

ID: W2034887836

TITLE: Latitudinal patterns in the abundance of major marine bacterioplankton groups

AUTHOR: ['Matthias Wietz', 'Lone Gram', 'Bo Barker Jørgensen', 'Andreas Schramm']

ABSTRACT:

The present study describes the abundance of major marine bacterioplankton groups and 2 bacterial genera (*Pseudoalteromonas* and *Vibrio*) in surface seawater at 24 stations around the world. Catalyzed reporter deposition-fluorescence in situ hybridization showed that Alphaproteobacteria (average relative abundance 37%, average absolute abundance 3.7×10^5 cells ml⁻¹) including SAR11 [30% / (3×10^5)], Gammaproteobacteria [14% / (1.2×10^5)] and Bacteroidetes [12% / (1.3×10^5)] globally dominated the bacterioplankton. The SAR86 clade [4.6% / (4.1×10^4)] and Actinobacteria [4.5% / (4×10^4)] were detected ubiquitously, whereas Archaea were scarce [0.6% / (4.2×10^3)]. The Roseobacter clade [averaging 3.8% / (3.5×10^4)], *Pseudoalteromonas* [2.6% / (2.1×10^4)] and *Vibrio* [1.5% / (1.3×10^4)] showed cosmopolitan occurrence. Principal component analysis revealed a latitudinal pattern in bacterial abundances by clustering samples according to lower and higher latitudes. This was related to significantly different relative abundances of Bacteroidetes (peaking at higher latitudes) and of unclassified Bacteria and *Vibrio* (both peaking at lower latitudes) between warmer and colder oceans. Relative abundances of Alphaproteobacteria (peaking at subtropical) and Gammaproteobacteria (polar stations) varied between major oceanic biomes, as did absolute abundances of Roseobacter (peaking at temperate and polar stations). For almost all groups, absolute abundances were positively correlated with nutrient concentrations in warmer oceans and negatively correlated with oxygen saturation in colder oceans. On a global scale, Roseobacter and SAR86 were correlated with chlorophyll a. Linkages of environmental parameters with relative abundances were more complex, with e.g. Bacteroidetes being associated with chlorophyll a. The finding of differing communities in warmer and colder oceans underlined the presence of biogeographical patterns among marine bacteria and the influence of environmental parameters on bacterial distribution.

SOURCE: Aquatic microbial ecology

PDF URL: <https://www.int-res.com/articles/ame2010/61/a061p179.pdf>

CITED BY COUNT: 98

PUBLICATION YEAR: 2010

TYPE: article

CONCEPTS: ['Bacterioplankton', 'Roseobacter', 'Gammaproteobacteria', 'Alphaproteobacteria', 'Bacteroidetes', 'Biology', 'Abundance (ecology)', 'Relative species abundance', 'Pseudoalteromonas', 'Ecology', 'Vibrio', 'Actinobacteria', 'Clade', 'Phytoplankton', 'Bacteria', '16S ribosomal RNA', 'Phylogenetics', 'Biochemistry', 'Genetics', 'Nutrient', 'Gene']