by

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(Under the Direction of Patricia Yager and Holly Bik)

ABSTRACT

In this study, we use 16 rRNA and taxonomic insights to understand that bacterial community in the Amundsen Sea Polynya, Antarctica. Polynyas are incredibly important to the Southern Ocean, accounting for most of the primary production of all the Southern Ocean, but only taking up a fraction of the size. These polynyas are relatively not understood, due to its remote location and difficult conditions. In this study, we analyze the bacterial community to understand how it shifts under different environmental conditions, like location and water mass. We found that communities were distinct based on water mass, as well as certain locations within the Amundsen Sea Polynya. Heterotrophic bacteria tend to dominate in the surface waters, near the bloom, while bottom water communities tend to vary based on location within the polynya.

INDEX WORDS:

by

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DEDICATION

. Kaitlyn/ Anderson famiwwy

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CHAPTER 1

ENTER TITLE HERE

Methods

We used the R package XXX for water mass categorization and the thresholds can be found in Table X. We excluded the continental shelf station, STN 198, in many of the microbial community analyses within the ASP, due to the distinctly different community, altering the ordination and Bray-Curtis analyses.

Results

* Looking at only deep CDW (2 figures), rel abund table
* Looking at inflow (adonis/indicator species), (rel abund table)

Discussion

PICRUSt

* At first we were looking at an iron story, we wanted to associate the taxa with known iron-related taxa, and we found no strong correlation with specific taxa. Attempting PICRUSt, we found that many iron metabolism related genes are expressed evenly throughout the polynya. Iron-related KO Numbers data was provided by Sun et. al, and the rest of the metabolism was provided by … et al. Looking at the free and particle associated taxa separately,

Photoshop jobs for Kaitlyn

* Temp-salinity lines  
  > changing names on picrust rel abund.

A graph with a blue tick

Description automatically generated

Inventories

> temp / salinity ranges, other nutrients, supp table, metadata, look at PCA, export

> water mass characterization

> ANOVA among water mass, tukey test for both free and particle-associated

PCA with location, PCA with watermass  
CCA with location, CCA with watermas

PICRUSt relabund with new metabolisms?

> adonis with watermass, tukey post hoc, for both communities

We found that both free-living and particle associated communities were both statistically significant, both >200 and <200m, based on the location within the polynya (F = , p < 0.001). When running a Tukey test, only the Dotson-OP category was significant in the upper 200m free-living communities (Table 1). The CCA of the communities show that the particle-associated is more related by the area within the polynya, while the surface communities are driven by bloom, as suggested in the typical communities found there. *Polaribacter* is a known algal-associated bacteria in high-latitude regions (pole-to-pole paper). Previous studies say that the bottom-water communities are heavily influenced by the surface communities, which are driven by the bloom. Our findings suggest that certain areas are in-fact driven by the bloom, like near the Dotson and Getz, but distinct communities in open polynya stations, especially in the free-living. The CDW communities are distinctly different based on the area in the polynya, suggesting that the presence of CDW is likely another factor driving the microbial community. *Pseudoalteromonas, of the Pseudomonadaceae* familyis only majorly present in STN2 and STN4, both stations that follow the Dotson Trough, were pure CDW has yet to be altered by meltwater and is likely not strictly influenced by bloom. Bloom markers near the Dotson are dominated by heterotrophic bacteria, mainly *Polaribacter spp., Nitrocolacae,*

STN89, an eastern notch station is distinctly different than bloom-marker communities, where the bloom was almost non-existent. The unique community underneath the bloom, found in Richert et al., mostly consists of opportunistic heterotrophic bacteria, like SUP05 clade, of the Thioglobacae family, or SAR 11 clade, known organoheterotrophs, capable of diverse genomic abilities due to their small genomes and horizontal transfer. (SAR11 and virsuses?). When comparing the communities together, Dotson-OP was significantly different in certain areas, particular stations, like STN 174, are different in each water mass, dominated by Saprinerceae, a known particle-associated taxa. The free-living and particle-associated communities don’t appear to be influenced by the location in the polynya, moreso the position in the water column in the mesopelagic, that includes both AASW and WW, where there are distinct nutrient and diversity shifts. The CDW, and only a few WW samples have *Pseudomonas*, a genomically diverse organism, a known pathogen or psychrophilic organism.   
 The community not only shifts because of the bloom, but also by DOC, potentially linked to the bloom, but also potentially by sloppy feeding, especially at stations like STN174, where the iron, cobalt, and magnesium are high at the bottom, and DOC is essentially depleted. In the surface waters, DOC follows the same gradient as temperature and oxygen, where sloppy feeding may play considerable role in the remineralization of organic matter, because of the microbial loop.

Though the inflow and outflow aren’t inherently different, the outflow might influence the communities by supplying more iron to the bloom, via the cavity at about ~400m at the ice shelf face. This water mixes with the fresher, colder water from the glacial melt, WW, and now a potentially significant, newly found coastal current, that may bring nutrients to the polynya. A Tukey test showed that both free-living and particle-associated communities were not different (F= , p < 0.5), and this could be because there isn’t enough time within the cavity for significant community changes, and instead the outflow more influences the communities that are following the coastal current in the surface, shown by the CCA, where western CC is distinctly different from the Dotson stations, including the outflow. Western CC and Dotson bottom-water stations do not include pure CDW, as it was likely categorized as WW-CDW, with the fresh meltwater addition, making it mCDW.

As previous studies, like Richert et al. suggest, the surface waters are dominated by opportunistic heterotrophic taxa, and leads to a less diverse community in the surface waters (rel\_abund\_plot). The particle-associated community in the upper 200m

Many of the previous bacterial studies in the ASP do not incorporate the inflow and outflow, and how the deep CDW travels into the ASP vis bathymetry.

Higher DOC in western CC, meaning higher sloppy feeding, or heterotrophy. Delmont et al. showed that free-living and particle-associated bacterial communities differ greatly within it ASP. Little to know Phaeocystis at the bottom of ASP (Delmont 2014). SAR 92 as a good marker for phaeocystis.

INFLOW/OUTFLOW

> dFe (after sea ice melt), remains under the shelf, and a major source of dFe is from under the cavities. We found that inflow/outflow communities were not significantly different in both the inflow, we ran an indicator species analysis on free-living + particle-associated to see if there were any taxa that were potentially added from the cavity. Based on a PERMANOVA and Tukey test, we found that the communities were not significant in either communities. The inflow, that comes from the bottom, off the continental shelf, does not seem to be affecting bacterial communities. Only a few species showed up in the indicator analysis (Table 1a).

(results). Outflow comes out of the DIS around >400m, then as the outflow continues out the shelf, it begins to

> meltwater pump

CDW OPEN POLYNYA COMMUNITIES

> the surface communities, there doeesnt seem to be much change based on location within the polynya. Under the AASW, where dFe tends to accumulate under the bloom, there seems to be a significant change in communities, along with this, nutrient-rich CDW

<https://journals.asm.org/doi/10.1128/iai.00577-19>

A chart of different colored tubes

Description automatically generated with medium confidence

Limitations:

* DNA
* Lot of uncultured
  + Many organisms do not go to genus level and are dominated by “uncultured” and “hydrothermal vent” genomes.
* Free-living community not as explored as particle associated.

From richert:

impacts both the epipelagic and the mesopelagic bacterial com- munity in this key region of the Southern Ocean. The increasing homogeneity of bacterial commu- nities as the algal bloom progresses appears to favor opportunistic heterotrophic taxa, leading to a less diverse bacterial community in the surface waters.

rel\_abund\_plot

Similar to other abundant marine heterotrophs, such as SAR11 and Roseobacter, heterotrophic Thioglobaceae use the dilute pool of osmolytes produced by phytoplankton for growth, including methylated amines and sulfonates.

* Here we use metagenomic and metatranscriptomic analyses to show that deep-sea populations of the SUP05 group of uncultured sulfur-oxidizing Gammaproteobacteria, which are abundant in widespread and diverse marine environments, contain and highly express genes encoding group 1 Ni, Fe hydrogenase enzymes for H2 oxidation.
* SUP05 transcripts for genes involved in H2 and sulfur oxidation are most abundant in hydrothermal plumes where these electron donors are enriched.

https://www.nature.com/articles/s41467-021-27769-5

* such as the Thioglobaceae (SUP05 and ARCTIC96BD-19) and UBA10353, which co-encode genes for the Calvin-Benson-Bassham cycle and heterotrophic metabolism. Consistently, RuBisCO genes (*rbcL*) affiliated to sulfur-oxidizing taxa (Supplementary Fig. [10](https://www.nature.com/articles/s41467-021-27769-5#MOESM1)) were transcribed at high levels throughout the water column (Supplementary Fig. [6](https://www.nature.com/articles/s41467-021-27769-5#MOESM1)). The potential of these lineages to fuel chemoautotrophy using reduced sulfur compounds as electron donors is supported by the presence and transcription of marker genes for sulfide oxidation (*sqr*, r-*dsrA*) and thiosulfate oxidation (*soxB*)
* The fuels for this pelagic primary production remain unknown, but recent studies show that ammonium ([3](https://www.pnas.org/doi/full/10.1073/pnas.1215340110?doi=10.1073%2Fpnas.1215340110#core-r3)) and sulfur ([8](https://www.pnas.org/doi/full/10.1073/pnas.1215340110?doi=10.1073%2Fpnas.1215340110#core-r8), [9](https://www.pnas.org/doi/full/10.1073/pnas.1215340110?doi=10.1073%2Fpnas.1215340110#core-r9)) are potential electron donors in the water column.
* DOC source, terrestrial and hydrothermal vent input, microbial production
* Pseudoalteromonas

Higher DOC in western CC because of the outflow, bringing DOC from the heterotrophs in deeper waters, and going back out into the polynya.

* Upper/lower 200m free/part for species and watermass
* Upper/lower 200m free/part for watermass and location
* Do alpha/beta diversity with the different locations
  + CDW/upper 200, lower 200
* Cluster anaylsis (indicator) based on water mass
  + For different with rhodobacterae and saprinerceae, found in 198 and 174.

Watermass table characterization

Once the outflow begins to mix with the polynya, we begin to see many bacterial-bloom signatures.

* explain beta diversity to crowd