

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

Van Oostende Nicolas and Koen Sabbe

Universiteit Gent, Vakgroep Biologie, Afdeling Protistologie en Aquatische Ecologie  
Krijgslaan 281 - S8, B-9000 Gent, Belgium  
E-mail: [Nicolas.VanOostende@UGent.be](mailto:Nicolas.VanOostende@UGent.be)

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.