

BACTERIAL COMMUNITY STRUCTURE DURING A COCCOLITHOPHORID BLOOM IN THE NORTHERN GULF OF BISCAY

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As part of a study on the ecosystem dynamics and carbon fluxes (PEACE project) during a coccolithophorid (Prymnesiophyceae, Haptophyta) bloom, DNA samples were taken to assess the bacterial community structure associated with the bloom. Here we report on the bacterial community profiles, generated by DGGE fingerprinting of PCR products derived from 16S rRNA encoding genes, of seven different oceanographic stations located near the shelf slope area in the northern part of the Gulf of Biscay, each sampled at six different depths. Both the particle-associated ($>3\mu\text{m}$) and the free-living size fraction ($<3\mu\text{m}$) were analysed, showing a marked difference in bacterial community composition between the two size fractions. The bacterial assemblages tend to be specific for a particular oceanographic station, even after a one week sampling interval. Depth related variation in bacterial community profiles appeared only in two of the stations sampled. The influence of environmental variables, such as chlorophyll a, TEP (Transparent Exopolymeric Particles), POC, and PIC concentrations, on the observed variation in bacterial community structure is assessed as well.