

Oceanic connections and marine microbial eukaryotes: can we monitor change?

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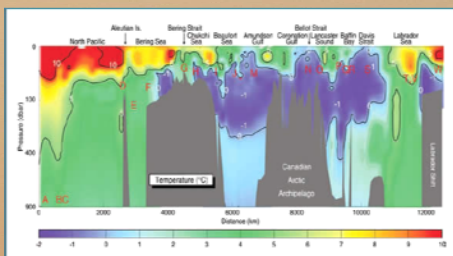
Most of the biological diversity of the planet is within single celled organisms that are visible only using microscopy. For example, many thousands of species of marine microbial eukaryotes; phytoplankton and heterotrophic protists have been reported from microscopy studies. More recently, high-throughput nucleic acid sequencing has revealed many more likely species of small flagellates, representing a previously hidden reservoir of genetic and taxonomic richness. Over the past 10 years we have participated in over 20 missions in the Arctic and sampled microbial DNA and RNA, which we use for amplicon multiplex tag sequencing to identify microbial eukaryotes. This data is yielding a pan-arctic view of diversity over time and space. The goal is to establish the biogeography and temporal distributions of indicator taxa, which will provide the needed context to detect local and basin wide changes in biodiversity in the Arctic Ocean. Here we provide the first pan-arctic view of heterotrophic flagellates (HF) that are usually considered a single functional group, despite belonging to different phyla. Overall, the different groups were indicative of specific conditions and several species complexes may be candidates for indicator taxa, which could be incorporated into national biodiversity monitoring programs.



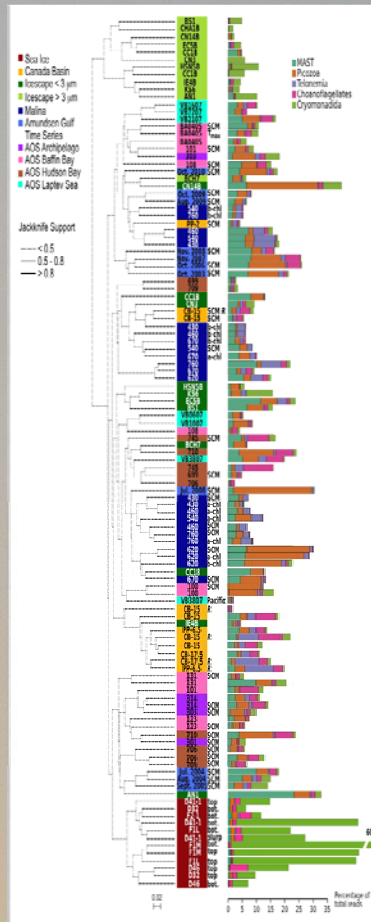
Google map of stations used for the survey.



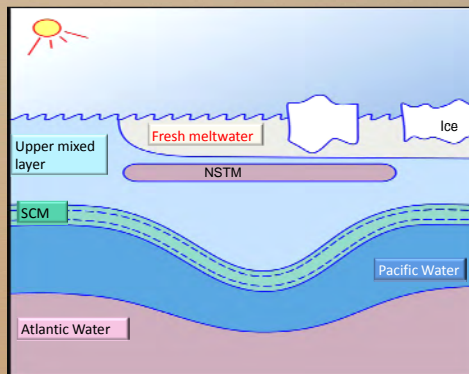
Major oceanic provinces in the Arctic used to define focal marine areas that are targeted for eventual monitoring by 6 circumpolar nations (Canada, USA, Russia, Norway and Denmark-Greenland and Iceland).



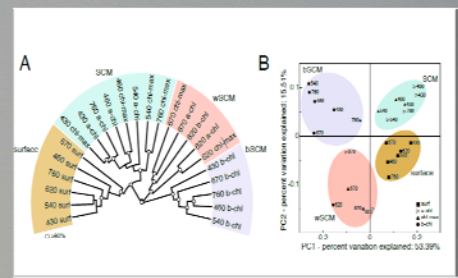
Composite section from Canada's Three Oceans summer of 2007, extending from Victoria in the Pacific to Halifax in the Atlantic reveals ocean temperatures ranging from -28C (dark blue) to 10C (dark red) from the North Pacific to the Labrador Sea. Unlike the adjacent Atlantic and Pacific Oceans, in the Arctic, cold water can overlie warmer water because of salinity stratification. Measurements were taken at depths of up to 900 dbars (1 dbar equals about a meter),



UniFrac unweighted distance tree of HF communities from 9 separate studies (Thaler & Lovejoy in press) The bars on the right indicate first: the total % of reads that were HFs and second the proportion of the different HF in each sample. Refer to the map for the location of the samples. The qualifiers listed in the center indicate: subsurface chlorophyll maximum (SCM), just above the SCM (a-chl), just below the SCM (b-chl), deeper Pacific water (Pacific; see Figure below). Samples from the surface do not have a qualifier. All samples from DNA, except where indicated R (for RNA). For the ice samples bottom (bot) is from the first 100 mm of an ice core. Top is from 100-400 mm, and slurp is the under ice community collected by a diver.



Complex water columns occur at sites of ice edge disintegration, including fresh meltwater, lenses of near surface temperature maximum (NSTM) water from daily solar heating, a low-nitrate upper mixed layer Subsurface chlorophyll maximum (SCM), Nitrate replete Pacific Water from Bering Strait, Atlantic Water from Fram Strait. Cartoon from Eddy Carmack



Whole community clustering of the 4 depths from 6 Beaufort Shelf stations collected in 2009. The SCM, below SCM and surface samples all clustered separately, except at two stations from the Mackenzie Trough characterized by a poorly defined SCM.



Relative abundance heatmap of the 25 most abundant taxa (genera, family or 'groups' depending on available taxonomic information) in the Beaufort Sea sequence datasets. Relative abundances were centered-scaled and corresponding z-score and the scale is displayed as a color gradient (green: abundant; red: rare). Taxonomic lineages of the 25 taxa are indicated by colored dots. Row dendrogram represents results from a hierarchical clustering of taxa relative abundances; columns were regrouped based on the Beaufort Sea community clusters in the community clustering above

Workplan

1. Explore boundaries-geo & watermass
2. Explore diversity-current, past
3. Select indicator taxa
4. Define protocols & standards
5. Create protocols and sampling kits.



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