SURFACE-DEPTH AND COASTAL-OCEAN GRADIENTS IN DIVERSITY AND ACTIVITY OF PROKARYOTES IN THE CANARY CTZ REGION

Federico Baltar[1], Javier Arístegui[1], Gerhard J. Herndl[2], Josep M. Gasol[3], Santiago Hernández-León[1]

1 Facultad de Ciencias del Mar, Universidad de Las Palmas de Gran Canaria
2 Royal Netherlands Institute for Sea Research (NIOZ), Texel, The Netherlands
3 Institut de Ciències del Mar – (CSIC), Barcelona

Prokaryotes are an important component of the marine plankton playing a key role in mediating a range of biogeochemical cycles in the ocean. However, very few studies have addressed their patterns of distribution, or the relative importance of bulk and groupspecific prokaryotic activity in the dark ocean. Here we report results of the differential distribution in the water column of the major prokaryotic groups, including Archaea and Bacteria (Crenarchaeota, Euryarchaeota, SAR 11, Roseobacter, Gammaproteobacteria and Cytophaga-Flavobacterium), along a transect stretching from the eutrophic waters of the NW Africa upwelling to the oligotrophic waters of the Canary Coastal Transition Zone (CTZ) region. We used the catalyzed reported deposition FISH (CARD-FISH) technique, together with measurements of leucine incorporation, to look at coastal-ocean and surfacedepth patterns of distribution in the abundance and metabolism of Bacteria and Archaea, related to the hydrography and presence of distinct water masses in this heterogeneous region. From surface to depth a marked substitution between SAR11 (ranging from 42% to 4% in the Deep Chlorophyll Maximum (DCM) and 2000 m depth respectively) and Crenarchaeota (ranging from 1% to 39% in the DCM and Oxygen Minimum (OM) respectively) was observed. A clear influence of the different intermediate water masses was also observed in the prokaryotic bulk heterotrophic activity, with lower values at the stations where Antarctic Intermediate Water was detected. Crenarchaeota and gammaproteobacteria increased in abundance in the OM, presumably due to nitrification processes. Along the coastal-ocean gradient we found -at the DCM level- a substitution in all the community assemblage, together with decreasing rates in the bulk prokaryotic heterotrophic activity. The slow-growing groups (Crenarchaeota, Euryarchaeota, SAR11), better adapted to oligotrophic environments, were substituted by the fast-growing groups (Cytophaga-Flavobacterium, Roseobacter, Gammaproteobacteria) better adapted to eutrophic conditions. To our knowledge this is the first detailed report showing a clear substitution of Archaea and different groups of Bacteria along a coastal-ocean gradient.