



## **Bacterial and archaeal diversity and function in the major deep water masses of the North Atlantic**

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In the frame of the International Census of Marine Microbes (ICoMM) as part of CoML, EUR-OCEANS and EuroDEEP, the relation between the physical structure of the major deep-water masses of the North Atlantic and the diversity of the prokaryotic community is examined in relation to the main biogeochemical cycles. During the previous TRANSAT and ARCHIMEDES cruises, the abundance and cell production of Archaea and Bacteria in the meso- and bathypelagic North Atlantic were determined along a S-N transect from 65°N to 7°S following the North Atlantic Deep Water. Using catalyzed reporter deposition-FISH (CARD-FISH) and specific oligonucleotide probes, Archaea were found to be consistently more abundant than Bacteria below 100 m depth. Combining microautoradiography with CARD-FISH (MICRO-CARD-FISH) revealed that the percentage of *Eury-* and *Crenarchaeota* taking up leucine did not follow a specific trend with depth. The fraction of *Crenarchaeota* taking up inorganic carbon increased with depth, while *Euryarchaeota* taking up inorganic carbon decreased from 200 m to 3000 m depth. The ability of Archaea to take up inorganic carbon was used as a proxy to estimate archaeal cell production. We estimate that archaeal production in the meso- and bathypelagic North Atlantic contributes between 10-84 % to the total prokaryotic production in the deep Atlantic water masses. The recently emerging notion that *Crenarchaeota* are ammonia oxidizers was tested using RT-PCR to quantify the *amoA* gene copy numbers. Crenarchaeal *amoA* copy numbers decreased from the bottom of the euphotic layer to the bathypelagic realm by three orders of magnitude while the abundance of *Crenarchaeota* determined by MICRO-CARD-FISH and RT-PCR decreased only by one order of magnitude over this depth range. Thus, we conclude that bathypelagic *Crenarchaeota* are actively growing in the dark ocean, however, it is likely that, in contrast to recent observation on *Crenar-*

*chaeota* from the upper water column, bathypelagic *Crenarchaeota* are not oxidizing ammonia in significant amounts. Sequence information on the 16S rRNA gene of the *crenarchaeotal* community indicates that those potentially harboring the *amoA* gene and those lacking it are very closely related.