Oceanirhabdus sediminicola gen. nov., sp. nov., an anaerobic bacterium isolated from sea sediment

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A novel anaerobic bacterium, designated NH-JN4T was isolated from a sediment sample collected in the South China Sea. Cells were Gram-stain-positive, spore-forming, peritrichous and rod-shaped (0.5–1.2×2.2–7 μm). The temperature and pH ranges for growth were 22–42 °C and pH 6.0–8.5. Optimal growth occurred at 34–38 °C and pH 6.5–7.0. The NaCl concentration range for growth was 0.5–6 % (w/v) with an optimum of 2.5 %. Catalase and oxidase were not produced. Substrates which could be utilized were peptone, tryptone, yeast extract, beef extract and glycerine. Main fermentation products from PYG medium were formate, acetate, butyrate and ethanol. Strain NH-JN4T could utilize sodium sulfite as an electron acceptor. No respiratory quinone was detected. The predominant fatty acids were anteiso-C<sub>15</sub>:0, C<sub>16</sub>:0, iso-C<sub>15</sub>:0, anteiso-C<sub>17</sub>:0 and C<sub>16</sub>:0 DMA. The major polar lipids were diphosphatidylglycerol, phosphatidylglycerol and glycolipids. The DNA G+C content was 35.8 mol%. Phylogenetic analysis based on the 16S rRNA gene sequence revealed that strain NH-JN4T was a member of family Clostridiaceae, and was most closely related to Clostridium limosum ATCC 25620<sup>T</sup>, Clostridium proteolyticum DSM 3090<sup>T</sup>, Clostridium histolyticum ATCC 19401<sup>T</sup> and Clostridium tepidiprofundii SG 508<sup>T</sup>, showing 94.0, 93.0, 92.9 and 92.3 % sequence similarity, respectively. On the basis of phenotypic, genotypic and chemotaxonomic properties, strain NH-JN4T represents a novel species of a new genus in the family Clostridiaceae, for which the name Oceanirhabdus sediminicola gen. nov., sp. nov. is proposed. The type strain of the type species is NH-JN4T (=JCM 18501<sup>T</sup>=CCTCC AB 2013103<sup>T</sup>=KCTC 15322<sup>T</sup>).
purify strains at least twice before preservation at −80 °C with 20% (v/v) glycerol and in dry-ice ampoules. One of the strains, designated NH-JN4T, was further analysed. *Clostridium tepidiprofundi* DSM 19306T and *Clostridium proteolyticum* DSM 3090T were used as reference strains.

Colonies of strain NH-JN4T were white and semi-transparent with a smooth surface. They were circular with a diameter of 0.5–1 mm on CJW slopes after 24 h incubation at 37 °C. Cell morphology was examined using optical microscopy (BX40; Olympus) and transmission electron microscopy (JEM-1230; JEOL) during stationary growth phase (Tan et al., 2012). Cells were rods (0.5–1.2 × 2.2–7 μm) and peritrichous (Fig. S1, available in IJSEM Online). In the stationary phase of growth, the rods formed terminal endospores. Specific sporulation genes ssp and spo0A were found in strain NH-JN4T by the PCR method (Brill & Wiegel, 1997). *Escherichia coli* and *Bacillus subtilis* were used as negative and positive controls, respectively. Gram staining was performed, and the strain was Gram-stain-positive. Ultra-thin section electron micrographs also revealed a typical Gram-positive cell wall structure (Fig. S1).

Genomic DNA was extracted and the 16S rRNA gene was amplified by PCR using the universal bacterial 16S rRNA gene amplification primers 27F (5′-AGAGTTTGATCC-TGGCTCAG-3′) and 1492R (5′-GGTTACCTTGTTAC-GACTT-3′); the annealing temperature for PCR was 55 °C. PCR products were ligated into T-vector and the 16S rRNA gene was sequenced. The sequence was compared with closely related sequences of reference organisms in the database of the Eztaxon-e using Eztaxon-e’s identifying function (Kim et al., 2012). Sequence data of the most closely related species and strain NH-JN4T were aligned using CLUSTAL W (Thompson et al., 1994). Neighbour-joining (Saitou & Nei, 1987), maximum-parsimony (Fitch, 1971) and maximum-likelihood (Felsenstein, 1981) methods in the MEGA 5 software package (Tamura et al., 2011) were used to reconstruct the phylogenetic trees. Evolutionary distances were calculated with a bootstrap value of 1000 for the neighbour-joining method. The algorithm of the Jukes–Cantor model was used according to the function of model selection in MEGA 5. An almost-complete 16S rRNA gene sequence (1473 nt) was obtained from strain NH-JN4T. Phylogenetic analysis based on this 16S rRNA gene sequence suggested that strain NH-JN4T was a member of family *Clostridiaceae* and was closely related to the genus *Clostridium* (Fig. 1). This result was also supported by the maximum-parsimony and maximum-likelihood trees both with bootstrap values of 1000 (Fig. S3). The results revealed that strain NH-JN4T was most closely related to *C. tepidiprofundi* SG 508T and *C. proteolyticum* DSM 3090T, which belong to Cluster I and Cluster II of the genus *Clostridium*, respectively (Collins et al., 1994; Slobodkina et al., 2008). The DNA G+C content of strain NH-JN4T determined by the HPLC method (Mesbah & Whitman, 1989) was 35.8 mol% using salmon sperm DNA as the calibration standard.

To test the growth range and optimal growth conditions, the strain was cultured in CJW medium at 4, 15, 19, 22, 28, 30, 32, 34, 36, 38, 40, 42, 46 and 50 °C as well as at pH 5.5, 6, 6.5, 7, 7.5, 8, 8.5 and 8.8. MES (for pH 5.5–6.5), PIPES (pH 6.1–7.5) or Tricine (pH 7.5–8.8) were added at a concentration of 25 mM to maintain a stable pH. To test the NaCl concentration growth range and optimum, sodium and chloride ions were removed from CJW medium. NaCl concentrations (w/v) of the medium were adjusted to 0, 0.5, 1, 1.5, 2, 2.5, 3, 3.5, 4, 4.5, 5, 6, 7 and 7.5%. All tests were performed in triplicate. Optimal growth of strain NH-JN4T was at 34–38 °C (range 22–42 °C), pH 6.5–7 (range 6.0–8.5) and with 2.5% NaCl (range 0.5–6%). No growth was observed when the strain was cultured below 22 °C or above 42 °C after incubation for 10 days. No growth was observed below pH 6.0 or above pH 8.5, or when the NaCl concentration (w/v) was higher than 6% or in the absence of NaCl. Strain NH-JN4T did not grow in aerobic medium, which indicated that it was an obligate anaerobic strain. Catalase and oxidase tests were also performed (Zhu et al., 2011). Catalase activity was detected with 3% hydrogen peroxide. Oxidase activity was detected with tetramethyl-p-phenylenediamine. Catalase and oxidase activities were negative.

To test utilization of carbon sources, basal medium based on CJW medium with yeast extract (Difco) and tryptone (Difco) removed was used. Complex proteinaceous substrates (10 g l⁻¹) such as Casamino acids and peptone and glycerol were added into basal medium which was then autoclaved for 20 min at 121 °C. Sugars and amino acids powder were sterilized by UV light overnight before added into the medium as described by Tan et al. (2012). Growth was observed in the presence of peptone (10 g l⁻¹), tryptone (10 g l⁻¹), yeast extract (10 g l⁻¹), beef extract (10 g l⁻¹) and glycine (20 mM). Growth was not observed in the presence of starch (10 g l⁻¹), pyruvate (25 mM), L-valine (25 mM), DL-alanine (20 mM), L-proline (10 mM), DL-alanine (20 mM) + L-proline (10 mM), L-arginine (25 mM), glucose (25 mM), maltose (25 mM), arabinose (25 mM), fructose (25 mM), xylose (25 mM), cellobiose (25 mM), sucrose (25 mM), formate (20 mM), acetate (20 mM), butyrate (20 mM), fumarate (20 mM), olive oil (10 g l⁻¹), carboxymethyl cellulose (10 g l⁻¹), filter paper (10 g l⁻¹), chitin (10 g l⁻¹), Casamino acids (10 g l⁻¹) or glycerol (20 mM). The major fermentation products detected by the HPLC method (Ehrlich et al., 1981) in PYG medium after incubation for 48 h were formate, acetate, butyrate and ethanol. The results of these phenotypic tests are given in Table 1 and in the species description.

Chemotaxonomic analysis was performed on strain NH-JN4T, *C. tepidiprofundi* DSM 19306T and *C. proteolyticum* DSM 3090T. Cells were cultivated in PYG medium at 37 °C until the culture reached late exponential phase. Fatty acids methyl esters (FAMEs) were obtained as described by Kuykendall et al. (1988). Identification and qualification of the FAMEs were automatically performed by the Sherlock
Clostridium histolyticum ATCC 19401T (M59094)  
Clostridium limosum ATCC 25620T (FR870444)  
Clostridium proteolyticum DSM 3090T (X73448)  
Oceanirhabdus sediminicola NH-JN4T (JQ771468)  
Clostridium tepidiprofundi SG 508T (EF197795)  
Clostridium argentinense ATCC 27322T (X68316)  
Clostridium oceanicum DSM 1290T (FR749923)  
Clostridium sporogenes ATCC 3584T (X68189)  
Clostridium butylicum ATCC 25763T (L37585)  
Eubacterium combesi ATCC 25545T (AY533380)  
Clostridium perfringens ATCC 13124T (CP000246)  
Clostridium butyricum ATCC 19398T (AB075768)

Fig. 1. Neighbour-joining phylogenetic tree based on a comparison of the 16S rRNA gene sequences of strain NH-JN4T and its closest relatives. GenBank accession numbers are given in parentheses. Percentages of bootstrap support are shown at branch nodes. Bootstrap value is 1000. Bar, 0.01 substitutions per nucleotide position.

Microbial Identification System with the standard MIS Library Generation Software (Microbial ID Inc.) and the results were matched with the ANAEROBE MOORE 3.90 library. The main fatty acids of strain NH-JN4T were anteiso-C_{15:0} (18.1 %), C_{16:0} (13.6 %), iso-C_{15:0} (12.0 %), anteiso-C_{17:0} (8.7 %) and C_{16:0} DMA (8.2 %). Significant differences existed in the proportion and major compositions of fatty acids of strain NH-JN4, C. tepidiprofundi 19306T and C. proteolyticum DSM 3090T (Table 2).

The polar lipids of strain NH-JN4T, C. tepidiprofundi 19306T and C. proteolyticum DSM 3090T were extracted, separated on silica gel plates (10 × 10 cm, Merck 5554) and further analysed (Minnikin et al., 1984). Concentrated sulfuric acid and 5 % ethanolic molybdatophosphoric acid were used to reveal total lipids, ninhydrin for aminolipids, x-naphthol for glycolipids and Zinzadze’s reagent for phospholipids (Fang et al., 2012). The results suggested that the major polar lipids of strain NH-JN4T were diphosphatidylglycerol, phosphatidylglycerol and a diversity of glycolipids (Fig. S2, panel 1).

Isoprenoid quinones were extracted using the method described by Minnikin et al. (1984), and were analysed by HPLC as described by Tindall (1990). No quinone was detected in strain NH-JN4T.

To analyse the reduction of electron acceptors, sodium thiosulfate (20 mM), sodium sulfite (5 mM), sodium sulfate (20 mM), sodium nitrate (5 mM) and sodium nitrite (20 mM) were added from filter-sterilized solutions to the basal medium (CJW medium lacking L-cysteine and resazurin). Amorphous iron (III) oxyhydroxide (90 mM) and elemental sulfur (1 %) were added into basal medium before autoclaving. Iron (III) citrate (20 mM) was sterilized by UV light overnight. Reduction of elemental sulfur, sodium thiosulfate, sodium sulfate and sodium sulfate were tested using the method of Ramamoorthy et al. (2006). Additional 0.5 % ammonium iron (II) sulfate was added into the cultural tubes after the cells reached stationary phase and tubes were scored positive if black iron (II) sulfide precipitation formed. The reduction of nitrate to nitrite was determined by using Griess reagent; tubes were scored positive if the Griess reagent turned red. The reduction of nitrite to nitrogen gas was determined with Durham tubes as described by Ogg & Patel (2009); tubes were scored positive if gas levels in Durham tubes were larger than that of control group. The reduction of amorphous iron (III) oxyhydroxide was inferred when a transformation of the reddish-brown colour of the iron (II) oxide to a dark precipitate [iron (II)] and a clearing of the media was observed (Ogg & Patel, 2009). The reduction of iron (III) citrate was inferred when the amount of solid iron (III) citrate decreased and the medium turned green. Strain NH-JN4T could utilize sodium sulfite as the electron acceptor when peptone (10 g l^{-1}) was used as the electron donor. It could not utilize elemental sulfur, sodium thiosulfate, sodium sulfate, sodium nitrate, sodium nitrite, amorphous iron (III) oxyhydroxide and iron (III) citrate as electron acceptors.

16S rRNA gene sequence analysis indicated that strain NH-JN4T was related to the family Clostridiaceae and was most closely related to six uncultured bacterial clones which were retrieved from Caribbean coral (GenBank accession numbers FJ202830, FJ202578, FJ425601, GU118553 and GU118556; similarity value 99 %) and Cedar Key, Florida (EU488325; similarity value 99 %). The novel strain NH-JN4T formed a separate branch on the phylogenetic tree and showed significant phylogenetic divergence from C. limosum ATCC 25620T, C. proteolyticum DSM 3090T, C. histolyticum ATCC 19401T and C. tepidiprofundi SG 508T (94.0, 93.0, 92.9 and 92.3 % 16S rRNA gene sequence similarity, respectively). The DNA G+C content of strain NH-JN4T was significantly higher (35.8 mol%) than those
Table 1. Differential phenotypic, physiological and genotypic characteristics of strain NH-JN4\textsuperscript{T} and its closest phylogenetic relatives

<table>
<thead>
<tr>
<th>Characteristic</th>
<th>1</th>
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<th>3</th>
<th>4</th>
<th>5</th>
<th>6</th>
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<tr>
<td>Isolation source</td>
<td>Sea sediment</td>
<td>Deep-sea hydrothermal vent</td>
<td>Chicken manure</td>
<td>Gas gangrene in humans</td>
<td>Mud</td>
<td>Soil</td>
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<tr>
<td>Cell width ((\mu)m)</td>
<td>0.5–1.2</td>
<td>0.4–0.6</td>
<td>0.5</td>
<td>0.5–0.9</td>
<td>0.6–1.6</td>
<td>0.5–1.7</td>
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<tr>
<td>Cell length ((\mu)m)</td>
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<td>2.0–3.0</td>
<td>2.2</td>
<td>1.3–9.2</td>
<td>1.7–16</td>
<td>2.4–7.6</td>
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<tr>
<td>Motility</td>
<td>+</td>
<td>+</td>
<td>–</td>
<td>±</td>
<td>±</td>
<td>±</td>
</tr>
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<td>Temperature ((^\circ) C)</td>
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<td>50</td>
<td>30–37</td>
<td>37</td>
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<td>22–45*</td>
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<td>ND</td>
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<td>6.0–8.0</td>
<td>ND</td>
<td>ND</td>
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<td>Range</td>
<td>6.0–8.5</td>
<td>4.0–8.5</td>
<td>5.5–9.0*</td>
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<td>ND</td>
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<td>NaCl concentration (%)</td>
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<td>2.5</td>
<td>0*</td>
<td>ND</td>
<td>ND</td>
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<tr>
<td></td>
<td>Range</td>
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<td>1–6</td>
<td>0–3.5*</td>
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<td>ND</td>
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<td>DNA G+C content (mol%)</td>
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<td>30.9</td>
<td>29.5</td>
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<tr>
<td>Glucose</td>
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<td>–</td>
<td>ND</td>
<td>±</td>
<td>ND</td>
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<tr>
<td>Maltose</td>
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<td>+</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>+</td>
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<tr>
<td>Amino acid fermentation</td>
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<tr>
<td>Glycine</td>
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<td>–</td>
<td>+</td>
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<td>ND</td>
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<td>Reduction of electron acceptors</td>
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<td>–*</td>
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<td>ND</td>
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<td>Sodium sulfite</td>
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<td>–*</td>
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<tr>
<td>Sodium nitrate</td>
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<td>–</td>
<td>+*</td>
<td>ND</td>
<td>ND</td>
<td>ND</td>
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<td>16S rRNA gene sequence similarity to strain NH-JN4\textsuperscript{T} (%)</td>
<td>100</td>
<td>92.3</td>
<td>93.0</td>
<td>92.9</td>
<td>94.0</td>
<td>90.0</td>
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</table>

*Data from this study.
\daggerFermentation products: F, formate; A, acetate; B, butyrate; E, ethanol; M, methanol; S, succinate; L, lactate.
Table 2. Fatty acid contents of strain NH-JN4<sup>T</sup> and its closest phylogenetic relatives

Taxa: 1, strain NH-JN4<sup>T</sup>; 2, C. tepidiprofundi DSM 19306<sup>T</sup>; 3, C. proteolyticum DSM 3090<sup>T</sup>. Data are from this study. Values are percentages of total fatty acids. Fatty acids representing >5% of the total fatty acids are in bold. –, Not detected.

<table>
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<th>Fatty acid</th>
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<td>–</td>
<td>–</td>
</tr>
<tr>
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<td>0.2</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>C&lt;sub&gt;13&lt;/sub&gt;:0 iso</td>
<td>1.3</td>
<td>1.1</td>
<td>–</td>
</tr>
<tr>
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<td>–</td>
<td>0.2</td>
<td>–</td>
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<td>0.5</td>
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<td>0.5</td>
<td>–</td>
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<tr>
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<td>3.6</td>
<td>19.7</td>
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<td>–</td>
<td>0.6</td>
<td>–</td>
</tr>
<tr>
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<td>–</td>
<td>0.9</td>
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<td>C&lt;sub&gt;15&lt;/sub&gt;:0 iso</td>
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<td>38.4</td>
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<td>2.4</td>
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<td>4.1</td>
<td>11.4</td>
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<td>–</td>
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<td>–</td>
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<td>C&lt;sub&gt;18&lt;/sub&gt;:1 cis 11/t9/t6</td>
<td>–</td>
<td>–</td>
<td>9.2</td>
</tr>
<tr>
<td>C&lt;sub&gt;18&lt;/sub&gt;:1 cis 13</td>
<td>–</td>
<td>–</td>
<td>20.5</td>
</tr>
<tr>
<td>C&lt;sub&gt;19&lt;/sub&gt;:0 anteiso</td>
<td>1.2</td>
<td>–</td>
<td>0.8</td>
</tr>
<tr>
<td>C&lt;sub&gt;20&lt;/sub&gt;:0</td>
<td>–</td>
<td>–</td>
<td>–</td>
</tr>
</tbody>
</table>

of C. limosum ATCC 25620<sup>T</sup> (24 mol%), C. proteolyticum DSM 3090<sup>T</sup> (29.5 mol%) and C. tepidiprofundi SG 508<sup>T</sup> (30.9 mol%).

Moreover, C. tepidiprofundi DSM 19306<sup>T</sup> is a moderately thermophilic bacterium with an optimal growth temperature of 50°C and endospore formed only below pH 5.5 (Slobodkina et al., 2008), whereas the upper growth temperature of strain NH-JN4<sup>T</sup> was 42°C and endospore formed in the optimal environment. Both strain NH-JN4<sup>T</sup> and C. tepidiprofundi DSM 19306<sup>T</sup> were tolerant to high NaCl concentrations (6%) while C. proteolyticum DSM 3090<sup>T</sup> could not grow when the NaCl concentration was above 4%. Strain NH-JN4<sup>T</sup> utilized glycine as its sole carbon source while C. tepidiprofundi DSM 19306<sup>T</sup> was not observed to utilize any amino acid (Slobodkina et al., 2008). However, C. tepidiprofundi DSM 19306<sup>T</sup> could use some kinds of common mono- and disaccharides (Slobodkina et al., 2008) while strain NH-JN4<sup>T</sup> could not. As for C. proteolyticum DSM 3090<sup>T</sup>, it can use neither carbohydrates nor amino acids (Wiegell, 2009). The fermentation products of strain NH-JN4<sup>T</sup> in PYG medium were mainly formate, acetate, butyrate and ethanol. In contrast, end products of fermentation in PYG medium were acetate and methanol for C. proteolyticum DSM 3090<sup>T</sup> and butyrate and ethanol for C. tepidiprofundi DSM 19306<sup>T</sup>. Strain NH-JN4<sup>T</sup> could only utilize sulfur dioxide as an electron acceptor, while C. tepidiprofundi DSM 19306<sup>T</sup> used elemental sulfur (Slobodkina et al., 2008) and C. proteolyticum DSM 3090<sup>T</sup> used sodium nitrate. Genomic and phenotypic traits suggest that strain NH-JN4<sup>T</sup> is distinct from its most related genus Clostridium.

Finally, the evidence from chemotaxonomy also showed distant relatedness among strain NH-JN4<sup>T</sup>, C. proteolyticum DSM 3090<sup>T</sup> and C. tepidiprofundi DSM 19306<sup>T</sup>. The most abundant FAME of strain NH-JN4<sup>T</sup> was anteiso-C<sub>15</sub>:0 (18.1%) while those of C. proteolyticum DSM 3090<sup>T</sup> and C. tepidiprofundi DSM 19306<sup>T</sup> were C<sub>16</sub>:0 (31.6%) and iso-C<sub>15</sub>:0 (38.4%), respectively. Strain NH-JN4<sup>T</sup> possessed anteiso-C<sub>19</sub>:0 and C<sub>20</sub>:0 while other two strains lacked these fatty acids. Additionally, cis-C<sub>18</sub>:1 11 DMA (20.5%) and C<sub>18</sub>:1 cis 11/t9/t6 were present in cell extracts of C. proteolyticum DSM 3090<sup>T</sup> but were not detected in cell extracts of strain NH-JN4<sup>T</sup> or C. tepidiprofundi DSM 19306<sup>T</sup>. Significant differences among strain NH-JN4<sup>T</sup>, C. tepidiprofundi DSM 19306<sup>T</sup> and C. proteolyticum DSM 3090<sup>T</sup> also existed in the composition of polar lipids. Strain NH-JN4<sup>T</sup> had a variety of glycolipids whereas C. tepidiprofundi DSM 19306<sup>T</sup> as well as C. proteolyticum DSM 3090<sup>T</sup> had some aminolipids and a diversity of phospholipids (Fig. S2).

On the basis of the genotypic and phenotypic differences, and the large phylogenetic distance separating strain NH-JN4<sup>T</sup> from the most closely related genus Clostridium of the family Clostridiaceae, it is proposed that the strain represents a novel species of a new genus, for which the name Oceanirhabdus sediminicola gen. nov., sp. nov. is proposed.

Description of Oceanirhabdus gen. nov.

Oceanirhabdus (O.ce.a.nlhabs.dus. L. n. oceanus ocean; Gr. fem. n. rhabdos rod; N.L. fem. n. Oceanirhabdus a rod of the ocean).

Cells are obligatory anaerobic, spore-forming rods and stain Gram-positive. Catalase and oxidase were not produced. Species of this genus can utilize complex...
proteinaceous substrates as carbon and energy source. The major cellular fatty acids are anteiso-C_{15:0}, C_{16:0}, iso-C_{15:0}, anteiso-C_{17:0} and C_{16:0} DMA. No isoprenoid quinone is detected. The major polar lipids are diphasphatidylglycerol, phosphatidylglycerol and glycolipids. The DNA G+C content of the only known strain of the type, and only known, species is 35.8 mol%. 16S rRNA gene sequence analysis indicates that the genus is a member of the family Clostridiaceae and is most closely related to the genus Clostridium. The type species is Oceanirhabdus sediminicola.

**Description of Oceanirhabdus sediminicola sp. nov.**

Oceanirhabdus sediminicola [se.di.mi.ni’co.la. L. n. sedimen -inis sediment; L. suff. -cola (from L. n. incola) inhabitant, dweller; N.L. n. sediminicola sediment dweller.]

Cells are 0.5–1.2 × 2.2–7.0 μm and peritrichous. Growth is observed at 22–42 °C (optimum 34–38 °C), at pH 6.0–8.5 (optimum 6.5–7.0) and with 0.5–6% (w/v) NaCl (optimum 2.5%). The substrates used are peptone, tryptone, yeast extract, beef extract and glycine. Growth can be observed in the presence of peptone, tryptone, yeast extract, beef extract and glycine. Growth is not observed in the presence of starch, pyruvate, L-valine, DL-alanine, L-proline, DL-alanine + L-proline, L-arginine, glucose, maltose, arabinose, fructose, xylose, cellobiose, sucrose, formate, acetate, butyrate, fumarate, olive oil, CM-cellulose, filter paper, chitin, Casamino acids or glycerol. The major fermentation products from PYG medium are formate, acetate, butyrate and ethanol. Sodium sulfite can be utilized as an electron acceptor but not elemental sulfur, sodium thiosulfate, sodium sulfate, sodium nitrate, sodium nitrite, ammonium iron (III) oxyhydroxide or iron (III) citrate.

The type strain, NH-JN4^T (=JCM 18501^T=KCTC 15322^T) was isolated from a sediment sample of the South China Sea. The DNA G+C content of the type strain is 35.8 mol%.

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**References**


