DEGRADATION OF DISSOLVED ORGANIC MATTER: CHEMICAL CHANGES AND THE STRUCTURE OF THE MICROBIAL COMMUNITY

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Abstract

Marine dissolved organic matter (DOM) represents a wide spectrum of biological reactivity. The aim of this study was to examine the bioavailability of high molecular weight DOM (>1000 Dalton) by measuring concurrent changes in chemical composition and microbial community structure. Sampling was carried out in the NW Mediterranean Sea at 0 m, 500 m and 1500 m and a series of incubations were subsequently carried out. The changes in chemical composition of DOM observed during incubations may reflect the nature of DOM at different depths, while flow cytometry and phylogenetic analysis revealed large variations in the abundance and structure of the microbial community. These results suggest potential links between community composition and DOM degradation.

Keywords : Organic Matter, Bacteria, Chemical Analysis.

Marine dissolved organic mater (DOM) displays a continuum of biological lability, from refractory material turning over on time scales of centuries to millennia to labile material turning over on time scales of minutes to days [3]. Despite a wide range for depth-integrated primary production (PP) in the world ocean [4], marine DOM concentrations are maintained in a remarkably narrow range in the upper 1000 m of the open ocean [2]. Given that DOM production can be a significant fraction of the total PP, this striking offset between the range in PP rates and dissolved organic carbon (DOC) concentrations indicates that there is a very tightly-controlled feedback between production and sinks. Previous studies added important knowledge on the utilization of bulk DOM and monomers by prokaryotes (e.g. [2], [1], [6]), however controls on the biovailability of DOM components remain poorly understood. The aim of this study is to examine the biological reactivity of high molecular weight DOM (HMW; >1000 Dalton) by studying changes in its chemical composition during degradation, while at the same time examining the subsequent changes in the structure of the microbial community.

Sampling was carried out at site DYFAMED (NW Mediterranean) in December 2004. Seawater samples (200L each) were collected at 0 m, 500 m and 1500 m and processed through a tangential flow filtration system in order to provide a HMW DOM concentrate. Unfiltered samples from the same depths served as an inoculum of natural microbial populations. A 30-day long experiment, consisting of 3 replicate incubations per depth and one control per depth (0.2 micron-filtered seawater added to the DOM concentrate, rather than unfiltered inoculum) were carried out between April and May 2005. The following analyses were carried out on the time-series samples: DOC, amino acids, flow cytometry and Restriction Fragment Length Polymorphism (T-RFLP: phylogenetic analysis).

The experiment revealed variations between incubations, even when samples collected at the same location and depth were considered, highlighting the complex nature of the DOM degradation processes. For the surface samples, DOC concentration appeared to decrease by $\sim$20% in the first ten days of the incubation remaining largely stable for the remaining of the incubation time. The 500 m and 1500 m samples on the contrary showed no significant change in DOC concentrations throughout the incubation, potentially reflecting difference in the nature of DOM between surface and the deep ocean. Surface water controls also experienced degradation suggesting that the bulk of the organisms responsible for the changes observed were smaller than 0.2 micron or that microbial population were introduced after the start of the incubations.

Amino acid enantiomer analysis suggested that the bacterial contribution to the amino acid pool shows an initial increase during the incubation for surface water samples. In two out of the four 500 m incubations, peptidoglycan amino acid nitrogen (PG-AA-N) remained stable in the duration of the experiment, while the remaining showed a marked decrease from a PG-AA-N of $\sim$12% to 6%. Three out of four 1500 m incubations also showed a significant decrease in PG-AA-N, while one remained stable.

Flow cytometry analysis showed a strong variability of bacterial and viral abundances ranging from 1.9×10^5 to 2.1×10^6 ml^{-1} and 4.2×10^6 to 1.7×10^8 ml^{-1}, respectively. A large increase in bacterial and viral numbers was observed in the first ten days of the incubations, as well as changes in the relative importance of different population sub-groups. Finally, preliminary T-RFLP results confirmed a large change in the structure of the microbial community throughout the incubation. This suggests tight links between DOM degradation and microbial community composition.

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