



## Horizontal and vertical complexity of attached and free-living bacteria of the eastern Mediterranean Sea, determined by 16S rDNA and 16S rRNA fingerprints

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Limnol. Oceanogr., 46(1), 2001, 95-107 | DOI: 10.4319/lo.2001.46.1.0095

**ABSTRACT:** The community structure of attached and free-living bacteria in the Aegean Sea (eastern Mediterranean Sea) was analyzed with use of terminal-restriction fragment length polymorphism (T-RFLP) fingerprinting. Since the Aegean Sea is characterized by rather small temperature fluctuations between surface and deep-water layers, it represents an ideal study site to determine the variations in the community structure of bacteria with depth, since environmental factors other than temperature are likely to determine depth zonation of bacteria. The analysis of 132 T-RFLP electropherograms indicated pronounced differences among the attached and free-living bacterial communities defined as operational taxonomic units (OTUs). Distinct vertical differences of attached and free-living OTUs were found between mesopelagic waters (>200 m depth) and the upper mixed water column (~10-200 m). Attached and free-living OTUs differed considerably throughout the water column, with only ~35% for the South Aegean and ~24% for the North Aegean of all OTUs in both free-living and attached OTUs. Approximately 50% of attached and free-living OTUs were present throughout the water column. Fingerprinting analysis using 16S rRNA indicated that only ~14% of the attached and ~33% of the free-living OTUs were identical to the 16S rDNA fingerprints. The distribution of free-living versus attached bacteria as obtained in this study suggests that even in the absence of temperature as a major selective factor, a distinct deep-water bacterial community exists (particularly in the free-living mode). The deep-water free-living bacterial community appears to be as compositionally complex as the surface water free-living bacterial community.

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