



Bacterial and archaeal diversity in the meso- and bathypelagic waters of the eastern North Atlantic basin

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The biogeography and diversity of prokaryotic deep-water communities were investigated in the Canary and Cap Verde basin of the eastern North Atlantic Ocean. The aim of this study was to determine whether patterns of bacterial and archaeal diversity correspond to individual water masses or whether depth is a more important determinant of prokaryotic community composition. To examine the variation between bacterial and archaeal assemblages at different stations, depths and water masses, we studied the less conserved internal transcribed spacer (ITS) region of the ribosomal operon. ITS gene fragments provide a higher taxonomic resolution than the 16S rRNA gene and served, in this study, as a molecular indicator for prokaryotic diversity in the deep water masses of the North Atlantic. Within a distinct water mass, the composition of bacterial community was relatively homogenous among stations. Bacterioplankton communities exhibited the highest taxa-richness in intermediate waters (200-1000m depth) and lowest richness in the lower deep water (3000-4500m depth). Archaeal communities were generally less diverse than bacterial communities. Specific bacterial and archaeal taxa were characteristic for distinct water masses while others were ubiquitously distributed over the entire water column. These data show that the phylogenetic composition of prokaryotes is not only based on depth but also on water masses which are physically and chemically distinct entities. The specific composition of bacterial communities in the same water masses is largely maintained even over large distances. Based on our analyses, we conclude that for deep-water prokaryotic biogeography the water masses exert more influence on the prokaryotic community composition than simply depth.