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Patterns of bacterial and archaeal production and diversity in the deep water masses of the North Atlantic

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The formation of the North Atlantic Deep Water in the Greenland-Iceland-Norwegian Sea is one of the major driving forces of the meridional ocean circulation. Over the last decades, oceanographers have identified the general flow patterns of the main water masses of the Atlantic Ocean and their physical properties. Biological oceanography, however, traditionally focuses on the vertical transport of matter from the surface to the deep ocean and the deep water masses are not considered as an entity as they are in physical oceanography. There is no reason to assume, however, that the deep water masses distinct by their physical characteristics would not also have distinct biogeochemical signatures and consequently, distinct microbial signatures. We present measurements of prokaryotic abundance, production and community structure along a more than 7,000 km transect covering meso- and bathypelagic layers of the North Atlantic Ocean.

Generally Bacteria were lower in abundance than Archaea in the layers below 200 m depth throughout the North Atlantic although archaeal growth rates were about one order of magnitude lower than those of Bacteria. Archaea were taking up bicarbonate indicating that there is a thus far unrecognized chemoautotrophy in the deep ocean raising the question on the energy source of these deep ocean Archaea. While Archaea in the oxygen minimum zone had a gene typical for ammonia oxidation, *amoA*, encoding for ammonium monooxygenase, *amoA* gene abundance was essentially undetectable in the layers below 1000 m depth. This indicates that particularly Crenarchaea are ammonia oxidizers in the oxygen minimum layer while in deep layers, they are apparently deriving their energy from other sources. Phylogenetic analysis of the crenarchaeotal community throughout the water column confirmed the different nature of the crenarchaeal communities between oxygen minimum layers and the deeper layers.

Moreover, the different water masses were found to harbor characteristic prokaryotic communities with some prokaryotes being specific to certain water masses reflecting the subtle changes in the biogeochemical signatures of the different major North Atlantic deep water masses.