Microbial studies of aggregate dynamics in the benthic boundary layer (BBL).

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In summer 1996 particle composition, microbial activities and the genetic structure of the microbial communities were studied across the east Atlantic continental margin at 47°N. At six sampling locations in the Whittard Canyon, ranging from 170 to 3700 m water depth, samples were taken in the euphotic zone, the intermediate water column, in the benthic boundary layer and the sediments. Measurements of bacterial production and bacterial protein production were restricted to water samples. For the identification of the genetic composition of the microbial communities additional samples from the surface sediments were retrieved.

The preliminary results suggest that microbial activities and particle composition in the BBL differ significantly from the intermediate and upper water column. The rates of bacterial production ranged from 0.004 to 1.9 $mgCm^{-3}$ d^{-1}, with highest measured in the euphotic zone. However, similar to other areas the median microbial activities in the benthic boundary layer were higher than in the intermediate water column, 0.31 compared to 0.006 $mgCm^{-3}$ d^{-1}, respectively. Due to the significant differences in bacterial abundances between the euphotic zone and the deeper water layers, the highest cell specific bacterial production rates of 0.36 fg $cell^{-1}d^{-1}$ were observed in the benthic boundary layer. Leucine incorporation rates displayed a similar vertical pattern and ranged from 0.08 to 13.1 µg m^{-3} d^{-1}.The difference in median rates between the BBL (0.34 µg m^{-3} d^{-1}) and the intermediate water column (0.14 µg m^{-3} d^{-1}) was less pronounced compared to the rates of bacterial production. In the BBL, bacterial production rates were significantly related to the concentrations of particulate organic carbon and chl. Equivalents (Kendall's τ, for POC $\tau = 0.39$, $p < 0.0425$, for chl. equivs. $\tau = 0.58$, $p < 0.0025$). Leucine incorporation rates in the BBL were only related to the concentrations of chl. equivalents Kendall's t, $t = 0.60$, $p < 0.0018$). In all other samples the microbial activities appeared to be independent of particle composition.

For the first time, a new approach of analysing the genetic structure of the microbial communities was applied to water samples from three different depth layers and the sediments at most of the visited stations. This approach combines various molecular techniques to resolve the genetic composition of the community of nitrifying bacteria. After DNA extraction and amplification of 16S rDNA sequences with specific primers for nitrifying bacteria, Density Gradient Gel Electrophoresis (DGGE) was used to resolve the genetic structure of the bacterial community and to compare with the genetic information of well defined species of nitrifying bacteria. In general, the band patterns of the DGGE suggest that the nitrifying bacterial communities in the different water bodies were different and that in the sediments all populations from the overlaying waters were represented. Furtheron, a distinct population of nitrifying bacteria was observed in the BBL. This population was genetically different from so far known cultured species. rRNA-sequences of *Nitrosomonas europaea* and *Nitrosospira briensis* were identified in the samples from the euphotic zone and the sediment. The genetic structure differed significantly not only within vertical water layers but also between the different stations.