MARS Themes:

Understanding natural and anthropogenic drivers of change

Title:

Marine microbiome responses to Fe supplementation

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Abstract:

Iron (Fe), an essential micronutrient for microorganisms, is known to be low in marine environments, limiting microbial primary productivity. Currently, we lack an understanding of how prokaryotic communities respond to Fe fertilization, especially in high nutrient low chlorophyll regions such as the Southern Ocean (SO). Here, we attempted to elucidate how prokaryotic communities respond to Fe supplementation, particularly in the subsurface. Samples were collected in the SO during Winter and Spring in the mesopelagic and bathypelagic zones. A mesocosm study was conducted where the effects of Fe fertilization at different time points (0 hours, 1 hour, 36 hours and 96 hours) and Fe concentrations (0 nM, 0.5 nM and 1.0 nM) were evaluated. 16S rRNA gene amplicon sequencing and shotgun metagenomics were used to investigate community and genome level differences, with a focus on Fe metabolism. Enzymatic activity, nutrient analysis and flow cytometry were included as part of the analyses. The findings showed patterns of fluctuating enzymatic activity of alkaline phosphatase and β -glucosidase following fertilization and revealed marked community differences between the two seasons and depths. Results suggest that Fe fertilization does not elicit major changes in community structure and composition at higher taxonomic levels. However, significant changes in relative abundance were seen among specific taxa such as SAR 202 clade and Marinimicrobia at lower taxonomic levels. The results also showed potential for Fe cycling in mesopelagic and bathypelagic zones of the ocean, particularly in the synthesis and exudation of siderophores. This suggests that siderophores may be the prevailing strategy used by microbes for the acquisition of Fe in these SO microbiomes. Taken together, this work adds insight into understanding the response subsurface marine microbes to Fe environmental perturbations and their overall contribution to biogeochemical cycling.

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