SESSION: Ecosystems, Biodiversity and Biodiscovery

MARS Themes:

Understanding natural and anthropogenic drivers of change

Title:

Nutrient co-limitation of iron and manganese effects on bacterial communities within the sub-Antarctic

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Abstract:

The role and quantitative contribution of chemoautotrophic microbial (picoplanktonic) communities in ocean systems is largely unknown. Previous studies have shown that iron fertilization results in increased productivity of marine phytoplankton. However, little work has been done to elucidate the effect of iron on deep-sea microbes. While the chemical form of iron in high nutrient low chlorophyll (HNLC) regions such as the Southern Ocean remains unknown, it is well established that molecular speciation affects microbial competition for iron uptake. The importance of iron and manganese for marine ecosystems and its role in the fixation of CO 2 makes the study of this trace metal of great interest. An on-board mesocosm experiment was set up to observe induced changes in iron and manganese concentrations in microbial communities from two distinct depths. Seawater samples (280L in total) collected at two depths (50m and 500m) at station OD2 using GOFlo – trace metal free bottles. 10L samples were incubated in 26 X 10 L acid washed carboys for a total duration of 168 hours. Per depth, 5 mesocosms were treated with 0.5 nM FeCl 3 , 5 with 1 nM FeCl 3 with 5 non-iron containing controls for the total experiment. Mesocosms were incubated in the dark at 4°C, with sub-sampling taking place after 1 hour, 36 hours and at the termination point of the experiment. 125 mL of the seawater incubation was collected from each mesocosm in order to measure dissolved iron. Water from each mesocosm was aliquoted for downstream analysis for flow cytometry (preserved in formaldehyde at a final concentration of 2%), single cell genome sequencing (preserved in glycerol Tris-EDTA buffer) and enzyme activity assays. These samples were stored at -20°C for downstream analysis. Remaining water up to a volume of 3 L was filtered via a dual filtration mechanism and vacuum pump through a 0.22 µm Polyethersulfone (PES) filter and the filters stored at -20°C for microbial community analysis at both the DNA and RNA level.

Format:

e-poster

Keywords:

Microbial diversity; Southern Ocean, Picoplankton; Fe/Mn supplementation