Microbial diversity in marine sediments from Sagami Bay and Tokyo Bay, Japan, as determined by 16S rRNA gene analysis

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16S rDNA clone libraries were analysed to investigate the microbial diversity in marine sediments from Sagami Bay (stations SA, water depth of 1159 m, and SB, 1516 m) and Tokyo Bay (station TK, 43 m). A total of 197 clones was examined by amplified rDNA restriction analysis (ARDRA) using three four-base-specific restriction enzymes (HhaI, RsaI and HaeIII). In SA, 57 RFLP types were detected from 77 clones. In SB, 17 RFLP types were detected from 62 clones. In TK, 21 RFLP types were detected from 58 clones. The genotypic diversity among the three sampling sites was 0.958, 0.636 and 0.821, respectively, indicating that the microbial diversity of SA was higher than at the other two stations. At SA, the most abundant RFLP type constituted 10% of all clones. The samples from SB and TK had dominant RFLP types which constituted 60% and 38% of the total clone libraries, respectively. The community structure of SA included many single-type clones, which were found only once in the clone libraries. This structure contrasted with that of the other two stations. Thirty-seven clones were selected and sequenced according to dendrograms derived from ARDRA, to cover most of the microbial diversity in the clone libraries. No clones were identical to any of the known 16S rDNA sequences or to each other. All sequences had 84-8% similarity to rDNA sequences retrieved from the DNA databases. Sequenced clones fell into five major lineages of the domain Bacteria: the gamma, delta and epsilon Proteobacteria, Gram-positive bacteria and the division Verrucomicrobia. At SA, the Verrucomicrobia and the three subclasses of the Proteobacteria were found. Most clone sequences belonged to the gamma Proteobacteria. The high-GC Gram-positive bacteria and the gamma subclass of the Proteobacteria were common at both SB and TK. Although the depths of SB and TK were very different, the community diversity inferred from ARDRA and the taxonomic position of the dominant clones were similar. All clones belonging to the high-GC Gram-positive bacteria collected from both SB and TK fell into the same cluster and are regarded as members of an unknown actinomycete group. The clone compositions were different at each sampling site, and clones of the gamma Proteobacteria and high-GC Gram-positive bacteria were dominant.

Keywords: microbial diversity, marine sediment, 16S rDNA, amplified rDNA restriction analysis (ARDRA), RFLP

INTRODUCTION

During the past decade, the development of molecular techniques using nucleic acids has led to many new findings in studies of microbial ecology (Amann et al., 1995). As a basic approach to clarifying microbial communities, 16S rDNAs are amplified by PCR from nucleic acids extracted from environmental samples, and then the PCR products are cloned and sequenced. This approach can avoid the limitation of the traditional culturing techniques for assessing the microbial diversity in natural environments and has been applied to water columns (Britschgi & Giovannoni, 1991; DeLong, 1992;
DeLong et al., 1994; Fuhrman et al., 1992, 1993; Fuhrman & Davis, 1997; Giovannoni et al., 1990; Mullins et al., 1995), hot springs (Barns et al., 1994; Hugenholtz et al., 1998; Ward et al., 1990), soils (Kuske et al., 1997; Liesack & Stackebrandt, 1992; Ueda et al., 1995), sediments (Schleper et al., 1997; Wise et al., 1997), deep subsurface environments (Boivin-Jahns et al., 1995), hydrothermal vents (Moyer et al., 1995) and the gut of animals (McInerney et al., 1995; Ohkuma & Kudo, 1996).

Both sediment and soil probably represent some of the most complex microbial habitats on Earth. There may be several thousand species of bacteria in 1 g soil (Torsvik et al., 1990). To study the genetic diversity and to analyse the members of mixed microbial populations are two of the most important steps in microbial community studies. However, little research has been done on microbial diversity in marine sediments, and little information is currently available (Gray & Herwig, 1996).

We analysed 16S rDNA clone libraries to investigate the genetic diversity of microbial communities in marine sediments from Sagami Bay and Tokyo Bay. Clonal types were initially grouped on the basis of amplified rDNA restriction analysis (ARDRA). The 16S rDNA sequences from representatives of different RFLP groups were then determined and compared with those available from the DNA databases.

**METHODS**

**Study areas.** Fig. 1 shows sampling sites. Sampling was done in February 1996 at two stations in Sagami Bay, SA (35° 4′ 0" N, 139° 14′ 5" E, water depth of 1159 m) and SB (35° 0′ 2" N, 139° 20′ 5" E, 1516 m), and at one station in Tokyo Bay, TK (35° 20′ 8" N, 139° 47′ 1" E, 43 m), by the R/V Tansei-Maru of the Ocean Research Institute, University of Tokyo. Tokyo Bay is located almost in the centre of Japan, and has an area of 1000 km². The mean depth is about 17 m. Industrial and domestic waste discharged from the large human population enters the bay mostly via four big rivers. Too much waste, aided by a low water exchange rate, has caused significant eutrophication (Coastal Oceanography Research Committee, The Oceanographical Society of Japan, 1985). Sagami Bay is located in the south-west of Tokyo Bay. Water exchange is good, because this bay is well-connected to the Pacific Ocean and the Kuroshio Current flows strongly offshore. The maximum depth of the bay is more than 2000 m. The Western part of the bay is a steep fault escarpment flanking the north-eastern portion of Izu Peninsula. SA is near the bottom of the escarpment. A gentle slope continues from the SA area to the centre of the bay and, SB lies on this slope (Coastal Oceanography Research Committee, The Oceanographical Society of Japan, 1985).

**Sampling procedures and physical and chemical characteristics of marine sediments.** Sediment samples were collected with a multiple-core sampler (Rigosha). The sampler enabled us to take samples without any disturbance of surface sediments or contamination from surrounding seawater. Cores (82 mm in diameter) were aseptically sliced on board into 1 cm intervals with a stainless-steel core cutter (Rigosha). Sliced samples were transferred into plastic bags, sealed with a thermo-sealer, and stored at −20 °C on board and at −80 °C in the laboratory until DNA extraction. The uppermost 1 cm sediment layer was used for further analysis. Sediment dry weights were measured after drying at 105 °C for 48 h. Total organic carbon and nitrogen were measured by a CHN analyser (NA1500NCS; Fisons Instruments).

Samples for direct counting were aseptically taken and placed into a plastic syringe (5 ml). One cubic centimetre of the sample was suspended in 9 ml filtered (0.22 µm) and autoclaved seawater and fixed with filtered formaldehyde (final concentration 4%) on board and stored at 4 °C. Sodium pyrophosphate solution was added to the samples (0.001 M final concentration), which were then sonicated and mixed (Velji & Albright, 1986). The total number of microorganisms was determined by counting cells stained with 4′,6-diamidino-2-phenylindole (DAPI; 5 µg ml⁻¹ final concentration) (Schallenberg et al., 1989) under an epifluorescent microscope (BH-2; Olympus), as described by Porter & Feig (1980). At least 15 fields and more than 350 cells for total bacterial number were counted. Redox potential was measured with an ORP meter (RM-10P; TOA electronics).

**DNA extraction and purification.** The DNA extraction method described by Ueda et al. (1995) was used with some modifications. Forty grams of sediment was mixed with an equal volume of 120 mM sodium phosphate buffer (pH 8.0) containing 5% SDS by vigorous shaking in a plastic bottle for 40 min at 40 °C. Then, 0.6 cm³ of the mixture was transferred to 2.0 cm³ plastic tubes and treated with seven cycles of freezing in liquid nitrogen and thawing in boiling water. The lysate was then purified by a SepaGene DNA extraction kit (Sankyo Junyaku). Electrophoresis on a 1% agarose gel (agarose 1600; Wako Pure Chemical Industries) was used to remove low-molecular-mass nucleic acids. DNA fragments larger than 9 kb were cut out and recovered with a GeneClean II kit (Bio 101) as recommended by the manufacturer.

**PCR amplification and cloning of 16S rDNA.** The primers used for amplification of bacterial 16S rDNA were 519f (5′-CAGCMGCCGCGTATTC-3′; positions 519–536 of Escherichia coli 16S rDNA numbering; Brosius et al., 1978) (Lane et al., 1985) and 1492r (5′-GGTACCTTGGTACCTT-3′; positions 1510–1492) (Eden et al., 1991). The PCR mixtures were prepared as described by Urakawa et al. (1997). DNA amplification was done in a DNA thermal cycle (PTC-
Table 1. Sediment characteristics

<table>
<thead>
<tr>
<th>Station</th>
<th>$E_h$ (mV)</th>
<th>C (%)</th>
<th>N (%)</th>
<th>C:N (mol)</th>
<th>Moisture content (%)</th>
<th>$10^{-9} \times$ No. of bacterial cells (dry g$^{-1}$)</th>
</tr>
</thead>
<tbody>
<tr>
<td>SA</td>
<td>15</td>
<td>1.128</td>
<td>0.103</td>
<td>12.8</td>
<td>68.5</td>
<td>3.2</td>
</tr>
<tr>
<td>SB</td>
<td>84</td>
<td>2.350</td>
<td>0.266</td>
<td>10.3</td>
<td>88.8</td>
<td>1.2</td>
</tr>
<tr>
<td>TK</td>
<td>–60</td>
<td>1.158</td>
<td>0.037</td>
<td>11.9</td>
<td>44.8</td>
<td>ND</td>
</tr>
</tbody>
</table>

ND, Not determined.

Table 2. Summary of amplified rDNA restriction analysis

<table>
<thead>
<tr>
<th>Station</th>
<th>No. of clones</th>
<th>No. of RFLP types</th>
<th>RFLP type to clone number ratio</th>
<th>Genotypic diversity</th>
<th>Coverage</th>
<th>Number of restriction patterns when digested with:</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>HhaI     Rsal    HaeIII</td>
</tr>
<tr>
<td>SA</td>
<td>77</td>
<td>57</td>
<td>0.74</td>
<td>0.958</td>
<td>0.45</td>
<td>20        39        49</td>
</tr>
<tr>
<td>SB</td>
<td>62</td>
<td>17</td>
<td>0.27</td>
<td>0.636</td>
<td>0.84</td>
<td>8         7         7</td>
</tr>
<tr>
<td>TK</td>
<td>38</td>
<td>21</td>
<td>0.36</td>
<td>0.821</td>
<td>0.74</td>
<td>10        12        9</td>
</tr>
</tbody>
</table>

Amplified rDNA restriction analysis. To examine the RFLP patterns, 2 µl of a 1:10 dilution of the PCR product amplified by the M13 primers was reamplified by using the 519f and 1492r primers with the same PCR program as described above. Six to eight microlitres of each PCR product was separately digested with three four-base-specific restriction enzymes (HhaI, Rsal and HaeIII) (Toyobo) at 37 °C for 120 min. Restricted DNAs were analysed by horizontal electrophoresis in 1% agarose gel in TAE buffer. Two microlitres of amplified DNA was examined by horizontal electrophoresis on 1% agarose gel in TAE buffer.

Determinant of nucleotide sequences. To determine the rDNA sequences, the PCR product amplified by the M13 primers was reamplified by using the 519f and 1492r primers with the same PCR program as described above. The PCR product was purified and concentrated with a Microcon-100 microconcentrator (Amicon).

Thirty-seven clones were selected according to the dendrograms derived from the results of ARDRA, and sequenced with a SequiTherm Long-Read Cycle Sequencing kit (Epicentre Technologies) and an automated sequencer (ALF DNA Sequencer; Amersham Pharmacia Biotech) as prescribed by Urakawa et al. (1998b). Primers for the sequencing described by Lane (1991) were used, and partial sequences corresponding to positions 600–1400 of E. coli were determined for each clone. These sequences were checked for chimeric artefacts by the check_chimeras program of the Ribosomal Database Project (RDP) (Maidak et al., 1997), and compared with similar rDNA sequences retrieved from the DNA databases, by using the BLAST search program in the National Centre for Biotechnology Information (NCBI), and the RDP SIMILARITY_RANK program.

Phylogenetic analysis. Sequences were aligned using the clustal w program (ver. 1.60) (Thompson et al., 1994) and then realigned manually as previously described (Urakawa et al., 1999). Nucleotide positions where there were ambiguous alignments and gaps were omitted from subsequent phylogenetic analysis. Neighbour-joining (NJ) analysis (Saitou & Nei, 1987) was also performed by using clustal w. The NJ tree was constructed from the distance matrix calculated by the algorithm of Kimura’s two-parameter model (Kimura, 1980). Bootstrap confidence values were obtained with 1000 resamplings.

RESULTS AND DISCUSSION

Sample collection and DNA extraction

Nucleic acids were successfully extracted from the sediment samples without polyvinylpolypyrrolidone purification, which has been used for extracting DNA
Fig. 2. Relationship between 16S rDNA RFLP types and number of clones. (a) Genotype compositions. ST, single-type clones, which were found only once in the clone library. (b) Dendrograms constructed from ARDRA. Dots show the positions of sequenced clones.

from rich humic acid samples (Holben et al., 1988) for PCR amplification. The freeze–thaw technique used in this study was helpful in extracting DNA from marine sediment with little damage.

Recently, many investigators have raised questions about possible problems associated with PCR of the 16S rRNA gene for the phylogenetic analysis of microbial communities. As an increment of cycles of PCR could bias the clone composition obtained, we used 25 cycles in the PCR step to minimize bias (Sekiguchi et al., 1998; Suzuki & Giovannoni, 1996; Wilson & Blitchington, 1996). Primers for PCR amplification were selected to lessen a levelling effect of amplification (Suzuki & Giovannoni, 1996). Strong biases may be introduced by the copy number of 16S rRNA genes (Kerkhof & Speck, 1997) and the differential PCR amplification efficacy of DNA from heterogeneous templates (Chandler et al., 1997; Farrelly et al., 1995). These possible effects may mean that the proportions found in the clone libraries do not always represent the 16S rDNA proportions found in the original samples. However, the limitation of culture techniques (Amann et al., 1995) means that sequence-based phylogenetic techniques may provide a
**Table 3. Nearest neighbour of the 16S rDNA clones**

<table>
<thead>
<tr>
<th>Clone</th>
<th>Length of sequence (bp)</th>
<th>Phylogenetic group</th>
<th>Accession no. of nearest neighbour</th>
<th>Nearest neighbour*</th>
<th>Similarity (%)</th>
<th>No. of clones included in the same restriction pattern</th>
</tr>
</thead>
<tbody>
<tr>
<td>SA14</td>
<td>771</td>
<td>Chlamydia/</td>
<td>X99392</td>
<td>Verrucomicrobium sp.</td>
<td>84.8</td>
<td>2</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Verrucomicrobium</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>SA15</td>
<td>582</td>
<td>Gamma</td>
<td>M26631</td>
<td>Arhodomonas aqaeolei</td>
<td>88.4</td>
<td>1</td>
</tr>
<tr>
<td>SA16</td>
<td>759</td>
<td>Gamma</td>
<td>X74724</td>
<td>Vibrio splendidus</td>
<td>98.2</td>
<td>6</td>
</tr>
<tr>
<td>SA28</td>
<td>821</td>
<td>Gamma</td>
<td>X84980</td>
<td>Lucina pectinata symbiont</td>
<td>94.3</td>
<td>1</td>
</tr>
<tr>
<td>SA41</td>
<td>848</td>
<td>Gamma</td>
<td>X74724</td>
<td>Vibrio splendidus</td>
<td>97.5</td>
<td>8</td>
</tr>
<tr>
<td>SA50</td>
<td>606</td>
<td>Gamma</td>
<td>U77478</td>
<td>Riftia pachyptila endosymbiont</td>
<td>94.1</td>
<td>1</td>
</tr>
<tr>
<td>SA51</td>
<td>764</td>
<td>Gamma</td>
<td>L25711</td>
<td>Anodontia phillipiana gill symbiont</td>
<td>89.4</td>
<td>1</td>
</tr>
<tr>
<td>SA56</td>
<td>809</td>
<td>Delta</td>
<td>M34407</td>
<td>Desulfosarcina variabilis</td>
<td>91.7</td>
<td>1</td>
</tr>
<tr>
<td>SA59</td>
<td>749</td>
<td>Gamma</td>
<td>X74724</td>
<td>Vibrio splendidus</td>
<td>98.3</td>
<td>5</td>
</tr>
<tr>
<td>SA63</td>
<td>634</td>
<td>Epsilon</td>
<td>L35520</td>
<td>Alumella pompejana epibiont</td>
<td>91.0</td>
<td>1</td>
</tr>
<tr>
<td>SA68</td>
<td>680</td>
<td>Gamma</td>
<td>U57919</td>
<td>Vibrio sp.</td>
<td>98.1</td>
<td>1</td>
</tr>
<tr>
<td>SA71</td>
<td>709</td>
<td>Delta</td>
<td>L35504</td>
<td>Nitrospina gracilis</td>
<td>87.0</td>
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<tr>
<td>SA73</td>
<td>651</td>
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<td>U57919</td>
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<tr>
<td>SA79</td>
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<td>Gamma</td>
<td>X74724</td>
<td>Vibrio splendidus</td>
<td>97.5</td>
<td>1</td>
</tr>
<tr>
<td>SA82</td>
<td>822</td>
<td>Delta</td>
<td>Y13672</td>
<td>‘Desulfovacea sulfoxidens’</td>
<td>90.2</td>
<td>1</td>
</tr>
<tr>
<td>SB01</td>
<td>657</td>
<td>Gram-positive</td>
<td>U09762</td>
<td>Clavibacter michiganisn</td>
<td>92.2</td>
<td>1</td>
</tr>
<tr>
<td>SB06</td>
<td>654</td>
<td>Gamma</td>
<td>AF030381</td>
<td>Pseudoalteromonas sp.</td>
<td>96.0</td>
<td>1</td>
</tr>
<tr>
<td>SB09</td>
<td>672</td>
<td>Gamma</td>
<td>L25707</td>
<td>Lucina floridana gill symbiont</td>
<td>90.4</td>
<td>1</td>
</tr>
<tr>
<td>SB11</td>
<td>731</td>
<td>Gram-positive</td>
<td>X77443</td>
<td>Microbacterium arborescens</td>
<td>92.0</td>
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</tr>
<tr>
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<td>842</td>
<td>Gram-positive</td>
<td>X77435</td>
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<td>93.9</td>
<td>37</td>
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<tr>
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<td>728</td>
<td>Gram-positive</td>
<td>X77443</td>
<td>Microbacterium arborescens</td>
<td>93.7</td>
<td>3</td>
</tr>
<tr>
<td>SB21</td>
<td>712</td>
<td>Gamma</td>
<td>D89792</td>
<td>Coxiella burnetti</td>
<td>88.9</td>
<td>1</td>
</tr>
<tr>
<td>SB26</td>
<td>812</td>
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<td>U09762</td>
<td>Clavibacter michiganisn</td>
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<td>SB33</td>
<td>644</td>
<td>Gram-positive</td>
<td>AB015562</td>
<td>Unidentified actinomycete</td>
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<td>X77443</td>
<td>Microbacterium arborescens</td>
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<td>3</td>
</tr>
<tr>
<td>SB53</td>
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<td>Gram-positive</td>
<td>X77443</td>
<td>Microbacterium arborescens</td>
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<td>3</td>
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<td>X77443</td>
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<tr>
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<td>94.0</td>
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</tr>
<tr>
<td>TK02</td>
<td>604</td>
<td>Delta</td>
<td>M34407</td>
<td>Desulfosarcina variabilis</td>
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<td>1</td>
</tr>
<tr>
<td>TK12</td>
<td>748</td>
<td>Gamma</td>
<td>L01575</td>
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<tr>
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<td>844</td>
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<td>X77435</td>
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<td>X77443</td>
<td>Microbacterium arborescens</td>
<td>93.2</td>
<td>22</td>
</tr>
</tbody>
</table>

* The closest matching sequence from a cultivated and characterized strain was identified using the fasta search available in the DDBJ. In some cases, higher similarities were found with environmental rDNA clones, or uncharacterized strains.

less biased picture of community composition than would any single cultivation technique.

**Amplified rDNA restriction analysis**

The summary of ARDRA is listed in Table 2. At SA, 57 RFLP types were detected from 77 clones. At SB, 17 RFLP types were detected from 62 clones. At TK, 21 RFLP types were detected from 58 clones. The genotypic diversity of SA was higher (0.958) than that at SB (0.636) and TK (0.821). Fig. 2(a) shows the relationships between RFLP types and number of clones. At SA, the most abundant RFLP type constituted 10% of all clones. In contrast, the most abundant RFLP types at the other two sites constituted 60% (SB) and 38% (TK) of the total clone libraries. Single-type clones, which occurred only once, were abundant at SA (66%), but were much less common at SB (16%) and TK (26%).

Moyer *et al.* (1994) examined a microbial mat community at a deep-sea hydrothermal vent by ARDRA.
They obtained 12 RFLP types from 48 clones by using four four-base-specific restriction enzymes and found two dominant clone types. We made some calculations from their data; the genotypic diversity was 0-70%, between those of SB and TK; the most abundant RFLP type in their data constituted 48% of all clones. Mullins et al. (1995) estimated the coverage of an rDNA clone library of the Sargasso Sea to be 81% and they also reported the coverage to be 68% by analysis of SAR and ALO clone libraries reported by Schmidt et al. (1991), which were constructed from rDNAs collected from the open ocean. Coverage values from our SB and TK libraries were similar (Table 2), but the value from the SA library was much lower. Rath et al. (1998) also used coverage value to estimate the microbial diversity in marine snow samples as 5-3%, the lowest value reported.

Sequencing analysis of 16S rDNA clones

Thirty-seven clones were selected and sequenced according to dendrograms derived from ARDRA (Fig. 2b), so as to cover most of the microbial diversity in the clone libraries. We obtained 580-847 nucleotide sequences (mean size 702 bp) corresponding to approximately positions 520-1400 of E. coli numbering (Brosius et al., 1978). One clone looked suspiciously chimeric when examined with the check_chimera program. One part was similar to Gram-positive bacteria, the other part to the gamma Proteobacteria. This sequence was not used for further phylogenetic analysis (data not shown).

Table 3 summarizes the clones sequenced. No clones were identical to any of the known 16S rRNA sequences from cultured organisms, environmental clones, or to each other in the library. All sequences had more than 84-8% similarity to rDNA sequences in the DNA databases. Sequenced clones fell into five major lineages of the domain Bacteria: the gamma, delta and epsilon Proteobacteria, Gram-positive bacteria and the division Verrucomicrobia (Hedlund et al., 1997) (Figs 3 and 4).

The community structure of SA contained many single-type clones, in contrast to the other two stations (Fig. 2a). As shown in Table 3, the Verrucomicrobia and the three subclasses of the Proteobacteria were found. The most frequently collected clones were the gamma Proteobacteria.

Community structures from SB and TK included dominant clones (Fig. 2a). 16S rDNA sequencing analysis showed that the high-GC Gram-positive bacteria and the gamma Proteobacteria were common to both (Table 3). Interestingly, in spite of very different depths at SB and TK, the dendrograms and the affiliations of sequenced clones were similar (Fig. 2b; Table 3). As shown in Fig. 4, clones belonging to the high-GC Gram-positive bacteria collected from both sites fell completely into the same cluster.

Delta subclass of the Proteobacteria

Four clones (SA56, SA71, SA82 and TK02) were included in the delta Proteobacteria (Table 3). Phylogenetic analysis showed that SA56, SA82 and TK02 were related to the sulfate-reducing bacteria (Fig. 3). The redox potential at SB was higher than at the other stations (Table 1), and sulfate-reducing bacteria were found at
TK and SA, but not at SB. SA6 and TK02 were most similar (91–92% similarity) to Desulfoarculus variabilis (Table 3; Fig. 3). SA82 was most similar to ‘Desulfoocapsa sulfuroxigens’ (90% similarity) by a FASTA search. SA71 was most similar to Nitrospina gracilis (87% similarity). This relationship is also supported by an 83% bootstrap confidence value on the phylogenetic tree (Fig. 3).

**Gamma subclass of the Proteobacteria**

One frequently encountered group, consisting of five clones (SA16, 41, 59, 68 and 79) (Fig. 3), was apparently affiliated with the genus Vibrio (97–99% similarity) by 100% bootstrap confidence values. Vibrio splendidus was the closest species. SB06 was affiliated with Pseudoalteromonas sp. (96% similarity) (Table 3). TK75 was most similar (94.2%) to E. coli by a FASTA search. It was found only from Tokyo Bay (Table 3; Fig. 1).

SA15 was most similar to the sequence of Arhodomonas aquaeolei (the 16S rDNA sequence is registered as A. oleiferhydrans in the DNA databases), isolated from fluid of a petroleum production reservoir (Adkins et al., 1993), by a FASTA search (88.4% similarity) (Table 3). SA51 had higher similarity to an Anodontia phillipiana gill symbiont (89.4%) (Table 3). Phylogenetic analysis showed that this clone was closely related to Coxiella burnetii (Fig. 3). SB21 branched deeply within the gamma Proteobacteria lineage. The similarity values of SA15, SA51 and SB21 to other known species or clones were less than 90%. As phylogenetic relationships shown in Fig. 3 were not supported by high bootstrap values, it was difficult to speculate on the phenotypic features of these diverse clones.

Five clones (SA28, SA50, SB09, TK12 and TK99) showed a close relationship to sulfur-oxidizing bacterial endosymbionts by a FASTA search (Table 3). Phylogenetic analysis showed that two of these clones (SA28 and SA50) were clustered with the symbiotic thioautotrophs, which are known to be distributed across a broad range of host taxa in marine environments (Annelida, Mol lusca, Pogonophora and Vestimentifera) (Durand & Gros, 1996), but are distinguished from Thiomicrospira species, which are free-living, obligately chemolitho trophic micro-organisms (Distel & Wood, 1992) (Fig. 3). However, the bootstrap support for most clades within the sulfur-oxidizing bacteria was low. SA28 was most similar (94.3%) to a sequence of Lucina pectinata endosymbiont (Table 3). SA50 was most similar (94.1%) to the endosymbiont of tube worm, Riftia pachyptila (Edwards & Nelson, 1991; Feldman et al., 1997).

The other three clones (SB09, TK12 and TK99) were clustered together with the marine snow clone agg47 reported by DeLong et al. (1993) (Fig. 3). Although detailed phylogenetic affiliation of this clone was not discussed in their report (DeLong et al., 1993), this clone has been treated as the sulfur-oxidizing bacterial group in the RDP. Thus these three clones are also included in this group. Gray & Herwig (1996) also found the sulfur-oxidizing bacterial group in coastal marine sediment. However, their sequence position is different from ours and cannot be compared.

**Epsilon subclass of the Proteobacteria**

One clone, SA63, was affiliated with the epsilon Proteobacteria (Table 3; Fig. 3). It was most similar (91.0%) to an endosymbiont of a polychaete, Alvinella pompejana, found at deep-sea hydrothermal vents, by a FASTA search (Cary et al., 1997; Haddad et al., 1995) (Table 3). This relationship was also supported on the phylogenetic tree by a 91% bootstrap confidence value (Fig. 3).

Moyer et al. (1995) reported the existence of epsilon Proteobacteria in a microbial mat community at Pele’s Vent, a hydrothermal vent on Loihi Seamount, Hawaii. Recently, distribution of the Alvinella pompejana ectosymbiont, a member of the epsilon Proteobacteria, was examined at a hydrothermal vent and reported by Cary et al. (1997). Cary et al. (1997) concluded that the chemosynthetic symbiomatic gamma and epsilon Proteobacteria are likely to play an important role in the ecology of hydrothermal vent ecosystems.

*Calyptogena*-vestimentiferan tube worm communities were observed for roughly 7 km along the foot of the Hatsushima escarpment, Sagami Bay, between depths of 900 and 1200 m (Hashimoto et al., 1989; Kim et al., 1995). SA, at a depth of 1159 m, is close to this cold seep area. The total number of organisms at SA was higher than at SB (Table 1) and the redox potential of the sediment was lower than that at SB. Although it is difficult to conclude whether the symbiont-like clones are true members of this area, the community structure of SA might be affected by this area. Our results show that the symbiont-like gamma and epsilon Proteobacteria might be distributed in marine sediment as members of the community. Jones & Gardiner (1989) and Feldman et al. (1997) suggested that vestimentiferans acquire endosymbionts from the free-living bacterial community. Our result might contribute to studies of the evolutionary origin and acquisition of these endosymbionts. Little information is available about this symbiont-like group; further investigation is needed for clarifying its nature.

**Verrucomicrobia**

One clone, SA14, was affiliated with the division Verrucomicrobia (Hedlund et al., 1997) (Table 3). This clone was most similar (84.8%) to Verrucomicrobi um sp. strain VeSm13, found in the anoxic soil of flooded rice microcosms (Janssen et al., 1997). The phylogenetic tree also supports their close relationship with a 93% bootstrap confidence value (Fig. 4). Novitsky (1990) reported that marine sedimenting particles may influence sediment bacterial communities. This phylogenetic group was also found in marine sedimenting particles (Rath et al., 1998). From these reports, we have to assume two different habitats, marine snow and...
sediment, for this phylogenetic group in marine environments.

**Gram-positive bacteria**

The most abundant sequences from SB and TK were the high-GC Gram-positive bacteria (Table 3). Fourteen clones showed close relationships to each other (93.0–99.8% similarity) and formed one large cluster supported by 100% bootstrap confidence values (Fig. 4). This group was dominant in the SB and TK clone libraries but was not found in SA. *Microbacterium arborescens*, *Clavibacter michiganensis* and an unidentified actinomycete were the closest species by a BLAST search (Table 3). It has been unclear for a long time whether the Gram-positive bacteria isolated from marine sediments are indigenous members of the microbial community in the sediments or whether they are carried from land by river flow. As shown in Fig. 4, new clones have been sequenced that are only distantly related to terrestrial isolates and this observation does indeed support the idea that this taxonomic group is separate from a previously known terrestrial group included in the family *Microbacteriaceae*. Moran et al. (1995) detected the presence of indigenous *Streptomyces* populations in marine sediments with the 16S rRNA probing technique. They concluded that true marine indigenous actinomycetes were present. Jensen & Fenical (1995) reported that 82% of the Gram-positive bacteria isolated from marine environments showed an obligate seawater requirement for growth. This result supports the conclusion of Moran et al. (1995). Quantitative analyses based on nucleic acid hybridization (Stahl & Amann, 1991), fatty acid analysis (Rajendran et al., 1994) or quinone profile analysis (Hiraishi et al., 1998) of these unknown Gram-positive bacteria are needed.

**Concluding remarks**

The clone compositions were different at each sampling site. Sequenced clones fell into five major lineages of the domain **Bacteria**: the gamma, delta and epsilon **Proteobacteria**, Gram-positive bacteria and **Verrucomicrobia**. The gamma **Proteobacteria** and Gram-positive bacteria dominated in our clone libraries. Gray & Herwig (1996) detected six major lineages of the domain **Bacteria** and reported the dominance of the gamma **Proteobacteria** and Gram-positive bacteria in a marine sediment sample. This result also supports our data. However, alpha **Proteobacteria**, dominant or nearly dominant in various soil (Stackebrandt et al., 1993; Zhou et al., 1997) and seawater samples (Mullins et al., 1995; Fuhrman & Davis, 1997), were not found.

Zhou et al. (1997) examined 43 16S rDNA clones from Siberian tundra soil, and found its diversity remarkable, because all clones had different RFLP patterns. We found that, in comparison with microbial communities observed in terrestrial soils (Kuske et al., 1997; Ueda et al., 1995; Zhou et al., 1997), microbial communities in marine sediments (Gray & Herwig, 1996) were less...
variable and simple at the phylum or class level, because marine sediments are covered with seawater. Such stability is also observed in microbial communities in the open ocean (Mullins et al., 1995). Further phylogenetic studies and functional analyses are required for understanding the microbial diversity and community structure in marine sediments. Other kinds of studies are necessarily required to supplement phylogenetic studies (Stahl & Amann, 1991; Rajendran et al., 1994; Hiraishi et al., 1998).

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