<table>
<thead>
<tr>
<th>Title</th>
<th>Vertical distribution of major sulfate-reducing bacteria in a shallow eutrophic meromictic lake</th>
</tr>
</thead>
<tbody>
<tr>
<td>Author(s)</td>
<td>Kubo, Kyoko; Kojima, Hisaya; Fukui, Manabu</td>
</tr>
<tr>
<td>Citation</td>
<td>Systematic and Applied Microbiology, 37(7): 510-519</td>
</tr>
<tr>
<td>Issue Date</td>
<td>2014-10</td>
</tr>
<tr>
<td>DOI</td>
<td></td>
</tr>
<tr>
<td>Doc URL</td>
<td><a href="http://hdl.handle.net/2115/57661">http://hdl.handle.net/2115/57661</a></td>
</tr>
<tr>
<td>Type</td>
<td>article (author version)</td>
</tr>
<tr>
<td>Additional Information</td>
<td>There are other files related to this item in HUSCAP. Check the above URL.</td>
</tr>
</tbody>
</table>
Supplementary material

**Vertical distribution of major sulfate-reducing bacteria in a eutrophic shallow meromictic lake**

Kyoko Kubo*, Hisaya Kojima* and Manabu Fukui

The Institute of Low Temperature Science, Hokkaido University, Kita-19, Nishi-8, Kita-ku, Sapporo 060-0819, Japan
<table>
<thead>
<tr>
<th>Probe</th>
<th>Specificity</th>
<th>Probe Sequence (5' - 3')</th>
<th>Position</th>
<th>FA (%)**</th>
<th>Probe concentration (final µl⁻¹)***</th>
<th>Reference</th>
</tr>
</thead>
<tbody>
<tr>
<td>EUB338-I</td>
<td>Most Bacteria</td>
<td>GCTGCTCCCTCCGGTGGAGT</td>
<td>338 - 355</td>
<td>35</td>
<td>28</td>
<td>[1]</td>
</tr>
<tr>
<td>NON338</td>
<td>Control probe complementary to EUB338</td>
<td>ACTCTACGGGAGGCAGC</td>
<td>338 - 355</td>
<td>35</td>
<td>28</td>
<td>[7]</td>
</tr>
<tr>
<td>Delta495a</td>
<td>Most Deltaproteobacteria</td>
<td>AGTTAGCGGTGCTTCTT</td>
<td>495 - 512</td>
<td>35</td>
<td>28</td>
<td>[3]</td>
</tr>
<tr>
<td>cDelta495a</td>
<td>Competitor for Delta495a</td>
<td>AGTTAGCGGTGCTTCTT</td>
<td>495 - 512</td>
<td>35</td>
<td>28</td>
<td>[4]</td>
</tr>
<tr>
<td>DSS658</td>
<td>Most Desulfobacteraceae</td>
<td>TCCACTTCTCTCTCCCCAT</td>
<td>658 - 675</td>
<td>50</td>
<td>28</td>
<td>[5]</td>
</tr>
<tr>
<td>SEEP1d-468*</td>
<td>Some SEEP SRB-1d bacteria</td>
<td>ACCGTAGTGCAAGATGG</td>
<td>468 - 485</td>
<td>40</td>
<td>60</td>
<td>This study</td>
</tr>
<tr>
<td>SEEP1d-1420*</td>
<td>SEEP-SRB1d group</td>
<td>CAA CTG GTA CAG CCA</td>
<td>1420-1437</td>
<td>40</td>
<td>60</td>
<td>[6]</td>
</tr>
<tr>
<td>cSEEP1d-1420*</td>
<td>Competitor for SEEP1d-1420</td>
<td>CAA CTG GTA CAA CCA</td>
<td>1420-1437</td>
<td>40</td>
<td>60</td>
<td>[6]</td>
</tr>
</tbody>
</table>

* Hybridization and washing temperatures were at 35°C.
** Formamide concentrations in the hybridization buffer (v/v).
*** Probe concentration in the hybridization buffer (v/v).
Supplementary figure captions

Fig. S1  Single cells of sulfate-reducing bacteria in Lake Harutori anoxic water column, visualized by CARD-FISH. A. DSS cells (probe DSS658, green). B. SEEP SRB-1d cells (probe SEEP1d-468, green). DAPI signals are in blue. Scale bars $= 10 \mu m$

Fig. S2  Partial alignment of the DSS658 probe targeting position and the sequences of *Desulfosarcina-Desulfococcus* specific clone library. Base position is according to *Escherichia coli*. Identical bases are shown in dots. Sequences in gray-shaded boxes have no mismatch to the probe DSS658.

Fig. S3  A magnified phylogenetic tree based on deduced AprA amino acid sequences of sulfur-oxidizing bacteria retrieved from the water column of Lake Harutori. The tree was constructed based on a distance matrix (119 amino acid positions) by using the neighbor-joining method. Bootstrap value estimation was based on 1000 replicates (only values above 50% are shown). Numbers of sequences obtained in each clone library were indicated in parentheses; 3.0 m, 3.5 m, and 4.0 m in that order. SOP1 and 2 means the different lineages of AprA. The bar represents 5% estimated sequence divergence.

Fig. S4  Alignment of 263 deduced AprA amino acid sequences used in this study. The amino acid sequences were aligned using ClustalW implemented in MEGA5.05 software.
Fig. S1
Kubo et al.
<table>
<thead>
<tr>
<th>Target sequence</th>
<th>658</th>
<th>675</th>
<th>No. of clones</th>
</tr>
</thead>
<tbody>
<tr>
<td>OTU1* T G A G T . . . . . . . . . . . . . . . . A T T C C</td>
<td>13</td>
<td></td>
<td></td>
</tr>
<tr>
<td>OTU2 T G A G T . . . . . . . . . . . . . . . . A T T C C</td>
<td>4</td>
<td></td>
<td></td>
</tr>
<tr>
<td>OTU3 T G A G T . . . . . . . . . . . . . . . . A T T C C</td>
<td>2</td>
<td></td>
<td></td>
</tr>
<tr>
<td>OTU4 T G A G T . . . . . . . . . . . . . . . . A T T C C</td>
<td>2</td>
<td></td>
<td></td>
</tr>
<tr>
<td>OTU5 T G A G T . . . . . . . . . . . . . . . . C . . A T T C C</td>
<td>1</td>
<td></td>
<td></td>
</tr>
<tr>
<td>OTU6 T G A G T . . . . . . . . . . . . . . . . C . . A T T C C</td>
<td>1</td>
<td></td>
<td></td>
</tr>
<tr>
<td>OTU8 T G A G T . . . . . . . . . . . . . . . . A T T C C</td>
<td>1</td>
<td></td>
<td></td>
</tr>
<tr>
<td>OTU9 T G A G T . . . . . . . . . . . . . . . . A T T C C</td>
<td>1</td>
<td></td>
<td></td>
</tr>
<tr>
<td>OTU10 T G A G T . . . . . . . . . . . . . . . . C . . A T T C C</td>
<td>1</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

*Sequence HADCC-54 (Accession No. AB894641) in OTU1 has a single terminal mismatch to the probe DSS658.

Fig. S2
Kubo et al.
<table>
<thead>
<tr>
<th>Species</th>
<th>Accession Numbers</th>
<th>GenBank</th>
<th>ETEC</th>
<th>EHEC</th>
<th>STEC</th>
<th>Shiga-like</th>
<th>S. Typhi</th>
<th>S. Paratyphi A</th>
<th>S. Paratyphi B</th>
<th>S. Paratyphi C</th>
</tr>
</thead>
<tbody>
<tr>
<td><em>Proteus</em> stuartii</td>
<td>U25620.1</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td><em>Escherichia coli</em></td>
<td>U02723.1</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td><em>Salmonella typhimurium</em></td>
<td>M9212.1</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td><em>Shigella flexneri</em></td>
<td>M9212.1</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

Fig. S4 contd.
Kubo et al.
References


