



54th Northeast Algal Symposium • Syracuse, New York

54th Annual Northeast Algal Symposium



**GENESEE GRANDE
HOTEL**

**Syracuse, NY
17-19 April 2015**

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2015 Northeast Algal Symposium Sponsors



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Acknowledgements

The co-conveners acknowledge the generous support of our sponsors for this event, McDevitt Center for Creativity and Innovation at Le Moyne College, Le Moyne College Student Research Committee, and Great Lakes Research Consortium. We thank Stéphane Marty for designing the 2015 NEAS logo used for the t-shirts, Katie Hurley for providing the original *Ascophyllum* illustrations that provides the backdrop, and Le Moyne undergraduate students Allison Lurz and Lucas Smith for their assistance with registration and AV support. We also thank Kathryn Hennigan of the McDevitt Center (Le Moyne College), and Christine Tucciarone and Jodi O'Key at the Genesee Grande Hotel for all of their logistical support and assistance planning this year's meeting, and Theresa Baker at the Great Lakes Research Consortium for assistance with the student travel awards. We extend our gratitude to the judges for the student presentation awards: Mary Bisson, Sam Bowser, John Hall, Caroline Longtin (Robert T. Wilce Graduate Oral Award Committee), John Wehr, Diba Khan-Bureau, Lindsay Green, Dion Durford (Francis R. Trainor Graduate Poster Award Committee), and Dale Holen, Laura Von Rosk, Piotr Domaszczynski, Craig Aumack (NEAS President's Undergraduate Oral and Poster Award), and to the session moderators who helped keep the momentum: Louise Lewis, Meghann Bruce, Thea Popolizio, and Naomi Phillips. Finally, we are especially grateful for our invited opening speaker, Steve Effler (Upstate Freshwater Institute), and our mini-symposium speakers, Craig Aumack, Ronald Hoham, Louise Lewis and Lynn Rothschild, for their time and excitement to share their expertise on extreme algae with the NEAS membership.

With sincere thanks from your co-Conveners,

Hilary McManus
Le Moyne College

Greg Boyer
SUNY ESF

Molly Letsch
Le Moyne College

Welcome to Syracuse and the 54th Annual Northeast Algal Symposium!

We are excited you made the voyage to NEAS's most westerly venue. We hope this weekend will provide a great opportunity to exchange ideas with your fellow phycologists in the beautiful setting of the Genesee Grande Hotel in Syracuse, NY. Join us Friday evening at the social mixer in the Bistro from 6-7:30 p.m., during which you will have the opportunity to re-unite with and meet new phycological acquaintances representing 4 countries and 10 states and provinces. Steve Effler from the Upstate Freshwater Institute will talk from 7:30-8:30 p.m. about the unique history of Central New York's Onondaga Lake.

Saturday morning sessions will begin at 8:45 a.m. with opening remarks and welcome by Dr. Jennifer Gurley of Le Moyne College, followed by the graduate student scientific program at 9:15 a.m. The poster session and mixer will take place from 4:00 p.m. to 6:00 p.m. with a cash bar, followed by the banquet and infamous auction to be held in the Tiffany Room. Come bid often as we will be able to accept credit card payments for the auction items this year!

The mini-symposium on Sunday morning is "Algae in Extreme Environments" and will highlight four keynote speakers: Dr. Craig Aumack (Lamont-Doherty Earth Observatory at Columbia University), Dr. Ron Hoham (Colgate University), Dr. Louise Lewis (University of Connecticut), and Dr. Lynn Rothschild (NASA-Ames). We will learn about algae growing in a wide range of habitats. An opportunity to discuss the topic with the speakers will follow their talks.

The General Business Meeting and lunch will conclude the conference, where all members have an opportunity to share ideas and contribute to the society. The election results for our next fearless leader and Member-at-Large will be announced, and we will learn about the venue for next year's gathering. For those interested, there will be a guided walk along Onondaga Lake on Sunday afternoon.

We hope you enjoy your weekend with phycological friends in upstate NY!

Hilary McManus, Greg Boyer & Molly Letsch
2015 Co-conveners

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	<p>Samuel Drerup Ohio University sd136405@ohio.edu</p>	2014-2015

Friday, 17 April

4:00 pm – 6:00 pm	Afternoon Registration - Lobby
6:00 pm – 8:00 pm	Evening Registration & NEAS Welcome Mixer Lobby and Bistro
7:40 pm – 8:20 pm	Invited Presentation - <u>Steve Effler</u> THE CULTURAL EUTROPHICATION OF ONONDAGA LAKE Tiffany Room

Saturday, 18 April

8:00 am – 8:45 am	Continental Breakfast, Morning Registration, Poster Set-up, & Auction Donation Salon A&B and Lobby
8:00 am – 8:30 am	Session I & II load presentations
8:45 am – 9:15 am	Welcome & Opening Remarks Tiffany Room

Session I **STUDENT PRESENTATIONS, Moderator: Louise Lewis** Tiffany Room

9:15 am–9:30 am	Wilce Award Candidate <u>Chris Paight</u> , Sergio A. Muñoz-Gómez, Mary Beth Saffo, Claudio Slamovits, and Chris Lane COMMUNITY GENOMICS: DISENTANGLING THE ENDOSYMBIONTS OF THE MOLGULID RENAL SAC
9:30 am–9:45 am	Wilce Award Candidate <u>Catharina R. Grubaugh</u> and J. D. Wehr LAYING THE GROUNDWORK FOR USING ACUTODESMUS OBLIQUUS AND MOLECULAR TECHNIQUES TO ANSWER ECOLOGICAL QUESTIONS.
9:45 am –10:00 am	Wilce Award Candidate <u>Gina V. Filloramo</u> and G.W. Saunders. DNA BARCODE ASSESSMENT OF THE GENUS <i>RHODYMENIA</i> (RHODYMENIACEAE, RHODYMENIALES) FROM AUSTRALIA REVEALS CRYPTIC AND OVERLOOKED SPECIES DIVERSITY.
10:00 am–10:15 am	Wilce Award Candidate <u>Sarah B. DeVaul</u> and Robert W. Sanders TEMPERATURE-DEPENDENT PHAGOTROPHY AND PHOTOTROPHY IN A MIXOTROPHIC CHRYSOPHYTE.

10:15 am–10:30 am	<i>Coffee Break</i> Salon A&B
Session II	STUDENT PRESENTATIONS, Moderator: Meghann Bruce Tiffany Room
10:30 am–10:45 am	Wilce Award Candidate <u>Thea R. Popolizio</u> , Craig W. Schneider and Christopher E. Lane. MOLECULAR ANALYSIS RESOLVES THE TAXONOMY OF THE <i>LAURENCIA</i> COMPLEX (RHODOMELACEAE, CERAMIALES) IN BERMUDA AND UNCOVERS NOVEL SPECIES IN THE WESTERN ATLANTIC OCEAN.
10:45 am–11:00 am	Wilce Award Candidate <u>Eric D. Salomaki</u> and Christopher E. Lane THE PRICE OF PARASITISM: COMPARATIVE -OMICS OF A RED ALGAL PARASITE AND ITS HOST.
11:00 am–11:15 am	Wilce Award Candidate <u>Katherine A. Perri</u> , Susan B. Watson, and Gregory L. Boyer PRODUCTION OF SIDEROPHORES BY FRESHWATER CYANOBACTERIA IN THE LOWER LAURENTIAL GREAT LAKES.
11:15 am–11:30 am	Wilce Award Candidate <u>Robin S. Sleith</u> , Amy J. Havens, Robert A. Stewart and Kenneth G. Karol DISTRIBUTION OF NITELLOPSIS OBTUSA IN NEW YORK, U.S.A.
11:30 am–11:45 am	President's Award Candidate <u>Joshua R. Evans</u> and Gary. W. Saunders. MOLECULAR 'FISHING' REVEALS <i>KALLYMENICOLA</i> GEN. NOV. INCLUDING THREE NEW HOST-SPECIFIC ENDO/EPIPHYTIC SPECIES OF MEIODISCACEAE (PALMARIALES, RHODOPHYTA).
11:45 am–12:00 pm	President's Award Candidate <u>Ivy Burns</u> , Lindsay Green, Deniz Ersegun, Jason Dahl, and Carol Thornber. HOLE-Y ULVA! EXAMINING THE ROLE OF HOLES IN SPECIES OF BLOOM-FORMING MACROALGAE.
12:00 pm–1:30 pm	Lunch - Bistro Executive Committee Luncheon - Capital Club Room
1:00 pm–1:30 pm	Session III & IV Speakers load presentations

Session III	Student and Contributed Presentations Moderator: Thea Popolizio, Tiffany Room
1:30 pm–1:45 pm	<u>Stephen D. Gottschalk</u> and Kenneth G. Karol. THE PLASTID GENOMES OF <i>SCHERFFELIA</i> AND <i>TETRASELMIS</i> .
1:45 pm–2:00 pm	<u>Sarah B. Whorley</u> and John D. Wehr. PERIPHYTON COMMUNITY COMPOSITION AND CARBON AND NITROGEN STABLE ISOTOPE PATTERNS IN AGRICULTURALLY IMPACTED STREAMS.
2:00 pm–2:15 pm	<u>Samuel S. Bowser</u> , Amy Leventer, Stacy Kim, Andrew Thurber, and Paul K. Dayton. MASSIVE DIATOM FLUX FOLLOWING BREAKOUT OF MULTI-YEAR SEA ICE, SALMON BAY, ANTARCTICA.
2:15 pm–2:30 pm	<u>Gordon Ober</u> and Carol Thornber GROWING PAINS: THE RESPONSE OF <i>ULVA LACTUCA</i> AND <i>FUCUS VESICULOSUS</i> TO THE COMBINED EFFECTS OF OCEAN ACIDIFICATION AND EUTROPHICATION
2:30 pm–2:45 pm	<u>Jonathan A.D. Neilson</u> , and Dion G Durnford. ANALYSIS OF THE LHC/LIL PROTEIN FAMILY WITHOUT MULTIPLE SEQUENCE ALIGNMENTS.
2:45 pm–3:00 pm	<i>Coffee Break</i> Salon A & B
Session IV	Student and Contributed Presentations, Moderator: Naomi Phillips Tiffany Room
3:00 pm–3:15 pm	<u>M.B. Bruce</u> and G.W. Saunders. INVESTIGATING SPECIES DIVERSITY, BIOGEOGRAPHY AND TAXONOMY WITHIN THE RED ALGAL GENERA <i>ANTITHAMNIONELLA</i> , <i>HOLLENBERGIA</i> AND <i>SCAGELIA</i> (CERAMIALES, RHODOPHYTA) IN CANADA.
3:15 pm–3:30 pm	<u>John Hall</u> , Rosalina Hristova Stancheva, Klaus Herburger, Louise Lewis, Richard McCourt, Robert Sheath and Andreas Holzinger. A REVIEW OF ZYGOGONIUM: ITS MORPHOLOGY, ECOLOGY AND OCCURRENCE IN NORTH AMERICA.

3:30 pm–3:45 pm	<u>Lindsay Green</u> , Carol Thornber, and Stephen Licht. THREE SPECIES OF BLADE-FORMING <i>ULVA</i> INHIBIT THE GROWTH OF CO-OCCURRING MACROALGAE THROUGH ALLELOPATHIC COMPOUNDS.
3:45 pm–4:00 pm	<u>Chris Neefus</u> . THE MACROALGAL HERBARIUM DIGITIZATION PROJECT
Session V 4:00 pm–6:30 pm	Student & Professional Contributed Posters Session & Mixer Salon A & B
7:00 pm–11:00 pm	NEAS Banquet, Awards & Live Auction Tiffany Room
Sunday, 19 April	
8:00 am–8:45 am	Light Breakfast & Poster Removal Salon A&B (Please remove posters by noon on Sunday)
8:30 am–8:45 am	Invited speaks load presentations Tiffany Room
Session VI	Invited Presentations, Moderator: Hilary McManus Tiffany Room
8:45 am–9:00 am	Announcements
9:00 am–9:30 am	<u>Craig Aumack</u> , Andrew Juhl, and Susanne Neuer. THE ARCTIC'S SECRET GARDEN: LANDFAST SEA ICE COMMUNITIES AND THEIR CONTRIBUTION TO THE UNDERLYING MARINE ECOSYSTEM
9:30 am–10:00 am	<u>Ron Hoham</u> . SNOW ECOLOGY: ALGAE IN AN EXTREME ENVIRONMENT.
10:00 am–10:30 am	<u>Louise Lewis</u> . THE DRIER SIDE OF GREEN ALGAE.
10:30 am–10:45 am	<i>Coffee Break</i>
10:45 am–11:30 am	<u>Lynn Rothschild</u> . EXTREMOPHILES AND THE SEARCH FOR LIFE IN THE UNIVERSE.
11:30 am–12:00 am	Invited Speaker Q&A and Closing Remarks
12:00 pm–1:30 pm	Lunch Pick-up & General Business Meeting Salon A&B and Tiffany Room
1:30 pm–3:00 pm	Onondaga Lake Field Trip Meet in the Tiffany Room at the close of the Business Meeting

**Invited Presentation
Friday, 17th April 2015**

7:30-8:30 PM

THE CULTURAL EUTROPHICATION OF ONONDAGA LAKE

Steven Effler, Upstate Freshwater Institute, Syracuse NY

Onondaga Lake is located along the northern edge of the City of Syracuse. Site of an early Jesuit mission in the 1656 and birthplace of the Haudenosaunee Confederacy, the lake has been closely tied to the city of Syracuse for more than 200 years. Commercial salt mining in the late 1700's led to the development of the Erie Canal and by the late 1800's Onondaga Lake was a popular tourist attraction with beaches, resorts and amusement parks to lure residents from New York City to the area. Unfortunately this did not last. The Solvay process was located along its shores to take advantage of the natural salt brines and easy transportation. The sewage treatment plant for the growing city of Syracuse was built in 1925 and discharged its primary effluent directly into the lake until it was upgraded in the 1950s. Steel and other heavy industries were also located along the lake shore. Allied Chemical started chlorine production in the 1940 using electrochemical cells which inadvertently discharged as much as 20 lbs of mercury per day into the lake. By 1940, swimming was banned in the lake and in 1968, a Federal lake study declared Onondaga Lake the most polluted lake within the Lake Ontario basin. The lake was declared a Federal and State superfund site in 1994 due to the combined nutrient and industrial pollution. In the last 30 years, Onondaga Lake has made a remarkable comeback from one of the most polluted lakes in the nation to where it now serves as an international demonstration site for lake restoration.



**Student and Contributed Presentations
Saturday 18th April 2015**

ABSTRACTS

9:15 – 9:30 am

COMMUNITY GENOMICS: DISENTANGLING THE ENDOSYMBIONTS OF THE MOLGULID RENAL SAC Chris Paight¹, Sergio A. Muñoz-Gómez², Mary Beth Saffo¹, Claudio Slamovits, Chris Lane¹ ¹ Department of Biological Sciences, University of Rhode Island, Kingston, RI, 02881, U.S.A. ² Department of Biochemistry and Molecular Biology, Dalhousie University, Halifax, NS, B3H4R2, Canada

Despite their photosynthetic roots, apicomplexans are highly successful parasites, infecting every major metazoan lineage. Apicomplexans are primarily intracellular parasites targeting blood cells or forming tissue cysts. However, species in the genus *Nephromyces* are beneficial endosymbionts, inhabiting all members of the tunicate family Molgulidae. Specifically, *Nephromyces* inhabits the renal sac, an organ unique to the Molgulidae. The renal sac contains high levels of urate, but its function is currently unknown. Completing this complex biological system are the bacterial endosymbionts with *Nephromyces* species, which introduce additional metabolic complexity. We have performed preliminary sequencing of the *Nephromyces* genome to determine the metabolic pathways that enabled *Nephromyces* to become an endosymbiont. Our sequence data revealed several *Nephromyces* species inhabiting a single tunicate host, greatly complicating sequence analysis. To facilitate further sequencing, a single *Nephromyces* species has been isolated and maintained in tunicate culture in the lab. The metabolic capabilities of both *Nephromyces* and its bacterial endosymbiont will be discussed with a focus on purine and carbon metabolism.

9:30 – 9:45 am

LAYING THE GROUNDWORK FOR USING ACUTODESMUS OBLIQUUS AND MOLECULAR TECHNIQUES TO ANSWER ECOLOGICAL QUESTIONS.

Catharina R. Grubaugh¹ & J. D. Wehr¹. ¹Louis Calder Biological Field Station and Department of Biological Sciences, Fordham University, Armonk, New York, 10504, USA.

Recent developments in molecular techniques have revolutionized the study of algal evolution and systematics and generated massive nucleic acid datasets. These powerful techniques also have great, but largely untapped, potential in many fields of ecology, including inter- and intraspecific competition, trophic dynamics, and ecosystem function. This talk will present initial findings that lay the groundwork for using molecular techniques and *Acutodesmus* (formerly *Scenedesmus*) *obliquus*, a well-studied chlorophyte, in ecological research. Our preliminary data show that molecular markers can be used to trace *A. obliquus* individuals through closed systems. We will discuss the application of these molecular techniques to our current research goal: to determine whether aquatic invertebrate grazers have the ability to selectively feed on algal cells of the same species (i.e., similar size and morphology) that differ solely in nutritional quality. Another molecular technique, the quantification

of various RNA transcripts with RT-PCR, may be used to examine expression patterns of ecologically relevant genes. We have begun to characterize fatty acid desaturase genes in *A. obliquus* to better understand how different culture conditions can affect the nutritional of this alga.

9:45 – 10:00 am

DNA BARCODE ASSESSMENT OF THE GENUS *RHODYMENIA* (RHODYMENIACEAE, RHODYMENIALES) FROM AUSTRALIA REVEALS CRYPTIC AND OVERLOOKED SPECIES DIVERSITY. Gina V. Filloramo & G.W. Saunders. Centre for Environmental & Molecular Algal Research, Biology, University of New Brunswick, Fredericton, NB E3B 5A3, Canada.

Previously published DNA barcode surveys of red macroalgae in Australia have revealed significant cryptic and overlooked diversity for the genus *Rhodymenia* with recognition of *R. novahollandica*, *R. prolificans*, *R. stenoglossa*, *R. wilsonis* and an additional four genetic species groups resolved to *Rhodymenia* that were represented by too few specimens for proper characterization. Since that study, robust sampling efforts in Australia have warranted reassessment and reinvestigation of the taxonomic status of species currently included in the genus *Rhodymenia*. Using the DNA barcode (COI-5P) the present study assigned approximately 200 Australian specimens to the genus *Rhodymenia* with these resolved as 12 genetic species groups. Molecular data confirmed the previously recognized *R. novahollandica*, *R. prolificans*, *R. stenoglossa* and *R. wilsonis* as distinct entities while some collections from Lord Howe Island, New South Wales were morphologically assigned to *R. novazelandica* Dawson from New Zealand. The remaining seven genetic groups were established as novel species. Morphological features for distinguishing the recognized Australian species of *Rhodymenia*, as well as biogeographical distribution patterns will be discussed.

10:00 – 10:15 am

TEMPERATURE-DEPENDENT PHAGOTROPHY AND PHOTOTROPHY IN A MIXOTROPHIC CHRYSOPHYTE. Sarah B. DeVaul & Robert W. Sanders. Department of Biology, Temple University, Philadelphia, PA 19122

Species of the genus *Dinobryon* are a significant component of the phytoplankton community in oligotrophic lakes. This mixotrophic chrysophyte defies traditional classifications of protists into discrete trophic modes by utilizing both phototrophy and heterotrophy. *Dinobryon* has been shown to contribute significantly to bacterial grazing, yet has an obligate requirement for light and restricts ingestion and growth in darkness. The balance between trophic modes, as well as efficiency of each, is influenced by a number of biotic and abiotic factors. We conducted a series of experiments to elucidate the role of temperature, light intensity and prey availability on bacterial ingestion rate and primary productivity in cultures of *Dinobryon* sp. Replicate flasks of non-axenic culture were incubated at two light intensities ($130 \mu\text{E m}^{-2} \text{s}^{-1}$ and $66 \mu\text{E m}^{-2} \text{s}^{-1}$) and under four temperatures: 8°C , 12°C , 16°C and 20°C . Bacterial ingestion rate was determined by uptake of fluorescently labeled tracers and primary production was measured by incorporation of radioactive ^{14}C . We found that rates of both grazing and photosynthesis by

Dinobryon sp. increased between 8°C and 16°C, and declined at 20 °C. Maximum bacterial ingestion rate (1.9 bacteria cell⁻¹ hr⁻¹) and primary production (1.5 pg C cell⁻¹ hr⁻¹) occurred at 16 °C under high light conditions. Photosynthesis vs. irradiance curves at 16 °C indicated that this mixotroph reached a higher maximum photosynthetic rate at a lower optimum light intensity relative to other temperatures. Calculations of carbon allocation from each trophic mode showed that *Dinobryon* sp. acquired 69-98% of its carbon from photosynthesis under the experimental conditions. These results have implications for the distribution and abundance of *Dinobryon* in aquatic systems where they play a role in carbon cycling by participating in primary productivity and remineralization of nutrients by grazing on bacteria.

10:15 – 10:30 Coffee Break

10:30 – 10:45 am

MOLECULAR ANALYSIS RESOLVES THE TAXONOMY OF THE *LAURENCIA* COMPLEX (RHODOMELACEAE, CERAMIALES) IN BERMUDA AND UNCOVERS NOVEL SPECIES IN THE WESTERN ATLANTIC OCEAN. [Thea R. Popolizio](#)¹, Craig W. Schneider² & Christopher E. Lane.¹ ¹ Biological Sciences, University of Rhode Island, Kingston, RI 02881, U.S.A.; ²Biology, Trinity College, Hartford, CT 06106, U.S.A.

In the last decade, molecular tools have revealed significant miscalculation of Bermuda's macroalgal biodiversity, especially among the red algae (Rhodophyta). A number of species have been persistently misidentified based on morphological similarities to species described from other localities. Some have been assigned to existing taxa not previously reported for the islands, and many have been determined to be novel species. Of late, researchers have substantially modified the '*Laurencia* complex' in several regions around the globe. In Bermuda, we have confirmed the presence of 5 of the 6 genera that currently comprise the complex—*Laurencia*, *Chondrophyucus*, *Palisada*, *Yuzurua* and *Laurenciella*. Our data does not support the century-old designation of *Laurencia obtusa* for the islands. Both *rbcl* and COI-5P data support the recognition of at least two species for what has historically been labeled *L. obtusa*, grouping with *L. dendroidea* and *L. catarinensis* in phylogenetic analyses. We also evaluate the relationship between the common intertidal species *L. microcladia* from the western Atlantic and its most closely related congeners. In the genus *Chondrophyucus*, we have identified one novel taxon. This species represents the first report of the genus in the western Atlantic that has been verified with molecular data. Additionally, we have uncovered a new species in the *Laurenciella* clade that is genetically and morphologically distinct from the monotypic *L. marilzae*.

10:45 – 11:00 am

THE PRICE OF PARASITISM: COMPARATIVE -OMICS OF A RED ALGAL PARASITE AND ITS HOST.

Eric D. Salomaki¹ & Christopher E. Lane¹. ¹Department of Biological Sciences, University of Rhode Island, Kingston, Rhode Island, USA.

Parasitism is a life strategy that has evolved in numerous lineages across the eukaryotic tree of life. Devastating human pathogens including malaria and toxoplasmosis have evolved from a photosynthetic ancestor. Genomic studies have revealed that non-essential genes have been lost in these highly derived parasites as they increasingly rely on a host for energy and nutrition. Because most parasitic lineages are distantly related from a free-living taxon, the initial effects of an organism transitioning from a photosynthetic to a parasitic life strategy remain mostly unknown. Parasitism has independently evolved numerous times among the red algae providing a framework for making direct comparisons between a parasitic and a free-living red alga which share a recent common ancestor. Previous research on red algal adelphoparasites (parasites that infect close relatives) demonstrated that the parasites had lost their own plastid and instead would incorporate a dedifferentiated host plastid when packaging its spores. Recently we sequenced a highly reduced native plastid from the alloparsite *Choreocolax polysiphoniae* that has lost genes involved in photosynthesis. Here we present data from genomic and transcriptomic sequencing of the *C. polysiphoniae* and its free-living host *Vertebrata lanosa*. These data show a reduction in the expression of nuclear-encoded plastid-targeted genes that encode proteins involved in manufacturing the phycobilisome and other photosynthesis related functions. Additional comparative data from *V. lanosa* and *C. polysiphoniae* will be presented and the genomic consequences and implications for the evolution of parasitism in red algae will be discussed.

11:00 – 11:15 am

PRODUCTION OF SIDEROPHORES BY FRESHWATER CYANOBACTERIA IN THE LOWER LAURENTIAL GREAT LAKES.

Katherine A. Perri¹, Susan B. Watson², & Gregory L. Boyer¹. ¹State University of New York – College of Environmental Science and Forestry, Syracuse, NY 13210 U.S.A., ²Watershed Hydrology and Ecology Research Division, Environment Canada, Burlington, ON, L7R 4A6, Canada

Cyanobacteria generally have higher iron requirements than most eukaryotic algae, and culture studies have shown that some cyanobacteria produce strong ferric iron chelators (siderophores) to facilitate iron uptake under iron-limited conditions. However, this mechanism has not been well characterized in natural systems, due largely to limitations in methodology. To evaluate the importance of siderophores to natural plankton assemblages in the Laurentian Great Lakes, a novel solid-phase extraction was used for shipboard extractions on samples collected across a range of trophic conditions and cyanobacterial densities. A total of 70 samples were collected from Lake Erie (10 sites) and Lake Ontario (8 sites) between 2012-2014. Eluents from the SPEs were later analyzed for hydroxamate siderophores using two methods: the Csáky test and LC-MS. Although many of the sites were dominated by cyanobacteria, *in situ* production of hydroxamate siderophores was detected at only one highly eutrophic site in Lake Erie (Sandusky

Bay). These results suggest that plankton at offshore sites in Lake Erie and all locations in Lake Ontario were not iron limited, that non-hydroxamate siderophores were produced, or that the biomass was insufficient to generate detectable levels of iron-binding compounds.

11:15 – 11:30 am

HOLE-Y ULVA! EXAMINING THE ROLE OF HOLES IN SPECIES OF BLOOM-FORMING MACROALGAE. Ivy Burns¹, Lindsay Green¹, Deniz Ersegun², Jason Dahl², and Carol Thornber¹. ¹University of Rhode Island, Dept. of Biological Sciences, 120 Flagg Road, Kingston, RI 02881; ²University of Rhode Island, Dept. of Ocean Engineering, 15 Receiving Road, Narragansett, RI 02882

Species of the genus *Ulva* are key contributors to macroalgal blooms and generally propagate asexually via fragmentation. The dominant species of *Ulva* in Narragansett Bay are *Ulva rigida* (blade contain holes) and *Ulva compressa* (blade lacks holes). We formed two testable hypotheses to test the role of holes in *Ulva rigida*. First, we hypothesized that the holes in *Ulva rigida* aid in propagation via fragmentation. To test this hypothesis, we compared tissue toughness and tensile strength of *Ulva rigida* and *Ulva compressa*. *Ulva rigida* had higher tensile strength than *U. compressa* and observations indicated that tearing in *U. rigida* generally occurred near the holes. There was also a slight difference between the tissue toughness of the species, although it was not statistically different. Our second hypothesis was that the holes in *Ulva rigida* may increase turbulent flow on the blade surface, thus increasing nutrient uptake and growth. We used digital particle image velocimetry to determine the boundary layer of both *U. rigida* and *U. compressa* and this data will be presented.

11:30 – 11:45 am

MOLECULAR 'FISHING' REVEALS KALLYMENICOLA GEN. NOV. INCLUDING THREE NEW HOST-SPECIFIC ENDO/EPIPHYTIC SPECIES OF MEIODISCACEAE (PALMARIALES, RHODOPHYTA). Joshua R. Evans & Gary. W. Saunders. Centre for Environmental & Molecular Algal Research, Biology, University of New Brunswick, Fredericton, NB E3B 5A3, Canada

Contaminant sequences generated during routine COI-5P DNA barcoding of British Columbia Kallymeniaceae had affinities to Meiodiscaceae, Palmariales. To further explore the source, frequency and diversity of the species associated with these sequences in west coast Kallymeniaceae, primers to amplify specifically *rbcL* from Meiodiscaceae were developed. Ultimately 284 kallymeniacean specimens representing 17 species were screened with 12 specimens from three species yielding positive PCR amplifications, which after sequencing resolved as three distinct host-specific genetic groups. Combined *rbcL* + COI-5P phylogenetic analyses confirmed assignment of the three genetic groups to a novel lineage in the Meiodiscaceae as a relatively distant sister to the genera *Meiodiscus* and *Rubrointrusa* necessitating a distinct genus for these taxa, *Kallymenicola* gen. nov. Anatomical studies of these 12 specimens revealed endo/epiphytic species with palmariallean attributes (notably asexual reproduction from tetrasporangia with regenerative stalk cells) that were assigned to the three species *Kallymenicola*

invisibilis sp. nov. (host = *Pugetia fragilissima* Kylin), *K. penetrans* sp. nov. (host = *Erythrophyllum delesserioides* J. Agardh) and *K. superficialis* sp. nov. (host = *Euthora timburtonii* Clarkston & G.W. Saunders).

11:45 am – 12:00 pm

DISTRIBUTION OF NITELLOPSIS OBTUSA IN NEW YORK, U.S.A. Robin S. Sleith^{1,2}, Amy J. Havens¹, Robert A. Stewart¹ & Kenneth G. Karol¹. ¹Lewis B. and Dorothy Cullman Program for Molecular Systematics, The New York Botanical Garden, Bronx, New York 10458, U.S.A.; ²The Graduate Center, CUNY, 365 Fifth Avenue, New York, NY 10016 U.S.A.

The charophytic green alga *Nitellopsis obtusa* (Characeae: Charophyta) was first reported in the New World in the St. Lawrence River in 1978. Since that time, *N. obtusa* has been reported from inland lakes throughout Michigan, northern Indiana, and western New York and has been listed as an aggressive invasive species by the United States Geological Survey. We studied the distribution of *N. obtusa* by surveying 390 waterbodies throughout New York. Previous reports were confirmed and new localities will be presented, including new reports from five counties (Franklin, Ontario, Seneca, Wayne, and Yates). In total, *N. obtusa* was found in 17 counties at 31 sites, including 16 inland lakes, seven sites in the St. Lawrence River, and eight sites in Lake Ontario. Much of the distribution pattern of *N. obtusa* in New York is correlated with human activity and water chemistry data. Among sites with Characeae (174), water chemistry parameters differed significantly between sites with *N. obtusa* and those without. Further work is needed to understand how environmental variables and human activities contribute to the current distribution of *N. obtusa* in North America.

12:00 – 1:30 pm Lunch Break

1:30 – 1:45 pm

THE PLASTID GENOMES OF SCHERFFELIA AND TETRASELMIS. Stephen D. Gottschalk^{1,2} & Kenneth G. Karol². ¹Department of Biological Sciences, Fordham University, Bronx, New York, 10458, U.S.A. ²The Lewis B. and Dorothy Cullman Program for Molecular Systematics, The New York Botanical Garden, Bronx, New York, 10458, U.S.A.

Recent studies have established a portion of the unicellular planktonic green algae — the portion referred to as prasinophytes — as a paraphyletic assemblage within the Chlorophyta. At least seven distinct clades are now thought to comprise the prasinophytes. Six of these clades have had representative plastid genomes sequenced. The genera *Scherffelia* and *Tetraselmis* are members of the remaining clade, Chlorellales, and lack sequenced genomes. Using next generation sequencing data we have made *de novo* assemblies of the plastid genomes for a representative of each of these two genera. The genomes of *Scherffelia* and *Tetraselmis* are 137,163 bp and 176,680 bp in length respectively. Each genome contains a large single copy, a small single copy and an inverted repeat. The small single copy is reduced to 3,385 bp in *Scherffelia* and 1,350 bp in *Tetraselmis*. Genes have been identified and rearrangements of at least six gene regions have occurred

between the two taxa. Structural comparisons between the genomes of these and other chlorophytic taxa are ongoing. These analyses shed light on the evolution of green algae plastid genomes and help to address important phylogenetic questions in the Chlorophyta.

1:45 – 2:00 pm

PERIPHYTON COMMUNITY COMPOSITION AND CARBON AND NITROGEN STABLE ISOTOPE PATTERNS IN AGRICULTURALLY IMPACTED STREAMS.

Sarah B. Whorley and John D. Wehr. Louis Calder Center – Biological Field Station and Department of Biological Sciences, Fordham University, Armonk, NY 10504.

Stable isotopes are increasingly used as indicators of environmental disturbance. We examined the taxonomic composition of benthic algae in conjunction with the use of $\delta^{13}\text{C}$ and $\delta^{15}\text{N}$ of stream water and periphyton, to determine the effectiveness of Best Management Practices (BMPs) used to mitigate agricultural disturbance in headwater streams in NY State. Stream water and periphyton were collected from five streams in each of four land-use categories: recently applied BMP treatments, long-standing BMPs, lacking BMPs, and minimally disturbed reference streams. Stream water and periphyton were sampled April through November 2013 and analyzed for $\delta^{13}\text{C}$ and $\delta^{15}\text{N}$ content. Enriched stream water $\delta^{13}\text{C}$ (-12‰) and $\delta^{15}\text{N}$ (9‰) explained low proportions of chlorophyte, rhodophyte, and xanthophyte algal groups, as well as low taxa richness. Conversely, depleted periphytic $\delta^{13}\text{C}$ (-20‰) was explained by low proportions of chlorophytes, diatoms, and low taxa richness. Enriched $\delta^{15}\text{N}$ (9‰) was similarly explained by chlorophyte, rhodophyte, and xanthophyte algal groups, as well as low taxa richness. Stream water and periphyton $\delta^{13}\text{C}$ in agricultural streams was 13.4% and 12.2%, respectively, greater than in reference streams, with no difference between BMP categories. $\delta^{15}\text{N}$ values in stream water in agricultural streams lacking mitigation averaged 33.9% greater than in reference streams, but varied little between BMP categories. Periphyton $\delta^{15}\text{N}$ in agricultural streams averaged 48.1% greater than reference periphyton, suggesting that algal assemblages indicated elevated N inputs from the landscape, despite BMP presence. These results suggest there was a significant effect of agriculture on stream water and periphyton biochemical properties, even following BMP mitigation. Results from this study suggest that current agricultural mitigation steps have not been fully effective at remediation.

2:00 – 2:15 pm

MASSIVE DIATOM FLUX FOLLOWING BREAKOUT OF MULTI-YEAR SEA ICE, SALMON BAY, ANTARCTICA. Samuel S. Bowser¹, Amy Leventer², Stacy Kim³,

Andrew Thurber⁴, & Paul K. Dayton⁵. ¹Wadsworth Center, NY State Dept. Health, Albany, NY 12201; ²Geology Department, Colgate University, Hamilton, NY 13346;

³Moss Landing Marine Laboratories, Moss Landing, CA 95039; ⁴College of Earth, Ocean, and Atmospheric Sciences, Oregon State University, Corvallis, OR 97331;

⁵Scripps Institution of Oceanography, La Jolla, CA 92037

Few records exist regarding the breakout of multi-year ice in Antarctica. During February 2011, McMurdo Sound experienced an unusually strong storm,

resulting in the breakout of decades-old ice at Salmon Bay (S 77° 55.708; E 164° 31.962) on the western side of the sound. The following spring, this weather event triggered the dense growth of algal strands, presumably tube-dwelling diatoms, on the underside of the new ice. Comparative photo/video records by divers (1988-89, 2004, 2011) and the remotely-operated vehicle SCINI (2010) show a depauperate benthic community in the bay, and dramatic input of phytodetritus associated with the November 2011 bloom. The diatoms deposited are similar to those observed by Watanabe (1988) in macroscopically-comparable, sub-ice algal strands from a coastal site in East Antarctica. Elsewhere, including shallow waters on the eastern side of McMurdo, localized deposition of organic material from under-ice and phytoplankton blooms occasionally exceeds the capability of the benthic community to decompose the algae without exhausting available oxygen. This can lead to organic-rich, highly sulfidic patchy habitats that impact the distribution of mega- and macrofaunal communities (pers. obs., Thurber, Kim, Smith et al. 2012). During the 2011 bloom, the Salmon Bay sediment surface had not yet become anoxic, although we posit that its impoverished macrofauna will be unable to process the large organic input and thus shift the habitat toward a sulfidic, bacteria-dominated community. With continuing climate change, the loss of multi-year sea ice is likely to become a common event in Antarctica, with associated organic disturbance and consequences for benthic communities.

2:15 – 2:30 pm

GROWING PAINS: THE RESPONSE OF *ULVA LACTUCA* AND *FUCUS VESICULOSUS* TO THE COMBINED EFFECTS OF OCEAN ACIDIFICATION AND EUTROPHICATION Gordon Ober¹ and Carol Thornber¹. ¹Biological Sciences, University of Rhode Island, Kingston, RI.

Ocean acidification and eutrophication are two important facets of global change. Their individual impacts have been well documented and are typically associated with detrimental effects on species and ecosystems. While troubling for many marine organisms, ocean acidification and eutrophication may benefit algae by providing increased resources. Here, I experimentally tested the response of algal growth and surface area to volume ratio to ocean acidification (increased pCO₂) and eutrophication (increased nutrient loading). Two common, intertidal algal species (*Ulva lactuca* and *Fucus vesiculosus*) with different life history strategies and evolutionary histories were used as test species. Individual algal thalli were placed in flow-through seawater systems with one of four experimental conditions: high pCO₂ (~1100 ppm) or background pCO₂ (~390 ppm) and high nutrients (200 μM TN) or low nutrients (10 μM TN), in a fully factorial design. Three experiments were run: the first two investigated the response of *U. lactuca* and *F. vesiculosus* in monocultures; the third tested the response of both species cultured together. This allowed us to determine the effect of the treatments on individuals as well as communities. Each experiment lasted three weeks, with mass, surface area, and tissue clippings for C:H:N analysis assessed weekly. We found that both ocean acidification and eutrophication impacted the growth rates and surface area to volume ratios in the fast-growing, opportunistic *U. lactuca*. Growth rates were significantly higher with increased pCO₂ and nutrients and the factors combined resulted in growth rates

more than four times higher than in controls. High pCO₂ also resulted in smaller surface area to volume ratios in *U. lactuca*. Growth rates in the long-lived *F. vesiculosus* were not affected by environmental conditions. We assess our findings of the resilience of these marine macrophytes in light of predicted environmental shifts in coastal systems.

2:30 – 2:45 pm

Analysis of the LHC/LIL protein family without multiple sequence alignments.

Jonathan A.D. Neilson, Dion G Durnford. University of New Brunswick

Traditional phylogenetics relies on multiple sequence alignments from which a phylogenetic tree is constructed representing the evolutionary relatedness of sequences in the alignment. These trees may represent the evolutionary history of an individual gene or protein, a gene or protein family, or be used as a proxy for species level relatedness. Certain assumptions go into multiple sequence alignment based phylogenetics. Chiefly among them is the assumption of homology where sequences included in the alignment are assumed to be homologous. This is not the case in many protein families, related through functional or structural domains, that contain non-homologous regions. One example is the extended LHC and LIL protein. LHC (light-harvesting complex) and LIL (light-harvesting-like) proteins are thylakoid membrane proteins that contain chlorophyll-binding domains. One-helix LILs originally evolved in cyanobacteria and were transferred to eukaryotes through endosymbiosis. They have one to four transmembrane helices, containing one or two chlorophyll-binding domains, and are involved in light-harvesting, regulating pigment synthesis and photoprotection. As such they all contain homologous (i.e. chlorophyll-binding domains) and non-homologous regions. Analyzing the entire LHC/LIL protein family using multiple sequence alignments is fraught with difficulties. The researcher must either subset their dataset to only include what is determined to be homologous sequences or decide which regions are homologous and ignore those that are not. In the current study we present two methods to examine the entire LHC/LIL protein family without the need for multiple sequence alignments. The first uses reciprocal BLAST all-vs-all queries to plot a protein similarity network. The second utilizes a motif discovery suite to identify short motifs in the dataset from which a distance matrix was generated and used to plot a neighbor-joining tree. The usefulness of the three approaches along with pros and cons will be discussed. Using these different techniques we propose a model for the evolution of the LHC/LIL protein family.

2:45 – 3:00 pm *Coffee Break*

3:00 – 3:15 pm

INVESTIGATING SPECIES DIVERSITY, BIOGEOGRAPHY AND TAXONOMY WITHIN THE RED ALGAL GENERA *ANTITHAMNIONELLA*, *HOLLENBERGIA* AND *SCAGELIA* (CERAMIALES, RHODOPHYTA) IN CANADA. M.B. Bruce and G.W. Saunders. Centre for Environmental & Molecular Algal Research, Department of Biology, University of New Brunswick, Fredericton, NB, Canada

The aim of this investigation was to resolve taxonomic, nomenclatural and distributional uncertainty surrounding species of the red algal genera *Antithamnionella*, *Hollenbergia* and *Scagelia* reported for Canadian coasts. Whereas only two species of *Antithamnionella* are currently recognized in the northeast Pacific, *A. pacifica* and *A. spirographidis*, we have confirmed the presence of an additional species, *A. floccosa*. Contrary to published accounts, *A. floccosa* is more widespread on the Canadian west coast than the morphologically similar *A. pacifica*. For the genus *Hollenbergia* in the northeast Pacific, analyses of genetic data are consistent with the two currently reported species (*H. subulata* and *H. nigricans*), however, we present genetic evidence that *H. nigricans* is more closely allied to the genus *Scagelia* than the type species of *Hollenbergia*, *H. subulata*. Finally, while *Scagelia occidentale* is currently reported in the Pacific and *Scagelia pylaisaei* is considered to be present in the Arctic and Atlantic, our analyses of both COI-5P and ITS resolved two closely related genetic groups with mixing of these populations in the Arctic. We argue that the two closely related genetic groups represent a single species, for which *S. pylaisaei* has priority, and that populations of this species have experienced past isolation (putative incipient speciation) followed by a collapse in barriers.

3:15 – 3:30 pm

A REVIEW OF ZYGOGONIUM: ITS MORPHOLOGY, ECOLOGY AND OCCURRENCE IN NORTH AMERICA. John Hall¹, Rosalina Hristova Stancheva², Klaus Herburger³, Louise Lewis⁴, Richard McCourt⁵ Robert Sheath² and Andreas Holzinger³. ¹Plant Science and Landscape Architecture, University of Maryland, College Park, MD, USA; ²Department of Biological Sciences, California State University, San Marcos, CA, USA; ³Institute of Botany, University of Innsbruck, Innsbruck, Austria; ⁴Department of Ecology and Evolutionary Biology, University of Connecticut, Storrs, CT, USA; ⁵Department of Botany, Academy of Natural Sciences of Drexel University, Philadelphia, PA, USA.

Differentiating the genera *Zygodonium* and *Zygnema* (Zygnematophyceae) has long been problematic. Many of their morphological characteristics overlap, and taxonomic experts have drawn different conclusions about the relationship between these genera. We investigated a sample of *Zygodonium ericetorum* Ktz. (the type species) from Austria. The species is phylogenetically distinct from the genus *Zygnema*, forming an early branch in the Zygnematophyceae. This sample of *Zygodonium* showed irregular branching, thickened cell walls, purple cytoplasm and discoid or globular chloroplasts but lacked a cellulosic wall separating the aplanospore from the sporangium. Although these characteristics had been considered diagnostic of *Zygodonium*, we found all of these characteristics except for the discoid chloroplasts in *Zygnema* as well. Thus we conclude that *Zygodonium*

is distinct from *Zygnema*, but most species previously assigned to *Zygogonium* are better treated as *Zygnema*. The occurrence and distribution of *Zygogonium* in North America will be discussed.

3:30 – 3:45 pm

THREE SPECIES OF BLADE-FORMING *ULVA* INHIBIT THE GROWTH OF CO-OCCURRING MACROALGAE THROUGH ALLELOPATHIC COMPOUNDS.

Lindsay Green¹, Carol Thornber¹, & Stephen Licht². ¹Department of Biological Sciences, University of Rhode Island, 120 Flagg Road, Kingston, RI 02881, U.S.A.

²Department of Ocean Engineering, University of Rhode Island, 120 Flagg Road, Kingston, RI 02881, U.S.A.

Narragansett Bay has been plagued with frequent ‘green tides’ dominated by blade-forming *Ulva* for over a decade. These blooms can have deleterious ecological and economic consequences by depleting oxygen and disrupting commercial and recreational fisheries. Evidence from other systems has suggested that *Ulva* can negatively impact the growth of co-occurring species through the formation and release of allelopathic compounds. *Gracilaria* is commonly found co-occurring with *Ulva* in estuarine habitats and in bloom mats and may encounter allelopathic chemicals released by *Ulva*. We tested the hypothesis that three species of blade-forming *Ulva* (*U. compressa*, *U. rigida*, and *U. lactuca*) inhibit the growth of *Gracilaria* through allelopathy. Tips of *Gracilaria* were grown in divided 1 L mesocosms with either *U. compressa*, *U. rigida*, or *U. lactuca* (1 g/L) for 8 days at 22°C and 110 $\mu\text{mol photons m}^{-2} \text{s}^{-1}$. *Gracilaria* only controls were also included. The blotted-dry wet mass of *Gracilaria* was recorded on day 0, 2, 4, 6, and 8 and relative growth rate was calculated for each 2-day period. Our results show that all three species of *Ulva* significantly inhibited the growth of *Gracilaria*, although the effect was dependent on time ($F_{9,156}=1.99$, $P=0.0436$). There was no significant difference in the growth rate of *Gracilaria* between treatments at day 2, 4, or 6. However, at day 8 *Gracilaria* co-cultured with *U. compressa*, *U. rigida*, and *U. lactuca* had significantly lower growth rates than the control. Further, the growth rate of *Gracilaria* co-cultured with *U. compressa* ($0.5 \pm 1.6 \%$ day⁻¹) was significantly lower than *Gracilaria* co-cultured with *U. lactuca* ($3.7 \pm 1.4 \%$ day⁻¹). Our results indicate that *Ulva* can inhibit the growth of co-occurring macroalgae when present at concentrations of 1 g/L which are regularly encountered in natural habitats and bloom mats.

3:45 – 4:00 pm

THE MACROALGAL HERBARIUM DIGITIZATION PROJECT. Chris Neefus.

Department of Biological Sciences, University of New Hampshire, Durham NH, 03824.

Through the NSF Advancing Digitization of Biological Collections (ADBC) program, funding has been provided to digitize all of the macroalgal specimens in U.S. herbaria and to make the information accessible online. Currently over 1 million specimens in 50 collections at universities, botanical gardens, museums, and field stations are being digitized. Images of each specimen are being captured using high resolution photography. Specimen label information is being transcribed, and where locality information is provided, the collection location is being georeferenced

to facilitate mapping. Data is accessible through the project's portal <http://macroalgae.org>. A brief overview of the digitization methodology will be presented along with a demonstration of how the data portal can be used to study changes in species distribution and algal community structure over time. The NSF ADBC program includes a mechanism to apply for funding to include additional collections in the project. Herbarium personnel and phycologists associated with macroalgal collection that are not currently part of the project are encouraged contact the presenter. People interested in using the project data portal for their research are invited to make suggestions on new features that would facilitate data extraction and visualization.

LE MOYNE

SPIRIT. INQUIRY. LEADERSHIP. *JESUIT.*

**Invited Presentations
Sunday, 19th April 2015**

ABSTRACTS

9:00 - 9:30 am

THE ARCTIC'S SECRET GARDEN: LANDFAST SEA ICE COMMUNITIES AND THEIR CONTRIBUTION TO THE UNDERLYING MARINE ECOSYSTEM

Craig Aumack¹, Andrew Juhl¹, and Susanne Neuer². ¹*Lamont-Doherty Earth Observatory at Columbia University NY.* ²*School of Life Sciences, Arizona State University, AZ.*

Sea-ice environments support a diverse interstitial algal community that contributes to annual polar production and, upon export, provides nutritious material to underlying ecosystems prior to spring bloom development in the open water. However, both the ecological and biogeochemical connections between sea ice derived material and the underlying marine systems are relatively unknown. In Spring 2011-2014, a series of field and laboratory experiments were conducted to further investigate community dynamics within the sea ice along with the ultimate fate of this material once it leaves the ice. Whether materials exported are primarily consumed by pelagic or benthic organisms is related to residence time in the water column, a capricious characteristic that can be influenced both by biotic (algal composition, EPS concentration) and abiotic (nutrient dynamics, overlying snow cover) factors. Results indicate that community composition, vertical orientation within the ice, and sinking velocity are all related to overlying snow depth and distance from the ice-water interface. This suggests that algal production within sea ice, carbon flux from sea ice, and the availability of this material to various marine organisms can be significantly influenced by local climate related shifts in temperature and precipitation.

9:30-10:00 am

SNOW ECOLOGY: ALGAE IN AN EXTREME ENVIRONMENT.

Ron Hoham, Department of Biology, Colgate University, Hamilton, NY 13346.

Snow algae occupy one of the most extreme habitats for life in temperatures near 0° C, extreme irradiance levels, usually acidic pH and low nutrients, and desiccation after snow melt. Most snow algae are chlamydomonad Volvocalean green algal flagellates that color the snow red, green, or orange; however, golden-brown snow is caused by chrysophytes. Green chlamydomonad cells are composed mostly of saturated fatty acids; whereas in red cells they are mostly monounsaturated. Orange cysts of *Chloromonas (Cr.) polyptera* have a higher percentage of

carotenoids than chlorophylls, are photosynthetically active, and contain water stress compounds during freezes and dehydration (Remias *et al.*, 2013). The chlamydomonad life cycle correlates with snow melt, light penetration, cyst germination, large populations, nutrient depletion, and new cysts prior to snowmelt. Molecular phylogenies reveal that chlamydomonad flagellates have invaded the snow habitat at least three times. Three temperate species of *Chloromonas* from upstate NY will be emphasized, *Cr. rosae* v. *psychrophila*, *Cr. tughillensis*, and *Cr. chenangoensis*, looking at temperature and pH optima, effects of coniferous leachates on growth, differences between strains (isolates), and the effects of light (spectral composition, irradiance level, and photoperiod) on sexual reproduction. Comparisons between these three species are made with the polar Antarctic snow alga, *Cr. polyptera*. Several micro- and macroscopic life forms live in or beneath snow or burrow through snow forming food chains and food webs. The future of snow algal research will be considered.

10:00-10:30 am

THE DRIER SIDE OF GREEN ALGAE.

Louise A. Lewis. University of Connecticut, Department of Ecology and Evolutionary Biology, Storrs, CT, 06269, USA.

Since the pioneering work characterizing algae of arid habitats, much progress has been made toward understanding the diversity, evolution, and underlying physiological and cellular mechanisms used by algae living in terrestrial habitats. I will first discuss our growing understanding of the diversity of green algae from aquatic to terrestrial habitats. Numerous invasions of the land have occurred across the green algae, and increased sampling provides a better understanding of algal geographic distributions and indicates multiple independent transitions even within certain genera. Some terrestrial invasions may be evolutionarily ancient whereas others are younger. Second, I will focus on the many ways that green algae tolerate/survive on land. Physiological studies show behavior indicative of vegetative desiccation tolerance (poikilohydry) although a range of different mechanisms have been demonstrated. New approaches promise to reveal answers to important questions such as, “How quickly do adaptations to land evolve?” and “Are the mechanisms of tolerance ancestral or derived?”

10:45-11:30 am

EXTREMOPHILES AND THE SEARCH FOR LIFE IN THE UNIVERSE.

Lynn J. Rothschild. NASA Ames Research Center. Moffett Field, CA 94035 USA

The search for life in the universe relies on defining the limits for life, and then finding suitable conditions for its origin and evolution elsewhere. From the biological perspective, a conservative approach uses life on Earth to set constraints on the environments in which life can live. Thus, we will describe what is known about conditions for the origin of life and limits to life on Earth as a template for life elsewhere, with a particular emphasis on such physical and chemical parameters as temperature, pH, salinity, desiccation and radiation. But, other life forms could exist, thus extending the theoretical possibility for life elsewhere. By utilizing new experimental tool sets such as synthetic biology, we are extending the range for the potential environments for life. At the same time, planetary missions in our own Solar System have greatly enlarged our knowledge habitable niches in our neighborhood, while Kepler and other telescopes are uncovering extrasolar Earth-like planets providing the first hint at habitable bodies outside of our Solar System.



**Contributed Posters Session
4:00-6:30 pm Saturday 18th April 2015**

ABSTRACTS

1.

Chrysophyte Stomatocyst Production in Laboratory Culture and Descriptions of Seven Cyst Morphotypes. Dale A. Holen. Penn State University, Dunmore, Pennsylvania, 18512, U.S.A.

There is an extensive literature on chrysophyte stomatocysts from diverse habitats and their use as paleolimnetic indicators of past environmental conditions in lakes. The majority of these cysts are unidentified and more laboratory studies are needed to link stomatocyst morphotypes to vegetative stages. A laboratory procedure that resulted in stomatocyst production in the chrysophyte alga *Ochromonas pinguis* (Chrysophyceae) was tested to determine if the protocol would also stimulate the production of stomatocysts in six other chrysophytes. *Chrysolepidomonas dendrolepidota*, *Dermatochrysis* sp., two different strains of *Synura* cf. *petersenii* and a second species of *Ochromonas* all produced stomatocysts within two to three weeks. Morphology of the stomatocyst was described using SEM. This was the first report of stomatocysts from *Chrysosaccus* and the first SEM description of *O. pinguis* cysts. Chrysophyte autecological studies on stomatocysts assure a greater linkage between sediment stomatocysts and their biological origin. This not only strengthens the interpretive value of these microfossils but also broadens our understanding of chrysophyte biogeography.

2.

HYDROPEAKING AND SUBSTRATE LIMIT PERIPHYTON NUTRITIONAL QUALITY IN AN ALPINE STREAM

¹Cashman, M.J., ²Bruno, M.C., ²Maiolini, B., ¹Harvey, G.L., ¹Wharton, G. ¹School of Geography, Queen Mary, University of London, London, UK. ²Fondazione Edmund Mach, Research and Innovation Centre. S. Michele all'Adige, Italy.

The fluctuating discharge from hydroelectric dams, known as hydropeaking, has been shown to cause catastrophic drift in aquatic communities and limit secondary production. We hypothesized that rivers undergoing hydropeaking may have suppressed periphyton biomass and especially nutritional quality (*i.e.* essential fatty acids). Since periphyton nutritional quality, especially fatty acid content, has been suggested to be a limiting resource on production in aquatic systems, this may result in an indirect and potentially overlooked limiting effect on aquatic consumers in hydropower-impacted alpine streams. We further hypothesized that substrates available in the channel, particularly wood, may mitigate the effect of hydropeaking due to its hydraulic effect on flow. We simulated daily 5-hour hydropeak events over the course of 5 days in an *in situ*, open air, experimental flume system fed by a pristine 2nd order stream in the Italian Alps. Hydropeaking resulted in decreased periphyton biomass growing on tiles, but there was no corresponding decrease in periphyton growing on wood. Changes in periphyton C:N stoichiometry, but not C:P, varied with substrate type. Essential fatty acids and ω 3: ω 6 ratios decreased on both

substrates, but there was less loss on wood. Ordination of the total fatty acid profiles indicated different periphyton fatty acid profiles before and after hydropeaking, and also by substrate type. These results suggests that hydropeaking may limit production via depressing primary biomass and nutritional quality, and that the availability of wood substrates may mitigate this effect.

3.

COMMUNITY ECOLOGY ASSOCIATED WITH THE INVASIVE MARINE ALGA *GRATELOUPIA TURUTURU*. Emily Bishop, Carol Thornber. University of Rhode Island, Dept. of Biological Sciences, 120 Flagg Road, Kingston, RI 02881

Invasive species have the ability to outcompete natives, and can create a monoculture if not mitigated by herbivores or some other mechanism. Limited information exists on the ecology of the invasive macroalgae *Grateloupia turuturu*, and the effect that herbivores have on its presence. Using laboratory mesocosm experiments, we investigated the ability of two invasive herbivore species common in Rhode Island, the snail *Littorina littorea* and Asian shore crab *Hemigrapsus sanguineus*, to control *Grateloupia* populations. In the first trial, *Grateloupia* was provided to a single herbivore (either *Littorina* or *Hemigrapsus*) or both herbivores together. *Grateloupia* controls were in the same mesocosms as each treatment, but were separated by a mesh partition to allow water flow and account for possible facilitation by herbivore presence. Preliminary results indicate that *Littorina* do indeed graze on *Grateloupia*, with an average decrease in mass of 37% after 6 days. There was no change in mass of *Grateloupia* in the presence of *Hemigrapsus* only or with *Littorina* and *Hemigrapsus* together. Upcoming trials will include two common species of marine macroalgae along with the *Grateloupia*, to investigate herbivore feeding preference when exposed to multiple food choices. The ultimate results of these trials are intended to indicate the success of the continued invasion of *Grateloupia* in Rhode Island waters, and predict the role of invasive herbivores in controlling *Grateloupia* populations.

4.

MOLECULAR-ASSISTED ESTIMATE OF GREEN ALGAL DIVERSITY IN RHODE ISLAND. Kelly DeMolles¹, Brian Wysor¹, & Chris Lane². Department of Biology, Marine Biology & Environmental Science, Roger Williams University, Bristol, RI, 02809, USA; ²Department of Biological Sciences, University of Rhode Island, Kingston, RI, 02881, USA.

Understanding the combined threats of global climate change and biological invasions requires a comprehensive understanding of species richness patterns across the diversity of life. For many groups of organisms, molecular validation of species richness is required to account for cryptic diversity, which underestimates richness, and phenotypic plasticity, which overestimates richness. Based on a survey of the literature we project that species richness of marine macroalgae in RI might approach 300 species, but a systematic, molecular-based evaluation of species richness has not been undertaken despite the recognition of important environmental changes occurring throughout region. Based on literature reports 86 species of marine Chlorophyta have a distribution that includes RI, but only 33

species have been specifically documented in RI waters. Here we present an updated account of green algal diversity in RI based on DNA Barcoding and morphological examination of recently collected specimens. Our molecular-based inventory from *tufA* data to-date confirms the presence of 26 green algal species, which includes several species that have no close sequence match in public databases and therefore might represent new distributional records for the state. Continued morphological and molecular examination will help to resolve species identities and evaluate whether these species represent marine floristic changes resulting from anthropogenic change to marine communities or simply the elucidation of true patterns of diversity using more sensitive methods.

5.

LOCI DISCOVERY IN HETEROKONT LINEAGES. Chelsea Colón, Jasmine Peake, and Naomi Phillips. ¹Biology Department, Arcadia University, Glenside Pa ²Zoology Department, University of Florida, Gainesville, FL

Some of the most diverse and ecologically important primary producers in marine systems are members of the Heterokonts. However, phylogenetic relationships among heterokont lineages remain poorly resolved partly due to a limited number of available phylogenetic markers. The goal of this research is to develop nuclear loci through bioinformatic mining of available genomic data and PCR screening of mined loci. We have mined over 3000 loci that are common among brown algae and other heterokonts. Approximately 300 of these loci were PCR screened, cloned and sequenced. To date, only two of these loci have recovered the same gene as the mined locus. This is an extremely low recovery rate and in sharp contrast to results in animal systems. Some of the challenges for algal systems are discussed along with next steps for developing nuclear loci for important primary producers.

6.

A COMPARATIVE ANALYSIS OF CHARACEAE NODE ANATOMY. Dario J. Cavaliere¹ & Kenneth G. Karol¹. ¹The Lewis B. and Dorothy Cullman Program for Molecular Systematics, The New York Botanical Garden, Bronx, NY, 10458, U.S.A.

Characeae is a group of freshwater green macroalgae distributed throughout the world in both tropical and temperate regions. The thallus is composed of an axis that is punctuated by a series of alternating nodes and internodes. Nodes are the site of branching and are composed of a complex of cells arranged in a ring around a variable number of central cells. Nodal anatomy is taxonomically informative and has been used to differentiate between *Chara*, *Lamprothamnium*, and *Nitella*. In the present study, we employ the use of classic histological techniques to analyze Characeae nodal anatomy. Six distantly related species within *Chara* were sampled—we confirmed that members of this genus consistently have two central cells. We also confirmed two central cells in *Nitellopsis obtusa*. Previous investigations of species within *Nitella* subgenus *Nitella* identified a variable number of central cells through observations of two dioecious species, *Nitella mirabilis* (four central cells) and *Nitella opaca* (five/eight central cells). We confirmed this variability within subgenus *Nitella* through analysis of a monoecious species, *Nitella flexilis* (six/eight

central cells). In this study, *Nitella* subgenus *Tieffallenia* was represented by the monoecious species, *Nitella hyalina* (four central cells). Comparative analyses of Characeae node anatomy can inform subsequent developmental and taxonomic studies. Future research will increase sampling across *Lamprothamnium*, *Lycnothamnus*, *Nitella*, and *Tolypella*.

7.

DETERMINING THE STABILITY OF ALLELOPATHIC COMPOUNDS PRODUCED AND RELEASED BY THREE SPECIES OF *ULVA*. Kyle Carpentier, Lindsay Green, & Carol Thornber. Department of Biological Sciences, University of Rhode Island, 120 Flagg Road, Kingston, RI 02881, U.S.A.

The bloom-forming green macroalgal species *Ulva compressa*, *U. rigida*, and *U. lactuca* continue to persist in Greenwich Bay, RI. Algal blooms are known to cause anoxic conditions and are detrimental to local fishing industries. The allelopathic effects of these green macroalgae species on *Cystoclonium* and *Gracilaria* has previously been shown in co-culture experiments. However, the stability of these allelopathic compounds is unknown. This study aimed to determine the stability of the allelopathic compounds produced and released by *Ulva compressa*, *U. rigida*, and *U. lactuca*. We grew tips of *Cystoclonium* and *Gracilaria* for 6 days in filtered nutrient enriched thalli-free medium of *Ulva compressa*, *U. rigida*, and *U. lactuca* that had been cultured for 72 hours at concentrations of 2g/L and 1g/L. Nitrate concentrations were measured and replenished when necessary on days 2 and 5 to ensure growth was not nutrient-limited. Blotted-dry fresh weight of tips was recorded daily and photographs were taken to determine changes in surface area over time. We expect that if the allelopathic compounds produced by *Ulva* are stable, we will see a negative impact on the growth rates of *Cystoclonium* and *Gracilaria* cultured in thalli-free medium. The results of our ongoing trials will be presented and the implications of the stability of allelopathic compounds will be discussed within the context of macroalgal blooms in Narragansett Bay.

8.

UNDERSTANDING THE ORIGINS OF THE CANADIAN ARCTIC ALGAL FLORA THROUGH DNA BARCODING. Trevor T. Bringloe and Gary W. Saunders. Centre for Environmental & Molecular Algal Research, Biology, University of New Brunswick, Fredericton, NB E3B 5A3, Canada.

The contemporary Arctic algal flora is believed to have recolonized from the Atlantic following the last glacial maximum (~10,000 years ago). DNA sequence data, however, are revealing the underlying population structure of algal species suggesting that the Pacific has made a substantial contribution. Our research objectives are to: 1) further clarify the origins of the modern day Canadian Arctic flora (biogeography – what are the relative contributions of Atlantic and Pacific basins?); and 2) determine the frequency and periodicity (due to glaciation cycles) of movement of species between these basins since the Bering Strait opened, and if this movement and subsequent isolation has led to speciation events (phylogeography). To answer these questions marine algae will be sampled from key locations and a standardized gene fragment will be sequenced from each specimen

(i.e. DNA barcoding; mitochondrial COI) and added to a large and growing database of collections from throughout the Arctic. In addition, a more variable marker (i.e. cox2-3 intergenic spacer) will be used to elucidate further population level migration patterns. Identifying past migration corridors has direct implications for predicting future westward and northward expansion of species ranges, and sets a baseline for detecting invasion events. In a time of rapid climate change, these baseline data are critical in our efforts to understand and document changes to the Canadian Arctic.

9.

INCREMENTAL ADAPTATION OF *PLEUROCLADIA LACUSTRIS* (PHAEOPHYCEAE) TO BRACKISH MEDIA OF INCREASING SALINITIES.

Nicholas R. Ballor and John D. Wehr. Louis Calder Center – Biological Field Station and Department of Biological Sciences, Fordham University, Armonk, NY 10504.

Of the approximately 2000 species of brown algae, only seven freshwater species (six genera) are currently recognized, which corresponds to less than 0.5% of all known members of the Phaeophyceae. The evolutionary origin and physiological characteristics of this unique group of freshwater taxa remain poorly understood. The sparse global distribution of freshwater brown algae and the small number of known species supports the hypothesis that they may represent an evolutionarily recent event within the class. We are testing the hypothesis that *Pleurocladia lacustris*, a freshwater brown alga, is a recent evolutionary development and may retain the capacity for adaptation to or survival in saline environments. *P. lacustris* has been reported in a few brackish and intermittently-marine environments, suggesting a moderate salinity tolerance. To evaluate the tolerance of and adaptation to saline environments, we are incrementally introducing increased concentrations of NaCl to the medium (MiEB₁₂) in which a freshwater population has been maintained. We have found that *P. lacustris* grown in MiEB₁₂ media shows an apparent range of salinity tolerance limited at present to between 0-3 ppt NaCl and that the same alga once adapted to MiEB₁₂ medium supplemented with 1.5 ppt NaCl can tolerate medium containing 3.0 ppt NaCl (approximately 10% seawater). Ongoing experiments are in place to assess the limits of *P. lacustris*' capacity to tolerate and adapt to salt stress and work is in progress to elucidate the physiological and genetic correlates of these adaptations. We have demonstrated that *P. lacustris* has the capacity to adapt to oligohaline media and that this adaptability has a limited capacity to accommodate sudden step-wise changes in NaCl concentrations of more than a few ppt.

10.

A NEW BEGINNING: *CHOREOCOLAX POLYSIPHONIAE* PROVIDES INSIGHT TO ALLOPARASITE EVOLUTION.

Katie R. Nickles¹, Eric D. Salomaki¹ & Christopher E. Lane¹. ¹Department of Biological Sciences, University of Rhode Island, Kingston, Rhode Island, USA.

Red algal parasites likely exist primarily due to their unique ability to create secondary pit connections. Generally, infection occurs when a parasite forms a secondary pit connection with the host and deposits its nucleus and organelles into the host cell, subsequently spreading throughout the host via these cell-cell

connections. Studies from the 1990's demonstrated that the parasites do not maintain their own plastid, but rather abscond with a dedifferentiated host plastid as they pack up spores for dispersal. -However, nearly all previous studies focused on interactions between adelphoparasites and their hosts. In our study, we examined sequence data from the alloparasite *Choreocolax polysiphoniae* and its host *Vertebrata lanosa* for differences in coding capacity. We identified and annotated the *V. lanosa* plastid, which is shorter than most florideophyte plastids at 167 kilobases, but still maintains the usual florideophyte genes and arrangement. We also identified the ~90,000 base pair plastid genome from the *C. polysiphoniae* which includes 71 protein-coding genes, 3 rRNAs, and 24 tRNAs. The *C. polysiphoniae* plastid is the first known non-photosynthetic red algal plastid, however genes involved in amino acid, fatty acid, and protein biosynthesis, transcription and translation as well as other cellular maintenance are conserved. The presence of a native plastid in *C. polysiphoniae* forces a re-interpretation of parasite evolution in red algae.

11.

A MORPHOLOGICAL AND MOLECULAR SURVEY OF ULVALES

(CHLOROPHYTA) SPECIES IN THE BAY OF FUNDY REGION. Kirby Morrill & Gary W. Saunders. Centre For Environmental & Molecular Algal Research, Department of Biology, University of New Brunswick, Fredericton, NB, E3B 5A3, Canada.

A floristic survey of green macroalgae has not been conducted in the Bay of Fundy (New Brunswick, Canada) since DNA barcoding became readily accessible. Collections available in the Connell Memorial Herbarium (University of New Brunswick) suggest that there are probably 26 unique species of the order Ulvales present in the Bay of Fundy – this in stark contrast to reports in previous floristic surveys. Clearly a full account of the Bay of Fundy ulvlean flora using molecular techniques is overdue. Unfortunately this task is complicated by contradictions within molecular databases such as GenBank® regarding the application of names associated with morphospecies relative to genetic groups – unique genetic groups have been granted multiple morphospecies names, while reciprocally individual morphospecies have been linked to many genetic groups. These inconsistencies render molecular identification via sequence comparison to extant records in the various molecular databases unreliable. To alleviate this problem, our study will generate a detailed morphological description of each specimen collected from the Bay of Fundy to augment the standard DNA data. Using morphological descriptions in comparison with corresponding type descriptions, as well as considering the presence of a genetic group in the type locality, we intend to apply meaningful morphospecies names to the genetic groups present in the Bay of Fundy.

12.

MOLECULAR-ASSISTED ESTIMATE OF BROWN ALGAL DIVERSITY IN RHODE ISLAND WATERS. Joseph Martin¹, Brian Wysor¹, & Chris Lane². Department of Biology, Marine Biology & Environmental Science, Roger Williams University, Bristol, RI, 02809, USA; ²Department of Biological Sciences, University of Rhode Island, Kingston, RI, 02881, USA.

In the western North Atlantic Ocean, increasing sea surface temperatures associated with global climate change has resulted in the re-distribution of numerous marine species, and some ecological models project significant changes in the abundance of habitat forming species over the next century. The loss of significant intertidal habitat, combined with organismal range expansions foreshadows changes to species composition and ecosystem functioning that will be difficult to predict or monitor without a comprehensive, molecularly-informed foundation for species richness against which new species inventories can be evaluated. Here, we present an updated checklist of brown algae in RI based on DNA barcoding and morphological examinations of recently collected specimens. Our molecular-based inventory confirms the presence of 31 brown algal species, including 14 (45%) that have no close sequence match in public databases and therefore might represent new distributional records for the state or region. While some 133 brown algal species are reported to have a distribution that includes RI (i.e., Long Island Sound to the Gulf of Maine), only 43 species have been specifically reported for RI waters in the literature. Thus, we regard the current estimate of brown algal diversity for RI waters as conservative and very likely to change as identification and molecular characterization continues.

13.

THE UTILITY OF DNA BAR-CODING IN SARGASSUM. Aimee Malzahn¹, Naomi Phillips¹, Brian Wysor².¹Biology Department, Arcadia University, Glenside, PA ²Biology Department, Roger Williams University, Bristol, RI.

Sargassum is one of the most ecologically important and widespread brown algal genera. The genus commonly forms either pelagic floating beds or large coastal stands in tropical to subtropical oceans. However, there is still much to be discovered about its evolutionary history and phylogeny. Progress is hampered by high rates of phenotypic plasticity as well as a lack of in depth studies of Caribbean *Sargassum*. This is especially true for coastal areas of Panama, where the estimates of diversity suggest that the region has many undiscovered species. The development of DNA barcoding regions for *Sargassum* would solve the problems with morphological identification and enable phylogenetic analysis. The goal of this project is to compare three gene regions for barcoding utility, and use this data to contribute to the resolution of *Sargassum*'s phylogeny. Twenty-one samples from the Caribbean Sea and the Pacific Ocean in areas surrounding Panama were obtained. Samples were extracted using a modified CTAB method and whole genome amplified using Genomiphi methods to archive DNA. Several gene regions were selected, amplified (e.g. LSU, rbcL and ITS-2) and sequenced. All 21 samples were successfully extracted and whole genome amplified to be archived. Master

alignments for individual gene regions are being built for the genus using new and GenBank data. Phylogenetic analyses will follow.

14.

CHEMICAL WARFARE IN NARRAGANSETT BAY: DETERMINING THE ALLELOPATHIC EFFECTS OF *ULVA*.

Fiona MacKechnie, Lindsay Green & Carol Thornber. ¹Department of Biological Sciences, University of Rhode Island, 120 Flagg Road, Kingston, RI 02881, U.S.A

Several species of *Ulva* are commonly found in the waters of Narragansett Bay, especially in eutrophic waters, where they can form fast growing blooms that can have ecological and economical consequences. The formation and release of allelopathic chemicals has been previously documented in some species of *Ulva*, including *Ulva lactuca*. Three species of blade-forming *Ulva* are commonly found in Narragansett Bay and coastal Rhode Island, namely, *U. compressa*, *U. lactuca*, and *U. rigida*. We aimed to determine if these three species of *Ulva* had allelopathic effects by testing their impacts on the growth of other macroalgae. In the first trial, *Cystoclonium purpureum* tips were grown alone (control) or with either *U. compressa*, *U. rigida*, or *U. lactuca* in mesocosms separated by mesh for eight days. The blotted-dry fresh weight of *Cystoclonium* was recorded every other day and tips were photographed for surface area analysis in ImageJ. Nutrients were checked daily using NO₃ as a proxy and adjusted to prevent nutrient limitation. All three species of *Ulva* had a significant negative effect on the growth of *Cystoclonium*, although the effect was dependent on time. The largest negative effect was seen in the *U. compressa* and *U. rigida* treatments, where overall mass loss appeared after 6 days of co-culture. *U. lactuca* had a smaller negative effect on growth, with the average *Cystoclonium* growth rate after 8 days of co-culture (2.9 ± 0.9 % day⁻¹), significantly below controls (5.0 ± 0.8 % day⁻¹). Our results indicate that *U. compressa*, *U. lactuca*, and *U. rigida* can significantly inhibit the growth of other macroalgae. The results of experiments that investigated allelopathic effects of *Ulva* on the adult and sporeling stages of the common epiphytic macroalgae *Ceramium virgatum* will also be presented.

15.

THE DEVELOPMENT OF THE RED SEAWEED *PALMARIA PALMATA* AS AN INTEGRATED MULTI-TROPHIC AQUACULTURE (IMTA) SPECIES.

Caroline Longtin, Constanza Chianale Cerda & Thierry Chopin. Canadian Integrated Multi-Trophic Aquaculture Network (CIMTAN), University of New Brunswick, Saint John, NB, E2L 4L5, Canada.

Since 2001, the kelps *Saccharina latissima* and *Alaria esculenta* have been cultivated as the inorganic extractive component of the Integrated Multi-Trophic Aquaculture (IMTA) system from fall until early summer on Canada's east coast. The absence of year round crops at the sites, and the need to increase the biomitigative capacity of the IMTA system during summer, led us to investigate the development of the cultivation of *Palmaria palmata*. Being present in summer, accumulating high levels of nitrogen, and having an established commercial value, makes *P. palmata* an ideal candidate as a summer species for dissolved nutrient biomitigation,

especially at a time when local cases of overharvesting have been reported. While *P. palmata* has been harvested for centuries for human consumption, its large-scale cultivation has never been successful. The problem is that *P. palmata* has a complex life history, alternating an asexual tetrasporophyte phase with a sexual gametophyte phase; moreover, female gametophytes are microscopic crusts, while male gametophytes are macroscopic and indistinguishable from tetrasporophytes when they are not reproductive. The fact that sexual reproduction depends on females being fertilized by males of the previous generation, in combination with the observation that mature tetrasporophytes are present in high abundances during all seasons, suggests that there may be an unknown asexual life history phase. We plan to investigate this possibility, which could benefit culturing practices by eliminating the need for sexual reproduction to create multiple generations in culture, thereby reducing the pressure on natural populations. We have had recent success in the laboratory on the cultivation of *P. palmata* and we plan to perform a tetraspore release in April to seed a number of ropes, which will be deployed at IMTA sites after the kelp harvest in June.

16.

ISOTOPIC INFLUX OF CADMIUM INTO *CHARA AUSTRALIS* (R. BR.)

INTERNODAL CELLS. Nicole LoCascio, Claudia Aghaie, Mary A Bisson.

Department of Biological Sciences, University at Buffalo, New York.

Cadmium (Cd), a toxic heavy metal, occurs in the environment from weathering of Cd-containing sediment as well as agricultural and industrial actions. The fresh water alga *Chara australis* has the ability to take up Cd from the water and from the sediment, from it can be transported from the rhizoids to other plant tissues. The tissues can then be harvested, suggesting a potential for *C. australis* in phytoremediation. In order to determine the cellular mechanism of Cd transport into *Chara* internodal cells, we developed an experimental technique using radioactive ^{109}Cd to determine uptake mechanism. Isolated *Chara* internodal cells were exposed to different concentrations of Cd spiked with .449 Ci/mole ^{109}Cd , incubated for 5 s to 20 minutes, and rinsed in cold solution containing 8 mM CaCl_2 + 10 mM LaCl_3 for five minutes to remove excess Cd from the cell wall. Internodes were then counted in a gamma counter and influx determined. Cd flux has been determined in concentrations up to 1 ppm (8.9 μM) Cd. If Cd transport into the cytoplasm occurs by carrier-mediated transport, we predict the relationship will be hyperbolic due to the saturation of all carriers. Competition with nutrients that are also divalent cations such as zinc, calcium, and iron, will suggest which nutrient transport system admits Cd into the cell.

17.

DRIFT ALGAE – SEAGRASS- EPIPHYTE INTERACTIONS IN TWO TEMPERATE

SEAGRASS MEADOWS IN BARNEGAT BAY, NEW JERSEY. Elizabeth Lacey,

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Seasonal macroalgal blooms create canopies which reduce light availability to other macrophytes, causing significant declines in ecosystem health. Current

research suggests that the negative consequences of these blooms may be reduced if bloom residence is short as the decreased light availability reduces filamentous macroalgal load, thus increasing overall light availability when compared to exposed sites with higher epiphytic loads. During the Summer 2014 bloom period, two sites were monitored within Barnegat Bay, New Jersey as part of a long-term project assessing the impact of blooms on nearshore communities. During this bloom event, which lasted from May to August, Barrel Island had higher algal and amphipod biomass while Seaside Heights had higher epiphytic biomass. There was no significant difference in seagrass density, habitat complexity or photosynthetic performance between sites. At Barrel, we hypothesize that the reduction of epiphytes was caused by bloom-hitchhiking epiphytic grazers, which increased relative light availability, while the lack of drift macroalgae at Seaside Heights had a similarly high light availability. Reduction of light from epiphytes versus blooming macroalgae may have a similar overall impact to seagrass health; however, further research is necessary to test this new hypothesis.

18.

EXAMINING THE MOLECULAR PHYLOGENY AND TAXONOMY OF THE RED ALGAL ORDER HALYMENIALES (FLORIDEOPHYCEAE, RHODOPHYTA) IN AUSTRALIA TO BETTER CONCEIVE ITS BIODIVERSITY. Lesleigh Kraft & Gary W. Saunders. Centre for Environmental and Molecular Algal Research, Department of Biology, University of New Brunswick, Fredericton, NB, E3B 5A3, Canada.

Data presented here represent the culmination of four years of work on members of the red algal order Halymeniales from Australia. Taxonomic perspectives regarding the Australian benthic marine red algal flora suffer from a residual bias towards European species, as European references were used to identify most of the flora in the early days of Australian marine Botany. Using the DNA barcode, molecular phylogenetics and traditional alpha taxonomy, the species diversity of this order was investigated. Cluster analysis of barcode data indicated that our collections expanded the order past the known species diversity as represented in the literature. Molecular and morphological data show that both novel and overlooked species are contributing to this spike in observed biodiversity. Novel diversity has been found within every genus within the Halymeniales represented in Australia that was studied here, with the molecular record uncovering diversity in excess of currently described genera. Among our findings, this study: confirms that Australian species assigned to the genera *Cryptonemia*, *Grateloupia* and *Halymenia* do not themselves form monophyletic lineages, the various lines not remotely associated with generitypes reflecting the need for revision on a global scale; clarifies the currently incorrect assignments of Australian representatives of the genus *Aeodes*; resolves Australian species assigned to the genera *Pachymenia* and *Grateloupia* in a new genus *Macromenia*; and establishes that species diversity within the rare genus *Tsengia* is much richer than previously thought.

19.

EXAMINATION OF SODIUM EXPORT GENES: THEIR EXPRESSION AND ROLE IN SALT ADAPTATION FOR *CHARA LONGIFOLIA* (R. BR.) AND *CHARA AUSTRALIS* (R. BR.).

Shaunna Kraatz, Mary A Bisson· Department of Biological Sciences, University at Buffalo, New York

Many species within the genus *Chara* have a range of tolerances when exposed to or cultured in varying salinities. We examine potential genes (SOS1, ACA4, AHA9, PpENA) potentially related to sodium export that have been previously established in embryophytes. We will determine their potential role in the export of Na⁺ in salt-tolerant *C. longifolia* and salt-sensitive *C. australis*. Since *Chara* is more closely related to embryophytes than other green algae, these genes are likely candidates for the mechanism behind sodium export in *Chara*. Both *C. longifolia* and *C. australis* were exposed to a range of saline treatments: freshwater culture, saltwater culture, or during adaptation from freshwater to saltwater. We will examine sequences of genes homologous to these four genes in the unpublished genome of *Chara braunii*. RNA extractions for the treatments will be analyzed through next generation Illumina sequencing to determine the gene expression and sequence for the specified genes. Primers are generated from these sequences to determine by quantitative-PCR expression levels in the salt-sensitive *C. australis* and the salt-tolerant species *C. longifolia*. We hypothesize that the expression of these genes would be greater in the *C. longifolia* than in *C. australis* for all treatments, greater in higher salinities, and greatest during adaptation to higher salt.

20.

DEVELOPMENT OF A SECONDARY SCHOOL CURRICULUM FOR

***SACCHARINA LATISSIMA* (SUGAR KELP) PRODUCTION**, Holly Turner¹, Kirk Shadle¹, Kenneth Tober¹, Elizabeth Kranyik¹, **Jang K. Kim**², Charles Yarish^{2,3},

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²Departments of Ecology and Evolutionary Biology and Marine Sciences, University of Connecticut, CT 06901.

The students and the staff Bridgeport Regional Aquaculture Science and Technology Education Center (B.R.A.S.T.E.C.) have been involved in a hands-on seaweed research project for the past five years. Throughout this time, the collaborative team has assisted in the development of: techniques to seed seaweed (*Sacharrina latissima*) line; design a farm site and gain appropriate permits for the site on Long Island Sound; grown, harvested, and processed the sugar kelp according to a Hazard Analysis Critical Control Point (H.A.C.C.P) plan created and implemented by the team. The kelp grown, harvested and processed by the students and staff has been available for sale at B.R.A.S.T.E.C's market, Angie's at Aqua. To provide a model for possible expansion of these techniques a secondary school level curriculum was developed. The development of this curriculum was pursued to facilitate student awareness of environmental function and potential anthropogenic impacts of coastal human development. Additionally, a cost effective and potentially high yield growth industry, sugar kelp production, was integrated as a

measure for long term ecosystem sustainability. Coupled with the sugar kelp cultivation methodology throughout this STEM, Science Technology Engineering Mathematics, based curriculum students were instructed on the environmental functionality of the nitrogen cycle as it pertains to coastal ecosystems. Students then implemented this background knowledge into a community awareness/action plan. This extension beyond the initial sugar kelp production immerses the students into the sugar kelp production industry and encourages them to develop skill sets for policy development as it directly relates to their community.

21.

A PROPOSED METHOD TO ASSESS VALVE SHAPE EVOLUTION IN *EUNOTIA* USING MORPHOLOGY AND PHYLOGENY. Jordan Bishop¹, Louise Lewis¹, Peter Siver², & Anne Lizarralde². ¹Department of Ecology and Evolutionary Biology, University of Connecticut, Storrs, CT, 06269, U.S.A. ²Department of Botany, Connecticut College, New London, CT, 06320, U.S.A.

A Middle Eocene maar located within Canada's Northwest Territories features deep sediments, including roughly 68m of stratified mudstone with abundant microfossils. Known as the "Giraffe Pipe", this sediment core contains the oldest known remains of the freshwater diatom genus *Eunotia* and is well represented within the core where the lake becomes shallow and acidic. Characterized by a "strong back" and lunate-shaped frustules, *Eunotia* is asymmetrical in valve view. This pilot study proposes a combined approach utilizing siliceous microfossils and extant taxa of the freshwater *Eunotia* to reconstruct a phylogeny of the genus. First, geometric morphometrics will be used to analyze shape variation within *Eunotia*. Previous work utilizing a combined dataset of over 250 taxa showed that fossils specimens feature a simple morphology compared to the wide variability in ornamentation characteristic of modern flora. This initial survey focused upon North American and European taxa. To expand this dataset, we will use the holdings of the Diatom Herbarium at the Academy of Natural Sciences of Drexel University. Specimens from a variety of locales, including type specimens, will be examined to thoroughly assess the changes in valve shape. Secondly, we will expand upon the morphological phylogeny of *Eunotia* by Souza (2004) with the inclusion of additional character traits and fossil taxa. The goal of this proposed study is to construct a phylogeny to assess the pattern and timing of morphological shape evolution of *Eunotia*.

22.

PHYCOLOGY WITHOUT APOLOGY: INVITING STUDENTS TO THE DISCIPLINE BY UNVEILING AN OCEAN GARDEN. Brian Wysor. Department of Biology, Marine Biology & Environmental Science, Roger Williams University, Bristol, RI 02809.

The lure of Phycology rarely captures the imaginations of students interested in careers in biology and marine biology the way that other organismal disciplines do. Marine mammals, even invertebrates, hold greater allure funneling students into marine mammalogy, ichthyology or invertebrate zoology. There is a dearth of exposure to the discipline through mainstream media, natural history museums or general biology coursework, such that when students do arrive to Phycology

courses, either by degree requirement or curiosity, they are *neophycs* in the truest sense. Indeed, most graduate and undergraduate courses in phycology that are ever taught are an introduction to the discipline for the majority of participants and the integration of discipline-specific vocabulary is often perceived as a daunting prospect for these beginning students. A few well-known textbooks serve as important supplements to phycology instruction, but these are few in number, and students often find them challenging to navigate without a functional vocabulary. An affordable alternative to these traditional textbooks is Josie Iselin's *An Ocean Garden: The Secret Life of Seaweed*, in which the biology and biodiversity of seaweeds is documented through an exquisite exposé of technically accurate prose and complementary, full color and artfully arranged photographs of eastern North Pacific and western North Atlantic marine macroalgae. Iselin offers personal narratives, but provides meaningful scientific context that instills excitement among students and invites them to ask good questions about the biology of algae. Student reflections on the adoption of Iselin's *An Ocean Garden*, will be presented as well as a technical index of the book for phycology instruction.

23.

DNA EXTRACTION OF MICROSCOPIC RED ALGAE. Katelyn Wadland¹ & Chris Lane¹. ¹*Department of Biology, University of Rhode Island, Kingston, RI 02881, USA*

Red algae demonstrate significant phenotypic plasticity and convergent evolution among the different species making morphological identification difficult, especially among diminutive red algae. However, genetic data facilitates the differentiation between morphologically similar red algae. Within the past decade, the field of single cell genomics has been growing and novel methods have been created to analyze minute quantities of DNA from freshly acquired microscopic samples. One method developed to overcome low DNA yield is multiple displacement amplification (MDA). To find the lower limits of MDA for fresh and dried red algal material, we have used an estimated sample size of 30 red algal cells from a variety of known red algal species, including *Porphyra*, *Vertebrata lanosa*, *Chondrus crispus*, and *Grateloupia turuturu*. The samples were first lysed by utilizing lysis buffer in combination with either heat or agitation. Following cell lysis an MDA was performed using the GenomiPhi HyDNA kit. Samples with detectable MDA product bands, using gel electrophoresis, were then PCR amplified for either 18S, *rbcL*, or COX1. PCR products were sent off for Sanger Sequencing to determine whether the MDA amplification was successful and detect errors resulting from amplification. We were able to successfully amplify *Grateloupia turuturu* for 18S and *rbcL* and *Porphyra* for 18S. We are currently in the process of decreasing the sample quantity to discover if this methodology is still applicable with fewer cells

24.

EVALUATING HETEROTROPHIC GROWTH CAPABILITIES OF TWO GREEN ALGAE THAT SYMBIOSE WITH SPOTTED SALAMANDERS. Nikolaus E. Schultz & Louise A. Lewis. University of Connecticut, Department of Ecology and Evolutionary Biology, Storrs, CT, 06269, USA.

Chlamydomonadalean algae of the *Oophila* clade are well known symbionts of spotted salamanders, *Ambystoma maculatum*. Blooms form within embryonic egg capsules and recently it was demonstrated that algae even occur within tissues and cells of embryos. Despite this intimate association, little is known about the establishment of the interaction. Molecular work has revealed non-monophyly of the symbionts, however algae from eggs of a given clutch are genetically more similar than algae among clutches of a single pond. A more diverse range of inhabitants would be expected if they simply entered eggs from the external environment. This may indicate selectivity for a particular type of algae at the clutch level and thus we propose a maternal component. It is possible that algal symbionts are taken up by females with male spermatophores, live within the female's reproductive tract and are provisioned to her embryos each generation, prior to egg encapsulation. If this were the case, algae must survive within a female's reproductive tract without photosynthesis. To evaluate this possibility, two distinct symbiotic strains isolated from salamander eggs of one pond were grown under heterotrophic conditions. Each strain was cultured from a starting population of 25,000 cells/ml, in three different media: BBM, BBM + 1% glucose, BBM + 1% sodium acetate, and under two different photoregimes: 16:8 L:D or 0:24 L:D. Each treatment consisted of four replicates and was grown for 16 days. Cultures were agitated every day, and populations quantified every two days. Our results show both strains grew best on BBM + 1% glucose media under both photoregimes. Our pilot study demonstrated that these algae are capable of heterotrophic growth and suggests further investigation of other symbiotic algae of spotted salamanders.

25.

EISENIA ARBOREA SUBTIDAL POPULATIONS IN CALIFORNIA: SPECIATION OR ADAPTION? Megan Roche¹, Brian Murphy¹, Jim Coyer², Naomi Phillips¹.

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Kelp forests are very productive ecosystems in temperate subtidal communities around the world. Past research suggests that water flow and hydrodynamic pressure differences between the shallow subtidal and deep subtidal zones may shape algal morphology. *Eisenia arborea* is an example of a kelp species with populations in the shallow subtidal deep subtidal zones near Catalina Island with distinct morphological differentiations. Whether the morphological differentiation is caused by phenotypic plasticity or genetic differences remains unclear. The goal of this research is to determine whether these populations are still one species adapted to different environments or have diverged into two distinct species. Samples representative of the two populations were collected and total genomic DNA extracted. The Z fragment of the large subunit of ribosomal cistron (LSU) and

mitochondrial COI gene region were amplified. Based on the difference in polysaccharide content from the DNA extractions; distinction between these two populations is evident. Both gene regions have sufficient variation to be used to determine population differences in *Eisenia*. Sequencing and phylogenetic analyses of both gene regions for the two populations are in progress with exciting results to follow.

26.

EXTREMOPHILE ALGAE ARE ADAPTED BY MANIFOLD METABOLIC

CHANGES. Daniel Remias¹, Johann Wastian², Belina De Carli² Cornelius Lütz² & Andreas Holzinger². ¹School of Engineering and Environmental Sciences, University of Applied Sciences Upper Austria, 4600 Wels, Austria; ²Institute of Botany, University of Innsbruck, 6020 Innsbruck, Austria.

Algae living in alpine or arctic terrestrial habitats, in snow fields or on glacial ice, are subject to extreme environmental conditions like high irradiation, desiccation or freezing events. Cellular mechanisms to maintain or restore viability are required. Different strategies evolved in chlorophytic- (e.g. *Chloromonas nivalis*, *Chlamydomonas nivalis*, *Chlainomonas* sp.) and streptophytic green algae (e.g. *Mesotaenium* sp., *Zygnema* sp.). Cytoarchitecture of species from exposed habitats shows that the cytoplasm is occupied either by lipid bodies or highly vacuolated. These lipid bodies and vacuoles contain abundantly either glycosylated polyphenolics (mainly in Zygnematophyceae) or secondary carotenoids esterified with fatty acids (mainly in Chlorophyceae). Such compounds act as protecting pigments, most likely to shade chloroplasts or the nucleus against excessive visible or UV irradiation. For example, the snow alga *Chlainomonas* sp., where the peripheral chloroplasts are not sheltered from light by astaxanthin like in many other snow algae, contains more than 20-fold alpha-tocopherol compared to *Chlamydomonas nivalis*. Desiccation and freezing tolerant organisms may either have rigid cell walls (snow algae: *Chlamydomonas*, *Chloromonas*, semi terrestrial algae: *Zygnema*) or thin and flexible cell walls (soil algae: *Klebsormidium* sp.). Especially in persistent cells like cyst stages, the morphology of chloroplasts can be modified, thus optimizing the volume to surface ratio (e.g. for better substrate exchange). Psychrophilic species tentatively accumulate soluble carbohydrates for decreasing the intracellular freezing-point. Osmolytic compounds like glycerol or sugar-alcohols also support the 'liquid state' in case of desiccation and extracellular freezing. Summarizing, these protecting and avoidance mechanisms enable algae from different phylogenetic lineages to survive in desiccated or cold habitats in combination with high irradiation. The study was supported by FWF grants P20810 to C.L. and in part by FWF grant P24242-B16 to AH.

27.

ROLE OF ZINC IN ALLEVIATING CADMIUM TOXICITY IN *CHARA AUSTRALIS*

(R. BR.). Stacia Wegst-Uhrich¹, Prasanna Ranganathan², Grace Craigie², Kaitlynn Donahue², Diana Aga¹, Mary A Bisson². ¹Department of Chemistry and ²Department of Biological Sciences, University at Buffalo, New York.

Characean algae have been proposed for use in phytoremediation of heavy metals because of their high biomass and cation uptake capacity. We previously showed that *C. australis* can take up cadmium up to 72 mg (kg DW)⁻¹. Since effective phytoremediators must be resistant to metal toxicity, we explored Cd toxicity in *C. australis*. We showed that 2 ppm (18 μM) Cd in solution is toxic, but adding 5 ppm (76 μM) zinc decreased mortality by 8 to 41%. Both treatments resulted in equivalent Cd uptake, so decreased Cd concentration was not the cause of reduced mortality. Heavy metals cause an increase in damaging reactive oxygen species (ROS) in other systems. We therefore hypothesized that Cd induces an ROS increase, which is limited in the presence of Zn due to increased glutathione. Glutathione plays an important role in controlling the redox potential of the cytoplasm by shifting between its reduced and oxidized forms (GSH and GSSG) and therefore altering ROS levels. Between 0.5 and 24 h, ROS in metal-stressed cells was always less than controls, with values ranging between 33% and 6.5% of controls. Neither GSH nor GSSG was different than control in the first 4 hours of exposure. However, at 24 h, GSH increased in Cd-stressed plants (12 X control). With Cd + Zn, the increase in GSH (32 X control at 24 h) was greater than in the Cd-stressed system. GSSG did not increase in plants treated with Cd only, but increased by 350% over controls with Cd + Zn. This suggests that Zn effects on Cd toxicity are mediated by GSH, but not necessarily due to its effect on ROS. We explore alternative theories for the role Cd and GSH in reducing Cd toxicity.

28.

THE REPRODUCTIVE PHENOLOGY AND DEVELOPMENT FOR AQUACULTURE OF THREE SEA VEGETABLE CROPS IN MAINE.

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Understanding the natural reproductive cycles of algae is crucial for their development as new sea vegetable crops. This information is required to plan when to collect wild strains and distribute seeded lines/nets to coastal farmers for grow-out. We conducted bimonthly phenology surveys to assess the seasonal reproductive stages of three sea vegetable species (laver, dulse, and alaria) at three locations (Lubec, Schoodic, Pemaquid) in Maine. We ran two transects (1-7 km apart) at each location. We considered laver (*Porphyra umbilicalis*) reproductive when a neutral spore margin was visible, and confirmed field determinations with microscopic examinations for subsets. We classified dulse (*Palmaria palmata*) into two reproductive categories: male (spermatia-producing) or tetrasporic (tetraspores present). We deemed alaria (*Alaria esculenta*) reproductive if basal sporophylls contained sorus tissue with zoospores. Whenever field calls were uncertain, microscopic determinations were made. We have posted phenology protocols of these three species as a mission on GMRI's Vital Signs' website, and are eager to have citizen scientists in New England add to the database at other locations. Our reproductive phenology data are guiding the next phase of our study: the grow-out of seeded lines at experimental lease sites in Maine. We attached spores of native

strains of each species to kuralon lines and deployed them into the field for growth assessment. Growth comparisons will be made based on the time of deployment and natural reproductive cycles of these potential sea vegetable crops (Supported by Maine Sea Grant and the Maine Aquaculture Innovation Center).

29.

NO EXPECTATIONS: A MODEL FOR ART/SCIENCE COLLABORATION IN

ANTARCTICA. Laura Von Rosk, Samuel S. Bowser, Henry Kaiser & Hilary Hudson. Wadsworth Center, NY State Dept. Health, Albany, NY 12201.

Art/Science collaboration has become a widely accepted way of communicating the mysteries, discoveries, potentials, and pitfalls of science (e.g., www.ASCI.org). The U.S. Antarctic Program has a longstanding tradition of providing logistic support for artists and writers (A&W) interested in experiencing the Antarctic continent to produce a body of work. The process for selecting A&W participants is similar to that of a research proposal: “tell us what you want to do, tell us how you will do it, justify its significance to your profession, and tell us where your work will be presented.” A panel of experts evaluates each application, and awardees visit field camps and research stations where scientists share their knowledge and logistic expertise. This approach certainly works, but does it nurture or hinder creative processes? Can an expert panel adequately assess the compatibility of an A&W project with a research team? What other options are available? We discuss our experience with embedding an artist in a science team as a salaried research assistant. This approach frees both scientist and artist from the necessity of producing a defined product. Instead, such an art/science partnership explores ideas in situ, unhindered, as they work toward their goals of “doing good science” and conveying their shared experiences to better inform the public.

30.

PHYCOLOGY CROWD-SOURCING: ASSESSING DIVERSITY IN A COMPLEX COMMUNITY. Maria Pappas,¹ Sonja Hausmann² and Richard M. McCourt¹.

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Identification of microalgae from microscopic images of naturally occurring communities is a widespread practice but fraught with difficulties. DNA fingerprinting or other analysis of similar-looking taxa uncovers cryptic diversity in samples of diverse--or even seemingly homogeneous--communities. Nevertheless, morphological characterization is often the first step in characterizing morphotypic diversity in a sample. Identifications are often made by one or a few observers and species lists compiled. We encountered a great deal of diversity and uncertainty of identification in a sample from an interesting community of algae associated with *Ophrydium versatile*, a freshwater colonial mixotrophic ciliate peritrich that was found in a New Jersey Lake. The colonies occur in the form of a gelatinous matrix, presumably secreted by the ciliates. We were able to distinguish numerous morphologically different taxa of microalgae in several divisions. Rather than present a simple species list, we propose to crowd-source our characterization of this community. This technique has been used in previously to track cyanobacterial

blooms (<http://www.cyanotracker.uga.edu/>) and to identify freshwater fish from Guyana (<http://www.sciencedaily.com/releases/2011/05/110513204526.htm>). For the NEAS poster session, we will present a series of microphotographs on our poster and provide paper and online documents for poster session observers to record putative identities of taxa in the microphotographs. The results will be analyzed and reported to all participants who sign up.

31.

FOUR MITOCHONDRIAL GENOMES FROM THE GREEN ALGAL FAMILY HYDRODICTYACEAE (SPHAEROPLEALES, CHLOROPHYCEAE).

Audrey A. Farwagi¹, Karolina Fučíková², Hilary A. McManus¹. ¹Department of Biological Sciences, Le Moyne College, Syracuse, NY, USA. ²Ecology and Evolutionary Biology, University of Connecticut, Storrs, CT, USA.

Green algal mitochondrial genomes are known to be quite variable in size, gene content, and gene order. The sampling of mt genomes from the class Chlorophyceae come predominantly from the order Volvocales, and the study of green algal mt genomes is lacking on a finer taxonomic scale leaving a gap in our understanding of green algal genome evolution. This study comprises the first within-family investigation of mt genome diversity. We report four completely sequenced mitochondrial genomes from the family Hydrodictyaceae (order Sphaeropleales) spanning three taxa and four phylogenetic groups, *Stauridium tetras*, *Pseudopediastrum boryanum*, and *Pediastrum duplex*, the first complete genomes to be sequenced from Hydrodictyaceae. The size range of 37,723 bp to 53,560 bp is attributed to intergenic region expansion while intron diversity and gene rearrangements appear to follow phylogenetic patterns. While these data provide insight and support for phylogenetic relationships among Hydrodictyaceae, further taxon sampling could contribute to resolving systematic questions surrounding this family.

32.

OPTIMIZING CULTIVATION TECHNIQUES FOR *SACCHARINA LATISSIMA* FORMA *ANGUSTISSIMA* (F. S. COLLINS) MATHIESON.

Simona Augyte¹, Jang K. Kim², Sarah Redmond³ and Charles Yarish⁴. ¹University of Connecticut, Dept. of Ecology & Evolutionary Biology, 75 N. Eagleville, Storrs, CT 06269, USA ²University of Connecticut, Dept. of Marine Sciences, 1 University Place, Stamford, CT 06901, USA ³SeaGrant, Center for Cooperative Aquaculture Research, 33 Salmon Farm Rd, Franklin, ME 04634, USA ⁴University of Connecticut, Depts. of Ecology & Evolutionary Biology and Marine Sciences, 1 University Place, Stamford, CT 06901, USA

Saccharina latissima forma *angustissima* (F. S. Collins) Mathieson is a morphologically unique kelp with a distribution restricted to exposed ledges in the low intertidal of mid-coastal Maine. Efforts have been made to resolve the taxonomic placement of this phenotypically plastic kelp, as well as to initiate the domestication process. Results of field and lab experiments done on both the microscopic and macroscopic stages of the life-cycle will be presented. In order to optimize cultivation conditions for the seedstock nursery, an initial 4 week experiment was run, testing

the effects of variable light and temperature conditions on germination, gametophyte growth, and juvenile sporophyte growth. At the three photosynthetically active radiation (PAR) levels tested (20, 40, 80 $\mu\text{mol photons m}^{-2} \text{ s}^{-1}$) we did not find any statistically significant differences in sporophyte growth. However, germination rates were below 90% at some of the highest PAR levels. Our results suggest temperature was a significant controlling factor for sporophyte growth. Optimal juvenile sporophytes grew at 12°C and 15°C, however, at the highest temperature tested (17°C), the sporophytes failed to develop. The 17°C treatment also appeared to promote vegetative cell growth of male and female gametophytes while inhibiting gamete formation. Culture trials at 2 different open-water farms in Maine are ongoing to evaluate this species as a possible new crop. Environmental parameters and morphometric data are being collected throughout the growing season, with an expected harvest in May or June. From initial observations, the narrow-bladed kelp is retaining its unique morphology in terms of its width and length, but blades are growing thinner compared to the wild population. These results are part of a larger study focused on the phenotypic plasticity seen in this morphologically distinct kelp.

33.

PARASITES OF THE GIGARTINALES: KNOWN AND NEW RED ALGAL

PARASITES FROM THE ARCTIC Jillian Freese, Chris Lane, Dept. of Biological Sciences, University of Rhode Island, Kingston, RI, USA

Florideophyceae red algae are prone to infection from related red algal parasites, also within the Florideophyceae, described as adelphoparasites or alloparasites. Adelphoparasites have close relationship to their host, whereas alloparasites are often from different families. Two previously undescribed parasites were collected on the host *Fimbrifolium dichotomum* (Lepechin) G.I.Hansen. One parasite has a single base attachment, a short stipe, is highly branched, and remains pigmented. The other parasite is not pigmented and composed of a number of globular segments. *Coccotylus hartzii* (Rosenvinge) L.Le Gall & G.W.Saunders, parasitic on *Coccotylus truncatus* (Pallas) M.J.Wynne & J.N.Heine was also collected. *C. hartzii* has a short stipe, multiple spheroidal growths that branch off and remains pigmented. Future work includes identifying the parasite and explaining the host-parasite relationship.

34.

DEFINING THE DIVERSITY OF THE GREEN ALGAL FAMILY

HYDRODICTYACEAE IN CENTRAL NEW YORK. Afsah Chohan & Hilary A.

McManus. Department of Biology, Le Moyne College, Syracuse, NY 13214, U.S.A.

The purpose of this study is to examine the diversity of the freshwater green algal family Hydrodictyaceae within Central New York. Collections were made during the summers of 2013 and 2014 from bodies of freshwater in the central New York state area. From the 26 samples collected, 16 hydrodictyaceae strains were successfully isolated and grown and 14 were included in analyses. DNA was obtained from the isolates and the chloroplast gene, ribulose 1, 5 bisphosphate carboxylase/oxygenase large subunit (*rbcL*), was amplified and sequenced. The *rbcL* data sets were analyzed phylogenetically using the maximum likelihood

criterion in the program MEGA. The resulting trees indicate there is a range of diversity among the Hydrodictyaceae family in Central New York, with isolates spanning four genera (*Hydrodictyon*, *Pediastrum*, *Pseudopediastrum*, *Stauridium*). One of the isolates grouped with *Neochloris*, indicating that it is likely in the family Neochloridaceae rather than Hydrodictyaceae.



SUNDAY FIELD TRIP

Guided walk along Onondaga Lake

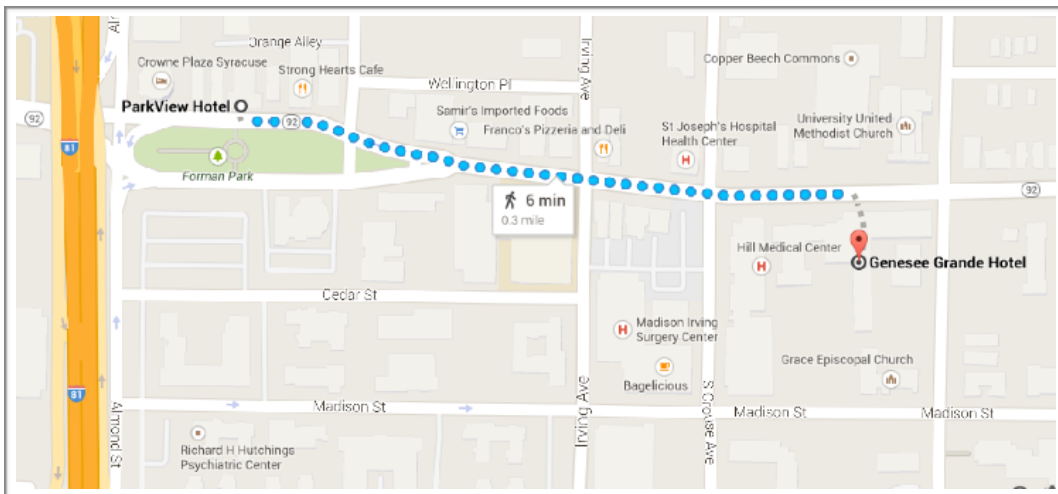
In the last 30 years, Onondaga Lake has made a remarkable comeback from one of the most polluted lakes in the nation to where it now serves as an international demonstration site for lake restoration. Join us for a walk along the newly built West Side trail to examine some of the insults and successes in the history of Onondaga Lake. The trail runs along the lake bluffs but is paved. Comfortable walking shoes are suggested.

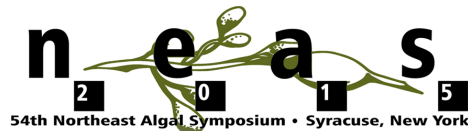
Interested participants should meet in the Tiffany Room after the business meeting concludes. Attendees will drive themselves or car pool to the parking lot of the West Side trail where the field trip will begin.

MEETING VENUE INFORMATION AND MAP

Woodbine Hospitality has a hotel experience for every type of stay. The Genesee Grande Hotel is the flagship property of the hotel group and includes 79 suites and the 1060 Restaurant and Lounge is noted in Wine Spectator Magazine. The hotel also includes a state-of-the-art fitness facility, complimentary wireless internet, complimentary parking and shuttle service to/from the airport, train and bus stations. Our sister properties, the ParkView Hotel and Hotel Skyler also located at the edge of Syracuse University's campus are buildings that have been repurposed into hotel properties. The ParkView Hotel was a former medical/dental arts building and the Hotel Skyler was a former temple and is one of three in the country at a Platinum Level of LEED Certification from the US Green Building Council. The final property is an elementary school turned lodge! Located on the world-renowned Salmon River, the 42-room property features 2,000+ feet of exclusive fishing access to the river, the Tailwater Restaurant and Bar, breakfast inclusive, a meeting space for up to 100. We've been expecting you!

Walk from ParkView to Genesee Grande - 0.3 miles





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HOTEL**