

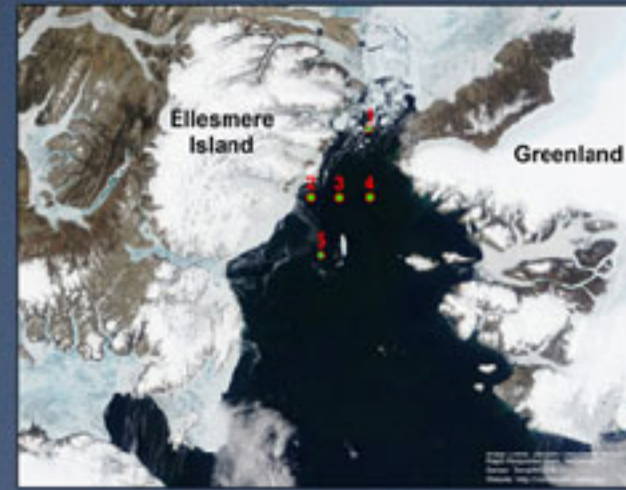
Vertical segmentation of microbial communities in a cold ocean ecosystem

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Introduction:

Life on earth is overwhelmingly dominated by microbes, both in abundance and biomass, and all higher trophic levels are dependent on microbial processes for survival. Yet, despite their importance very little is known about basic aspects of microbial ecology, especially in the marine environment. Previous studies have suggested that vertically segmented layers in the water column, caused by interleaving of water masses with distinct temperature/salinity characteristics, create a heterogeneous environment with unique microbial assemblages associated with each layer (1). The relationship between physical conditions, which are climate driven, and marine microbial diversity will effect ecosystem functioning, with strong implications for carbon, nutrient, and energy fluxes in the ocean.



North Water Polynya:

A region of open ocean surrounded by sea-ice for most of the year, the North Water Polynya (NOW), situated between Ellesmere Island and Greenland, is one of the most productive marine ecosystems in the Arctic (2). Due to the direct influence of climate driven physical forces (temperature, salinity, ice cover) on the physical water column structure in high latitude regions, coupled with its high productivity, the NOW is an excellent region to examine how microbial diversity is related to habitat heterogeneity.

Hypothesis:

Biological diversity increases with habitat complexity - A higher degree of physical water mass interleaving and layering (complex habitat) will be associated with a more diverse microbial community.

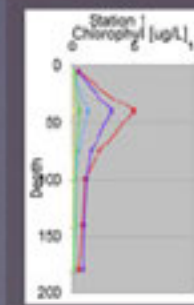
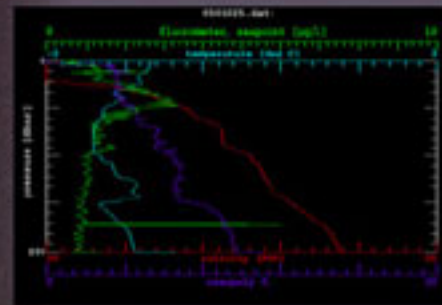
Physics:

The hydrography of the NorthWater Polynya between Greenland and Ellesmere Island was determined from 27 CTD casts in August 2005. Raw CTD profiles (uncalibrated) show a range of water column interleaving (interleaving indicated by temperature inversions), from minor (e.g. Station 1) to strong interleaving (e.g. Station 5). The origin of water mass layers in this region is influenced by ice presence, ice melt and formation, coastal runoff, and the convergence of southward flowing cold fresh Arctic water and northward flowing warm saline Atlantic water.

Biology:

To investigate the microbial communities associated with distinct layers we sampled 6 depths at 5 sites, focusing sampling on layers and lenses with unique temperature-salinity (TS) characteristics. To describe the microbial community we collected samples for size fractionated chlorophyll and genetic analysis. Although picoplankton (<3µm) are extremely abundant and important contributors to food webs in marine ecosystems, they remain relative understudied due to the difficulty of identification with standard microscopy. To describe the species composition and diversity of the picoplankton community we utilized molecular genetic techniques.

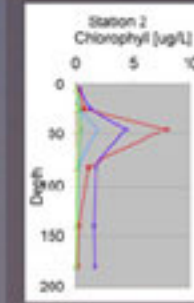
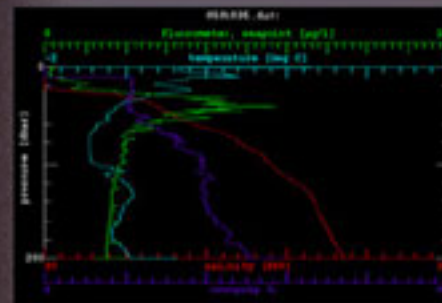
Station 1



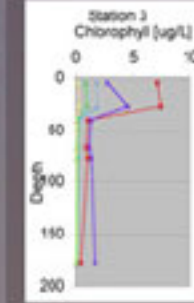
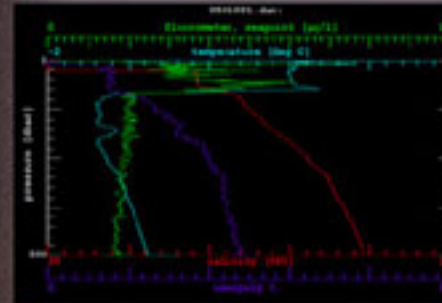
UV Image of DNA in DGGE Gel



Station 2



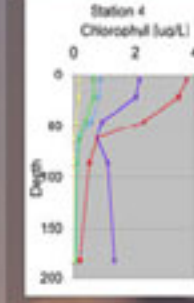
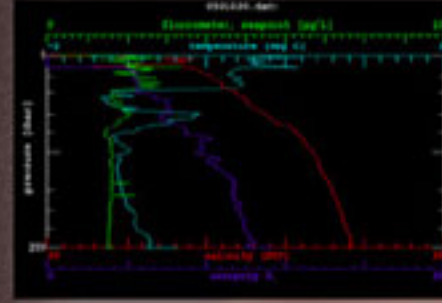
Station 3



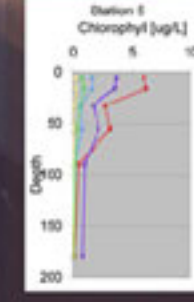
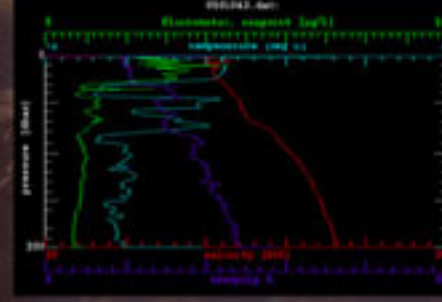
Denaturing gradient gel electrophoresis (DGGE) images (above and below) of polymerase chain reaction (PCR) amplified picoeukaryotic DNA. An environmental sample of extracted DNA from a specific depth is loaded into each lane of the DGGE gel. Due to minor differences in genetic sequence, DNA from each distinct species present separates out into a distinct band (3).

>>Station 3 DGGE not yet acquired.

Station 4



Station 5



Synthesis:

Basic ecological theory necessitates an understanding of the interactions between organisms and their environment. The nature of the oceanic realm requires that we take a 3-dimensional approach to ecology; integration of horizontal AND vertical complexity in the ocean will benefit our understanding of the processes shaping the diversity and distribution of organisms in the marine environment.

Physics - Next step:

Once the CTD data is calibrated the hydrography of the NOW polynya will be examined in greater detail. Identification of distinct water masses at depth using TS diagrams, and interpreting the origin and formation of these water masses from processes such as ice melt, coastal runoff, and advection of Arctic and Atlantic water will begin. The extent of interleaving at each station will be quantified to examine habitat heterogeneity in the water column.

Biology - Next step:

Optimization of the DGGE protocol will continue in order to maximize the resolution of distinct bands, enabling the utilization of imaging software to quantify the phylogenetic diversity of each sample. Specific bands from the DGGE gels will be extracted and sequenced to identify the species present in each sample. Identification of species present will permit interpretation of the functional role each organism has in the ecosystem.

References:

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- Diez, B., Pedros-Alio, C., Marsh, T. L. & Massana, R. Application of denaturing gradient gel electrophoresis (DGGE) to study the diversity of marine picoeukaryotic assemblages and comparison of DGGE with other molecular techniques. *Applied and Environmental Microbiology* 67, 2042-2051 (2001).