Cloud Cover over the Gulf Stream in Winter: Observational Evidence for Atmospheric Response to Changes in Upper Ocean Heat Content
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Mentor: LuAnne Thompson, Oceanography

Observational analyses have shown that changes in the overturning circulation of the Atlantic Ocean are tightly linked to changes in northward heat transport. Average ocean heat transport convergence is balanced locally by surface heat flux from the ocean to the atmosphere. Previous work has shown that this relationship holds interannually in the Gulf Stream region, where heat content variations are primarily driven by ocean heat transport convergence. In turn, surface heat fluxes are controlled by ocean heat content variations. The seasonal cycle of sea surface temperature, surface wind convergence and precipitation has been previously shown to be linked to cloud cover in the region with mid-level (2000-6000 meter) cloud fraction forced by surface wind convergence driven by sea surface temperature gradients. Here, we investigate the relationship between year-to-year changes in cloud fraction with variations in surface heat fluxes and heat content variations in the Gulf Stream region. We do this using satellite sea surface height measurement as a proxy for upper ocean heat content, sensible and latent heat fluxes, and satellite derived mid-level cloud fraction. We find that in January and February, mid-level cloud fraction anomalies are tightly coupled to surface heat flux anomalies. In addition, we find that sea surface height leads mid-level cloud fraction in December and January by as much as six months. This study shows direct evidence for an atmospheric response to heat content changes in the Gulf Stream region and that the changes in the atmosphere can be predicted several seasons in advance. Our continued research is focused on confirming these findings with additional satellite datasets.

Temporal Variation in Fatty Acid Composition of Migrating Alaskan Sockeye Salmon (Oncorhynchus nerka)
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Mentor: Gordon Holtgrieve, Aquatic and Fishery Sciences

Physiological condition contributes to the productivity of anadromous salmonids and is particularly relevant in species that include large-scale migrations in their life histories. Sockeye salmon (Oncorhynchus nerka) cease feeding before beginning their spawning migration to freshwaters and rely solely on energy storage for physiological function and survival. A considerable amount of energy is derived from lipids and previous research has highlighted the nutritional value of the eicosapentaenoic acid and docosahexaenoic acid (omega-3 fatty acids) for human health. Additionally there is now a broad recognition that salmonids play an integral part in coastal food webs and provide substantial energetic resource subsidies to numerous consumers such as bears, birds, and resident fishes. What remains largely unknown about salmon lipid physiology is an understanding if a temporal selection for the metabolism of specific fatty acids exists, and if so then to what extent. Here, we characterized lipid (fatty acid) profiles across three major stages in freshwater migration (freshwater entry, midway, and senescence). Fatty acids were isolated by following a modified Bligh-Dyer protocol. We used gas chromatography and modeling functions to identify and quantify fatty acid trends. Total fatty acids declined through the salmon run, but declines were not even across individual fatty acids. The proportion of several fatty acids (e.g. 24:1n-9) drastically decreased by senescence, while some fatty acid reserves were nearly completely metabolized (e.g. 18:3n-3). Our results have implications for understand-
ing the mechanism and extent that migrating salmonids utilize lipids, which may partially determine their overall reproductive success.

Physical and Microbial Drivers of Hypoxia in Bellingham Bay

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Bottom water hypoxia is a feature of many coastal embayments and fjords in the Salish Sea. Ongoing research in Bellingham Bay (Bellingham, WA) by Northwest Indian College and Western Washington University has identified a seasonally recurring area of low dissolved oxygen near the center of the bay. Similar to other regions of the Salish Sea, hypoxia in Bellingham Bay may be a naturally occurring phenomenon, yet the extent of eutrophication and anthropogenic nutrient loading’s influence on patterns of hypoxia are poorly understood. The present study has continued an established monitoring program documenting the range, duration and severity of hypoxia in Bellingham Bay, while adding an experimental component investigating factors that regulate respiration of heterotrophic bacterioplankton. Profiles of water column parameters and sample collection were performed on six regularly scheduled cruises per summer in 2013 and 2014. In 2014, an array of constant-monitoring water quality sensors were additionally deployed into the center of the bay to monitor dynamics of oxygen concentrations over several weeks and found that water layer-displacement in the bay strongly correlated with spring-neap tide cycling. Manipulative experiments were conducted on collected water samples to investigate effects of temperature and organic carbon on water column respiration. These experiments revealed that temperature had a negligible effect on water column respiration, while organic carbon stimulated oxygen consumption and was thus identified as a possible limiting factor. The study’s findings broaden our knowledge of factors regulating oxygen dynamics in coastal embayments of the Salish Sea and provide further insight into the potential effects of anthropogenic stressors and climate change on Salish Sea water quality.

High Resolution Effects of Frontal Forcing on Phytoplankton Diversity and Community Structure on the Kuroshio Front

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Mentor: Sophie Clayton, Oceanography

A fine-scale, biological survey of the Kuroshio Front, a front forming along a Western barrier current as it extends eastward from Japan, was undertaken in October 2009 and revealed great variability and patchiness in phytoplankton communities. Through data from microscopy counts of 190 samples from 5 transects with multiple depths, richness, the Shannon-Wiener Index, and evenness were calculated. I also conducted Euclidean distance cluster analyses to understand community differences. When compared to physical conditions such as temperature and salinity and plotted in three dimensional space, these diversity indexes and measurements of similarity provide a snapshot of frontal effects on the phytoplankton community structure. I investigated how phytoplankton communities responded to the front position, mixing, and differences in subtropical and subpolar water profiles on both sides of the front. My analysis revealed a region of high phytoplankton diversity in shallow, Kuroshio edge water. Large phytoplankton taxonomic groups played an important role in influencing community dynamics on the front while community composition did not correlate to the water profile species were found in. I conclude that as a community phytoplankton do have some ability to respond to their environment on the front despite rapid transport. Yet, dynamic frontal mixing is likely the most important factor in determining community composition rather than the physical profile of the water. I also hypothesize mechanisms for the observed impacts on phytoplankton community diversity and composition which merit further investigation. As one of few, fine-scale phytoplankton microscopy surveys of an oceanic front, this study provides new insights into phytoplankton community life in a highly productive, ever changing environment.

Investigating the Interactions between the Ciliate Mesodinium major and Cryptophyte Algae in the Columbia River Estuary

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Mentor: Virginia Armbrust, Oceanography
Mentor: Francois Ribalet, Oceanography
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Every summer or early fall, the single-celled ciliate *Mesodinium major* creates impressive non-toxic red blooms in the surface waters of the Columbia River estuary, an important regional fishery. The ciliates feed on cryptophyte algae and acquire the active red colored chloroplasts from their prey, allowing the ciliates to become photosynthetic. Our goal is to better characterize this unusual predator-prey interaction to understand how the dynamics of *M. major* blooms relate to cryptophyte cell production. Our approach utilizes SeaFlow, a novel flow cytometer that can continuously measure the abundance and size distribution of phytoplankton in situ, from which cell division rates are estimated using a size-structured matrix population model. SeaFlow was stationed in surface waters of the Columbia River for 30 days to estimate hourly cryptophyte cell production, while discrete samples for *M. major* cell counts and determination of cryptophyte species composition were additionally collected. In
this presentation, we will show preliminary results suggesting that M. major blooms are not limited by cryptophyte prey cell production and discuss how these findings fit into our overall understanding of the M. major-cryptophyte relationship in the Columbia River estuary, a system of ecological and economic importance to local communities.

Effects of Nutrient Limitations on Protein Production of the Marine Cyanobacterium Prochlorococcus MED4
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Mary Gates Scholar
Mentor: Gabrielle Rocap, Oceanography

Prochlorococcus is the most abundant photosynthetic organism responsible for 13-48% of gross primary productivity in oligotrophic regions. As a dominant primary producer, it plays a major role in the ocean by cycling nutrients throughout the water column, sequestering carbon, and producing oxygen. With the health of the ocean deteriorating due to anthropogenic influences, it is crucial to understand the response of Prochlorococcus to changing oceanic conditions. To examine the response to nutrient stress, Prochlorococcus strain MED4 was grown under various levels of nitrogen and phosphorus stress. To do this, MED4 was grown using different culturing techniques to produce a nitrogen or phosphorus replete, limited, or starved conditions. A proteomics analysis was conducted to explore cellular response under these different physiological growth states. I am examining the proteomics data set to produce a cell profile of differentially produced proteins under varying nutrient stressed environments. By taking the holistic approach of examining the entire proteome, I will obtain a better comprehension of the cell status. To accomplish this, I am using R, a programming language and software environment, to determine what genes are differentially expressed to produce the observed proteins. My end result will be a short list of proteins that are indicators of the nutrient environment Prochlorococcus inhabited. This information could then be plotted on a metabolic pathway diagram or on the chromosome to potentially understand the mechanisms driving the differential protein production. These findings will be helpful to the scientific community as a diagnostic tool to assess the health of Prochlorococcus in the ocean based on specific indicator proteins I will identify.

Bacterial Impacts on Viral Susceptibility in the Marine Diatom Pseudo-nitzschia
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Mentor: Gabrielle Rocap, Oceanography
Mentor: Michael Carlson, Oceanography

Diatoms are a group of phytoplankton that account for around 20% of global photosynthesis and play an important role as the base of many marine food webs. A model organism used to show diatom diversity and distribution is a genus called Pseudo-nitzschia. Many diatoms, including Pseudo-nitzschia, share a close relationship with bacteria and can even be found with diverse bacterial communities attached to their cells. Depending on bacterial species, the interaction between bacteria and diatom can range from mutualistic to parasitic. Viruses also participate in significant associations with diatoms, as the viral lysis of phytoplankton is an important factor in nutrient cycling. To better understand the relationship between viruses and Pseudo-nitzschia, a previous experiment measured how viral susceptibility varied between Pseudo-nitzschia isolated at different times and locations. The relationship between virus and Pseudo-nitzschia was found to be quite complex as even the viral susceptibilities of isolates with identical sequences for a certain genetic marker, the internal transcribed spacer (ITS) region, varied significantly. To determine why this variability exists, I explored the role bacterial presence plays in viral susceptibility. First, Automated Ribosomal Intergenic Spacer Analysis (ARISA), a community fingerprinting method, was conducted on the bacterial communities of the isolates with identical ITS sequences, identifying present bacteria by the length of 16S rDNA gene. If bacteria do play a role in susceptibility, similarities found between each isolate’s community will be found to correlate with similar susceptibilities of Pseudo-nitzschia isolates. The next step in this experiment will be to make the Pseudo-nitzschia cultures axenic, without bacteria, and expose them to various viral communities. By comparing the susceptibilities of axenic cultures to their non-axenic counterparts, we can gain more insight into the role that bacteria play in viral susceptibility.

Investigating Cyclic AMP as a Mediator of CO₂-Sensing in the Diatom Thalassiosira pseudonana
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Since the Industrial Revolution, CO₂ concentrations have risen from 280 to 400 ppm, and are expected to double by the century’s end. Approximately half of CO₂ emissions are absorbed into the oceans, where 50 Pg C/year are taken up by marine phytoplankton. The most productive group of phytoplankton are the diatoms, accounting for ~40% of marine primary production. The response of diatoms to increasing CO₂ is an important element in considering biogeochemical cycling of carbon. Recent full transcriptome analysis of the model diatom Thalassiosira pseudonana grown under elevated CO₂ identified several genes whose transcript abun-
dance is significantly reduced under increased extracellular CO₂ concentrations. Included in this set of genes is a carbonic anhydrase gene, \textit{delta-CA3}, which is thought to encode a component of the carbon concentrating mechanism. Research on a distantly related diatom, \textit{Phaeodactylum tricornutum}, suggests that CO₂-sensing is moderated by the secondary messenger cyclic AMP (cAMP). We hypothesize that cAMP is also a key intermediate messenger in the regulation of CO₂-responsive genes in \textit{T. pseudonana}. To test this, we grew \textit{T. pseudonana} in semi-continuous triplicate cultures under two CO₂ concentrations, approximating current ambient partial pressures of near 400ppm, and a high CO₂ treatment of near 1000ppm. Each culture was sampled with or without exposure to IBMX, a compound that inhibits the phosphodiesterase-mediated breakdown of cAMP. Treatment with IBMX raises intracellular cAMP concentrations.

Next, we will measure differential transcription of targeted CO₂-correlated genes using qRT-PCR. We anticipate that increased concentrations of cAMP in either the elevated CO₂ treatment or the presence of IBMX will result in a reduced abundance of cAMP-regulated transcripts compared to the abundance of control transcripts. The results of this research will be important in clarifying the role of cAMP as it pertains to CO₂-sensing in diatoms, allowing inference of diatom responses to changing ocean environments.