

BACTERIAL AND ARCHAEAL DIVERSITY IN THE MESO- AND BATHYPELAGIC WATERS OF THE EASTERN NORTH ATLANTIC BASIN

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Abstract

The biogeography and diversity of bacterial and archaeal deep-water communities was investigated in the eastern North Atlantic basin. The internal transcribed spacer (ITS) region was used as a relevant marker for this study. ITS gene fragments provide higher taxonomic resolution than the 16S rRNA gene and served as a molecular indicator for prokaryotic diversity in the deep water masses of the North Atlantic. The aim of this study was to determine whether patterns of prokaryotic diversity correspond to individual water masses or whether the depth is a more important determinant of prokaryotic community composition. 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. *Keywords* : *Bacteria, Biodiversity, Biogeography, Deep Waters, Intermediate Waters.*

We investigated the composition of the meso- and bathypelagic prokaryotic community at 31 stations in the Canary and Cape Verde basin of the eastern North Atlantic Ocean. Temperature, salinity, density and oxygen concentration were used to identify distinct water masses. The mesopelagic waters (200-1000 m depth) were characterized by two distinct water masses depending of the location of the station: the more saline Mediterranean Sea Outflow Water (MSOW) and the relatively fresh Antarctic Intermediate Water (AAIW). The Lower Deep Water (LDW) (3000-4500 m depth) is characterized by a lower salinity than MSOW and a low temperature. To examine the variation between bacterial and archaeal assemblage at different stations, depths and water masses, we studied the less conserved internal transcribed spacer (ITS) region of the ribosomal operon, which is characterized by a significant variability in the length (from 150 to 1200 bp) among different bacterial and archaeal genotypes [1, 2].

Within a same water mass, the composition of bacterial community was relatively homogenous among stations (Figure 1). Bacterioplankton communities of the MSOW were slightly different from communities of the AAIW although both water masses occupied the same depth range. Specific bacterial and archaeal taxa were specific for distinct water mass while others are ubiquitously distributed over the entire water column. Bacterioplankton communities exhibited the highest richness in taxa intermediate waters (MSOW and AAIW) and the lowest richness in the LDW. Archaeal communities were generally less diverse than bacterial communities. For Archaea, the OTU (operational taxonomic unit) composition varied among stations even within the same water mass.

distributed over large portions of bathypelagic ocean than the archaeal assemblages. 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 composition of prokaryotic communities in the same water masses is largely maintained even over large distances. Thus, for assessing the biogeography of deep water prokaryotic communities the water masses have to be identified and incorporated into analysis.

References

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Jaccard (UPGMA) (0.0% - 100.0%) (0.0% - 100.0%) (0.0% - 100.0%) (0.0% - 100.0%)

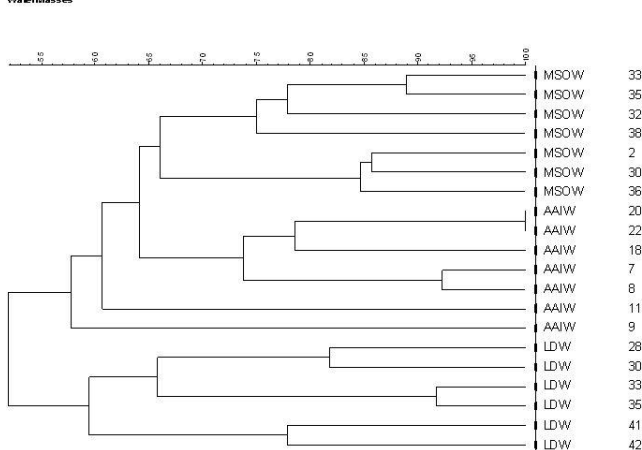


Fig. 1. Cluster analysis of bacterioplankton communities based upon all operational taxonomic units (OTUs) detected. Similarity is expressed as the Jaccard coefficient which compares the presence or absence of OTU when making pairwise comparison between communities. Cluster analysis was performed with the unweighted-pair-group mean average (UPGMA). For each sample, the water mass (MSOW, AAIW or LDW) and the station are indicated.

Bacterioplankton assemblages seem to be spatially more homogeneously