Geophysical Research Abstracts, Vol. 7, 09496, 2005
SRef-ID: 1607-7962/gra/EGU05-A-09496

Microbial community structure along the 18˚W transect of the POMME study area (NE Atlantic) in late summer 2001.

C. Fernández I. (1) , M. Thyssen (1) , M. Denis (1) , P. Raimbault (2)

(1) Laboratoire de Microbiologie, Géochimie et Ecologie Marines (LMGEM), (2) Laboratoire d'Océanographie et de Biogéochimie (LOB), Centre d'Océanologie de Marseille, 163 Av. de Luminy, Case 901, 13288 Marseille cedex 09, France.

(fernandez@com.univ-mrs.fr / Phone 0033491829114)

The influence of hydrodynamic features on biology could be fairly assessed during the POMME experiment (Programme Océanographique Multidisciplinaire Méso-Echelle), held in the northeast Atlantic Ocean.

The spatial and vertical distribution of heterotrophic bacteria and ultraphytoplankton ($< 10\ \mu$m) was investigated by flow cytometry along 18˚W, during the last cruise of the POMME experiment (October 2001). Three bacteria subpopulations (LNA, HNA1, HNA2) were distinguished after staining of their nucleic acids on the basis of their fluorescence and scattering properties. Four main phytoplankton groups were similarly resolved in unstained subsamples.

Bacterial abundances along 18˚W were higher north of 42˚N for HNA2 and LNA (up to 0.5 10^5 cells cm^{-3} and 6 10^5 cells cm^{-3} respectively).

The presence of an anticyclonic eddy (A1 at 43˚N; 18˚W) resulted in increased abundances of LNA and HNA2 in its centre, between surface and 150 m depth.

In contrast, HNA1 showed higher abundances in the southern area with maximal values of 4 10^5 cells cm^{-3}.

Prochlorococcus vertical distribution along 18˚W showed high spatial variability, with cells mainly distributed in the upper 150 m and average higher values observed at 50 m depth (30 10^3 cells cm^{-3}). A twofold increase in cell abundance was observed inside eddy A1 (up to 50 10^3 cells cm^{-3}).

Synechococcus abundance was lower than that of *Prochlorococcus*, with values in the range 2.5-12.5 10^3 cells cm^{-3}. Maximal values were generally observed inside eddy A1.

The contribution percentage of the bacteria carbon to total organic carbon along 18°W oscillated between minimal values of 60% at 44°N and maximal values of 77% at 42.5°N.

Prochlorococcus's contribution to total carbon was close to 5% at southern stations and decreased to 3% in the north, with the exception of stations located inside A1, where this group represented 7% of total carbon biomass.

The contribution of *Synechococcus* to total carbon biomass was lower than 3% in southern stations. However in the northern part area, values reached a maximal contribution of 8.9% to total carbon biomass.

Results show that the microbial community inside A1 was dominated by small size cells, typical of a highly regenerative environment. The higher numbers of bacteria inside the eddy compared to surrounding waters suggest that, during POMME 3, most of the activity was done by heterotrophic community, and that the high nutrient levels observed inside A1 were sustained by regenerative processes.