogenase gene), gyrB (gyrase subunit B gene), mreB (rod shaping protein gene), ftsZ and topA (topoisomerase I gene) (Sawabe et al., 2007). Therefore, in this study, four of the above five housekeeping genes (not ftsZ) were amplified for MLSA as described by Sawabe et al. (2007, 2013). Sequence data of the most closely related species of the genus Vibrio were obtained from GenBank and from the online electronic taxonomic scheme for vibrios (http://www.taxvibrio.lncc.br). These four genes and 16S rRNA gene sequences were concatenated. The concatenated gene sequences of strain DSG-S6T and closely related species were analysed as for the 16S rRNA gene sequences.

The sequences of gapA (775 nt), gyrB (1152 nt), mreB (976 nt) and topA (720 nt) genes were obtained and compared with those of related species. In the neighbour-joining phylogenetic tree (Fig. 2) based on the concatenated sequences of the four housekeeping genes and 16S rRNA gene (Table S2), strain DSG-S6T formed a robust cluster together with V. aestuarianus, V. anguillarum and V. ordalii, the three members of the Anguillarum clade, with highest similarity (87.8 %) to the type strain of V. aestuarianus. This topology was also recovered in both the maximum-parsimony and the maximum-likelihood trees as indicated in Fig. 2. The results clearly suggested that strain DSG-S6T is a member of the Anguillarum clade within the genus Vibrio. In addition, strain DSG-S6T could be distinguished from the type strains of V. anguillarum and V. ordalii based on very low 16S rRNA gene sequence similarities (both 95.0 %).

In addition to the phylogenetic data, strain DSG-S6T also showed important properties that were in agreement with those reported for the members of the genus Vibrio: Gram-stain-negative, rod-shaped, motile by means of a single polar flagellum, facultatively aerobic and capable of fermenting D-glucose. However, many other properties could be used to differentiate strain DSG-S6T from reference type strains of species of the genus Vibrio, such as H2S production, hydrolysis of L-arginine and starch, growth
conditions (NaCl concentration and temperature), activities of some enzymes, assimilation of some carbon substrates, resistance to some antibiotics and DNA G+C content (Table 1). To distinguish strain DSG-S6<sup>T</sup> further from the type strains of species of the genus *Vibrio* showing highest 16S rRNA gene sequence similarity, DNA–DNA hybridization was performed in triplicate by using the initial renaturation rate method of De Ley et al. (1970) as modified by Huss et al. (1983). Mean levels of DNA–DNA relatedness between strain DSG-S6<sup>T</sup> and *Vibrio* species are given in Table 2.

![Fig. 1. Neighbour-joining tree based on 16S rRNA gene sequences showing the phylogenetic position of strain DSG-S6<sup>T</sup> and related species. Bootstrap values (expressed as percentages of 1000 replications) >50% are shown at branch points. Filled circles indicate branches that were also recovered in both the maximum-likelihood and the maximum-parsimony trees; open circles indicate branches that were also recovered in the maximum-likelihood tree but not in the maximum-parsimony tree. *Alteromonas macleodii* DSM 6062<sup>T</sup> was used as an outgroup. Bar, evolutionary distance (K<sub>nucl</sub>) of 0.01.](image-url)
Diazotrophicus clade

Vibrio salilacus sp. nov.

D. clade

[Diagram showing phylogenetic position of strain DSG-S6T and related species]

V. pacini CGMCC 1.12557T and V. metchnikovii JCM 21189T were 20.6 ± 2.3, 38.1 ± 3.5 and 24.2 ± 2.8 %, respectively.

Combining the above phenotypic, chemotaxonomic and genotypic results, we conclude that strain DSG-S6T represents a novel species of the genus Vibrio, for which the name Vibrio salilacus sp. nov. is proposed.

Descriptions of Vibrio salilacus sp. nov.

Vibrio salilacus (sa.li.lac’us. L. n. sal salt; L. n. lacus lake; N. L. gen. masc. n. salilacus of a salt lake).

Facultatively aerobic, and oxidase- and catalase-positive. Cells are Gram-stain-negative, slightly bent rods, motile by means of a single polar flagellum, 0.6–0.9 μm wide and 1.5–2.0 μm long. Colonies are 1.0–2.0 mm in diameter, smooth, non-pigmented, transparent and glistening after cultivation on MA (pH 7.5) at 30 °C for 24 h. Positive for H2S production, D-glucose fermentation, and hydrolysis of L-tyrosine, aesculin and gelatin. Negative for nitrate reduction, indole production, and hydrolysis of urea, D- and L-arabinose, L-arabinose, D-xylose, D-xylose, D-adonitol, methyl β-D-xylopyranoside, D-galactose, D-mannose, L-sorbose, L-rhamnose, dulcitol, inositol, D-sorbitol, methyl α-D-mannopyranoside, methyl α-D-glucopyranoside, amygdalin, arbutin, salicin, cellulbiose, lactose, melibiose, inulin, melezitose, raffinose, xylitol, gentiobiose, turanose, D-lyxose, D-tagatose, D-fucose, L-fucose, D-arabitol, L-arabitol or potassium 5-ketogluconate. Positive for alkaline phosphatase, leucine arylamidase and acid phosphatase, but negative for esterase (C4), esterase lipase (C8), naphthol-AS-BI-phosphohydrolase, lipase (C14), valine arylamidase, cystine arylamidase, trypsin, α-chymotrypsin, α-galactosidase, β-galactosidase, β-glucuronidase, α-glucosidase, β-glucosidase, N-acetyl-β-glucosaminidase, α-mannosidase and α-fucosidase. The major fatty acids (>10%) are C16:0, C18:1ω7c and summed feature 3 (C16:1ω7c and/or C16:1ω6c). The polar lipid profile consists of phosphatidyethanolamine (PE), phosphatidylglycerol (PG), two unknown aminophospholipids and an uncharacterized phospholipid.

The type strain is DSG-S6T (=CGMCC 1.12427T = JCM 19265T), isolated from a water sample of a saline lake, Dasugan Lake in Qaidam basin, Qinghai Province, China. The DNA G+C content of the type strain is 46.8 mol% (Tm).

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References


