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Pressure effects on surface Mediterranean prokaryotes and biogenic silica dissolution during a diatom sinking experiment

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ABSTRACT: This study examined the effect of increasing pressure on biogenic silica dissolution and on prokaryotic assemblages associated with diatom detritus. Experiments were carried out in hyperbaric bottles subjected to a gradual increase in pressure and compared to incubations at atmospheric pressure. To examine only pressure effects and to simulate detritus degradation in the Mediterranean Sea, the incubation temperature was kept constant (13°C), while pressure was increased by 1.5 MPa d^{-1}, simulating a fall of particles at a sinking rate of 150 m d^{-1} over 8 d. Aminopeptidase activity was significantly lower (nearly 5-fold) under increasing pressure than under atmospheric pressure conditions. Lower aminopeptidase activity under increasing pressure affected biogenic silica dissolution, at least at the beginning of the incubation, corresponding to a simulated depth of the first 800 m of the water column. Silicic acid regeneration rates were very low (0.07 ± 0.02 µmol l^{-1} h^{-1}) under increasing pressure conditions during the first 4 d (i.e. between 200 and 800 m), while rates were much higher under atmospheric pressure (0.32 ± 0.05 µmol l^{-1} h^{-1}). However, orthosilicic acid concentrations in the incubations under increasing pressure approached those of the atmospheric pressure incubations by the end of the experiment. In contrast, the taxonomic composition of prokaryotic communities was not affected by increasing pressure, but the input of fresh diatom detritus led to an increase in the relative abundance of the *Cytophaga–Flavobacter* cluster and γ-*Proteobacteria*. These results suggest that hydrostatic pressure affects the function rather than the broad taxonomic structure of prokaryotic communities associated with sinking detrital particles.

KEY WORDS: Hydrostatic pressure · Particle sinking · Decomposition processes · Ectoenzymatic activity · Silica dissolution · Prokaryotic diversity · Mesopelagic waters · Bathypelagic waters

INTRODUCTION

Attached bacteria play an important biogeochemical role in the oceanic carbon flux and are implicated in the remineralization and enzymatic dissolution of particulate organic matter (POM) during its descent through the water column (Cho & Azam 1988, Turley & Mackie 1994, 1995). Remarkably little is known about the composition of POM as it sinks through mesopelagic and bathypelagic waters (Wakeham et al. 1997, Hedges et al. 2000). It is known that a large component of the sinking flux consists of diatoms, which dominate phytoplankton communities at specific times of the year in many oceanic systems (Honjo et al. 1995, Smith et al. 1996, Tréguer & Pondaven 2000).

The fate of sinking biogenic mineral particles depends on the remineralization of the organic matrix, as well as on the dissolution of the mineral matrix. Both processes could be mediated by microbial activities. Milliman et al. (1999), for instance, suggested the exis-

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