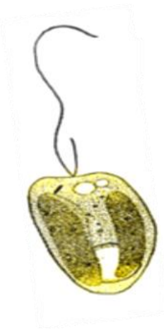
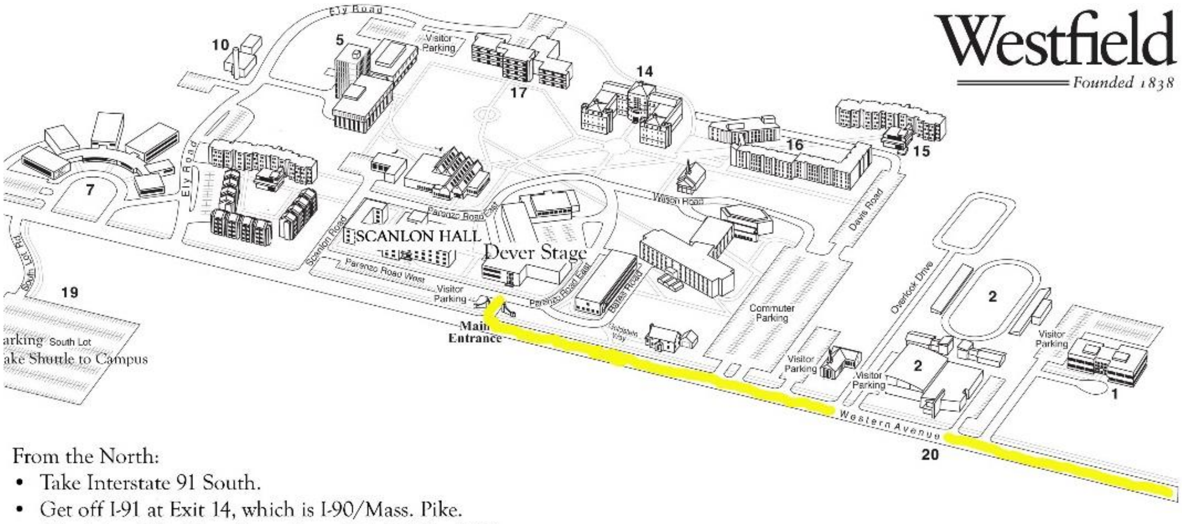
N E  S 2  1 6

NORTHEAST ALGAL SOCIETY
55th Annual Symposium
Westfield State University
Westfield, MA
April 22- 24, 2016

Campus Map



From the North:

- Take Interstate 91 South.
- Get off I-91 at Exit 14, which is I-90/Mass. Pike.
- Take Mass. Pike West five miles to Exit 3 (Westfield).
- Turn right onto routes 10/202 South, travel for about two miles through town to the Westfield Public Library (on your right).
- Turn right onto Court Street/Western Avenue and continue for 2.5 miles.
- Westfield State University is on your right.

From the South:

- Take Interstate 91 North.
- Follow directions from above.

From the East or West:

- Travel to I-90/Mass. Pike until you reach Exit 3.
- Follow directions from above.

Address:
Westfield State University, 577 Western Avenue, Westfield, MA 01086

NORTHEAST ALGAL SOCIETY 55TH ANNUAL SYMPOSIUM

Welcome to the 55th Annual Northeast Algal Society Meeting on the campus of Westfield State University! We hope that this annual gathering is both an intellectually stimulating exchange of information and ideas, and an opportunity to socialize with fellow phycologists.

This year's theme is "Alternative Nutritional Strategies" and as a distinguished speaker we are pleased to have Dr. Diane Stoecker, University of Maryland Center for Environmental Science, Horn Point Laboratory, Cambridge MD. The title of her talk is *Mixotrophy in Marine Plankton*.

As conveners for the meeting, we would like to acknowledge the generous financial and facilities support from Westfield State University and Penn State University - Worthington Scranton. At WSU, we would specifically like to acknowledge the assistance of Dr. Steven Adams (Academic Affairs), Joanne Bigelow (Events Management), Pete Goodreau and the Catering staff, the Westfield State University Foundation and the staff of the Copy Center. We gratefully acknowledge the contributions of several volunteers, including Mary Masse, Sarah Tomas, and Sarah Grobe. At PSU, we would like to thank Dr. Marwan Wafa (Chancellor) for his financial support, Kathy Holen and Lynn Fazio of the copy center for her assistance.

We also appreciate the presence and contributions of the following vendors: Scott Balogh and Balogh International, the Darling Marine Center, Micro-Tech Optical, Schweizerbart Publishing, and Sinauer Publishers. The contributions from members and friends of NEAS to our annual auction are also much appreciated.

We would like to thank the following moderators; Gina Filloramo, Simona Augyte, Thea Popolizio, Craig Schneider, Bob Sanders, Robert Thompson and judges; Harold Hoops, Lindsay Green, Ruth Schmitter, Allison Sherwood, Sarah Whorley, John Wehr, Bob Sanders, Nic Boudin, Brian Wysor and Peg Van Patten for kindly volunteering their services.

Finally, the assistance, advice, and support of all of the members of the NEAS Executive Board have been invaluable as we undertook the preparations for this meeting.

All events will be held in Scanlon Hall (see map) and parking on campus for the Friday night mixer and the events on Saturday and Sunday is unrestricted.

We hope that we have not overlooked anything terribly important as we prepared for this meeting, and we hope that you will be forgiving if you find anything that is lacking or has been omitted. Please let us know if there is anything that we can do to assist you or to correct a problem.

Carl Grobe & Dale Holen

Westfield
STATE UNIVERSITY
Founded 1838

PennState

55th ANNUAL NORTHEAST ALGAL SYMPOSIUM
WESTFIELD STATE UNIVERSITY
WESTFIELD, MA

FRIDAY, April 22, 2016

5:30 – 7:30 PM **Evening Registration, Check in and Auction Donation**
Speakers load presentations for Session I
(Scanlon Banquet Hall)
Poster Setup *(Scanlon Livingroom)*

6:00 – 9:00 PM **NEAS Welcome Mixer *(Scanlon Banquet Hall)***

SATURDAY, April 23, 2016

7:00 – 8:15 AM **Continental Breakfast *(Scanlon Banquet Hall)***
Session I speakers load your presentations
Poster setup *(Scanlon Livingroom)*
Morning Registration and Auction Donation

8:15 – 8:30 **Welcome and Introductory Remarks – Carl Grobe and Dale Holen**

SESSION I **STUDENT PRESSENTATIONS, Moderator: Simona Augyte *(Scanlon Banquet Hall)***

8:30 – 8:45 *Wilce Award Candidate*
Robin S. Sleith, Amy J. Havens, Robert A. Stewart, John Wehr & Kenneth G. Karol. IN CHARACEAE: "EVERYTHING IS EVERYWHERE, BUT THE ENVIRONMENT SELECTS."

8:45 – 9:00 *Wilce Award Candidate*
H.G. Reich, D.L. Robertson, & G. Goodbody-Gringley. SYMBIOSIS AND SURVIVAL: EVALUATING *SYMBIODINIUM* POPULATIONS DURING MATERNAL TRANSMISSION AND EARLY DEVELOPMENT IN THE CORAL *PORITES ASTREOIDES.*

9:00 – 9:15 *Wilce Award Candidate*
Kirby Morrill & Gary W. Saunders. AN INVESTIGATION OF BROADLY BLADED *ULVA* SPP. (CHLOROPHYTA) IN THE OUTER BAY OF FUNDY (NEW BRUNSWICK, CANADA).

9:15 – 9:30 *Wilce Award Candidate*
Alysha Putnam, Noemi Collazo & Paulette Peckol. INTERTIDAL BULLY: COMPETITIVE INTERFERENCE BY *LITTORINA LITTOREA* ON *L. OBTUSATA.*

9:30 – 9:45 *Wilce Award Candidate*
Gina V. Filloramo & Gary W. Saunders. MOLECULAR-ASSISTED ALPHA TAXONOMY OF THE ORDER RHODYMENIALES (RHODOPHYTA) FROM BRITISH COLUMBIA REVEALS OVERLOOKED AND CRYPTIC SPECIES DIVERSITY.

9:45 – 10:00 *Wilce Award Candidate*
Amber Paasch & Eunsoo Kim. BACTERIVORY IN THE PHAGO-MIXOTROPHIC GREEN ALGA *CYMBOMONAS* (PRASINOPHYCEAE) PROVIDES A COMPETITIVE ADVANTAGE IN PHOSPHATE-LIMITED ENVIRONMENTS ONLY.

10:00 – 10:15 *Wilce Award Candidate*
Trevor T. Bringloe & Gary W. Saunders. CONTEMPORARY MIGRATION OF FOUR SPECIES OF ALGAE THROUGH THE CANADIAN ARCTIC.

10:15 – 10:45 *Coffee Break, Session II Speakers load presentations*

SESSION II STUDENT PRESENTATIONS, Moderator: Thea Popolizio

10:45 – 11:00 *Wilce Award Candidate*
Simona Augyte & Charles Yarish. INSIGHTS INTO THE ECOPHYSIOLOGY AND TAXONOMY OF *SACCHARINA LATISSIMA* FORMA *ANGUSTISSIMA*, (LAMINARIALES, PHAEOPHYCEAE) FROM THE GULF OF MAINE.

11:00 – 11:15 *Wilce Award Candidate*
Rebecca Littlefield, Baxter Worthing, G. Jason Smith & Deborah Robertson. ANALYSIS OF THE FORMALDEHYDE DETOXIFICATION PATHWAY IN EUKARYOTES.

11:15 – 11:30 *Wilce Award Candidate*
Katelyn Wadland, Gary W. Saunders & Christopher E. Lane. PHYLOGENETIC ANALYSIS OF A CRYPTIC MICROSCOPIC RED ALGA.

11:30 – 11:45	*Wilce Award Candidate* Chris Paight, Sergio A. Muñoz-Gómez, Mary Beth Saffo, Claudio Slamovits & Christopher E Lane. WILL MAKE YOUR VITAMINS AND AMINO ACIDS FOR FOOD: ENDOSYMBIONT PATHWAY RESTORATION IN A LONG TIME PARASITE.
11:45 – 12:00	*Wilce Award Candidate* Eric Salomaki & Chris Lane. THE ORIGIN OF ORGANELLES IN RECENTLY DERIVED RED ALGAL PARASITES.
12:00 – 1:30	*Lunch (Scanlon Banquet Hall)* *Executive Committee Lunch (Scanlon Banquet Room)* *Session III speakers load presentations.*

SESSION III STUDENT PRESENTATIONS, Moderator: Gina Filloramo

1:30 – 1:45	*Wilce Award Candidate* Jillian Freese & Chris Lane. RED ALGAL PARASITISM: DEVELOPMENT OF AN INFECTION.
1:45 – 2:00	*Wilce Award Candidate* Ober, G.T. & Thornber, C.S. GRAZE UNDER PRESSURE: HOW THE INTERACTION OF OCEAN ACIDIFICATION AND EUTROPHICATION IMPACTS MACROALGAL CONSUMPTION BY MARINE SNAILS.
2:00 – 2:15	*Wilce Award Candidate* Yuanyu Cao, Lindsay Green, Renée Eriksen, & Anita S. Klein. IDENTIFICATION OF EXOME VARIANTS FROM RNA-SEQ OF *PORPHYRA UMBILICALIS* KÜTZING POPULATIONS IN THE NW ATLANTIC.
2:15 – 2:30	*Wilce Award Candidate* Amanda M. Savoie & Gary W. Saunders. UNDERSTANDING EVOLUTIONARY RELATIONSHIPS AND SPECIES DIVERSITY OF THE TRIBE PTEROSIPHONIEAE (CERAMIALES, RHODOPHYTA) IN THE NORTHEAST PACIFIC**.**
2:30 – 2:45	*President's Award Candidate* Nicholas J. Macoretta, Anna Curtin, Hilary A. McManus, Louise Lewis, & Kenneth G. Karol. THE DIVERSITY OF THE FRESHWATER GREEN ALGAL GENUS *HYDRODICTYON* (SPHAEROPLEALES, CHLOROPHYCEAE).
2:45 – 3:00	*Coffee break, Session IV speakers load their presentations*

SESSION IV — STUDENT PRESENTATIONS, Moderator: Craig Schneider

3:00 – 3:15
President’s Award Candidate
Walter M. Jongbloed, Craig W. Schneider & Christopher E. Lane. NEW GENETIC SPECIES OF *WRANGELIA* (WRANGELIACEAE, CERAMIALES) FROM BERMUDA, WESTERN ATLANTIC OCEAN.

3:15 – 3:30
President’s Award Candidate
Cody M. Brooks, Gary W. Saunders. LONG-DISTANCE KELP RAFTING OF RED ALGAE IN THE NORTHEAST PACIFIC.

3:30 – 3:45
President’s Award Candidate
Grant F. Kusick, Stephanie Newman & Harold Hoops. THE COLONIAL GREEN ALGA *ASTREPHOMENE GUBERNACULIFERA* (CHLOROPHYCEAE) PERFORMS CHEMOTAXIS BY AN EXTRACELLULAR CALCIUM-DEPENDENT TEMPORAL SENSING MECHANISM.

3:45 – 4:00
President’s Award Candidate
Kelly DeMolles & Brian Wysor. DNA BARCODING REVEALS NEW DISTRIBUTION RECORDS OF GREEN MACROALGAE (CHLOROPHYTA: ULVOPHYCEAE) IN RHODE ISLAND WATERS.

SESSION V — STUDENT & PROFESSIONAL POSTER SESSION & MIXER *(Scanlon Livingroom)*

4:00 – 5:30
Please take down posters by lunch on Sunday

SESSION VI — DISTINGUISHED SPEAKER *(Scanlon Banquet Hall)*

Introduction, Dr. Sarah Devaul

5:45 – 6:45
DR. DIANE STOECKER
MIXOTROPHY IN THE MARINE PLANKTON

7:00 – 10:00
NEAS BANQUET, AWARDS, & LIVE AUCTION
(Scanlon Banquet Hall)

SUNDAY, April 24th, 2016

8:30 – 9:30	**Continental Breakfast *(Scanlon Banquet Hall)*** **Session VI and VII Speakers can load their presentations.** **Please remove posters by 12:00 today.**
SESSION VI	**CONTRIBUTED PRESENTATIONS, Moderator: Bob Sanders *(Scanlon Banquet Hall)***
9:30 – 9:45	Sarah DeVaul & Robert Sanders. VERTICAL DISTRIBUTION OF MIXOTROPHIC NANOFLAGELLATES IN A MESOTROPHIC LAKE.
9:45 – 10:00	Paulette Peckol & Alysha Putnam. DEATH BY ULVA: DIFFERENTIAL TOXIC EFFECTS ON THE HERBIVOROUS SNAILS, *LITTORINA LITTOREA* AND *L. OBTUSATA.*
10:00 – 10:15	John D. Wehr, Kam Truhn & Nicholas R. Ballor. REDISCOVERY OF THE FRESHWATER BROWN ALGA *HERIBAUDIELLA FLUVIATILIS* IN CONNECTICUT.
10:15 – 10:30	Stephen D. Gottschalk & Kenneth G. Karol. A PROPOSED REVISION OF *CHARA* SUBSECTION *WILLDENOWIA.*
10:30 – 10:45	Lindsay A. Green & Carol S. Thornber. THE EFFECT OF WARMING OCEAN TEMPERATURES ON THE GROWTH AND SURVIVAL OF BLOOM-FORMING MACROALGAE (*ULVA* SPP.).
10:45 – 11:00	*Coffee break and poster removal*

SESSION VII	**CONTRIBUTED PRSENTATIONS, Moderator: Robert Thompson**
11:00 – 11:15	Yuanzi Huo, Jang Kyun Kim, Charles Yarish,Simona Augyte& Peimin He. ADAPTABILITY OF FREE-FLOATING GREEN TIDE ALGAE TO GRADIENTS OF TEMPERATURE AND LIGHT INTENSITY.
11:15 – 11:30	Lindsay A. Green & Carol S. Thornber. THE EFFECT OF WARMING OCEAN TEMPERATURES ON THE GROWTH AND SURVIVAL OF BLOOM-FORMING MACROALGAE (*ULVA* SPP.).
11:30 – 11:45	Larry M. Lewis. REFLECTIONS ON THE MEANING OF THE POLYSIPHONOUS STATE VIEWED THROUGH THE LENS OF *HETEROSIPHONIA.*

11:45 - 12:00 Price N.N., Donham E., Fachon E., Honisch B., Arnold S.N.
Record N., White M., Doan M., Neckles H.
CAN KEY NEW ENGLAND MACROPHYTES RAISE SEAWATER PH?

12:00 – 12:15 **CLOSING REMARKS, BUSINESS MEETING AND LUNCH**

ABSTRACTS

WILCE GRADUATE ORAL AWARD (WA)

(WA) INSIGHTS INTO THE ECOPHYSIOLOGY AND TAXONOMY OF *SACCHARINA LATISSIMA* FORMA *ANGUSTISSIMA*, (LAMINARIALES, PHAEOPHYCEAE) FROM THE GULF OF MAINE. Simona Augyte[1] and Charles Yarish[1] 1-University of Connecticut, Dept. of Ecology & Evolutionary Biology, 1 University Place, Stamford, CT U.S.A.

The narrow-bladed kelp, *Saccharina latissima* forma *angustissima* (F. S. Collins) Mathieson, was first described by Collins in 1880. This form is morphologically distinct with one strictly narrow (1.6 ± 0.7 cm wide) and long (average 1.8 ± 0.96 m, up to 4.4 m) blade with coalescent haptera having multiple stipes. The common sugar kelp, *S. latissima* grows a much wider (20-30 cm) blade that is usually shorter (about 2 m, up to 3.5 m) in length. Forma *angustissima* is restricted in distribution to mid-coastal Maine, spanning a radius of 8 nautical miles on ledges and islands in the low intertidal, exposed to high ocean swells. Based on a multi-locus approach, using mitochondrial (CO1), nuclear (ITS) and chloroplast (*rbc*L) genes, we did not find enough divergence between the two forms to designate species level differences. These loci have been used in previous studies to differentiate species in the order Laminariales. In collaboration with kelp farmers from *Maine Fresh Sea Farms* and *Maine Coast Sea Vegetables*, we successfully domesticated this kelp and grew it to full maturity on longlines. We then conducted a common garden experiment at these farms using parental material from each of the two forms. At maturity, we found significant differences in overall blade length, width, and stipe length. The narrow-bladed kelp retained its' long narrow morphology but lost its strap-like shape and formed bullations, a phenotypically plastic adaptation to slow-flow water movement. Further work is needed to identify population level differences and potential hybridization events.

(WA) CONTEMPORARY MIGRATION OF FOUR SPECIES OF ALGAE THROUGH THE CANADIAN ARCTIC.

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 algal flora of the Canadian Arctic is the result of recolonization since the retreat of glacial ice sheets within the past 10,000 years. This recolonization was hypothesized to be the result of the northward range extensions of Atlantic species. The ongoing accumulation of DNA sequence data, however, suggests a more complex history of migration events. Our research objective is to clarify the origins of modern day Canadian Arctic flora by studying, in detail, the population and migration history of several trans-arctic species. Preliminary results on four trans-arctic species of algae are presented here, including *Coccotylus truncatus*, *Odonthalia dentata*, *Rhodomela lycopodioides* f. *flagellaris,* and *Agarum clathratum*. These species have been collected via scuba from various locations in the Canadian Atlantic and Arctic basins, with recent collection in Prudhoe Bay (Alaska), and Haida Gwaii, British Columbia (in the case of *A. clathratum*). Mitochondrial COI-5P sequences have been generated or retrieved from the Barcode of Life Database and GenBank. A coalescent theory population genetic approach with a Bayesian search strategy is being used to infer asymmetric migration patterns and events through time. Though our results are preliminary, haplotype diversity suggests that several of these species travelled East through the Arctic, counter to the presumed North-Westward expansion from the Atlantic. *Coccotylus truncatus* likely has a more complex history of Arctic recolonization, with a possible European influence. Sampling in Norway in June is planned to explore putative European contributions. This research has implications for understanding historical marine migrations through the Arctic; in a field where single-species studies are common, we believe studying multiple species concurrently will provide a more comprehensive and accurate account of Arctic marine recolonization. Such baseline data are necessary to understand and document further changes in the Canadian Arctic.

(WA) IDENTIFICATION OF EXOME VARIANTS FROM RNA-SEQ OF *PORPHYRA UMBILICALIS* KÜTZING POPULATIONS IN THE NW ATLANTIC.

Yuanyu Cao[1], Lindsay Green[1,2], Renée Eriksen[1,3], Anita S. Klein[1] [1]Department of Molecular, Cellular, and biomedical Sciences , University of New Hampshire, Durham, NH U.S.A. [2]Department of Biological Sciences, University of Rhode Island, Kingston, RI U.S.A. [3]United States Department of Agriculture – Agricultural Research Service, 1636 East Alisal Street, Salinas, CA U.S.A.

Porphyra umbilicalis Kützing is a marine red alga, which is distributed along the rocky shores of the NW and NE Atlantic. The population structure of *P.umbilicalis* in the NW Atlantic is still unclear due to the conflicting results from previous surveys using AFLP and SSRs markers. With next-generation sequencing technology and bioinformatics analysis, putative single nucleotide polymorphisms (SNPs) markers of *P.umbilicalis* have been identified from five-transcriptome libraries. After stringent filtering, there are 534 putative SNPs present in all five libraries. Ten of these putative SNPs were validated using 5 individuals from 5 populations. Five polymorphic primers out of the ten tested were used to examine the population structure of five populations of *P.umbilicalis* in the NW Atlantic.

(WA) MOLECULAR-ASSISTED ALPHA TAXONOMY OF THE ORDER RHODYMENIALES (RHODOPHYTA) FROM BRITISH COLUMBIA REVEALS OVERLOOKED AND CRYPTIC SPECIES DIVERSITY.

Gina V. Filloramo & Gary W. Saunders. Centre for Environmental & Molecular Algal Research, Biology, University of New Brunswick, Fredericton, NB E3B 5A3, Canada.

Molecular-assisted alpha taxonomy using COI-5P and *rbc*L-3P was employed to reassess species diversity for the Rhodymeniales (Rhodophyta) in British Columbia. A total of 555 collections were resolved as 16 genetic species groups in 10 genera whereas 13 species in 10 genera were previously reported. Molecular data revealed cryptic and overlooked diversity for *Botryocladia, Fryeella, Gloiocladia* and *Rhodymenia* and warranted some genus level reassignments. Collections attributed to *B. pseudodichotoma* from British Columbia were resolved as distinct from collections of that species from California (type locality) and were assigned to *B. hawkesii* sp. nov. Molecular data resolved an additional species of *Fryeella* for which the combination *F. callophyllidoides* comb. nov. (= *Rhodymenia callophyllidoides*) was established. Although two species of *Gloiocladia* were recognized, genetic analyses resolved three: *G. fryeana, G. laciniata* and *G. vigenaultii* sp. nov. Data also resolved *G. media* comb. nov. from California. For the genus *Rhodymenia,* where two species were expected, molecular data resolved four. Both *R. californica* and *R. pacifica* were confirmed in British Columbia, while some collections field identified as *R. californica* resolved as a genetically distinct species group assigned to the novel species, *R. bamfieldensis* sp. nov., while some collections identified as *R. pacifica* also resolved as a distinct group assigned to the resurrected *R. rhizoides* E.Y. Dawson. Our investigation clarifies the number of rhodymenialean species in British Columbia and has resolved taxonomic and distributional uncertainties associated with some of these taxa.

(WA) RED ALGAL PARASITISM: DEVELOPMENT OF AN INFECTION

Jillian Freese, Chris Lane, Dept. of Biological Sciences, University of Rhode Island, Kingston, RI U.S.A.

Parasitism is a complete lifestyle change for an organism as they become entirely dependent upon their host. Up to ten percent of florideophyte red algae are parasitic on other red algae, reliant upon their host for photosynthate. The relationship between host and parasite has informed the delineation of red algal parasites into adelphoparasites and alloparasites. Adelphoparasites evolved from their current host or a taxon closely related to its modern host and typically only infect one to two closely related species. Alloparasites are potentially more indiscriminate, capable of infecting multiple hosts that are often distantly related. Most lineages of medically relevant parasites are hundreds of millions of years old and studying their genome fails to identify patterns in the early

stages of parasite evolution. Red algal parasites, however, have repeatedly evolved in independent lineages in the very recent past, making them an ideal system to track the progression of an ongoing transition from free-living to parasitic organisms. Fundamental questions regarding parasite infection mechanisms, parasite development, or its repercussions on the host remain incompletely answered for nearly every red algal parasite described. Maintaining two host-parasite pairs in culture and manipulating their environment to stimulate the release of spores and control parasite reinfection has allowed for the development of the parasite from spore to mature pustule to be monitored, and enabled the exploration of adelphoparasitic organelle inheritance. The application of further microscopy techniques and single cell transcriptomics will give a greater glimpse into the experiences of host and parasite cells during infection.

(WA) ANALYSIS OF THE FORMALDEHYDE DETOXIFICATION PATHWAY IN EUKARYOTES.

Rebecca Littlefield[1], Baxter Worthing[1], G. Jason Smith[2] & Deborah Robertson[1] [1]Biology, Clark University, Worcester, MA, 01610, U.S.A. [2]Moss Landing Marine Laboratory, Moss Landing, CA U.S.A.

Formaldehyde (CH_2O) is a naturally occurring organic compound that is produced by all cells as an intermediate in the breakdown of many carbon compounds as well as in the metabolism of amino acids. In both prokaryotic and eukaryotic cells, formaldehyde detoxification involves a spontaneous reaction between glutathione and formaldehyde producing S hydroxymethylglutathione, which is oxidized by formaldehyde dehydrogenase (FALDH) to S-formylglutathione. S-formylglutathione in turn is hydrolyzed to formate and glutathione by S-formylglutathione hydrolase (FGH). Formaldehyde has been used as an inexpensive selectable marker for genetic transformations of bacteria and yeast. The purpose of this study is to characterize the enzymes and regulation of the formaldehyde detoxification pathway in diatoms and determine if formaldehyde can be used as a selectable agent for genetic transformation. Several species of centric diatoms in the genera *Thalassiosira* and *Skeletonema* have two genes encoding FALDH; one gene is a fusion of the FGH and FALDH open reading frames (FGH::FALDH) and the other encodes only FALDH. Other members of the Stramenopiles had only the FGH::FALDH gene. Of note, two marine prasinophytes had a FGH::FALDH that was not observed in other green algae; this may have evolved via a horizontal gene transfer between stramenopiles and the prasinophytes. RT-PCR analyses revealed that both FGH::FALDH and FALDH genes are expressed in *Thalassiosira pseudonana* and ongoing experiments are examining expression of these genes in response to exogenously supplied formaldehyde. Comparison studies of diatoms with different copy numbers of FALDH genes are being done as well to identify whether an increase in endogenous genes encoding FALDH increases their resistance to formaldehyde.

(WA) AN INVESTIGATION OF BROADLY BLADED *ULVA* SPP. (CHLOROPHYTA) IN THE OUTER BAY OF FUNDY (NEW BRUNSWICK, CANADA). <u>Kirby Morrill</u> & Gary W. Saunders. Centre for Environmental & Molecular Algal Research, Biology, University of New Brunswick, Fredericton, N.B., E3B 5A3, Canada.

Genetic data for ulvalean specimens collected in the outer Bay of Fundy (New Brunswick, Canada) since 2005 indicate that previous floristic accounts of ulvalean diversity in the area underestimated total species richness. The Bay of Fundy ulvalean flora is therefore in need of reassessment. Using DNA barcoding to overcome the identification difficulties inherent in the simple morphologies of these algae, four species of *Ulva* with broadly bladed morphologies are recognized in contrast to the two previously reported species. Keeping biogeography in mind, *rbc*L and *tufA* data from the Bay of Fundy species were compared with data available on GenBank, and morphological examinations were completed for comparison to type descriptions to identify our four bladed *Ulva* species. While originally *U. lactuca* and *U. rigida* were the only reported species in our area, we recognize *U. fenestrata*, *U. gigantea*, *U. laetevirens*, and *U. procera*.

(WA) GRAZE UNDER PRESSURE: HOW THE INTERACTION OF OCEAN ACIDIFICATION AND EUTROPHICATION IMPACTS MACROALGAL CONSUMPTION BY MARINE SNAILS. <u>Ober, G.T.</u>* and Thornber, C.S. Biological Sciences, University of Rhode Island, Kingston, RI U.S.A.

While detrimental to many marine organisms, ocean acidification and eutrophication enhance the growth and abundance of opportunistic macroalgae by increasing concentrations of critical resources like carbon dioxide (CO_2) and nutrients. This enhanced growth could be troubling for many coastal ecosystems, but grazers may hold the key to mitigating algal growth and keeping ecosystems in balance. Here, we experimentally tested how the consumption rates and feeding preferences of a common marine snail (*Littorina littorea*) responds to the combined effects of ocean acidification and eutrophication. Snails were placed in treatment mesocosms and were exposed to high pCO_2 (~1200 ppm) and high nutrient conditions (~200 μM TN), along with ambient levels of pCO_2 (~400 ppm) and nutrients (10 μM TN) in a factorial design. Under these conditions, snails were given a choice of two common macroalgal species, *Ulva lactuca* and *Fucus vesiculosus*. Non-herbivore controls (mesocosms only containing the two algal species) were run simoultaneously in order to capture non-consumptive effects on macroalgae. Two consumption experiments were run, lasting seven days each. We found that high pCO_2 levels (ocean acidification) significantly reduced macroalgal consumption by about 50% and snails switched from a mixed algal diet to feeding exclusively on *U. lactuca*. To understand the decreased consumption, we measured respiration rates for *L. littorea*, finding significantly lower rates under high pCO_2. Fake food trials were run to help explain the preference change. We found no difference comparing consumption of the fake food, pointing to the preference shift being driven by algal tissue toughness. Coupled with enhanced macroalgal growth under acidification and eutrophication conditions, decreases in consumption could ultimately enhance algal abundance in coastal ecosystems.

(WA) WILL MAKE YOUR VITAMINS AND AMINO ACIDS FOR FOOD: ENDOSYMBIONT PATHWAY RESTORATION IN A LONG TIME PARASITE.

Chris Paight[1], Sergio A. Muñoz-Gómez[2], Mary Beth Saffo[1], Claudio Slamovits, Christopher E Lane[1] [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

Apicomplexans are highly successful parasites, infecting every major metazoan lineage. The genus *Nephromyces* has recently been described as having a mutualistic relationship to its host *Mogulid* tunicates (Saffo 2010). If true, *Nephromyces* would be the only known example of a mutualistic apicomplexan genus. Apicomplexans have reduced genomes and have lost the ability to make many essential metabolites. These essential metabolites are instead scavenged from their host. Species of *Nephromyces* are known to have three different bacterial endosymbionts. Our data show that the bacterial endosymbionts encode a number of essential pathways lost in Apicomplexans. Here we describe insights from the transcriptome from *Nephromyces,* all three bacterial emdosymbionts and the tunicate host. These data gives us a glimpse of the complex metabolic relationships and intertwined pathways of hosts and endosymbionts, with a particular focus on the biosynthesis of amino acids and vitamins.

(WA) BACTERIVORY IN THE PHAGO-MIXOTROPHIC GREEN ALGA *CYMBOMONAS* (PRASINOPHYCEAE) PROVIDES A COMPETITIVE ADVANTAGE IN PHOSPHATE-LIMITED ENVIRONMENTS ONLY.

Amber Paasch, Eunsoo Kim, American Museum of Natural History, NY U.S.A.

The lineage Chloroplastida (Viridiplantae), which includes green algae and land plants, began as a result of cyanobacterium ingestion. Yet nearly all members of this primary-plastid lineage lost the ability to ingest bacteria. Recently, however, *Cymbomonas tetramitiformis,* a prasinophyte green alga, was definitively confirmed with transmission electron microscopy to ingest bacteria into a large, permanent vacuole. Since then, other prasinophytes have been found to ingest fluorescently-tagged bacteria and synthetic particles. It is not clear what evolutionary pressure exists to retain the trait of bacterivory in the prasinophytes alone. The presented study examines the hypothesis that resource limitation encourages bacterivory in the phago-mixotrophic *Cymbomonas*. Cultures were grown under limited nitrogen, phosphate, and light regimes and offered bacteria as a rescue source of nutrients. Surprisingly, bacteria only rescued *Cymbomonas* growth under phosphate-limited conditions. The results suggest that *Cymbomonas* retains the ability to extract phosphorous source, but not the nitrogen or carbon from prey bacteria. The *Cymbomonas* genome was mined for genes involved in metabolic pathways related to C, N and P uptake and assimilation, aspects of which will be discussed.

(WA) INTERTIDAL BULLY: COMPETITIVE INTERFERENCE BY *LITTORINA LITTOREA* ON *L. OBTUSATA*.

Alysha Putnam, Noemi Collazo & Paulette Peckol. Biological Sciences, Smith College, Northampton MA U.S.A.

Herbivorous species such as *Littorina* spp. may have overlapping food and habitat requirements resulting in competitive interactions in temperate rocky intertidal areas. *L. littorea* is a habitat generalist, found on rocky shorelines, salt marshes and tidal flats, while *L. obtusata* is a specialist, relying on *Fucus vesiculosus* and *Ascophyllum nodosum* for food and habitat. We investigated intra- and interspecific interactions between these gastropods, focusing on food and density effects. In the field, removal of *L. littorea* from intertidal fucoid canopies resulted in significant density increases of *L. obtusata*. Paired-choice laboratory experiments revealed reduced grazing rates by both species on *A. nodosum* that had been "pre-grazed" (induced) by their congener. However, only *L. obtusata* showed lower grazing rates on *F. vesiculosus* pre-grazed by *L. littorea* compared with un-grazed fronds. Phlorotannin levels were elevated above constitutive values only when grazed by *L. obtusata*, suggesting that chemical induction was not the mechanism of interference by *L. littorea*. Growth rate measurements using *F. vesiculosus* and *A. nodosum* as the food source indicated that *L. obtusata* showed reduced growth rates in the presence of *L. littorea*, but not in the presence of high densities of its conspecific, further highlighting a negative interspecific effect. *L. littorea* demonstrated the opposite pattern: lower growth rates in the presence of its conspecific (intraspecific effect) but not congeneric, under low food availability. Taken together, these results indicate that *L. littorea* exerts competitive interference on *L. obtusata*, affecting grazing and growth rates. Due to the mobility of these gastropods and adequate food supply in most intertidal areas, these closely related species are able to coexist through resource partitioning, thus avoiding strong competitive interactions.

(WA) SYMBIOSIS AND SURVIVAL: EVALUATING *SYMBIODINIUM* POPULATIONS DURING MATERNAL TRANSMISSION AND EARLY DEVELOPMENT IN THE CORAL *PORITES ASTREOIDES*.

Reich, H.G. [1,2]; Robertson, D.L. [1]; Goodbody-Gringley, G.[2] [1]Clark University, Department of Biology, Worcester, MA U.S.A.; [2]Bermuda Institute of Ocean Sciences, St. George's, Bermuda GE01

Shallow water coral abundances are declining globally as a result of anthropogenic stressors, which has not been observed in mesophotic reefs (30-150m). The Deep Reef Refugia Hypothesis postulates that mesophotic taxa may provide a source of larvae to repopulate shallow communities. Comparing *Symbiodinium* (algal endosymbiont) population structure on reefs at different depths will provide insight into the connectivity between shallow and mesophotic reefs. This study examined whether *Symbiodinium* communities associated with shallow (10m) and upper mesophotic (30m) *Porites astreoides* (1) differ, (2) change during coral development and (3) influence survivorship and growth of mesophotic juveniles on shallow reefs. *Symbiodinium* ITS2 sequences were amplified and sequenced from *P. astreoides* adults, planulae, and juveniles to determine symbiont diversity. Initial results revealed that adults, planulae, and juveniles from both depths harbor primarily clade A *Symbiodinium*. In addition, there was no evidence that symbiont populations changed during coral development and there were no differences in survivorship and growth. Although further fine-scale analyses of *Symbiodinium* genetic structure is ongoing, the conservative relationship between symbiont genotype and *P. astreoides* across its bathymetric distribution and throughout development may enable the recruitment of mesophotic *P. astreoides* planulae to shallow reefs.

(WA) THE ORIGIN OF ORGANELLES IN RECENTLY DERIVED RED ALGAL PARASITES.

Eric Salomaki & Chris Lane, Dept. of Biological Sciences, University of Rhode Island, Kingston, RI U.S.A.

Although most red algae are free-living autotrophs, some Florideophytes have successfully abandoned photosynthesis in favor of a parasitic life strategy. Interestingly, red algae seem to provide fertile ground for parasite evolution with more than 100 different parasitic species being recognized across eight orders. Red algal parasites exclusively infect other photosynthetic red algae, and are classified by their evolutionary relationship to their host. One hypothesis about their evolution holds that red algal parasites start as adelphoparasites, infecting close relatives, and diversify into alloparasites which infect more distant and in some cases multiple hosts. These numerous independent events across an evolutionary gradient provide a framework to investigate genomic change as an organism transitions from a photosynthetic to a parasitic lifestyle. In the late 20th century, microscopy revealed that upon germination, the parasite spore would create a pit connection with the host and deposit its nucleus, mitochondrion and a plastid into the host cells. Subsequent molecular work demonstrated that red algal parasites maintained their own mitochondrion, but some adelphoparasites had lost their own plastid and instead would abscond with a host plastid when packaging its spores. We recently sequenced a native parasite plastid form an alloparasite, indicating that not all red algae follow the same path to parasitism. Here we present DNA and RNA sequence data from *Gonimophyllum skottsbergii* and *Janczewskia gardneri*, two adelphoparasites that have very recently transitioned towards parasitism. These data hint at the origin of organelles in red algal adelphoparasites and provide insight into the very early stages of speciation and the transition towards parasitism.

(WA) UNDERSTANDING EVOLUTIONARY RELATIONSHIPS AND SPECIES DIVERSITY OF THE TRIBE PTEROSIPHONIEAE (CERAMIALES, RHODOPHYTA) IN THE NORTHEAST PACIFIC.

Amanda M. Savoie and Gary W. Saunders. Centre for Environmental and Molecular Algal Research, Department of Biology, University of New Brunswick, Fredericton, NB, Canada E3B 5A3.

Sequence data (COI-5P and *rbc*L) for North American members of the tribe Pterosiphonieae (*Amplisiphonia* Hollenberg, *Pterosiphonia* Falkenberg, *Symphyocladia* Falkenberg, and *Tayloriella* Kylin) were compared to congeners from around the world (including Australia, Russia and South Africa). Phylogenetic analyses resolved the genus *Pterosiphonia* as polyphyletic relative to other members of the Pterosiphonieae, and many species required transfer to other genera. In our analyses *Pterosiphonia* sensu stricto included only the type species *P. cloiophylla* (C. Agardh) Falkenberg and *P. complanata* (Clemente) Falkenberg, as well as the newly described South African species *P. stegengae* sp. nov. Some Asian, European and North American species previously attributed to *Pterosiphonia* were transferred to *Symphyocladia* including *S. arenosa* (M.S. Kim & B. Kim) comb. nov., *S. baileyi* (Harvey) comb. nov., *S. dendroidea* (Montagne) comb. nov., *S. plumosa* nom. nov. (for *P. gracilis* Kylin), *S. parasitica* (Hudson) comb. nov., and *S. tanakae* (S. Uwai & M. Masuda) comb. nov. We also described two new species of *Symphyocladia* from the northeast Pacific, *S. brevicaulis* sp. nov., and *S. rosea* sp. nov. Other species previously attributed to *Polysiphonia* and *Pterosiphonia* formed a distinct and well-supported clade for which the genus name *Polyostea* Ruprecht was resurrected. Included in *Polyostea* were *P. arctica* (J. Agardh) comb. nov., *P. bipinnata* (Postels & Ruprecht) Ruprecht, *P. hamata* (E.S. Sinova) comb. nov., and *P. robusta* (N.L. Gardner) comb. nov.

(WA) IN CHARACEAE: "EVERYTHING IS EVERYWHERE, BUT THE ENVIRONMENT SELECTS.” Robin S. Sleith[1], Amy J. Havens[1], Robert A. Stewart[1], John Wehr[2] & Kenneth G. Karol[1]. [1]Cullman Program for Molecular Systematics, New York Botanical Garden, Bronx, NY, 10458, U.S.A.; [2]Fordham University, Bronx, NY U.S.A.

The Characeae, commonly called stoneworts or muskgrasses, are a group of freshwater green algae. Species in this family are integral parts of aquatic ecosystems: they provide forage for birds, invertebrates and fish, and are important for colonizing new habitats and stabilizing sediments. Previous studies have shown that the Northeast U.S.A. has a particularly rich Characeae flora. Over 25 species from four genera have been reported from New York and New England. The pattern of richness in Northeast lakes was complex: with equal sampling effort some lakes were found to have only a single species while at others up to seven species were found. Furthermore, certain species were found to cluster in geographic regions of New York and New England, while others were widespread. These differing distribution patterns have been hypothesized to be biological (e.g., waterfowl dispersal) or chemical (e.g., pH or conductivity). In 2014 and 2015 we surveyed 740 water bodies across New York and New England, collecting all species of Characeae encountered and water chemistry data for each site (pH, Conductivity, Dissolved Oxygen, Nitrogen, Phosphorous, Calcium, Magnesium). This dataset allows investigation of species richness using multivariate analyses and species distribution models. Species with uneven distributions (e.g., western New York and northern Maine) such as *Chara contraria* were very well supported by the species distribution models (AUC 0.98), while more evenly distributed species such as *Nitella flexilis* were poorly supported (AUC 0.67). Taken together, the twelve species analyzed for this study suggest that water chemistry constrains species in different ways, with generalist and specialist species identified. This information indicates that conservation efforts must work to protect a wide range of habitats to ensure the maintenance of diversity in this ecologically important group.

(WA) PHYLOGENETIC ANALYSIS OF A CRYPTIC MICROSCOPIC RED ALGA. Katelyn Wadland[1], Gary W. Saunders[2] & Christopher E. Lane[1]. [1]Department of Biological Sciences, University of Rhode Island, Kingston, RI 02881, USA. [2]Department of Biology, University of New Brunswick, NB, Canada

Red algae demonstrate significant phenotypic plasticity and convergent evolution, making morphological identification difficult, which is further complicated by their limited number of morphological features. An unidentified red algal epiphyte (minute in size and composed of only a few cells) growing on another red alga (*Camontagnea oxyclada*) was collected in Stanley, Tasmania, Australia, and accidentally detected during routine DNA barcoding surveys. The objective of our study was to sequence commonly used phylogenetic markers (*cox*1, *cob, rbc*L, *psa*B, *psa*A, *psb*A) from both the host and epiphyte to place them in a wider red algal phylogenetic context. DNA was extracted for the combined red algal host and epiphyte using a micro-phenol-chloroform method and sequenced on the Illumina Miseq platform. The phylogenetic markers for each organism were then located and aligned within a concatenated data set. Phylogenetic placement of our samples was determined using Bayesian and maximum likelihood methods. The robust placement of the host, *C. oxyclada*, as a sister genus to *Rhodothamniella*, Palmariales, Nemaliophycidae, was confirmed. The epiphyte, on the other hand, was firmly allied as sister to the genus *Ballia*, Balliales, also in the Nemaliophycidae, but at a large genetic distance. The phylogenetic placement of this new epiphyte in the red algal tree of life has helped to uncover a potentially new order and further clarify red algal diversity.

PRESIDENT'S UNDERGRADUATE ORAL AWARD (PA)

(PA) LONG-DISTANCE KELP RAFTING OF RED ALGAE IN THE NORTHEAST PACIFIC. Cody M. Brooks, Gary W. Saunders, Biology, University of New Brunswick, Fredericton, NB, E3B 5A3, Canada.

At the species level ~10% of the seaweed flora in Haida Gwaii (an archipelago in northern British Columbia) has a disjunct distribution – these species being found also in California but not in nearby southern British Columbia. The kelp conveyor hypothesis posits that giant kelps dislodged from the Californian coastline in the winter may be responsible for rafting turf-forming seaweed northward on the Davidson Current. If individuals are being rafted to Haida Gwaii, we expect to see some evidence of the kelp conveyor even in species with a continuous distribution along the entire Northeast Pacific coast. To test this hypothesis, population analyses were carried out on three red algal species growing variously in the mid to subtidal zones as we expect that kelp rafting will affect species in different zones to different degrees. We generated data for the mitochondrial cytochrome c oxidase I (COI) gene and the nuclear internal transcribed spacer (ITS) of the ribosomal cistron. These data were analysed with Migrate-N to model and rank the kelp conveyor hypothesis relative to other possible migration patterns for our three species. Our results provide the first test of the kelp conveyor hypothesis at the population level and an indication of the importance of this mode of long-distance dispersal in structuring benthic communities in the Northeast Pacific.

(PA) DNA BARCODING REVEALS NEW DISTRIBUTION RECORDS OF GREEN MACROALGAE (CHLOROPHYTA: ULVOPHYCEAE) IN RHODE ISLAND WATERS. Kelly DeMolles & Brian Wysor. Biology, Roger Williams University, Bristol, RI U.S.A.

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 I project that species richness of marine algae 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, 76 species of marine Chlorophyta have a distribution that includes RI, but only 20 species have been documented in RI. Here I present an updated account of green algal diversity in RI based on DNA Barcoding and morphological examination of recently collected specimens. The molecular-based inventory from *tuf*A, ITS, and LSU data confirms the presence of 36 species, which includes several species that have no close sequence match in public databases. Morphological and molecular examination has helped to resolve species identities and evaluate whether these species represent floristic changes resulting from anthropogenic stress or simply the elucidation of true patterns of diversity using more sensitive methods.

(PA) NEW GENETIC SPECIES OF *WRANGELIA* (WRANGELIACEAE, CERAMIALES) FROM BERMUDA, WESTERN ATLANTIC OCEAN. Walter M. Jongbloed[1], Craig W. Schneider[1] & Christopher E. Lane[2]. [1]Department of Biology, Trinity College, Hartford, CT U.S.A; [2]Department of Biological Sciences, University of Rhode Island, Kingston, RI U.S.A.

Currently there are 20 accepted species in the genus *Wrangelia* from warm waters of the world's oceans with four presently known from the western Atlantic: *W. argus, W. bicuspidata, W. gordoniae* and *W. penicillata.* A recent molecular and morphological investigation separated *W. gordoniae* (type locality, Puerto Rico) from what it had been earlier called, *W. penicillata* (type locality, Mediterranean Sea). Using similar techniques, our barcode and phylogenetic analyses (COI-5P, SSU rDNA) indicate the presence of six species of *Wrangelia* in Bermuda, three of which appear to be novel species in the *W. penicillata* complex. Anatomical and reproductive characters, as well as their gene sequences, are used to distinguish the new genetic species. Lack of complete rhizoidal cortication in *W. argus* and *W. bicuspidata* distinguish them from the four species in the *W. penicillata* complex in Bermuda. A key to the western Atlantic species of *Wrangelia* is provided.

(PA) THE COLONIAL GREEN ALGA *ASTREPHOMENE GUBERNACULIFERA* (CHLOROPHYCEAE) PERFORMS CHEMOTAXIS BY AN EXTRACELLULAR CALCIUM-DEPENDENT TEMPORAL SENSING MECHANISM.

Grant F. Kusick[1], Stephanie Newman[1] & Harold Hoops[1]. [1]Biology and Biochemistry, State University of New York College at Geneseo, Geneseo, NY U.S.A.

One challenge in the early evolution of multicellularity is the performance of collective behaviors. This transition is drastic within the volvocine algae: multi-celled members of the Volvocales exhibit many of the same behaviors as their unicellular relatives, but the mechanisms involved must be distinct. *Astrephomene gubernaculifera* is the only multi-celled volvocine alga that has been shown to perform chemotaxis: navigation along a chemical gradient. Since the discovery of this behavior, the signaling pathway involved and the physical means by which the alga changes its movement to navigate toward higher concentrations of its food source, acetate, have been obscure. We report that extracellular calcium is required for chemotaxis independent of general motility and at a different concentration than is required for phototaxis. This suggests that there is an influx of calcium in the chemoresponse separate from the photosensory pathway, as in *Chlamydomonas reinhardtii*. We also find that increasing the viscosity of the medium abrogates effective phototaxis but not chemotaxis. This finding demonstrates that the mechanisms of chemotaxis and phototaxis are fundamentally different, recommending that chemotactic sensing and response occur over time rather than instantaneously, as is the case in phototaxis.

(PA) THE DIVERSITY OF THE FRESHWATER GREEN ALGAL GENUS *HYDRODICTYON* (SPHAEROPLEALES, CHLOROPHYCEAE).

Nicholas J. Macoretta[1], Anna Curtin[1], Hilary A. McManus[1], Louise A. Lewis[2], and Kenneth G. Karol[3]. [1]Biology, Le Moyne College, Syracuse, NY U.S.A.; [2]Ecology and Evolutionary Biology, University of Connecticut, Storrs, CT U.S.A.; [3]The New York Botanical Garden, Bronx, NY U.S.A.

The freshwater green algal genus *Hydrodictyon* comprises of six identified species, of which only three have been previously studied in the context of a molecular phylogeny. One such species, *Hydrodictyon reticulatum*, is known for nuisance blooms in many freshwater lakes, ponds, and slow moving streams around the world, including but not limited to Australia, Southeast Asia, and the United States. Furthermore, this species has recently been observed in more northern freshwater lakes than previously recorded. Preliminary data have suggested that the genus *Hydrodictyon* may be more diverse than what is currently recognized based on morphology alone. For this project, samples of *Hydrodictyon* were obtained from field collections in the Central New York State area, herbarium specimens from The New York Botanical Garden and the Academy of Natural Sciences, and donations from the phycological community. Analysis included digital imaging of the samples, sequencing of the mitochondrial *nad2* and the chloroplast *rbc*L genes, and observations of life cycle stages. The resulting phylogenetic trees reveal that *Hydrodictyon reticulatum* is likely not monophyletic.

CONTRIBUTED ORAL

(C) VERTICAL DISTRIBUTION OF MIXOTROPHIC NANOFLAGELLATES IN A MESOTROPHIC LAKE. Sarah DeVaul & Robert Sanders. Department of Biology, Temple University, Philadelphia PA, 19122, U.S.A.

Heterotrophic nanoflagellates are fundamental members of the microbial food web as prey for zooplankton and predators of bacteria. Field studies have revealed that mixotrophic protists that combine phototrophy and phagotrophy are often numerically dominant in freshwater systems and can exhibit a greater grazing impact on the bacterial community than pure heterotrophs. Although the presence of mixotrophic nutrition among phytoflagellates has been well documented within a variety of aquatic ecosystems and in a range of taxa, few studies have focused on the influence of vertical habitat heterogeneity in shaping their depth-distribution and bacterial grazing impact across extended temporal scales. The combination of trophic modes utilized by mixotrophic protists may provide a competitive advantage along the vertical gradient of resources created as a result of thermal stratification in temperate lakes. Abundance and, as appropriate, bacterivory of phototrophic, heterotrophic and mixotrophic nanoflagellates were quantified at three depths over a 15-month period in Lake Lacawac (Pocono Mountains, Pennsylvania, USA) via microscopic analysis of ingested bacterial surrogates. The absolute and relative abundances of all nanoflagellate trophic groups varied with season and depth, likely as a result of differences in physiological tolerance. Whereas the abundance of phototrophic and heterotrophic nanoflagellates varied with depth in both the presence and absence of thermal stratification, mixotrophic protists were evenly distributed throughout the water column during mixis. The abundances of phototrophic and mixotrophic protists were significantly correlated, but only in surface waters during periods of thermal stratification. Grazing rate and consequent impact by bacterivorous nanoflagellates varied with depth across season, particularly during thermal stratification. Mixotrophic bacterivory exceeded that of heterotrophs in the epi- and metalimnion during stratification, removing a maximum of 80% of the bacterial standing stock day^{-1}. The relative contribution of heterotrophic nanoflagellates to community bacterivory increased with depth, even during mixis, and dominated the grazing impact in the hypolimnion.

(C) A PROPOSED REVISION OF *CHARA* SUBSECTION *WILLDENOWIA*. Stephen D. Gottschalk[1,2] & Kenneth G. Karol[2]. [1]Department of Biological Sciences, Fordham University, Bronx, NY U.S.A. [2]The Lewis B. and Dorothy Cullman Program for Molecular Systematics, New York Botanical Garden, Bronx, NY U.S.A.

In their 1964 revision of the Characeae, R. D. Wood and K. Imahori acknowledge 81 species, a number revised down from a previous estimate of 314 species in the family. This has resulted in the aggregation of numerous morphologically, taxonomically, and ecologically diverse *Chara* into just 19 species with previously recognized species relegated to varietal and formal synonymy. An example of this is *Chara* subsection *Willdenowia*, whose sole representative in Wood and Imahori's treatment is *Chara zeylanica*. In this treatment, *C. zeylanica* exhibits a diverse range of morphologies and traits including plants that are monoecious or dioecious, gametangia that are conjoined or sejoined, different structural and developmental characteristics of gametangia and zygotes, different chromosome numbers, and reproductive isolation. These differences are bolstered by molecular analysis of this geographically widespread taxon, an analysis that reveals that *C. zeylanica sensu* Wood and Imahori represents many distinct, sometimes cryptic, species. Presented here is an overview of the historical treatments of this group, and the current data that support a wholesale revision of *Chara* subsection *Willdenowia*.

(C) THE EFFECT OF WARMING OCEAN TEMPERATURES ON THE GROWTH AND SURVIVAL OF BLOOM-FORMING MACROALGAE (*ULVA* SPP.).

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

Narragansett Bay has been plagued with frequent 'green tides' comprised of blade-forming *Ulva* species for several decades. The mean annual water temperature of Narragansett Bay has increased by 1°C since 1960 and is predicted to warm another 1-4°C by 2100. We aimed to determine the effect of warming ocean temperatures on the survival and growth of bloom-forming *Ulva compressa* and *Ulva rigida* and the abundant but not bloom-forming *Ulva lactuca. Ulva compressa, U. lactuca,* and *U. rigida* were grown for 3 weeks under temperatures that represented current monthly averages during the summer bloom-forming season (15°, 18°, and 24°C), as well as a projected increase of 3°C (27°C) above the maximum monthly average. Percent survival of all species was >70% when grown between 15° and 24°C. At 27°C, survival of *U. lactuca* and *U. rigida* declined, while *U. compressa* maintained 100% survival up to 27°C. All species had lower growth rates at 27°C. *U. compressa* and *U. rigida* grew 27-78% faster on average than *U. lactuca* at all temperatures. The projected warming of Narragansett Bay is likely to negatively affect *U. lactuca* and *U. rigida* survival and growth and *U. compressa* growth during the current bloom-forming season.

(C) REFLECTIONS ON THE MEANING OF THE POLYSIPHONOUS STATE VIEWED THROUGH THE LENS OF *HETEROSIPHONIA*.

Larry M. Lewis. Biology, Salem State University, Salem. MA U.S.A.

Polysiphonous algae likely evolved from uniseriate forms; however the morphological meaning of the polysiphonous state my not be clear. The transition from one form to another occurs in the *Heterosiphonia japonica*, a common invasive organism in New England where one observes a main axis that can be many cells across and uniseriate branches that extend from the main axis. Measurements of the length to width ratio of the uniseriate cells are far less that the adjacent polysiphonous regions (cells average 62.8 µm x 38.2 µm compared with151.2 µm by 15.5 µm). Thus the polysiphonous state results in cells that are longer and narrower. The surface/volume ratio of the uniseriate cells measures 0.11 compared to the adjacent polysiphonous regions that measure 0.18. Thus, the evolution of the polysiphonous condition results in a thallus that is not only stronger but has an increased surface volume ratio.

(C) DEATH BY ULVA: DIFFERENTIAL TOXIC EFFECTS ON THE HERBIVOROUS SNAILS, *LITTORINA LITTOREA* AND *L. OBTUSATA*.

Paulette Peckol & Alysha Putnam. Biological Sciences, Smith College, Northampton, MA U.S.A.

Members of the genus *Ulva* are widespread and abundant in intertidal and shallow subtidal areas but there are conflicting data regarding its susceptibility to herbivory. While members of this genus are often favored by a diversity of marine herbivores, other studies have documented herbivore deterrence. We investigated grazing and growth rates of the littorinid species, *Littorina littorea* and *L. obtusata*, when offered *Fucus vesiculosus*, *Ascophyllum nodosum*, *Ulva lactuca* and *Chondrus crispus*, highlighting distinctive vulnerabilities to toxic effects of *U. lactuca*. *U. lactuca* was the preferred food of *L. littorea*, while *L. obtusata* showed no grazing on this ephemeral algal species. In contrast, *Fucus vesiculosus* was highly preferred by *L. obtusata*. Although *L. littorea* demonstrated a grazing preference for *U. lactuca*, growth rate of this gastropod species was nearly 3X greater when fed *F. vesiculosus*, suggesting a non-lethal, negative effect of *U. lactuca* on *L. littorea* with long-term exposure. When held in the presence of *U. lactuca*, *L. obtusata* suffered nearly 100% mortality within one week. However, few surviving *L. obtusata* died when transferred to clean water, suggesting recovery from the negative effects of *U. lactuca.* We conclude that a toxic exudate of *U. lactuca* had allelopathic properties, and is likely the water soluble acrylic acid. Observed differences in species susceptibility to *Ulva* toxicity may be related to contrasting physiological and population characteristics of the littorinid species.

(C) CAN KEY NEW ENGLAND MACROPHYTES RAISE SEAWATER PH?

Price N.N.[1]; Donham E.[1,2]; Fachon E.[1,3]; Honisch, B.[1]; Arnold, S.N.[4]; Record, N[1]; White, M.[1,5]; Doan M.[6]; Neckles, H.[7] [1] Bigelow Laboratory for Ocean Sciences, ME; [2] Moss Landing Marine Laboratory, CA; [3] Northeastern University, MA; [4] Island Institute, ME; [5] Bowdoin College, ME; [6] Friends of Casco Bay, ME; [7] USGS Patuxent Wildlife Research Center, ME U.S.A.

Marine macrophytes uptake CO_2 during photosynthesis and thus can reduce seawater acidity, but species vary in their capacity to remove and store inorganic carbon. We used literature values and lab experiments to compare instantaneous CO_2 capture rates among commercially and ecologically relevant New England macrophytes, followed by field campaigns to measure impacts of primary production on bulk seawater chemistry. In the lab, we exposed five species (*Saccharina latissima*, *Ascophyllum nodosum, Fucus vesiculosus*, *Ulva lactuca*, and *Zostera marina*) to six pCO_2 levels (280, 400, 520, 640, 880, and 1120 μatm) in 1.5 hr long metabolic assays (after acclimation). CO_2 consumption rates, photosynthetic quotient ($Q = CO_2$ consumed:O_2 evolved), and ability

to raise seawater pH and $\Omega_{aragonite}$ differed across species, but increased at higher pCO_2 treatments. These results generally agree with previous work, although reported intraspecific variation is large and likely dependent on differing light availability across studies. In Casco Bay, intact eelgrass meadows (*Z. marina*) raised seawater pH by 0.04 units (± 0.01) and dissolved oxygen by 60.7 µmol (± 4.9) on average each day relative to recently denuded coves, as measured with autonomous SeapHOx sensor packages. Likewise, farmed and edible sugar kelp (*S. latissima*) raised seawater pH by 0.05 units (± 0.003) and $\Omega_{aragonite}$ by 0.36 (± 0.05) each day relative to a nearby 'control' location 100s meters upstream (as determined by predominant tidal flux). Differences in photo-physiology and response to changing environmental conditions imply that certain species may be better candidates to mitigate coastal acidification and may provide an important ecosystem service while serving as an additional nutritional resource.

(C) REDISCOVERY OF THE FRESHWATER BROWN ALGA *HERIBAUDIELLA FLUVIATILIS* IN CONNECTICUT.

John D. Wehr, Kam Truhn, Nicholas R. Ballor. Louis Calder Center – Biological Station, Fordham University, Armonk, NY U.S.A.

The first record in North America of the freshwater brown alga *Heribaudiella fluviatilis* (Areschoug) Svedelius was reported by Collins, Holden and Setchell in *Phycotheca Boreali-Americana* (1895-1919), based on a collection by Isaac Holden on September 4, 1898 from Island Brook, in Bridgeport, CT (as *Lithoderma fluviatile* Areschoug). In 1950 G.M. Smith suggested Holden's material could have been the marine alga *Lithoderma fatiscens* Areschoug, as sample location was near the coast "a short distance" above the tide, and the species was removed from the U.S. flora.

No other collections of this species were reported from anywhere on the continent for another 80 years until a population was discovered in 1979 from a stream in British Columbia and confirmed by Pueschel & Stein in 1980. We have since collected > 30 populations of *Heribaudiella* from BC, WA, OR, and WY. Our molecular analyses based on mt and pt genes indicate these populations form one or more clades distinct from those in Europe and Japan.

While past authors cast doubt on the identity of Holden's CT material, our reexamination of the exsiccati have determined that diatoms associated with these samples were freshwater species, supporting the original record as a freshwater location. Resampling efforts in 1998 and 2014 at several sites along Island Brook, CT were unsuccessful in locating any specimens of *H. fluviatilis*, likely due to degraded water quality. However, additional sampling in 2015 of more pristine streams in western CT successfully located 5 newly identified populations of *H. fluviatilis.* The present study describes the macroscopic and microscopic morphology of the CT populations, and compares with those from Europe and western North America. DNA analyses are underway to examine the genetic relatedness between CT populations with those from distant locations.

(C) ADAPTABILITY OF FREE-FLOATING GREEN TIDE ALGAE TO GRADIENTS OF TEMPERATURE AND LIGHT INTENSITY. Yuanzi Huo[1,2], Jang Kyun Kim[1,3], Charles Yarish[1],Simona Augyte[1]& Peimin He[2].[1]Department of Ecology and Evolutionary Biology, University of Connecticut, 1University Place, Stamford, CT 06901, USA; [2]College of Fisheries and Life Sciences, Shanghai Ocean University, Shanghai 201306, China;[3]Incheon National University, 119 Academy-ro, Yeonsu-gu, Incheon, 22012, Korea

From 2008 to 2015, massive floating green macroalgal blooms caused by *Ulva* species occurred annually during the summer months in the Yellow Sea, China. The small patches of floating *Ulva* species drifted for about 1.5 months, and eventually developed into the world's largest green tide, reaching a maximum algal cover of 3489 km^2. The floating *Ulva* species grow quickly and accumulate huge biomass rapidly under favorable environmental conditions. The influence of temperature and light intensity on the germination, early development, and growth of four green tide algae, *U. prolifera*, *U. linza*, *U. compressa* and *U. flexuosa*, from the Yellow Sea were evaluated. Neither the gametes nor spores of these *Ulva* species germinated <3 ºC at 10 $\mu mol\ m^{-2}s^{-1}$ but could survive over two months as single cells. Germination and rapid growth took placed when the temperature increased more than 10 ºC. Only *U. prolifera* could germinate and grow into mature thalli at 30ºC at photon fluence rates of 10–200 $\mu mol\ m^{-2}s^{-1}$. The growth rate of sporelings was much higher than that of adults for the four species. The specific growth rate (*SGR*) of *U. prolifera* was 1.5–3.5 times greater than the other three species at 15–25 °C at 200–600 $\mu mol \cdot m^{-2} \cdot s^{-1}$. The average daily *SGR* of floating green tide algae was about 23.2–23.6 % d^{-1}during the growing season, and it reached up to 56.2 % d^{-1} in the exponential phase. These results further elucidate the dynamics of the green macroalgal blooms in the Yellow Sea.

POSTERS

C = Contributed; PA = Presidents Award; FA = Francis R. Trainer Award

1. (PA) EXAMINING THE EFFECT OF FLOW ON PERFORATIONS IN SPECIES OF BLOOM-FORMING MACROALGAE.

Ivy Burns, Lindsay Green, and Carol Thornber. University of Rhode Island, Dept. of Biological Sciences, 120 Flagg Road, Kingston, RI U.S.A.

Increased nutrient loading rate and projected ocean warming associated with anthropogenic climate change are likely to lead to an increase in macroalgal blooms. Blade-forming species of the genus *Ulva* are key contributors to macroalgal blooms and generally propagate asexually via fragmentation. The dominant blade-forming species of *Ulva* in Narragansett Bay are *Ulva rigida* (blade contains perforations) and *Ulva compressa* (blade lacks perforations). These perforations are naturally occurring and seem counterintuitive since they decrease the photosynthetic area of the algal blade. We hypothesized that the perforations may have evolved in *Ulva rigida* to increase turbulent flow over the blade surface, thus increasing nutrient uptake and growth in low water flow environments where blooms generally occur. To test this, both species were grown at three sites in Greenwich Bay that have flow rates ranging from low to high flow. Blades were also grown in outdoor flow-through mesocosms at high and low flow. Both species exhibited an increase in the percent of surface area comprised of perforations under high flow conditions in outdoor mesocosm trials, most likely due to their rapid growth rate, and this observed increase under high flow conditions was more than 10 times the increase observed under low flow conditions. These results were also observed at our high and medium flow field sites. Interestingly, the surface area to mass ratio of the blades grown in the outdoor mesocosms decreased under both high and low flow. This indicated that the blades were getting thicker. The decrease in surface area to mass ratio was more dramatic under high flow rates for *U. compressa* and these results were not observed at our field sites. Our results suggest that perforations in *Ulva* may be more closely linked to growth rate than to water flow conditions.

2. (PA) CHARACTERIZING THE CELL WALLS OF *KOSHICOLA* AND *CHAETOPELTIS (CHAETOPELTIDALES, CHLOROPHYCEAE)*.

Mariedonica Canieso[1], Louise A. Lewis[1] & Shin Watanabe[2]. [1]University of Connecticut, Department of Ecology and Evolutionary Biology, Storrs, CT 06269 U.S.A. [2]University of Toyama, Faculty of Science, Toyama, Japan.

The cell walls of green algae are tremendously diverse. Some species have walls that are very similar in composition to those of embryophytes (Zygnemophyceae, Charophyceae, and Coleochaetophyceae). Others have organic scales or walls derived from fused scales (e.g., prasinophytes and Chlorodendrophyceae), and others have glycoprotein-rich walls (e.g., *Chlamydomonas*). Most of what we know about the components of the cell walls of members of the class Chlorophyceae comes from a few species. Within the OCC lineage (Oedogoniales, Chaetopeltidales, Chaetophorales) little is known about the composition of the walls, except for *Oedogonium*. Recent investigations demonstrated surprising similarities of certain wall components of *Oedogonium* to those within the land plant lineage of algae. To expand knowledge about the cell walls in Chlorophyceae, and in particular within the OCC lineage, two

representatives of Chaetopeltidales were targeted. In aquatic habitats, the recently described genus *Koshicola* forms a loosely filamentous stage that is epiphytic. This species also produces packets of two to four thick-walled cells in more desiccating habitats, resembling the terrestrial relative *Hormotilopsis*. *Chaetopeltis* forms characteristic disk-shaped thalli as well as small packets of cells in culture. In light microscopy and transmission electron microscopy, the walls of *Koshicola* can be seen to comprise small, overlapping plates of what we suspect is cellulose, interspersed by other wall compounds. We are investigating the composition of the walls of *Koshicola* and *Chaetopeltis* using a combination of wall stains (Calcofluor white, Analine blue), enzymatic digestions, and fluorescence microscopy. An examination of cell walls of these two algae contributes to a better understanding of cell wall diversity in Chlorophyceae.

3. (PA) *SHIZOCLADIA ISCHIENSIS* ORGANELLAR GENOMES: OVERALL PATTERNS AND INSIGHTS.

Cheda, B.[1], Salomon, M.[2], Boore, J. L.[3], Braun, E. L.[4], Phillips, N.[5] Biology Department: [1,5]Arcadia University, Glenside, PA. [2,3]University of Southern California, Berkeley, CA. [4]University of Florida, Gainesville, FL U.S.A.

Brown algae (Phaeophyceae) are one of the most productive and ecologically important lineages in marine ecosystems and represent one of the last lineages in the Eukaryotic tree of life to shift to multicellularity. Members of these lineages (including other heterokonts) generate approximately half the world's oxygen. However, we are just beginning to understand their organellar genomes and architectural changes that accompany their transition to complexity. This presentation will examine the plastid and mitochondrial genomes of *Schizocladia* discuss insights gained from a project to closely related classes (Phaeophyceae). This project was initiated to understand the organellar genomes of these important primary producers and the genomic changes accompanying their shift to multicellularity. To assure the isolation of pure genomic DNA cultures were grown with GeO_2 to inhibit diatom growth before DNA extraction. Data from a separate HiSeq and Miseq run were collected and assembled. We report here on the size, structure, and gene content of this heterokont lineage and compare it to members of the brown algae. Lastly, we summarize insights these data provided into the evolutionary patterns in organellar genomes from heterokonts to brown algae.

4. (C) MOLECULAR DIVERSITY OF THE GREEN ALGAL FAMILY HYDRODICTYACEAE.

Anna Curtin & Hilary A. McManus. Department of Biology, Le Moyne College, Syracuse, NY U.S.A

Recent molecular phylogenetic studies of the freshwater green algal family Hydrodictyaceae (Sphaeropleales, Chlorophyceae) have revealed that the diversity of the family is poorly understood using morphology alone. The focus of this study is to continue to accumulate sequence data for the examination of the molecular diversity of the family within Central New York State. Members of the family were collected and isolated during the summers of 2013-2015. Thirty-three isolates representing four genera (*Hydrodictyon, Pediastrum, Pseudopediastrum*, and *Stauridium*) from the family Hydrodictyaceae were successfully cultured. Isolates were imaged and their genomic DNA extracted and used for amplification of the chloroplast *rbc*L gene using PCR. Sanger sequencing was used to obtain the nucleotide sequence of the successful amplicons. The sequence data were analyzed using phylogenetic methods to allow for species differentiation and diversity assessment. The addition of more isolates supports the conclusions of past data analyses for this project that there is a range of diversity within the family Hydrodictyaceae in Central New York State.

5. (PA) DETERMINING THE MECHANISM OF THERMOTAXIS IN ASTREPHOMENE GUBERNACULIFERA.

Stephanie Clookey, Naomi Wilson, & Harold Hoops. Biology, SUNY College at Geneseo, Geneseo, NY U.S.A.

Astrephomene gubernaculifera is a colonial, volvocine green alga. The colonies are hollow spheres of 32 - 64 cells, each with two flagella. These cells have no apparent means of communication with one another, and yet the colony responds as a unit to stimuli. Prior studies have demonstrated that *A. gubernaculifera* colonies accumulate at warmer temperatures in a steady-state temperature gradient. In theory, accumulation might result from colonies slowing at warmer absolute temperatures, but Amy Potter and Yuliya Muradova demonstrated that this was not the case. More complex models require the alga to sense the gradient, and to adjust to *changes* in temperature rather than the absolute temperature. For example, *A. gubernaculifera* colonies might respond to a temporal increase in temperature by swimming faster and/or making fewer (or shallower) turns. In an attempt to test these ideas, we tracked colonies in temperature regimes that mimic algae moving through a temperature gradient. Preliminary data suggests that there is no significant difference in the velocity of colonial movement between step-up response of 0.03 °C/s between 27.4 °C and 27.7 °C and step-down response to -0.02 °C/s between 28 °C and 27.8 °C. Therefore, changes in linear velocity in response to a temporal temperature gradient appear insufficient to explain thermotaxis. Further studies will investigate if step-up and step-down temperature regimes influence colonial turning frequency or magnitude.

6. (PA) SPECIES COMPOSITION AND DISTRIBUTION OF ULVOID BLOOMS IN NEW HAVEN HARBOR.

Kayla Delano, Jean-Paul Simjouw, and Amy Carlile. Department of Biology and Environmental Science, University of New Haven, West Haven, CT U.S.A.

Blooms of green algae, called ulvoid blooms, occur along shorelines worldwide, and can have harmful effects on the ecology and economy of the areas in which they persist. Due to their thick, dense nature they block sunlight from aquatic life below, and can create unsightly tourism deterrents. Species identification within ulvoid blooms by morphology alone is unreliable given their simple and overlapping characteristics; however, the development of DNA sequencing technology led to more accurate species characterizations. This study examines the species composition and distribution of ulvoid blooms that persist in New Haven Harbor, CT during summer months. The chloroplast encoded *rbcL* gene and nuclear internal transcribed spacer region (ITS) were sequenced and compared to publically available sequences in GenBank for species identification and population structure. Morphological characters were also noted in an effort to delimit physical differences between species. At least four species from the genus *Ulva* were found within blooms between June and August in 2015. *Ulva compressa* was the most abundant within large blooms; this was also found in a similar study conducted in Rhode Island. The number of species was not apparent based on morphology; samples collected were either large green blades with angular edges and perforations, or fine, thin tubes. The similarity of morphological characters found in our collections confirmed the difficulty and inaccuracy of identifying species without the use of molecular methods.

7. (C) MORE THAN MICROCYSTINS? ANALYTICAL METHODS FOR PARALYTIC SHELLFISH TOXINS IN FRESHWATER SYSTEMS. Zacharias Smith[1] & Gregory Boyer[1].

[1]State University of New York, College of Environmental Science and Forestry, Department of Chemistry, Syracuse NY U.S.A.

Most research on Harmful Algal Blooms in the US has focused on the occurrence of microcystins. However, toxin suits are known to vary significantly from region to region, and thus there may be a sizable presence of other cyanobacterial toxins. Paralytic Shellfish Toxins (PSTs) are produced by members of the genus Anabaena and Lyngbya – both common cyanobacteria in the Northeastern US. To develop a robust monitoring program for the occurrence of PSTs in the region, we examined three different methods for measurement of PSTs in New York State freshwaters. These include (1) the traditional HPLC with post-column oxidation and fluorescent detection developed by Oshima, (2) newer HILIC chromatography methods coupled with mass spectroscopy (MS or MS/MS) detection, and (3) commercially available ELISA assays for PSTs. Known PST-producing cyanobacteria were grown in laboratory culture, and water samples were collected from more than 125 lakes spread across New York. Samples were extracted using a unified sample extraction protocol and analyzed using all three methods. A comparison of the different methods will be presented.

8. (C) UTILIZATION OF PHYTATE IN DINOFLAGELLATES. Sprecher, Brittany N. & Lin, Senjie.

Marine Science Department, University of Connecticut, Groton, CT U.S.A.

Dinoflagellates are an important class of phytoplankton responsible for primary productivity in their environments. Depending on the environment, growth and proliferation are often limited by access to phosphorous (P). P is bioavailable in both dissolved inorganic (DIP) and organic (DOP) forms. DIP is preferred yet limited in many marine systems. Under these DIP limited conditions, dinoflagellates are able to sustain populations, which has been attributed to the utilization of DOP. Phytate is a plant product that most consumers cannot metabolize; its release via feces into aquatic ecosystems is potentially a source of DOP pollution. However, this most abundant DOP in soil has heretofore been understudied in response to dinoflagellate utilization. Phytase is the enzyme responsible for the hydrolysis of phytate and our preliminary data indicate the presence of its enconding gene in several dinoflagellates' genomes. We are proposing to apply molecular and biochemical techniques to determine if under DIP limited conditions, dinoflagellates will hydrolyze and exploit phytate as a source of P to sustain populations. This study will examine bacteria reduced cultures to determine growth rate and phytase gene expression levels under different DIP and DOP conditions. Key findings will provide a new and previously untouched aspect of P utilization in dinoflagellates. If phytate utilization is found, phytase can be used as a molecular marker for future studies to survey the phytate-utilizing ability in global phytoplankton communities.

9. (PA) THE ROLE OF DNA METHYLATION IN TEMPERATURE ACCLIMATION OF *CHONDRUS CRISPUS*.

Amanda DeLiberto & Amy Carlile. Department of Biology and Environmental Science, University of New Haven, West Haven, CT U.S.A.

Chondrus crispus is a temperate marine alga, typically found in regions with a temperature range of 5-25°C. With global climate change leading to increased temperatures, it is important to determine how organisms such as *C. crispus* will react to temperatures outside of their normal range. The ability of an organism to acclimate to new conditions is vital to survival; however, the mechanisms involved in acclimation responses are not well understood. One possible mechanism for acclimation is varying gene expression via DNA methylation. DNA methylation is often correlated with decreased gene expression; therefore it may play a role in temperature acclimation. The purpose of this study was to determine how *C. crispus* responds physiologically and epigenetically to increased temperatures, and if DNA methylation plays a role in its acclimation. *C. crispus* samples were exposed to temperatures of 15°C, 25°C and 35°C. Physiological acclimation was detected by measuring photosynthetic efficiency using a Pulse Amplitude Modulated (PAM) fluorometer. Repeated measurements were taken over the first 30 minutes until acclimation was observed, and again after 24 and 72 hours. Over the course of the PAM measurements, tissue samples were frozen for subsequent genomic DNA extraction. DNA methylation was measured using the methylation-sensitive amplified polymorphism (MSAP) method to determine if there were any changes in methylation. Physiologically, samples were able to acclimate more rapidly at 25°C than at 35°C. Photosynthetic rates were also higher at 25°C than at 35°C over the 30 minute period. This suggests that *C. crispus* is able to acclimate to increasing temperatures, which may be due to epigenetic mechanisms such as DNA methylation.

10. (C) FIELD AND GIS BASED EVALUATION OF ALGAL DIVERSITY AND LAND COVER IN THE QUINNIPIAC RIVER, CT, USA.

Joseph Eigenberg, Jean-Paul Simjouw, and Amy Carlile. Department of Biology and Environmental Science, University of New Haven, West Haven, CT U.S.A.

Urbanization has historically been associated with stream degradation and a loss of biodiversity in freshwater systems. The changes in land use associated with urbanization, such as the expansion of impervious surface area within a watershed, can negatively affect the chemistry and ecology of stream ecosystems. Biodiversity can be reduced as the aquatic community structure changes in response to deviations from optimal water conditions. This study was designed to evaluate the relationships between algal species diversity and land cover, as well as potential correlations between land cover and water quality. The Quinnipiac River, an urbanized river in south-central Connecticut, USA, was selected as the study stream because of its historical exposure to nutrient pollution and its diversity of land cover types. Algae samples and water quality data were obtained between May and September of 2015. Morphological and DNA sequencing analyses were performed to evaluate macroalgal species diversity. Spatial data containing land cover and impervious surface cover were attained and mapped using ArcGIS 10.1. The area of developed land cover and impervious surface cover were measured within various sized buffers, established by previous studies, (30m, 91m, and 152m) that radiated from both the sampling locations as well as the stream centerline. Regression models were then used to compare the amount of each type of cover to the amount of nitrate, phosphate, and species richness at each sampling location. Additionally, surface prediction models were created for nitrate, phosphate, and biodiversity index values. We found that although the river is heavily impacted, there are healthy algal communities. The results revealed minor correlations between most variables. Future studies should attempt to use microalgal diversity, in addition to macroalgal diversity, to gain a more complete view of the algal community structure.

11. (FA) EFFECTS OF NUTRIENT LIMITATION ON THE PHOTOSYNTHETIC EFFICIENCY OF MICROCYSTIS AERUGINOSA.

Dominique Derminio[1] and Gregory Boyer [1]
[1]Chemistry, State University of New York, College of Environmental Science and Forestry, Syracuse NY U.S.A.

Microcystis aeruginosa, a bloom-forming cyanobacterium, is responsible for many harmful algal blooms that occur in the embayments of the Great Lakes. Recent work has suggested that nitrogen, in addition to phosphorus, may be important in controlling the growth of Microcystis in the western basin of Lake Erie. Traditional field experiments to determine how nutrient limitation affects Microcystis are often convoluted due to its slow growth rate and presence of other species. Nutrient-induced fluorescence transients (NIFTs) may provide a faster means to assess the nutrient status of cyanobacteria in natural settings in the presence of other species. NIFTs record the changes in the photosynthetic efficiency of species with the addition of variable nutrients. *Chlorella vulgaris* and *M. aeruginosa* LE3 were grown in N- and/or P-limited and replete (Z8 media) cultures that were spiked at different time with 0.06mM phosphate and 1.4mM nitrate. Their fluorescence response was measured using a PhytoPAM active fluorometer and Phyto-Win Software V 1.45 for 10 minutes pre- and post-addition of nutrients. Initial results suggest that changes in the fluorescent efficiency of cultures were dependent on both the species and availability of nutrients. The suitability of using NIFT’s in capturing these changes will be investigated.

12. (C) RECENT DATA UNDERSCORES THE NEED FOR MOLECULAR SEQUENCING THAT TARGETS GENERITYPES AND TYPE LOCALITIES OF THE LIAGORACEAE AND OTHER NEMALIALEAN RED ALGAE.

Thea R. Popolizio[1] & Craig W. Schneider.[2] [1] Biology, Salem State University, Salem, MA U.S.A.; [2]Biology, Trinity College, Hartford, CT U.S.A.

The Liagoraceae is widely distributed in tropical and temperate seas, exhibiting the greatest diversity in warm waters. Until recently, no molecular studies targeted the western Atlantic, but our liagoroid data from Bermuda resolved far greater generic diversity in this part of the western Atlantic than previously reported. Specimens collected from St. Croix suggest diversity may be underestimated here as well. We have discovered at least one Caribbean liagoroid taxon that is distinct from all other genera in *rbc*L analysis, and distantly allied to *Dotyophycus* in COI analysis. Due to a lack of comparative sequence data, we are unable to place it definitively in the genus despite reproductive characteristics that conform to the species presently known. The generitype, *D. pacificus* was reported in Brazil, but morphological characteristics between these specimens and our Caribbean ones show differences. Sequence data of generitypes from their type localities have been critical for our work on western Atlantic Liagoraceae, and highlight the need for greater genetic sampling. With sequence data from a Caribbean specimen of *Liagora ceranoides*, we were able to demonstrate that Bermuda specimens were unique and undescribed. Using data from Australian and Hawaiian collections, we separated a novel species of *Yamadaella* in Bermuda from the Indo-Pacific generitype. Our movement of *Liagora pectinata* to *Hommersandiophycus*, a new genus for the western Atlantic, was made possible by published sequence data from the generitype. The presence of *Trichogloeopsis pedicellata* in Bermuda, not previously reported there, was confirmed as sequences from *T. pedicellata* collected in the Bahamas type locality were accessible. Conversely, our analyses show that *Ganonema farinosum* from around the world is not genetically uniform, suggesting that it may represent a species complex. But since sequences from the type locality are not yet available for comparison, it is not possible to place them in a proper taxonomic context. In addition to our Caribbean *Dotyophycus*, we have uncovered unique sequences ascribed to *Dichotomaria* and *Tricleocarpa* (Nemaliales) in this region. Clearly, future studies of liagoroids would benefit from a greater molecular sequencing effort, especially for localities like the Caribbean where little comparative data is available.

13. (PA) TESTING THE LIGHT: NUTRIENT HYPOTHESIS IN STREAM PERIPHYTON: DO CANOPY COVER AND NUTRIENT AVAILABILITY ALTER ELEMENTAL STOICHIOMETRY?

Ariana B. Dionisio[1], Catharina R. Grubaugh[2], Kam Truhn[2], John D. Wehr[2]. 1: Huxley College of the Environment, Western Washington University, Bellingham, WA 98225 USA; 2: Louis Calder Center – Biological Field station, Fordham University, Armonk, NY U.S.A.

Nutrients in periphyton (benthic algae) serve as the primary and basal nutrient source in aquatic food webs. Increased light exposure may lead to lower nutritional quality in periphyton, as carbon fixation can outpace nutrient acquisition. According to the light:nutrient hypothesis

(LNH), as the ratio of light to available nutrients increase, the nutrient content of primary producers decrease. The purpose of this study was to test the LNH with periphyton in naturally occurring streams. The nitrogen and phosphorus contents of periphyton were measured from 30 streams in New York State (USA) that varied in nutrient and light availabilities. Periphyton nitrogen content (µmol N/g AFDM) did not follow the predictions of the LNH. The ratio of light to available total inorganic nitrogen was not correlated with periphyton to nitrogen content ($r_s = -0.142$, $p > 0.50$). This is likely due to the mixture of periphyton consisting of not only primary producers but decomposers and detritus as well. It is speculated the decomposers in periphyton excrete nitrogen-rich humic acids, thus manipulating the ratios suggested by the LNH. Periphyton phosphorous content (µmol P/g AFDM) followed predictions of the LNH. The ratio of light to available total dissolved phosphorus was positively correlated with periphyton phosphorus content ($r_s = -0.499$, $p < 0.02$). However, light availability was likely the main driver of this correlation, as periphyton phosphorus content was correlated with light availability ($r_s = -0.492$, $0.20 < p < 0.05$) but not with total dissolved phosphorus availability ($r_s = 0.239$, $0.20 < p < 0.05$). These results suggest that carbon fixation plays a greater role than available nutrients in periphyton nutrient concentrations.

14. (C) UTILIZATION OF URIC ACID IN DINOFLAGELLATE *PROROCENTRUM DONGHAIENSE.*

Xiaoli Jing[1,2] & Senjie Lin[2]. [1]Marine Science Department, University of Connecticut, Groton, CT U.S.A. [2]College of Marine Life Science, Ocean University of China, Qingdao, 266003, China

Uric acid has been reported to be utilized by several algae as an organic nitrogen source for growth. Some recent studies have shown that assimilation of nitrate, ammonium, etc resulted in rapid incorporation of nitrogen into uric acid crystals, forming temporary N storage sites within the symbiotic dinoflagellate *Symbiodinium*. Moreover, abundant uric acid stores can be mobilized rapidly, thereby allowing the algal symbionts to flourish in an otherwise N-poor environment. Whether uric acid exists in other dinoflagellate species, such as *Prorocentrum donghaiense,* and how different nitrogen sources affect the progression of accumulation remains unclear. In the current study, we hope to examine how different sources and availability of N affect the growth of *P. donghaiense*. Specifically, we will focus on whether *P. donghaiense* is capable of storing N in uric acid when DIN is abundant and utilizing uric acid when DIN is limited. We plan to investigate if different DIN conditions will affect DNA content and CHN content of the cells and their correlation. This data will provide a new and previously unconsidered aspect of N metabolism in *P. donghaiense*.

15. (PA) GENETIC ANALYSIS OF HERBARIUM SPECIMENS: WHY SHOULD WE *CHARA?*

Sarah E. Glass[1,2], Christine de Roux[1,2], Amy J. Havens[1], Kenneth G. Karol[1].; [1]The Lewis B. and Dorothy Cullman Program for Molecular Systematics, New York Botanical Garden, Bronx, NY U.S.A.; [2]Sarah Lawrence College, Bronxville NY U.S.A.

Chara are a group of freshwater green algae found throughout the world. Many species are thought to have cosmopolitan distributions, while other species are geographically restricted. Morphological variation within species can often confuse identification and it is sometimes necessary to use DNA analysis to assist in making determinations. We analyzed DNA sequence data from four chloroplast-encoded genes in order to assist in making species determinations on historical specimens from the New York Botanical Garden's William and Lynda Steere Herbarium, some more than one hundred years old. Using this method, we were able to positively identify 26 *Chara* specimens; this includes ten previously described species as well as one potentially new species. We also provide evidence that the range of *Chara leiopitys* extends beyond its previously known range in South America to the African continent. Our work illustrates the historical distribution of *Chara* species across a broad geographic range, refining the understanding of diversity and distributions in this ecologically and evolutionarily important group of green algae.

16. (FA) METABOLIC LABELING OF RNA OPENS UP NEW HORIZONS IN THE STUDY OF GENE EXPRESSION IN DIATOMS.

Minoli Perera, Rebecca Littlefield, Deborah L. Robertson Clark University, Biology Department, 950 Main Street Worcester, MA U.S.A.

Cellular RNA levels represent the integration of RNA synthesis, processing, and degradation. *In vivo* metabolic labeling can be used to measure both global and gene-specific RNA transcription and degradation rates. The technique uses sulfur-substituted molecules that are rapidly taken up by cells and incorporated into RNA. The *Thalassiosira pseudonana* genome encodes both uracil phosphoribosyltransferase (UPRT) and uridine kinase (UK), which allow for the incorporation of 4-thiouracil (4tU) and 4-thiouridine (4sU), respectively. Both 4tU and 4sU were detected in *T. pseudonana* RNA after a 5 min incubation. To further examine changes in transcription in response to nitrogen availability, *T. pseudonana* cells grown in the presence and absence of nitrate were exposed to a 5 min pulse of 4tU (0.2 mM) and total RNA was extracted from cells. Newly synthesized (labeled) mRNA was separated from pre-existing pools using thiol-specific biotinylation and fractionation. Fractionated mRNA can be used for first strand synthesis and qRT-PCR to provide estimates of *de novo* transcription rates for genes involved in nitrogen assimilation. The method is currently being scaled up to determine whether it will yield sufficient quantities of fractionated mRNA for high throughput RNA sequencing. If successful, the method can be used to examine global changes in transcription and degradation rates in response to nutrient availability.

17. (C) DO INTRODUCED HERBIVORES PREFER INTRODUCED SEAWEEDS? TESTING THE PREFERENCE OF *LITTORINA LITTOREA*. Marguerite Kinsella, Lindsay Green & Carol Thornber. University of Rhode Island, Dept. of Biological Sciences, 120 Flagg Road, Kingston, RI U.S.A.

Changes in climatic conditions have many environmental and ecological ramifications including increasing the success of introduced specie. When non-natives species become established in new habitats they become competitors with native species and may have impacts on native populations. Non-native species may also impact other non-native species. We were interested in whether an introduced herbivore, the common periwinkle, *Littorina littorea*, preferred native seaweeds (*Chondrus crispus* and *Ulva* sp.) over the non-native *Grateloupia turuturu*. *Grateloupia* has spread throughout Narragansett Bay since its arrival in 1994 and serves as a threat to the native *C. crispus*. To test the food preference of *L. littorea* we conducted a series of food preference experiments in laboratory mesocosms. In the first trial, we offered *L. littorea* both *G. turuturu* and *C. crispus* (n=8) and measured consumption over time. In the second trial, we offered *L. littorea* three macroalgae, *G. turuturu, C. crispus,* and *Ulva* sp. (n=10). The results of the first trial showed that on average, both *Chondrus crispus* and *Grateloupia turuturu* gained mass over time (i.e. growth outpaced consumption). *C. crispus* was consumed in four mesocosms and *G. turuturu* in three mesocosms. In the second trial, the only macroalgae that *L. littorina* consumed on average was *G. turuturu* (0.03 mg per day), while growth of both *Ulva* sp. and *C. crispus* outpaced consumption. In this trial, consumption of *G. turuturu* occurred in five mesocosms, consumption of *C. crispus* in six mesocosms, and consumption of *Ulva* sp. in only two mesocosms. However, there was no statistical difference between the consumption of the three species due to a high level of variability. Our results suggest that the introduced periwinkle, *L. littorea* shows no preference for non-native or native macroalgae.

18. (PA) GENETIC BARCODING RESOLVES THE HISTORICALLY KNOWN RED ALGA *CHAMPIA PARVULA* FROM SOUTHERN NEW ENGLAND, USA, AS *C. FARLOWII* SP. NOV. (CHAMPIACEAE, RHODYMENIALES). Maura K. Griffith[1], Craig W. Schneider[1], Gary W. Saunders[2], Daniel I. Wolf[3] & Christopher E. Lane[3]. [1]Department of Biology, Trinity College, Hartford, CT U.S.A.; [2]Centre for Environmental and Molecular Algal Research, Department of Biology, University of New Brunswick, Fredericton, NB E3B 5A3, Canada; [3]Department of Biological Sciences, University of Rhode Island, Kingston, RI U.S.A.

Using mitochondrial COI-5P and choloroplast *rbc*L genetic markers, the red algal species historically known in southern New England, USA, as *Champia parvula* is found to be genetically distinct from the species to which it has historically been aligned, necessitating the description of a new species, *C. farlowii,* for plants from Rhode Island, Massachusetts, Connecticut and New York. The new species is morphologically compared with true European *C. parvula* and congeners, especially those with similar features previously aligned under the same species name. *Champia farlowii* is a morphologically cryptic species, the seventh in the expanded *C. parvula* complex, with overlapping characteristic measurements despite differences at the extremes when compared to *C. parvula*.

19. (C) MOLECULAR CHARACTERIZATION OF RHODE ISLAND *RHODOMELACEAE*.

Matthew Koch[1] & Brian Wysor. [1] Department of Biology, Marine Biology, and Environmental Science, Roger Williams University, Bristol, RI U.S.A.

Despite being one of the most well studied estuaries in the world, little attention has been given to establishing a modern, molecular-based macroalgal inventory for Narragansett Bay (Rhode Island, USA). To better understand marine macroalgal diversity, we sequenced the *rbc*L gene for over 100 specimens of the red algal family *Rhodomelaceae*, which is known for its high bioinvasion potential and difficulty in species identification. Molecular-assisted identification reveals at least 13 distinct species in the genera *Chondria*, *Neosiphonia*, *Polysiphonia*, and *Vertebrata*. While this species richness estimate approximates the historical, morphology-based species richness record of 17 species, it is not yet clear whether all molecular-identified species correspond strictly to those reported historically. Given the combined pressures of global climate change, biological invasions and coastal development, we anticipate that changes in species distributions will be reflected in an updated species inventory for RI waters, which will continue to serve as a baseline for future monitoring efforts.

20. (PA) COPPER CONTENT ANALYSIS OF ULVOID BLOOMS IN NEW HAVEN HARBOR.

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Anthropogenic input of heavy metals has become an increasing concern within many near shore coastal systems, including New Haven Harbor. Among these pollutants, copper is a prominent heavy metal being released into New Haven Harbor and can be found in the surface water as well as in the sediment. Between the months of May to September, ulvoids are present throughout New Haven Harbor creating large, thick biomass. Other studies have shown that ulvoids are effective at uptaking heavy metals, including lead and cadmium, as well as PCB's from the sediment whether attached or in close proximity to the substrate. The purpose of the research presented here is to examine the copper content, distribution, and relative biomass of ulvoid blooms in New Haven Harbor. Copper was measured in algal tissues and sediment samples using Energy Dispersive X-Ray Fluorescence (EDXRF); this instrument allows for direct sample measurements, eliminating the need for extractions or other extensive sample preparations. The results of this study show an uneven bloom distribution observed in the harbor with copper detected in the tissue of most ulvoid samples. Initial data revealed that samples in direct contact with the sediment contained higher quantities of copper in their tissue than ulvoids collected free-floating. In addition, ulvoid samples contained correspondingly more copper in areas where the sediment also had higher copper content, suggesting that algae may be uptaking copper from the sediment. With their ability to absorb copper from the surrounding environment, ulvoids have potential as a bioremediation tool in coastal ecosystems.

21. (C) DINOFLAGELLATE GENE EXPRESSION AND CORAL SYMBIOSIS UNFOLDED BY SYMBIODINIUM KAWAGUTII GENOME ANALYSIS. Senjie Lin. Marine Science Department, University of Connecticut, Groton, CT U.S.A.

Dinoflagellates are important components of marine ecosystems and essential coral symbionts, yet little is known about molecular underpinnings of many of their unique biological features and of symbiosis. By high-throughput sequencing we (an international team) analyzed the 1180-Mb genome and RNA of *Symbiodinium kawagutii*. No whole genome duplication was observed, but instead we found active (retro)transposition and gene family expansion, especially in processes important for successful symbiosis with corals. Comparative genomic analysis revealed a gain of 7663 gene families and a loss of 338 in *Symbiodinium* compared with common ancestor with apicomplexa, potentially related to symbiosis. We also identified genes potentially governing host recognition and symbiosis establishment and maintenance. Although dinoflagellates are well known to conduct sexual reproduction and form cysts, genes potentially governing these processes were identified for the first time. In agreement with previous documents, no TATA box or TATA box-binding protein were found, but TTTT and other previously unrecognized promoter elements were identified. More importantly, consistent with the scarcity of transcriptional regulation in dinoflagellates, we identified a microRNA system potentially regulating genes expression in both *Symbiodinium* and a host coral. All these provide a resource for studying protist genome evolution and the evolution of coral symbiosis.

22. (PA) THE “HOTEL CALIFORNIA” MODEL OF CHEMOTAXIS IN THE COLONIAL GREEN ALGA *ASTREPHOMENE GUBERNACULIFERA*. Stephanie Newman[1], Grant F. Kusick[1], Benjamin Yao & Harold Hoops[1]. [1]Biology and Physics, State University of New York College at Geneseo, Geneseo, NY U.S.A.

One challenge in the early evolution of multicellularity is the performance of collective behaviors. These collective behaviors are due to the robust ability to respond to changes in the environment. Multi-celled members of the Volvocine algae exhibit many of the same behaviors as their unicellular relatives, but the mechanisms involved must be distinct. *Astrephomene gubernaculifera* is the only multi-celled volvocine alga that has been shown to perform chemotaxis, which is navigation along a chemical gradient. We previously found evidence implying that *Astrephomene* somehow senses and adjusts its swimming based on changes over time in the local concentration of acetate, a food source. We sought to learn more about this mechanism of navigation. Qualitative observations recommended that *Astrephomene* colonies reverse direction when they swim from a region of high acetate concentration to a region of low acetate concentration. Using tools that we developed to analyze videomicroscopy data, we were able to quantitate this phenomenon. We report evidence from two different experimental systems that *Astrephomene* reorients in response to decreases in local acetate concentration. We term this the “Hotel California” model of chemotaxis, as algae become “trapped” wherever the acetate concentration is high.

23. (C) THE SILICA SECCHI DISK WEBSITE: TOOLS FOR RESEARCH INCLUDING EXTENSIVE SEARCHABLE DATABSES, WEB-BASED NON-HEIRARCHICAL USER-FRIENDLY KEYS, MOVIES, AND MORE.

Anne-Marie Lizarralde & Peter Siver. Botany Department, Connecticut College, New London, CT U.S.A.

The Silica Secchi Disk website (silicasecchidisk.conncoll.edu) was developed at Connecticut College, under the direction of Dr. Peter Siver. Created using FileMaker Pro, a versatile relational database software package, it includes several searchable image databases of scaled chrysophytes and diatoms from cores with associated location attributes, physical and chemical data for all collecting sites, and interactive maps. There are specimen image libraries and information on newly described species which aid in the identification. Currently, the database of over 4500 records includes information and images of chrysophyte scales, bristles, cysts, diatoms, testate amoebae, sponges, heliozoans, and several unknowns. Users can view all records or conduct customized searches in order to extract specific information. In addition, the site is the access point for an interactive, web-based, computerized identification key for freshwater algal genera using Lucid software. Users may answer questions in any order to quickly and efficiently narrow down a list of taxa to only those that match chosen characteristics. All characters and terms are clearly explained for ease of use by those unfamiliar with the algae. This non-hierarchical, user-friendly key is linked to web pages containing a wealth of resources, including images, movies, and information about the ecology, morphology, and reproduction of each organism. The movies incorporate titles, diagrams, and structural terminology to further familiarize students with the morphology and taxonomy of the algae and has been in use by multiple levels of scientist ranging from elementary school teachers to research scientists around the world. The Silica Secchi Disk also serves as the home site for the *"Giraffe Pipe Eocene Project"* and the Biotic Survey and Inventory Project on *"Scaled Chrysophytes and Diatoms in Seepage Lakes Along the Coast of the United States"* both sponsored by the National Science Foundation.

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

Shaunna Phipps, Mary A Bisson, Department of Biological Sciences, University at Buffalo, NY U.S.A.

Many species within the genus *Chara* have a range of tolerances when exposed to or cultured in varying salinities. We examine four potential genes (SOS1, ACA4, AHA9, PpENA) related to sodium export that have been previously established in embryophtes to determine their potential role in the export of Na^+ in salt tolerant *C. longifolia* and salt sensitive *C. australis.* Since Chara being more closely related to embryophytes than other green algae, we infer that similar genes will likely be the mechanism behind sodium export in *Chara.* Both *C. longifolia* and *C. australis* were exposed to a range of saline treatments: freshwater, saltwater, 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 have been analyzed through next generation Illumina sequencing to create transcriptome libraries for each of the examined species. These data will be used to determine the gene expression and sequence for the specified genes. Primers will be generated from these sequences for quantitative-PCR to determine 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, in higher salinities, and during adaptation to higher salt.

25. (C) DETERMINING CONDITIONS FOR BEST SEA VEGETABLE CROP PRODUCTION ON SEA FARMS IN COASTAL MAINE.

Sarah Redmond[1], Kyle Capistrant-Fossa[2], Robert Cushman[1], Charlotte T. C. Quigley[2] & Susan H. Brawley[2]. [1]Maine Sea Grant, Franklin, ME; [2]School of Marine Sciences, University of Maine, Orono, ME U.S.A.

An important part of developing a sea vegetable industry on the Maine coast is to understand where, when, and at what depth to grow different species. We examined grow-out of laver (*Porphyra umbilicalis*), dulse (*Palmaria palmata*), and winged kelp (*Alaria esculenta*) on two different experimental farms on the Maine coast from October 2015 to March 2016 with monthly sampling. Laver and dulse were seeded onto 3 m long dropper lines of kuralon twine at the University of Maine's Sea Vegetable Research Nursery at the Center for Cooperative Aquaculture Research. Three lines/species were placed on Farm 1 (open coastal site) and three lines/species were placed on Farm 2 (partially sheltered cove). Light levels were measured monthly, and subsamples at 0, 0.5, 1.0, 1.5, 2.0, 2.5, and 3.0 m depth were taken to measure individual lengths, widths, and surface areas with ImageJ (nih.gov). Laver length and width were correlated (R^2= 0.727, n=254 plants, Farm 1; R^2= 0.751, n= 260 plants, Farm 2) across depths and sampling dates. Laver growth was better in this trial at Farm 1 than at Farm 2, and was best between 0 m-1.0 m at Farm 1. A trend toward better growth of dulse at shallower depths was observed at Farm 2, whereas dulse grew well across depths at Farm 1. The effect of outplanting dates for *Alaria* is being investigated, with lines outplanted at two different times in the fall, early October and early November. Growth, size, condition, and yield will be obtained from both farms through May 2016. These results demonstrate varying site parameters to produce good crops on each site. (Supported by Maine Sea Grant (NOAA), Maine Coast Sea Vegetables, Ltd., and Maine Fresh Sea Farms, Ltd.).

26. (PA) INCREASED SALINITY AND NUTRIENT EFFECTS ON PHYTOPLANKTON IN A SUBURBAN LAKE.

Emily P. Pinckney[1, 2], Steve DiLonardo[2], and John D. Wehr[2] [1]Humboldt State University, Arcata, CA 95521 [2]Louis Calder Biological Field Station, Fordham University, Armonk, NY U.S.A.

Cyanobacteria blooms, often occurring in water bodies with elevated nitrogen and phosphorus, low turbulence, and warm temperatures are an increasingly significant environmental and public health issue. Past studies have suggested that other factors such as increased salinity, may enhance blooms. We studied the effects of increased nutrient and NaCl on algal production and nutrient uptake in North Lake, a suburban lake in Westchester County, NY. The phytoplankton

assemblage during the experiment was composed diatoms and green algae (15% cyanobacteria). The experiment was conducted in-situ in 1-L plastic containers using a 2 x 2 x 2 factorial design (N x P x NaCl; n = 3). The aim was to double ambient nitrogen, phosphorus and NaCl levels. Algal production was significantly enhanced by phosphorus, but not nitrogen, and was inhibited by NaCl. Rates of N and P nutrient uptake were unaffected by NaCl treatment, but final P content / Chl-a in P-amended microcosms was greater in + NaCl treatments. A follow-up experiment when will test these effects cyanobacteria are dominant. Implications of this study may influence nutrient and salinity management in lakes.

27. (C) COMPETITIVE INTERACTIONS OF TWO ANTARCTIC MIXOTROPHS WITH EITHER PHOTOTROPHIC OR PHAGOTROPHIC SPECIALISTS.

Zaid McKie-Krisberg[1] and Robert Sanders[2]. [1]Biology Department, Brooklyn College, Brooklyn. NY 11210; [2]Biology Department, Temple University, Philadelphia, PA U.S.A.

Competitive interactions provide a major biological filter through which natural selection can act on microbial populations. Microbial eukaryotes are involved in a complex network of interactions important for energy transfer, nutrient retention, and recycling. Utilization of a trophic strategy combining photosynthesis and phagotrophy (mixotrophy) has been shown in some theoretical and empirical studies to impart a competitive advantage over purely phototrophic and purely phagotrophic organisms. Here we present results of competitive assays of two species of Antarctic mixotrophic flagellates paired with either an obligate phototroph or an obligate phagotroph. In the first experiments, the cryptophyte *Geminigera cryophila* was grown with two solely Antarctic diatoms of contrasting sizes (*Fragilaria* sp. and *Fragilariopsis* sp.). In the second experiment, the prasinophyte *Pyramimonas tychotreta* is grown with the solely heterotrophic chrysophyte *Paraphysomonas antarctica*. Under the experimental conditions, the mixotrophic *G. cryophila* was a dominant competitor in the presence of either diatom, regardless of the size of the autotrophic competitor. However, the mixotrophic *P. tychotreta* was competitively inferior to the bacterivorous *P. antarctica*. In this case, the heterotrophic flagellate reduced prey density, probably to an effective abundance below the critical density for survival of the mixotrophic flagellates. These experiments show that in some cases, mixotrophs are able to access alternative resources to their advantage, while in other cases, the combination of acquisition strategies result in a loss of competitive ability when paired with a trophic specialist.

28. (C) PHYLOGENETIC ANALYSES OF THREE GENES OF PEDINOMONAS NOCTILUCAE, THE GREEN ENDOSYMBIONT OF THE MARINE DINOFLAGELLATE NOCTILUCA SCINTILLANS, REVEAL ITS AFFILIATION TO THE ORDER MARSUPIOMONADALES (CHLOROPHYTA, PEDINOPHYCEAE) UNDER THE REINSTATED NAME PROTOEUGLENA NOCTILUCAE.

Lu Wang[1, 3], Xin Lin[1], Joaquim I. Goes[2], and Senjie Lin[1, 3]. [1] Marine Biodiversity and Global Change Research Center and State Key Laboratory of Marine Environmental Science, Xiamen University, Xiamen 361005, China; [2] Lamont Doherty Earth Observatory at Columbia University, Palisades, NY U.S.A.; [3] Department of Marine Sciences, University of Connecticut, Groton, CT U.S.A.

In the last decade, field studies in the northern Arabian Sea showed a drastic shift from diatom-dominated phytoplankton blooms to thick and widespread blooms of the green dinoflagellate, *Noctiluca scintillans*. Unlike the exclusively heterotrophic red form, which occurs widely in tropical to temperate coastal waters, the green *Noctiluca* contains a large number of endosymbiotic algal cells that can perform photosynthesis. These symbiotic microalgae were first described under the genus *Protoeuglena* Subrahmanyan and further transferred to *Pedinomonas* as *P. noctilucae* Sweeney. In this study, we used the 18S rDNA, *rbc*L and chloroplast 16S rDNA as gene markers, in combination with the previously reported morphological features, to re-examine the phylogenetic position of this endosymbiotic algal species. Phylogenetic trees inferred from these genes consistently indicated that *P. noctilucae* is distantly related to the type species of *Pedinomonas.* The sequences formed a monophyletic clade sister to the clade of *Marsupiomonas* necessitating the placement of the algal symbionts as an independent genus within the family Marsupiomonadaceae. Based on the phylogenetic affiliation and ecological characteristics of this alga as well as the priority rule of nomenclature, we reinstate the genus *Protoeuglena* and reclassify the endosymbiont as *Protoeuglena noctilucae*.

29. (FA) A *PORPHYRA* NURSERY.

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Porphyra umbilicalis (Rhodophyta) is an important sea vegetable that is harvested for food across the North Atlantic. Neutral spores from a laver strain isolated (summer 2015) on the Maine coast were seeded onto glass beads and grown up in the laboratory to small blades that were transferred onto kuralon lines in the University of Maine's CCAR Research and Seeding Nursery at Franklin, ME, which is the first organic sea vegetable nursery in the State of Maine. A key factor in laver development as a commercial crop is control over the development and release of neutral spores in the nursery and establishment of adequate nursery stock to seed nets. We have cultured ~140 g (wet wt) to produce high spore release from this strain in the nursery; these spores were used to seed 26 m long nets on our seeding wheel (Sullivan Plastics, Sullivan, ME). This strain produces more spores per blade than an earlier trial strain (P.um.1) suggesting that, despite the apparent absence of sexual reproduction in these algae, there are substantially different traits between *Porphyra* individuals on the Maine coast. This is our second

demonstration of nursery seeding of clean, strain-defined laver. Freezing of ripe adult blades and trimmed tissues are techniques that can potentially extend the “shelf-life” of spore-producing plants, and eliminate the need for continuous culture of blades with nutrients and growth space in the net-seeding season. Trials with different freezing regimes are in progress, and the nursery seeded nets are in grow-out trials in a sea farm near CCAR. (*These authors made equal contributions. Supported by Maine Sea Grant and The Maine Technology Institute.)

30. (C) ALGAL INVENTORY OF TWO NATIONAL WILDLIFE REFUGES ON KAUA‘I, HAWAI’I, WITH AN EMPHASIS ON THE DIVERSITY OF *SPIROGYRA* (ZYGNEMATOPHYCEAE, CHAROPHYTA).

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An algal inventory of two National Wildlife Refuges (Hanalei and Hulē‘ia) on the island of Kaua‘i, Hawai‘i, was conducted in December 2014 and June 2015 with the aims of: 1) producing a checklist of algae for future biomonitoring activities, and 2) identifying potential toxin-producing algae that may be playing a role in recent outbreaks of avian botulism at the Refuges through lowered fecundity or survival of waterbirds. The two Refuges were originally established to provide protection for Hawai‘i’s endangered waterbirds (koloa maoli, Hawaiian duck, *Anas wyvilliana*; ae‘o, Hawaiian stilt, *Himantopus mexicanus knudseni*; ‘alae ‘ula, Hawaiian moorhen, *Gallinula chloropus sandvicensis*; ‘alae ke‘oke‘o, Hawaiian coot, *Fulica alai*). Algal identifications were made using microscopy and molecular phylogenetic analysis. A total of 100 taxa were identified from over 1,800 specimens, with representation from the cyanobacteria, green and red algae, diatoms, synurophytes, xanthophytes, euglenoids, and glaucophytes. Associations among sites based on algal community composition and physico-chemical measurements revealed no clear trends, although mapping of previous cases of avian botulism and identifications of potential toxin-producing algae (all cyanobacteria) demonstrated that in most cases, both occurred in the north units of the Hanalei Refuge. The green algal genus *Spirogyra* was one of the most common and abundant algae encountered during the survey, and a combination of morphological and molecular analyses of these specimens indicated that seven of the 12 clades of *Spirogyra* known from the Hawaiian Islands are present in these two National Wildlife Refuges. Details of the taxonomy and phylogenetic relationships among these clades will be presented.

31. (PA) THE CASE FOR TRUE MORPHOLOGICAL CRYPSIS: PACIFIC *DASYA ANASTOMOSANS* AND ATLANTIC *D. CRYPTICA* SP. NOV. (DASYACEAE, RHODOPHYTA).

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With the advent of routine genetic barcoding for taxonomic distinction a decade ago, descriptions of morphologically cryptic species have exploded in the macroalgal literature. Produced either by convergence of morphological characteristics for geographically distant species, or divergence of species from a common ancestor, cryptic species often can be distinguished by subtle anatomical or reproductive features. Some species pairs, however, remain indistinguishable with overlapping characteristics even upon close inspection. Such a case is demonstrated for two species differentiated by sequences of a portion of the *rbc*L chloroplast gene, *Dasya anastomosans* from the Indo-Pacific, and *D. cryptica* sp. nov. from the western Atlantic. After assembling morphological and anatomical data for the two species, no significant differences were detected between them, thus affording the usage of the epithet for the new species from a distant ocean basin than its congener.

32. (C) URBANIZATION ALTERS FATTY ACID CONCENTRATIONS OF STREAM FOOD WEBS WITHIN THE NARRAGANSETT BAY WATERSHED.

Sarah B. Whorley[1,4], Nathan J. Smucker[2], Anne Kuhn[3], & John D. Wehr[1] [1]Louis Calder Center, Fordham University, Armonk, NY 10504 [2]Environmental Protection Agency, Water Supply and Water Resources Division, Cincinnati, OH 45220 [3]Environmental Protection Agency, Atlantic Ecology Division, Narragansett, RI 02882 [4]Natural Sciences Department, Daemen College, Amherst, NY U.S.A.

Urbanization and associated human activities negatively affect stream algal and invertebrate assemblages, likely altering food webs. Our goal was to determine if urbanization affects food web essential fatty acids (EFAs) and if EFAs could be useful ecological indicators in monitoring efforts. Streams along a gradient of urbanization in the Narragansett Bay Watershed (USA) were sampled for water chemistry, benthic algae, and invertebrates. Metabolically important EFA compounds >18 carbons (C) were measured. Total algal EFA content increased from 0.63 mg/m^2 in rural streams to 1.09 mg/m2 in urbanized streams. Groups of biologically important omega-3 compounds increased 0.22 mg/m2, and omega-6 compounds decreased 0.10 mg/m^2 from rural to urban streams. However, these differences were not significantly different (ANOVA: Total EFA, P = 0.46; omega-3, P = 0.24; omega-6, P = 0.40). For invertebrate functional feeding groups, average total EFA content increased for collectors (0.83 mg/g) and omnivores (0.49 mg/g), was stable for predators (0.32 mg/g) with increasing urbanization, but decreased for shredders (1.07 mg/g). These results indicate that urbanization likely affects nutritional qualities of different trophic positions in stream food webs.

33. (PA) A METHOD TO QUANTIFY MOTILITY PATTERNS IN A COLONIAL GREEN ALGA.

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Astrephomene gubernaculifera is a colonial green alga that has the robust ability to perform chemotaxis, a directional movement that leads to the overall algal accumulation around acetate, a food source. However the mechanism for this is obscure. We developed a system to create and analyze videos of colonial motion. In order to test models of chemo-response, we needed to obtain values for speed, turning frequency and turn magnitude. Using the Tracker software program, we obtained the x,y coordinate positions as a function of time and velocity data, but quantifying turning is more difficult. To do this, we extract the polar angle, theta, and acceleration (theta A). Because theta A represents the angle of acceleration, a change in sign indicates a reversal in the direction of angular velocity and thus a “turn”. This value is obtained by taking a moving average of the theta velocity (provided by Tracker) as a function of time. Using the Cartesian coordinates, the distance travelled between any two time points can be determined using the Pythagorean Theorem. Based on these values, some of the possible calculated metrics include colony turn frequency, average distance traveled per frame, as well as total distance traveled, and final displacement.

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Professional Preparation

University of New Hampshire, Botany, BS l969
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State University of New York at Stony Brook, Ecology & Evolution, Ph. D. 1979
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Appointments

Professor, University of Maryland Center for Environmental Science 1995-present
Associate Professor, Center for Environmental & Estuarine Science, Univ. of Maryland System, 1991-1995
Associate Scientist, Woods Hole Oceanographic Institution, 1984-1991
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Research Interests

Ecology and physiology of marine dinoflagellates, ciliates and other protists; Use of alternate modes of nutrition (mixotrophy) among the plankton; Microzooplankton grazing and growth; Trophic interactions between the microbial and metazoan food webs.

Awards and Special Recognition

Fellow, Amercian Association for the Advancement of Science, 1996-present
University of Maryland, Regents Award for Scholarship, 2005

Recent Publications (2012-present)

Gao, Y, Cornwell JC, Stoecker DK, Owens, M. 2012. Effects of cyanobacterial driven pH increases on sediment nutrient fluxes and coupled nitrification-denitrification in a shallow fresh water estuary. Biogeosciences: 9:2697-2710.

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