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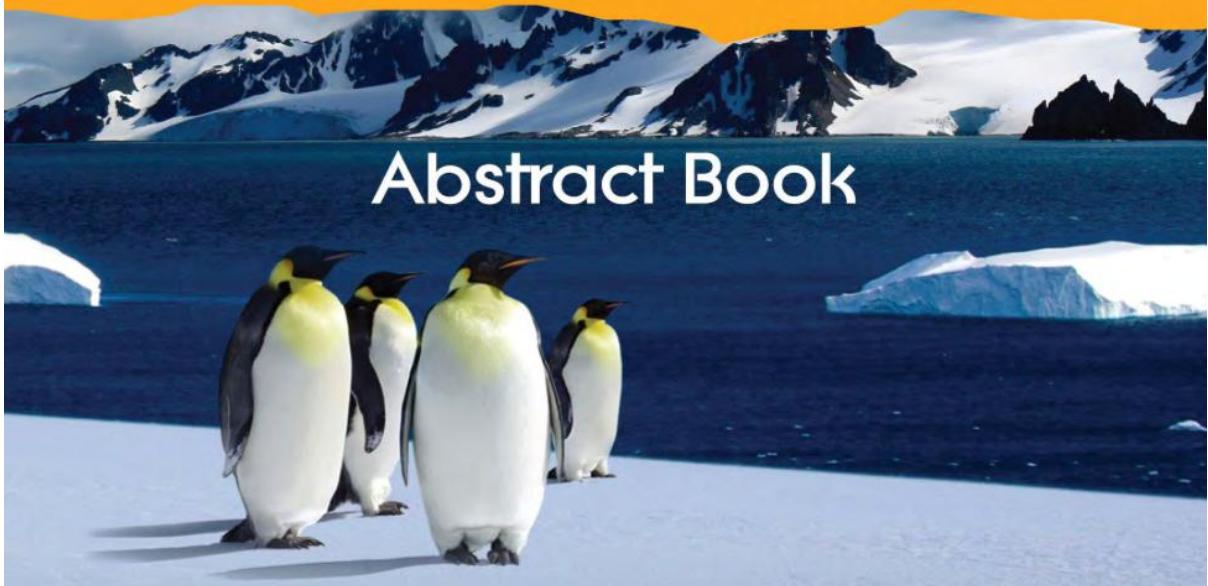


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ANTARCTICA IN THE GLOBAL EARTH SYSTEM:
FROM THE POLES TO THE TROPICS

Abstract Book



Assessing the impact of climate change on microbial diversity across environmental gradients in the southern ocean

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The Southern Ocean is characterized by a complex interplay of environmental variables that may influence the composition of the microbial communities. It is expected that microbes, which are the main drivers of the biogeochemical cycles and essential for ecosystems functioning, will be affected by climate change and anthropogenic impact. An increased understanding of the factors that drive the diversity of microbes is paramount to predict responses of this important biome to future changes. The polar regions are the most sensitive areas to climate change on Earth, and the Western Antarctic Peninsula is experiencing one of the fastest rates of warming, in contrast to regions in the Eastern Antarctic Peninsula (influenced by the Weddell Sea). So, the current conditions and future scenarios represent an unique opportunity to study the interactions between the climate change and the responses of the microbial communities in the Antarctic marine ecosystem. The main goals of this research were to: 1) Determine the composition, relative abundance and distribution of the microbial communities in different regions of the Southern Ocean: a) Along depth profiles, b) From coastal waters to the open ocean, c) Comparing different years; and 2) Identify the environmental parameters driving the microbial community structure. For the spatial approach we sampled the following areas: Bransfield and Gerlache Straits and the area influenced by the Bellingshausen Sea in the Western Antarctic Peninsula, and the Weddell Sea in the Eastern Antarctic Peninsula. We also sampled areas in front of glaciers melting and near the sea ice edge. Sampling depths were selected according to the CTD profiles. For the temporal approach, ten monitoring stations were selected in order to compare the microbial distribution annually (2013, 2014, 2015, 2016) and seasonally (contrasting the beginning and the end of the austral summers). We filtered 2 liters of seawater onto 0.2 µm Sterivex filters from which DNA was extracted and we used the Illumina sequencing-based profiling of archaeal and bacterial 16S rRNA genes to analyze the composition of the microbial community. We combined these results with environmental data such as temperature, salinity, dissolved oxygen, inorganic nutrients and chlorophyll-a. We used different softwares (QIIME, Cytoscape, ItoI and Ocean Data View) for statistical analyses and plotting for the data. In general, Flavobacteria and Alphaproteobacteria were very abundant in surface waters, depending on the geographic location on the sampling stations. In waters below 300 m, Alphaproteobacteria and Gammaproteobacteria were the most dominant groups, summing up more than 50%, followed by Thaumarchaeota with 15% of total abundance. Betaproteobacteria were especially prevalent near the sea ice edge, with 10% of relative abundance. A combination of oceanographic factors drive the microbial community composition. The results will be an invaluable contribution to understanding how the dynamic seascape of the Southern Ocean shapes the microbial community composition, considering both spatial and temporal approaches, in light of climate change. This research was made possible by a SCAR fellowship.