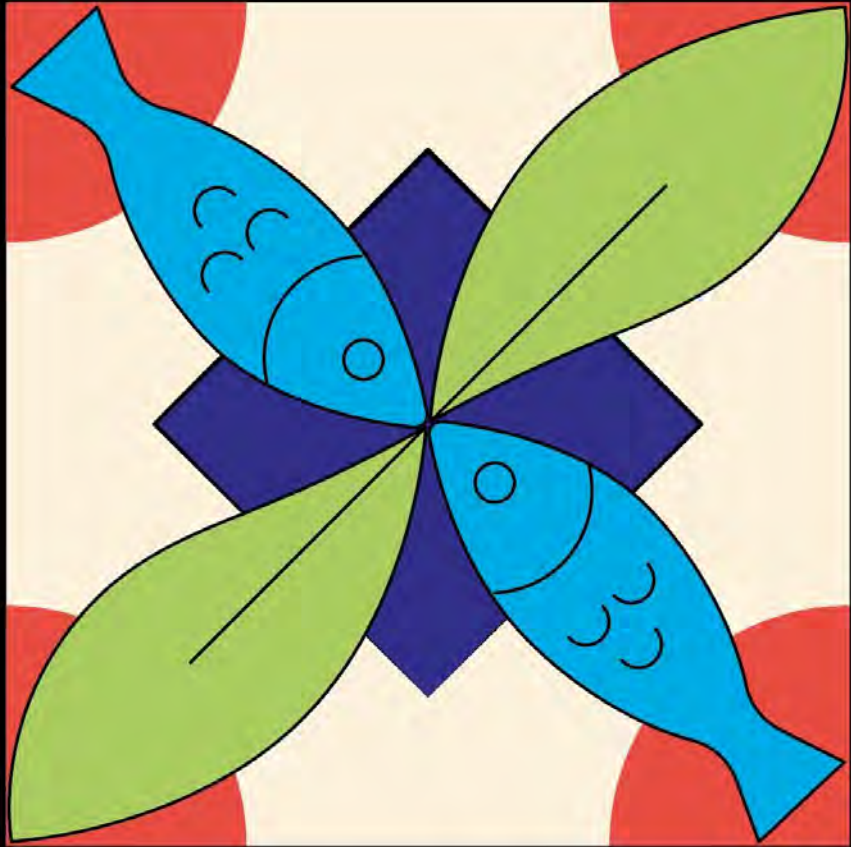



ABSTRACT BOOK



SIBECOL
AIL  **MEETING**
2022
3-8 JULY AVEIRO



Friday 8th July, Room 1, 09:45h

OC 229: A measure every strike of the clock: a high-resolution image of microbial community structure in the Bransfield strait and Bellingshausen Sea (Antarctica) by continuous flow cytometry

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Microbes are a fundamental part of the Antarctic marine ecosystem, and their study is essential for understanding the functioning of carbon, nutrient and pollutant biogeochemical cycles. However, there is a dearth of high-resolution data sets of their temporal and spatial abundance, size, distribution and phenotypic diversity. Here we present flow-cytometry data on total bacteria and small phytoplankton collected from surface waters during the ANTOM2 cruise, which sailed through the Bransfield Strait and Bellingshausen Sea during austral summer 2022. The cruise consisted in a north-south transect along the Antarctic peninsula coast and a second south-north transect along the edge of the continental shelf. Sea-water was taken by a faucet linked to a continuum pump (5 m depth) with an automatic sampler connected to a flow-cytometer that was sampling every 15 minutes during two weeks yielding a total of 2500 sampling points. Quality assurance and control of the data set was performed by contrasting approaches, including the comparison of microbial data with boat movement along its axis (pitch and roll) as well weather conditions, indicating these did not affect the measurements. Total small phytoplankton abundance ranged between 102 and 104 cells-ml⁻¹; with higher values along the coast. Total bacteria abundance ranged between 105 and 106 cells-ml⁻¹; abundance values tended to increase in the Bellingshausen Sea at latitudes between 68° and 71° S. In the Bransfield Strait, there was a maximum in bacterial abundance at Deception Island, probably due to several factors including stable human and animal presence, volcano emissions, and the limited water exchange with the open ocean. For each data point, we collected the mean of the forward light scatter emission which are surrogates of the relative size of the cells. Larger sized cells were observed in Marguerite Bay and at the edge of the shelf after crossing 65° South. Finally, the optical properties of each single cell, which are considered a phenotypic attribute, were used to identify through sub-populations of prokaryotes shared by different sample points. This type of fingerprinting indicates that prokaryotic phenotypic diversity varied throughout the entire cruise and could be related to some of the environmental oceanographic and meteorological variables. As far as we know, this is the first study using this spatial and temporal resolution in the maritime Antarctica.

Friday 8th July, Room 1, 10:30h

OC 230: Seasonal niche of planktonic prokaryotes inhabiting surface waters of the upwelling region off NW Iberia

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Prokaryotes play an important role in biogeochemical cycling in marine ecosystems, but little is known about their diversity and composition, and it's even less understood how they may contribute to the ecological functioning of highly variable coastal areas affected by upwelling. Between May 2016 and May 2018, we carried out 26 one-day samplings in the temperate northwestern Iberian upwelling system to investigate the temporal patterns of variability for prokaryotic abundance, diversity and community composition by combining flow cytometry and 16S RNA high-throughput sequencing. A marked seasonality was found for prokaryotic abundance, peaking during summer upwelling and relaxation season (≈May to September), when extracellular release of organic matter from phytoplanktonic blooms is a significant process, and decreasing in downwelling events (≈October to April). Those downwelling conditions, characterized by deeper mixed layers and a homogeneous water column, favored a higher abundance of the archaeal groups, Marine Group II (Euryarchaeota) and Nitrosopelagicus (Thaumarchaeota), as well as of Marinimicrobia bacterium (SAR406 clade) and the group Bacteria_Others. By contrast, upwelling and relaxation conditions characterized by enhanced vertical

stratification and hydrographic variability, included a community generally less diverse with core-phylogenotypes (occurring > 75% of the samples) proliferating, i.e. Flavobacteriaceae (Bacteroidetes), Chloroplast (Cyanobacteria) and Amylibacter (Proteobacteria). Overall, the environmental conditions explained 60% ($R^2=0.60$, $AIC=125.64$) of the prokaryotic community composition, being temperature, inorganic nutrients, chlorophyll and particulate organic nitrogen the variables that best explained the variation in the prokaryotic community composition ($r=0.40$). Additional efforts are currently underway on a fine-tuning composition assessment (oligotypes composition from particular core-phylogenotypes) to study if this variability along the temporal environmental gradient could be associated with the differentiation of ecotypes (oligotype's seasonality within particular phylogenotypes). Overall, the present study provides new insights into the barely explored seasonal niche partitioning of surface prokaryotic community driven by hydrodynamic forcing in an upwelling system, which may support further investigations on the role of bacterioplankton in the biogeochemistry of these ecosystems.

Friday 8th July, Room 1, 10:45h

OC 231: Seasonality of the marine microbiome in the Blanes Bay Microbial Observatory (NW Mediterranean)

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The oceans are ecosystems dominated by microbes, in which bacteria and archaea play key roles in biogeochemical cycling. In temperate oceans, seasonal changes in environmental conditions deeply influence the marine microbiome. Here, we analyse the seasonality of the marine microbiome of a coastal ocean site, using the long-term time series of the Blanes Bay Microbial Observatory (BBMO). First, using amplicons of the 16S rRNA gene, we evaluate the dynamics of the main bacterial groups in this coastal oligotrophic station during 11 years and test how similar the temporal niches of closely related taxa are, and what are the environmental parameters modulating their patterns of seasonality. We further explore how conserved the niche is at higher taxonomic levels. The community presents recurrent seasonality for 297 out of 6825 amplicon sequence variants (ASVs), which constitute almost half of the total relative abundance (47%). For certain genera, niche similarity decreases as nucleotide divergence in the 16S rRNA gene increases, a pattern compatible with the selection of similar taxa through environmental filtering. Additionally, we observe evidence of seasonal differentiation within various genera as seen by the distinct seasonal patterns of closely related taxa. Then, we focus on the seasonal patterns of a relevant functional group in the marine microbial food web, the aerobic anoxygenic phototrophic bacteria (AAPs), and evaluate their long-term temporal dynamics through multivariate and co-occurrence analyses. Diversity indices show a clear seasonal trend, with maximum values in winter, which is inverse to that of AAP abundance. Finally, we extend the seasonality analyses to 21 biogeochemical relevant functions by using 7 years of metagenomic data from the BBMO and identify the main taxa driving each function in each season. We show that, for some groups, the seasonality of bacterial families is different than that of their gene repertoire, so that different taxa within the same group present different functional specialization. Overall, this study provides new insights into the seasonal patterns of key taxonomic and functional groups in the coastal surface ocean through the integration of information obtained using several molecular techniques applied to a long-term time series.