

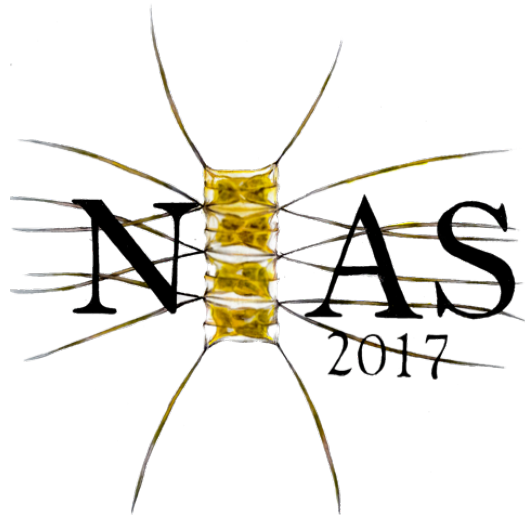
The Northeast Algal Society 56th Annual Symposium



**Mt. Washington Hotel,
Bretton Woods, New Hampshire**

21-23 April 2017





56th Northeast Algal Symposium

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56th Northeast Algal Symposium
Dedication

H. William “Bill” Johansen
(1932-2016)



Bretton Woods, New Hampshire
22 April 2017

We are very pleased to dedicate the 56th NEAS symposium to our friend and colleague Hans William ‘Bill’ Johansen, who passed away at age 84 in Holden, Massachusetts this past November. A long-time member, contributor and promoter of our society, Bill will be missed for his love for everything NEAS. Bill’s, warm, welcoming and friendly demeanor to veteran and newly arrived phycologists, and his enthusiastic support of students will be missed by all who gather annually at our meetings. Bill earned a B.A. at San Jose State University in 1955 and then taught science at San Mateo High School for four years. After earning a Master’s degree from San Francisco State University in 1961, he joined George F. Papenfuss’ lab at University of California, Berkeley, where he initiated his lifelong study of algae. Bill’s dissertation on Pacific western North American coralline red algae (1966) paved the way for a future research career, beginning with his post-doc at Rhodes University in Grahamstown, South Africa where he studied Indian Ocean corallines. In 1968, Bill accepted a position at Clark University in Worcester, Massachusetts, where he remained until retiring in 1999 as Professor of Biology Emeritus. Over his career, Bill published 34 papers, nearly all on corallines, 11 book chapters and his important 1981 book entitled “*Coralline Algae, a First Synthesis*”.

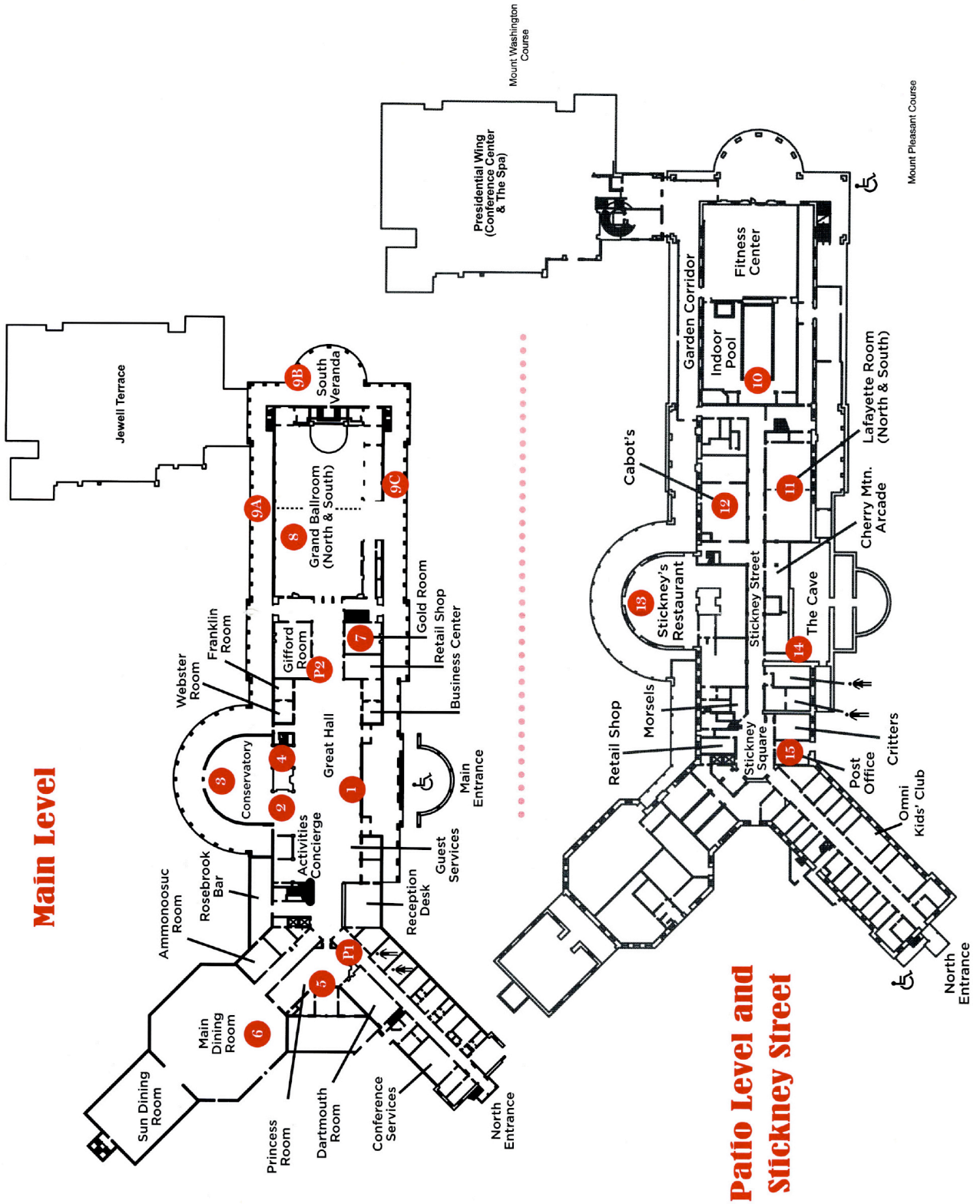
Bill was an integral member of the Northeast Algal Society (NEAS). He watched it grow from its inception as a formal organization with meeting abstract books prepared on ditto machines to what we know today. He first served NEAS by co-convening the 17th annual symposium in 1978 at Woods Hole, Massachusetts, with Steve Golubic, later returning to that role for the 48th Symposium at University of Massachusetts in 2009. From 1982–1987, Bill was the inaugural Secretary/Treasurer (the position later was divided in 1996 due to an excessive workload) of the NEAS Executive Committee, when he initiated the tax-free status for the new Development Committee (1984) that supports our student members. He was elected to two terms as NEAS President from 1987–1992. In 1998, Bill was honored with the Frank S. Collins Award for his long and valuable service to NEAS and then as Honorary Chairperson for the 45th Symposium at Marist College in Poughkeepsie, New York in 2006. Throughout his longtime association with NEAS, Bill became an un-official Society archivist. In 2011, along with Peter Bradley, Bill produced the *History of the Northeast Algal Society* (NEAS Contribution No. 4, online at <<http://www.e-neas.org/>>) for the 50th anniversary meeting at Woods Hole. Along with his other service to NEAS, this publication will remain a lasting legacy of Bill’s service to us all (the picture of Bill that precedes this dedication was taken at a symposium holding an annotated draft of his “*History*”).

After retirement Bill and his wife Fran traveled between Massachusetts and Vermont, where he became interested in the history of the small town of Bethel where Fran’s father had spent his youth and where her Italian grandparents had lived. After spending several years collecting data on the influx of Italian immigrants to Bethel in the early 20th century, Bill wrote a book on Bethel’s “Italian Era” from 1900–1940. This book was published just before he started weakening from cancer in September 2016. Bill will be greatly missed.



Louise Lewis, President
Christopher Neefus and Craig Schneider, Co-conveners
23 April 2017

Omni Mt. Washington Hotel Floor Plan, Bretton Woods, NH



General Program: 56th Northeast Algal Symposium, Mt. Washington Hotel

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Friday, April 21, 2017

- 5:00 – 8:00 pm** **Evening Registration/Poster Setup**
Presidential Ballroom Lobby, Mt. Washington Hotel
Poster setup, Adams Room
- 6:30 – 9:00** **NEAS Friday Night Social**
Presidential Ballroom

Saturday, April 22, 2017

- 7:00 – 8:30 am** **Breakfast**
Main Dining Room buffet
Poster setup, Grand Ballroom
Session I speakers load ppts on Presidential Ballroom computer
- 8:00 – 9:30** **Morning Registration**
Presidential Ballroom Lobby
- 8:30** **Meeting Group Photo**
Jewell Terrace
- SESSION I** **Student Presentations, Moderator – Lesleigh Kraft**
Presidential Ballroom
- 8:50 – 9:00** **Welcome and Opening Remarks – Chris Neefus**
- 9:00 – 9:15** *Wilce Award Candidate*
Cong Wang & Senjie Lin – Differential growth responses of marine phytoplankton to the herbicide glyphosphate (**Abstract 15, p. 16**)
- 9:15 – 9:30** *President’s Award Candidate*
Nathan T. Lanning, Jean-Paul Simjouw & Amy L. Carlile – Development of a method for copper quantification in ulvoid tissue (**Abstract 8, p. 13**)
- 9:30 – 9:45** *Wilce Award Candidate*
Trevor T. Bringloe & Gary W. Saunders – Molecular data reveal the postglacial origins of the Northwest Atlantic marine algal flora; assessing the European origins paradigm (**Abstract 2, p. 10**)
- 9:45 – 10:00** *Wilce Award Candidate*
Dominique S. Derminio & Gregory L. Boyer – Impacts of hydrogen peroxide on the growth of cyanobacteria and chlorophytes (**Abstract 3, p. 11**)
- 10:00 – 10:30** **Coffee Break**
Presidential Ballroom Foyer
Session II speakers load presentations on computer

- SESSION II** *Student Presentations, Moderator – Amanda Savoie*
 Presidential Ballroom
- 10:30– 10:45** *Wilce Award Candidate*
Danielle C. Perry, Carol Thornber & S. Moseman-Valtierra – Impacts of *Fucus* and bloom-forming *Ulva* on salt marsh vegetation and greenhouse gases (**Abstract 11, p. 14**)
- 10:45 – 11:00** *Wilce Award Candidate*
Kirby Morrill & Gary W. Saunders – Molecular-assisted alpha taxonomy reveals less diversity among tubular *Ulva spp.* in the Bay of Fundy (N.B., Canada) than previously reported (**Abstract 9, p. 13**)
- 11:00 – 11:15** *Wilce Award Candidate*
Chris Paight, Mary Beth Saffo & Christopher E. Lane – It takes a village: multispecies community dependence in the genus *Nephromyces* (**Abstract 10, p. 14**)
- 11:15 – 11:30** *Wilce Award Candidate*
Stephen D. Gottschalk & Kenneth G. Karol – Freeze out. Dry up. Testing the physiological limits of vegetative propagules in *Nitellopsis obtusa* (**Abstract 5, p. 11**)
- 11:30 – 11:45** *Wilce Award Candidate*
Jillian Freese & Christopher E. Lane – Microscopy of red algal parasites: features of infection (**Abstract 4, p. 11**)
- 11:45 – 12:00** *Wilce Award Candidate*
Eric D. Salomaki & Christopher E. Lane – Redefining red algal parasites (**Abstract 13, p. 15**)
- 12:00 – 1:30** *Lunch*
 Presidential Ballroom Foyer
Executive Committee Meeting
 Washington Board Room
Session III speakers load ppts on computer
- SESSION III** *Student & Contributed Presentations, Moderator – John Wehr*
 Adams Room
- 1:30 – 1:45** *Wilce Award Candidate*
Simona Augyte, Chris Neefus & Charles Yarish – Speciation in the extremely exposed intertidal: the case of *Saccharina angustissima* (Collins) Augyte, Yarish *et* Neefus *comb. nov. et stat. nov.* (**Abstract 1, p. 10**)
- 1:45 – 2:05** **Craig W. Schneider**, Thea R. Popolizio & Gary W. Saunders – Preliminary results of the benthic marine algae collected from the mesophotic zone on the 2016 Bermuda Nekton cruise of the R/V *Baseline Explorer* (**Abstract 14, p. 16**)

- 2:05 – 3:00** *Invited plenary lecture, Introduction – Craig Schneider*
Gary W. Saunders – To key or not to key? Tales of disjunct distributions, heteromorphy and taxonomic turmoil (**Abstract 12, p. 15**)
- 3:00** *Coffee Break*

SESSION IV *Poster Session*

- 3:15 – 4:30** **Student & Contributed Posters**
 Grand Ballroom
- 4:30 – 7:00** **Open period**
 Trail hiking, heated swimming, snow algal foray, colleague collaboration in hotel bar, spa &c.
- 7:00 – 10:00** **Social hour & Banquet, Awards, Silent & Live Auctions**
 Sun Dining Room

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Sunday, April 23, 2017

- 7:00 – 8:30 am** **Breakfast**
 Main Dining Room buffet
Session V speakers load ppts on computer

SESSION V *Contributed Papers, Moderator – Deb Robertson*
 Presidential Ballroom

- 8:55 – 9:00** *Morning Announcements – Chris Neefus*
- 9:15 – 9:30** **Ronald Hoham** – Snow algae and other snow microbes in Mt. Washington, New Hampshire (**Abstract 7, p. 12**)
- 9:30 – 9:45** **John D. Hall**, Jillian C. Adair & Richard M. McCourt – Taxonomy of *Cylindrocystis* with the description of two new species and a re-evaluation of the fossil records for Zygnematophyceae (**Abstract 6, p. 12**)
- 9:45 – 10:00** **John D. Wehr**, Sarah Steirer, Nicholas Ballor, Xian Wang & Kenneth G. Karol – A tale of two phaeophytes: new insights in freshwater brown algal evolution and ecology (**Abstract 16, p. 17**)
- 10:00 – 10:20** *Coffee Break*
- 10:20 – 11:00** *NEAS Annual Business Meeting – Louise Lewis*
 Presidential Ballroom
Boxed-lunches available in Presidential Ballroom Foyer only after the business meeting
- 11:00 am** *Room checkout*

Poster Presentations

Undergraduate Posters (President's Award)

- P1** – **Ravi N. Balasubramanian** – *Volvox barberi* likely uses weak forces to aggregate into optimally packed two-dimensional flocks (**Abstract p. 17**)
- P3** – **Isabel H. Bilek**, **Sarah E. Glass**, Joseph A. Sardina & Kenneth G. Karol – Testing historical morphology-based determinations of *Chara* using DNA sequence data from herbarium specimens (**Abstract p. 18**)
- P6** – **Timothy Earley** & Amy Carlile. DNA methylation as a possible control for morphological form in *Ulva compressa* (**Abstract p. 20**)
- P9** – **Seanna Gray**, Lindsay Green & Carol Thornber – The effects of caffeine on locally occurring Rhode Island seaweeds (**Abstract p. 21**)
- P12** – **Marguerite Kinsella**, Lindsay Green & Carol Thornber – The effects of future temperature projections on the growth and survival of non-native and native seaweeds (**Abstract, p. 23**)
- P14** – **Nate Morris**, Peter Siver & Anne Lizarralde – Potential impacts of climate on Candlewood Lake based on long-term monitoring records (**Abstract p. 23**)
- P20** – **Joseph A. Sardina** & Kenneth G. Karol – Intra- and inter-population comparison of *Chara brittonii* Allen ex Rob. organellar genomes (**Abstract p. 26**)

Graduate Student Posters (Trainor Award)

- P4** – **Yuanyu Cao**, Lindsay Green, Renée Eriksen & Anita S. Klein – A pilot study of genetic structure of *Porphyra umbilicalis* Kützinger in the Gulf of Maine using SNP markers from RNA-Seq (**Abstract p. 19**)
- P8** – **Stephen D. Gottschalk**, Richard M. McCourt, John D. Wehr & Kenneth G. Karol – Limited morphology conceals genetic differences in a group of *Chara* subsection *Willdenowia* (**Abstract p. 21**)
- P19** – **Jaclyn Robidoux** & Chris Neefus – Diversifying New England sea vegetable aquaculture: modifying kelp nursery and grow out technologies for nori production (**Abstract p. 26**)
- P21** – **Amanda Savoie** & Gary W. Saunders – Species diversity and evolutionary relationships of the taxonomically challenging red algal tribe Polysiphonieae (Rhodomelaceae) in Canada (**Abstract p. 27**)
- P22** – **Kristen Slodysko** & Gregory Boyer – Microcystin in fish tissue: a potential risk to consumers? (**Abstract p. 28**)
- P24** – **Lingjie Zhou**, Lingke Wang, Senjie Lin & Peimin He – Transcriptomic analysis of four green tide algae in the Yellow Sea, China (**Abstract p. 28**)

Contributed Posters

- P2 – Chris Benton**, Anita Klein, Matt MacManes & Kelley Thomas – The challenges of characterizing the transcriptome of the non-model organism, *Codium fragile* (**Abstract p. 18**)
- P5 – Amy L. Carlile**, Joseph Eigenberg, Kyla Kelly & Jean-Paul Simjouw – Copper uptake by macroalgae and the potential for bioremediation in the Quinnipiac River (**Abstract p. 19**)
- P7 – Karolina Fučíková**, Kenneth G. Karol, Paul O. Lewis & Louise A. Lewis – Chlorophyceae: will the last green algal stronghold of Linnaean ranks fall? (**Abstract p. 20**)
- P10 – Lindsay A. Green**, Marta Gomez-Chiarri, Hilary Ranson, David Rowley & Carol S. Thornber – The effects of allelochemicals from bloom-forming seaweeds (*Ulva compressa* and *Ulva rigida*) on shellfish larvae (**Abstract p. 21**)
- P11 – Nanjing Ji**, Lingxiao Lin, Ling Li, Hao Luo, Yaqun Zhang & Senjie Lin – Metatranscriptome analysis of the harmful alga *Heterosigma akashiwo* (Raphidophyceae) (**Abstract p. 22**)
- P13 – Lesleigh Kraft** & Gary W. Saunders – Recognition of two new Australian genera in the order Halymeniales (Floridiophyceae, Rhodophyta) reduces polyphyly in the genera *Cryptonemia* and *Halymenia* (**Abstract, p. 23**)
- P15 – Bahareh Nowruzi**, Taher Nehadsattari & Jouni Jokela – Identification of four different chlorophyll *a* allomers of *Nostoc* sp. by liquid chromatography mass spectrophotometry (LC MS) (**Abstract p. 24**)
- P16 – Bahareh Nowruzi**, Taher Nehadsattari & Jouni Jokela – Characterization of a new peptide-aldehyde compound from the terrestrial cyanobacterium *Nostoc* sp. Bahar M by LC MS and Marfey's analysis (**Abstract p. 24**)
- P17 – Chelsea M. Parise** – The challenges of databasing an historical herbarium collection (**Abstract p. 25**)
- P18 – Daniela Lopes Paim Pinto**, Tatiana Rynearson, Kristina Terpis & Christopher E. Lane – Diversity and distribution of microbial eukaryotes in Antarctic waters (**Abstract p. 25**)
- P23 – Christopher Neefus & Hannah Traggis** – The current status of digitization efforts within the Macroalgal Herbarium Consortium (**Abstract p. 28**)

ABSTRACTS

Oral Presentation Abstracts (in alphabetical order by presenting author)

1 – SPECIATION IN THE EXTREMELY EXPOSED INTERTIDAL: THE CASE OF SACCHARINA ANGUSTISSIMA (COLLINS) AUGYTE, YARISH ET NEEFUS COMB. NOV. ET STAT. NOV. **Simona Augyte**¹, Chris Neefus² and Charles Yarish¹. ¹University of Connecticut, Dept. of Ecology & Evolutionary Biology, 1 University Place, Stamford, CT 06901, USA; ²University of New Hampshire, Department of Biological Science, Durham, NH 03824, USA.

On the basis of new molecular evidence coupled with ecological and hybridization studies, we have elevated *Saccharina angustissima* (Collins) Augyte, Yarish & Neefus *comb. nov. et stat. nov.* from its former designation of *Saccharina latissima* forma *angustissima* (Collins) Mathieson. The basionym is *Laminaria agardhii* forma *angustissima* Collins, *Phycotheca Boreali-Americana* D: LXXXIII (1905). The designated lectotype (NY no. 02243824) was collected by Frank Collins, July 18th, 1903. This kelp forms dense beds found on flat, horizontal platforms and islands within the low intertidal to shallow subtidal zones (+0.5 to -0.5 m) of very exposed coast. Its distribution spans only eight nautical miles in Harpswell, Casco Bay, Maine, USA. Blades are up to 4.5 m long, strictly narrow at 1-5 cm wide, arising from hapterous bases, usually coalesced with multiple terete stipes of 9 cm in length, up to 36 cm long. Thalli are annuals with peak sorus production in October thru late November. Overall, there is as much or more genetic divergence between *S. latissima* and *S. angustissima* as there are between other taxonomically accepted species of *Saccharina* spp. In addition, our research has shown that *S. angustissima* and *S. latissima* are persistently morphologically distinct in a common garden experiment. *Saccharina angustissima* grown in culture maintains its parental narrow blade form even when grown in calm conditions, indicating that the trait is heritable.

2 – MOLECULAR DATA REVEAL THE POSTGLACIAL ORIGINS OF THE NORTHWEST ATLANTIC MARINE ALGAL FLORA: ASSESSING THE EUROPEAN ORIGINS PARADIGM. **Trevor T. Bringle** and Gary W. Saunders. Centre for Environmental & Molecular Algal Research, Biology, University of New Brunswick, Fredericton, NB E3B 5A3, Canada.

Following the last glacial maximum, the marine algal flora in the Northwest Atlantic was believed to have been recolonized from Northeast European refugia. Recent genetic evidence, however, has suggested that some species survived glaciation in the Northwest Atlantic. We investigated several species of red and brown macroalgae to determine whether or not molecular data were consistent with the recolonization from Europe hypothesis. We generated and gathered genetic data from the 5' end of the cytochrome *c* oxidase subunit I gene (COI-5P) in 1549 specimens representing 20 amphi-Atlantic species, and examined biogeographic distributions in mitotypes. Of the 20 species, only three showed mitotype variation consistent with recent recolonization of Northwest Atlantic populations from European counterparts. In contrast to the established paradigm, 40% showed clear signs of divergence between East and West populations, while the other 45% possessed amphi-Atlantic and private mitotypes in the Northwest Atlantic. Our results clearly reject the established hypothesis that the majority of the Northwest Atlantic marine flora was derived from European populations sometime within the past 10 ka. Rather, our results point to refugia, likely off the coasts of Newfoundland and Nova

Scotia, and/or trans-Arctic migration from the Pacific as the source populations for the Northwest Atlantic flora. By shedding light on the phylogeographic history of the Northwest Atlantic we can better understand the nature of postglacial recolonization and possibly forecast future changes to the Canadian Arctic.

3 – IMPACTS OF HYDROGEN PEROXIDE ON THE GROWTH OF CYANOBACTERIA AND CHLOROPHYTES. **Dominique S. Derminio** and Gregory L. Boyer. State University of New York College of Environmental Science and Forestry, 1 Forestry Dr., Syracuse, NY 13210, USA.

Algal blooms are increasing on a worldwide scale. This includes cyanobacteria blooms that produce toxins that impact recreation, human, and ecosystem health. Hydrogen peroxide (H_2O_2) has been proposed as a control method to limit the growth of these cyanobacteria blooms. Here, the sensitivity of different species of cyanobacteria and chlorophytes to H_2O_2 was examined. Cyanobacteria in the genera *Anabaena*, *Microcystis* and *Planktothrix*, and chlorophytes in the genera *Chlorella*, *Chlamydomonas* and *Scenedesmus*, were grown in Z8 media using a 12:12 light:dark cycle at 22°C with the addition of various concentrations of H_2O_2 . *In vivo* fluorescence, catalase activity and toxin production were measured at the beginning and end of each experiment. Different species, even within the same genus, reacted differently to the addition of H_2O_2 . This suggests that if H_2O_2 is to be used to control harmful cyanobacterial blooms, the genera and species present must be carefully considered.

4 – MICROSCOPY OF RED ALGAL PARASITES: FEATURES OF INFECTION. **Jillian Freese** and Christopher E. Lane. Department of Biological Sciences, University of Rhode Island, Kingston, RI 02881, USA.

Parasitic red algae evolve from a common ancestor with their hosts, infecting close relatives using cellular connections. These parasites have independently evolved over one hundred times within the red algal class Florideophyceae. Molecular and morphological studies led to the delineation of red algal parasites based on their relationship to their host. Adelphoparasites are phylogenetically close to their hosts, often infecting a sister species, whereas alloparasites are more distantly related to their hosts. Morphological examinations of mature and developing red algal parasites demonstrated variations in the infection process. From the limited number of parasite species that have been studied in depth, it is clear that each parasite does things a little differently with regard to cellular structure or organelle maintenance. Given the diversity of red algal parasites, it is necessary to examine a more comprehensive set of these organisms in order to fully understand how these parasites successfully use their host. Observing the details of the parasite infection mechanism and stages of parasite development will be essential in comparing parasites throughout their growth. The maintenance of multiple host-parasite pairs in culture and manipulation of spore release has enabled controlled re-infections for the development of the parasite to be monitored using microscopy. Utilization of traditional histological stains and fluorescence *in situ* hybridization has identified morphological features of adelphoparasite and alloparasite development. Combining these images with transcriptomes will facilitate comparisons between parasite species to determine similarities and differences in their infection process. The future integration of microscopy and molecular data will result in an improved understanding of host and parasite experiences throughout infection.

5 – FREEZE OUT. DRY UP. TESTING THE PHYSIOLOGICAL LIMITS OF VEGETATIVE PROPAGULES IN *NITELLOPSIS OBTUSA*. **Stephen D. Gottschalk**^{1,2} and Kenneth G. Karol².

¹Department of Biological Sciences, Fordham University, Bronx, NY 10458, USA; ²The Lewis B. and Dorothy Cullman Program for Molecular Systematics, The New York Botanical Garden, Bronx, NY 10458, USA.

Since the initial discovery of *Nitellopsis obtusa* (commonly called starry stonewort) in the St. Lawrence River in 1978, there has been a steady increase in the number of water bodies with this aquatic invasive. Invasions have been reported from Vermont to Minnesota and range from benign to aggressive. Lake and water management agencies are seeking methods to counter the spread of starry stonewort, and ideas include both chemical and environmental controls. Starry stonewort readily grows from star-shaped, starchy propagules called bulbils. As only male plants have been found so far in North America, it is thought that these bulbils are the primary propagule behind the invasions across the northeast and Great Lakes regions. Here we test the physiological limits of starry stonewort bulbils when exposed to freezing and desiccation treatments. Results from this baseline experiment will guide and inform management strategies for limiting the further spread of this aquatic invasive alga.

6 – TAXONOMY OF *CYLINDROCYSTIS* WITH THE DESCRIPTION OF TWO NEW SPECIES AND A RE-EVALUATION OF THE FOSSIL RECORDS FOR ZYGNEMATOPHYCEAE. **John D. Hall**¹, Jillian C. Adair² & Richard M. McCourt¹.

¹Department of Botany, Academy of Natural Sciences of Drexel University, Philadelphia, PA 19103, USA; ²Biodiversity, Earth and Environmental Science, Drexel University, Philadelphia, PA 19104, USA.

In an attempt to better understand the evolution and taxonomy of the species in the non-monophyletic genus *Cylindrocystis*, we undertook a laboratory study of all available strains of *Cylindrocystis* spp. We used microscopy, controlled growth experiments and molecular phylogenetic techniques to investigate their diversity and phylogenetic relationships. Taxonomy of *Cylindrocystis* relies in part on the characteristics of the zygospores they produce. Twenty-four strains of *Cylindrocystis* were investigated by light microscopy and subjected to culture methods to induce conjugation. Very few strains responded to our attempts. Nonetheless, two of the strains that did respond were found to be species new to science. Additionally, one of these strains produces spores that are indistinguishable from fossil spores historically assigned to a different, distantly related zygnematophyte. This indicates that the fossil record should be carefully reviewed because even structurally complex spores may represent phylogenetically distinct taxa. Our phylogenetic analysis confirmed that species assigned to the genus do not form a non-monophyletic lineage but we cannot determine which of the two major lineages of *Cylindrocystis* contains the type species – *C. brebissonii* – because both contain morphologically similar strains and none are from the type locality. Additional study is required to better understand the taxonomy of *Cylindrocystis*.

7 – SNOW ALGAE AND OTHER SNOW MICROBES ON MT. WASHINGTON, NEW HAMPSHIRE. **Ronald Hoham**, Department of Biology, Colgate University, Hamilton, NY 13346, USA.

Mt. Washington is the highest mountain in northeastern U.S.A. (1977 m; 6288') and is the location of Tuckerman's Ravine, an historic hiking and ski site. In this ski bowl several snow microbes have been identified including three Volvocalean green algae, *Chloromonas* (*Cr.*) *rosae* v. *psychrophila*, *Cr. brevispina*, and *Cr.* sp. that color snow green and orange. These three algae have been found in mountainous regions and ski areas of Maine, New Hampshire,

Vermont, Massachusetts, New York and Québec. The first two species have been studied extensively with respect to life cycles, pH, temperature, photoinhibition, conductivity, and molecular phylogenies. In the UTEX SNO Collection there are 24 axenic strains of *Cr. rosae* v. *psychrophila* from 5 location sites and 5 axenic strains of *Cr. brevispina* from 3 location sites. *Cr. rosae* v. *psychrophila* has been completely sequenced and its growth is stimulated by extracts from balsam fir. Over 20 IBP's have been identified in *Cr. brevispina* that reduce freeze damage. Other snow microbes found on Mt. Washington include fungi (*Chionaster nivalis* and *Selenotila nivalis*), a colorless euglenoid (*Notosolenus* sp.), bacteria, and primary consumers (ciliates and rotifers).

8 – DEVELOPMENT OF A METHOD FOR COPPER QUANTIFICATION IN ULVOID TISSUE. **Nathan T. Lanning**, Jean-Paul Simjouw and Amy L. Carlile. Department of Biology & Environmental Science, University of New Haven, West Haven, CT 06516, USA.

Legacy pollution is a concern within many coastal systems, specifically New Haven Harbor. One pollutant is copper, a critical micronutrient for many algae species and is considered the “Goldilocks Metal” where too much can be toxic, but too little can limit algal growth. Tissue analysis studies have been conducted for pollutants such as cadmium and PCBs; however, copper has been understudied. With copper being a potentially toxic heavy metal at increased concentrations, it is essential to measure its concentration within New Haven Harbor to make predications of its impact on biota. The aim of this study was to develop a method to quantify copper within the tissue of the algal genus *Ulva*. *Ulva* was chosen as the medium to examine copper because it is well documented to absorb copper and is found in abundance in the harbor. An Energy Dispersive X-Ray Fluorescence Instrument (EDXRF) was utilized to determine copper within ulvoid tissue because it eliminates the need for extractions or other extensive sampling preparations. Samples were cleaned with Nanopure filtered water before Cobalt (II) chloride was added to act as an internal standard. A standard addition calibration curve was constructed using Copper sulfate to allow for copper quantification within ulvoid samples. The results of this study provided quantitative concentrations of copper from samples throughout New Haven Harbor. Samples from sites in the inner harbor contained higher concentrations of copper than samples from the outer. This is the first study to quantify copper within ulvoid tissue using EDXRF.

9 – MOLECULAR-ASSISTED ALPHA TAXONOMY REVEALS LESS DIVERSITY AMONG TUBULAR *ULVA* SPP. IN THE BAY OF FUNDY (N.B., CANADA) THAN PREVIOUSLY REPORTED. **Kirby Morrill** and Gary W. Saunders. Centre for Environmental & Molecular Algal Research, Biology, University of New Brunswick, Fredericton, NB E3B 5A3, Canada.

Identifying members of the cosmopolitan genus *Ulva* (Ulvales, Chlorophyta) using morphological features alone is at best challenging and at times impossible due to the morphological plasticity and simple features exhibited by many members of the group. Even the most basic gross morphology (the growth of the thallus as a monostromatic tube, a distromatic blade, or a distromatic blade that splits into a monostromatic tube only at its margins) can vary between individuals within a species depending on varying environmental factors. DNA barcoding is a powerful tool for overcoming the frustrations of morphology-based identifications, but the taxonomy of *Ulva* is hardly a straightforward matter due to a history of taxonomic confusion and worldwide introductions from anthropogenic activity. In the current study we examine the species of *Ulva* that grow as *Enteromorpha*-like tubes in the Bay of

Fundy. The last published checklist of marine algae for this region (MacFarlane & Milligan 1965) reported eight species of *Enteromorpha* in our flora. Using the plastid barcode markers *rbcL* and *tufA* we can distinguish just seven unique genetic groups of *Enteromorpha*-like *Ulva* in the Bay of Fundy, and three of these commonly grow as blades as well. Using molecular-assisted alpha taxonomy, we present a contemporary re-evaluation of these *Ulva* spp. in our area.

10 – IT TAKES A VILLAGE: MULTISPECIES COMMUNITY DEPENDENCE IN THE GENUS *NEPHROMYCES*. **Chris Paight**, Mary Beth Saffo and Christopher E. Lane. Department of Biological Sciences, University of Rhode Island, Kingston, RI 02881, USA.

Nephromyces, a genus in the phylum Apicomplexa, has a mutualistic relationship with its host *Molgula* tunicates. The dynamics of this relationship are complicated by multiple *Nephromyces* species co-infecting a single host animal. Multi-species infections are common among other apicomplexans, however unlike other apicomplexans where co-infection is coincidental, co-infection appears to be mandatory for *Nephromyces*. No *Nephromyces* species has ever been found as an isolated infection and lab results demonstrate single-species infections fail to thrive. A combination of cloning, multi-gene amplicon sequencing, genomic sequencing, laboratory culturing, and single cell isolation have uncovered a highly complex, interdependent, endosymbiont community comprised of a single genus. This single genus community has evolved in relative isolation from competition and has developed into a mosaic of inter-dependent closely related species, which parallels the evolution of some extremophile microbial communities. The community structure, diversity, relationships, and genomic consequences of community dependence will be discussed.

11 – IMPACTS OF FUCUS AND BLOOM-FORMING ULVA ON SALT MARSH VEGETATION AND GREENHOUSE GASES. **Danielle C. Perry**¹, Carol Thornber¹ and S. Moseman-Valtierra². ¹Department of Natural Resources Science, University of Rhode Island, Kingston, RI 02881, USA; ²Department of Biological Sciences, University of Rhode Island, Kingston, RI 02881, USA.

Macroalgae is a natural component of salt marshes, but large accumulations on the marsh surface can have adverse effects on vegetation due to competition for light and space. Interactions among coastal algal species and the salt marsh plant, *Spartina alterniflora* will intensify as macroalgal abundance increases due to climate change effects. Through physiological processes, *S. alterniflora* and macroalgae can emit or absorb greenhouse gases at various rates. The purpose of this study was to determine how algal coverage of *Ulva* spp. and *Fucus* spp. affects the survival of *S. alterniflora* and associated greenhouse gas fluxes from vegetated mesocosms. Our experiment consisted of twenty-five 20 cm cores of *S. alterniflora* placed under five treatments (n=5 each). The treatments included: (1)-*S. alterniflora* cores covered with 210g/m² of *Ulva* spp., (2)-cores with 210g/m² of *Fucus* spp., (3)-cores with 105g/m² of *Ulva* spp. and 105g/m² of *Fucus* spp., (4)-cores with 210g/m² of *Ulva* spp. and 210g/m² of *Fucus* spp., and (5)-cores with no algal treatment as the control. The stem density, height, and photosynthetic efficiency were measured monthly and the methane (CH₄) and carbon dioxide (CO₂) gas fluxes of the cores were measured biweekly from June-September. The *Ulva* treatment showed a significant decrease in stem density compared to the other treatments. Algal treatments containing *Ulva* showed a trend of higher CH₄ and CO₂ emissions and a trend of lower photosynthetic efficiency by the end of the experiment. Future field studies will explore the effects of higher density algal accumulation on *S. alterniflora*.

12 – TO KEY OR NOT TO KEY? TALES OF DISJUNCT DISTRIBUTIONS, HETEROMORPHY AND TAXONOMIC TURMOIL. **Gary W. Saunders**, Centre for Environmental & Molecular Algal Research, Biology, University of New Brunswick, Fredericton, NB E3B 5A3, Canada.

At long last, an answer to that years old question, “when will Saunders provide the updated NEAS key?” Of course being science, one question only begets more questions. Fundamental questions such as what are the true origins of the NW algal flora? How many species do we actually have in common with the NE Atlantic, NE Pacific, or, for that matter, Australian floras, and how did they come to have disjunct distributions? What the heck is the conchocelis stage of *Fuscifolium papenfussii* doing in the Bay of Fundy, two oceans out of its previously reported range, and why have we not encountered its gametophyte? Geographically, spatially and temporally where and when do kelp gametophytes really live and how does this compare to the ranges of their respective sporophytes – does this even matter in preparing a key? What do we do with one-off genetically verified collections such as *Alaria crassifolia* and *A. marginata*? How many species are there in our flora and what are their true names and taxonomic assignments? For example, how could so many have had the identity of something as common as *Scytosiphon lomentaria* wrong for so long? Are there really species of *Kallymenia* in our waters? And finally, is nothing sacred in the eyes of us annoying algal taxonomists with our never-ending name changes? The answers to these, and other, questions will be explored and in some cases even provided.

13 – REDEFINING RED ALGAL PARASITES. **Eric D. Salomaki** and Christopher E. Lane. Department of Biological Sciences, University of Rhode Island, Kingston, RI 02881, USA.

The first parasitic red alga was described in 1845 with twenty-one additional species being described before the turn of the century. Today, more than 120 red algal parasites have been described from eight different orders within the Florideophyceae. Red algal parasites are predominately unpigmented and appear as erumpent pustules or irregular growths on their free-living red algal hosts. Despite their diminutive nature, parasitic red algae share morphological characteristics with other close relatives, allowing them to be assigned to tribes or families from their initial discovery. Historically parasites that have infected close relatives have been considered ‘adelphoparasites’, while those more distantly related to their hosts are called ‘alloparasites’. Molecular data has suggested that a gradient exists between adelphoparasites and alloparasites and therefore, these terms may no longer be suitable. Recent research has focused on the role of plastids in red algal parasite evolution. It is logical that selective pressure on genes involved in plastid functions will change as a parasite relies on its host for the products of photosynthesis. Accordingly, all ‘adelphoparasites’ that have been thoroughly investigated appear to have lost their native plastid and instead hijack a copy of the host plastid when packaging their spores. Furthermore, a highly reduced native plastid was recently sequenced from the ‘alloparasite’ *Choreocolax polysiphoniae*. Here we present transcriptomic and genomic data from nuclear-encoded plastid-targeted genes of three red algal parasites of varying evolutionary relationships to their hosts. We discuss the impacts of parasitism on genes and their expression involved in the carotenoid biosynthesis pathway, which produces pigments necessary for photosynthesis. Finally, we propose that developmental differences in may be a more appropriate characteristic for distinguishing and defining red algal parasites.

14 – PRELIMINARY RESULTS OF THE BENTHIC MARINE ALGAE COLLECTED FROM THE MESOPHOTIC ZONE ON THE 2016 BERMUDA NEKTON CRUISE OF THE R/V BASELINE EXPLORER. **Craig W. Schneider**¹, Thea R. Papolizio² and Gary W. Saunders³. ¹Department of Biology, Trinity College, Hartford, CT 06106, USA; ²Department of Biology, Salem State University, Salem, MA 01970, USA; ³Centre for Environmental & Molecular Algal Research, Department of Biology, University of New Brunswick, Fredericton, NB E3B 5A3, Canada.

Using technical divers and submersibles launched from the R/V *Baseline Explorer* in July-Aug. 2016, we were able to secure a number of benthic marine algae from waters of 56-178 m depths off Bermuda, including the two offshore seamounts, Argus and Challenger. The deepest living algae collected were large (to 10 cm diam.) rhodoliths from 178 m (585') depths, and the most abundant fleshy alga was *Sporochnus bolleanus* growing in dense meadows atop the Argus Bank. Although we are just beginning our genetic assessment of the collections, an initial screening with the mitochondrial COI-5P barcode marker has revealed six species in the Halymeniaceae (n=3) and Kallymeniaceae (n=3) that are largely aligned with Southern Hemisphere species, some in genera not previously known north of the equator. Other interesting finds highlighted include species of *Contarinia*, *Dasya*, *Gloiocladia*, *Halarachnion*, *Halopeltis*, *Microdictyon*, *Rhododictyon* and *Verdigellas* that are not found in the shallower habitats around Bermuda. A few of the newly collected species will be compared with specimens collected on the offshore seamounts by dredging and U.S. Navy lockout divers in 1960, now housed at the University of Michigan Herbarium.

15 – DIFFERENTIAL GROWTH RESPONSES OF MARINE PHYTOPLANKTON TO THE HERBICIDE GLYPHOSPHATE. **Cong Wang**^{1,2} and Senjie Lin^{1,2}. ¹State Key Laboratory of Marine Environmental Science and College of Ocean and Marine Biodiversity, Xiamen University, Xiamen, China; ²Department of Marine Sciences, University of Connecticut, Groton, CT 06340, USA.

Glyphosate is a globally popular herbicide to kill weeds and its wide applications may lead to accumulation in coastal oceans as a source of phosphorus (P) nutrient or growth inhibitor of phytoplankton. We studied the physiological effects of glyphosate on fourteen species representing five major coastal phytoplankton phyla (Haptophyta, Bacillariophyta, Dinoflagellata, Raphidophyta, and Chlorophyta). Based on growth responses to different concentrations of glyphosate under contrasting dissolved inorganic phosphorus (DIP) conditions, we found that phytoplankton species could be classified into five groups. Group I (*Emiliania huxleyi*, *Skeletonema costatum* and *Phaeodactylum tricorutum*) could utilize glyphosate as sole P-source to support growth in axenic culture, but in the presence of DIP, they were inhibited by both 36 μ M and 360 μ M glyphosate. Group II (*Karenia mikimotoi*, *Prorocentrum minimum*, *Dunaliella tertiolecta*, *Symbiodinium* sp., *Heterosigma akashiwo* and *Alexandrium catenella*) could not utilize glyphosate as sole P-source to support growth, and in the presence of DIP growth was not affected by 36 μ M but inhibited by 360 μ M glyphosate. Glyphosate consistently enhanced growth of Group III (*Isochrysis galbana*) and inhibited Group IV (*Thalassiosira weissflogii*, *Thalassiosira pseudonana* and *Chattonella marina*) regardless of DIP condition. Group V (*Amphidinium carterae*) exhibited no measurable response to glyphosate regardless of DIP condition. This grouping is not congruent with the phylogenetic relationships of the phytoplankton species suggesting functional differentiation driven by environmental pressure. We conclude that glyphosate could be used as P source by some species while is toxic to some other species and yet has no effects on others. The observed differential effects suggest that the

continued use of glyphosate and increasing concentration of this herbicide in the coastal waters will likely exert significant impact on coastal marine phytoplankton community structure.

16 – A TALE OF TWO PHAEOPHYTES: NEW INSIGHTS IN FRESHWATER BROWN ALGAL EVOLUTION AND ECOLOGY. **John D. Wehr**¹, Sarah Steirer¹, Nicholas Ballor¹, Xian Wang^{1,2} and Kenneth G. Karol². ¹Louis Calder Center, Biological Field Station, Fordham University, Armonk, NY, USA; ²The Lewis B. and Dorothy Cullman Program for Molecular Systematics, New York Botanical Garden, Bronx, NY, USA.

The Phaeophyceae is an overwhelmingly marine class of roughly 300 genera and at least 2000 species. For more than a century, reports on the few freshwater species have led to questions regarding their presumed rarity and evolution from marine to freshwater habitats. Of the 6 or 7 freshwater taxa, just two, *Heribaudiella fluviatilis* (Areschoug) Svedelius and *Pleurocladia lacustris* A. Braun, have been reported from scattered habitats. Each is known from freshwater streams and lakes on several continents, and each has been reported as “rare” or as a Red-List species in several publications. Newer data suggest that both have broad, possibly global distributions, although biogeographic patterns remain incomplete. Here we summarize some of our findings from field surveys, culture studies, and molecular analyses, which indicate their very different evolutionary histories and ecological requirements. While the two species even co-occur in a few locations, recent ecological and culture data indicate *Pleurocladia*, with a few documented populations from brackish-water habitats, but a narrow ecological freshwater niche, may be a more recent (centuries?) invader from the marine environment. Additionally, the species apparently has limited genetic variation among widely separated populations. In contrast, *Heribaudiella* has a fairly broad ecological range within freshwater habitats, no known brackish-water populations, and greater genetic variation among populations. These data thus far render a confusing evolutionary history for this freshwater alga.

Poster Abstracts (in alphabetical order by presenting author)

P1 – VOLVOX BARBERI LIKELY USES WEAK FORCES TO AGGREGATE INTO OPTIMALLY PACKED TWO-DIMENSIONAL FLOCKS. **Ravi N. Balasubramanian**, Harriton High School, Rosemont, PA 19010, USA. **(President’s Award candidate)**

Volvox barberi is a multicellular alga forming colonies of 10,000-50,000 cells. I established that typical colonies have diameters varying ten-fold from ~50 to ~500 μm , drawn from a log-normal distribution. I measured swimming speeds up to 600 $\mu\text{/sec}$, making this one of the fastest swimming *Volvox* species. I showed that *V. barberi* aggregates actively into “flocks” of two to more than 100 colonies that move and rotate collectively at high speeds. *Volvox* centers in flocks form a packed, irregular lattice. I hypothesized that the *Volvox* were dynamically finding the optimal packing for their size distribution. To test this, I built molecular dynamics simulations of spherical particles with a log-normal diameter distribution (matching the *Volvox*), and a weak long-range attractive force with strong local repulsion (to model mutual exclusion of colonies). Such “soft-spheres” are known to form random close-packed configurations that pack nearly optimally. I found that the lattice angle distribution in these close-packed configurations was identical to that of *Volvox* flocks. This suggests that *Volvox* achieves random optimal packing by exerting weak attractive forces on one another. My ongoing experiments test whether the forces

drawing *V. barberi* together arise from water currents produced by the rotation of colonies driven by the beating flagella of each colony's cells.

P2 – THE CHALLENGES OF CHARACTERIZING THE TRANSCRIPTOME OF THE NON-MODEL ORGANISM, *CODIUM FRAGILE*. **Chris Benton**¹, Anita Klein^{2,3}, Matt MacManes² and Kelley Thomas². ¹State of New Hampshire Public Health Laboratories, 29 Hazen Drive, Concord, NH 03301-9998, USA; ²Molecular Cellular and Biomedical Sciences, 46 College Road, University of New Hampshire, Durham, NH 03824-2618, USA; ³Department of Biological Sciences, University of New Hampshire, Durham, NH 03824, USA.

We investigated the phylogeography of the invasive alga *Codium fragile* in the Northwest Atlantic, observing haplotype variation among populations in Prince Edward Island (PEI), Canada. As chloroplast DNAs are too conserved for population study, and there were no available nuclear sequences for *Codium*, we constructed a partial transcriptome using RNA seq. This library yielded 163 million reads averaging 93 bp. Our assembly resulted in 125,000 contigs with 68,180 identified as coding sequences. Of these, 29,000 were complete exons. Identifying putative *Codium* sequences is of importance as the assembled transcriptome likely represents *Codium*'s microbiome. In order to identify which sequences likely belonged to *Codium*, multiple approaches were taken: coding sequences were queried against the BLAST non-redundant nucleotide database, while translated protein sequences were queried against the Pfam and Signal Peptide databases. The BLAST query resulted in 800 sequences (1.2%) matching other plants. The BLAST query also resulted in identifying sequences representing endophytic and epiphytic organisms common to algae in the marine environment. We found 36,000 sequences (53%) had matches to the Pfam database, and 8,000 sequences (12%) were determined to be either eukaryotic or prokaryotic based on signal peptide matches. The sorting of sequences by GC content was also attempted, though produced no useable result. The high number of sequences that remain unidentified by BLAST query is likely due to a lack of available nuclear sequence data for members of the Codiaceae. However, this could also be due to inadequate assembly. Due to this, and given the advancement of assembly programs, reassembly and subsequent annotation attempts with this data set are planned.

P3 – TESTING HISTORICAL MORPHOLOGY-BASED DETERMINATIONS OF *CHARA* USING DNA SEQUENCE DATA FROM HERBARIUM SPECIMENS. **Isabel H. Bilek**^{1,2}, **Sarah E. Glass**^{1,2}, Joseph A. Sardina¹ and Kenneth G. Karol¹. ¹Lewis B. and Dorothy Cullman Program for Molecular Systematics Studies, The New York Botanical Garden, Bronx, NY 10458, USA; ²Sarah Lawrence College, Bronxville, NY 10708, USA. **(President's Award candidates)**

Accurate and consistent species identification is vital for many areas of study ranging from biodiversity to conservation to evolutionary biology. Identification of specimens using morphological characters alone can be misleading, especially in groups containing cryptic species. One such group with the potential for cryptic species is the Characeae (Charophyceae, Charophyta), which is a group of fresh and brackish water green algae found on all continents except Antarctica. For example, morphology-based classification schemes of *Chara* subsection *Willdenowia* have recognized as many as 19 species, or as few as just one. Recently, at least 14 species have been recognized in this group using DNA-based phylogenetic methods. DNA was extracted from 397 herbarium specimens housed in the New York Botanical Garden's William and Lynda Steere Herbarium (NY), some collected more than 150 years ago. One hundred and ninety-three were previously determined based on morphology to be members of *Chara*

subsection *Willdenowia*, and the remaining were Characeae specimens that lacked species determinations. PCR was attempted for four chloroplast-encoded genes (*atpB*, *ndhD*, *psbC*, and *rbcL*) in order to either test morphology-based determinations of specimens, or to identify the indeterminate Characeae. The results and their implications on species concept and biodiversity within this ecologically important group will be discussed.

P4 – A PILOT STUDY OF GENETIC STRUCTURE OF *PORPHYRA UMBILICALIS* KÜTZING IN THE GULF OF MAINE USING SNP MARKERS FROM RNA-SEQ. **Yuanyu Cao**¹, Lindsay Green², Renée Eriksen³ and Anita S. Klein⁴. ¹Department of Molecular, Cellular, and Biomedical Sciences, University of New Hampshire, Durham, NH, 03824 USA; ²Dept. of Biological Sciences, University of Rhode Island, Kingston, RI 02881, USA; ³Agricultural Research Service, United States Department of Agriculture, USA; ⁴Department of Biological Sciences, University of New Hampshire, Durham NH 03824, USA. (**Trainor Award candidate**)

Porphyra umbilicalis KÜTZING is a marine red alga with a wide distribution from the Northeast Atlantic to Northwest Atlantic. In the Northeast Atlantic, *P. umbilicalis* is dioecious and reproduces both sexually and asexually, while in the Northwest Atlantic only the asexual reproduction has been observed. Northwest Atlantic populations of the alga were likely extirpated during the last glacial maximum, and then replaced by migration from Northeast Atlantic refugia. We would like to learn more about the population structure of *P. umbilicalis* but this has been difficult due to limited variable molecular markers for *P. umbilicalis*. In this study, transcriptomes were mined to identify putative single nucleotide polymorphisms (SNP). A computational pipeline was developed that accounts for the specific characteristics of transcriptome dataset, filtered against available red algae genome and *P. umbilicalis* EST library to eliminate microbial contamination. A total of 538 single nucleotide polymorphisms (SNPs) were found within a single population (Schoodic Point, ME). Five of these SNP markers were further applied in a pilot study of population diversity and structure of six *P. umbilicalis* populations in the Gulf of Maine. Results of this pilot study showed that the genetic diversity is highest in the two northern populations along the northwest Atlantic coast (Schoodic Point, ME and Lubec, ME). The genetic diversity is lowest in the two estuary populations (Wiscasset, ME and Dover Point, NH) and Reid State Park population. The genetic differentiation is the highest among Reid State Park compared to other populations. Possible bias resulting from means of SNP discovery will be discussed.

P5 – COPPER UPTAKE BY MACROALGAE AND THE POTENTIAL FOR BIOREMEDIATION IN THE QUINNIPIAC RIVER. **Amy L. Carlile**, Joseph Eigenberg, Kyla Kelly and Jean-Paul Simjouw. Department of Biology & Environmental Science, University of New Haven, West Haven, CT 06516, USA.

The Quinnipiac River in south-central Connecticut flows through predominantly urban areas and historically has been exposed to nutrient and heavy metal pollution, including copper. Our previous work has examined the biodiversity and copper contamination of benthic algal communities along the salinity and land use gradients present in the river. Copper was detected in algal tissue throughout the river, particularly in those samples from Hanover Pond, a site known to have elevated copper levels in the sediment. With copper contamination persisting in the Quinnipiac River, methods for heavy metal removal would promote the health of the system while being beneficial for various recreational uses of the river. Here, we present data from mesocosm copper uptake experiments where we tested the bioremediation potential of algal species found in polluted sites. Our results showed that *Hydrodictyon reticulatum* was effective

at copper uptake at a range of copper concentrations, while *Spirogyra* spp. showed some copper uptake but did not survive mesocosm trials beyond several days, even in the 0 ppm copper control. These preliminary results indicate that bioremediation using *Hydrodictyon reticulatum* found at Hanover Pond might be possible.

P6 – DNA METHYLATION AS A POSSIBLE CONTROL FOR MORPHOLOGICAL FORM IN *ULVA COMPRESSA*. Timothy Earley and Amy Carlile. Department of Biology & Environmental Science, University of New Haven, West Haven, CT 06516, USA. (President's Award candidate)

Epigenetics describes changes made to an organism's phenotype that result from a change in gene expression and not in genotype. Such changes likely play a key role in phenotypic plasticity, the ability of a single genotype to express a range of phenotypes. DNA methylation, one of the most understood controls of gene expression, is thought to be a major mechanism behind this plasticity. *Ulva* is a genus of green macroalgae found worldwide that is known to form blooms with large environmental and economic impacts. *Ulva compressa*, a species common in Long Island Sound, is one of these bloom-forming species. Research indicates that *U. compressa* occurs in the two morphological forms found in this genus: a flattened blade and a tube form. This project aims to test the hypothesis that the morphological form of *U. compressa* is epigenetically controlled and can be assessed through examination of DNA methylation patterns. It is predicted that the two morphological forms will have distinct methylation patterns. This is being tested using methylation sensitive amplification polymorphism (MSAP), a molecular technique that allows one to detect genome-wide methylation without a need to know which genes are being targeted. The assay involves a restriction digest of genomic DNA using a pair of isoschizomers that will selectively cut the DNA based on the presence or absence of methyl groups, followed by pre-selective and selective PCRs to amplify the fragments and allow for visualization of differences in methylation patterns. As the restriction digest requires a high amount of DNA, extraction protocols had to be modified with lower elution volumes and higher tissue samples to compensate. The pre-selective PCR also needed to be adjusted to account for lower quantities of DNA. In spite of these challenges, MSAP is still a strong tool for examining methylation because it does not require any prior genomic data. Future studies might consider trying to induce a form switch in *U. compressa* by exposing it to various environmental stressors, such as different salinities, in order to determine the underlying cause of this switch.

P7 – CHLOROPHYCEAE: WILL THE LAST GREEN ALGAL STRONGHOLD OF LINNAEAN RANKS FALL? Karolina Fučíková¹, Kenneth G. Karol², Paul O. Lewis³ and Louise A. Lewis³.¹Natural Sciences, Assumption College, Worcester, MA 01609, USA; ²Cullman Program for Molecular Systematics, The New York Botanical Garden, Bronx, NY 10458, USA; ³Ecology and Evolutionary Biology, University of Connecticut, Storrs, CT 06963, USA.

Chlorophyceae is one of the three most species-rich classes in core Chlorophyta and the only class whose monophyly remains uncontested as gene and taxon sampling improves. However, the relationships within the class are becoming less clear-cut as more data become available. The present study combined genome-scale chloroplast data and rich taxon sampling in an attempt to resolve the higher classification in Chlorophyceae. The traditional division into Volvocales, Sphaeropleales, and the OCC clade was of particular interest, as well as the placement of several *incertae sedis* taxa. Concatenated analyses yielded at least two well-supported phylogenies: nucleotide data supported the traditional classification with the inclusion of the enigmatic clade

Treubarinia into Sphaeropleales *sensu lato*. However, amino acid data yielded equally strong support for a topology that rendered Sphaeropleaceae sister to Volvocales, the rest of the taxa traditionally classified in Sphaeropleales in a separate clade, and Treubarinia as sister to all of the above. Single-gene analyses did not provide insights into this conflict, and both phylogenetic hypotheses should be therefore considered viable. Given this uncertainty as well as the higher-taxonomic mayhem seen in other algal groups, it is possible that adhering to well-defined Linnaean orders will soon be a thing of the past in Chlorophyceae as well.

P8 – LIMITED MORPHOLOGY CONCEALS GENETIC DIFFERENCES IN A GROUP OF CHARA SUBSECTION WILLDENOWIA. **Stephen D. Gottschalk**^{1, 2}, Richard M. McCourt³, John D. Wehr² and Kenneth G. Karol². ¹Department of Biological Sciences, Fordham University, Bronx, NY 10458, USA; ²The Lewis B. and Dorothy Cullman Program for Molecular Systematics, The New York Botanical Garden, Bronx, NY 10458, USA; ³Academy of Natural Sciences of Drexel University, Philadelphia, PA 19104, USA. **(Trainor Award candidate)**

As in other groups of green algae, morphologically based revisions in the 20th century have obfuscated the underlying genetic diversity of the macrophytic green algal group *Chara* subsection *Willdenowia*. The morphological characters considered in previous taxonomic treatments excluded related algae from this group, and lumped the others into one species: *Chara zeylanica*. Furthermore, important morphological characters, such as gametangial positioning, were dismissed as representing “minor genetic variation,” and subsequent tests have shown that some of these ignored characters are indicative of biological and genetic isolation. DNA sequencing and phylogenetic analyses demonstrate that members with similar gametangial positioning (in this case sejoined members) are themselves genetically isolated and distinct from one another. With a focused consideration of ecological, morphological and genetic data, we reexamine the species boundaries of *Chara foliolosa*.

P9 – THE EFFECTS OF CAFFEINE ON LOCALLY OCCURRING RHODE ISLAND SEAWEEDS. **Seanna Gray**, Lindsay Green and Carol Thornber. Department of Natural Resources Science, University of Rhode Island, Kingston, RI 02881, USA. **(President’s Award candidate)**

Pharmaceuticals are entering aquatic ecosystems through many pathways, such as accidental spillage, improper disposal, leakage, and wastewater. Wastewater management does not completely filter all pharmaceutical contaminants from sewage. Some drugs, such as caffeine, are actively removed, but a large percentage still makes it through to the aquatic environment. In fact, caffeine is one of the most commonly found pharmaceuticals in water and is usually found in relatively high concentrations. In this study we determined the effects of different concentrations of caffeine on the growth of two species of locally occurring macroalgae. We cultured *Chondrus crispus* and *Codium fragile* subsp. *fragile* in 0, 125 and 250 mg/L caffeine for a period of two weeks and assessed growth weekly. Caffeine significantly affected the growth rate of both *Codium fragile* subsp. *fragile* and *Chondrus crispus*. *Codium fragile* subsp. *fragile* tips exposed to ≥ 125 mg/L of caffeine began to lose mass after 1 week. There was no significant difference in the growth rates of *Chondrus crispus* tips cultured in 0 and 100 mg/L of caffeine, but tips cultured in 200 mg/L lost mass. Overall our results suggest that seaweeds are negatively impacted by caffeine in the aquatic environment in a species-specific manner.

P10 – THE EFFECTS OF ALLELOCHEMICALS FROM BLOOM-FORMING SEAWEEDS (ULVA COMPRESSA AND ULVA RIGIDA) ON SHELLFISH LARVAE. **Lindsay A. Green**¹,

Marta Gomez-Chiari², Hilary Ranson³, David Rowley³ and Carol S. Thornber¹. ¹Department of Natural Resources Science, University of Rhode Island, Kingston, RI 02881, USA; ²Department of Fisheries, Animal, and Veterinary Sciences, University of Rhode Island, Kingston, RI 02881, USA; ³Department of Biomedical and Pharmaceutical Sciences, University of Rhode Island, Kingston, RI 02881, USA.

Seaweed blooms have been increasing in frequency and severity worldwide due to anthropogenic activities. Narragansett Bay has experienced seaweed blooms dominated by blade-forming *Ulva* for over a century. Previous research has shown that *Ulva* can produce allelochemicals that negatively affect other seaweeds. The objective of this study was to determine whether allelochemicals from the dominant bloom-forming species of *Ulva* in Narragansett Bay affect survival or behavior of oyster larvae through a series of laboratory challenge experiments. Oyster larvae (2-11 days old) were exposed to crude extract from cultured *Ulva compressa* or *U. rigida* (5 g/L) that was either nutrient replete or deplete and their survival was determined over one week. We found a significant negative effect of *Ulva* extract on oyster survival, which depended on both the *Ulva* species and the nutrient condition. Survival of larvae exposed to nutrient replete *Ulva compressa* extract dramatically decreased over time, with less than 25% survival after one week. Larval survival was not significantly affected by nutrient deplete *Ulva* extract, although larvae exposed to this extract had a slower swimming speed. Our results suggest that *Ulva* blooms may cause oyster larval mortality under eutrophic conditions, which are common in coastal ecosystems.

P11 – METATRANSCRIPTOME ANALYSIS OF THE HARMFUL ALGA *HETEROSIGMA AKASHIWO* (RAPHIDOPHYCEAE). Nanjing Ji¹, Lingxiao Lin¹, Ling Li¹, Hao Luo¹, Yaqun Zhang¹ and Senjie Lin^{1,2}. ¹State Key Laboratory of Marine Environmental Science, Xiamen University, Xiamen, Fujian 361005, China; ²Department of Marine Sciences, University of Connecticut, Groton, CT 06340, USA.

Harmful algal blooms (HABs) have serious impacts on fisheries, tourism, public health and ecosystem in many coastal regions. To form a bloom, the causative algal species may own a unique strategy with which to more efficiently utilize available resources and increase its population more rapidly than the co-occurring species. However, such a strategy is poorly understood. Here, we studied a bloom of the raphidophyte *Heterosigma akashiwo*, a globally distributed HAB species, whose bloom has been associated with massive mortality of cultivated fish. Two bloom and one pre-bloom samples were collected in the course of a HAB outbreak in the East China Sea in 2014. 18S rDNA and metatranscriptome Next-Generation sequencing in combination with environmental factors were used to reveal the conditions that might have trigger and regulate the bloom. Our results suggested that silicate-limitation might have caused the decline of a diatom bloom (*H. akashiwo* pre-bloom) and benefited *H. akashiwo* and dinoflagellates. We noted a sharp decrease in dissolved inorganic phosphate concentration and simultaneous remarkable up-regulation of phosphate and dissolved organic phosphorus uptake genes under bloom conditions. Also up-regulated during the bloom were genes related to the carbon dioxide-concentrating mechanism. Most strikingly, the majority of the differentially expressed genes, including DNA replication, nitrogen metabolism, amino acid synthesis and citrate cycle, were regulated by photoperiod, indicating *H. akashiwo* regulates genes associated with the vital metabolic processes diurnally. Our findings provide new insight into how *H. akashiwo* operates gene regulation during a bloom, and underscores the importance to consider circadian timing of sampling in field studies.

P12 – THE EFFECTS OF FUTURE TEMPERATURE PROJECTIONS ON THE GROWTH AND SURVIVAL OF NON-NATIVE AND NATIVE SEAWEEDS. Marguerite Kinsella, Lindsay Green and Carol Thornber. Department of Natural Resources Science, University of Rhode Island, Kingston, RI 02881, USA. (President’s Award candidate)

The non-native seaweed *Grateloupia turuturu*, which is indigenous to Japan, was introduced to Rhode Island in 1994 through the ballast water of ships. This invasive alga prefers to live in shallow, protected subtidal waters and competes for space (i.e. rocks to attach to) with native algal species including *Chondrus crispus*. *Chondrus crispus* is an economically and ecologically vital species that provides habitat for invertebrates and contains commercially important compounds (i.e. carrageenan). Previous research has examined the environmental tolerance of the spore stage of these algae and indicated that *G. turuturu* spores have a broader tolerance than *C. crispus*. The goal of this experiment was to determine the impact of current and projected ocean temperatures in Narragansett Bay on adult thalli of *Grateloupia turuturu* and *Chondrus crispus*. We grew *G. turuturu* and *C. crispus* at the current average temperature in fall when *G. turuturu* is most abundant (14°C) and at a projected future temperature (17°C). Our results indicated that there was no difference in the average growth rate between species or temperatures. *Chondrus crispus* had a growth rate of 6.28 ± 1.36 at 14°C and 5.84 ± 1.36 at 17°C, while *G. turuturu* had a growth rate of 4.59 ± 1.36 at 14°C and 4.72 ± 1.36 at 17°C. Future research will determine whether there is a difference in growth rate of adult thalli of *G. turuturu* and *C. crispus* at temperature above 20°C.

P13 – RECOGNITION OF TWO NEW AUSTRALIAN GENERA IN THE ORDER HALYMENIALES (FLORIDEOPHYCEAE, RHODOPHYTA) REDUCES POLYPHYLY IN THE GENERA CRYPTONEMIA AND HALYMENIA. Lesleigh Kraft and Gary W. Saunders. Centre for Environmental and Molecular Algal Research, Department of Biology, University of New Brunswick, Fredericton, NB E3B 5A3, Canada.

Previous work using the DNA barcode, molecular phylogenetics, and traditional alpha taxonomy was undertaken to explore species diversity of this large and varied order in Australia. Results revealed that Australian species assigned to the genera *Cryptonemia*, *Grateloupia*, *Halymenia* and *Pachymenia* did not associate with their respective generic types, reflecting the need for global revision. The genus *Macromenia* was erected to accommodate the Australian species *Grateloupia ovata* and *Pachymenia orbicularis*, thereby reducing non-monophyly for these genera. Here, we turn our attention to Australian species assigned to the genera *Cryptonemia* and *Halymenia*. *Halymeniophyllum* gen. nov. is established for a well-supported clade that includes *Halymenia kraftii*, *H. plana*, and two potentially cryptic species resembling *Cryptonemia kallymenioides* (as well as the South Pacific *H. maculata*). Another well-supported clade containing *Cryptonemia nitophylloides* and two novel ‘cryptonemia’-like species will be transferred to *Irideofolium* gen. nov. The Peruvian *H. elongata* forms a novel clade with an unidentified halymeniacean specimen from Australia, likely requiring the erection of a third novel genus, but we defer that decision to the future. Our phylogenetic results also indicate that *H. abyssicola* and *H. californica* are better assigned to the genus *Amalthea*, highlighting the need for similar systematic work in other regions.

P14 – POTENTIAL IMPACTS OF CLIMATE ON CANDLEWOOD LAKE BASED ON LONG-TERM MONITORING RECORDS. Nate Morris, Peter Siver and Anne Lizarralde. Botany Department, Connecticut College, New London, CT 06320, USA. (President’s Award candidate)

Candlewood Lake is the largest water body in Connecticut, spanning 18 km in length and covering 21.9 km². A long-term monitoring program was initiated in 1985 to track changes in lake conditions that now spans over 30 years. In this study we will use the monitoring data to examine shifts in temperature and summer stratification structure at four sites, and correlate findings with regional climate data (air temperature, precipitation and wind speed). Relative thermal resistance to mixing (RTRM) was used to evaluate changes in stratification. Hypotheses include: (1) Climate warming has increased the surface temperature at all sites over the last three decades; (2) Stratification has increased over time forming a stronger thermocline which in turn reduces mixing; (3) Warmer surface temperatures coupled with stronger stratification would favor cyanobacteria at the expense of planktonic diatom populations. Although we are still processing data and assembling wind speed information, several preliminary findings are noteworthy. First, there is a clear positive relationship between the epilimnetic temperature and total RTRM that holds for all sites. The RTRM doubles from 200 to 400 with an increase in temperature from 23°C and 28°C. The combination of warmer surface waters and greater stratification would foster growth of blue-greens. Despite the clear relationship between surface temperature and RTRM of the water column, there were no significant trends in surface temperature or RTRM over time at any sites. The lack of an upward trend in summer lake temperature since 1985 is supported by the climate data, which also shows no increase in summer air temperature over the same time period. Interestingly, the hypolimnion temperature has significantly decreased by 3°C over the last three decades with the majority occurring during the first decade and possibly caused by a shift in wind characteristics. Future work will be discussed.

P15 – IDENTIFICATION OF FOUR DIFFERENT CHLOROPHYLL A ALLOMERS OF *NOSTOC* SP. BY LIQUID CHROMATOGRAPHY MASS SPECTROPHOTOMETRY (LC MS). Bahareh Nowruzi¹, Taher Nehadsattari¹ and Jouni Jokela². ¹Department of Biology, Science and Research Branch, Islamic Azad University, Tehran, Iran; ²Division of Microbiology, Department of Food and Environmental Sciences, University of Helsinki, Finland.

Cyanobacteria (blue-green algae) differ from other types of bacteria in that they have chlorophyll *a*, a pigment lacking in other photosynthetic bacteria. In this study, liquid chromatography mass spectrophotometry (LC MS) has been used for identification of the four different allomers of chlorophyll *a* (HO-chl *a*, MeO-chl *a* and MeO-lact-chl *a*), the hydroxy allomer of chlorophyll *a* (HO-chl *a*) and the hydroxy and methoxylactone allomers of chlorophyll *a* (HO- chlorophyll *a* and MeO-lact- chlorophyll *a*) from *Nostoc* sp. isolated from Iran. The differences in mass spectrometric fragmentation of extracted ion chromatogram can be used as a diagnostic tool for the assignment of the configuration of four different chlorophyll allomers. This case is the first documented of identification of four different chlorophyll *a* allomers from *Nostoc* sp. in Iran.

P16 – CHARACTERIZATION OF A NEW PEPTIDE-ALDEHYDE COMPOUND FROM THE TERRESTRIAL CYANOBACTERIUM *NOSTOC* SP. BAHAR_M BY LC MS AND MARFEY'S ANALYSIS. Bahareh Nowruzi¹, Taher Nehadsattari¹ and Jouni Jokela². ¹Department of Biology, Science and Research Branch, Islamic Azad University, Tehran, Iran; ²Division of Microbiology, Department of Food and Environmental Sciences, University of Helsinki, Finland.

Cyanobacteria are a diverse and ancient group of photosynthetic prokaryotic organisms that inhabit a wide range of environments including extreme conditions such as hot springs, desert

soils and the Antarctic. They are abundant producers of natural products and well recognized for their bioactivity and utility in drug discovery and biotechnology applications. Novel intracellular and extracellular compounds from various cultured and field cyanobacteria with diverse biological activities and a wide range of chemical classes have considerable potential for development of pharmaceuticals and other biomedical applications. However, cyanobacteria are still viewed as unexplored source of potential drugs. Collections of cyanobacterial strains are still largely unexplored from rice paddy fields of north Iran where biodiversity is high. We investigated one *Nostoc* strain isolated from soil samples that were frequently collected from rice fields in Golestan province of Iran to search for new compounds. The chemical structure of a new identified metabolite was elucidated by liquid chromatography mass spectrophotometer (LC MS) and Marfey's analysis of the degradation products. We discovered a new peptide aldehyde compound from a hydrophilic extract of *Nostoc* sp. Bahar_M, which was composed of three subunits, 2-hydroxy-4-(4-hydroxyphenyl) butanoic acid (Hhpba), L-Ile, and L-argininal. According to the structural information, we made the prediction that the new peptide-aldehyde compounds might be trypsin inhibitors. The presented results show that soil cyanobacteria are a promising source to yield chemically- and pharmaceutically-interesting compounds.

P17 – THE CHALLENGES OF DATABASING AN HISTORICAL HERBARIUM COLLECTION. **Chelsea M. Parise.** Farlow Herbarium of Cryptogamic Botany, Harvard University Herbaria, Cambridge, MA 02138, USA.

The Farlow Herbarium (FH) of the Harvard University Herbarium is a participating member of the MacroAlgal Herbarium Consortium Digitization Thematic Collection Network Project funded by the National Science Foundation. The project produces algal specimen images and georeferenced label transcription data. This data is made available to the global public through the MacroAlgal Web Portal, where it can be used to inform climate change studies and other research. It is imperative that herbarium specimen digitization data is transcribed as accurately as possible in order to secure robust research results, improve data searchability, and increase institutional collaboration. Recent statistics revealed that over half of the FH specimens databased were collected pre-1900 and over 90% before the 1950s. Historical collections pose unique challenges for interpretation and accuracy in transcriptions. The majority of the FH labels are handwritten and the legibility varies dramatically based on quality of paper, pen, handwriting and typography. Locality data can prove difficult to confirm due to shifting geo-political boundaries, archaic or disused classical locations, and synonymous locality names in multiple countries or states. Nearly a third of the FH specimens are of European origin, thus their labels are often written in German, French or Latin as well as Russian, Italian and Icelandic. The FH has streamlined the databasing process by creating a handwriting reference key. We frequently use both web and paper resources to trace names, locations and habitat information. As of March 2017, the FH has contributed 13,000 specimen label data and 29,000 images to the MacroAlgal Herbarium Portal.

P18 – DIVERSITY AND DISTRIBUTION OF MICROBIAL EUKARYOTES IN ANTARCTIC WATERS. **Daniela Lopes Paim Pinto**¹, Tatiana Rynearson², Kristina Terpis¹ and Christopher E. Lane¹. ¹Department of Biological Sciences, University of Rhode Island, Kingston RI, 02881, USA; ²Coastal Institute, University of Rhode Island, Narragansett Bay Campus, Narragansett RI, 02882, USA.

Besides playing crucial roles in a variety of ecosystems, microbial eukaryotes are key actors for understanding the evolution and diversity of eukaryotic life. Notwithstanding the intensive efforts to unveil their biodiversity, some lineages remain poorly known. Using Illumina reads of the 18S rDNA hypervariable region V9, obtained from 30 samples collected at different depths and latitudes in the Antarctic waters, we surveyed the diversity and distribution pattern of eukaryotic microbes focusing on particularly unexplored lineages within the SAR (Stramenopile, Alveolate, Rhizaria) clade. After alignment, quality checks (including chimera removal) and clustering at 98% similarity, a total of 6881 operational taxonomic units (OTUs) were identified. The OTUs were taxonomically annotated using Mothur in combination with the SILVA SSU Ref datasets. OTUs that could not be assigned to any of the known eukaryotic groups are currently being manually investigated using phylogenetic analysis to determine if they represent new lineages of eukaryote microbes. On average, SAR groups constitute 80.5% of the eukaryotic diversity of all combined samples using our PCR primers, where 38.5% are represented by Stramenopile, 39.83% Alveolate and 2.31% Rhizaria. However, the distribution of these different groups across different samples (different, depth, latitude and filter size) is highly variable. We identified a large proportion of different MAST (MARine STRamenopiles) groups in different samples, as well as a variety of other rare taxa. The results obtained shed light on the scarce biodiversity information of microbial eukaryotes expanding our knowledge particularly in underrepresented areas of the SAR tree.

P19 – DIVERSIFYING NEW ENGLAND SEA VEGETABLE AQUACULTURE: MODIFYING KELP NURSERY AND GROW OUT TECHNOLOGIES FOR NORI PRODUCTION. **Jaelyn Robidoux** and Chris Neefus. University of New Hampshire, Durham, NH 03824, USA. (**Trainor Award candidate**)

The emerging New England sea vegetable aquaculture industry is currently based on the long-line production of kelp. Seeking to promote greater industry stability and sustainability, our research will contribute to diversification of aquaculture in the Gulf of Maine by adapting kelp technologies for the production of nori. Of the nori species that occur in New England, *Wildemanian amplissima* Foslie (1891) has been chosen as the ideal candidate for long-line production due to its size, seasonality, geographic range, ammonia removal efficiency, and exceptional growth rates. Field collections of *W. amplissima* were conducted along the New Hampshire and Maine coastlines and three experimental zygospore isolation techniques were used to successfully establish conchocelis-phase nursery cultures. Optimum environmental conditions for vegetative conchocelis growth and conchospore release are being investigated by growing conchocelis cultures under various combinations of light level, temperature and photoperiod. Further investigations will focus on developing nursery techniques for string seeding and modifications of existing kelp long-line grow-out operations. Field trials will be conducted at lease sites in Casco Bay, Maine, and the UNH Aquaculture Farm off Newcastle, New Hampshire. This research plays a key role in the development of nursery systems and species specific technologies that will provide the platform for commercial nori production in the Gulf of Maine.

P20 – INTRA- AND INTER-POPULATION COMPARISON OF *CHARA BRITTONII* ALLEN EX ROB. ORGANELLAR GENOMES. **Joseph A. Sardina** and Kenneth G. Karol. Lewis B. and Dorothy Cullman Program for Molecular Systematics Studies, The New York Botanical Garden, Bronx, NY 10458, USA. (**President's Award candidate**)

The Characeae (Charophyceae, Charophyta) contains six genera (*Chara*, *Lamprothamnium*, *Lychnothamnus*, *Nitella*, *Nitellopsis* and *Tolypella*), and are found in fresh and brackish waters worldwide. While many species in this family are common, there are several examples of rare taxa in the New World. *Chara brittonii* Allen ex Rob. is one such example and is perhaps one of the more rare members of the Characeae in North America. *Chara brittonii* is one of two completely ecostriate species in the genus in North America (*C. braunii* being the other), and reportedly has antheridia composed of four scute cells while eight scute cells are typical for the family. Complete sequencing of the mitochondrial (mt) and plastid (pt) genomes of four *C. brittonii* specimens was attempted using Next-Generation Sequencing. Two were collected from Lawrence Lake, Michigan (Sept., 2001), and two represent the lectotype and an isolectotype collected near Sparta, New Jersey (Sept., 1887). Both the mt genomes (62,817 bp, on average) and pt genomes (188,342 bp, on average) of the Lawrence Lake individuals completely assembled, varying slightly in size between the two individuals. The mt genomes of both individuals collected near Sparta, NJ completely assembled and were identical to each other (62,812 bp); however, the pt genomes only partially assembled into several large contigs. These pt contigs covered approximately 97% of the complete pt genomes of the Lawrence Lake individuals. Gene content and gene order of the *C. brittonii* organellar genomes were identical to those published for *C. vulgaris*. Polymorphisms were detected within and among the *C. brittonii* organellar genomes including single nucleotide polymorphisms, inversions, and insertion-deletion events. An analysis of these polymorphisms and their implications on intra- and inter-population organellar genome evolution will be presented.

P21 – SPECIES DIVERSITY AND EVOLUTIONARY RELATIONSHIPS OF THE TAXONOMI-CALLY CHALLENGING RED ALGAL TRIBE POLYSIPHONIEAE (RHODOMELACEAE) IN CANADA. Amanda Savoie and Gary W. Saunders. Centre for Environmental & Molecular Algal Research, Biology, University of New Brunswick, Fredericton, NB E3B 5A3, Canada. (Trainor Award candidate)

Sequence data generated during a DNA barcode survey (COI-5P) of the Polysiphonieae, a large and taxonomically challenging tribe of red algae, revealed taxonomic confusion and hidden species diversity in Canada. Four common species (*Polysiphonia pacifica*, *P. paniculata*, *P. stricta* and *Vertebrata fucoides*) were revealed as complexes of two or more genetically distinct yet cryptic species, with one variety of *P. pacifica* elevated to species rank, *P. determinata* (Hollenberg) stat. nov. Several new additions to the Canadian flora were recorded including *Acanthosiphonia echinata* (Harvey) gen. et comb. nov., *Polysiphonia kapraunii*, and *P. morrowii*. Subsequent multigene (COI-5P, LSU, and *rbcL*) phylogenetic analyses confirmed that the genus *Polysiphonia* was polyphyletic, and *Polysiphonia sensu stricto* was restricted to a group of species that formed a monophyletic lineage with the type, *Polysiphonia stricta*. The genus *Carradoriella* was resurrected for the South African species *Carradoriella virgata*, and now includes *C. elongata* (Hudson) comb. nov. The monotypic genus *Leptosiphonia* was expanded to include *L. fibrillosa* (Dillwyn) comb. nov. and *L. flexicaulis* (Harvey) comb. nov., while the genus *Vertebrata* was expanded by returning *V. ericoides* (Harvey) Kuntze and *V. woodii* (Harvey) Kuntze, as well as the addition of *V. hendryi* (N.L.Gardner) comb. nov. Three new genera were described for species previously attributed to *Polysiphonia*: *Acanthosiphonia* gen. nov. for *A. echinata* (Harvey) comb. nov., *Eutrichosiphonia* gen. nov. for *E. inconspicua* (Hollenberg) comb. nov. and *E. sabulosia* (B.Kim et M.S.Kim) comb. nov. and *Kapraunia* gen. nov., which includes *K. schneideri* (B.Stuercke et D.W.Freshwater) comb. nov., *K. amplacapilli*

(B.Kim *et* M.S.Kim) comb. nov., *K. morroides* (B.Kim *et* M.S.Kim) comb. nov., and *K. pentamera* (Hollenberg) comb. nov.

P22 – MICROCYSTIN IN FISH TISSUE: A POTENTIAL RISK TO CONSUMERS? Kristen Slodysko and Gregory Boyer. State University of New York, College of Environmental Science and Forestry, Syracuse, NY 13210, USA. (**Trainor Award candidate**)

Microcystins (MCs), a class of cyclic heptapeptide toxins produced by cyanobacteria, present a variety of risk factors to consumers. While the risk of exposure to MCs through drinking water is well characterized, less is known about fish consumption as an exposure pathway. The World Health Organization (WHO) has established a tolerable daily intake (TDI) for the public of 0.04 μg MC-LR per kilogram of body weight. It is unknown if fish from lakes with blooms would contain amounts of MC that would exceed the 0.04 μg TDI if consumed. Lake Champlain has a documented history of cyanoblooms especially in embayments like Missisquoi Bay. Muscle and liver tissues were collected and tested for MCs from three Lake Champlain fish species. Different extraction methods and purification protocols were tested including solid phase extraction. All samples were analyzed using tandem mass spectroscopy (LC-MS/MS). Concentrations of MCs in fish were found to be highly variable. MC concentrations in relation to their human health implications will be discussed.

P23 – THE CURRENT STATUS OF DIGITIZATION EFFORTS WITHIN THE MACROALGAL HERBARIUM CONSORTIUM. Christopher Neefus¹ and **Hannah Traggis**².
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Macroalgae are a diverse group of aquatic photosynthetic organisms from four divisions spanning two kingdoms. They serve as the basis for nearly every benthic habitat, providing food, shelter and substrata for other organisms. Globally, they are important primary producers and essential participants in ecosystem nutrient cycling. They are an important food source for humans and extractable colloids are used in pharmaceuticals and cosmetics. Worldwide, herbaria have housed plant and algal collections for 400 years providing a priceless record of distribution and ecology for local and visiting scientists. Recently, there has been an enormous collective effort to digitize herbarium and biological collections worldwide, making the information therein available online, open-access to scientists and citizens alike. Funded by the NSF ADBC Program, the Macroalgal Herbarium Consortium (MHC) was formed, bringing together 49 universities, museums, botanical gardens and field stations from 26 states and U.S. possessions across the globe. The MHC collectively contains more than 1.1 million recent and historic algal specimens. Digitization efforts, including high-resolution imaging, transcription of label information and georeferencing collection sites based on locality information, have been underway for three years. Images and data are accessible through the MHC web portal (www.macroalgae.org) as well as iDigBio, GBIF, and other data integration portals worldwide. This information is already being used extensively in research today. We present the current status of our ongoing efforts to fully digitize these collections and discuss the already realized implications of having this data globally available in an open access form.

P24 – TRANSCRIPTOMIC ANALYSIS OF FOUR GREEN TIDE ALGAE IN THE YELLOW SEA, CHINA. **Lingjie Zhou**¹, Lingke Wang², Senjie Lin¹ and Peimin He². ¹Department of Marine Sciences, University of Connecticut, Groton, CT 06340, USA; ²College of Fisheries and Life Science, Shanghai Ocean University, Shanghai 201306, China.

Green tide has become a global environmental problem, which not only exerts impacts on the marine ecosystem but also on regional economy. Since 2007, green tide has happened every year in the Yellow Sea, China, where it is caused by four green algae, *Ulva prolifera*, *U. compressa*, *U. linza* and *U. flexuosa*. Usually, *U. prolifera* persistently dominates the bloom period while the other three species gradually decline and fall in the middle-late stages of the bloom. While numerous physiological and ecological studies have been conducted, ‘omics studies are still limited despite its potential to enable unlocking the mechanisms behind the green tide of these algae. Here, we launched a large-scale comparative transcriptomic study for the 4 species grown under 9 different light-temperature conditions for each species, 1 optimum condition and 8 stress conditions. Through transcriptomic analysis, we obtained 64931, 52679, 61580, 38459 annotated unigenes for *U. prolifera*, *U. compressa*, *U. linza* and *U. flexuosa*, respectively. The result showed that these four green tide algae all had complete C4 pathway, which suggests a highly efficient photosynthetic carbon fixation. Analyses of the differentially expressed genes (DEGs) showed that the green tide algae were more sensitive to temperature. Additionally, the stress responsive genes were mostly related to photosynthesis, antioxidant activity, photoprotection, among other processes. Finally, we identified the genes most highly expressed in *U. prolifera* compared with the other three species, including genes encoding catalase, xanthine dehydrogenase, dehydrogenase, monodehydroascorbate reductase, light-harvesting complex, ElipL2, carotene biosynthesis related (CBR) proteins, and SEPALLATA (SEP). Most of these genes are related to photoprotection, which illustrated that the photoprotection mechanism played a significant role in the process of resisting abiotic stress in the green tide dominating species.

NOTES

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