Oden science: Sea ice ecology in the Amundsen and Eastern Ross Sea

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The primary objective of this research will be to extensively sample the microbial community throughout the large expanse of sea ice that is located between the Bellingshausen Sea and the Ross Sea, Antarctica. During this transit, we will address the following hypotheses:

Hypothesis 1. Community composition of the Amundsen Sea polynya phytoplankton bloom will closely resemble that of the adjacent sea ice. The phytoplankton bloom in the Amundsen Sea polynya generally peaks in January. Given the fixed cruise schedule, we will sample the polynya during the early stages of the bloom. This will provide an excellent opportunity to compare the phytoplankton community composition of the sea ice and water column at a time when the sea ice is beginning to melt but before any single species (e.g. *P. antarctica*) has had an opportunity to dominate the pelagic phytoplankton community and possibly exclude minor components of the population. Ideally, we will sample along a transect through the sea ice perpendicular to the Antarctic coast and terminating within the Amundsen Sea polynya. Sea ice stations should be located every 0.5-1.0° of latitude (depending on ice extent and requirements of other participants) along the transect and samples will be collected for enumeration of algal species composition, as well as for DNA extraction and amplification of the 18S rRNA gene to describe the eukaryotic community composition. In conjunction with these measurements, we will also measure physical characteristics of the sea ice (ice and snow thickness, ice type, temperature, salinity, irradiance), as well as total algal biomass (e.g. Chl *a*, POC, PON) and physiological parameters (e.g. P-E, Fv/Fm).

Hypothesis 2. ^{13}C enrichment of POC in the sea ice is due to algal utilization of bicarbonate during photosynthesis, as a result of depleted CO2 concentrations. At the beginning of each *Oden* cruise (e.g. November), the sea ice algal community will be in its early stages of development. Throughout December and January, as the sea ice microbial community continues to develop, we expect that CO2 concentrations in the sea ice will diminish considerably. Therefore, we expect to sample sea ice with concentrations of aqueous CO2 ranging from supersaturation to significant depletion. As we sample this CO2 gradient, we will assay the relative importance of bicarbonate and CO2 as inorganic C sources for photosynthesis by ice algae, as well as the expression levels of various CA isoforms. This should help us to understand the extent to which CO2 concentrations in sea ice regulate cellular physiology and rates of primary production. We will also collect samples for DNA extraction to map the diversity of CCM target genes using degenerate primers in sea ice populations. In concert, we will isolate RNA to quantify expression levels of CCM genes uncovered in our DNA analysis using gene-specific primers. These novel measurements will be augmented with standard assays for algal biomass, community composition and 18S rRNA gene diversity, and photophysiology

Hypothesis 3. Production of DMSP by sea ice algae will correlate more strongly with high salinity than with algal species composition or other types of stressors (e.g. supersaturating irradiance, nutrient depletion), suggesting that the primary function of DMSP is as an osmolyte. Using a underway membrane inlet mass spectrometer (MIMS), we will identify regions within the ice pack where production of DMS (and perhaps DMSP) is high. In addition to this “hot spot” sampling, we will sample sea ice over a wide range of ice and snow thicknesses, ice surface temperatures, and stages of algal bloom development, to maximize the different types of stress conditions we encounter. Snow depth, and to a lesser extent, sea ice thickness, controls the amount of incident irradiance that reaches the algal community. If DMSP is used to regulate oxidative stress due to excess excitation energy being absorbed by the photosynthetic apparatus, we expect its concentrations to be higher when snow cover is reduced. Conversely, if DMSP is used as an osmolyte, we would expect its concentrations to be greatest in cold sea ice where brine salinity is high. At each station, we will use the gene sequence of the MTHB S-methyltransferase enzyme as a target in the DMSP production pathway to identify 1) the haplotypes/taxa that possess this pathway and 2) the relative strength of gene expression these haplotypes.