Bigelow Laboratory for Ocean Sciences

Research Experience for Undergraduates
The Gulf of Maine and the World Ocean

REU Symposium Program & Abstracts
Thursday, August 15, 2013

Program

10:00 Opening Remarks

10:15 **Yesmalie Alemán Resto -** Universidad Metropolitana, San Juan, Puerto Rico
SCREENING OF THE MMV CHEMICAL LIBARARY FOR COMPOUNDS INHIBITING THE OYSTER PROTOZOAN PARASITE *PERKINS MARINUS*.
Mentor: Dr. José Antonio Fernández Robledo

10:30 **Elizabeth M. Johnsey** - University of South Florida
QUANTIFYING DNA, RNA, AND PROTEIN CONTENT IN PHYTOPLANKTON BY FLOW CYTOMETRY
Mentor: LeAnn Whitney, Michael Lomas

10:45 **Mary E. Mathyer** - Kalamazoo College,
CARBON AND NITROGEN CYCLING BY *NITROSPINA* IN THE DARK OCEAN
Mentors: Brandon K. Swan, Ramunas Stepanauskas

11:00 **Charlotte A. Francisco** – Lewis and Clark College
THE RESPIRATION RATES OF ACARTIA TONSA IN RESPONSE TO CHANGING TEMPERATURE AND SALINITY
Mentors: David Fields, Alex Vermont, Jesica Waller

11:15 **Wilton Burn**s - University of North Carolina at Chapel Hill
GROWTH AND GRAZING DYNAMICS OF PHOTOTROPHIC PROTISTS IN BOOTH BAY, MAINE
Mentor Mike Sieracki, Nicole Poulton

11:30 **Ryan Yan -** College of William and Mary
DO HUMIC COMPOUNDS INHIBIT THE AEROSOLIZATION OF CHLOROPHYLL *A* AND BREVETOXINS?
Mentors: Cynthia Heil, Steve Archer

11:45 Break (45 minutes) *************************************

12:30 **Victoria Abel** – Colby College
LIGHT DEPENDENCY OF CALCIFICATION AND IMPACTS OF VARYING PH LEVELS IN THE COCCOLITHOPHORID *PLEUROCHRYSIS CARTERAE*
Mentors: William Balch, Merideth White.

12:45 **Kara Voss** - RSMAS University of Miami
EFFECTS OF OCEAN ACIDIFICATION ON DMS AND DMSP PRODUCTION BY THE DINOFLAGELLATE *H. TRIQUETRIA*
Mentors: Patricia Matrai, Steve Archer

13:00 **Sean Anderson** – Bigelow Laboratory
GROWTH AND GRAZING OF *SYNECHOCOCCUS* IN BOOTH BAY, MAINE
Mentors: Mike Sieracki, Nicole Poulton

13:15 **Kayla Erf** – Colby College
ANALYZING THE POPULATION DIVERSITY OF *SYNECHOCOCCUS* DURING THE 2013 SUMMER BLOOM PERIOD IN THE WEST BOOTH BAY OF MAINE
Mentors: Pete Countway, Mike Sieracki, Nicole Poulton

13:30 **Audrey E. Lyman** - Colby College
BIOINFORMATIC ANALYSES OF EPSILONPROTEOBACTERIA AND THE POTENTIAL INTERACTIONS WITH ZETAPROTEOBACTERIA
Mentors: Erin K. Field, Dave Emerson

**13:45 Break (15 minutes) **

14:00 **Campbell Belisle Haley** - University of Maine
WEAVING THE MICROBIAL TAPESTRY: THE IDENTIFICATION OF A CORE MICROBIOME IN FRESHWATER IRON SEEPS
Mentors: Jarrod Scott, Emily Fleming, David Emerson

14:15 **Kim Dempsey** - Bowdoin College
GROWTH & DEVELOPMENT OF *ZETAPROTEOBACTERIA* SP. DIS-1 BIOFILM ON MILD STEEL
Mentors: Adam Mumford and David Emerson

14:30 **Alice Chapman –** Wiliams College
REGENERATION OF FE(II) BY PROTIST GRAZING IN THE OCEAN
Mentors: Ben Twining, Jochen Nuester

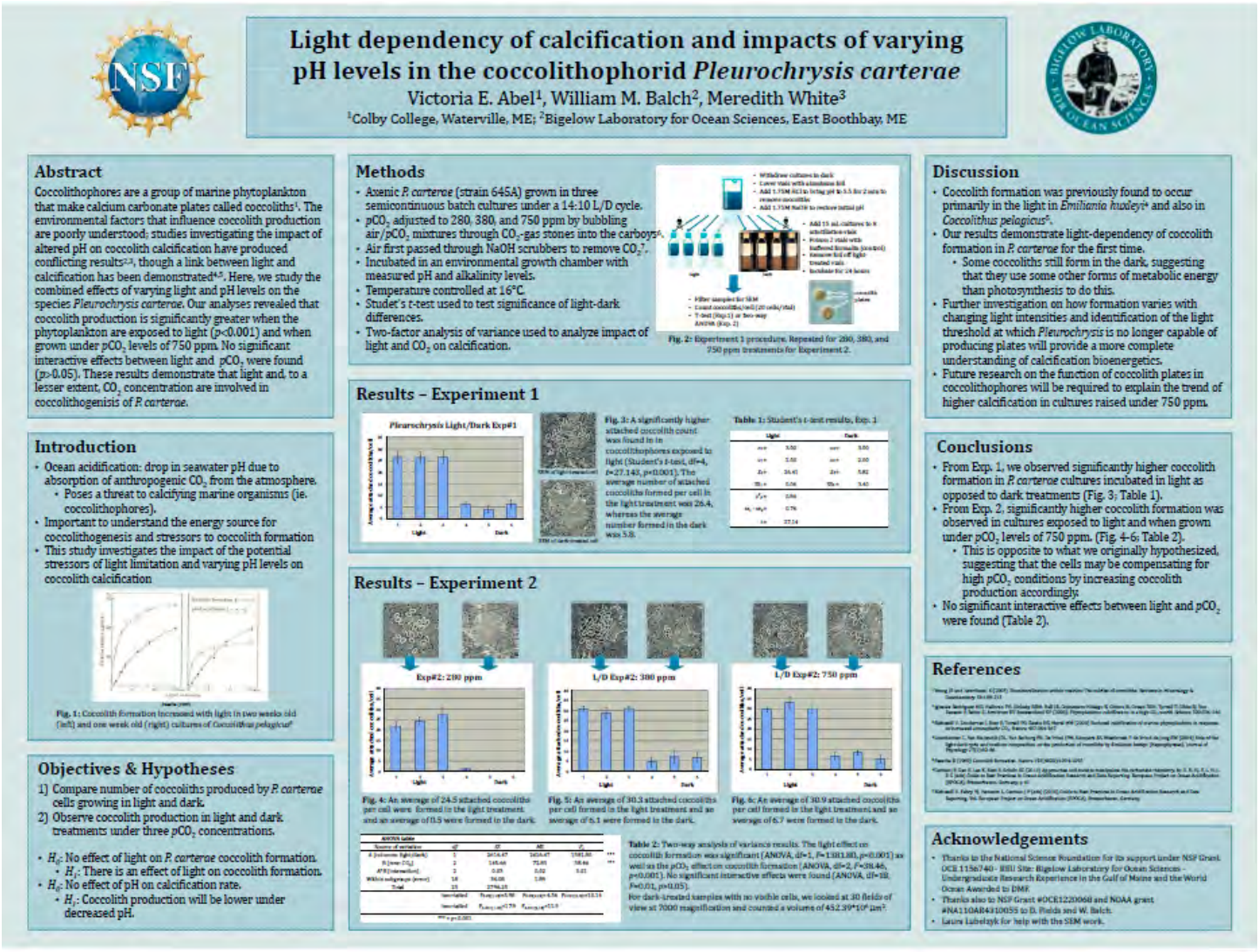
14:45 **Amy Duarte** - Humboldt State University
DIVERSITY OF LARGE MARINE VIRUSES IN THE GULF OF MAINE
Mentors: Ilana Gilg, Willie Wilson

Abstracts

Light dependency of calcification and impacts of varying pH levels in the coccolithophorid *Pleurochrysis carterae*

Victoria E. Abel [1,2], William M. Balch[2], Meredith White[2]
[1]Colby College, Waterville, ME; [2]Bigelow Laboratory for Ocean Sciences, East Boothbay, ME

Coccolithophores are a group of marine phytoplankton that make calcium carbonate plates called coccoliths. The environmental factors that influence coccolith production are poorly understood; studies investigating the impact of altered pH on coccolith formation have produced conflicting results, though a link between light and calcification has been demonstrated. Here, we study the combined effects of varying light and pH levels on the species *Pleurochrysis carterae*. A plating strain of P. carterae grown under three different pCO_2 levels was bottled for 24 hours in light and dark treatments and filtered for SEM comparison of coccolith formation. A t-test was used to determine significance of light-dark differences in calcification rate and a two-factor analysis of variance was performed to analyze the combined impact of light and pCO_2. Our analyses revealed that coccolith production is significantly greater when the phytoplankton are exposed to light ($p<0.001$) and when grown under pCO_2 ($p=0.05$) levels of 750 ppm. No significant interactive effects between light and pCO_2 were found ($p=0.05$). These results demonstrate that light and, to a lesser extent, pCO_2 concentration are involved in coccolithogenisis of *P. carterae*.

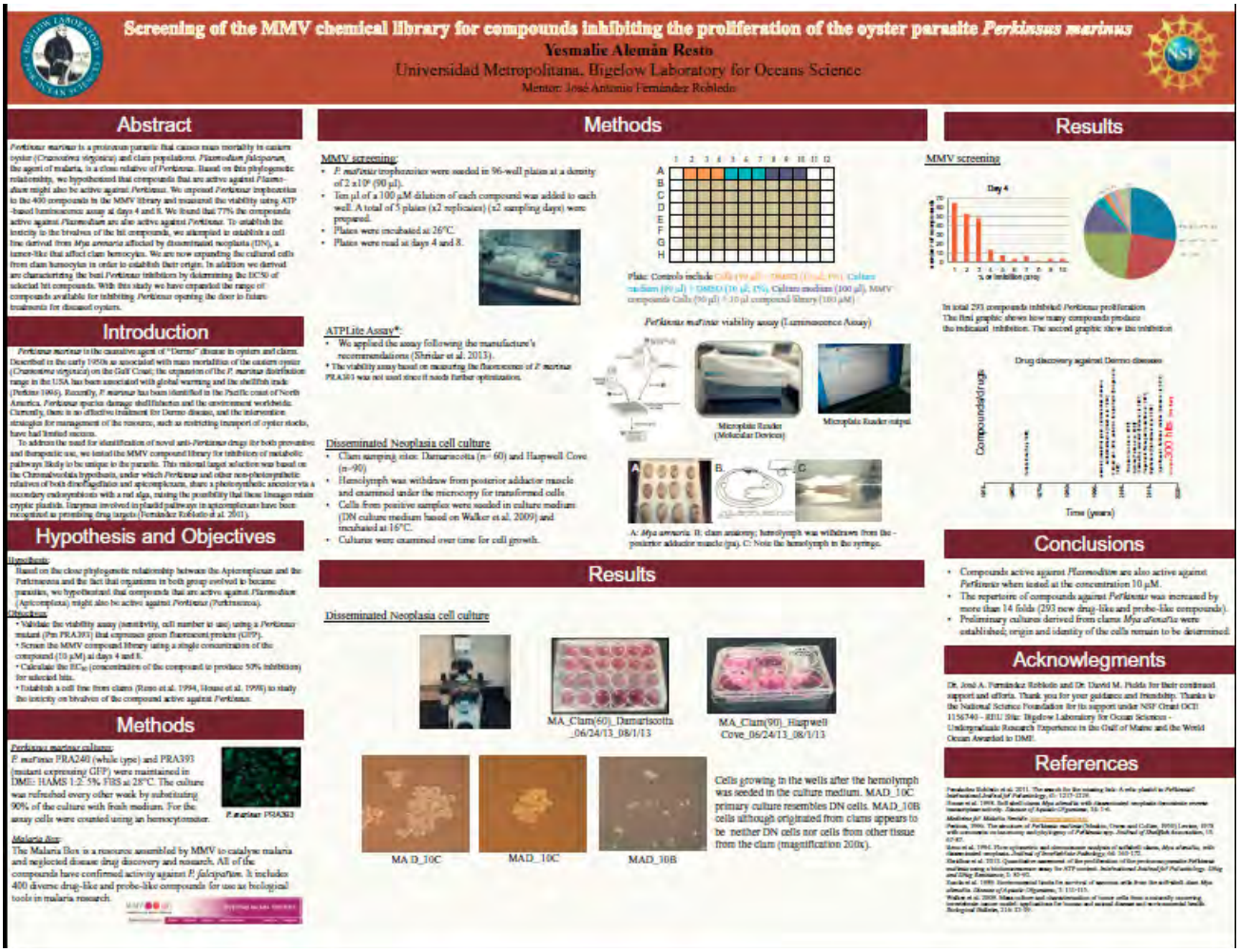


Screening of the MMV Chemical Library for Compounds Inhibiting the Proliferation of the Oyster Protozoan Parasite *Perkinsus marinus*

Yesmalie Alemán Resto, Universidad Metropolitana, San Juan, Puerto Rico
Mentor: Dr. José Antonio Fernández Robledo
Bigelow Laboratory for Ocean Sciences, REU Program

Abstract

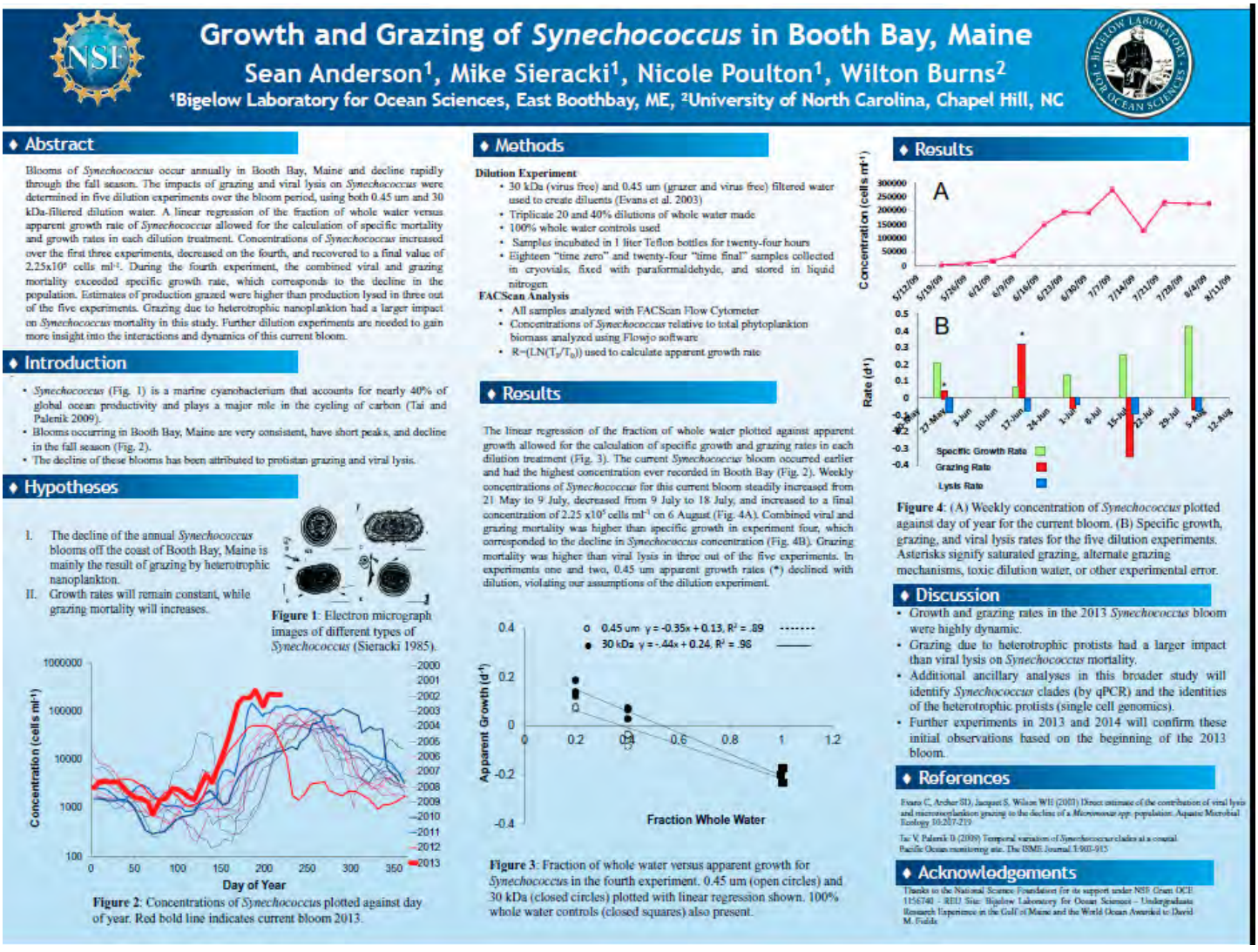
Perkinsus marinus is a protozoan parasite that causes mass mortality in eastern oyster (*Crassostrea virginica)* and clam populations. *Plasmodium falciparum,* the agent of malaria, is a close relative of *Perkinsus*. Based on this phylogenetic relationship, it was hypothesized that compounds that are active against *Plasmodium* might also be active against *Perkinsus*. We exposed *Perkinsus trophozoites* to the 400 compounds in the MMV library and measured the viability using ATP-based luminescence assay at days 4 and 8. We found that 77% the compounds active against *Plasmodium* are also active against *Perkinsus*. To establish the toxicity to the bivalves of the hit compounds, we attempted to establish a cell line derived from *Mya arenaria* affected by disseminated neoplasia (DN) a tumor that affect clam hemocytes. We are now expanding the cultured cells derived from clam hemocytes in order to establish their origin. In addition we are characterizing the best *Perkinsus* inhibitors by determining the EC50 of selected hit compounds. With this study we have expanded the range of compounds available for inhibiting *Perkinsus* opening the door to future treatments for diseased oysters.



GROWTH AND GRAZING OF *SYNECHOCOCCUS* IN BOOTH BAY, MAINE

Sean Anderson[1], Mike Sieracki[1], Nicole Poulton [1], Wilton Burns[2]
[1]Bigelow Laboratory for Ocean Sciences, East Boothbay, ME
[2]University of North Carolina, Chapel Hill, NC

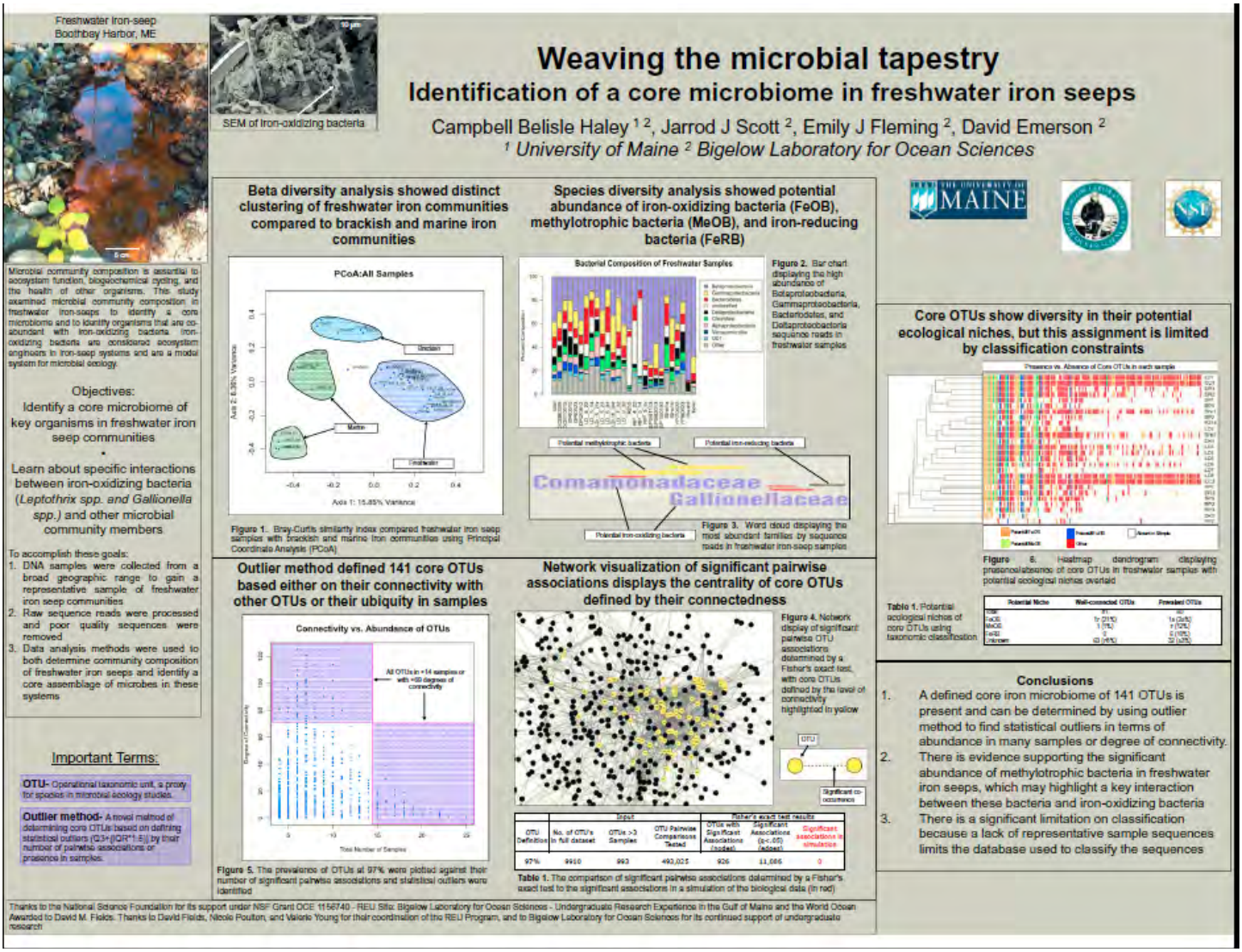
Blooms of *Synechococcus* occur annually in Booth Bay, Maine and decline rapidly through the fall season. The impacts of grazing and viral lysis on *Synechococcus* were determined in five dilution experiments over the bloom period, using both 0.45 um and 30 kDa-filtered dilution water. A linear regression of the fraction of whole water versus apparent growth rate of *Synechococcus* allowed for the calculation of specific mortality and growth rates in each dilution treatment. Concentrations of *Synechococcus* increased over the first three experiments, decreased on the fourth, and recovered to a final value of $2.25x10^5$ cells ml^{-1}. During the fourth experiment, the combined viral and grazing mortality exceeded specific growth rate, which corresponds to the decline in the population. Estimates of production grazed were higher than production lysed in three out of the five experiments. Grazing due to heterotrophic nanoplankton had a larger impact on *Synechococcus* mortality in this study. Further dilution experiments are needed to gain more insight into the interactions and dynamics of this current bloom.



WEAVING THE MICROBIAL TAPESTRY: THE IDENTIFICATION OF A CORE MICROBIOME IN FRESHWATER IRON SEEPS

Campbell Belisle Haley[1,2], Dr. Jarrod Scott[2], Dr. Emily Fleming[2], Dr. David Emerson[2]
[1]University of Maine, [2]Bigelow Laboratory for Ocean Sciences

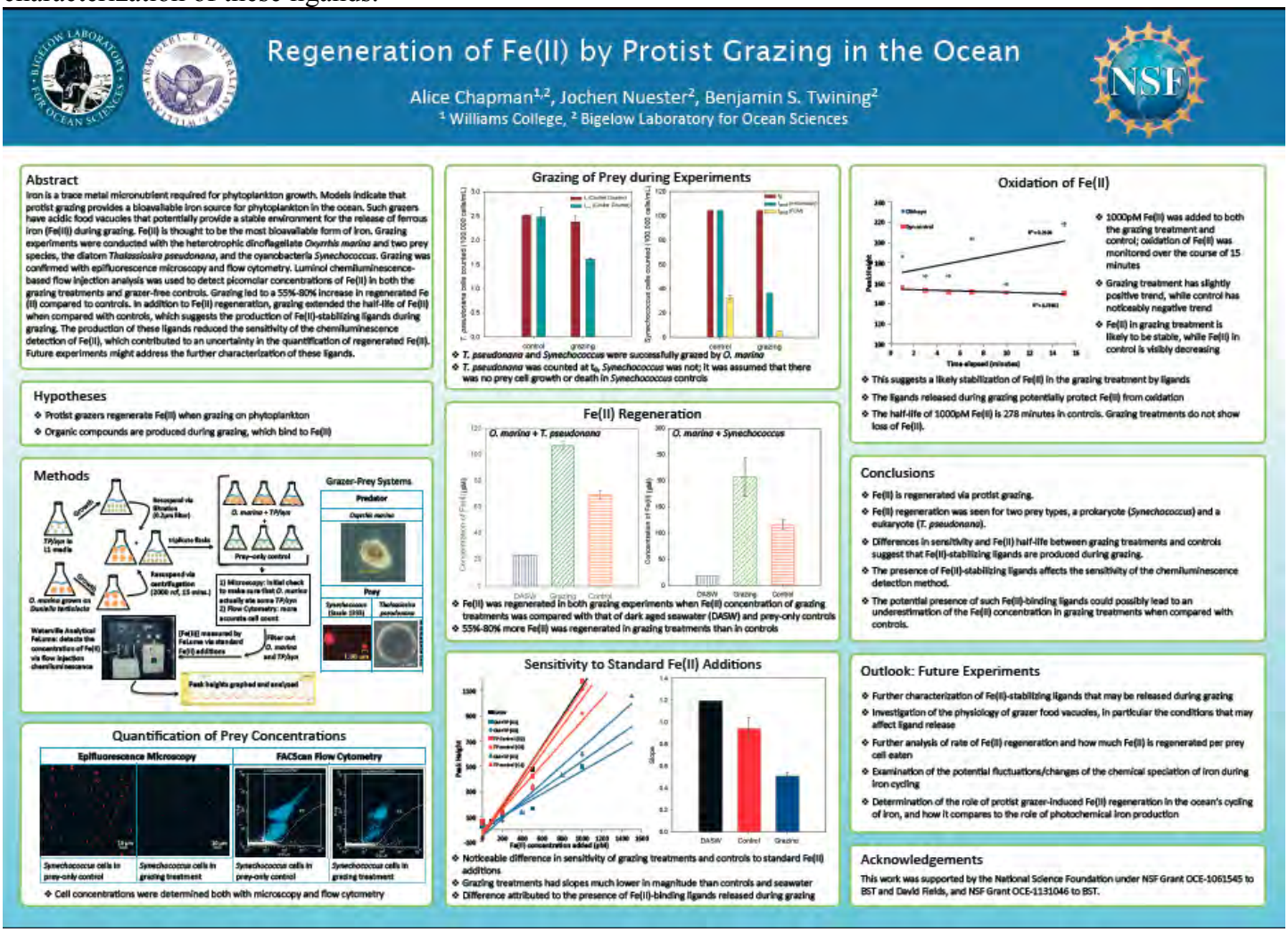
Microbial community composition is essential to ecosystem function, biogeochemical cycling, and the health of local organisms. This study examined microbial community composition in freshwater iron-seeps to identify a core microbiome that represents an assemblage of specific microbes and their potential ecological niches. 32 DNA samples were collected from a broad geographic range to gain a representative sampling of microbial communities in these systems. After targeted 16S rRNA gene pyrosequencing of the V4-V6 region, samples were processed and subsequently analyzed for species diversity. Comamonadaceae, Gallionellaceae, Methylococcaceae, and Crenotrichaceae were the most abundant groups identified in freshwater samples. These families contain most studied freshwater iron-oxidizing bacteria and methylotrophic bacteria, and this co-abundance suggests a potentially important relationship. Also, a Fisher's exact test identified 11086 significant pairwise co-occurrence associations ($q<0.05$) between 926 operational taxonomic units (OTUs) in freshwater samples. 141 OTUs were statistical outliers (Q3+(IQR*1.5)) in either their ubiquity across samples or total associations from the co-occurrence analysis. This outlier method identified an assemblage of potential core microbes in freshwater iron-seeps and elucidated methods for defining the key members of microbial communities.



REGENERATION OF FE(II) BY PROTIST GRAZING IN THE OCEAN

Alice Chapman[1,2], Dr. Ben Twining[2] & Dr. Jochen Neuster[2]
[1]Williams College, [2] Bigelow Laboratory for Ocean Sciences

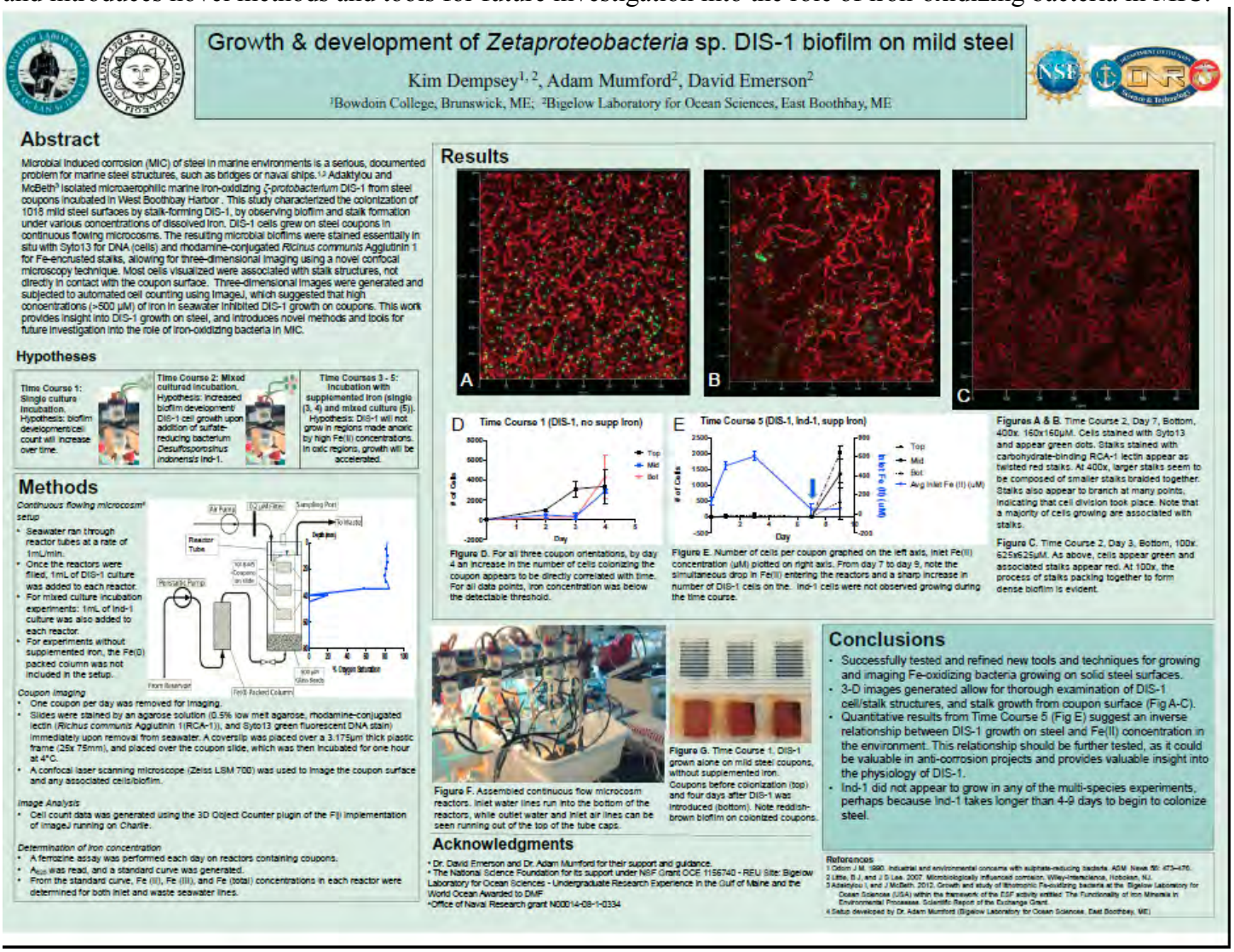
Iron is a micronutrient required for phytoplankton growth. Models indicate that protist grazing provides a bioavailable iron source for phytoplankton in the ocean. Such grazers have acidic food vacuoles that potentially provide a stable environment for the release of ferrous iron (Fe(II)) during grazing. Fe(II) is thought to be the most bioavailable form of iron. Grazing experiments were conducted with the heterotrophic dinoflagellate *Oxyrrhis marina* and two prey species, the diatom *Thalassiosira pseudonana*, and the cyanobacteria *Synechococcus*. Grazing was confirmed with epifluorescence microscopy and flow cytometry. Luminol chemiluminescence-based flow injection analysis was used to detect picomolar concentrations of Fe(II) in both the grazing treatments and grazer-free controls. Grazing led to a 55% - 80% increase in regenerated Fe(II) compared to controls. In addition to Fe(II) regeneration, grazing extended the half-life of Fe(II) when compared with controls, which suggests the production of Fe(II)-stabilizing ligands during grazing. The production of these ligands reduced the sensitivity of the chemiluminescence detection of Fe(II), which contributed to an uncertainty in the quantification of regenerated Fe(II). Future experiments might address the further characterization of these ligands.



GROWTH & DEVELOPMENT OF *ZETAPROTEOBACTERIA* SP. DIS-1 BIOFILM ON MILD STEEL

Kim Dempsey[1,2] Adam Mumford[2] and David Emerson[2]
[1]Bowdoin College, Brunswick ME; [2]Bigelow Laboratory for Ocean Sciences, East Boothbay, ME

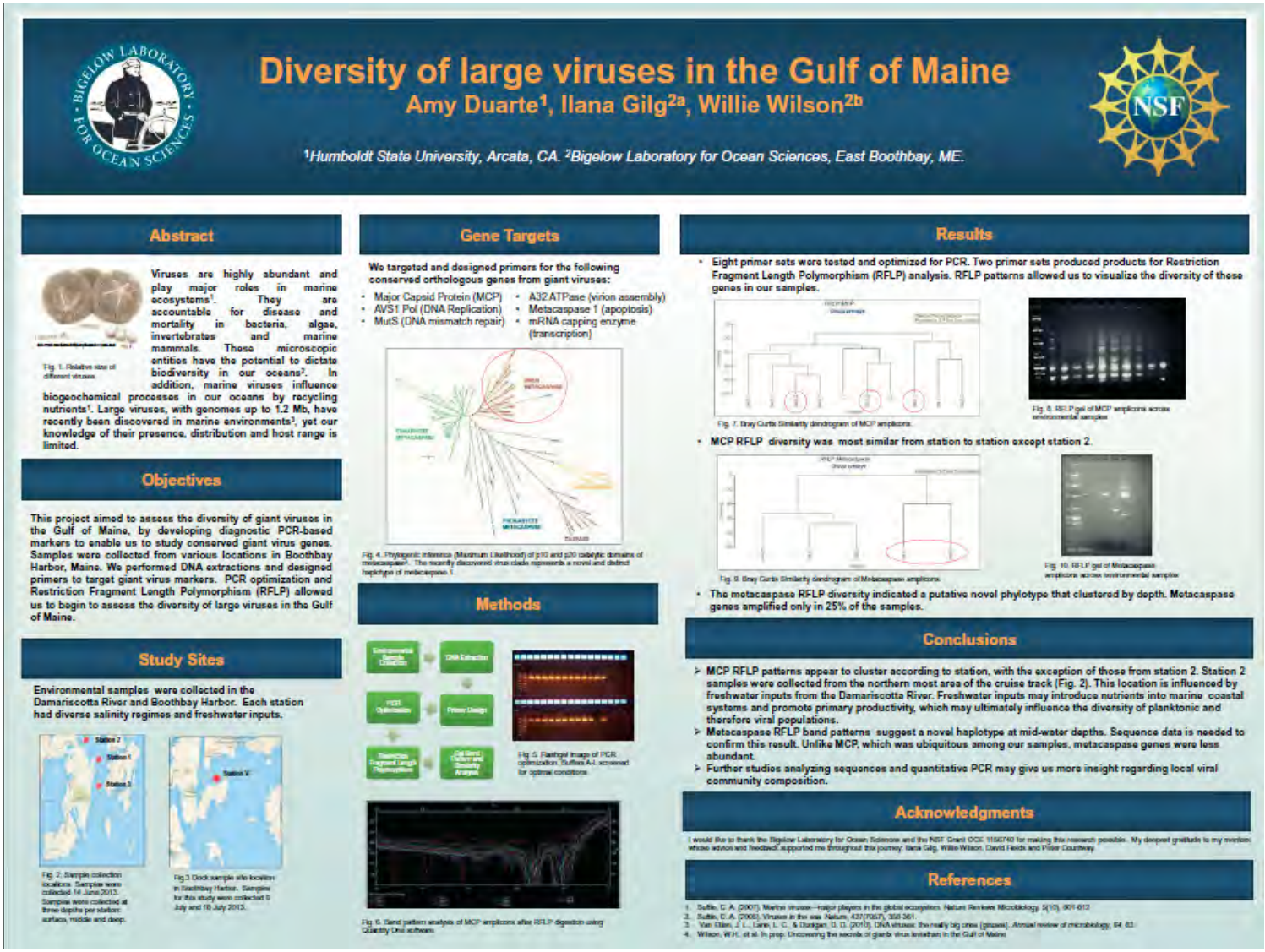
Microbial induced corrosion (MIC) of steel in marine environments is a serious, documented problem for marine steel structures, such as bridges or naval ships. Recently microaerophilic marine iron-oxidizing *Zetaprotobacterium* DIS-1 was isolated from steel coupons incubated in West Boothbay Harbor. This study characterized the colonization of 1018 mild steel surfaces by stalk-forming DIS-1, by observing biofilm and stalk formation under various concentrations of dissolved iron. DIS-1 cells grew on steel coupons in continuous flowing microcosms. The resulting microbial biofilms were stained essentially *in situ* with Syto13 for DNA (cells) and rhodamine-conjugated *Ricinus communis* Agglutinin 1 for Fe-encrusted stalks, allowing for three-dimensional imaging using a novel confocal microscopy technique. Most cells visualized were associated with stalk structures, not directly in contact with the coupon surface. Three-dimensional images were generated and subjected to automated cell counting using ImageJ, which suggested that high concentrations (>500 & microM) of iron in seawater inhibited DIS-1 growth on coupons. This work provides insight into DIS-1 growth on steel, and introduces novel methods and tools for future investigation into the role of iron-oxidizing bacteria in MIC.



DIVERSITY OF LARGE MARINE VIRUSES IN THE GULF OF MAINE

Amy Duarte [1], Ilana Gilgi[2], Willie Wilson[2]
[1]Humboldt State University, [2] Bigelow Laboratory for Oceans Sciences

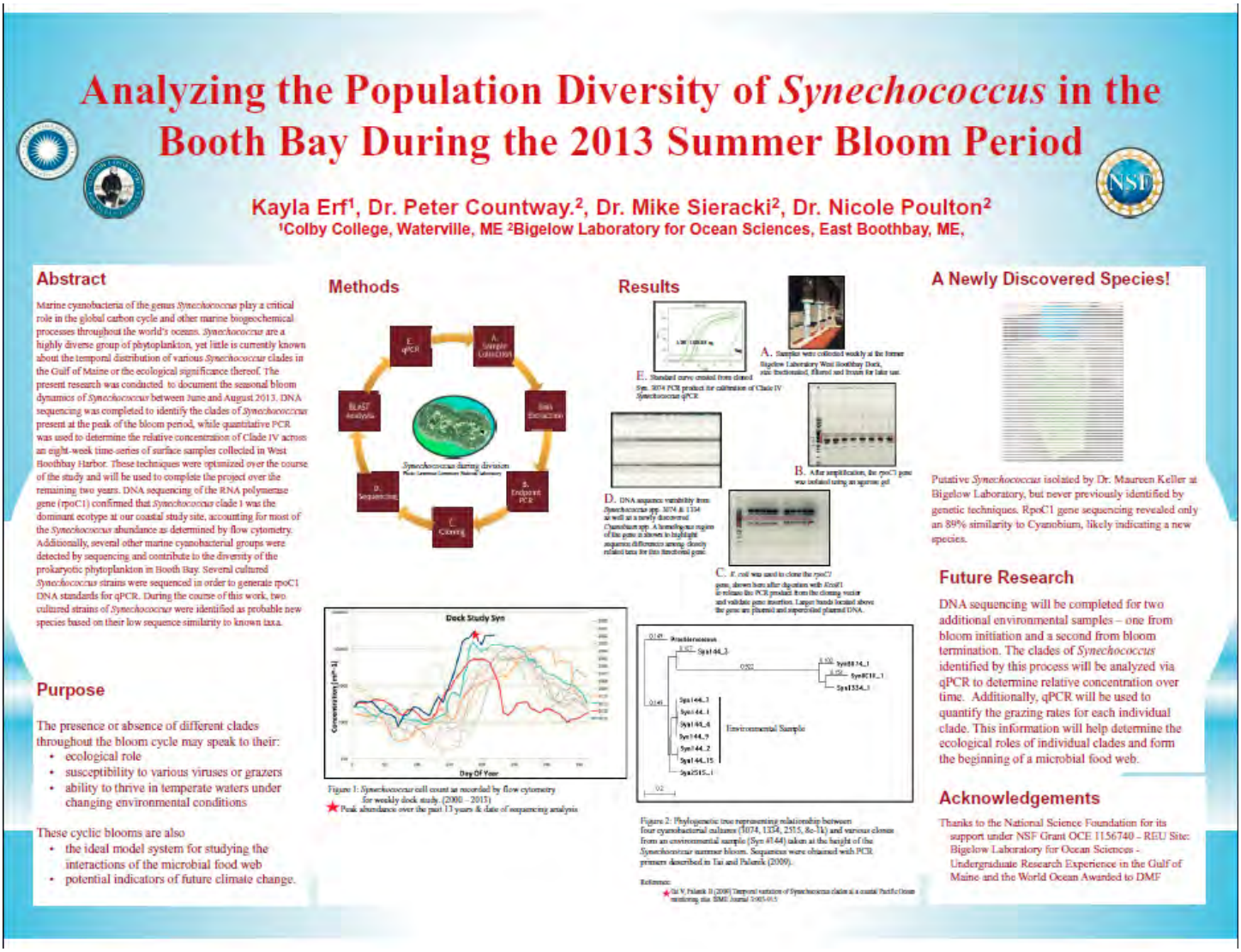
Viruses are highly abundant and play major roles in marine ecosystems. They are accountable for disease and mortality in bacteria, algae, invertebrates and marine mammals. These microscopic entities have the potential to dictate biodiversity in our oceans. In addition, marine viruses influence biogeochemical processes in our oceans by recycling nutrients. Large viruses, with genomes up to 1.2 Mb, have recently been discovered in marine environments, yet our knowledge of their presence, distribution and host range is limited. Nothing is known about the large virus population in the Gulf of Maine. This project aimed to assess the diversity of giant viruses in the Gulf of Maine, by developing diagnostic PCR-based markers to enable us to study conserved giant virus genes. Samples were collected from various regions around Boothbay Harbor, Maine. We performed DNA extractions and designed primers to target giant virus markers. PCR optimization and Restriction Fragment Length Polymorphism (RFLP) allowed us to identify and to begin to assess the diversity of large viruses in the Gulf of Maine.



ANALYZING THE POPULATION DIVERSITY OF *SYNECHOCOCCUS* DURING THE 2013 SUMMER BLOOM PERIOD IN THE WEST BOOTH BAY OF MAINE

Erf, K.M.[1], Countway, P.D.[2], Sieracki, M.[2], Poulton, N.[2]
[1]Colby College, Waterville, ME [2]Center for Ocean Health, Bigelow Laboratory for Ocean Sciences, East Boothbay, ME

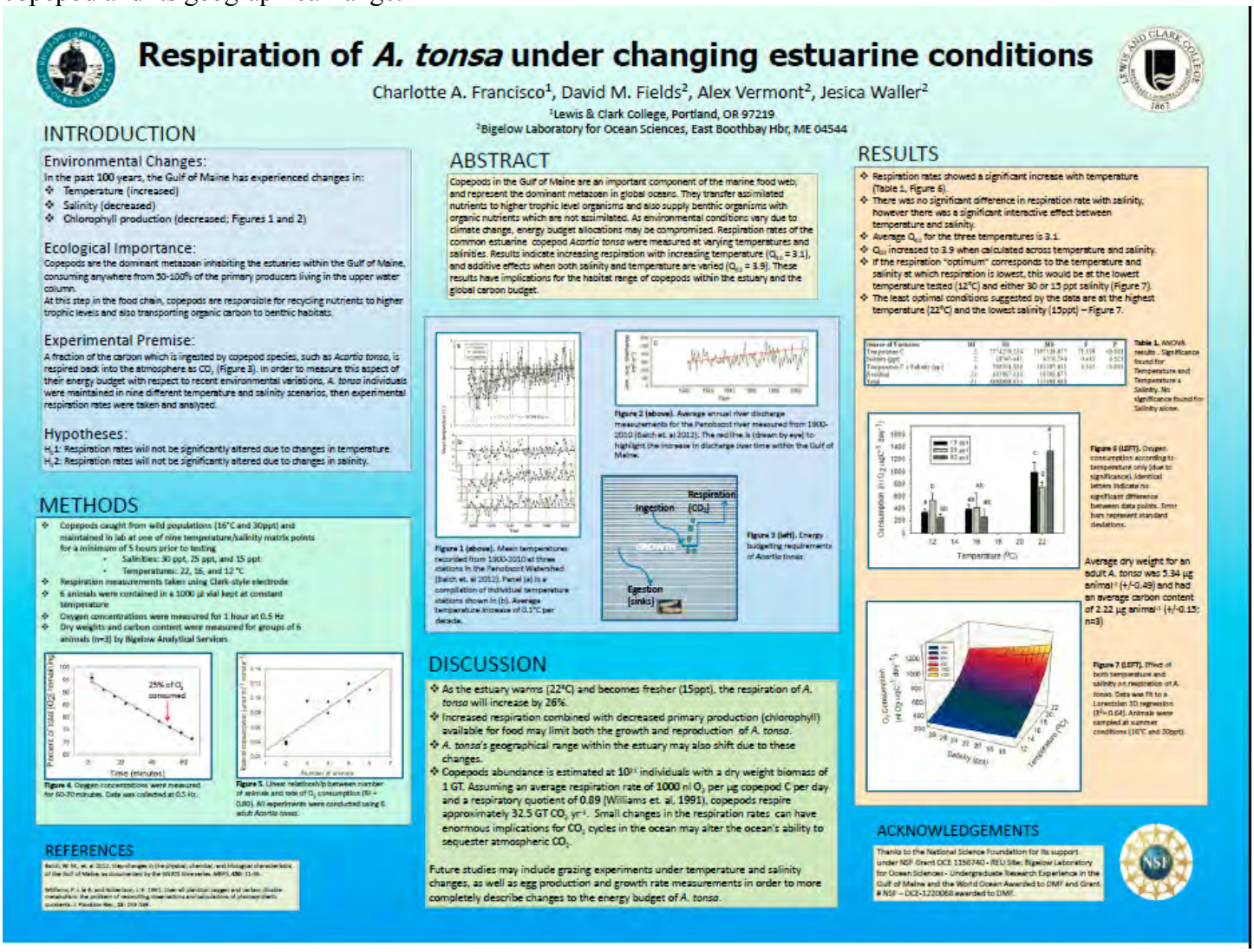
Marine cyanobacteria of the genus *Synechococcus* play a critical role in the global carbon cycle and other marine biogeochemical processes throughout the world's oceans. *Synechococcus* are a highly diverse group of phytoplankton, yet little is currently known about the temporal distribution of various *Synechococcus* clades in the Gulf of Maine or the ecological significance thereof. The present research was conducted to document the seasonal bloom dynamics of *Synechococcus* between June and August 2013. DNA sequencing was completed to identify the clades of *Synechococccus* present at the peak of the bloom period, while quantitative PCR was used to determine the relative concentration of Clade IV across an eight-week time-series of surface samples collected in West Boothbay Harbor. These techniques were optimized over the course of the study and will be used to complete the project over the remaining two years. DNA sequencing of the RNA polymerase gene (rpoC1) confirmed that *Synechococcus* clades I and IV were the dominant ecotypes at our coastal study site, accounting for most of the *Synechococcus* abundance as determined by flow cytometry.



THE RESPIRATION RATES OF ACARTIA TONSA IN RESPONSE TO CHANGING TEMPERATURE AND SALINITY

Charlotte A. Francisco[1,2], David M. Fields[2], Alex Vermont[2], Jesica Waller[2]
[1]Lewis and Clarck, [2]Bigelow Laboratory for Ocean Sciences

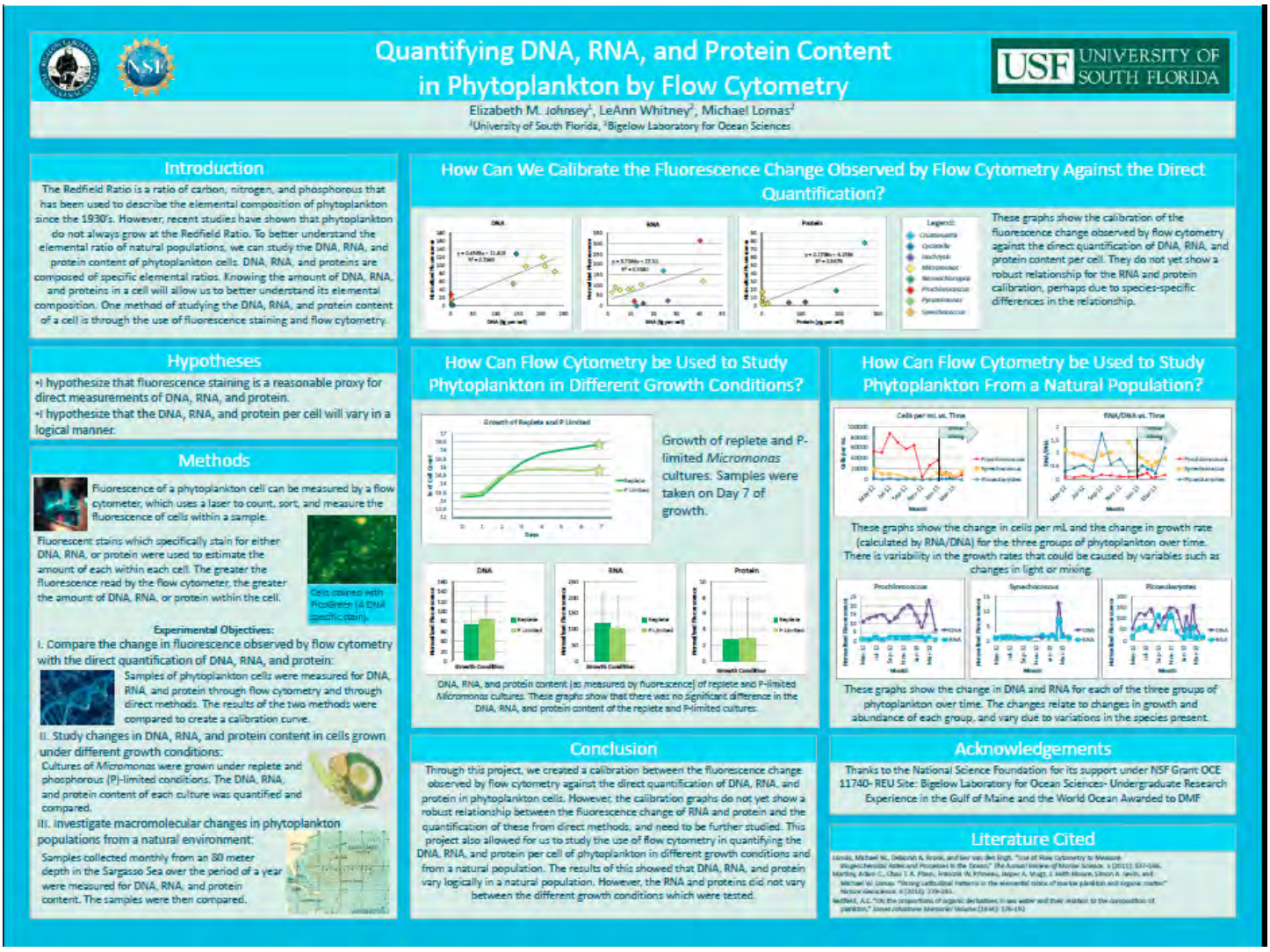
In the past century, increased temperatures, decreased salinity, and decreased chlorophyll concentrations have occurred within Gulf of Maine estuaries. Copepods, the dominant metazoans on the planet, are an important component of marine ecosystems, bridging the gap between phytoplankton and higher trophic level organisms, recycling nutrients, and transporting carbon to the benthos. The respiration rates of adult *Acartia tonsa* (a principal estuarine copepod) were measured under nine temperature and salinity scenarios using microrespirometry techniques. Oxygen concentrations were measured at 0.5 Hz for one hour in 1000 µl chambers. A two-way ANOVA showed a significant relationship between respiration rates and temperature and a significant interactive effect of temperature and salinity on respiration. The average Q10 for respiration was 3.1 which increased to 3.9 over the salinity range used in this study. These results suggest that as the estuaries warm and become fresher, the respiration rates of *Acartia tonsa* will increase by 26%. The increased respiration rates combined with decreasing rates of primary productivity may limit the growth and reproduction of this copepod and its geographical range.



QUANTIFYING DNA, RNA, AND PROTEIN CONTENT IN PHYTOPLANKTON BY FLOW CYTOMETRY

Elizabeth M. Johnsey[1], LeAnn Whitney[2], Michael Lomas[2]
[1]University of South Florida, [2]Bigelow Laboratory for Ocean Sciences

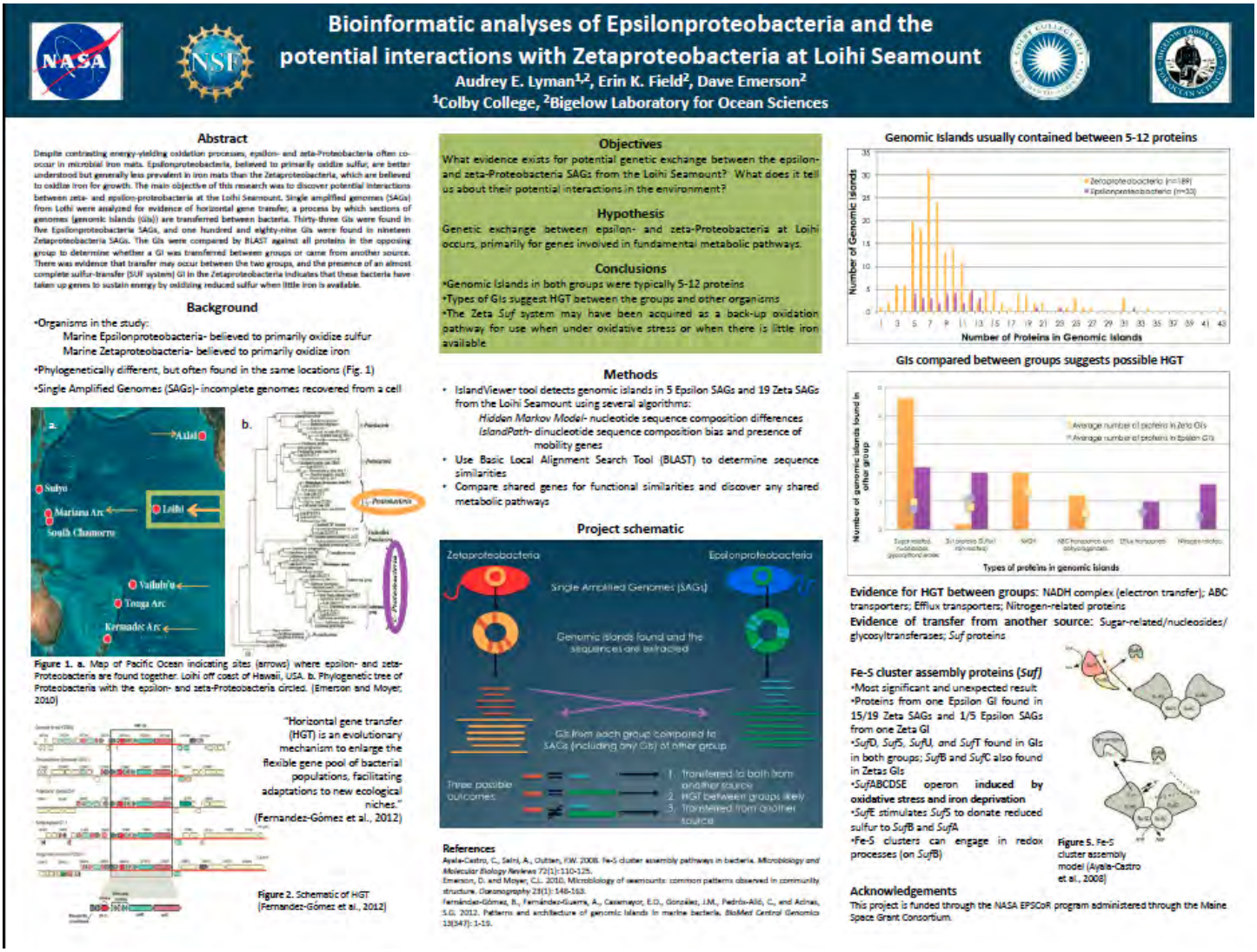
The Redfield ratio has been used to describe the elemental composition of phytoplankton since the 1930s. Recent studies have shown deviations from this ratio, indicating that we don't understand how and why these deviations occur. Studying the DNA, RNA, and protein content of phytoplankton cells will allow us to better understand their elemental composition as these biochemicals have well constrained elemental ratios and comprise the bulk of phytoplankton organic material. We coupled fluorescence staining and flow cytometry to investigate the macromolecular composition of phytoplankton. Our goals were to determine whether fluorescence staining is a reasonable proxy for direct measurements of DNA, RNA, and protein per cell and whether DNA, RNA, and protein per cell varies in a predictable manner. We calibrated the fluorescence observed by flow cytometry against direct quantification of DNA, RNA, and protein per cell. Macromolecular composition was also measured in phytoplankton grown under different growth conditions as well as from a natural sample. Data collected thus far do not yet show a predictable relationship between fluorescence and quantification from direct methods, and need further study.



BIOINFORMATIC ANALYSES OF EPSILONPROTEOBACTERIA AND THE POTENTIAL INTERACTIONS WITH ZETAPROTEOBACTERIA

Audrey E. Lyman[1,2], Erin K. Field[2], Dave Emerson[2]
[1]Colby College, [2]Bigelow Laboratory for Ocean Sciences

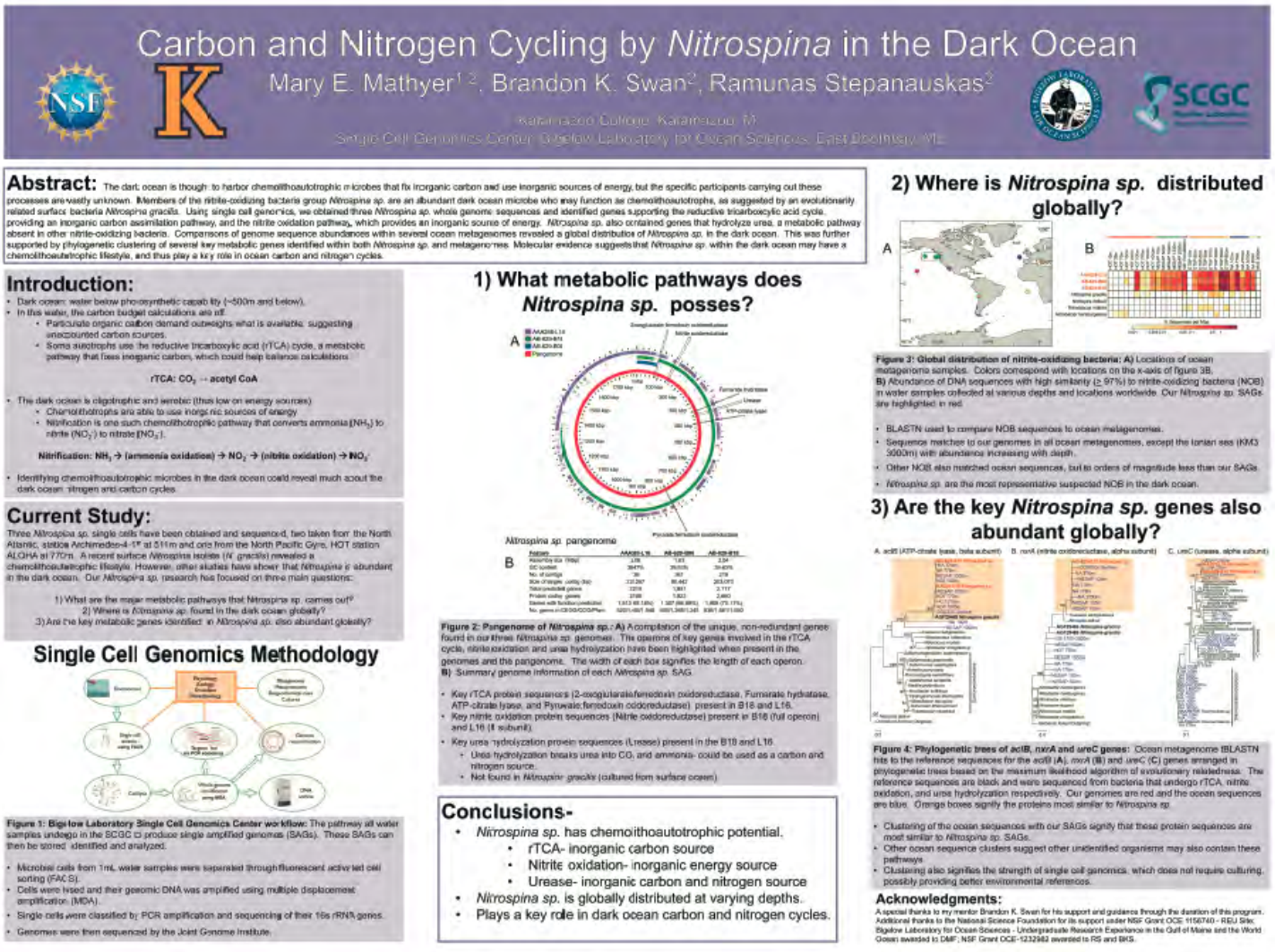
Despite contrasting energy-yielding oxidation processes, epsilon- and zeta-Proteobacteria often co-occur in microbial iron mats. Epsilonproteobacteria, believed to primarily oxidize sulfur, are better understood but generally less prevalent in iron mats than the Zetaproteobacteria, which are believed to oxidize iron for growth. The main objective of this research was to discover potential interactions between zeta- and epsilon-proteobacteria at the Loihi Seamount. Single amplified genomes (SAGs) from Loihi were analyzed for evidence of horizontal gene transfer, a process by which sections of genomes (genomic islands (GIs)) are transferred between bacteria. Thirty-three GIs were found in five Epsilonproteobacteria SAGs, and one hundred and eighty-nine GIs were found in nineteen Zetaproteobacteria SAGs. The GIs were compared by BLAST against all proteins in the opposing group to determine whether a GI was transferred between groups or came from another source. There was evidence that transfer may occur between the two groups, and the presence of an almost complete sulfur-transfer (SUF system) GI in the Zetaproteobacteria indicates that these bacteria have taken up genes to sustain energy by oxidizing reduced sulfur when little iron is available.



CARBON AND NITROGEN CYCLING BY *NITROSPINA* IN THE DARK OCEAN

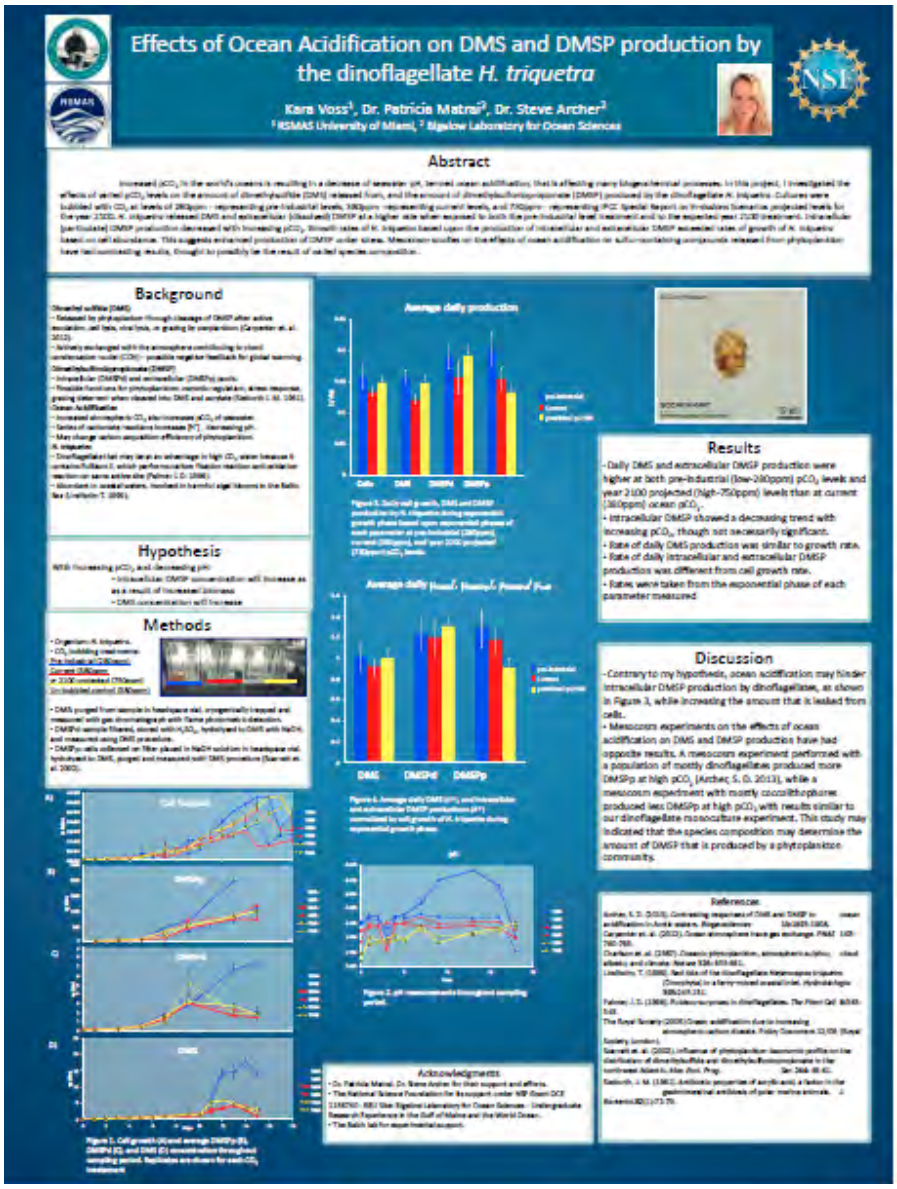
Mary E. Mathyer[1,2], Brandon K. Swan[2], Ramunas Stepanauskas[2]
[1,]Kalamazoo College, Kalamazoo, MI, [2]Bigelow Laboratory for Ocean Sciences, East Boothbay, ME

The dark ocean is thought to harbor chemolithoautotrophic microbes that fix inorganic carbon and use inorganic sources of energy, but the specific participants carrying out these processes are vastly unknown. Members of the nitrite-oxidizing bacteria group *Nitrospina sp*. are an abundant dark ocean microbe who may function as chemolithoautotrophs, as suggested by an evolutionarily related surface bacteria *Nitrospina gracilis*. Using single cell genomics, we obtained three *Nitrospina sp*. whole genome sequences and identified genes supporting the reductive tricarboxcylic acid cycle, providing an inorganic carbon assimilation pathway, and the nitrite oxidation pathway, which provides an inorganic source of energy. Nitrospina sp. also contained genes that hydrolyze urea, a metabolic pathway absent in other nitrite oxidizing bacteria. Comparisons of genome sequence abundances within several ocean metagenomes revealed a global distribution of *Nitrospina sp*. in the dark ocean. This was further supported by phylogenetic clustering of several key metabolic genes identified within both *Nitrospina sp*. and metagenomes. Molecular evidence suggests that *Nitrospina sp.* within the dark ocean may have a chemolithoautotrophic lifestyle, and thus play a key role in ocean carbon and nitrogen cycles.



EFFECTS OF OCEAN ACIDIFICATION ON DMS AND DMSP PRODUCTION BY THE DINOFLAGELLATE *H. TRIQUETRIA*

Kara Voss[1], Patricia Matrai[2], Steve Archer[2]
[1]RSMAS University of Miami, [2]Bigelow Laboratory for Ocean Sciences

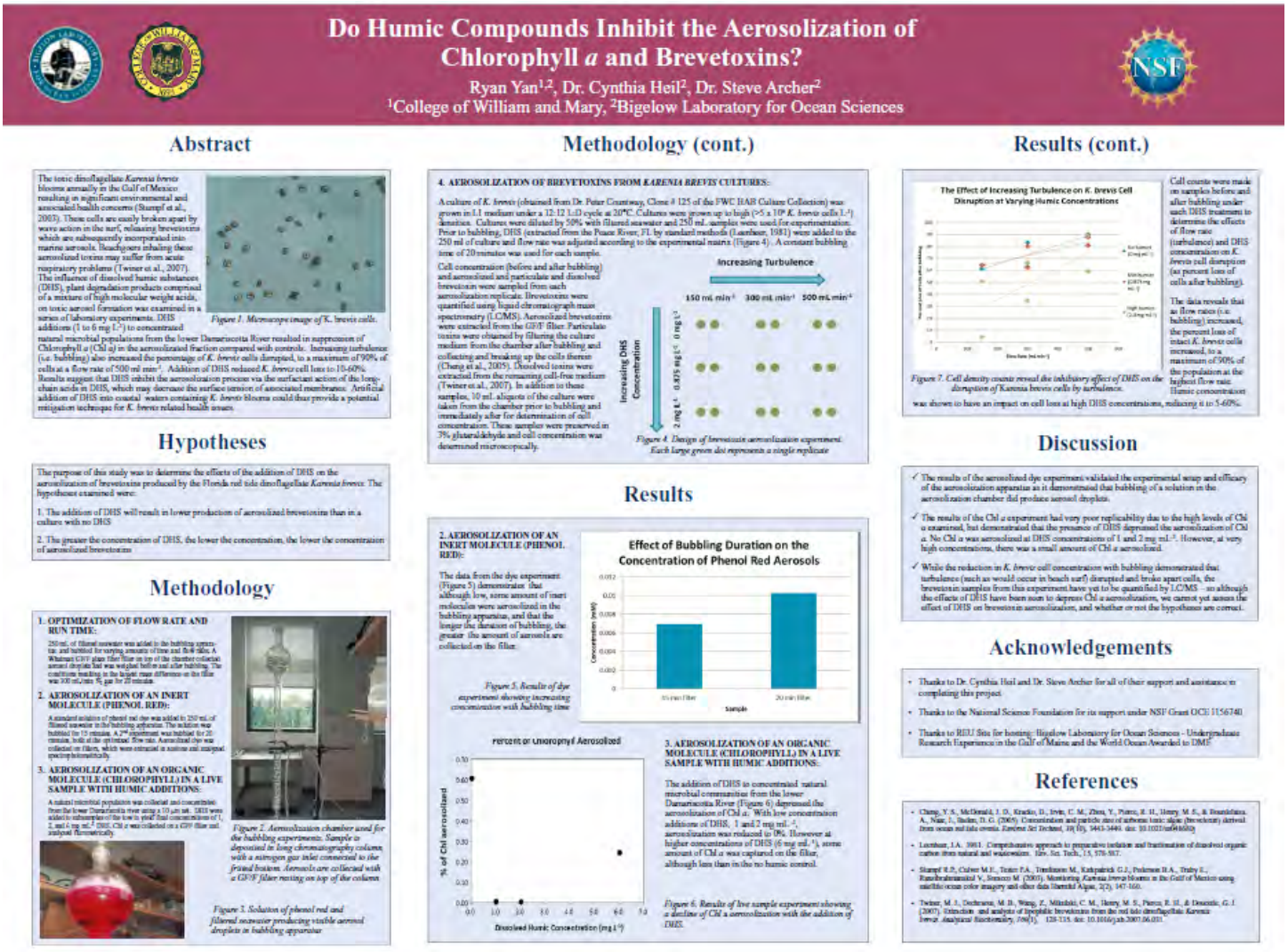


Increased pCO_2 in the world's oceans is resulting in a decrease of seawater pH, termed ocean acidification, that is affecting many biogeochemical processes. In this project, I investigated the effects of varied pCO_2 levels on the amount of dimethylsulfide (DMS) released from, and the amount of dimethylsulfoniopropionate (DMSP) produced by the dinoflagellate *Heterocapsa triquetria*. Cultures were bubbled with CO_2 at levels of 280ppm - representing pre-industrial levels, 380ppm -representing current levels, and 750ppm - representing IPCC Special Report on Emissions Scenarios projected levels for the year 2100. *H. triquetria* released DMS and extracellular (dissolved) DMSP at a higher rate when exposed to both the pre-industrial level treatment and to the expected year 2100 treatment. Intracellular (particulate) DMSP production decreased with increasing pCO_2. Growth rates of *H. triquetria* based upon the production of intracellular and extracellular DMSP were higher than growth rates based on cell abundance. This suggests enhanced production of DMSP. Mesocosm studies on the effects of ocean acidification on sulfur containing compounds released from phytoplankton have had contrasting results, thought to possibly be the result of varied species composition (Archer, S. D. 2010).

DO HUMIC COMPOUNDS INHIBIT THE AEROSOLIZATION OF CHLOROPHYLL *A* AND BREVETOXINS?

Ryan Yan[1,2], Dr. Cynthia Heil[2], Dr. Steve Archer[2]
[1]College of William and Mary, [2]Bigelow Laboratory for Ocean Sciences

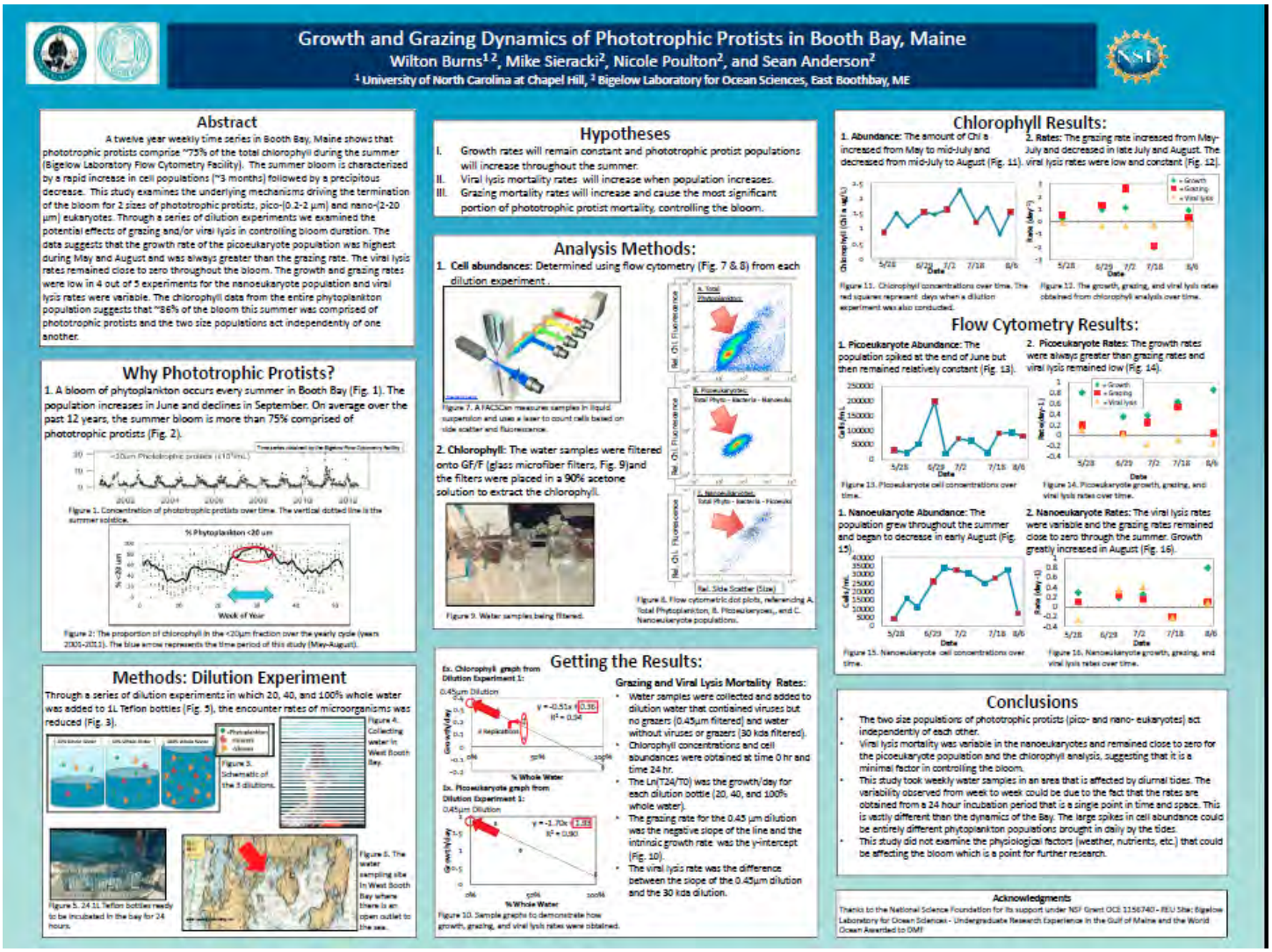
The toxic dinoflagellate *Karenia brevis* blooms annually in the Gulf of Mexico resulting in significant environmental and associated health concerns (Stumpf et al., 2003). These cells are easily broken apart in the surf, releasing brevetoxins which are subsequently incorporated into marine aerosols. Beachgoers inhaling these aerosolized toxins may suffer from acute respiratory problems (Twiner et al., 2007). The influence of dissolved humic substances (DHS), plant degradation products comprised of a mixture of high molecular weight acids, on aerosol formation was examined in a series of laboratory experiments. DHS additions to microbial populations from the lower Damariscotta River resulted in suppression of Chlorophyll *a* in the aerosolized fraction compared with controls. Increasing turbulence also increased the percentage of *K. brevis* cells disrupted, to a maximum of 90% of cells at a flow rate of 500 ml min^{-1}. Addition of DHS reduced *K. brevis* cell loss to 10-60%. Results suggest that DHS inhibit the aerosolization process via the surfactant action of the long-chain acids in DHS, which may decrease the surface tension of associated membranes. Artificial addition of DHS into coastal waters containing *K. brevis* blooms could thus provide a potential mitigation technique for bloom related health issues.



GROWTH AND GRAZING DYNAMICS OF PHOTOTROPHIC PROTISTS IN BOOTH BAY, MAINE

Wilton Burns[1,2] Mike Sieracki[2]
[1]University of North Carolina at Chapel Hill, [2]Bigelow Laboratory for Ocean Sciences

This study focuses on two sizes of phototrophic protists that bloom every summer in Booth Bay, Maine. Phototrophic protists are unicellular eukaryotes that have compromised over 75% of the total chlorophyll for the past 10 years during the bloom (from a time series done by the Bigelow Flow Cytometry Lab). Every year the bloom is controlled around September and through a series of dilution experiments in which 20, 40, and 100% whole water are added to water containing just viruses and water without viruses and grazers, the encounter rates of the microorganisms are altered and it can be determined whether viral lysis or grazing by predators is more important in the termination of the bloom. The picoeukaryote population declined, the growth and grazing rates increased, and the viral lysis rates remained low. The viral lysis and grazing rates of the nanoeukaryotes stayed relatively constant but the population grew throughout the summer. The chlorophyll data showed that 86% of the total chlorophyll came from phototrophic protists and it did not reflect the individual populations, as they act independently from each other.



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