

COCCOLIHTOPHORE BLOOM DYNAMICS SHAPE BACTERIOPLANKTON COMMUNITY IN THE NORTHERN BAY OF BISCAY

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This is the first study to apply a comparative analysis of environmental parameters, phytoplankton pigment data, and bacterioplankton community structure combined with 16S rRNA clone libraries in an *Emiliana huxleyi* bloom (Prymnesiophyceae). We found a clear difference between the free-living and the particle-associated bacterial assemblage, as revealed by denaturing gradient gel electrophoresis (DGGE) and clone libraries. With the majority of the DGGE phylotypes identified, domination by Flavobacteria in the particle-associated bacterial assemblage and by Alphaproteobacteria and SAR86 in the free-living bacterial assemblage was apparent. Stations showed distinct bacterial assemblages, as indicated by ordination of the bacterial community composition. Moreover, changes in particle-associated bacterial assemblage detected by DGGE were weakly yet significantly correlated with changes in phytoplankton community composition.