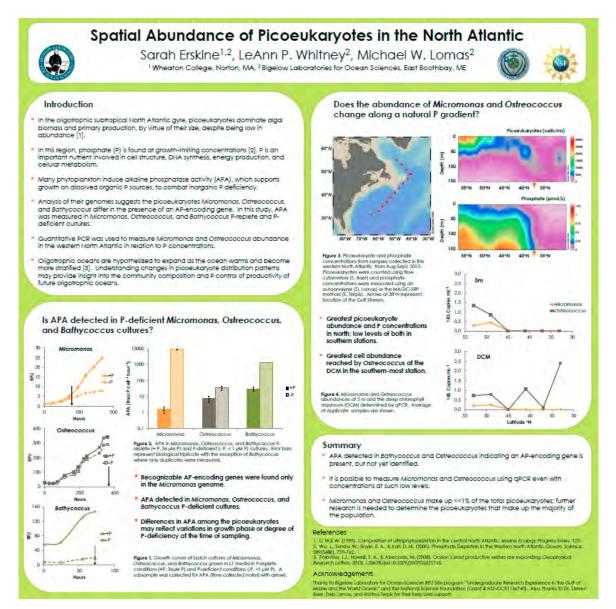
#### SPATIAL ABUNDANCE OF PICOEUKARYOTES IN THE NORTH ATLANTIC

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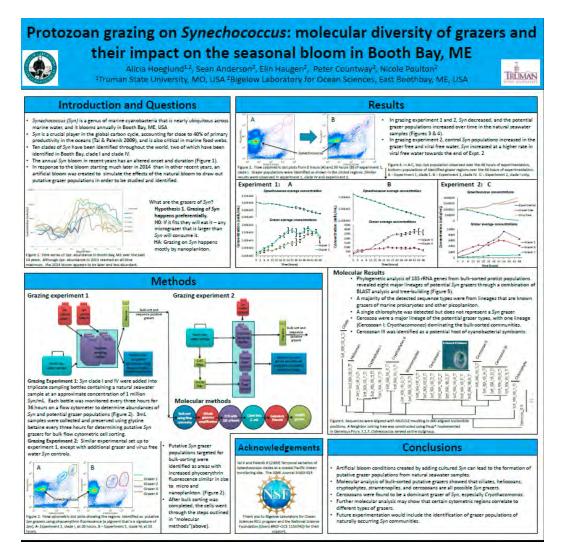
Picoeukaryotes are a diverse group of primary producers that have only recently been recognized for their importance in primary production in oligotrophic gyres. With the hypothesized expansion of these regions with global warming, research into how different picoeukaryote strains respond to phosphate (P) limitation may provide insight into the future of nutrient controlled production in oligotrophic gyres. We measured alkaline phosphatase activity (APA), the enzyme that hydrolyzes P-esters, in P-deficient Micromonas pusilla, Ostreococcus tauri, and Bathycoccus prasinos cultures; picoeukaryotes common to the North Atlantic. Enhanced APA was detected in all three picoeukaryotes though a recognizable AP-encoding gene was only identified in Micromonas. Micromonas and Ostreococcus cell abundances were estimated in samples collected from the North Atlantic across a natural P gradient. In general, Ostreococcus was more abundant than Micromonas, and abundance increased with decreasing P concentrations; Micromonas showed the opposite pattern. Their contribution to the absolute picoeukaryote population was less than 1%. Further research is needed to identify the picoeukaryotes that make up the majority of the population to better understand the impacts of future ocean conditions on oligotrophic gyres.



## PROTOZOAN GRAZING ON *SYNECHOCOCCUS*: MOLECULAR DIVERSITY OF GRAZERS & THEIR IMPACT ON THE SEASONAL BLOOM IN BOOTH BAY, ME

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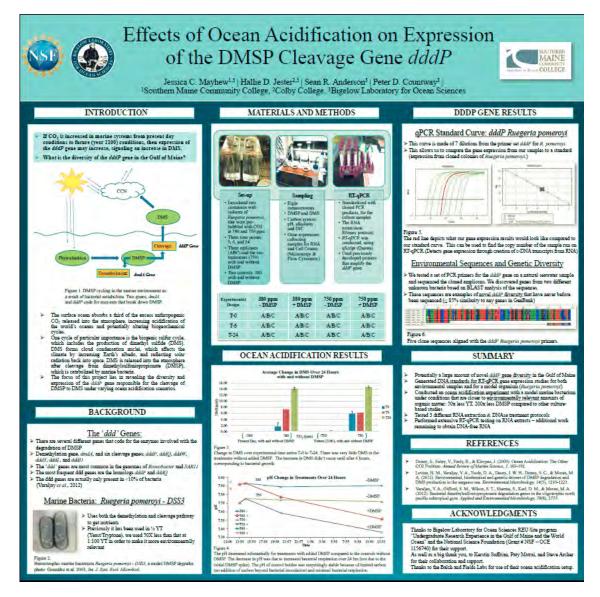
*Synechococcus* is a genus of marine cyanobacteria that accounts for nearly 40% of primary productivity in the ocean and blooms annually in Boothbay Harbor, ME, USA. A *Synechococcus* bloom was simulated to elicit a grazing response from heterotrophic protists in natural seawater samples. Seawater samples were spiked with cultured *Synechococcus*, clades I and IV, and monitored for 36-48 hours in an attempt to identify putative grazer populations through a hybrid approach between community diversity analyses and single-cell genomics. The concentration of *Synechococcus* decreased due to grazing, and potential populations of grazers formed over the 48 hours of experimentation as revealed by increased abundance in particular regions of cytometric plots. Control bottles showed an increase in *Synechococcus*, towards the end of the experiment. The *Synechococcus* concentration increased faster in a control that contained no viruses, compared to the control that had a full complement of viruses. After bulk cell sorting and 18S rRNA gene sequence analysis from putative grazer regions in cytometric dot plots, ciliates, heliozoans, cryptophyptes, stramenopiles and cercozoans were identified as the potential grazers of *Synechococcus* in Booth Bay.



## EFFECTS OF OCEAN ACIDIFICATION ON EXPRESSION OF THE DMSP CLEAVAGE GENE DDDP

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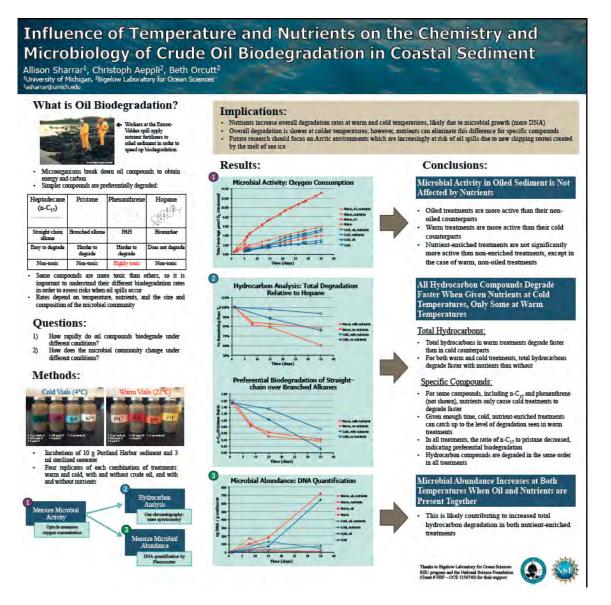
The surface ocean absorbs a third of the excess anthropogenic CO2 released into the atmosphere, increasing acidification of the world's oceans and potentially altering biogeochemical cycles. One cycle of particular importance is the biogenic sulfur cycle, which includes the production of dimethyl sulfide (DMS). DMS forms cloud condensation nuclei, which affects the climate by increasing Earth's albedo, and reflecting solar radiation back into space. DMS is released into the atmosphere after cleavage from dimethylsulfoniopropionate (DMSP), which is catabolized by marine bacteria. The focus of this project lies in revealing the diversity and expression of the dddP gene responsible for the cleavage of DMSP to DMS under varying ocean acidification scenarios. We observed the abundance and expression of this gene within a cultured Roseobacter species, Rugeria pomeroyi. We compared dddP expression under present day CO2, to predicted CO2 concentration (and the resulting increase in ocean acidity) for the year 2100. Additionally, we spiked DMSP into these cultures and then observed changes in gene expression. We applied RT-qPCR of RNA extractions to look at changes in gene expression for the dddP gene.



### INFLUENCE OF TEMPERATURE AND NUTRIENTS ON THE CHEMISTRY AND MICROBIOLOGY OF CRUDE OIL BIODEGRADATION IN COASTAL SEDIMENT

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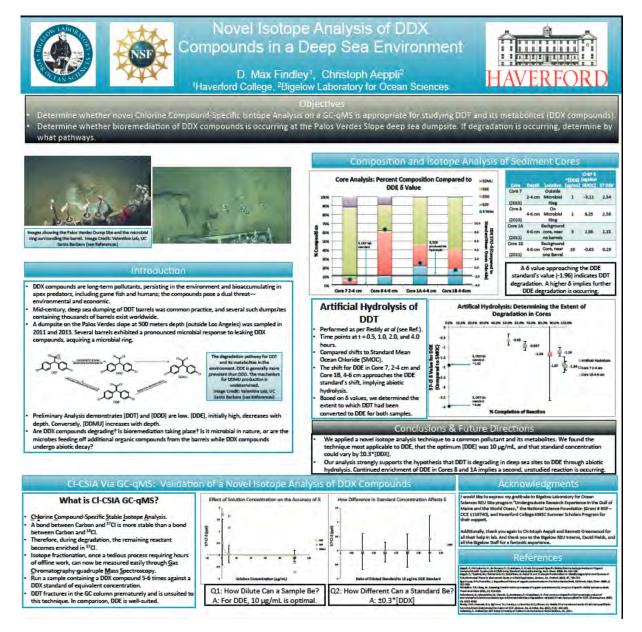
Although marine environments are susceptible to oil spills, marine microorganisms are able to degrade many of the compounds in crude oil. Some compounds are more toxic than others; therefore, it is important to be able to predict the degradation rates of different compounds in different environments. To test the effects of temperature and nutrients on crude oil degradation rates and microbial abundance, we incubated Portland Harbor sediment with eight different combinations of oil (with or without), temperature (4°C or 20°C), and nutrient treatments (with or without N and P). Oxygen consumption was used as a measure of bulk microbial abundance was assayed by quantifying DNA. We found that at both temperatures, microbial abundance increases when oil and nutrients are present together; otherwise, it does not change. Nutrients cause all compounds to degrade faster at cold temperatures and only some compounds to degrade faster at warm temperatures. In general, we found that overall degradation is 2-3x slower at colder temperatures; however, nutrients can eliminate this difference for specific compounds.



### NOVEL ISOTOPE ANALYSIS OF DDX COMPOUNDS IN A DEEP SEA ENVIRONMENT

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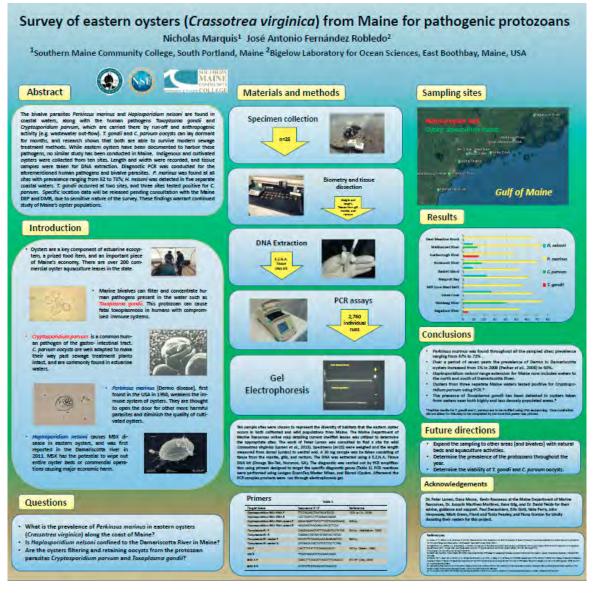
DDT—a chlorinated pesticide—and its metabolites (DDX compounds) are ubiquitous pollutants, despite bans in most developed nations in the 1970s. DDX compounds bioaccumulate and persist in apex predators, threatening marine wildlife and, by proxy, innumerable industries. Natural attenuation, particularly in the deep sea, where several hundred thousand barrels were deposited throughout the mid-20th century, is not well understood. To identify transformation pathways, we analyzed DDX extracts from several cores from the Palos Verdes Slope by Chlorine Compound-Specific Stable Isotope Analysis (CI-CSIA) using Gas Chromatographyquadropole Mass Spectroscopy (GC-qMS). We found, due to fragmentation, that DDT was unsuited to the technique. Instead, we utilized DDE, the degradation product of DDT, which provided reliable measurements down to 100 nanograms per gram of sediment. We compared isotope fractionation from DDE produced by artificial hydrolysis of DDT to fractionation in DDE from sediment cores. Our analysis indicates abiotic hydrolysis of DDT is occurring at the Palos Verdes Slope. Furthermore, DDE degrades further to DDMU, likely through microbe-mediated reductive dechlorination.



### A SURVEY OF EASTERN OYSTERS (CRASSOSTREA VIRGINICA) IN MAINE FOR PATHOGENIC PROTOZOA

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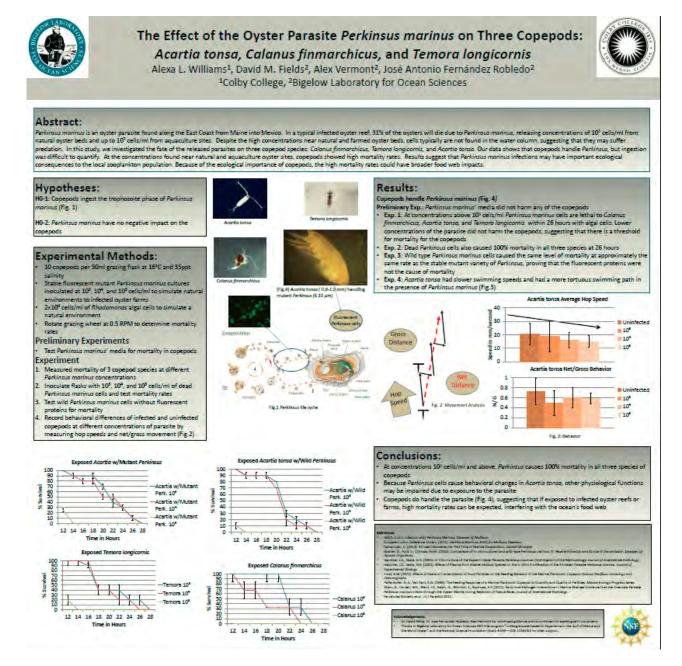
The bivalve parasites Perkinsus marinus and Haplosporidium nelsoni are found in coastal waters, along with the human pathogens Toxoplasma gondii and Cryptosporidium parvum, which are carried there by run-off and anthropogenic activity (e.g. wastewater out-flow). T. gondii and C. parvum oocysts can lay dormant for months, and research shows that both are able to survive modern sewage treatment methods. While eastern oysters have been documented to harbor these pathogens, no similar study has been conducted in Maine. Indigenous and cultivated oysters were collected from ten sites. Length and width were recorded, and tissue samples were taken for DNA extraction. Diagnostic PCR was conducted for the aforementioned human pathogens and bivalve parasites. P. marinus was found at all sites with prevalence ranging from 52 to 73 percent;, H. nelsoni was detected in five separate coastal waters. T. gondii occurred at two sites, and three sites tested positive for C. parvum. Specific location data will be released pending consultation with the Maine DEP and DMR, due to sensitive nature of the survey. These findings warrant continued study of Maine's oyster populations.



# THE EFFECT OF THE OYSTER PARASITE *PERKINSUS MARINUS* ON THREE COPEPODS: *ACARTIA TONSA*, *CALANUS FINMARCHICUS*, AND *TEMORA LONGICORNIS*

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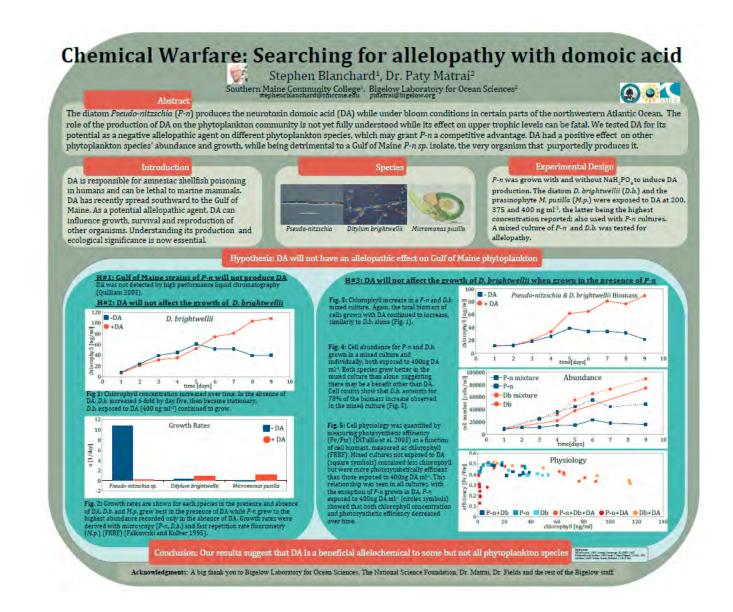
*Perkinsus marinus* is an oyster parasite found along the East Coast from Maine into Mexico. In a typical infected oyster reef, 31% of the oysters will die due to *Perkinsus marinus*, releasing concentrations of 10^3 cells/ml from natural oyster beds and up to 10^7 cells/ml from aquaculture sites. Despite the high concentrations near natural and farmed oyster beds, cells typically are not found in the water column, suggesting that they may suffer predation. In this study, we investigated the fate of the released parasites on three copepod species: *Calanus finmarchicus, Temora longicornis,* and *Acartia tonsa*. Our data shows that copepods handle *Perkinsus*, but ingestion rates were difficult to quantify because at the concentrations found near natural and aquaculture oyster sites, copepods suffered high mortality rates. Results suggest that *Perkinsus marinus* infections may have important ecological consequences to the local zooplankton population. Because of the ecological importance of copepods, the high mortality rates could have broader food web impacts.



### CHEMICAL WARFARE: SEARCHING FOR ALLELOPATHY WITH DOMOIC ACID

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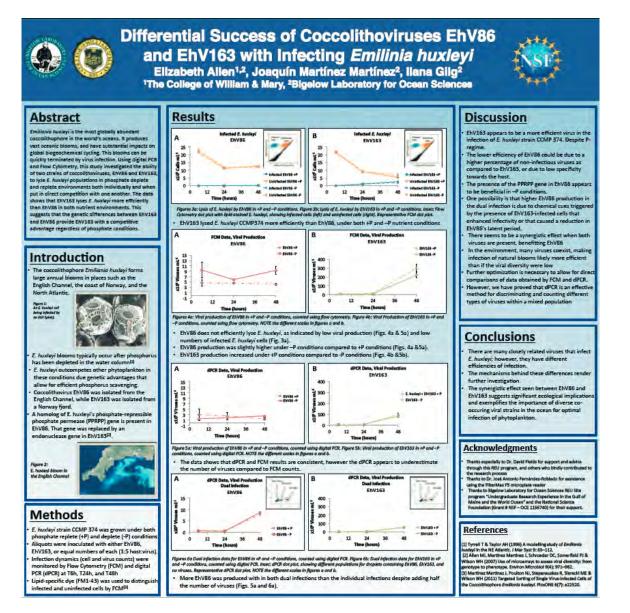
The diatom Pseudo-nitzschia (P-n) produces the neurotoxin domoic acid (DA) while under bloom conditions in certain parts of the northwestern Atlantic Ocean. The role of the production of DA on the phytoplankton community is not yet fully understood while its effect on upper trophic levels can be fatal. We tested DA for its potential as a negative allelopathic agent on different phytoplankton species, which may grant P-n a competitive advantage. DA had a positive effect on other phytoplankton species' abundance and growth, while being detrimental to a Gulf of Maine P-n sp. isolate, the very organism that purportedly produces it.



## DIFFERENTIAL SUCCESS OF COCCOLITHOVIRUSES EHV86 AND EHV163 WITH INFECTING EMILIANIA HUXLEYI

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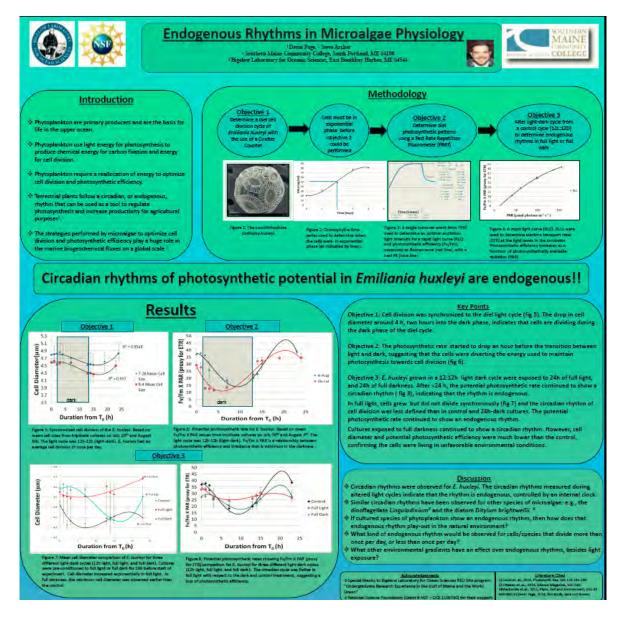
Emiliania huxleyi is the most globally abundant coccolithophore in the world's oceans. It produces vast oceanic blooms, and have substantial impacts on global biogeochemical cycling. This blooms can be quickly terminated by virus infection. Using digital PCR and Flow Cytometry, this study investigated the ability of two strains of coccolithoviruses, EhV86 and EhV163, to lyse E. huxleyi populations in phosphate deplete and replete environments both individually and when put in direct competition with one another. The data shows that EhV163 lyses E. huxleyi more efficiently than EhV86 in both nutrient environments. This suggests that the genetic differences between EhV163 and EhV86 provide EhV163 with a competitive advantage regardless of phosphate conditions.



### ENDOGENOUS RHYTHMS IN MICROALGAE PHYSIOLOGY

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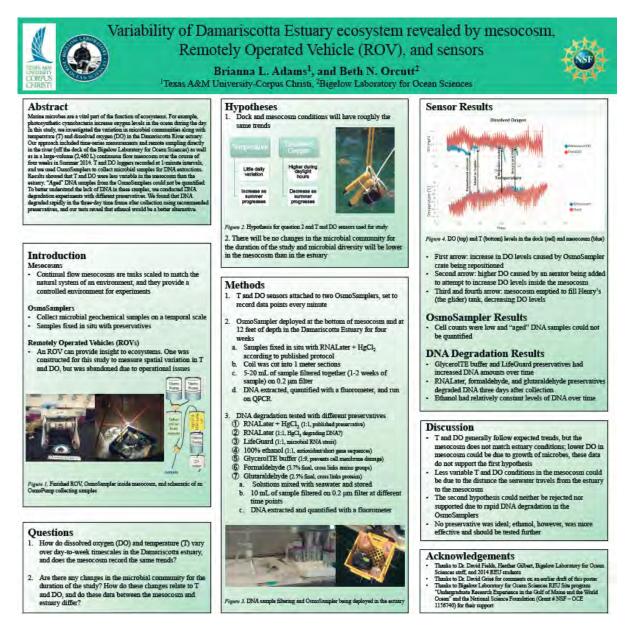
Phytoplankton need to balance energy required to optimize cell division and maintain photosynthetic efficiency. Using basic methods to determine cell size and fast rate repetition fluorometry (FRRf), circadian rhythms were observed for the phytoplankton *Emiliania huxleyi* in exponentially growing cultures. Cell division and potential photosynthetic rate showed distinct circadian rhythms for cultures maintained in 12:12h diel light-dark cycles. Potential photosynthetic rate decreased two hours before transition into the dark phase of the diel cycle. Two hours into the dark phase cell diameter decreased indicating cell division proceeded through the dark phase. Cultures were then exposed to either 24h light or 24h dark for two diel cycles (48h). Under full light and full dark, the variation in potential photosynthetic rates over the diel cycle decreased but the circadian pattern was still apparent. In contrast, the pattern of cell diameter decreased and no circadian pattern of division was apparent. Overall, *E. huxleyi* possesses an endogenous rhythm of photosynthetic physiology, possibly independent of cell division.



### VARIABILITY OF DAMARISCOTTA ESTUARY ECOSYSTEM REVEALED BY MESOCOSM, REMOTELY OPERATED VEHICLE (ROV), AND SENSORS

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Marine microbes are a vital part of the function of ecosystems. For example, photosynthetic cyanobacteria increase oxygen levels in the ocean during the day. In this study, we investigated the variation in microbial communities along with temperature (T) and dissolved oxygen (DO) in the Damariscotta River estuary. Our approach included time-series measurements and remote sampling directly in the river (off the dock of the Bigelow Laboratory for Ocean Sciences) as well as in a large-volume (2,460 L) continuous flow mesocosm over the course of four weeks in Summer 2014. T and DO loggers recorded at 1-minute intervals, and we used OsmoSamplers to collect microbial samples for DNA extractions. Results showed that T and DO were less variable in the mesocosm than the estuary. "Aged" DNA samples from the OsmoSamplers could not be quantified. To better understand the lack of DNA in these samples, we conducted DNA degradation experiments with different preservatives. We found that DNA degraded rapidly in the three-day time frame after collection using recommended preservatives, and our tests reveal that ethanol would be a better alternative.

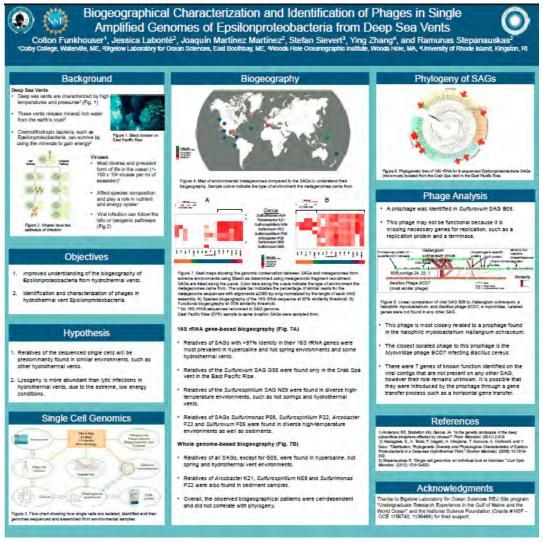


### BIOGEOGRAPHICAL CHARACTERIZATION AND IDENTIFICATION OF PHAGES IN SINGLE AMPLIFIED GENOMES OF EPSILONPROTEOBACTERIA FROM DEEP SEA VENTS

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Deep-sea vents are characterized by extreme and dynamic conditions with high temperatures and pressures. In these mineral rich locations, chemolithotropic bacteria are able to survive through inorganic processes such as sulfur oxidation and nitrogen fixation. One objective of this project was to examine the biogeography of ten single amplified genomes of Epsilonproteobacteria from the East Pacific Rise vent by comparing them to metagenomes from various extreme environments.

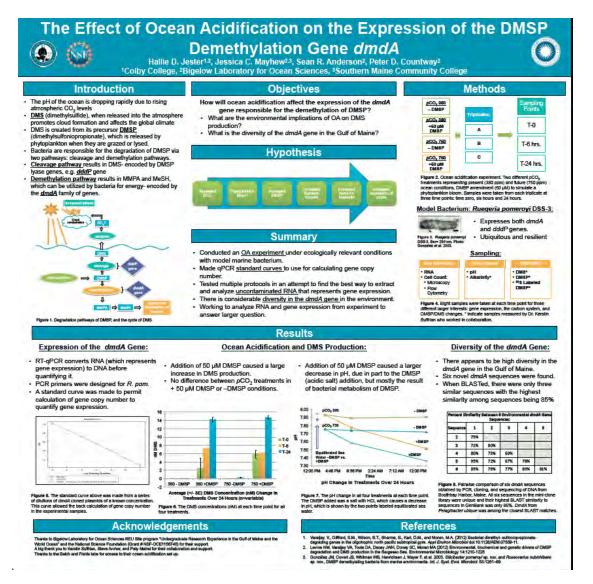
Genomic similarities were found between SAGs and metagenomes from other hydrothermal vents, hypersaline environments, hot springs and sediments. However, the observed patterns were cell-dependent and did not correlate with phylogeny. The second objective was to examine the SAGs for the presence of phages. Using multiple bioinformatics tools, we found one prophage, sharing phage genes with another prophage found in *Haliangium ochraceum*. Seven genes of known functions were identified on the viral contigs that are not present on any other SAG. It is possible that they were introduced by the prophage through a horizontal gene transfer process called transduction.



## THE EFFECT OF OCEAN ACIDIFICATION ON THE EXPRESSION OF THE DMSP DEGRADATION GENE DMDA

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Anthropogenic contributions to atmospheric carbon dioxide levels are causing a rapid drop in the pH of the ocean. The effects of ocean acidification on the marine sulfur cycle, remain largely unknown. Biogenic sulfur in the form of dimethylsulfide (DMS) escapes from the ocean and can lead to an increase in Earth's albedo via enhancement of cloud formation. DMS is formed primarily by the degradation of phytoplankton-derived dimethylsulfoniopropionate (DMSP). However, most DMSP is processed by marine bacteria via the demethylation pathway to obtain carbon and sulfur, resulting in methylmercapto-proprionate (MMPA) and methanethiol (MeSH). The demethylation pathway is encoded by dmdA genes, which are highly diverse in the marine environment, including coastal Maine. Using a model heterotrophic bacterium, Ruegeria pomeroyi DSS-3, we investigated dmdA gene expression under two different pCO2 treatments, 380 ppm and 750 ppm. Treatments included control (no DMSP) and DMSP amendments (50 uM DMSP). Bacterial abundance, DMS, and DMSP levels were monitored over time. Gene expression of dmdA transcripts was measured by RT-qPCR but preliminary results were somewhat inconclusive due to persistent DNA contamination in RNA extracts.

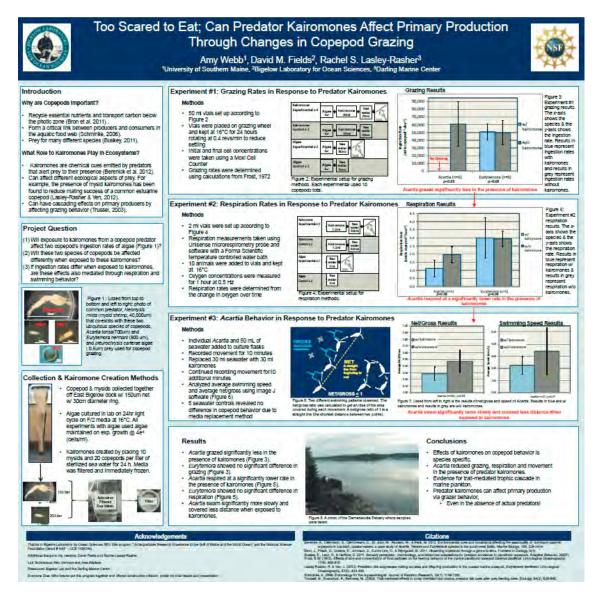


## TOO SCARED TO EAT; CAN PREDATOR KAIROMONES AFFECT PRIMARY PRODUCTION THROUGH CHANGES IN COPEPOD GRAZING?

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Copepods form a critical link between producers and consumers in the aquatic food web. To reduce predation, copepods have evolved a wide range of sensory and morphological adaptations. One mechanism for reducing predation is through the detection of chemical cues (kairomones) emitted by predators that alert prey to their presence. In this study we investigated the effects of predator kairomones from a local predator, *Neomysis mixta* on grazing, respiration and swimming behavior of two common estuarine copepods, *Acartia tonsa* and *Eurytemora herdmani*.

*Acartia* significantly reduced grazing, respiration, swimming speed and distance traveled in the presence of predator kairomones (p<0.05). *Eurytemora* showed no significant differences in grazing or respiration (p>0.05). These results indicate that the effects of kairomones on copepod behavior is species specific. This research suggests that predator kairomones can affect primary production via grazer behavior, even in the absence of actual predators.



### A MODEL OF POPULATION DYNAMICS FOR THE LIFE STAGES OF SALPA FUSIFORMA IN THE GULF OF MAINE

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Gelatinous zooplankton species are coming into the public spotlight as large blooms are noticed throughout the world. This new attention has emphasized the problem that we do not have enough data on many species of gelatinous zooplankton to fully understand their blooming processes. Models are useful in data-sparse situations, so we have updated a model for a particular type of gelatinous zooplankton: salps. The model reproduces the salp's seasonal cycle extremely well and does an acceptable job generating the interannual variation. It predicts a 34% increase in the size of large annual blooms, and a 68% increase in mean salp population over the course of the year for possible future conditions of an average temperature increase of 3 degrees C and double the amount of chlorophyll during the annual fall phytoplankton bloom.

