53rd Annual
Northeast Algal Symposium

SALVE REGINA UNIVERSITY

Newport, RI
25-27 April 2014

2014 Northeast Algal Symposium Sponsors

Roger Williams University

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The 2014 NEAS logos were designed by Kathryn Hurley. Hurley graduated from Roger Williams University in 2012 with a B.A. in Marine Biology and a minor in Visual Arts, focusing on scientific illustration. Directly after graduation, she became an Aquarist and Trainer at the Maritime Aquarium in Norwalk, Connecticut. She has recently moved back to Plymouth Massachusetts where she is an Assistant Biologist for Smithers Viscient. http://kathrynhurleyartwork.blogspot.com.

Table of Contents

Acknowledgements

The co-conveners acknowledge the generous support of our sponsors for this event, Salve Regina University, Roger Williams University (Feinstein School of Arts & Sciences, and the Department of Biology, Marine Biology & Environmental Science), and FMC (Erick Ask). We thank Katie Hurley for providing the rockweed illustrations that adorn the NEAS communications and symposium memorabilia this year, as well as undergraduate volunteers from RWU, RIC and SRU for their assistance in registration and AV support. We also thank Events Coordinator Mariann Maida from Salve Regina University and Nancy Rusiloski at the Hotel Viking for logistical support for this meeting. For their careful review of presentations, we thank the NEAS Student Award Judges: Greg Boyer, Mark Cock, Ken Karol, and Ursula Röse (Wilce Graduate Oral Award Committee), Kyatt Dixon, Larry Liddle, and Amy Carlile (Trainor (Graduate Poster Award Committee), David Domozych, Karolina Fučíková, Carol Thornber, and John Wehr (President's Undergraduate Presentation (oral & poster) Award Committee). We also wish to thank session moderators: Louise Lewis, Gina Filloramo, Meghann Bruce, Morgan Vis, Craig Schneider, and Curt Pueschel. Finally, we are especially grateful to our mini-symposium speakers, J. Mark Cock, David Domozych, and Alexander Jüterbock who have traveled far and wide to share their expertise with the NEAS membership.

With sincere thanks from your co-Conveners,

Brian Wysor,	Eric Roberts,	JD Swanson,
Roger Williams University	Rhode Island College	Salve Regina University

Welcome to Newport and the 53rd Annual Northeast Algal Symposium! We're glad you are here! We have an exciting professional and social program lined up to exchange ideas and share your latest research findings on all things algae. The social program commences on Friday night from 6-9pm. With participation from phycologists representing 5 countries and 12 states and provinces, this will be a great time to re-unite with colleagues and make new friends, while sharing Hors d'oeuvres at the beautiful Ochre Court. If the weather is nice, you can enjoy the terrace overlooking the Atlantic Ocean and visit the famous Cliff Walk.

The scientific program kicks off on Saturday morning @ 8:15am with opening remarks and we will commence graduate student oral presentations at 8:30 am. The afternoon will be capped with a Poster mixer including a one-hour cash bar, before we settle in at the Hotel Viking for an elegant dinner and the *famous* NEAS auction. This event is a major source of revenue for student activities that NEAS funds. Please participate liberally and spend with reckless abandon!

The theme of the Sunday morning mini-symposium is "*Algae as model systems*" and we are excited to have as keynote speakers Dr. J. Mark Cock (Algal Genetics Group, Station Biologique de Roscoff, France), Dr. David Domozych, (Skidmore College Microscopy Imaging Center) and Dr. Alexander Jüterbock (Marine Ecology Research Group, Faculty of Biosciences and Aquaculture, University of Nordland, Norway). Our speakers will share their expertise on the evolution of complexity in plants, the biosynthesis of cell walls, and global climate change in marine communities from the perspective of *algae as model systems*, and everyone is invited to participate in a panel discussion immediately following the delivery of keynote talks.

The meeting will close, as usual, with the business meeting where all members will have an opportunity to voice their ideas regarding NEAS missions. Our meeting will conclude with the annual Business Meeting on Sunday, followed by lunch before we meet again in 2015. Please take time to vote in society elections and consider serving NEAS in an elected role in the future. Please see p. 6-7 for your ballot, and remember all meeting participants are members and therefore eligible to vote.

Best wishes for a wonderful weekend!

Brian Wysor, Eric Roberts & JD Swanson
2014 Co-conveners

NEAS EXECUTIVE COMMITTEE & OFFICERS 2013-2014

Office	Officer	Term
President	Peter A. Siver Connecticut College pasiv@conncoll.edu	2011-2012 as Vice President 2012-2014 as President
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	Jonathan Neilson University of New Brunswick f5yrn@unb.ca	2013-2014

THE NORTHEAST ALGAL SOCIETY ELECTION BALLOT (APRIL 25 – 27, 2014)

I am a student member	
I am a non-student member	

Candidates for Nominations Committee Chair

1. Sean Grace	
1. Dale Holen	
1. Molly Letsch	
1. Sarah Redmond	
1. I don't want to vote for any candidate above because	**2**

2. I don't know the candidates	**3**
2. I can't find an appropriate candidate for the position	
2. I simply don't care	

3. I would have voted if more information about candidates were provided	
3. I would have voted only if someone I knew directly was nominated	
3. I would have voted if… (your comments here)	

SEAN GRACE: I am an associate professor and the graduate coordinator in the Department of Biology at Southern Connecticut State University in New Haven, CT. I graduated from the University of Rhode Island with a Ph.D. in Biological Sciences (Marine Ecology/Biology). My research focused on the subtidal competition between the temperate coral *Astrangia poculata* and macroalgae (both *Chondrus crispus* and *Saccharina latissima*). As a graduate student, I benefited through NEAS directly with a Wilce Award that allowed me to complete some of my field work. Since then, I have had several graduate students who have completed work on macroalgae and have benefited directly from NEAS through presentations at the yearly meetings. I like what NEAS has accomplished, enjoy the meetings when I can attend and look forward to the future of the society. Currently, I am the only marine ecologist at SCSU's Biology Department which means my research lab has been full of students with varied research interests, though I maintain my own interests in the ecology of near-shore shallow water marine communities (corals and macroalgae). It would be an honor to be chosen and I will do my best to serve and represent NEAS and all the positive qualities that it embodies.

DALE HOLEN: I am an Associate Professor of Biology at Penn State University – Worthington Scranton and am starting my 20th year in academia. I teach courses in microbiology, evolution, cell biology and lake and stream ecology. My research interests pertain to mixotrophic algae/protists and their functional role in lakes. More specifically I study the relative contributions of phagotrophy and phototrophy to growth of these ubiquitous microorganisms. More recently I've begun to study stomatocyst production in chrysophyte algae as little is known about the environmental factors associated with cyst induction. As only 5% of the stomatocysts have been identified, inducing cyst formation in known species while in laboratory culture enables the coupling of stomatocyst morphotypes to their biological origin. I live Dalton, PA a small rural community of 1400 that is almost like living in Mayberry, for those old enough to remember. I'm married with two children and twin grandchildren. We co-habit with two dogs and three cats. For leisure I enjoy reading, running, working in the yard, restoring old furniture and chasing with my grandchildren. I first became a NEAS member around the mid-1990s.

MOLLY LETSCH: I have been a member of the Northeast Algal Society since 2004. I participated in my first NEAS meeting as an undergraduate student and continued to attend every year as a graduate student. I was the Graduate Student Board member in 2010-2011 and appreciated getting to know more about how NEAS is run. I would be pleased to serve as the Nominations Chair for the society. I completed my Ph.D. in Ecology and Evolution at the University of Connecticut in the fall of 2011 and I am currently an adjunct professor in the department of Biological Sciences at Le Moyne College, Syracuse, NY. I was recently recruited to assist in organizing NEAS 2015.

SARAH REDMOND: Sarah Redmond is a seaweed-lover working in her home state of Maine as a Sea Grant Marine Extension Agent, providing education, outreach, and research for these valuable and amazing sea-plants. She works extensively both with the wild harvest seaweed fishery in Maine and with the new developing seaweed aquaculture industry. She operates a seaweed research nursery at the University of Maine's Center for Cooperative Aquaculture Research, where she is working with Dr. Susan Brawley to develop culture techniques for native sea vegetables. She received her Bachelor of Science in aquaculture from the University of Maine, and then studied under Dr. Charles Yarish at the Seaweed Marine Biotechnology Laboratory at the University of Connecticut. She enjoys sharing the beauty and joy of seaweed with others.

53rd Annual Northeast Algal Symposium
Salve Regina University

	Friday, 25 April 2014
10:00 am – 4:00 pm	Laboratory Manual Workshop at Roger Williams University (contact bwysor@rwu.edu for details)
TBD	Pre-Symposium Collecting Trip (contact clane@uri.edu for details)
6:00 pm – 9:00 pm	NEAS Welcome Mixer, Evening Registration & Auction Donation Ochre Court, Salve Regina University. (Parking on Webster Street)

	Saturday, 26 April 2014
7:00 am–8:00 am	Continental Breakfast, Morning Registration, Poster Set-up, & Auction Donation Antone Academic Center
7:30 am–8:00 am	Session I & II load presentations
8:15 am–8:30 am	Welcome & Opening Remarks – Brian Wysor, Eric Roberts & JD Swanson Antone Academic Center
Session I	**STUDENT PRESENTATIONS, Moderator: Louise Lewis**
8:30 am–8:45 am	*Wilce Award Candidate* Caroline Longtin & Gary W. Saunders. ON THE UTILITY OF MUCILAGE DUCTS AS A TAXONOMIC CHARACTER IN *LAMINARIA* AND *SACCHARINA*—THE CONUNDRUM OF *S. GROENLANDICA*.
8:45 am–9:00 am	*Wilce Award Candidate* Gina V. Filloramo & Gary W. Saunders. USING MULTIGENE PHYLOGENETCS AND NOVEL RECONSTRUCTION TECHNIQUES TO IMPROVE SUPRAGENERIC RESOLUTION IN RHODYMENIALES.

9:00 am–9:15 am	*Wilce Award Candidate* Samuel A. Drerup & Morgan L. Vis. ACID MINE DRAINAGE REMEDIATION ASSESSMENT USING BIOFILM STRUCTURE AND FUNCTION.
9:15 am–9:30 am	*Wilce Award Candidate* Elaine E. Potter, Carol S. Thornber, J.D. Swanson & Katharine Egan. LIFE CYCLE DYNAMICS OF *ULVA* SPP. IN NARRAGANSETT BAY, RI.
9:30 am–9:45 am	*Wilce Award Candidate* Robin Sleith, J.D. Hall, R.M. McCourt & K.G. Karol. THE INVASIVE MACROALGA *NITELLOPSIS OBTUSA* (N. A. DESVAUX) J. GROVES (CHARACEAE, CHAROPHYCEAE) IN NEW YORK STATE.
9:45 am–10:00 am	*Wilce Award Candidate* Eric Salomaki & Chris Lane. A GENOMIC SURVEY OF THE PARASITIC RHODOPHYTE *CHOREOCOLAX POLYSIPHONIAE* AND ITS HOST *VERTEBRATA LANOSA*.
10:00 am–10:15 am	*Wilce Award Candidate* Aleatha X. Lee & Aurora M. Nedelcu. *VOLVOX CARTERI* AS A MODEL-SYSTEM FOR CANCER RESEARCH.
10:15 am–10:30 am	*Coffee Break*
Session II	**STUDENT PRESENTATIONS, Moderator: Gina Filloramo**
10:30 am–10:45 am	*Wilce Award Candidate* Lesleigh Kraft & Gary W. Saunders. THE GENUS *TSENGIA* IN TROPICAL AND TEMPERATE AUSTRALIAN WATERS.
10:45 am–11:00 am	*Wilce Award Candidate* Lindsay A. Green & Christopher D. Neefus. THE EFFECTS OF LONG-TERM FREEZING ON *PORPHYRA UMBILICALIS* KÜTZING (BANGIALES, RHODOPHYTA) BLADE VIABILITY.

11:00 am–11:15 am *Wilce Award Candidate*
Amanda Savoie & Gary W. Saunders. THE EVIDENCE FOR INTROGRESSION BETWEEN AN INTRODUCED RED ALGA AND A CLOSELY RELATED NATIVE SPECIES (*NEOSIPHONIA JAPONICA* AND *N. HARVEY*I) IN THE NORTHWEST ATLANTIC.

11:15 am–11:30 am *Wilce Award Candidate*
Thea R. Popolizio, Craig W. Schneider & Christopher E. Lane. NEMALIALES (RHODOPHYTA) OF THE BERMUDA ISLANDS: MORE ADDITIONS TO A SMALL ARCHIPELAGO'S ACCUMULATING MACROALGAL DIVERSITY**.**

11:30 am–11:45 am *Wilce Award Candidate*
Jonathan Neilson & Dion Durnford. DECIPHERING THE COMPLEXITIES OF ANTENNA EVOLUTION: A NEW APPROACH FOR RECOGNIZING AND ANALYZING THE LHC PROTEIN FAMILY.

11:45 am–12:00 pm *Wilce Award Candidate*
Meghann B. Bruce & Gary W. Saunders. A MOLECULAR-ASSISTED INVESTIGATION OF DIVERSITY, BIOGEOGRAPHY AND EVOLUTIONARY RELATIONSHIPS FOR SPECIES OF *NEOPTILOTA* AND *PTILOTA* (WRANGELIACEAE, RHODOPHYTA) IN CANADIAN WATERS.

12:00 pm–1:30 pm Lunch at Miley Hall
Executive Committee Luncheon in Antone Academic Center

1:00 pm–1:30 pm Session III & IV Speakers load presentations

Session III **Student Presentations, Moderator: Meghann Bruce**
Antone Academic Center

1:30 pm–1:45 pm *Wilce Award Candidate*
Sarah B. Whorley & John D. Wehr. INTERANNUAL VARIATION OF PERIPHYTON TAXONOMIC COMPOSITION AND FATTY ACID PROFILES UNDER AGRICULTURAL STRESS.

1:45 pm–2:00 pm *Wilce Award Candidate*
Christine Newton, Annick Drouin & Matthew E.S. Bracken. CHANGES IN ALGAL BIODIVERSITY ALTER CRITICAL ECOSYSTEM FUNCTIONS AFTER RECENT INVASION OF *HETEROSIPHONIA JAPONICA* IN NEAR-SHORE ENVIRONMENTS.

2:00 pm–2:15 pm	*Wilce Award Candidate* Renée L. Eriksen, Lindsay A. Green & Anita S. Klein. POPULATION DIFFERENCES AND ORGANISM-ENVIRONMENT INTERACTIONS IN NATURAL ASEXUAL POPULATIONS OF *PORPHYRA UMBILICALIS* KÜTZING RHODOPHYTA.
2:15 pm–2:30 pm	*President's Award Candidate* Amy Havens, Amy Carlile & Alison Sherwood. MOLECULAR PHYLOGENY AND MORPHOLOGICAL ANALYSIS OF THE GENUS *RHIZOCLONIUM* (CLADOPHORALES, CHLOROPHYTA) IN HAWAII.
2:30 pm–2:45 pm	*President's Award Candidate* Nels Christensen, Peter A. Siver, Anne-Marie Lott & Alex P. Wolfe. POTENTIAL USE OF CHRYSOPHYTE CYST MORPHOMETRICS AS A TOOL FOR RECONSTRUCTING ARCTIC EOCENE ENVIRONMENTS.
2:45 pm–3:00 pm	*Coffee Break*
Session IV	**Contributed Presentations, Moderator: Morgan Vis**
3:00 pm–3:15 pm	*President's Award Candidate* Afsah Chohan, John D. Hall & Hilary A. McManus**.** DEFINING THE DIVERSITY OF *BOTRYOCOCCUS* (TREBOUXIOPHYCEAE, CHLOROPHYTA).
3:15 pm–3:30 pm	*President's Award Candidate* Nikolaus E. Schultz, Craig W. Schneider, Christopher E. Lane, Line Le Gall, Florence Rousseau & Bruno de Reviers**.** MOLECULAR-ASSISTED ALPHA TAXONOMY REVEALS NEW GENETIC SPECIES OF THE GENUS *LOBOPHORA* (DICTYOTALES, PHAEOPHYCEAE) IN THE TROPICAL WESTERN ATLANTIC.
3:30 pm–3:45 pm	*President's Award Candidate* Noe B. Mercado, Timothy S. Roosa, Tania Aires, Hope Allen, Carol S. Thornber & J.D. Swanson. ELUCIDATION OF *LhcSR* GENE EXPRESSION IN THE MACROALGAE, *ULVA RIGIDA* AND *ULVA COMPRESSA*.
3:45 pm–4:00 pm	*President's Award Candidate* Shennel Gelin, Carol S. Thornber & J.D. Swanson. TRANSCRIPTOME ANALYSIS OF THE GENETIC MAKEUP OF MACROALGAL *ULVA* BLOOMS.
4:00 pm–4:15 pm	Jordan Bishop, Peter Siver & Anne-Marie Lott. EVALUATING TRENDS IN VALVE SHAPE IN EUNOTIA BY COMPARING FOSSIL AND MODERN

	SPECIES.
4:15 pm–4:30 pm	Daniel J. Sanchez & Hilary A. McManus. EXAMINING CHLOROPLAST GENOMES IN THE ORDER SPHAEROPLEALES.

Session V	**Student & Professional Contributed Posters Session & Mixer**
4:30 pm–6:30 pm	**Antone Academic Center**
4:30 pm–5:30 pm	Open Bar
5:30 pm–6:30 pm	Cash Bar

7:00 pm–11:00 pm	NEAS Banquet, Awards & Live Auction Hotel Viking

Sunday, 27 April 2014

7:00 am–8:00 am	Continental Breakfast & Poster Removal (Please remove posters by noon on Sunday)
7:30 am–8:00 am	Session VI & VII speakers load presentations
8:00 am–8:10 am	Announcements – Brian Wysor, Eric Roberts & JD Swanson

Session VI	**Mini-Symposium: *Algae as Model Systems*** **Moderator: Craig Schneider**
8:10 am–8:50 am	David S. Domozych. DECIPHERING THE SECRETS OF THE PLANT CELL WALL THROUGH THE CHAROPHYTE MODEL ORGANISM, *PENIUM MARGARITACEUM*.
8:50 am–9:30 am	J. Mark Cock. LIFE CYCLE REGULATION AND THE EMERGENCE OF COMPLEX MULTICELLULARITY IN THE BROWN ALGAE.
9:30 am–10:10 am	Alexander Jüterbock. SEAWEED MEADOWS IN THE LIGHT OF GLOBAL CLIMATE CHANGE.
10:10 am–10:50 am	Panel Discussion: *Algae as Model Systems* Mark Cock, David Domozych, Alexander Jüterbock
10:50 am–11:00 am	*Coffee Break*

Session VII	**Contributed Presentations, Moderator: Curt Pueschel**
11:00 am–11:15 am	Stephen D. Gottschalk, Naveed Davoodian, Sarah N. Dutton, Juli A. Janis, Beryl C. M. Kahn, Theodore D. Kirkinis, Eli Min, Jonathan W. Toll & Kenneth G. Karol**.** THE MACROALGAE DIGITIZATION PROJECT: ADVANCING ONLINE ALGAL COLLECTIONS AT THE NEW YORK BOTANICAL GARDEN AND BEYOND.
11:15 am–11:30 am	José A. Zertuche-González, D. Craig Barilotti, José M. Guzmán-Calderón, Zarko Altamirano-Gómez, Mariana Sánchez-Barredo & Isaí Pacheco-Ruiz. SITE EVALUATION AND THE DEVELOPMENT OF METHODS FOR FARMING *MACROCYSTIS PYRIFERA* OFF THE PACIFIC COAST OF BAJA CALIFORNIA.
11:30 am–11:45 am	Kyatt Dixon & Gary W. Saunders. ASSESSING MONOPHYLY IN THE DUMONTIACEAE WITH AN EMPHASIS ON CRUSTOSE MEMBERS.
11:45 am–12:00 pm	Ursula S.R. Röse & Janithri Wickramanayake. EMISSION OF VOLATILE COMPOUNDS IN *FUCUS VESICULOSUS*.
12:00 pm–12:15 pm	Jang K. Kim, George P. Kraemer & Charles Yarish. SUGAR KELP AQUACULTURE: A COASTAL MANAGEMENT TOOL AND NEW BUSINESS OPPORTUNITIES IN LONG ISLAND SOUND AND NEW YORK COASTAL WATERS.
12:15 pm–1:30 pm	Closing Remarks & General Business Meeting Lunch at Miley Hall

ABSTRACTS

(WA[1]) 8:30 – 8:45 pm **ON THE UTILITY OF MUCILAGE DUCTS AS A TAXONOMIC CHARACTER IN *LAMINARIA* AND *SACCHARINA*—THE CONUNDRUM OF *S. GROENLANDICA*.** Caroline Longtin & Gary W. Saunders. Centre for Environmental & Molecular Algal Research, Department of Biology, University of New Brunswick, Fredericton, NB, E3B 5A3, Canada.
The use of mucilage ducts as a taxonomic character in *Laminaria* and *Saccharina* has been a source of confusion for years. For example, two of four plants in Rosenvinge's type collection of *S. groenlandica* were subsequently considered to be *S. latissima* despite these species reportedly having distinct mucilage duct features. The objectives of this study were to: 1) determine whether mucilage ducts are a useful taxonomic character for species differentiation in these genera emphasizing the North Atlantic flora; 2) verify the taxonomic status of *S. groenlandica* and the appropriateness of its current application to a North American genetic species; and 3) determine the full geographic range of the last mentioned genetic group. Through microscopy of genetically verified collections we have determined that the presence/ absence of mucilage ducts in the blade is variable and thus not taxonomically useful, whereas their presence/ absence and distribution in the stipe is species specific. Examination of type material reveals that *S. groenlandica* is synonymous with *S. latissima,* reported mucilage ducts in the former are actually manifestations of infections. Examination of *L. nigripes* type material revealed a combination of misidentified *L. digitata* and one specimen that matched the North American genetic material currently attributed to *S. groenlandica*. We thus assign the North American genetic group currently attributed to *S. groenlandica* to *Saccharina nigripes* (J. Agardh) C. Longtin et G.W. Saunders comb. nov.—a species distributed in the Northeast Pacific, Canadian Arctic, Northwest Atlantic, and Northern Europe.

(*WA*) 8:45 – 9:00 am **USING MULTIGENE PHYLOGENETCS AND NOVEL RECONSTRUCTION TECHNIQUES TO IMPROVE SUPRAGENERIC RESOLUTION IN RHODYMENIALES.** Gina V. Filloramo & Gary W. Saunders. Centre for Environmental & Molecular Algal Research, Department of Biology, University of New Brunswick, Fredericton, New Brunswick, Canada.

Schmitz established the Rhodymeniales in 1892 for procarpic Florideophyceae with outward carposporophyte development. Since inception, numerous taxonomic revisions were proposed based on the subjective interpretation of vegetative and reproductive characteristics. Application of molecular tools subsequently provided an objective means to test the classical morphology-based taxonomy. The first molecular assessment used small subunit ribosomal DNA, which confirmed monophyly for the order, but failed to resolve family-level relationships. Subsequent studies combined large subunit ribosomal DNA and elongation factor2 sequences to distinguish the six currently recognized families, viz., Rhodymeniaceae, Lomentariaceae, Champiaceae, Faucheaceae, Hymenocladiaceae and Fryeellaceae, establishing a more natural system of classification. However, relationships among most families remained unresolved. In conjunction with the RedToL project, the objective of the current study was to reassess rhodymenialean systematics by adding taxa

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[1] WA = Wilce Graduate Oral Award

and using a more robust multigene dataset of plastid, mitochondrial and nuclear markers. To prevent phylogenetic inference problems associated with substitution saturation, a series of progressively more conservative alignments was generated and analyzed using Maximum Likelihood. Results will be discussed with particular emphasis on the systematic affiliations of taxa whose family-level assignments are currently unclear.

(*WA*) 9:00 – 9:15 am **ACID MINE DRAINAGE REMEDIATION ASSESSMENT USING BIOFILM STRUCTURE AND FUNCTION.** Samuel A. Drerup & Morgan L. Vis. Environmental and Plant Biology, Ohio University, Athens, Ohio, 45701, USA.

Acid mine drainage (AMD) impacts many streams throughout the Appalachian region. Remediation efforts have been successful in ameliorating water quality with elevated pH and decreased dissolved metals. In many streams, there has been biological recovery in terms of restored algal, invertebrate, and fish assemblages, but success is not universal. The goal of restoration is to improve not only biological diversity, but also stream function. We compared biofilm community structure using phospholipid fatty acid (PLFA) profiles and biofilm function (productivity and respiration, extracellular enzyme activity, and C:N:P) from three stream categories (5 unimpaired, 5 AMD-impaired, and 5 AMD-remediated) in southeastern Ohio. Biofilm communities in unimpaired and AMD-impaired streams were successfully separated using PLFA profiles. However, AMD-remediated streams showed similarities to both unimpaired and AMD-impaired communities. AMD-impaired and AMD-remediated sites had the lowest concentrations of chlorophyll a and the lowest rates of productivity and respiration. Interestingly, no significant difference was observed in microbial biomass or ash free dry mass between stream categories. AMD-impacted and AMD-remediated sites had significantly lower soluble reactive phosphorus concentration as well as biofilm phosphorus content compared to unimpaired sites. Extracellular enzyme activities showed and increase in the ratio of phosphorous:nitrogen acquiring enzymes in impaired and AMD-remediated sites. Our results suggest phosphorus limitation is occurring AMD-impaired and AMD-remediated streams, potentially limiting or delaying biotic recovery.

(*WA*) 9:15 – 9:30 am **LIFE CYCLE DYNAMICS OF *ULVA* SPP. IN NARRAGANSETT BAY, RI.** Elaine E. Potter[1], Carol S. Thornber[1], J.D. Swanson[2] & Katharine Egan[1]. [1]Biological Sciences, University of Rhode Island, Kingston, RI, 02881, USA; [2]Biology and Biomedical Sciences, Salve Regina University, Newport, RI, 02840, USA.

Macroalgal blooms occur worldwide and have the potential to cause severe ecological and economic damage. Narragansett Bay, RI is a eutrophic system that experiences summer macroalgal blooms composed mostly of *Ulva compressa* and *Ulva rigida*. All *Ulva* species have isomorphic, biphasic life cycles, and the relative contribution of the haploid and diploid life history stages to bloom formation is poorly understood. We first developed flow cytometry protocols to assess the ploidy of individual *Ulva* thalli. We then assessed the ploidy levels of *U. compressa* and *U. rigida* populations from five sites in Narragansett Bay, RI in June through October 2013. For each species during each month we sampled, both haploid gametophytes and diploid sporophytes were present. We found a large variability among sites, but our data do not match modeling predictions of gametophyte dominance when the phases are ecologically identical. In addition to ploidy analysis, we conducted growth and cell size experiments to investigate ecological differences among ploidy levels. We found no differences in growth rates between ploidy levels. However, we found differences between cell sizes, with the diploid sporophyte having significantly larger cells than the haploid gametophyte in *U. compressa*. This is the first study to identify gametophytes and sporophyte population-level data for *Ulva* in Narragansett Bay.

(*WA*) 9:30 – 9:45 am **THE INVASIVE MACROALGA *NITELLOPSIS OBTUSA* (N. A. DESVAUX) J. GROVES (CHARACEAE, CHAROPHYCEAE) IN NEW YORK STATE.** Robin Sleith[1], John D. Hall[2], Richard M. McCourt[3] & Kenneth G. Karol[1]. [1]The New York Botanical Garden, Bronx, NY, 10458, USA; [2]The University of Maryland, College Park, MD, 20742, USA; [3]Drexel University, Philadelphia, PA, 19104, USA.

Nitellopsis obtusa (Characeae) is a freshwater green alga rare in its native Eurasian range but considered invasive in North America. *Nitellopsis* was first reported in the Saint Lawrence River, NY in 1978, and by 1983 it was recorded in Lake St. Clair, MI. Recent reports include inland lakes in Michigan, northern Indiana, and northern New York. *Nitellopsis* outcompetes native aquatic vegetation and inhibits fish spawning. It is a nuisance in lakes with recreational value, clogging swimming areas and fouling boat motors. We assessed Characeae diversity across New York in areas with and without *Nitellopsis* to better understand the impact of this exotic on native communities. We combined recent collections with historic and published records to report *Nitellopsis* in 17 counties in NY. Our efforts added one county (Yates) and four lakes previously not known to contain *Nitellopsis*. We used niche modeling to test how abiotic factors are correlated with the presence or absence of *Nitellopsis* and will discuss how these results can be used by lake managers and conservationists to understand and control the spread of *Nitellopsis*.

(*WA*) 9:45 – 10:00 am **A GENOMIC SURVEY OF THE PARASITIC RHODOPHYTE *CHOREOCOLAX POLYSIPHONIAE* AND ITS HOST *VERTEBRATA LANOSA*.** Eric Salomaki & Chris Lane. Department of Biological Sciences, University of Rhode Island, Kingston, RI, 02881, USA.

Parasitism is a life strategy that has independently evolved countless times throughout the eukaryotic tree of life, however most parasitic lineages are distantly related from a free-living taxon making comparative studies difficult. Rhodophytes have an evolutionary gradient of parasites and their free-living hosts, providing an ideal framework to study the genomic consequences of an organism shifting from a free-living to a parasitic life strategy. Additionally, red algal parasites do not maintain their own plastid and instead hijack and maintain a photosynthetically inactive plastid from the host. In typical eukaryotic parasites non-essential genes are lost, as they rely on a host for energy and nutrition. Red algal parasites have never been examined at the genome level and mechanisms for their lifestyle change are unknown. To gain insight into the evolution of parasitism we are conducting a genomic survey of a parasite and host pair from the Rhodomelaceae. Genomic data from *Choreocolax polysiphoniae* and its host *Vertebrata lanosa* and the implications for the evolution of parasitism will be discussed, including the loss of genes related to plastid maintenance in the parasite.

(WA) 10:00 – 10:15 am ***VOLVOX CARTERI* AS A MODEL-SYSTEM FOR CANCER RESEARCH.** Aleatha X. Lee & Aurora M. Nedelcu. University of New Brunswick, Fredericton, NB, E3B 1Y9 Canada.

The stability of all multicellular organisms is dependent on cooperation among the various cell types. However, cooperation sets the stage for cheating, and cancer is a premier example of selfishness at the cell level. To prevent cheating, a variety of mechanisms have evolved in multicellular organisms. One mechanism that can favor/stabilize cooperation is antagonistic pleiotropy. Specifically, cooperation is more likely to be stable if cooperation genes influence two traits in opposite ways, such that the loss of the cooperative trait will negatively affect the other trait. As cancer cells are mutated in one or more cooperation genes, we hypothesize that cancer cells' short-term gain in terms of replication comes with a cost in other aspects of fitness. To address this hypothesis we are using *Volvox carteri*—a simple multicellular alga comprised of only two cell types: reproductive (immortal) cells and non-dividing somatic (mortal) cells. One gene—*reg*A—appears to be necessary and sufficient to suppress the replication of somatic cells; single mutations in this gene render the somatic cells immortal (cancer-like cells). In this context, *reg*A can be considered both a cooperation gene and a tumor suppressor gene. Under the above hypothesis, we predict that although mutations in *reg*A have a positive effect on cell reproduction, they will negatively affect cell survival in certain settings. Once such conditions are identified, they can be used to decrease the fitness of these *V. carteri reg*A mutants. We are currently using two *reg*A mutants and are assessing the effect of various environmental stresses on their fitness relative to the wild-type. Our preliminary data suggest that, relative to the wild-type, *reg*A mutants are more sensitive to changes in environmental conditions. These results support our hypothesis and provide proof of principle for developing therapeutic strategies that take advantage of the evolutionary vulnerabilities of cancer cells by exposing their weaknesses. As such, *V. carteri* can be used as a model-system for cancer research.

10:15 – 10:30 Coffee Break

(WA) 10:30 – 10:45 am **THE GENUS *TSENGIA* IN TROPICAL AND TEMPERATE AUSTRALIAN WATERS.** Lesleigh Kraft & Gary W. Saunders. Centre for Environmental and Molecular Algal Research, Department of Biology, University of New Brunswick, Fredericton, NB, E3B 5A3, Canada.

Since 1994, the genus *Tsengia* in Australia has been represented in the literature by three species: *T. comosa*, *T. feredayae* and *T. laingii*; the two former having type localities from Victoria and Tasmania, respectively, and the last mentioned with a New Zealand type locality. However, a DNA barcode survey of 43 *Tsengia* samples collected from South Australia and Tasmania in the temperate southeast to Lord Howe and Norfolk Islands off the eastern coast of Australia revealed eight genetic species groups, including the three species currently recorded from Australia. Two of the novel genetic species groups were collected exclusively from Lord Howe Island, a location well established as a hotspot for red-algal species discovery and endemism in Australia. A further two genetic species groups were restricted to Tasmania. Tasmania is fast emerging as a location of rich rhodophyte biodiversity and species discovery, especially for halymenialean taxa. Presented here is an examination of the genus *Tsengia* in Australia, with an emphasis on species discovery, and with some nomenclatural suggestions.

(*WA*) 10:45 – 11:00 am **THE EFFECTS OF LONG-TERM FREEZING ON *PORPHYRA UMBILICALIS* KÜTZING (BANGIALES, RHODOPHYTA) BLADE VIABILITY.** Lindsay A. Green & Christopher D. Neefus. Department of Biological Sciences, University of New Hampshire, 46 College Road, Durham, NH, 03824, USA.

Seaweeds inhabiting the upper intertidal zone are subjected to a wide variety of temperature, light, and water stresses and vertical distribution has been correlated to environmental tolerance. *Porphyra umbilicalis* Kützing is an aseasonal red alga inhabiting the upper intertidal zone in temperate and subarctic regions of the North Atlantic. It is a member of the economically important group of foliose Bangiales, and has been the focus of research aimed at the development of an aquaculture industry in New England. The goal of this study was to assess whether frozen storage is a practical method of preservation for mass quantities of seed stock of *P. umbilicalis* by determining the effects of long-term freezing on blade viability. Cultured blades of *P. umbilicalis* (4.8 ±0.22 mg) were air dried to 30% or 5% absolute water content (AWC) and frozen for 1, 3, 6, or 12 months at -20°C or -80°C. Following freezing, blades were rehydrated and growth rate was measured weekly for 4 weeks. Photosynthetic efficiency (F_V/F_M) was assessed for each blade 3 hours and 4 weeks post-rehydration. AWC significantly affected growth rates but the effect was dependent on both freezing temperature and the length of freezing. Blades frozen at -80°C and 5% AWC showed the highest overall growth rate (8.03 ±0.16% day^{-1}), while blades frozen for 1 month at 5% AWC grew significantly slower (7.06 ±0.16% day^{-1}) than blades frozen for 3, 6, or 12 months at either AWC. Growth rates peaked two weeks post-rehydration followed by a small decline in weeks 3 and 4. Length of freezing significantly affected F_V/F_M 4 weeks post-rehydration with blades frozen for 6 months performing better than blades frozen for 12 months. There was 100% blade survival and both growth rates and F_V/F_M were equivalent to those recorded in non-frozen blades. Overall, these results indicate that long-term frozen storage has little physiological effect on blades of *P. umbilicalis* and is a practical method of preservation for mass quantities of seed stock.

(*WA*) 11:00 – 11:15 am **THE EVIDENCE FOR INTROGRESSION BETWEEN AN INTRODUCED RED ALGA AND A CLOSELY RELATED NATIVE SPECIES (*NEOSIPHONIA JAPONICA* AND *N. HARVEYI)* IN THE NORTHWEST ATLANTIC.** Amanda Savoie & Gary W. Saunders. Center for Environmental & Molecular Algal Research, Department of Biology, University of New Brunswick, Fredericton, N.B., E3B 5A3, Canada.

The Asian red alga *Neosiphonia japonica* was collected in Narragansett Bay, Rhode Island; this species is likely introduced to the Northwest Atlantic. In Japan, *N. japonica* is often epiphytic on *Grateloupia turuturu*, an invasive species that is well established in New England waters. Interestingly, three of five New England collections of *N. japonica* were found growing on *G. turuturu,* possibly indicating a co-introduction. The presence of *N.*

japonica in Rhode Island may have been overlooked because it is morphologically similar to the native species *N. harveyi*. We sequenced COI-5P and ITS for seven collections of *N. japonica* from Rhode Island and the Northwest Pacific, and for 45 collections of *N. harveyi* from New England and Atlantic Canada. We also sequenced *rbc*L for seven *N. harveyi* and four *N. japonica* collections to facilitate comparison to data available on GenBank. All three of these markers indicate that *N. harveyi* and *N. japonica* are separate but closely related species. However, the ITS sequences for some *N. harveyi* individuals show mixed patterns and additivity indicating introgression of nuclear DNA from *N. japonica*. Introgression of DNA from an introduced species to a native species (i.e. "genetic pollution") is often listed as one of the possible negative impacts of species introductions. Previously recorded in land plants and brown algae, we believe this is the first documented evidence for "genetic pollution" in red algae.

(*WA*) 11:15 – 11:30 am **NEMALIALES (RHODOPHYTA) OF THE BERMUDA ISLANDS: MORE ADDITIONS TO A SMALL ARCHIPELAGO'S ACCUMULATING MACROALGAL DIVERSITY.** Thea R. Popolizio[1], Craig W. Schneider[2] & Christopher E. Lane[1]. [1]Biological Sciences, University of Rhode Island, Kingston, RI, 02881, USA; [2]Department of Biology, Trinity College, Hartford, CT, 06106, USA.

Historically, seasonal water temperature oscillations (18°-28°C) in the Bermuda Islands have yielded an assemblage of warm-water tolerant, temperate North Atlantic species and largely cool-water tolerant Caribbean species carried northward via the Gulf Stream. Prior studies have demonstrated that macroalgal biodiversity is notably underestimated for the archipelago. We have undertaken a comprehensive, molecular-assisted alpha-taxonomic examination of the rhodophyte order Nemaliales, a group that has not previously been targeted for molecular studies of Bermuda's flora. Sequence data from several molecular markers indicate that taxonomic revisions are required for this group. These include the addition of three genera to the Liagoraceae in the Bermuda flora—*Yamadaella*, *Trichogloeopsis*, and putatively, the newly described *Hommersandiophycus*. The genus *Yamadaella* in Bermuda is represented by a novel species phylogenetically and morphologically distinct from the monotypic, Indo-Pacific *Y. caenomyce*. Sequences of *Trichogloeopsis pedicellata* from the type locality (Bahamas I. grouping) demonstrate the presence of this species in Bermuda. We have discovered that *Liagora pectinata* (type locality = Bermuda), first reported by Collins and Hervey (1917) is genetically allied with the Indo-Pacific genus *Hommersandiophycus*. Additionally, we have reassessed the historically reported species *Liagora ceranoides* for the islands, and find it to be genetically distinct from specimens collected in Florida and the Indo-Pacific. Sequence data has also revealed an unreported species in this clade, possibly a long-distance new record from the Indo-Pacific. In the Galaxauraceae, molecular data reveal *Dichotomaria marginata* from the Caribbean (type locality = Bahamas) to be polyphyletic and suggest that Bermuda specimens are a novel species. Our analyses indicate a single species each of *Helminthocladia, Ganonema*, *Gloiocallis*, *Trichogloea*, *Titanophycus*, *Galaxaura* and *Scinaia* in Bermuda. *Tricleocarpa* has not been confirmed in our molecular survey of the flora, despite reports of two species here in the past.

(WA) 11:30 – 11:45 am **DECIPHERING THE COMPLEXITIES OF ANTENNA EVOLUTION: A NEW APPROACH FOR RECOGNIZING AND ANALYZING THE LHC PROTEIN FAMILY.** Jonathan Neilson & Dion Durnford. Department of Biology, University of New Brunswick, Fredericton, NB, E3B 5A3, Canada.

Photosynthetic eukaryotes have a membrane intrinsic, light-harvesting antenna system composed of proteins called Light-Harvesting Complexes (LHCs). A structural hallmark of these proteins is the presence of two conserved chlorophyll-binding domains that are responsible for coordinating the pigments that direct captured light energy to reaction centres for photosynthesis. LHCs are part of a larger protein family that includes the Light-Harvesting-Like (LIL) proteins. These are a diverse group of proteins united by the presence of a chlorophyll-binding domain, but otherwise having considerable structural diversity compared to the LHCs. Because of the presence of LIL proteins in cyanobacteria and early eukaryotes, they are commonly thought to be “intermediates” in LHC evolution and a number of evolutionary scenarios involving internal duplications or shuffling of chlorophyll-binding domains have been proposed. A common approach to infer the relatedness of LHC and LIL proteins is to align proteins and conduct a phylogenetic analysis. However, it has become abundantly clear that classification and alignment based on structural features, such as number of membrane-spanning helices, violates the assumption of homology. To address this issue we have taken an approach that utilizes multiple, pairwise alignments and creates a protein similarity network. From the network, clusters of similar proteins are extracted and aligned for subsequent phylogenetic analysis. Using this approach we are able to identify homologous regions of LHCs and LILs outside the chlorophyll-binding domain, discover new members of the LHC/LIL protein family and uncover hidden homology between different classes of LILs. From this data we propose a new hypothesis for the evolution of this diverse protein family.

(WA) 11:45 – 12:00 pm **A MOLECULAR-ASSISTED INVESTIGATION OF DIVERSITY, BIOGEOGRAPHY AND EVOLUTIONARY RELATIONSHIPS FOR SPECIES OF *NEOPTILOTA* AND *PTILOTA* (WRANGELIACEAE, RHODOPHYTA) IN CANADIAN WATERS.** Meghann B. Bruce & Gary W. Saunders. Centre for Environmental & Molecular Algal Research, Department of Biology, University of New Brunswick, Fredericton, NB, Canada.

Traditional morphology-based investigations of the red algal genera *Neoptilota* and *Ptilota* have struggled to provide consistent accounts of diversity, distributions and evolutionary relationships for the species reported in Canadian waters. Consequently, there is much disagreement and taxonomic uncertainty surrounding several species within these genera. To resolve these issues we conducted a molecular-assisted investigation that included both a DNA barcode (COI-5P) survey, as well as the first multigene (COI-5P, *psa*A, *rbc*L) phylogenetic analyses for species of *Neoptilota* and *Ptilota*, as well as closely related genera. Our analyses indicate that: 1) species diversity is currently underestimated, indicated by the presence of cryptic species complexes and novel species; 2) the previously reported biogeographical distributions are incorrect for some taxa; and lastly, 3) currently held hypothesis of evolutionary relationships among members of these genera are incorrect, necessitating taxonomic revisions. The implications of these results will be discussed.

12:00 – 1:30 pm Lunch Break

(WA) 1:30 – 1:45 pm **INTERANNUAL VARIATION OF PERIPHYTON TAXONOMIC COMPOSITION AND FATTY ACID PROFILES UNDER AGRICULTURAL STRESS.** Sarah B. Whorley & John D. Wehr. Louis Calder Center—Biological Field Station, Fordham University, 53 Whippoorwill Road, Armonk, NY, 10504, USA.

Agricultural activities affect water quality, which can alter the biological properties that constitute healthy stream ecosystems. We evaluated the effects of stream management, known as Best Management Practices (BMPs), on algal community composition and their fatty acid (FA) content in agricultural streams in Delaware County NY. We employed a multi-year, time-series design with varying BMP treatments and duration. This study examines taxonomic and associated biochemical changes as affected by BMPs, and compares these patterns between 2012 and 2013. During a dry 2012, periphyton assemblages were dominated by diatoms, with the proportion of chlorophytes and cyanobacteria declining throughout the year. However, periphyton in unimpacted streams consisted of 20% fewer diatoms than communities in agriculturally altered streams. Diatoms in unimpacted (reference) streams consisted mostly of araphid and monoraphid taxa (e.g. *Cocconeis* and *Synedra*), while streams with no BMPs (greatest impacts) consisted primarily of motile, biraphid taxa (e.g. *Navicula, Cymbella*, and *Gomphoneis*). With these differences, there were also significant seasonal changes in both total FA quantity and composition (RM ANOVA $p < 0.05$). Significant differences were observed for FA concentration and composition (types of FAs), when stream category and season were taken into account (RM ANOVA $p < 0.05$). Fatty acid concentrations increased throughout the year despite a summer decline in algal biomass (chl-*a* mg/m^2). Seasonally, differences were observed in the amount of conversion of a-linolenic acid (ALA 18:3w3) to eicosapentaenoic acid (EPA 20:5w3) (RM ANOVA $p < 0.05$), but there was no effect of stream management category. This increase in overall FA concentrations as well as concentrations of EPA throughout the year coincides with an increase in the proportion of diatoms. However, 2013 was a much wetter year; we predict that changing hydrological conditions will alter periphyton taxonomic composition and thus FA content, and may also alter periphyton response to BMP treatments. As such, our data suggests that biochemical properties of periphyton may be more sensitive indicators of ecosystem disturbance than traditional response variables such as biomass.

(WA) 1:45 – 2:00 pm **CHANGES IN ALGAL BIODIVERSITY ALTER CRITICAL ECOSYSTEM FUNCTIONS AFTER RECENT INVASION OF *HETEROSIPHONIA JAPONICA* IN NEAR-SHORE ENVIRONMENTS.** Christine Newton[1], Annick Drouin[2,3] & Matthew E.S. Bracken[4]**.** [1]Marine Science Center, Northeastern University, Nahant, MA, 01908, USA; [2]Institut Maurice Lamontagne, Fisheries and Océans Canada, Québec, G5H 3Z4, Canada; [3]Institut des Sciences de la Mer, Université du Québec à Rimouski, Québec, G5L 3A1, Canada; [4]University of California, Irvine, CA, 92697, USA.

Marine invasions have become a primary focus of scientific research over the past decade due to the enormous ecological impacts these species can have in recipient communities. However, empirical evidence of how these invaders affect biodiversity and ecosystem functioning is lacking. In this study, we incorporate realistic biodiversity changes to examine the impacts a recent algal invader has had on critical ecosystem functions of growth-limiting nutrients. A recent invader to the western North Atlantic Ocean, *Heterosiphonia japonica* is particularly abundant in areas with lower diversity, suggesting invasion-related changes in biodiversity, as well as on community composition. The effects of these biodiversity changes on ecosystem functioning were examined using nitrate uptake experiments to assess whether the invasion of *Heterosiphonia* has altered the mechanisms underlying critical nutrient dynamics in recipient subtidal communities. We found evidence that *Heterosiphonia* not only alters the community composition and biodiversity of recipient communities, but also exceeds the nutrient uptake rates of recipient communities upon introduction, which may contribute to the success of this invader. However, upon the invaders establishment and incorporation into the recipient community, the nutrient dynamics within communities stabilize suggesting this *Heterosiphonia* plays a dominant role in regulating nutrient dynamics, thus fundamentally altering critical ecosystem functioning in recipient communities.

(WA) 2:00 – 2:15 pm **POPULATION DIFFERENCES AND ORGANISM-ENVIRONMENT INTERACTIONS IN NATURAL ASEXUAL POPULATIONS OF *PORPHYRA UMBILICALIS* KÜTZING RHODOPHYTA.** Renée L. Eriksen, Lindsay A. Green & Anita S. Klein**.** Department of Biological Sciences, 46 College Road, University of New Hampshire, Durham, NH, 03824-2618, USA.

Because plants are non-motile, those that live in marginal or unusual environments must adjust their physiology to cope with environmental change either by acclimating or adapting to various stress factors. *Porphyra umbilicalis* Kützing (Rhodophyta) is a highly stress tolerant species of marine macroalga that most often lives in the upper intertidal regions of open-coastal rocky shores, but can also be found in estuarine tidal rapid sites along the NW Atlantic coast. In the NW Atlantic, populations are not known to reproduce sexually. We used EST-SSR markers to identify six genotypes among eight populations from intertidal habitats in the Gulf of Maine from northern Maine to New Hampshire. Some of these genotypes are unique to certain populations. We measured quantitative phenotypic traits such as chlorophyll and phycobilin concentrations, and growth rates of individuals of single genotypes from these populations. We find differences among populations in phycobilin concentrations and growth rates, but not in total chlorophyll concentrations. We also describe differences in gene expression patterns from RNA-seq libraries derived from samples taken from open-coastal and estuarine tidal rapid environments, and we assess the expression patterns of an ammonium transporter gene under experimental high and low nitrogen conditions using qPCR. Our goal is to elucidate organism-environment interactions by describing the mechanisms by which this species acclimates or has adapted to different nutrient conditions that are experienced in marginal or unusual habitat.

(PA[2]) 2:15 – 2:30 pm **MOLECULAR PHYLOGENY AND MORPHOLOGICAL ANALYSIS OF THE GENUS *RHIZOCLONIUM* (CLADOPHORALES, CHLOROPHYTA) IN HAWAII.** Amy Havens[1], Amy Carlile[1] & Alison Sherwood[2]. [1]University of New Haven, West Haven, CT, 06516, USA; [2]University of Hawaii, Honolulu, HI, 96822, USA.

Molecular work on various algal groups has revealed new lineages that contradict traditional taxonomic classification based on morphology. The genus *Rhizoclonium* has been shown to be polyphyletic, and its simple morphology of uniseriate, unbranched filaments with lateral rhizoids has evolved several times independently in marine and freshwater cladophoraleans. This study analyzed the nuclear large subunit rRNA gene and the internal transcribed spacer sequences of non-marine putative *Rhizoclonium* in Hawaii. The traditionally used morphological characters of cell length, cell width, cell wall thickness, rhizoid presence, and rhizoid structure were also measured in order to determine their diagnostic value and phylogenetic relevance. This study found two distantly related lineages, including a divergent cryptic lineage that likely represents a new genus. The two lineages are indistinguishable at the light microscopic level.

(PA) 2:30 – 2:45 pm **POTENTIAL USE OF CHRYSOPHYTE CYST MORPHOMETRICS AS A TOOL FOR RECONSTRUCTING ARCTIC EOCENE ENVIRONMENTS.** Nels Christensen[1], Peter A. Siver[1], Anne-Marie Lott[1] & Alex P. Wolfe[2]. [1]Botany, Connecticut College, New London, CT, 06320, USA; [2]Biology, University of Alberta, Edmonton, AB, T6G 2R3, Canada.

Chrysophycean algae produce a siliceous resting stage, the cyst, within the confines of the cell that ranges in diameter from about 3 to 30 µm. Cyst morphology is species-specific and they serve as valuable bioindicators in paleolimnological studies. We have uncovered massive numbers of fossil cysts from an Arctic maar lake that existed during the globally-warm middle Eocene. The exquisite preservation of microfossils makes the locality an especially valuable site for understanding impacts of warming on Arctic waterbodies. We have devised a method to extract cysts from the core, and then enumerate and measure morphometric characters on hundreds to thousands of specimens using a FlowCAM. Our goals are to a) characterize the size distributions of cysts over the existence of the lake and, b) use this information to aid in reconstructing lake history. We have now characterized over 25,000 cysts ranging in diameter from 2.6 to 32 µm, and correlated size frequency distributions at specific core sections with other fossil bioindicators. Through comparisons to other proxies from the sediment sequence, our findings indicate that cyst morphometric data can advance our understanding of lake ontogeny under warm climate conditions.

2:45 – 3:00 pm Coffee Break

(PA) 3:00 – 3:15 pm **DEFINING THE DIVERSITY OF *BOTRYOCOCCUS* (TREBOUXIOPHYCEAE, CHLOROPHYTA).** Afsah Chohan[1], John D. Hall[2] & Hilary A. McManus[1]. [1]Department of Biology, Le Moyne College, Syracuse, NY, 13214, USA; [2]Norton-Brown Herbarium, College of Agricultural and Natural Resources, University of Maryland, College Park, MD, 20742, USA.

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[2] PA = President's Undergraduate Presentation (oral and poster)

Botryococcus Kützing 1849 is a genus of green algae that is found in freshwater worldwide. The species *B. braunii* is used in biofuel production because it has a high concentration of lipids and can yield products such as gas, diesel, and kerosene when processed by the same methods used to form petroleum. Currently, the diversity of *B. braunii* is not well understood. Preliminary phylogenetic analyses that included multiple representatives of *B. braunii* indicated the species is diverse and may encompass several different species. The purpose of this study is to increase our understanding of the diversity of *B. braunii* and more accurately define the species by incorporating additional representatives in phylogenetic analyses. The chloroplast gene, ribulose 1, 5 bisphosphate carboxylase/oxygenase large subunit (*rbc*L), was analyzed in isolates obtained from field samples in Florida. By comparing these data we can determine the phylogenetic relationships that will provide a more accurate picture of the diversity of the species.

(PA) 3:15 – 3:30 pm **MOLECULAR-ASSISTED ALPHA TAXONOMY REVEALS NEW GENETIC SPECIES OF THE GENUS *LOBOPHORA* (DICTYOTALES, PHAEOPHYCEAE) IN THE TROPICAL WESTERN ATLANTIC.** Nikolaus E. Schultz[1], Craig W. Schneider[1], Christopher E. Lane[2], Line Le Gall[3], Florence Rousseau[3] & Bruno de Reviers[3]. [1]Department of Biology, Trinity College, Hartford, CT, 06106, USA; [2]Department of Biological Sciences, University of Rhode Island, Kingston, RI, 02881, USA; [3]Institut de Systematique, Evolution, Biodiversite (UMR7205 CNRS, EPHE, MNHN, UPMC), Museum National d'Histoire Naturelle, CP 39, 57 rue Cuvier, 75231 Paris cedex 05, France.

In the western Atlantic Ocean, the brown algal genus *Lobophora* is currently represented by a single species, *L. variegata,* with a type locality given by Lamouroux as 'Antilles.' In this study, we use molecular-assisted alpha taxonomy (MAAT) to assess species diversity of *Lobophora* in Bermuda, the Florida Keys and Guadeloupe (Lesser Antilles). Using COI-5P sequences as a genetic marker, at least four genetic species of *Lobophora* have been identified from these areas, all being identified in the past as forms of *L. variegata*. Our morphological and habitat studies have revealed unique characters for each of these genetic species, including cellular arrangements, as well as different depth ranges for some species. Finally, we have been able to utilize Lamouroux's holotype of *Dictyota variegata* to reassess a detailed anatomy for this species and align this early taxon to one of our genetic species from the western Atlantic.

(PA) 3:30 – 3:45 pm **ELUCIDATION OF *LhcSR* GENE EXPRESSION IN THE MACROALGAE, *ULVA RIGIDA* AND *ULVA COMPRESSA*.** Noe B. Mercado[1], Timothy S. Roosa[1], Tania Aires[1,2], Hope Allen[1], Carol S. Thornber[2] & JD Swanson[1]. [1]Department of Biology and Biomedical Sciences, Salve Regina University, Newport, RI, 02840, USA; [2]Department of Biological Sciences, The University of Rhode Island, Kingston, RI, 02881, USA.

Macroalgal blooms can cause serious negative economic and ecological impacts given the proper environmental conditions, such as light, temperature, and nutrients. Anthropogenic activity along with climate change may result in an increase in the duration and magnitude of these algal blooms. Although algal blooms provide food, habitat, and refuge for several marine organisms, they can also cause harm by depleting oxygen levels in the water column. Moreover, information about the genetic make-up and functional biology of these algal blooms is severely lacking. This study analyzed the expression patterns of a specific gene (*LhcSR*), known to play an important role in the photo-protective mechanisms of green algae. Quantitative PCR was performed on *U. rigida* and *U. compressa* tissue samples collected from Narragansett Bay in 2013 during pre-bloom, bloom, and post-bloom periods. In previous studies *LhcSR* gene expression has been shown to be greater during warmer time periods and also high light intensities. In this study, two housekeeping genes (Histone 2 and 18S) were used as controls to normalize the expression of the target gene (*LhcSR*). Expression patterns were compared between different bloom periods (May, July, and September) in three different *U. rigida* and *U. compressa* populations in Narragansett Bay (Chepiwanoxet, Sandy Point, and Oakland Beach). In addition, the samples were compared between the two tidal levels where the tissues were collected (intertidal and subtidal). The *LhcSR* gene expression analysis for the intertidal zones between the two species revealed that the target gene was more expressed in all *U. compressa* samples compared to *U. rigida*. Furthermore, in the subtidal zones a lower normalized fold expression was observed for the target gene in all three sites (Chepiwanoxet, Sandy Point, and Oakland Beach). The site comparison data demonstrated that the target gene (*LhcSR*) was upregulated in the intertidal zones compared to the subtidal zones in all *U. compressa* and *U. rigida* populations. Further analysis considering temperature and salinity records for these locations may help understand the difference in gene expression for these bloom-forming algae.

(PA) 3:45 – 4:00 pm **TRANSCRIPTOME ANALYSIS OF THE GENETIC MAKEUP OF MACROALGAL *ULVA* BLOOMS.** Shennel Gelin, Carol S. Thornber & J.D. Swanson. Department of Biology and Biomedical Sciences, Salve Regina University, Newport, RI, 02840, USA.

Ulva compressa and *Ulva rigida* are common species of sea lettuce found around the Narragansett Bay area. When in bloom, they tend to form harmful aggregates, which negatively impact the surrounding community in an ecological and economical manner. Up until recently, very little was known about its genetic make-up and functionality; this information could be used to correlate bloom dynamics to environmental changes, especially in light of recent climate changes. To start understanding the genomics of this genus, we sampled both species of *Ulva* and performed a genome-wide analysis on them, accompanied by transcriptome analysis, which could potentially link gene expression to bloom formation. The samples were taken from three different sites in Narragansett Bay at significant stages in the bloom cycle during cell growth. RNA was then extracted from the samples and sequenced using HiSeq 2000 NGS technology. After, the sequence was assembled and annotated using both Geneious and Blast2go software respectively. Around 300,000 genes were identified per sample and their expression levels were analyzed. The resulting data showed changes in gene expression throughout the year, which could be linked to the formation of aggregates. This leads to the first understanding of the functional genomics of this species, which could later be used to predict bloom formation.

4:00 – 4:15 pm **EVALUATING TRENDS IN VALVE SHAPE IN *EUNOTIA* BY COMPARING FOSSIL AND MODERN SPECIES.** Jordan Bishop, Peter Siver & Anne-Marie Lott. Department of Botany, Connecticut College, New London, CT, 06320, USA.

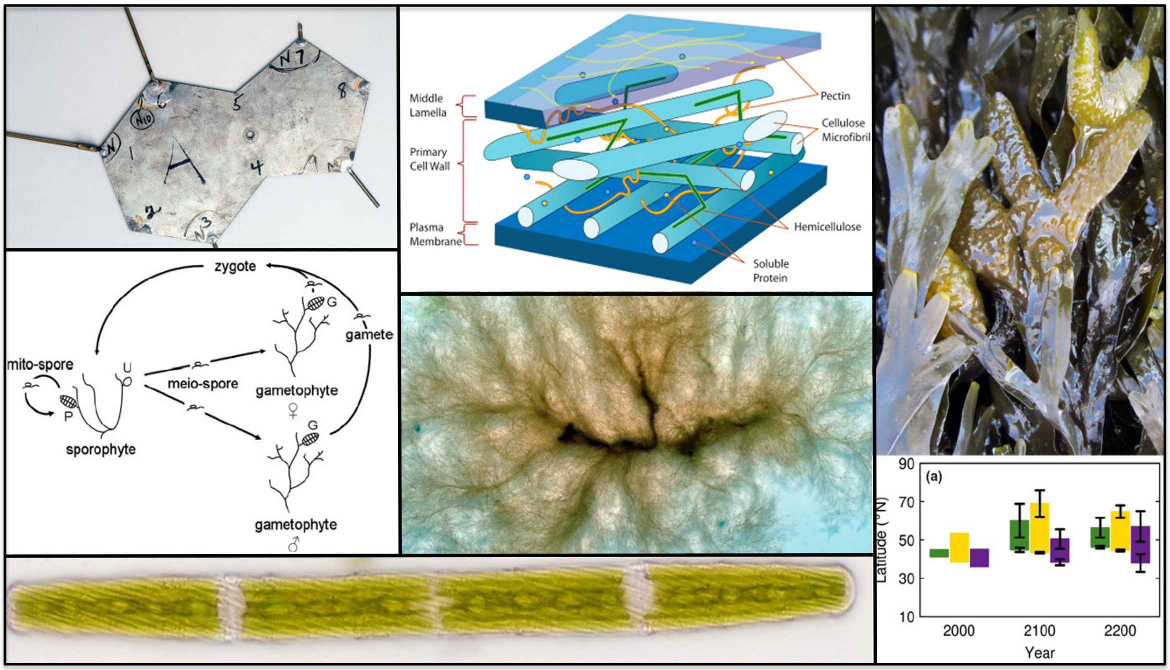
Siliceous microfossils abound in lake sediments deposited in the Giraffe kimberlite diatreme, a Middle Eocene maar situated in the Northwest Territories of Canada. The lake persisted between the time of kimberlite emplacement at 48 Ma and final paludification at 40 Ma, as constrained by ^{87}Rb/^{87}Sr and fission-track ages. An exploration drill core taken from the crater in 1999 contains 113.1 m of organic sediment, including 44.8 m of peaty material underlain by 68.3 m of stratified lacustrine mudstone, in many places finely laminated, and rich in siliceous microfossils. The Giraffe core contains the oldest known fossil remains of the freshwater diatom genus *Eunotia*, a taxon characterized by lunate-shaped frustules that are asymmetrical in valve view, short raphe slits positioned on the ventral mantle and the presence of rimoportulae. *Eunotia* is well represented within the core where the lake becomes shallow and acidic. The objective of this study is to characterize the range in valve shape of the fossil specimens relative to the modern flora. We used geometric morphometrics to characterize valve shape and identify the primary trends in shape for both modern and fossil taxa. Over 250 specimens are included in the analysis, including approximately 150 fossil specimens and over 100 modern species as represented in Patrick & Reimer (1966) and Siver & Hamilton (2012). Changes in valve morphology that account for the majority of shape variation were similar for fossil and modern species, however, the modern flora contains a significantly larger array of shapes. Based on initial findings, fossil shapes are constrained within the shape space represented by modern species. It is likely that significant changes in valve shape in *Eunotia* have occurred since the Middle Eocene, but we can't rule out the possibility that fossil species with more elaborate shapes have yet to be uncovered in the fossil record.

4:15 – 4:30 pm **EXAMINING CHLOROPLAST GENOMES IN THE ORDER SPHAEROPLEALES.** Daniel J. Sanchez & Hilary A. McManus. Department of Biology, Le Moyne College, Syracuse, NY, 13214, USA.

Since next-generation sequencing technology availability and efficiency have increased, whole genome sequencing can now be used to compare closely related organisms at the genomic level. This method is becoming more prevalent as it provides the opportunity to observe genome architecture and identify gene rearrangements in genomes of closely related organisms. Currently, only one chloroplast genome has been characterized within the order Sphaeropleales, *Acutodesmus obliquus*, of the family Scenedesmaceae. This completed genome has served as the representative of the Sphaeropleales since its publication in 2006. Recent comparisons of plastid genomes across and within the green algal lineages for which chloroplast genome data are available have revealed extensive variations in gene order and content, even within the same genus (*Elliptochloris*). To increase the number of chloroplast genomes sequenced within the Sphaeropleales, and therefore improve our understanding of chloroplast evolution in the order, we have collected data from a second family of Sphaeropleales, Hydrodictyaceae. A comparison of the sphaeroplealean chloroplast genomes provides information regarding gene content, reorganizations, and individual gene variation.

NEAS Mini-Symposium & Panel Discussion
Sunday, 27 April 2014

Algae as Model Systems



DECIPHERING THE SECRETS OF THE PLANT CELL WALL THROUGH THE CHAROPHYTE MODEL ORGANISM, *PENIUM MARGARITACEUM*

David S. Domozych

LIFE CYCLE REGULATION AND THE EMERGENCE OF COMPLEX MULTICELLULARITY IN THE BROWN ALGAE

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SEAWEED MEADOWS IN THE LIGHT OF GLOBAL CLIMATE CHANGE

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DECIPHERING THE SECRETS OF THE PLANT CELL WALL THROUGH THE CHAROPHYTE MODEL ORGANISM, *PENIUM MARGARITACEUM*.

David S. Domozych

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The cell wall of plants contributes profoundly to the life of the plant cell functioning prominently in physical defense, absorption, adhesion and communication with external biota. Cell walls also represent a major source of renewable biomass and are used extensively in the food, building, textile and biofuels industries. Over the past two decades, the emergence of new technologies has provided critical insight into the structure, function and development of the cell wall and central to these studies, are model organisms including such taxa as *Arabidopsis* and *Physcomitrella*. Recently, several studies have revealed that the cell walls of charophyte or streptophyte green algae, specifically late divergent taxa, have cell walls whose constituents are remarkably similar to those of land plants. This supports the supposition that the ancestors of charophytes were uniquely positioned to successfully invade terrestrial habitats 450-500 million years ago because wall biochemistry and other features afforded a degree of pre-adaptation to life on land. Also, this has stimulated the search amongst modern charophytes for potential model organisms for the study of the biology and evolution of cell walls. Recently, a consortium of several laboratories has begun extensive studies of the cell wall of a unicellular charophyte, *Penium margaritaceum*, a common placoderm desmid. *Penium* is a powerful tool for cell wall studies in that it has easily recognized and probed wall polymers including pectins, cellulose, hemicellulosic macromolecules and glycosylated proteins. The alga grows quickly in culture and is easily adapted for rapid microarray screening of specific pharmacological agents. Specific wall polymers may be live-labeled with an extensive arsenal of cell wall antibodies and carbohydrate binding modules, returned to culture and subsequently monitored for developmental events. Recent high-resolution imaging with various microscopy-based technologies has allowed for detailed 3-dimensional modeling of the wall. Most importantly, the first stable transformed cell lines have been developed that are allowing for specific analyses of subcellular systems involved in the biosynthesis of specific cell wall polymers.

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LIFE CYCLE REGULATION AND THE EMERGENCE OF COMPLEX MULTICELLULARITY IN THE BROWN ALGAE.

J. Mark Cock

Algal Genetics Group
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Roscoff, France

The brown algae are members of the supergroup chromalveolata, and as such are very distantly related both to animals and to green plants. This group of seaweeds evolved complex multicellularity independently of the plants and animals and is one of only a small number of eukaryotic groups that has acquired this level of developmental complexity[1]. Analysis of the genome sequence of the model brown alga *Ectocarpus* has revealed a number of features that may be linked to the emergence of complex multicellularity in this lineage, including a family of membrane-localised receptor kinases that evolved independently in brown algae but strongly resemble the receptor kinases of green plants and animals[2]. Genome analysis has therefore provided some clues about the molecular mechanisms that underlie multicellular development in the brown algae but more meaningful comparisons with other multicellular lineages will only be possible if we can obtain a deeper, experimental understanding of these molecular mechanisms. To address this problem, we have proposed and are developing the filamentous brown alga *Ectocarpus* as a model system for the brown algae[3] and are using this system to investigate the genetic basis of specific developmental processes. This work currently focuses on two key aspects of this organism's reproductive biology, life cycle regulation and sex determination.

The life cycle of *Ectocarpus* involves an alternation between two independent multicellular organisms, the sporophyte and the gametophyte. We have shown that the identities of the two generations are not determined by ploidy, but rather are determined genetically. Several life cycle mutants are currently being studied[4,5], including the *ouroboros* mutant, which exhibits complete conversion of the sporophyte generation into a gametophyte. The *ouroboros* mutation not only identifies a key developmental regulator in *Ectocarpus* but also represents a new class of homeotic mutant in which there is a switch between developmental programs at the level of the whole organism rather than at the organ or tissue level. Characterisation of *Ectocarpus* life cycle mutants at the molecular level is providing insights into how multicellular development programs may have been built on to pre-existing regulatory networks controlling life cycle progression.

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2. Cock, J. M. *et al.* (2010) The *Ectocarpus* genome and the independent evolution of multicellularity in brown algae. Nature, 465, 617-621.
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5. Peters, A. F. *et al.* (2008) Life-cycle-generation-specific developmental processes are modified in the *immediate upright* mutant of the brown alga *Ectocarpus siliculosus*. Development, 135, 1503-1512.

SEAWEED MEADOWS IN THE LIGHT OF GLOBAL CLIMATE CHANGE

Alexander Jüterbock

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8049 Bodø, Norway

Coastal ecosystems in general and intertidal systems in particular, are likely to be profoundly affected by climate change. On temperate rocky shores, the responses of foundational seaweed species to climate change have the potential to trigger major changes in the entire intertidal ecosystem. We studied the impact of climate change on seaweeds meadows in the North-Atlantic rocky intertidal with focus on the brown canopy-forming macroalga *Fucus serratus*. More specifically, we aimed to identify the impact of climate change on 1) the geographical distribution, 2) the thermal tolerance, and 3) the genetic changes of fucoid seaweeds. Ecological Niche Model predictions suggest that suitable environments for fucoid seaweeds are opening up in the Arctic along the southern coasts of Greenland, Iceland and Spitzbergen. At the same time, our models predict that fucoid seaweeds will face extinction from rocky shores in southern Europe before year 2200. The negative impact of climate change on the southern edge populations of fucoid seaweeds is not only a prediction but is already supported by empirical findings. For example, we recorded a significant loss of allelic richness and an abundance decline of about 90 % in a Spanish southern edge population of *F. serratus* over the past decade. The threatened southern-edge populations of many temperate seaweeds are ancient glacial refugia and centers of genetic diversity. Thus, a remaining key question is, whether the plastic or adaptive capacities of these populations are sufficient to survive climate change or if temperate seaweeds are at risk to lose their centers of adaptive potential to future environmental change.

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2. Jüterbock, A., Tyberghein, L., Verbruggen, H., Coyer, J. A., Olsen, J. L. & Hoarau, G. 2013. Climate change impact on seaweed meadow distribution in the North Atlantic rocky intertidal. *Ecol Evol* **3**:1356-73.

11:00 – 11:15 am **THE MACROALGAE DIGITIZATION PROJECT: ADVANCING ONLINE ALGAL COLLECTIONS AT THE NEW YORK BOTANICAL GARDEN AND BEYOND.** Stephen D. Gottschalk[1], Naveed Davoodian[1], Sarah N. Dutton[1], Juli A. Janis[1], Beryl C.M. Kahn[1], Theodore D. Kirkinis[1], Eli Min[1], Jonathan W. Toll[1] & Kenneth G. Karol[2]. [1]The William and Lynda Steere Herbarium, The New York Botanical Garden, Bronx, NY, 10458, USA; [2]The Lewis B. and Dorothy Cullman Program for Molecular Systematics, The New York Botanical Garden, Bronx, NY, 10458, USA.

The Macroalgal Herbarium Consortium (MHC) was formed in 2013 to facilitate the access to institutional collections of algae across the United States. The aim of this consortium is to make digitally available more than 1,143,000 specimens representing all major algae lineages (e.g., browns, greens, reds) through a four-year thematic collections network (TCN) grant sponsored by the National Science Foundation. The New York Botanical Garden (NYBG) is one of the 49 collaborating institutions and will contribute to this TCN as one of six primary digitization centers (PDCs). NYBG collections have been acquired both by active staff and through the incorporation of outside herbaria. These include some historically important collections made by Frank S. Collins, Marshall A. Howe, Nicolas Pike, Richard D. Wood and others. Additionally, the NYBG Herbarium includes 2,900 algal type specimens, a number that continues to grow as the collection is thoroughly examined during this project. Taxonomic, geographic, and temporal data will be accessible online for every specimen in the collection as both a digital image and textual transcription. Unlocking the more than 150 years of data stored in this collection will allow for more extensive climate change, human impact, bioinvasion, and systematics research from institutions and individuals worldwide. The increased accessibility to these data will not only benefit scientific research, but will serve to engage and educate the public. In addition to discussing the goals of this project, we will address the challenges of digitizing a collection of this magnitude, historical scope, and taxonomic complexity.

11:15 – 11:30 am **SITE EVALUATION AND THE DEVELOPMENT OF METHODS FOR FARMING *MACROCYSTIS PYRIFERA* OFF THE PACIFIC COAST OF BAJA CALIFORNIA.** José A. Zertuche-González, D. Craig Barilotti, José M. Guzmán-Calderón, Zarko Altamirano-Gómez, Mariana Sánchez-Barredo & Isaí Pacheco-Ruiz. Instituto de Investigaciones Oceanológicas, UABC, Carretera Tijuana-Ensenada No. 3917. Ensenada, B.C., 22860, México.

To further the development of abalone aquaculture in Baja California, we've been conducting research that focuses on developing farming methods for growing *Macrocystis pyrifera* (giant kelp) that small vessel fishermen can use. Our research approach was to conduct "proof of concept" studies with small scale testing of all stages of the kelp life history, with our major emphasis on post laboratory outplant and vegetative grow-out in semi-protected coastal water. Giant kelp zoospores were obtained from mature sporophylls in the laboratory. Zoospores that settled and attached to nylon string wrapped on PVC (3.8 cm diameter) spools were maintained in nutrient enriched, filtered seawater until the juvenile outplants plants had grown to 2-5 mm in length. Lengths of nylon string about 30 cm long with the juvenile outplants growing on them were tied to the plastic mesh that covered 3.8 l plastic bottles (referred to as growth centers) to provide greater surface area for the holdfasts as the they grew in size. The use of buoyant growth center avoids the entanglement of plants growing on a long-line while the plants grow and develop their own buoyancy. The growth centers were then outplanted to the long-lines anchored at three different depths (4, 8 and 12 m relative to the tidal datum of MLLW) in a semi-exposed bay (Santa Maria bay). After three months, growth was evaluated. Fully developed plants, were observed at 4 and 8 m. Plants at 12 m were strongly affected by large presence of caprellids and the availability of light. Surviving plants from all depths and other sites that were in the same cohort of plants grown from zoospores, were replanted at 8 m. Seven months after outplanting, some plants had fronds on them that were over 16 m in length and had a plant biomass up to 14 kg (wet) per growth center. There was major variation in frond length and plant biomass associated with caprellid abundance.

11:30 – 11:45 am **ASSESSING MONOPHYLY IN THE DUMONTIACEAE WITH AN EMPHASIS ON CRUSTOSE MEMBERS.** Kyatt Dixon[1] & Gary W. Saunders[1]. [1]Centre for Environmental & Molecular Algal Research, Biology, University of New Brunswick, Fredericton, NB, E3B 5A3, Canada.

Efforts to resolve genus-level relationships within the Dumontiaceae have failed to yield definitive results for many members, typically suffering from poor resolution of key nodes due to a lack of both comprehensive gene and taxon representation. This has led to several conflicting hypotheses regarding the evolution of the family and its close relatives, namely the Rhizophyllidaceae, Kallymeniaceae and Gainiaceae. We employed a multigene phylogenetic approach to study relationships among comprehensively sampled Dumontiaceae, Kallymeniaceae, Rhizophyllidaceae and Gainiaceae including a number of previously unsequenced members and several unidentified crusts that were associated with these families based on preliminary COI-5P data. Our phylogenetic results revealed several inconsistencies with the current classification of these groups, the implications of which are discussed. We also investigated the biogeography of this four-family complex and evolution of the crustose growth form, both as the heteromorphic sporophyte phase of species with erect gametophytes, and as obligate crusts.

11:45 am – 12:00 pm **EMISSION OF VOLATILE COMPOUNDS IN *FUCUS VESICULOSUS*.** Ursula S.R. Röse & Janithri Wickramanayake. Department of Biology, University of New England, Biddeford, ME, 04005, USA.

Brown macroalgae are known to release a variety of volatile compounds, some of which are thought to be emitted in response to oxidative stress. We investigated the emission of volatiles by the brown macroalgae *F. vesiculosus* collected from the intertidal zones in Biddeford Pool, ME, USA Algae were exposed to several directly applied stressors and headspace volatiles were collected over 6 days. Volatiles were collected from algae exposed to herbivory by the gastropod *Littorina littorea* and the isopod *Idotea baltica*, as well as in response to mechanical injury. Herbivory and mechanical injury were compared to volatile emissions in response to treatment with the plant signaling compound methyl jasmonate or arachidonic acid as well as control algae. We found that *F. vesiculosus* released two halogenated compounds, tribromomethane and diiodomethane in response to all treatments, with a high production of diiodomethane on in response to methyl jasmonate and arachidonic acid. These compounds may have antibacterial and antiherbivore properties or may be emitted as byproducts of the detoxification of reactive oxygen species.

12:00 – 12:15 pm **SUGAR KELP AQUACULTURE: A COASTAL MANAGEMENT TOOL AND NEW BUSINESS OPPORTUNITIES IN LONG ISLAND SOUND AND NEW YORK COASTAL WATERS.** Jang K. Kim[1], George P. Kraemer[2] & Charles Yarish[3]. [1]Department of Marine Sciences, University of Connecticut, CT, 06901, USA; [2]Environmental Studies Program, Purchase College, Purchase, NY, 10577, USA; [3]Department of Ecology & Evolutionary Biology, University of Connecticut, CT, 06901, USA.

Saccharina latissima (sugar kelp) was cultivated and harvested at the mouth of the Bronx River estuary (BRE), western Long Island Sound (Fairfield, CT; WLIS) and central Long Island Sound (Branford, CT; CLIS) during winter and spring of 2012– 2013. These sites differ in salinity and inorganic nutrients. The salinities were 22-29 (BRE), 30-32 (WLIS), and 26-33 ppt (CLIS), respectively. Inorganic nitrogen and phosphorus concentrations at the BRE site were 4.1-11.6 times and 1.6-3.3 times higher, respectively, than those at WLIS or CLIS during winter months (Dec.–Feb.). During the spring months (Mar. – May), the nutrient concentrations at the WLIS and CLIS sites dropped below 0.5 μM N and 1.0 μM P, while the nutrient concentration at the BRE site remained high (5.7 – 14.9 μM N and 3.0-3.6 μM P). The tissue nitrogen contents at the final harvest were 3.26% (BRE), 1.07% (WLIS) and 1.04% (CLIS), respectively. Estimated biomass yields were 62, 61 and 37 kg MT FW ha^{-1} at the BRE, WLIS, and CLIS sites, respectively. A hypothetical nutrient bioextraction farm of one hectare at each site would remove an estimated 183, 74 and 35 kg N, respectively. The economic value of N removal was as high as \$2,020 ha^{-1} (BRE), \$817 ha^{-1} (WLIS) and \$386 ha^{-1} (CLIS). These values would represent additional income for seaweed aquaculturalists beyond the value of seaweed products. All sugar kelp harvested from CLIS were sold to NYC's premium restaurants. The sugar kelp from WLIS was tested for other applications, including organic fertilizer, cosmetic products and production in microbreweries. The findings in this study showed that kelp aquaculture could be included as part of a suite of management tools to minimize nutrient impacts in urbanized coastal waters, while providing a new business opportunity for seaweed aquaculturalists.

POSTERS

1. *(PA)* **GRAZING EFFECTS ON BIOFILMS ALONG AN ACID MINE DRAINAGE REMEDIATION GRADIENT.** Jessica Lindner[1], Samuel A. Drerup[1], Kelly S. Johnson[2] & Morgan L. Vis[1]. [1]Environmental and Plant Biology, Ohio University, Athens, OH, 45701, USA; [2]Biological Sciences, Ohio University, Athens, OH, 45701, USA.

In stream ecosystems benthic biofilms are an important source of energy, which higher trophic levels depend upon. Two factors that can substantially affect biofilm function are macroinvertebrate grazing and acid mine drainage (AMD). Grazing by macroinvertebrates has been shown to decrease periphyton biomass while increasing rates of production. AMD, even after remediation, typically results in decreases in biomass and production rates of biofilms. In this research, grazing along an AMD remediation gradient was studied to determine the interactive effects on periphyton productivity. Tiles pre-colonized with a mature biofilm were placed in containers with and without grazers in a reference stream and three sites along a remediated AMD stream for 72 hours. The field experiment was replicated in greenhouse mesocosms. Biofilm ash free dry mass, chlorophyll a, and productivity were measured as well as grazer biomass. Significant ($P < 0.05$) reductions in primary productivity were found between the reference and remediated sites in field and mesocosm experiments. There was no effect of grazers or grazer biomass in the field experiment. Even in the short duration of this study, there was a sharp drop in primary production and respiration related to AMD severity. Possible implications for biofilm-grazer dynamics in AMD remediated streams will be discussed. Our results suggest that the extreme environmental conditions in remediated AMD impacted streams have a more severe impact on biofilm function than grazing pressure.

2. **EVALUATING TRENDS IN VALVE SHAPE IN *EUNOTIA* BY COMPARING FOSSIL AND MODERN SPECIES.** Jordan Bishop, Peter Siver & Anne-Marie Lott. Department of Botany, Connecticut College, New London, CT, 06320, USA.

Siliceous microfossils abound in lake sediments deposited in the Giraffe kimberlite diatreme, a Middle Eocene maar situated in the Northwest Territories of Canada. The lake persisted between the time of kimberlite emplacement at 48 Ma and final paludification at 40 Ma, as constrained by $^{87}Rb/^{87}Sr$ and fission-track ages. An exploration drill core taken from the crater in 1999 contains 113.1 m of organic sediment, including 44.8 m of peaty material underlain by 68.3 m of stratified lacustrine mudstone, in many places finely laminated, and rich in siliceous microfossils. The Giraffe core contains the oldest known fossil remains of the freshwater diatom genus *Eunotia*, a taxon characterized by lunate-shaped frustules that are asymmetrical in valve view, short raphe slits positioned on the ventral mantle and the presence of rimoportulae. *Eunotia* is well represented within the core where the lake becomes shallow and acidic. The objective of this study is to characterize the range in valve shape of the fossil specimens relative to the modern flora. We used geometric morphometrics to characterize valve shape and identify the primary trends in shape for both modern and fossil taxa. Over 250 specimens are included in the analysis, including approximately 150 fossil specimens and over 100 modern species as represented in Patrick & Reimer (1966) and Siver & Hamilton (2012). Changes in valve

morphology that account for the majority of shape variation were similar for fossil and modern species, however, the modern flora contains a significantly larger array of shapes. Based on initial findings, fossil shapes are constrained within the shape space represented by modern species. It is likely that significant changes in valve shape in *Eunotia* have occurred since the Middle Eocene, but we can't rule out the possibility that fossil species with more elaborate shapes have yet to be uncovered in the fossil record.

3. *(PA)* **COMPARITIVE PHYLOGEOGRAPHY OF *BATRACHOSPERMUM GELATINOSUM* (BATRACHOSPERMALES, RHODOPHYTA) IN EUROPE AND NORTH AMERICA.** Emily J. Keil[1], Taylor R. Macy[1], Janina Kwandrans[2], Pertti Eloranta[3], P. Tomás[4], Marina Aboal[5] & Morgan L. Vis[1]. [1]Department of Environmental and Plant Biology, Ohio University, Athens, OH, USA; [2]Institute of Nature Conservation, Department of Freshwater Biology, Kraków, Poland; [3]Jyväskylä, Finland; [4]Laboratorio de Ensayos Técnicos ENSAYA, Zaragoza, Spain; [5]Departamento de Biología Vegetal, Facultad de Biología, Universidad de Murcia, Murcia, Spain.

The freshwater red alga, *Batrachospermum gelatinosum* (L.) DC., inhabits streams of Europe and North America having been collected frequently on both continents. A study of this species showed evidence of a glacial refugium in the southeastern US with little genetic variation throughout its more northern range in eastern North America. This study was initiated to investigate its phylogeography throughout Europe in order to compare with North America. Specimens were collected from Belgium, Estonia, Finland, France, Great Britain, Italy, Latvia, Lithuania, Poland and Spain. Of the 70 individuals analyzed, there were 12 COI haplotypes. In addition, ITS variation of 66 individuals was surveyed and showed 22 haplotypes. The haplotype network of COI data showed 54 individuals distributed among three common haplotypes. The other nine haplotypes only differed from the commons ones by 1–2 base pair and were represented by 1–5 individuals. For the ITS data, the network had a star appearance with common haplotype (16 individuals) and many closely related haplotypes with few individuals per haplotype. Compared to North America (5 COI haplotypes), there are many more haplotypes present in Europe and the relationship among haplotypes is more complex. The geographic distribution of haplotypes did not appear to follow a glaciation pattern as was the case in North America, but rather the common haplotypes were widely spread suggesting a recent expansion.

4. **INTERACTING INFLUENCE OF LOW SALINITY AND NUTRIENT PULSES ON THE GROWTH OF BLOOM-FORMING *ULVA COMPRESSA*.** Michele Guidone & LaTina Steele. Department of Biology, Sacred Heart University, Fairfield, CT, 06825, USA.

For the eastern US, it is predicted that climate change will increase the frequency of severe rainstorms, inundating coastal areas with pulses of freshwater that will reduce salinity but also temporarily increase nutrients through sewage overflow and storm runoff. In an effort to predict how this may influence the frequency and severity of macroalgal blooms, this study examined the interacting effect of salinity and nutrient supply on bloom-forming *Ulva compressa.* In laboratory experiments with constant nutrient supply, *U. compressa* showed decreased growth at low salinities; however, this decrease was not detectable until the fifth day of treatment. Moreover, *U. compressa* demonstrated an extraordinary tolerance for freshwater, surviving for 48 hours without nutrients at 0 PSU. When exposed to pulses of freshwater (0 PSU) and varying nutrient levels (none, low, high) lasting either 0.5, 4, or 8 hours, *U. compressa* growth was negatively impacted in the treatment without nutrients and positively impacted by the low and high nutrient treatments. Furthermore, thalli in the high nutrient treatment showed increased growth with increased pulse time. These findings, combined with observations of *U. compressa*'s tolerance for high temperatures, suggest *Ulva* blooms will not decrease in frequency or severity with a change in precipitation patterns.

5. *(PA)* **INVESTIGATING THE POPULATION GENETICS OF SUSEPTIBILITY TO RED ALGAL PARASITIC INVASION.** Taylor Clement, Eric Salomaki & Chris Lane. Department of Biological Sciences, University of Rhode Island, Kingston, RI, 02881, USA.

Rhodophytes are prone to parasitism from congeners, seemingly due to their characteristic pit plugs, by which parasites deposit their cellular components into the host. While the method of infection is becoming more understood, there is little known about what makes some hosts more susceptible than others, and what determines the geographic distribution of the parasite on both a smaller and larger scale. To gain insight into population dynamics of parasites and their hosts, we are using two species in Rhodomelaceae, *Vertebrata lanosa,* and its obligate parasite, *Choreocolax polysiphoniae* as model species. *Choreocolax polysiphoniae* invades *V. lanosa* cells, forming erumpent pustules on the host's thallus. This system is made more intricate by the fact that *V. lanosa* is an obligate epiphyte of *Ascophyllum nodosum*, a brown alga. While previous studies have focused on the genetic variability of *A. nodosum* within the mtDNA-IGS and mtTrnW loci, no research has been published on the relationships between *V. lanosa* and *Choreocolax* in regards to their geographic diversity. Samples continue to be collected from different areas throughout the North Atlantic, with a current focus on Rhode Island and Maine, utilizing data within the cox1 and cox2-3 spacer, in order to look for haplotype distinction. This study of the population genetics involving these three species will offer insight as to the dynamics within this system of algae, and ultimately determine whether there is a correlation between parasite prevalence and genotype.

6. **USING NEXTGEN TRANSCRIPTOME SEQUENCING TO RESOLVE ORDINAL RELATIONSHIPS IN THE NEMALIOPHYCIDAE: FIRST STEPS AND FUTURE DIRECTIONS.** Chris Jackson & Gary W. Saunders. Centre for Environmental and Molecular Algal Research, Department of Biology, University of New Brunswick, Fredericton, NB, E3B 5A3, Canada.

Phylogenetic analyses of the red algae have highlighted five poorly supported regions. Here we investigate one of these – ordinal relationships within the subclass Nemaliophycidae. Considerable additional sequence data are likely required to resolve this conundrum with good statistical support and thus standard multigene approaches are not the best path forward. To resolve this shortcoming, we are generating transcriptomes from select taxa from diverse orders within the Nemaliophycidae. To date successes include three taxa from the Palmariales (*Devaleraea ramentacea*, *Meiodiscus spetsbergensis* and *Rhodothamniella floridula*), and two taxa from the Acrochaetiales (*Grania efflorescens* and *Rhodochorton* sp.). For each species total RNA was extracted, and strand-specific cDNA libraries were generated and sequenced using Illumina sequencing technology (100 bp paired-end reads, HiSeq 2500, Genome Quebec). We assembled a transcriptome for each species using the assembler Trinity (Broad Institute), and annotated the resulting mRNA sequences by BLAST searching against a database of all available Glaucophyta, Rhodophyta and Viridiplantae proteins. Using an annotation BLAST e-value cut-off off e^{-100}, we recovered 920 genes in each of the five transcriptomes selecting 821 that were present as single copies for further analyses. For each gene, a neighbor-joining tree was generated from a trimmed alignment, with ~550 genes producing congruent topologies. We are currently generating additional transcriptomes from other representative taxa, and exploring RNA extraction and transcriptome sequencing from herbarium samples stored in silica.

7. *(TA)* **COMPARATIVE GENOMIC SEQUENCING OF *NEPHROMYCES* AND ITS SISTER TAXA.** Chris Paight, Mary Beth Saffo & Chris Lane. Department of Biological Sciences, University of Rhode Island, Kingston, RI, 02881, USA.

Though no longer photosynthetic, many apicomplexans still possess a derived version of the same red algal plastid that enables brown algae to photosynthesize. Despite their photosynthetic roots, apicomplexans are highly successful and often devastating parasites, infecting every major metazoan lineage. Until recently it was believed the apicomplexan phylum was entirely composed of parasites, but species in the genus *Nephromyces* have been shown to be a tunicate endosymbiont inhabiting all of the members of the Molgulidae family. We have performed preliminary sequencing of the *Nephromyces* genome to determine the metabolic pathways that enabled *Nephromyces* to become an endosymbiont. Our sequence data support an earlier claim that *Nephromyces* harbor bacterial endosymbionts, further complicating the metabolic picture. The metabolic capabilities of both *Nephromyces* and its bacterial endosymbiont will be discussed, along with the relationship they have with the tunicate host.

8. *(PA)* **TIMING OF THE PRODUCTION OF INDUCIBLE COMPOUNDS IN BROWN MACROALGAE *FUCUS VESICULOSUS.*** Janithri Wickramanayake & Ursula S.R. Röse**.** Department of Biology, University of New England, Biddeford, ME, 04005, USA.

In response to herbivory and other stress, brown macroalgae may respond with the synthesis of inducible compounds. We investigated the inducibility of compounds in the brown macroalga *Fucus vesiculosus* (L.) in response to herbivory, mechanical injury, and the signaling compounds arachidonic acid and methyl jasmonate. Samples of visibly uninjured *F. vesiculosus* were collected during low tide from the intertidal zone of Biddeford Pool, ME, U.S.A. and either periwinkles (*Littorina littorea)* or isopods (*Idotea baltica)* were allowed to feed on algae over 6 days. The effects of herbivory were compared to treatments with either methyl jasmonate or mechanical injury, and samples were harvested after 1 day, 3 days and 6 days in the field. For arachidonic acid treatments, *F. vesiculosus* samples were exposed to arachidonic acid in the laboratory and harvested 3 days and 6 days post treatment. Samples were extracted with pentane and analyzed by GC-MS. Six days post treatment, an increase in the synthesis of at least two compounds, tocopherol and fucosterol was observed in response to herbivory, arachidonic acid, and in significant amounts in response to mechanical injury and methyl jasmonate exposure. Tocopherol and fucosterol are reported to have antioxidant properties, which may provide protection against oxidative stress. The results of this study advance our understanding of the strategies employed by algae to cope with herbivores and possible oxidative stress in their marine environment.

9. ***SPIROGYRA*, *MOUGEOTIA* AND *ZYGNEMA*: A MULTISCALE COMPARISON OF GENETIC VARIATION AND GEOGRAPHICAL DISTANCE.** Maria Pappas[1], John D. Hall[2] & Richard M. McCourt[1]**.** [1]Academy of Natural Sciences of Drexel University, Philadelphia, PA, 19118, USA; [2]The University of Maryland, College Park, MD, 20742, USA.

Filamentous conjugating green algae (Class Zygnematophyceae) are common in freshwater habitats worldwide. Knowledge of the distribution and ecology of particular species of these algae is hindered by the difficulty of identifying strains to species. Species identification is based on sexually produced zygospores, which are found in only a small percentage of field collections. Instead we used gene sequence data to identify related strains of *Spirogyra*, *Mougeotia* and *Zygnema* from the northeastern United States and placed them in a larger phylogeny of the genera. In addition, we tested for patterns of genetic divergence relative to between-habitat distance. Given the limited dispersal abilities and separation of habitats of freshwater algae, we predict that geographic distance is correlated with genetic distance on broader spatial scales and not on smaller, within habitat scales. We tested the hypothesis that this pattern holds for these genera of algae by comparing sequence divergence in *rbcL* to geographic distance between collections in the northeastern U.S., as well as published data from collections across the U.S.

10. *(PA)* **HOST RANGE ANALYSIS OF *SYNECHOCOCCUS*-INFECTING PODOVIRUSES FROM SOUTHERN NEW ENGLAND.** Alex Veglia & Marcie Marston. Department of Biology and Marine Biology, Roger Williams University, Bristol, RI, 02809, USA.

Synechococcus, a genus of unicellular cyanobacteria, is an important primary producer in coastal marine ecosystems. Viruses called cyanophages can influence the abundance and composition of *Synechococcus* communities by infecting and killing particular cyanobacteria. Cyanophages belonging to the Myoviridae family have large genomes (~170,000 bp) and typically have broad host ranges while cyanophages in the Podoviridae family have much smaller genomes (~45,000 bp) and narrower host ranges. In this study, we examined the host range and full genome sequences of 29 podoviruses to try to identify the genes responsible for determining host range. *Synechococcus*-infecting podoviruses were isolated from seawater samples collected in Narragansett Bay, Rhode Island and along the shores of Long Island. The 29 podoviral isolates fall into three phylogenetic clusters (RIP1, RIP4, and RIP5) based on viral DNA polymerase gene sequences. Although all the isolates within a cluster have very similar DNA polymerase gene sequences (>98% sequence identity), differences in gene content, particularly in regions associated with tail fiber genes, were observed among isolates within a cluster. As in other studies, the 29 podoviruses all had narrow host ranges, with each isolate only infecting one to two *Synechococcus* strains. All of the isolates in the RIP4 cluster had identical host ranges; however, isolates belonging to the RIP1 and RIP5 clusters differed in the hosts that they could infect. These results suggest that phylogenetically similar podoviruses can differ in host range, perhaps due to small changes in gene content. Next, we plan to examine if there are phenotypic differences in the infection kinetics (e.g., rate of absorption, burst size) of isolates infecting the same host. Knowledge of the host range dynamics and the genes responsible for host interactions will help us to determine the effects that podoviruses may have on local *Synechococcus* communities.

11. *(TA [3])* **THE RESPONSE OF *GRACILARIA VERMICULOPHYLLA* TO ACIDIFICATION, EUTROPHICATION, AND GRAZING PRESSURE IN COASTAL RHODE ISLAND**. Gordon Ober & Carol S. Thornber. Department of Biological Sciences, University of Rhode Island, Kingston, RI, 02881, USA.

Coasts and estuaries are sites of great societal value and ecosystems services, but these systems are under environmental pressure from a myriad of sources. In order to appropriately quantify ecosystem and community response under a changing climate, research based around multiple stressors is necessary. Ocean acidification and eutrophication represent two major sources of influence in these zones. In this study I have tested the response of algal growth and herbivore feeding behavior to increased carbon dioxide and nutrients in a common invasive red macroalga. Here, we used *Gracilaria vermiculophylla* from Narragansett Bay, Rhode Island as our model species. Individual algal thalli were placed in flow-through seawater systems with one of four experimental conditions: high pCO_2 (~560 ppm) or background pCO_2 (~390 ppm) and high nutrients (40 µM TN) or low nutrients (20 µM TN), in a fully factorial design. After two weeks, we found no differences in algal growth rates among treatments. We then introduced the common snail *Littorina littorea* to all experimental aquaria and assessed their feeding preferences and behavior over 4 days. Under high pCO_2, feeding behavior was not altered, but under low pCO_2 snail feeding was two times more frequent with high nutrients. However, herbivore impacts on algal biomass did not significantly vary among treatments, although these results may be confounded by the settlement of epiphytic algae in our experimental system.

12. **GIS MODELING OF POTENTIAL AQUACULTURE SITES IN LONG ISLAND SOUND FOR NUTRIENT BIO-EXTRACTION.** Daniel J. Koval[1], Jang K. Kim[2], George P. Kraemer[3] & Charles Yarish[4]. [1]Environmental Studies Program, Purchase College, Purchase, NY, 10577, USA; [2]Department of Marine Sciences, University of Connecticut, CT, 06901, USA; [3]Environmental Studies Program, Purchase College, Purchase, NY, 10577, USA; [4]Department of Ecology & Evolutionary Biology, University of Connecticut, Stamford, CT, 06901, USA.

Nitrogen run off into Long Island Sound (LIS) and resulting eutrophication-driven hypoxia could be effectively mitigated with year round seaweed aquaculture. Geographic information systems (GIS) offer an invaluable tool for optimizing site selection. In order to maximize both nutrient removal and crop biomass, two species (sugar kelp *Saccharina latissima* and the red seaweed *Gracilaria tikvaiae*) were examined in this model. The unrestricted farmable areas of LIS were first identified. These areas were then examined for water column nitrogen concentration, temperature, dissolved oxygen level, chlorophyll

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[3] TA = Trainor Graduate Poster Award

level, turbidity, and salinity. Seasonal and monthly variations in these water quality parameters allow planners to identify optimum planting times and areas as well as determine site specific crop biomass and nutrient removal capacity.

13. *(TA)* **TREHALOSE IDENTIFIED IN *PORPHYRA UMBILICALIS* USING GC-MS**. Yuanyu (Helen) Cao[1], Andy Hanneman[2] & Anita S. Klein[1]. [1]Molecular, Cellular, Biomedical Sciences, University of New Hampshire, NH, 03824, USA; [2]Glycomics Center, University of New Hampshire, NH, 03824, USA.

Trehalose is a non-reducing disaccharide in plants that functions to protect against multiple abiotic stresses (i.e. desiccation, salinity, and extreme temperature). The intertidal macroalga *Porphyra umbilicalis* was analyzed for the occurrence of trehalose because of its high resilience to desiccation. Chemotaxonomy studies identified trehalose in species of the *Ceramiales*, but not in *Porphyra* (Karsten et al. 2007). Their observation conflicts with the occurrence of a putative gene for the key enzyme in trehalose synthesis, trehalose-phosphate-synthase in several messenger *Porphyra* RNA libraries. Using an ethanol extraction followed by separation on solid phase extraction (SPE) column and gas chromatography – mass spectrophotometer (GC-MS), trehalose was identified in the extracts from the *Porphyra* samples. The concentration of trehalose in *Porphyra* is quite low (<< millimolar) which suggests trehalose may serve as a signal molecule to regulate overall metabolism instead of osmotic protector. The research will help elucidate the role(s) of trehalose metabolism in *P. umbilicalis*.

14. *(TA)* **PROTEIN AND TOTAL NITROGEN CONTENTS OF PERIPHYTON IN STREAMS WITH DIFFERING INORGANIC N & P SUPPLIES.** Catharina Grubaugh & John D. Wehr. Biological Sciences, Louis Calder Center—Biological Field Station, Fordham University, 53 Whippoorwill Road, Armonk, NY, 10504, USA.

Total nitrogen (TN) content of a food resource is often used as an indicator of its nutritional quality, as dietary protein is thought to affect growth rates in consumers. Protein content has long been estimated from a theoretical nitrogen-to-protein conversion factor of 6.25. However, algal cells can store cellular nitrogen in inorganic as well as organic forms. Therefore, total nitrogen content of periphyton may overestimate the true protein content of this basal food resource. Because the size of inorganic nitrogen pools in algal cells changes with concentrations of nitrogen available to the cells, increased nitrogen concentrations in aquatic ecosystems may increase the total nitrogen content of algae without affecting its protein content or nutritional quality for upper trophic levels. This study (1) quantifies true protein and TN contents of periphyton from streams in southeastern New York and (2) evaluates the use of nitrogen content to estimate the protein content of periphyton in streams with differing concentrations of available inorganic nitrogen and phosphorus.

15. *(PA)* **PHYLOGENETIC INVESTIGATION OF GREEN ALGAE THAT SYMBIOSE WITH SALAMANDER EGGS.** Crystal Xue, Louise A. Lewis, Mark C. Urban & Kurt Schwenk. University of Connecticut, Department of Ecology and Evolutionary Biology, Storrs, CT, 06269, USA.

The green alga *Oophila amblystomatis* Lambert ex Wille was described in 1909 for green algae that symbiose with salamanders in the egg stage. These algae were shown to provide oxygen and carbon to the developing salamanders. The source of the algae is under debate. Early studies concluded that the algae enter the eggs from the surrounding water once they are laid. Yet, an intimate association of green algae and their salamander partners has been described in which the algae occur inside tissues and even cells of embryonic salamanders, suggesting that there is maternal contribution. It is also known that male salamanders deposit spermatophores on pond vegetation, after which the spermatophores are used by females for internal fertilization. Thus, we investigated possible sources of the salamander green algae in one small pond in Connecticut, USA, by comparing *rbc*L sequences of algae cultured from spermatophores, cloacal swabs of male salamanders, egg mass jelly, and eggs. The sequences of algae from eggs were distributed into five phylogenetic lineages. Sequences of algae from jelly, cloacal swabs and spermatophores were found in three lineages, two of which were shared with sequences of egg algae. We also examined the level of genetic variation within and among egg clutches, as we sampled algae from multiple eggs across clutches. Variation was found among eggs in some clutches but not in others. We cannot exclude either the maternal transmission or the environmental acquisition hypothesis, suggesting that both sources may contribute to the presence of algae in salamander eggs.

16. **PHYCO-FLASHCARDS, AN EDUCATIONAL TOOL TO INCREASE ALGAE AWARENESS.** Courtney Anderson & Brian Wysor. Department of Biology, Marine Biology and Environmental Science, Roger Williams University, Bristol, RI, 02809, USA.

Outside of this venue, algae are commonly misunderstood as slimy, smelly, or gross; in short, a problem to be remedied, an ailment to be treated, or a scourge to be eradicated. This sentiment is unlikely to be the result of an ecological smear campaign, rather an honest lack of appreciation and attention to the many services these organisms provide. In order to highlight the resources that marine macroalgae represent, we have produced a set of flashcards that highlight morphological features, habitat, and cellular structures of algae in the Rhode Island marine flora. The intent is to share these *Phycology Phlashcards* with students new to the discipline of phycology and outreach organizations that might not, as a matter of course, emphasize the value of the marine flora as source of oxygen, habitat and food. We envision using *Phycology Phlashcards* as a matching game in which various features of macroalgae such as branching pattern, pigment composition, life history strategy or other features are used as criteria on which to match organisms represented in the card deck. What makes this card game particularly fun, is that it is flexible to the creativity of user-defined match criteria. For example, young children might enjoy identifying similarities in color or branching patterns, while more advanced students could match on life history attributes, pigment composition, taxonomy, phylogeny or functional morphology. This memory game is a fun, interactive way to introduce the biodiversity of a commonly overlooked group of organisms to diverse audiences in a short amount of time.

17. *(PA)* **EFFECTS OF SALINE ENVIRONMENT ON FRESHWATER GREEN ALGAL SPECIES *MONACTINUS SIMPLEX* AND *PEDIASTRUM DUPLEX* (HYDRODICTYACEAE, CHLOROPHYCEAE).** India Dancil & Hilary McManus**.** Le Moyne College, Department of Biology, Syracuse, NY, 13214, USA.

The green algal family Hydrodictyaceae of the order Sphaeropleales is typically defined as consisting of species that grow in freshwater habitats. However, studies have indicated that *Monactinus simplex* and *Pediastrum duplex,* along with other algae from the taxonomic class Chlorophyceae, have been thriving in natural waterways with moderate to high salinity levels. Reported occurrences of these two species growing in brackish and high salinity include multiple lakes in Poland and in the Ebro River of Spain. To explore the possibility of euryhaline behaviour in *M. simplex* and *P. duplex*, both strains were grown in various salinities ranging from 0.62 mS/cm to 9.02 mS/cm. Colony volume of the species was measured on a weekly basis and compared with growth rates of cultures grown in the traditional freshwater medium, BBM+micronutrients+soilwater.

18. **METAGENOMIC ANALYSIS OF SUMMER PHYTOPLANKTON AND MICROZOOPLANKTON IN LOWER HUDSON RIVER SURFACE WATER.** A. Liberato[1], A. Yang[1], B. Sprung[1], E. Kim[1], S. Scheinbach[1] & M. Levandowsky[1,2,3]. [1]American Museum of Natural History, New York, 10023, USA; [2]Pace University, New York, NY, 10038, USA; [3]The River Project, New York, NY, 10001, USA.

We extracted DNA from a sample of saline surface water of the lower Hudson River taken in June 2013. Two size fractions, 80–20 mm and 20–0.2 mm, were obtained by sequential filtration of a liter of river water. DNA was extracted and amplified by Polymerase Chain Reaction (PCR) using 2 primer sets for the 18S small subunit ribosomal gene regions, and then sequenced using the Illumina MiSeq platform. The 2 primer sets yielded similar results, and many taxa were found in both size fractions; however dinoflagellates only appeared in the larger fraction. Greatest species richness was found in diatoms, ciliates and Rhizaria (chiefly cercozoa). About 200,000 paired end reads per sample were quality trimmed, merged and clustered using automated data processing pipelines, with a 97% identity threshold for clustering. Sequence clustering and annotation were based on a tool called USEARCH and the reference 18S SILVA database. This resulted in 250 - 350 clusters per set. We focus here on the 50 largest clusters in each set. For comparison, we also analyzed net plankton from a plankton tow with a 20 mm mesh net. This material was examined live using phase contrast microscopy and 16 taxa were noted, mostly diatoms. Hydrographic variables were also measured *in situ*.

19. *(TA)* **PHYSIOLOGICAL Fe SPARING IN CHLOROPLASTIC PHOTOPROTECTIVE MECHANISMS DURING IRON DEPRIVATION OF *DUNALIELLA TERTIOLECTA*.** Hannah Traggis. Department of Biological Sciences, University of New Hampshire, Durham, NH, 03824, USA.

Iron limitation is a major factor controlling primary productivity in large portions of the oceans. Yet some species of phytoplankton are able to persist and dominate community structures. Understanding the physiology behind this persistence is critical to predicting how our changing ocean climate, both acidification and warming, may affect these communities and the global carbon cycle. Previous studies in this lab have documented apparent iron-sparing by substitution of ascorbate peroxidase activities with an increased cellular pool of ascorbate and increased monodehydroascorbate reductase activity. Current investigations are underway to determine possible further iron sparing mechanisms with the superoxide dismutase system. Physiological assay of FeSOD and MnSOD coupled with Western blot with chemiluminescent detection analysis of cell fractions will be presented. Catalase activities under iron deprivation and xanthophyll cycle pigments will also be discussed.

20. **PHYSIOLOGICAL INFLUENCE OF ORGANIC FERTILIZER, TEMPERATURE AND PHOTOPERIOD ON *GRACILARIA TIKVAHIAE*, MCLACHLAN (GRACILARIALES, RHODOPHYTA).** Jennifer Savicky[1], Jang K. Kim[2], Scott Lindell[3] & Charles Yarish[1]**.** [1]Department of Ecology and Evolutionary Biology, University of Connecticut, 1 University Place, Stamford, CT, 06901, USA; [2]Department of Marine Sciences, University of Connecticut, 1 University Place, Stamford, CT, 06901, USA; [3]Marine Biological Laboratory, 7 MBL St., Woods Hole, MA, 02543, USA.

Inorganic nutrients have been primarily used in land based *Gracilaria* cultivation systems. We compared an organic fertilizer to inorganic fertilizer for *G. tikvahiae* culture, which might enable it to receive an organic food designation. *Gracilaria* was cultured at three different conditions: 20 °C with 16:8 L:D or 12:12 L:D photoperiod, and 25 °C with a 16:8 L:D photoperiod. Concentrations of the organic nutrients used were 250, 500 and 1000 µM of nitrogen in comparison to 500 µM of nitrogen supplied by the inorganic fertilizer. There was no clear effect of photoperiod or temperature on the growth rate of *Gracilaria*. *Gracilaria* exhibited a higher growth rate with the addition of organic fertilizer in comparison to inorganic fertilizer. The highest average growth rate at all temperatures and photoperiods was found at 1000 µM N organic fertilizer with an average of 14.4 % d^{-1}. The average growth rate of *Gracilaria* grown in the inorganic fertilizer at all temperatures and photoperiods was 8.6 % d^{-1}. *Gracilaria* grown in 1000 µM N organic fertilizer had the highest tissue nitrogen concentration with an average of 2.16%. The carbon to nitrogen ratio was the highest in the 250 µM N organic fertilizer with an average ratio of 26:1, suggesting nitrogen limitation at this condition. The lowest ratio was seen in 1000 µM N organic concentration with an average ratio of 13:1. The highest biomass yield was seen in 1000 µM N organic fertilizer with an average of 0.72 g L^{-1} d^{-1} at all temperatures and photoperiods. The inorganic fertilizer produced an average biomass yield of 0.49 g L^{-1} d^{-1} in all temperatures and photoperiods. If *Gracilaria* can be grown in an organic fertilizer it may qualify as “organic” designation for human consumption.

21. *(TA)* **INSIGHTS INTO THE DEVELOPMENT OF THE ENDEMIC NARROW-BLADE KELP *SACCHARINA LATISSIMA* FORMA *ANGUSTISSIMA* (LAMINARIALES, PHAEOPHYCEAE)**. Simona Augyte[1], Jang Kim[2] & Charles Yarish[1,2]. [1]Department of Ecology & Evolutionary Biology, University of Connecticut, CT, 06269, USA; [2]Department of Marine Sciences, University of Connecticut, CT, 06901, USA.

The narrow-blade kelp *Saccharina latissima* forma *angustissima* (F. S. Collins) Mathieson was first described by F. S. Collins in 1880. This form of *S. latissima* is morphologically distinct from the common variety (20-30 cm wide and ~ 2 m in length blades) in that it has one strictly narrow (1-2 cm wide) and long (> 4.0 m) blade with coalescent haptera with multiple stipes. The endemic narrow-blade kelp has been reported to have a restricted distribution in mid-coastal Maine, although additional reports throughout the Gulf of Maine and Southern New England need to be examined further. This form occurs in the low intertidal in areas exposed to high ocean swells such as flat ledges and islands in comparison to the common form that is found in the low and subtidal environments with low wave energy. Preliminary molecular analysis of sequences of the nuclear 18S ITS and mitochondrial cytochrome c-oxidase regions show high similarity to the common *S. latissima*. Common garden experiments in wave-impacted and calm environments as well as reciprocal crosses are proposed to identify ecotypic or ecophenotypic variation in both kelp. Distribution of this form will be investigated to understand vertical zonation limits. Manipulation of early stages of gametogenesis including gametophyte and young sporophyte development should provide insight into how ecological parameters affect morphology. Lastly, genetic variation between the morphologically distinct populations will be investigated.

22. **PHYLOGENETIC COMPARISON OF RUBISCO LARGE SUBUNIT (*rbc*L) GENE IN *SPIROGYRA* SPECIES: GEOGRAPHY, MORPHOLOGY AND DNA SEQUENCE COMPARISONS.** Christine Brown[1], John D. Hall[2] & Richard McCourt[1]. [1]Academy of Natural Sciences of Drexel University, Philadelphia, PA, 19118, USA; [2]The University of Maryland, College Park, MD, 20742, USA.

Filamentous conjugating green algae (Class Zygnematophyceae) are common in freshwater habitats worldwide. Knowledge of the distribution and ecology of particular species of these algae is hindered by the difficulty of identifying strains to species. Species identification is based on sexually produced zygospores, which are found in only a small percentage of field collections. Instead we used gene sequence data to identify related strains of *Spirogyra*, *Mougeotia* and *Zygnema* from the North Eastern United States and place them in a larger phylogeny of the genus. In addition, we tested for patterns of genetic divergence relative to between-habitat distance. Given the limited dispersal abilities and separation of habitats of freshwater algae, we predict that geographic distance is correlated with genetic distance on broader spatial scales and not on smaller, within habitat scales. We tested the hypothesis that this pattern holds for these genera of algae by comparing sequence divergence in rbcL to geographic distance between collections in the Northeastern U.S., as well as published data from collections across the U.S.

23. *(TA)* **INTEGRATED MULTI-TROPHIC AQUACULTURE IN THE GREAT BAY ESTUARY DURHAM, NH.** Katherine Hladki, Kyrstin Ward, Ray Grizzle & Christopher Neefus**.** Department of Biological Sciences, University of New Hampshire, Durham, NH, 03824, USA.

Aquaculture produces nearly half the world's seafood. Most current aquaculture production comes from monoculture systems that are often associated with negative environmental impacts such as eutrophication from increased nutrients. Integrated multi-trophic aquaculture (IMTA) is an emerging technology that can mitigate some of the environmental issues of aquaculture. Integrated aquaculture systems utilize waste from a primary species as food for a secondary species, turning waste nutrients that would otherwise be considered pollution, into a valuable resource. The Great Bay is located in Durham, NH. Called the hidden coast, it is one of the most inland estuaries in the world. Over the last several decades The Great Bay Estuary has suffered from several environmental issues, most notably eutrophication from nitrogen inputs. Currently, the waters of Great Bay are considered to have eutrophic or hypertrophic nitrogen levels. Other environmental concerns include habitat loss. For example, oyster beds in Great Bay have declined by nearly 90 percent since the 1970s (www.nature.org). Oyster beds are essential for estuary health as they provide habitat for juvenile fish and naturally filter the water. In this study integrated multi-trophic aquaculture in Great Bay is proposed as a way to generate economic growth in the area without further threatening the fragile estuary ecosystem. In the summer of 2013 an IMTA project was deployed in Great Bay using the eastern oyster (*Crassostrea virginica*) and *Gracilaria tikvahiae.* The purpose of this study was to determine if aquaculture method (IMTA vs. monoculture) had any impact on the growth, epiphyte cover, and nitrogen content of *Gracilaria tikvahiae.*

24. **SPECIES RICHNESS OF RED ALGAL ACCUMULATIONS ON SACHUEST BEACH, MIDDLETOWN, RI, USA.** Kelly DeMolles, James Flynn, Nicholas Hammerman, Benjamin Korry & Brian Wysor. Department of Biology, Marine Biology and Environmental Science, Roger Williams University, Bristol, RI, 02809, USA.

Sachuest Beach is a popular summer tourist destination on the southern shore of Rhode Island that seems to have experienced a long history of algal biomass accumulations. This phenomenon does not appear to be the product of an algal bloom *per se*; rather, local current and wind patterns, appear to retain drifting populations of marine algae in a semi-protected embayment. Locally referred to as "red tides," the water at Sachuest Beach can become crimson-hued due to the density of planktonic populations of the primary constituent, the filamentous *Spermothamnion repens* (Rhodophyta: Ceramiales). The incidence of significant algal biomass accumulations has escalated to problematic proportions in recent years, where it has deterred beach-goers and impacted the local economy. While *Spermothamnion* dominates the suspended populations, drift accumulations deposited on-shore are species rich. As a first step towards characterizing this biomass accumulation problem at the species level, and as part of the larger Rhode Island Seaweed Biodiversity Project, we attempted to elucidate red algal species richness based on morphological examinations and DNA Barcoding. To date, over 30 species have been documented as part of Sachuest Beach depositions.

25. **THE MACROALGAL HERBARIUM CONSORTIUM DIGITIZATION PROJECT.** Hannah Traggis & Christopher Neefus. University of New Hampshire, Department of Biological Sciences, Durham, NH, 03824, USA.

Macroalgae are a diverse group of aquatic photosynthetic organisms from four divisions spanning two kingdoms. They serve as the basis for nearly every benthic habitat providing food, shelter and substrata for other organisms. Globally, they are important primary producers and essential participants in ecosystem nutrient cycling. They are an important food source for humans and extractable colloids are used in pharmaceuticals and cosmetics. Worldwide, herbaria have housed plant and algal collections for 400 years providing a priceless record of distribution and ecology for local and visiting scientists. Recently, there has been an enormous collective effort to digitize herbarium and museum collections worldwide making the information therein available online, open-access to scientists and citizens alike. Funded by the NSF ADBC Program, the Macroalgal Herbarium Consortium (MHC) was formed, bringing together 49 universities, museums, botanical gardens and field stations from 26 states and U.S. possessions. The MHC collectively contains more than 1.1 million recent and historic specimens that will be digitized over the next four years. Digitization includes high resolution imaging, transcription of label information and georeferencing the collection site based on locality information. Images and data will be accessible through the MHC web portal (macroalgae.org) as well as iDigBio, GBIF, and other data integration portals. These databases are fully searchable by a number of criteria including taxonomy, collection date, geographic location and collector's name. These historic records will aid the study of bioinvasions, human impact and climate change effects on benthic community structures. Today, the project overview, sample workflow and geo-referenced samples will be presented.

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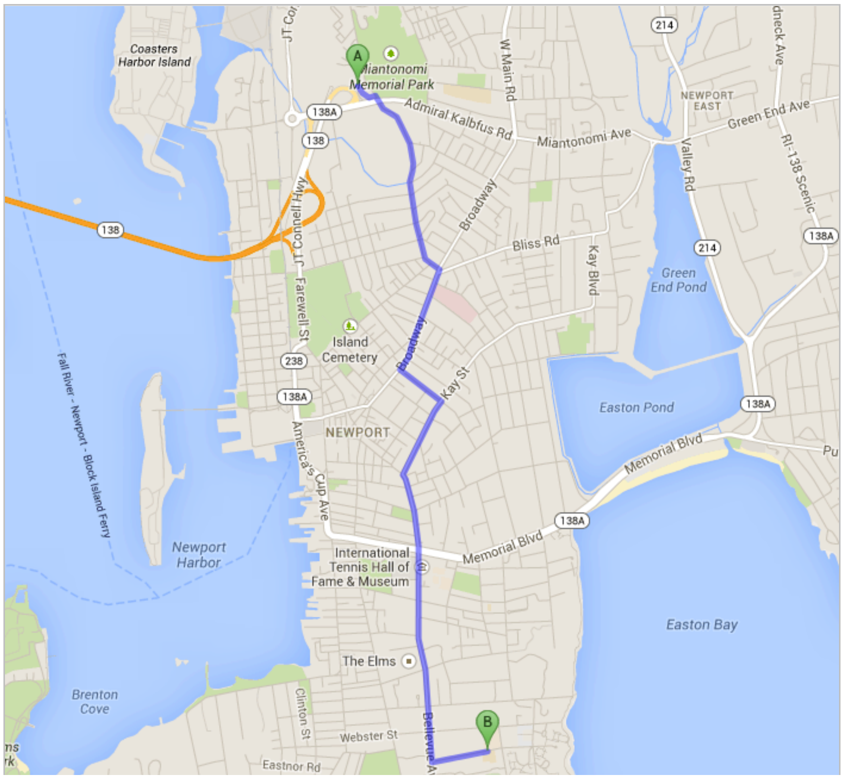
1. OCHRE COURT (parking along Webster St.)
    a. Friday Welcome Mixer

2. ANTONE ACADEMIC CENTER
    a. Continental breakfast, coffee breaks & vendors
    b. All presentations
    c. Poster mixer

3. Miley Hall
    a. Lunch on Saturday & Sunday (please bring lunch tickets provided in your registration packet)

Google

Directions to Leroy Ave, Newport, RI 02840
3.0 mi – about **10 mins**
Best Western Mainstay Inn to Antone Academic Center, Salve Regina University

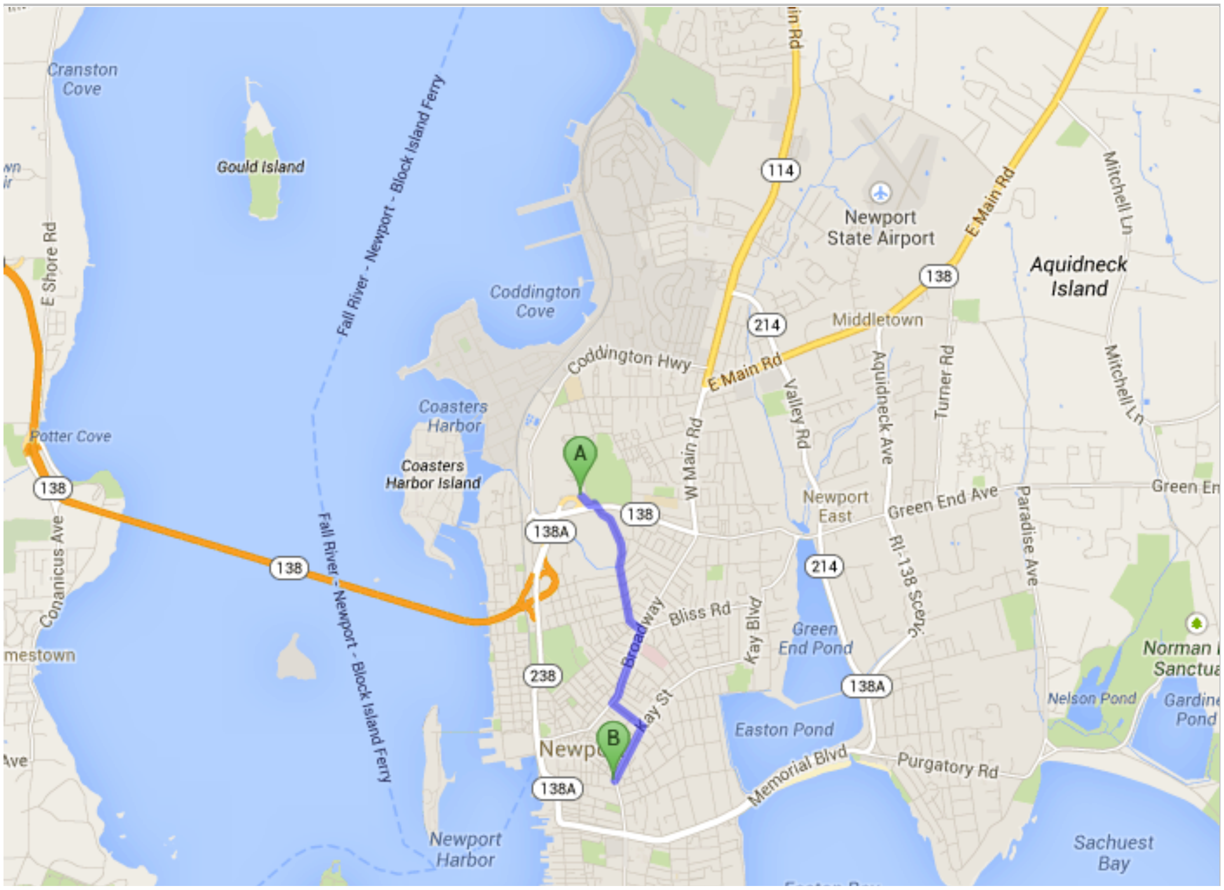


Best Western the Mainstay Inn
151 Admiral Kalbfus Rd, Newport, RI 02840

	1. Head **southeast** toward **Girard Ave**	go 463 ft total 463 ft
↱	2. Turn right onto **Girard Ave**	go 148 ft total 0.1 mi
	3. Continue onto **Malbone Rd** About 3 mins	go 0.7 mi total 0.8 mi
↱	4. Turn right onto **Broadway** About 1 min	go 0.4 mi total 1.2 mi
↰	5. Turn left onto **Ayrault St**	go 0.2 mi total 1.4 mi
↱	6. Take the 2nd right onto **Kay St** About 48 secs	go 0.3 mi total 1.7 mi
↰	7. Turn left onto **Bellevue Ave** About 3 mins	go 1.1 mi total 2.8 mi
↰	8. Turn left onto **Leroy Ave** About 54 secs	go 0.2 mi total 3.0 mi

Leroy Ave, Newport, RI 02840

Directions to 1 Bellevue Ave, Newport, RI 02840
1.7 mi – about **6 mins**
From Best Western Mainstay Inn to Hotel Viking

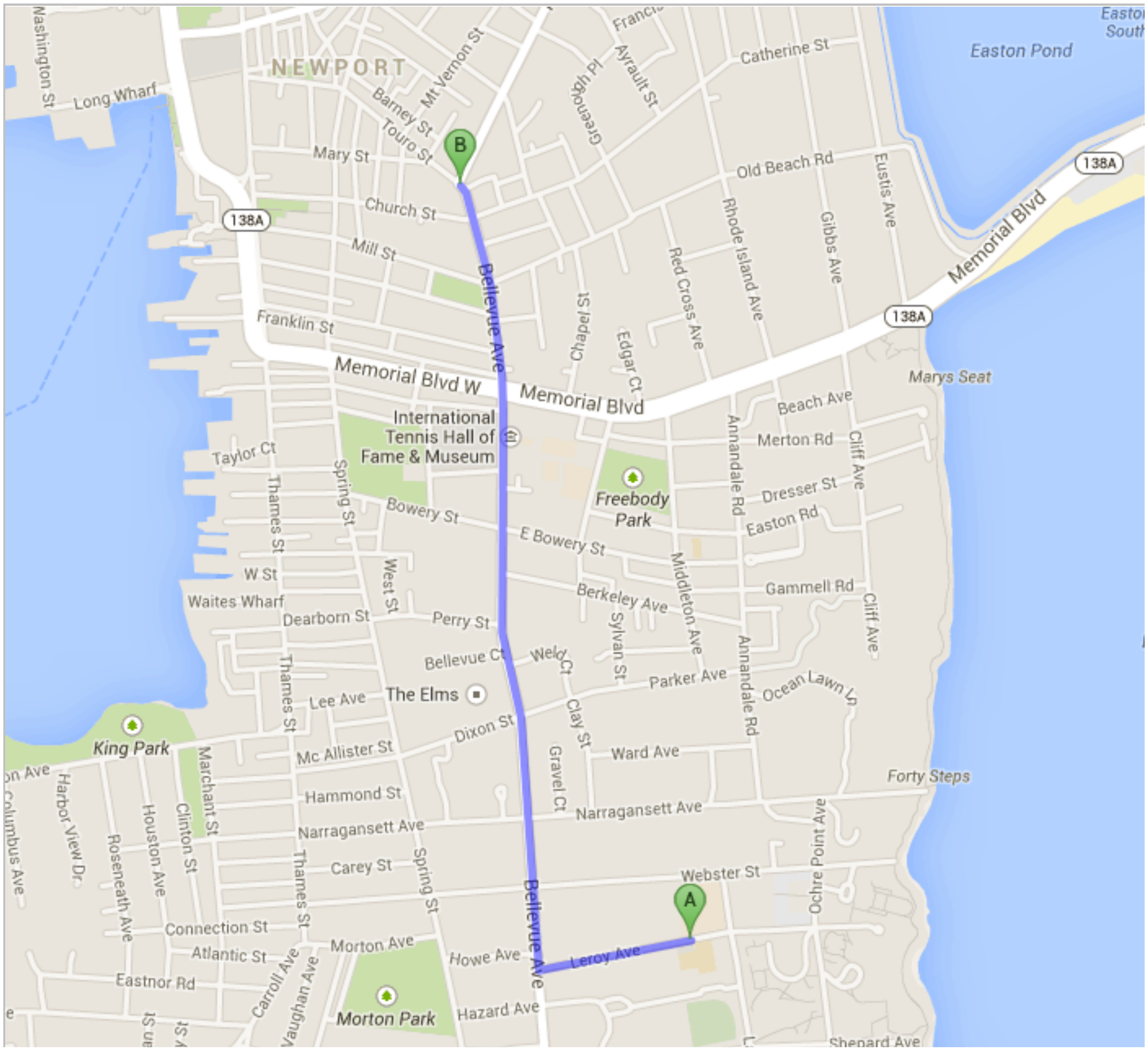


A 151 Admiral Kalbfus Rd, Newport, RI 02840

	1. Head **southeast** toward **Girard Ave**	go 463 ft total 463 ft
↱	2. Turn right onto **Girard Ave**	go 148 ft total 0.1 mi
	3. Continue onto **Malbone Rd** About 3 mins	go 0.7 mi total 0.8 mi
↱	4. Turn right onto **Broadway** About 1 min	go 0.4 mi total 1.2 mi
↰	5. Turn left onto **Ayrault St**	go 0.2 mi total 1.4 mi
↱	6. Take the 2nd right onto **Kay St** About 48 secs	go 0.3 mi total 1.7 mi
↰	7. Turn left onto **Bellevue Ave** Destination will be on the right	go 16 ft total 1.7 mi

B 1 Bellevue Ave, Newport, RI 02840

Directions to 1 Bellevue Ave, Newport, RI 02840
1.3 mi – about **4 mins**
Antone Academic Center to Hotel Viking



A Leroy Ave, Newport, RI 02840

	1. Head **west** on **Leroy Ave** toward **Bellevue Ave**	go 0.2 mi total 0.2 mi
↱	2. Turn right onto **Bellevue Ave** Destination will be on the left About 4 mins	go 1.1 mi total 1.3 mi

B 1 Bellevue Ave, Newport, RI 02840

53rd Annual
Northeast Algal Symposium

SALVE REGINA UNIVERSITY

Newport, RI
25-27 April 2014