Association of Marine Archaea with the Digestive Tracts of Two Marine Fish Species

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Recent studies have shown that archaea which were always thought to live under strict anoxic or extreme environmental conditions are also present in cold, oxygenated seawater, soils, the digestive tract of a holothurian deep-sea-deposit feeder, and a marine sponge. In this study, we show, by using PCR-mediated screening in other marine eukaryotes, that marine archaea are also present in the digestive tracts of flounder and grey mullet, two fish species common in the North Sea, in fecal samples of flounder, and in suspended particulate matter of the North Sea water column. No marine archaea could be detected in the digestive tracts of mussels or the fecal pellets of a copepod species. The archaeal 16S rRNA gene sequences of archaea in cold, oxygenated seawater (3, 4, 8, 9), it became clear that archaea might be more widely distributed. In coastal waters of the Atlantic and Pacific oceans, marine archaea constitute between 2 and 8% of the prokaryotic community (3, 17). Occasionally they can be very abundant and contribute up to 34% of the prokaryotic biomass as was found for Antarctic waters (4). Archaea present in ocean water are designated marine archaea and can be divided into three phylogenetic lineages (3, 7, 8). The first lineage includes the group I marine archaea belonging to the subdomain of the Crenarchaeota, which includes extreme thermophilic species. The second lineage is the group II marine archaea and is part of the subdomain Euryarchaeota, which includes thermophiles, sulfur-metabolizing microorganisms, and all known methanogens. The third lineage of marine archaea comprises clones that have been obtained from deep-water samples (7); closely related archaeal sequences have been retrieved from coastal (19) and continental shelf sediments (27). A recent study on water samples from the Santa Barbara Channel showed that the group I and II marine archaea have different vertical distributions (16). Group II is dominant in the surface layer, while group I becomes abundant at depths of 100 m (16), thus suggesting that representatives of the two groups have different ecological traits. Not-yet-cultivated archaea have also been found in other habitats. Currently, crenarchaeotal 16S rRNA gene sequences have been detected in agricultural and forest soils (2, 12, 25), freshwater and coastal sediments (15, 19, 23), and deep-sea sediment (13).

The difference in membrane lipid composition between bacteria and archaea (10) has been used to specifically look for archaeal lipids that cannot be assigned to known cultivated members of the Archaea. An unknown C40-ether-bound lipid, which was assigned to a planktonic marine archaeon, was detected in particulate organic matter of the Cariaco Trench and the Black sea water column (11). Compound-specific isotope analysis of the carbon skeleton of this lipid suggested that this marine archaeon utilizes an isotopically heavy carbon source, such as algal carbohydrates or dissolved bicarbonate (11). Recently, the identification of specific lipids associated with group I marine archaea has been reported by DeLong et al. (5). The only other studies on marine archaea showed that members of group I marine archaea were found in the gut contents of a deep-sea-deposit feeder (18) and in a marine sponge (21). To extend knowledge on the distribution of marine archaea in marine animals, we screened digestive tract and fecal samples of two marine fish species, common mussels, and a copepod species for the presence and diversity of marine archaea. Here we report on the association of group I and II marine archaea with the digestive tracts of flounder and grey mullet,
two fish species which are commonly found in the North Sea. It was also shown that feces of flounder and suspended particulate matter of the North Sea water column contain group I and II marine archaea. These clones were closely related to the ones found in the digestive tract contents. The data suggest that certain marine fish species host marine archaea in their digestive tracts and that the feces of these fish could be a source of particle-associated marine archaea.

Hybridization experiments. The distribution of group I and II marine archaea among the different clonal libraries was determined by slot blot hybridization with chemiluminescently labelled oligonucleotide probes, which have been described previously by Massana et al. (16). One hundred microfilariae of plasmid DNA from 1,000 times was spotted and fixed with 100 mM NaCl. The DNA was denatured at 95°C for 3 min and immediately put on ice. Electrophoresis of the substrate CSPD (Boehringer) with alkaline phosphatase and capture phosphatase had been attached, bound probe was detected through the conversion of the light signal on X-ray film.

Fingerprinting by terminal restriction fragment length polymorphism. Archaeal community composition was analyzed by terminal restriction fragment length polymorphism as described by Liu et al. (14). The 16S rDNA of the archaeal community was amplified with the same primers as those described above for the amplification and cloning experiments. However, the Arch958R primer was extended by several washing steps and binding of a digoxigenin antibody to which alkaline phosphatase had been attached, bound probe was detected through the conversion of the substrate CSPD (Boehringer) with alkaline phosphatase and capture of the light signal on X-ray film.
PCR products were analyzed in 1% agarose and stained with ethidium bromide. Community DNA from flounder digestive-tract contents; lane 3, 100-bp ladder. Arch2F and Arch958R. Lane 1, community DNA from flounder feces; lane 2, originate from the seawater in which the fish lives and are symbiotic members of the fish intestines or whether they are marine archaea found in the digestive tract and fecal samples in this study, it cannot be concluded exclusively whether the phylogenetic analysis. Preliminary determination of the phylogenetic affiliation of the clones consisted of a BLAST analysis (1) with the National Center for Biotechnology Information database. A number of sequences from the BLAST similarity ranking list were chosen for detailed phylogenetic analysis. The clone sequences were aligned with those from the database with the Dedicated Comparative Sequence Editor software program of de Rijk and de Wachter (6). Phylogenetic trees were generated and bootstrap analysis (100 replicates) was performed with the TREECON software package (20) by the algorithm described by Kimura and the neighbor joining method.

Nucleotide sequence accession numbers. The sequences discussed in this study have been deposited in GenBank under accession no. AF052943 to AF052954.

RESULTS AND DISCUSSION

Marine archaeal 16S rDNA sequences have been found in the gut of a deep-sea-deposit feeder (18) and associated with a marine sponge (21). To investigate whether marine archaea are also present in other marine animals, digestive tract contents and feces were collected from a number of eukaryotic animals which are common in the North Sea. After extraction of DNA from these samples, PCRs with two archaea-specific 16S rDNA primers (3) were performed. Amplification products with the expected size of 950 bp were obtained with DNA extracted from the feces of flounder and the digestive tract contents of flounder and grey mullet (Fig. 2). After these amplification products were cloned into the p-GEM-T vector and transformed into competent E. coli cells, the plasmids of up to 30 randomly chosen white colonies were isolated for further analysis. The partial 16S rRNA gene insert of three clones, one from the digestive tract of flounder (FIN625), one from grey mullet digestive tract contents (GIN492), and two from flounder feces (FF619 and FF620), were sequenced. Phylogenetic analysis of these sequences showed that they clustered within the group II marine archaea (Fig. 3). The clones derived from flounder digestive tract and feces form a separate group within the lineage of the group II marine archaea and had only 76.7 to 89.8% similarity to the previously described group II marine archaea. The closest related sequences are clone PVAOTU1 (90.0 to 93.2% similarity), from a hydrothermal vent microbial community, Antarctic 5 (89.0 to 89.8% similarity), from Antarctic surface waters, and WHARN (87.7 to 88.5% similarity), from the coastal waters of the Atlantic Ocean near Woods Hole, Mass. (3). From the data presented in this study, it cannot be concluded exclusively whether the marine archaea found in the digestive tract and fecal samples are symbiotic members of the fish intestines or whether they originate from the seawater in which the fish lives and are passaged through the fish as it feeds. No amplification products were obtained from copepod fecal pellets or from the digestive tract contents of mussels with archaeal primers, whereas a PCR product was obtained with the universal primers S*-Univ-50-a-S-19 and S*-Univ-1492-a-A-22. Therefore, it appears that no archaeal DNA was recovered from the copepod and mussel samples. No amplification product was found when DNA of E. coli was used with the same archaea-specific primers and PCR conditions, indicating that the primers and the PCR conditions were specific for archaea and not bacteria.

Phylogenetic analysis of four clones from the fish digestive tract or fecal DNA showed that they are group II marine archaea. To determine the affiliation of other clones, hybridization experiments were carried out with chemiluminescently labelled group I and II probes. All 29 clones of the flounder

<table>
<thead>
<tr>
<th>Community</th>
<th>No. of clones</th>
<th>No. of clones hybridizing with:</th>
<th>No. of restriction groups with:</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td>Group I</td>
<td>Group II</td>
</tr>
<tr>
<td>Flounder feces</td>
<td>29</td>
<td>0</td>
<td>29</td>
</tr>
<tr>
<td>Flounder digestive tract</td>
<td>29</td>
<td>7</td>
<td>22</td>
</tr>
<tr>
<td>Grey mullet digestive tract</td>
<td>23</td>
<td>0</td>
<td>23</td>
</tr>
</tbody>
</table>

ND, not determined.
community present in the digestive tract and the feces of flounder were similar and showed four different fragments (Fig. 4A and B). To learn more about the potential origin of the prominent 249-bp fragment (no. 2), a simulated restriction analysis of 16S rRNA gene sequences in the database was performed (14). This method calculates the expected size of a labelled fragment for 16S rDNA sequences when the fluorescently labelled Arch958R primer and the restriction enzyme HhaI are used. A total of 35 archaeal 16S rDNA sequences, including all the sequences found in this study, were used for simulated restriction analysis. Of the 10 group II marine archaea sequences, 6 yielded a simulated restriction product of 248 bp. One sequence (WHARN) had a simulated product of 247 bp, two sequences of 249 bp (TS10C294 and TS235C302), and one sequence of 250 bp (TS10C298). The other 23 archaeal sequences, including 13 sequences of group I marine archaea, 6 sequences of methanogenic archaea, and 4 sequences of halophilic archaea, all had simulated HhaI digests of different sizes. Only the sequence of the hyperthermophilic archaeon ES1, isolated from a hydrothermal vent, and that of Methanobacterium bryantii, a methanogen isolated from a bovine rumen, had a simulated HhaI restriction product of 249 bp. Based on the results of the simulated restriction analysis, it is concluded that the 249-bp peak of the digestive tract and fecal samples is likely derived from group II marine archaea. The possibility that the 249-bp fragment originated from an unknown fish digestive tract methanogen very closely related to M. bryantii cannot be excluded but seems unlikely because methanogenesis has been demonstrated only with the digestive tract contents of Dover sole and black cod (20), and no isolates of methanogenic archaea from marine fish digestive tract have been described.

It is possible that the marine archaea present in the digestive tracts of marine fish are liberated into the water column and subsequently contribute to the marine archaeal community of suspended particulate matter. To investigate this, we isolated DNA from suspended particulate matter of the North Sea, which was retained on a GF/C filter, and used it for PCR detection, because until now all the studies on marine archaea have analyzed the fraction of the water that passes through a GF/C filter (3, 4, 8, 16, 17). From suspended particulate matter of two stations in the North Sea (see Materials and Methods for the exact locations), a PCR product of 950 bp was obtained. After the cloning of this amplification product, a number of clones were randomly selected and the sequences of the partial 16S rDNA inserts of these clones were determined. Four clones from station TS10, designated TS10C286, TS10C294, TS10C298, and TS10C299, and three from station TS235, designated TS235C302, TS235C306, and TS235C310, were found to cluster with the group I and II marine archaea (Fig. 1) and were related to the clones obtained from the fish digestive tract or fecal samples. The terminal restriction fragment length polymorphism analysis of the archaeal community of suspended particulate matter of the two stations showed the same fragment pattern, similar to those obtained for the archaeal community for the flounder digestive tract and feces (Fig. 4C and D), indicating a high similarity between the archaeal communities of fish digestive tracts, feces, and suspended particulate matter. What the physiological characteristics of the fish-associated marine archaea are and whether or not they are actively present in suspended particulate matter cannot be concluded on the basis of the 16S rDNA sequences. The exact nature of fish-associated marine archaea remains unknown as long as no stable enrichments or pure cultures are available.

FIG. 4. Terminal restriction fragment length polymorphism analysis of 16S rRNA genes derived from flounder feces (A), digestive tract (B), and suspended particulate matter from stations TS 10 (C) and TS235 (D) with the PCR primers Arch2F and fluorescently labelled Arch958R, followed by restriction with HhaI.
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