Metabarcoding Zooplankton Diversity in the Sargasso Sea – Taxonomy and Functionality

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Understanding the responses and evolution over space and time of any community requires a deep knowledge of the species present at each location and their interactions. Where taxonomy turned out to be challenging, as it is the case of zooplankton, supra-species grouping is a common resource, at the price of limiting the depth of our study, and with the risk of mixing different species' organismal responses. The development of DNA-based identification protocols during the last decades are rapidly driving these limitations away, increasing our understanding of the existing complexity of even very close taxa to different stressors or environmental conditions. Beyond the mere taxonomic discrimination of the analyzed community, the use of DNA sequences allow for the rapid integration of phylogenetic measurements and related indexes to the functional and identity components. In this presentation, we show our first results tackling one of the regions with the highest zooplankton diversity, the Subtropical North Atlantic at the Bermuda Atlantic Time-Series Study (BATS) site. The chosen Metabarcoding region was the hypervariable V9 region of the 18S rRNA gene. In this first approach, we establish the baseline information needed for further and more comprehensive analyses on the time series: minimum coverage depth per sample, taxonomic and phylogenetic diversity of the community and effect of the Diel Vertical Migration in the epipelagic community. We also analyze the limitations to the species identification in relation to the variability of the V9 region within and between species.