

NEAS



Mystic, Connecticut 2013

Table of Contents & Acknowledgements

Welcome note	2
General program	3-7
Poster presentation summary	8-10
Oral abstracts (in order of presentation)	11-25
Poster abstracts (numbered presentation boards)	26-38
Biographies of our distinguished speakers: James Carlton, Mark Edlund, Alan Steinman	39

Sincere appreciation

The co-conveners acknowledge the generous support of our sponsors for this event, Woods Hole Sea Grant, Dominion Resources, Connecticut Sea Grant. Our vendors include Balogh Books (Scott Balogh), Environmental Proteomics (Jackie Zorz), Microtech Optical (Mark Specht), Reed Mariculture (Eric Henry), Saltwater Studio (Mary Jameson), and Willywaw (Ashley Van Etten). We thank our student volunteers: Shelby Rinehart, Meg McConville, Emily Bishop (U. Rhode Island) and Catharina Grubaugh, Sarah Whorley, and Xian Wang (Fordham U.) for their assistance in registration and meeting audio/visual support. We thank the award judges for the Wilce Graduate Oral Award Committee (Brian Wysor (Chair), Nic Blouin, Ursula Röse), Trainor Graduate Poster Award Committee (Karolina Fučíková (Chair), Charles O'Kelly, Michele Guidone, Ruth Schmitter) and President's Undergraduate Presentation (oral & poster) Award Committee (Anita Klein (Chair), Julie Koester, Dion Durnford, Kyatt Dixon, Ken Hamel). We also thank the session moderators: Jessie Muhlin, Lorraine Janus, Anne-Marie Lizarralde, Dale Holen, Hilary McManus, and Amy Carlile. We are grateful to our invited speakers Jim Carlton, Mark Edlund, and Alan Steinman. We extend sincere gratitude to Bridgette Clarkston, who designed the 50th NEAS logo and Nic Blouin for modifying that logo for this meeting, and the staff at the Mystic Hilton, particularly Eileen Menard, for providing logistical support for this meeting.



Balogh International Inc

Booksellers & Distributors of International Publishers

NEAS



Mystic, Connecticut 2013

Welcome to the 52nd Northeast Algal Symposium!

We are delighted to welcome everyone to Mystic, Connecticut, and the Mystic Hilton. We extend a special welcome to all new student and professional attendees. We think the venue lends itself to a most productive and relaxing conference! We hope you enjoy the beauty and serenity of this area and take the time to visit some nearby attractions. Following NEAS tradition, we celebrate all students of phycology and seek to foster understanding and appreciation for the multitude of algal research we collectively study. With nearly 60 combined talks and posters, along with a panel discussion, the schedule is packed with interesting presentations from locations near and far.

This year's theme is "**Impacts of invasive species: invaders in freshwater and marine systems**". Our distinguished speakers Sunday morning are **Dr. James Carlton, Dr. Mark Edlund, and Dr. Alan Steinman**, with a panel discussion following these talks. We also have attempted, whenever possible, to cluster together contributed invasive species presentations to further facilitate this theme.

If you are giving an oral presentation, please be sure to have your talk loaded well before your session. Someone will be available to assist you during breaks and before the start of talks each day. Posters can be set up anytime Friday evening and Saturday morning. Please look for the poster board that corresponds to the number next to your title in the following schedule. Posters must be taken down by lunchtime on Sunday.

The banquet will include a special tribute to Francis R. Trainor (1929-2013) as well as the *famous* NEAS auction. This event is a major source of revenue for student activities that NEAS funds. Please participate liberally and spend with reckless abandon!

Our meeting will conclude with the annual Business Meeting on Sunday, followed by lunch before we meet again in 2014. Please take time to vote in society elections and consider serving NEAS in an elected role.

Best wishes for a wonderful weekend!

Carol Thornber and John Wehr
2013 Co-conveners

General Program: 52nd Northeast Algal Symposium
Mystic, CT Hilton

Friday, April 19, 2013

- 5:00 – 9:00 pm** **Evening Registration, Check-in & Auction Donation**
Lobby/Hallway
Speakers load presentations, *Lobby/Hallway*
Poster setup, *Maritime Ballroom*
- 7:00 – 9:00 pm** **NEAS Welcome Mixer**
Grand Ballroom
-

Saturday, April 20, 2013

- 6:30 – 8:00 am** **Continental Breakfast**
Soundings Lounge
Poster setup, *Maritime Ballroom*
- 8:00 – 8:30 am** **Morning Registration & Auction Donation**
Lobby/Hallway
Session I, II speakers load presentations
- 8:30 – 8:45 am** **Welcome and Opening Remarks – Carol Thornber and John Wehr**
Grand Ballroom
- SESSION I** **STUDENT PRESENTATIONS, Moderator: Jessie Muhlin**
Grand Ballroom
- 8:45 – 9:00** *Wilce Award Candidate*
Jennifer A Jeans, Mia Hoogenboom & Douglas A Campbell.
DINOFLAGELLATE SYMBIONTS OF THE CORAL *STYLOPHORA*
PISTILLATA INCREASE DEPENDENCE ON PHOTOSYSTEM II REPAIR
WHEN ACCLIMATED TO HIGHER LIGHT LEVELS.
- 9:00 – 9:15** *Wilce Award Candidate*
Xian Wang, John D. Wehr & Kenneth G. Karol. PHYLOGENETIC
RELATIONSHIPS AMONG DIFFERENT POPULATIONS OF
FRESHWATER BROWN ALGAE *HERIBAUDIELLA FLUVIATILIS* AND
BODANELLA LAUTERBORNII.
- 9:15 – 9:30** *Wilce Award Candidate*
Gina V. Filloramo & Gary W. Saunders. ASSESSMENT OF THE RED
ALGAL ORDER RHODYMENIALES USING A MULTIGENE
PHYLOGENETIC APPROACH.

9:30 – 9:45 *Wilce Award Candidate*
Renée Eriksen, Lindsay A. Green & Anita Klein. ORGANISM-ENVIRONMENT INTERACTIONS IN NATURAL ASEXUAL POPULATIONS OF *PORPHYRA UMBILICALIS* KÜTZING RHODOPHYTA.

9:45 – 10:00 *Wilce Award Candidate*
Jennifer E. Dingman & Dion G. Durnford. CYST FORMATION IN HETEROSIGMA AKASHIWO, RAPHIOPHYCEAE, DURING INFECTION WITH HaV.

10:00 – 10:15 *Wilce Award Candidate*
Caroline Longtin & Gary W. Saunders. OBSERVATIONS ON THE LAMINARIACEAE IN THE BAY OF FUNDY, WITH EMPHASIS ON *SACCHARINA GROENLANDICA*.

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

SESSION II **STUDENT PRESENTATIONS, Moderator: Lorraine Janus**
Grand Ballroom

10:45- 11:00 *Wilce Award Candidate*
Amanda Savoie & Gary. W. Saunders. USING MOLECULAR TOOLS TO RESOLVE THE *NEOSIPHONIA JAPONICA/NEOSIPHONIA HARVEYI* SPECIES COMPLEX IN NEW ENGLAND.

11:00 – 11:15 *Wilce Award Candidate*
Christine Newton, Matthew E.S. Bracken, Megan McConville, Katherine Rodrigue & Carol S. Thornber. INVASION OF THE RED ALGA *HETEROSIPHONIA JAPONICA* IN THE WESTERN NORTH ATLANTIC OCEAN.

11:15 – 11:30 *Wilce Award Candidate*
Chris Benton & Anita Klein. EVALUATING THE GENETIC DIVERSITY OF *CODIUM FRAGILE* IN THE NW ATLANTIC.

11:30 – 11:45 *Wilce Award Candidate*
Meghann Bruce & Gary W. Saunders. POPULATION GENETIC ANALYSES CONFIRM THE INTRODUCTION OF *CERAMIUM SECUNDATUM* (CERAMIACEAE, RHODOPHYTA) TO RHODE ISLAND.

11:45-12:00 *President's Award Candidate*
Shaunna R. Kraatz, Alison R. Sherwood & Amy L. Carlile. PHYSIOLOGICAL RESPONSE TO CHANGES IN SALINITY: AN EXAMINATION OF A BROADLY DISTRIBUTED *CLADOPHORA* IN THE HAWAIIAN ISLANDS.

12:00 – 1:30

*Lunch (Soundings Lounge), Executive Committee Lunch (West Ballroom)
Session III, IV speakers load presentations*

SESSION III

STUDENT & CONTRIBUTED PRESENTATIONS

Moderator: Anne-Marie Lizarralde

Grand Ballroom

1:30 – 1:45

President's Award Candidate

Shelby Rinehart, Michele Guidone & Carol Thornber. OVERWINTERING STRATEGIES OF *ULVA* SPP. IN NARRAGANSETT BAY, RI.

1:45 – 2:00

President's Award Candidate

Benjamin Korry, Brian Wysor & Charles J. O'Kelly. DETERMINING THE DIVERSITY OF MICROFILAMENTOUS GREEN ALGAE IN PANAMA USING A DNA BARCODING APPROACH.

2:00 – 2:15

President's Award Candidate

Nick Hammerman, Brian Wysor & Heroen Verbruggen. DNA BARCODING REVEALS INCREASES IN *CODIUM* (ULVOPHYCEAE: BRYOPSISDALES) SPECIES RICHNESS FOR CARIBBEAN AND PACIFIC PANAMA.

2:15 – 2:30

Contributed paper

Kyatt Dixon, Gary Saunders & John Huisman. THE MARINE BENTHIC FLORA OF NORTHWESTERN AUSTRALIA: ADDITIONS TO THE PEYSSONNELIACEAE AND RHIZOPHYLLIDACEAE (RHODOPHYTA).

2:30 – 2:45

Contributed paper

Thea R. Popolizio, Craig W. Schneider & Christopher E. Lane. FIRST REPORT OF THE GENUS *YAMADAELLA* (LIAGORACEAE, RHODOPHYTA) IN BERMUDA.

2:45 – 3:00

Coffee Break

SESSION IV

CONTRIBUTED PRESENTATIONS

Moderator: Dale Holen

Grand Ballroom

3:00 – 3:15

Nicolas A. Blouin, Elizabeth Sullivan & Christopher E. Lane. THE *GRACILARIOPSIS ANDERSONII* PLASTID: CONSERVATION IN RED ALGAL PLASTID EVOLUTION.

3:15 – 3:30

Jang K. Kim, George P. Kraemer & Charles Yarish. NUTRIENT BIOEXTRACTION VIA SEAWEED AQUACULTURE IN LONG ISLAND SOUND AND THE URBANIZED BRONX RIVER ESTUARIES.

3:30 – 3:45 **Julie A Koester**, Willie J. Swanson & E. Virginia Armbrust. EXPRESSION OF POSITIVELY SELECTED GENES IN *THALASSIOSIRA PSEUDONANA* SUGGESTS A LINK BETWEEN GENOTYPE AND PHENOTYPE.

3:45 – 4:00 **Eric Salomaki** & Chris Lane. COMPARATIVE GENOMICS OF FREE-LIVING AND PARASITIC RHODOPHYTE MITOCHONDRIA.

SESSION V **POSTER SESSION & MIXER**
Maritime Ballroom & Lobby

4:00 – 6:00 **Student and Professional Contributed Posters**
Please take down posters by lunch on Sunday,

6:30 – 10:00 **NEAS Banquet, Awards & Live Auction, including special Tribute to Frank Trainor**
Grand Ballroom

Sunday, April 21, 2013

6:30 – 8:00 am **Continental Breakfast**
Soundings Lounge

7:30– 8:00 am **Morning Registration**
Lobby/Hallway
Session VI, VII speakers load presentations

SESSION VI **DISTINGUISHED SPEAKERS**
Moderator: Hilary McManus
Grand Ballroom

8:00 – 8:10 am **Announcements – Carol Thornber/John Wehr**

8:10 – 8:50 **James Carlton.** DEEP (PHYTO-) INVASION ECOLOGY AND THE ASSEMBLY OF MARINE COMMUNITIES IN HISTORICAL TIME.

8:50 – 9:30 **Alan D. Steinman.** EUTROPHICATION, RESTORATION, AND ALGAE IN GREAT LAKES COASTAL ECOSYSTEMS.

9:30 – 10:10 **Mark Edlund.** SILICEOUS INVADERS: WHEN THE LEAST AMONG US GO BAD.

10:10 – 10:25 **Coffee Break**
Session VII speakers load presentations

SESSION VII **PANEL DISCUSSION AND CONTRIBUTED PAPERS**
Moderator: Amy Carlile
Grand Ballroom

10:25 – 11:05 **PANEL DISCUSSION: IMPACTS OF INVASIVE SPECIES**
Panel: Jim Carlton, Mark Edlund, Alan Steinman

Contributed papers

11:05 – 11:20 **Jim Foertch**, John Swenarton, Don Landers & Deb Pacileo. SOME IMPACTS OF AN INVASIVE ALGA (“*HETEROSIPHONIA*” *JAPONICA*) ON INDUSTRY IN LONG ISLAND SOUND.

11:20 – 11:35 **Tania Aires**, Ester A. Serrao, Carlos M. Duarte & Sophie Arnaud-Haond. BIOTIC INTERACTIONS AND THE SUCCESS OF INVASIONS: BACTERIAL COMMUNITIES IN INVASIVE *VERSUS* NATIVE SPECIES OF ALGAE (*CAULERPA* SP.).

11:35 – 11:50 **Charles J. O’Kelly**, Geneva J. Mottet, Sylvain Santoni & Aline Tribollet. CULTURE-BASED STUDIES ON THE CARBONATE MICROBORING CHLOROPHYTE *OSTREOBIMUM* (ULVOPHYCEAE, BRYOPSIDALES) REVEAL NOVEL DIVERSITY IN TEMPERATE MARINE WATERS.

11:50 – 12:05 **Gary W. Saunders**. NEAS KEY V3 THROUGH THE LOOKING GLASS: AN ALTERNATIVE PERSPECTIVE ON SEAWEED DIVERSITY IN THE NORTHEAST AND HOW TO BEST MANAGE AND SHARE THAT KNOWLEDGE.

12:05 – 12:35 **Closing Remarks and General Business Meeting**
Grand Ballroom

12:35 – 1:30 **Lunch**
Soundings Lounge

Poster Presentation Summary (By Category)

(Poster No.) Authors/Title (Abstracts can be found on page 27)

Undergraduate Posters (President's Award)

(P4) Megan McConville, Katherine Rodrigue, Matthew Bracken, Christine Newton & Carol Thornber. INVASION HISTORY AND POPULAR PRESS COVERAGE OF THE RED ALGA *HETEROSIPHONIA JAPONICA* IN THE WESTERN NORTH ATLANTIC OCEAN.

(P8) Alyssa Rogers, Thea Popilizio, Craig Schneider & Christopher Lane. BROWN ALGAL DIVERSITY IN BERMUDA REVEALED USING DNA BARCODING.

(P9) Laura Dushkin & Marcie Marston. GENETIC ANALYSIS OF A COMMON MARINE CYANOPHAGE STRAIN (RIM12) IN SOUTHERN NEW ENGLAND.

(P11) Jordan Bishop, Peter Siver & Anne Lizarralde, VALVE SHAPE IN *EUNOTIA*: COMPARING MODERN AND FOSSIL FLORAS.

(P15) Matthew Breseman, Shennel Gelin, Amy Battocletti, Carol Thornber & JD Swanson. ELUCIDATION OF POLYMORPHIC MICROSATELLITE MARKERS IN *ULVA RIGIDA* AND *ULVA COMPRESSA*.

(P16) Amy Battocletti, Emily Bishop, Tanja Schollmeier, Shennel Gelin, Matthew Breseman, J.D. Swanson, Tania Aires & Carol Thornber. INVESTIGATING *ULVA RIGIDA* BLOOM FORMATION IN NARRAGANSETT BAY, RI.

Graduate Student Posters (Trainor Award)

(P1) Simona Augyte, Louise A. Lewis & Charles Yarish. NON-NATIVE *BRYOPSIS MAXIMA* (ULVOPHYCEAE, CHLOROPHYTA) INTRODUCTION TO LONG ISLAND SOUND.

(P2) Diba Khan-Bureau, Mike Beauchene & Louise A. Lewis. MONITORING THE DISTRIBUTION OF *DIDYMOSPHENIA GEMINATA* AND OTHER "ROCK SNOT" SPECIES IN THE FARMINGTON RIVER IN CONNECTICUT.

(P3) Lesleigh Kraft & Gary W. Saunders. A SYSTEMATIC INVESTIGATION OF THE RED ALGAL ORDER HALYMENIALES (FLORIDEOPHYCEAE, RHODOPHYTA) IN AUSTRALIA.

(P5) Katherine Hladki & Christopher D. Neefus. AMMONIUM UPTAKE BY *GRACILARIA* SPECIES FOR POTENTIAL USE IN INTEGRATED MULTI-TROPHIC AQUACULTURE.

(P17) E. Bishop, **E. E. Potter**, J.D. Swanson & Carol S. Thornber. DEVELOPING A PROTOCOL FOR ANALYSIS OF ALGAL CELLS USING FLOW CYTOMETRY.

(P18) **Sarah B. Whorley** & John D. Wehr. EFFECTS OF AGRICULTURAL BMPs ON PERIPHYTON COMMUNITIES AND NUTRITIONAL QUALITY IN STREAM ECOSYSTEMS.

(P21) **Gordon Ober** & Guillermo Diaz-Pulido. TURF WARS: HOW OCEAN ACIDIFICATION IS IMPACTING THE GROWTH AND DIVERSITY OF TROPICAL TURF ALGAL COMMUNITIES.

(P26) **Hannah Traggis**. IRON LIMITATION EFFECTS A MASSIVE SHIFT IN IRON AND FLAVIN BASED ANTIOXIDANT ENZYME SYSTEMS AND THEIR SUBSTRATES IN THE CHLOROPHYTE ALGA *DUNALIELLA TERTIOLECTA*.

(P27) **Minoli Perera**, Jessica Alexander, Sohini Ghoshroy & Deborah Robertson. POSTTRANSCRIPTIONAL REGULATION OF NITROGEN ASSIMILATION IN MARINE DIATOMS – THE ROLE OF RNA-BINDING PROTEINS.

Contributed Posters

(P6) **Jacquelyn Schaub**, Craig Frysinger & Hilary A. McManus. MOLECULAR AND MORPHOLOGICAL VARIATION IN SELECTED *PEDIASTRUM* STRAINS.

(P7) **Craig W. Schneider**, Gary W. Saunders & Christopher E. Lane. A NEW SPECIES OF *MEREDITHIA* (KALLYMENIACEAE, GIGARTINALES) FROM BERMUDA BASED UPON *KALLYMENIA LIMMINGHEI* MONT. *SENSU* W.R. TAYLOR.

(P10) **Dana Baltrusitis** & Hilary A. McManus. TESTING THE DIVERSITY OF THE GREEN ALGA *BOTRYOCOCCUS* (TREBOUXIOPHYCEAE).

(P12) **Joseph Holbeche** & Marcie Marston. GENETIC DIVERSITY OF *SYNECHOCOCCUS* SPP. FOUND IN RHODE ISLAND COASTAL WATERS.

(P13) **Elizabeth Sullivan**, Nicolas Blouin & Christopher Lane. THE PLASTID GENOME SEQUENCE OF THE RED MACRO ALGA *GRACILARIOPSIS ANDERSONII*.

(P14) **Hiroshi Kawai**, Takeaki Hanyuda, Atsushi Kai, Takahiro Yamagishi, Gary W. Saunders, Chris Lane, Dan McDevit & Frithjof C. Küpper. LIFE HISTORY, MOLECULAR PHYLOGENY AND TAXONOMIC REVISION OF *PLATYSIPHON VERTICILLATUS* (PHAEOPHYCEAE).

(P19) **Ursula S.R. Röse**, Kyle Martin & Janithri Wickramanayake. INDUCIBILITY OF VOLATILE AND NON-VOLATILE COMPOUNDS IN BROWN MACROALGAE AND THEIR EFFECT ON HERBIVORE BEHAVIOR.

(P20) Michele Guidone, Tanja Schollmeier & Carol S. Thornber. COMPETITION BETWEEN TWO BLOOM-FORMING *ULVA* SPECIES UNDER DIFFERENT NUTRIENT REGIMES.

(P22) Louise A. Lewis, Tobias Landberg, Chien Lo & Andrew Fuller. NATURAL HISTORY OF THE GREEN ALGAE - SPOTTED SALAMANDER SYMBIOSIS.

(P23) George P. Kraemer, G. Yunxiang Mao, Jang Kim & Charles Yarish. COMPARISON OF LED AND FLUORESCENT LIGHTING IN THE CULTURE OF WILD AND GREEN MUTANT STRAINS OF *GRACILARIA TIKVAHIAE*.

(P24) Sarah Redmond, Dana Morse, Charles Yarish, Jang Kim, George Kraemer & Anoushka Concepcion. OPPORTUNITIES AND CHALLENGES FOR THE DEVELOPING SEAWEED CULTURE INDUSTRY IN NEW ENGLAND.

(P25) Lindsay A. Green & Christopher D. Neefus. A COMPARISON OF THE TANK-BASED AQUACULTURE POTENTIAL OF TWO LOCAL SPECIES OF NORI.

(P28) Dale A. Holen. PHAGOTROPHY IN THE SCALED CHRYSOPHYTE *CHRYSOLEPIDOMONAS DENDROLEPIDOTA*.

(P29) Lorraine L. Janus, Gerry Marzec, Rich Van Dreason, Jim Mayfield, & Mark Zion. ALGAL BLOOMS AND THEIR MANAGEMENT IN NYC RESERVOIRS.

ABSTRACTS

Oral Presentations (In order of presentation)

(C= Contributed; I = Invited; WA= Wilce Award Candidate; UP= Undergraduate President's Award Candidate)

Session I

(1 WA) DINOFLAGELLATE SYMBIONTS OF THE CORAL *STYLOPHORA PISTILLATA* INCREASE DEPENDENCE ON PHOTOSYSTEM II REPAIR WHEN ACCLIMATED TO HIGHER LIGHT LEVELS. Jennifer A Jeans¹, Mia Hoogenboom², & Douglas A Campbell¹. ¹Mount Allison University, Sackville NB Canada, ²James Cook University, Townsville, QLD, Australia.

Scleractinian corals maintain a symbiosis with photosynthetic dinoflagellates (*Symbiodinium*) which is vital to reef growth and productivity. When *Symbiodinium* are exposed to high irradiances, they must up-regulate the rate of photosystem II repair to counter increased photoinactivation of photosystem II or they will fall into net photoinhibition, potentially leading to expulsion from the host (coral bleaching). We examined *Symbiodinium* Photosystem II function to determine the effect of the external light environment of the coral on the repair cycle of photosystem II. Colonies of *Stylophora pistillata* were collected from moderate light environments on the Lizard Island reef (Queensland, Australia) and transported to a field station where they were assigned to high or low light regimes for two weeks. Following this photoacclimation, the low-light acclimated corals showed greater symbiont density, greater chlorophyll per symbiont cell, and a lower maximum photosynthetic yield than high-light acclimated corals. At the end of the two-week acclimation period, the corals were treated with lincomycin (an inhibitor of chloroplastic protein synthesis) and exposed to the same high light treatment to isolate the effect of *de novo* protein synthesis in PSII repair. Both high-light and low-light acclimated corals showed a decline in maximum quantum yield of photosynthesis and PSII protein content (PsbA) in the presence of lincomycin. These lincomycin effects were greater in the high-light acclimated corals, which therefore showed increased reliance on the PSII repair cycle.

(2 WA) PHYLOGENETIC RELATIONSHIPS AMONG DIFFERENT POPULATIONS OF FRESHWATER BROWN ALGAE *HERIBAUDIELLA FLUVIATILIS* AND *BODANELLA LAUTERBORNI*. Xian Wang^{1,2}, John D. Wehr¹, & Kenneth G. Karol². ¹Biology department, Fordham University, Bronx, NY, 10458, U.S.A.; ²The Lewis B. and Dorothy Cullman Program for Molecular Systematics, The New York Botanical Garden, Bronx, NY, 10458, U.S.A.

Of an estimated 2,000 brown algae species (Phaeophyceae), less than 1% occur in freshwater habitats. Freshwater brown algae have been known for more than 150 years, but the phylogenetic relationships and taxonomic placement of some species remains unclear. Currently, there are no comprehensive molecular phylogenetic studies of freshwater brown algae, which would provide additional insight into evolution within this class. This study aims to resolve the phylogenetic positions and better understand the relationships among populations of the freshwater brown algae *Heribaudiella fluviatilis* (Areschoug) Svedelius (1930) and *Bodanella lauterborni* Zimmermann (1927). *Heribaudiella fluviatilis* has been reported in Europe, Asia, and North America, and *B. lauterborni* has been found only in Europe.

Although quite different morphologically, these two species were found to be relatively similar genetically. Variable regions from the organellar genomes of these two species were selected as molecular markers to compare different individuals of *H. fluviatilis* collected from North America and from Europe, and *B. lauterborni* from Europe. Phylogenetic relationship generated using both mitochondrial and plastid markers support *H. fluviatilis* from North America as sister to *B. lauterborni* from Europe, and *H. fluviatilis* from Europe sister to these. Three possible taxonomic conclusions inferred from this result will be discussed, including: (1) although *B. lauterborni* is morphologically distinct from *H. fluviatilis*, the *B. lauterborni* lineage and the two *H. fluviatilis* lineages might represent different phenotypes of one polymorphic species (*H. fluviatilis sensu lato*); (2) these lineages might represent three distinct species within *Heribaudiella*; (3) these three lineages might each warrant separate generic status (*Bodanella*, *Heribaudiella*, and *gen. nov.*).

(3 WA) ASSESSMENT OF THE RED ALGAL ORDER RHODYMENIALES USING A MULTIGENE PHYLOGENETIC APPROACH. Gina V. Filloramo & Gary W. Saunders. Centre for Environmental & Molecular Algal Research, Department of Biology, University of New Brunswick, Fredericton, NB E3B 5A3, Canada.

The Rhodymeniales was established by Schmitz (1889) to include florideophycean taxa that were procarpic (i.e. having the carpogonium in close proximity to the auxiliary cells from which the zygote develops following fertilization). Since the order's inception, analyses of vegetative and reproductive characteristics have resulted in numerous taxonomic revisions and extensive suprageneric systematic changes throughout the early to mid 1900's. Despite its utility, morphology-based classification also has a variety of limitations and shortcomings, including its highly subjective nature. This has resulted in the increased use of molecular tools, which enable more objective investigations into red algal systematics and evolution. The first molecular phylogenetic assessment of the Rhodymeniales employed the small subunit ribosomal gene, which confirmed monophyly for the order but failed to resolve most of the infraordinal relationships (Saunders et al. 1999). More recently Le Gall et al. (2008) combined large subunit ribosomal and elongation factor2 sequences to resolve the six families that are currently recognized within the order, viz., Rhodymeniaceae, Lomentariaceae, Champiaceae, Faucheaceae, Hymenocladaceae and Fryeellaceae. The combination of more taxa and additional sequence data in their study provided increased phylogenetic resolution and evolutionary insight, although some aspects of rhodymenialean relationships remain poorly resolved. The objective of the current study was to reassess rhodymenialean systematics with a more robust multigene dataset of plastid, mitochondrial and plastid markers. Taxa included in this study represented ~80% of the recognized genera of the Rhodymeniales making it the most comprehensive phylogenetic study of this order to date. Preliminary results will be discussed with particular emphasis on the systematic affiliations of taxa whose family-level assignments are currently unclear. Overall, this study aims to improve phylogenetic resolution among the major lineages of the Rhodymeniales for a greater understanding of the group's evolutionary history.

(4 WA) ORGANISM-ENVIRONMENT INTERACTIONS IN NATURAL ASEXUAL POPULATIONS OF *PORPHYRA UMBILICALIS* KÜTZING RHODOPHYTA. Renée Eriksen, Lindsay A. Green, & Anita Klein. Department of Biological Sciences, 46 College Road, University of New Hampshire, Durham NH 03824-2618, U.S.A.

Because plants are non-motile, those that live in marginal or unusual environments must adjust their physiology to cope with environmental change either by acclimating or adapting to various stress factors. *Porphyra umbilicalis* Kützing (Rhodophyta) is a highly stress tolerant species of marine macroalga that most often lives in the upper intertidal regions of open-coastal rocky shores, but can also be found in estuarine tidal rapid sites along the NW Atlantic coast. In the NW Atlantic, populations are not known to reproduce sexually. Two stress factors that *P. umbilicalis* from open-coastal and estuarine habitats experience are differential nutrient loads and salinity. Using EST-SSR markers, we have identified considerable genotypic variation within and among populations in the Gulf of Maine. By assessing ammonium uptake rates and chlorophyll fluorescence measurements under varying salinity levels, we have identified populations that differ in physiological responses to these specific abiotic stress factors. We have also used RNA-seq technology to describe differential gene expression patterns among open-coastal and estuarine populations in order to formulate hypotheses about the expression of specific genes related to ammonium uptake and low salinity tolerance. These hypotheses will next be tested among population-specific genotypes in culture under controlled environmental conditions. My goal is to elucidate organism-environment interactions by describing the mechanisms by which this species acclimates or has adapted to specific abiotic stress factors that are experienced in marginal or unusual habitat.

(5 WA) CYST FORMATION IN HETEROSIGMA AKASHIWO, RAPHIOPHYCEAE, DURING INFECTION WITH HaV. Jennifer E. Dingman & Dion G. Durnford. Department of Biology, University of New Brunswick, Fredericton. NB E3B 5A3, Canada.

Heterosigma akashiwo belongs to a small group of nuisance or harmful algae, Raphidophyceae. In large blooms, raphidophytes can cause toxicity in sea urchins, oysters and finfish, possibly leading to death. This group is especially dangerous because three marine genera, *Heterosigma*, *Chattonella*, and *Fibrocapsa* have two life history phases: a vegetative and a cyst phase. In the vegetative phase, cells are metabolically active and free swimming, often recognizable by visible red or brown blooms in the water column. Conversely, cysts or resting cells are non-motile and can reside in the sediment for many months. *Heterosigma* is unique because it does not require a long mandatory dormancy period (<2 weeks) before cysts germinate into vegetative cells, allowing them to quickly switch life phases as nutrient, temperature and light availability change. In this study, we examined *Heterosigma akashiwo* cells for cyst formation during cold-dark conditions (known to cause cyst formation) and also during lytic viral infection with HaV. During infection, the majority of *H. akashiwo* cells died and the cells lysed, however, a small but significant proportion survived as vegetative cells or cysts. In the presence of a caspase inhibitor (z-VAD-FMK), cyst formation was delayed or significantly reduced when triggered by cold-dark conditions or HaV infection, respectively. Surviving vegetative cells were immune to future infections with HaV, suggesting an acquired immunity. Conversely, the cysts (after germination) were immediately susceptible to subsequent exposure to HaV. Additionally, when infected cultures were exposed to cold-dark conditions 24 h post infection, the lytic cycle was delayed and cyst formation occurred. When cultures were returned to normal growth conditions, the lytic cycle resumed. Our evidence suggests that cyst

formation may represent a short-term strategy for evading viral infection, a mechanism that likely involves caspases-like enzymes.

(6 WA) OBSERVATIONS ON THE LAMINARIACEAE IN THE BAY OF FUNDY, WITH EMPHASIS ON *SACCHARINA GROENLANDICA*. Caroline Longtin & Gary W. Saunders. Centre for Environmental & Molecular Algal Research, Department of Biology, University of New Brunswick, Fredericton, NB E3B 5A3, Canada.

Until recently, only two members of the Laminariaceae were reported from the Maritime Provinces of Canada (*Saccharina latissima* and *Laminaria digitata*); however, a third species, *Saccharina groenlandica*, was revealed using molecular techniques. *Saccharina groenlandica* can display either a digitate morphology (similar to *L. digitata*) or a non-digitate morphology (similar to *S. latissima*). As a result of this morphological variation and likeness to both of the Atlantic species, *Saccharina groenlandica* has gone undetected and has been incorrectly lumped with either *S. latissima* and/or *L. digitata* in ecological studies of these two latter species in our region. We have determined that *S. groenlandica* typically displays the digitate morphology in the Bay of Fundy, while the non-digitate phenology is very rare (9% of total *S. groenlandica*). *Saccharina groenlandica* is most abundant at moderately exposed and wave-exposed sites, and predominantly absent from sheltered sites. We also observed that *S. groenlandica* was twice as abundant as *L. digitata* in the Bay of Fundy, when averaged across all wave exposures and years. However, we noticed a decrease in abundance of *S. groenlandica* in 2012 compared with 2010 and 2011. We have also studied the Laminariaceae (*S. groenlandica*, *S. latissima* and *L. digitata*) community composition at sites of differing fetch distances to establish distribution patterns. The kelp communities observed at similar fetch distances had similar composition, with sites of greater fetch distances having a high abundance of digitate individuals (*S. groenlandica* and *L. digitata*), while sites with lower fetch distances were mainly composed of *S. latissima*. We are currently studying the seasonality and phenology of all three kelp species as previous reports, especially for *L. digitata*, will be based on data from more than one species.

Session II

(7 WA) USING MOLECULAR TOOLS TO RESOLVE THE *NEOSIPHONIA JAPONICA*/ *NEOSIPHONIA HARVEYI* SPECIES COMPLEX IN NEW ENGLAND. Amanda Savoie & Gary W. Saunders. Center for Environmental & Molecular Algal Research, Department of Biology, University of New Brunswick, Fredericton, N.B., E3B 5A3, Canada.

Since 2007 we have collected five plants from Rhode Island that are a genetic and morphological match to *Neosiphonia japonica*, indicating that this species has been introduced to the Northwest Atlantic. In Japan, *N. japonica* is often epiphytic on *Grateloupia turuturu*, an invasive species that was introduced to Rhode Island through ballast water or hull fouling and is now established from Long Island Sound to the Gulf of Maine. Interestingly three of our collections of *N. japonica* from New England were found growing on *G. turuturu* possibly indicating a co-introduction. *Neosiphonia japonica* may have been overlooked by researchers because it is closely related to the native species *Neosiphonia harveyi*. In fact, there have been conflicting reports in the literature in reference to these two species. McIvor et al. (2001) concluded that these two species were conspecific using *rbcL* sequences and breeding experiments.

However, in 2006, Kim and Yang published contrary conclusions using *rbcL* and *cpeA/B* sequences. Their results indicated that *N. japonica* and *N. harveyi* were separate, although closely related, species. To provide additional insights into this ongoing debate and to resolve this complex for Northeastern North America, we have sequenced COI-5P and ITS for all five collections of *N. japonica* from Rhode Island, as well as for 32 collections of *N. harveyi* from New England and New Brunswick, Canada. We have also sequenced COI and ITS for six collections of *N. japonica* from Korea and Australia (where it is likely also introduced). COI sequence data indicate that *N. japonica* and *N. harveyi* are genetically distinct, however, our ITS sequence data indicate that these two species are hybridizing in New England, between Cape Neddick, Maine and Fort Wetherill, Rhode Island.

(8 WA) INVASION OF THE RED ALGA *HETEROSIPHONIA JAPONICA* IN THE WESTERN NORTH ATLANTIC OCEAN. Christine Newton¹, Matthew E.S. Bracken¹, Megan McConville², Katherine Rodrigue², & Carol S. Thornber². ¹Marine Science Center, Northeastern University, Nahant, MA, U.S.A.; ²University of Rhode Island, Kingston, RI, U.S.A.

Native to the western North Pacific Ocean, the red alga *Heterosiphonia japonica* has recently invaded the western North Atlantic Ocean. Initial reports in 2007 and 2009 limited the geographic range of this invader to Rhode Island, however, through subsequent subtidal surveys, we have extended the invaded range of this species to include a continuous distribution from Maine through New York, USA; a distance of over 700 km and spanning a well-known biogeographical barrier at Cape Cod, Massachusetts. Despite unique community structures north and south of Cape Cod, we found *Heterosiphonia* at all but two of 31 sites surveyed in both biogeographic provinces, where it comprised, on average, 14% of the subtidal macroalgal benthic community. However, the invader comprised nearly 80% of cover at some locations, and our data suggest that this invader is capable of rapid expansion over broad geographic ranges. We found a significant negative correlation between species richness and *Heterosiphonia* abundance across sites, suggesting that *Heterosiphonia* may be causing distinct changes in subtidal community structure. In addition, drifting *Heterosiphonia* is frequently deposited on beaches, where it can comprise up to 65% of the intertidal wrack biomass; this has created a public nuisance due to its accumulation and subsequent decomposition. From the temperature and salinity tolerances of genetically identical European populations of *Heterosiphonia*, we believe this alga has the potential to invade coastal communities from Florida to Newfoundland in the western North Atlantic. Furthermore, based on our work to characterize its ecological interactions, *Heterosiphonia* has the potential to greatly impact subtidal communities in which it becomes established.

(9 WA) EVALUATING THE GENETIC DIVERSITY OF *CODIUM FRAGILE* IN THE NW ATLANTIC. Chris Benton¹ & Anita Klein^{1,2}. ¹Molecular, Cellular and Biomedical Sciences, ²Department of Biological Sciences, Rudman Hall, 46 College Road, University of New Hampshire, Durham NH 03824-2618, U.S.A.

Codium fragile subsp. *fragile* (Suringar) Hariot was first observed in Long Island Sound in the 1950's, and spread to the Gulf of Maine and the Canadian Maritime Provinces. Our initial studies identified two chloroplast haplotypes in populations of *C. fragile* from Malpeque Bay Prince Edward Island (PEI); these populations previously were described as having two distinct morphotypes (Hubbard and Garbary 2002). These observations lead to two alternate hypotheses: The 2nd haplotype in PEI represents an independent

introduction of *Codium* in the NW Atlantic; or the alternate morphotype results from the accumulation of somatic mutations in an asexual lineage of *Codium fragile* in situ. To distinguish between these alternatives we have developed nuclear markers for *C. fragile*. In order to have access to nuclear gene sequences, we constructed a partial transcriptome using RNA seq. This library yielded 163 million reads averaging 93 bp that were assembled into 129,000 contigs. To distinguish cDNAs that are most likely associated with *Codium* genes rather than *Codium* epiphytes and endophytes, the contigs were examined by BLAST analysis against the NCBI non-redundant protein database, and two *Bryopsis* EST libraries provided by Heroen Verbruggen (University of Melbourne) and Gwang Hoon Kim (Kongju National University). From the BLAST matches, several hundred microsatellite and SNP-containing contigs were analyzed for PCR primer design; of the 49 primer pairs we constructed, two amplified polymorphic loci. These two microsatellite markers as well as the previously mentioned chloroplast polymorphism appear to distinguish some Malpeque Bay PEI populations from other populations in the Northwest Atlantic. These new markers will be used to survey additional PEI and NW Atlantic populations of *Codium fragile* for evidence of genetic variation.

(10 WA) POPULATION GENETIC ANALYSES CONFIRM THE INTRODUCTION OF CERAMIUM SECUNDATUM (CERAMIACEAE, RHODOPHYTA) TO RHODE ISLAND. Meghann Bruce & Gary W. Saunders. Centre for Environmental and Molecular Algal Research, Department of Biology, University of New Brunswick, Fredericton, NB, E3B 5A3, Canada.

Environmental monitoring of marine algal floras is critical to detect biological changes in localized areas of our oceans and for establishing marine conservation priorities. During surveys of the macroalgal flora along the northwest Atlantic coast we discovered a population of *Ceramium secundatum* in Rhode Island, USA. This species is regarded as common and widespread in the northeast Atlantic, ranging from Norway to Morocco, but until now has not been reported from the western Atlantic. Several lines of evidence suggest that *C. secundatum* may be introduced to Rhode Island: 1) despite extensive collecting effort, specimens have only been obtained from a very limited geographic range in the northwest Atlantic; 2) this species is an acknowledged introduction to South Africa and New Zealand (Christine Maggs, pers. comm.); 3) three other non-indigenous seaweed species have been reported for this region, suggesting the area may be an “introduction hotspot”. If *C. secundatum* is indeed introduced, we would expect genetic variation in the Rhode Island population to be low compared to that of populations within its native range. To investigate this we applied population genetic analyses (using the *cox2-3* spacer) to compare genetic variation within the Rhode Island *C. secundatum* population relative to native populations in the Republic of Ireland and the United Kingdom. Collectively, the morphological, biogeographical and molecular data analyzed support the hypothesis that *C. secundatum* is a recent introduction to Rhode Island. The implications of this discovery will be discussed.

(11 UP) PHYSIOLOGICAL RESPONSE TO CHANGES IN SALINITY: AN EXAMINATION OF A BROADLY DISTRIBUTED *CLADOPHORA* IN THE HAWAIIAN ISLANDS. Shaunna R. Kraatz¹, Alison R. Sherwood², & Amy L. Carlile¹. ¹University of New Haven, West Haven, CT, 06515, U.S.A.; ²University of Hawaii at Manoa, Honolulu, HI, 96822, U.S.A.

Cladophora is a widely distributed green alga that is found in both marine and freshwater environments worldwide. Molecular data from the large subunit ribosomal RNA (LSU rRNA) previously obtained from collections throughout the Hawaiian Islands revealed a broadly distributed clade of *Cladophora* that has been collected from freshwater, brackish, and marine habitats. In this study, specimens belonging to this clade were DNA barcoded using the more variable Internal Transcribed Spacer (ITS rRNA) to infer whether members of the clade represent the same species. Analyses of these data revealed multiple clades, likely representing at least two species. With this finer resolution, there remained a clade containing freshwater, brackish, and marine collections. The physiological tolerance of freshwater collections from this clade was tested by culturing samples in 0ppt (control), 15ppt (brackish), and 35ppt (seawater) water. Physiological response to changes in salinity was measured using a combination of pulse amplitude fluorometry (PAM) and photosynthetic oxygen evolution. Growth rate was measured via wet weight. Morphological changes in response to culture medium salinity were evaluated through cell length and width comparisons prior to and after experimental trials. Despite a predicted broad salinity tolerance in this taxon, growth rate and physiological measurements indicated that freshwater collections die in 35ppt salinity exposure and decline, but do not die, in all metrics when exposed to brackish conditions in comparison to freshwater controls. Knowledge of this alga's capacity to respond to changes in salinity is key to understanding its success in habitat shifts, either due to natural dispersal events or habitat alteration (such as stream channelization). Further possibilities for study include exposing *Cladophora* gradually to salt stress to determine the possibility of incremental acclimation and recovery from physiological stress.

Session III

(12 UP) OVERWINTERING STRATEGIES OF *ULVA* SPP. IN NARRAGANSETT BAY, RI. Shelby Rinehart¹, Michele Guidone^{1,2}, and Carol Thornber¹. ¹Department of Biological Sciences, University of Rhode Island, Kingston, RI, 02881, U.S.A.; ²Department of Biology, Sacred Heart University, Fairfield, CT, 06825, U.S.A.

Ulva spp. blooms negatively impact marine coastal organisms, commerce, and recreation. In order to fully understand how *Ulva* spp. blooms begin to proliferate in the spring, we need to understand their overwintering strategies. Previous studies showed that *Ulva* spp. can overwinter as fragments, germlings and/or microscopic propagules. In our study, we examined the winter abundance of *Ulva* species as fragments, germlings, and microscopic propagules on top of and within sediments at multiple bloom-impacted sites in Narragansett Bay, RI. We found that distromatic *Ulva* fragments were present in the water column and the sediment throughout the winter months. The density of fragments in sediment cores did not differ significantly among months or sites, indicating a relatively consistent fragment pool. Settlement tiles placed in the field for varying lengths of time contained distromatic *Ulva* spp., confirming their presence throughout the winter months; however, *Ulva* germlings were significantly less abundant than germlings of other native macroalgal species. Tiles moved from the field and subsequently cultivated

in the laboratory showed that under simulated spring conditions, *Ulva* spp. begin to propagate, suggesting that *Ulva* spp. may be overwintering as microscopic propagules until favorable conditions arise during spring months. Additionally, fragments within the sediments may act as a 'seed bank' during years of reduced propagule recruitment. Our data give increased support to the hypothesis that bloom-forming *Ulva* may utilize multiple reproductive strategies, thereby increasing its chances of survival during harsh winter months.

(13 UP) DETERMINING THE DIVERSITY OF MICROFILAMENTOUS GREEN ALGAE IN PANAMA USING A DNA BARCODING APPROACH. Benjamin Korry¹, Brian Wysor¹, and Charles J. O'Kelly². ¹Department of Biology, Marine Biology & Environmental Science, Roger Williams University, Bristol, Rhode Island, 02889, U.S.A.; ²Friday Harbor Labs, University of Washington, Friday Harbor, Washington, 98250, U.S.A.

Microfilamentous green algae are ubiquitous components of marine floras world wide, where they may serve as microhabitats, food and/or substrata for other organisms. Despite these important roles, they are rarely characterized in floristic accounts of tropical localities, likely due to their diminutive size, need to culture live specimens, and paucity of concrete morphological characters. In an attempt to circumvent these problems, and as part of ongoing marine floristic studies in Panama, microfilamentous green algae isolated from fouled surfaces in Caribbean and Pacific waters were subjected to DNA barcoding. Comparison of 67 *tufA* sequences in UPGMA analysis placed 38 within the microfilamentous green algal family *Ulvellaceae*. Within this family, nine distinct clusters were revealed, only three of which (*Ulvella endozoica*, *U. leptochaete*, and a previously recognized but undescribed species) overlap existing molecular concepts for other species in the family. Four molecular clusters were limited to the Pacific, while three other clusters contained solely Caribbean representatives. The remaining two molecular groups contained identical Pacific and Caribbean genotypes. All of these records represent new distributional records for Caribbean and Atlantic Panama.

(14 UP) DNA BARCODING REVEALS INCREASES IN *CODIUM* (ULVOPHYCEAE: BRYOPSIDALES) SPECIES RICHNESS FOR CARIBBEAN AND PACIFIC PANAMA. Nick Hammerman¹, Brian Wysor¹ & Heroen Verbruggen². ¹Department of Biology, Marine Biology & Environmental Science, Roger Williams University, Bristol, RI, 02809, U.S.A.; ²School of Botany, University of Melbourne, Victoria, 3010, Australia.

Morphological convergence and phenotypic plasticity render species determinations challenging in the green algal genus *Codium* Stackhouse. In order to circumvent these problems, and as part of ongoing studies to elucidate the biodiversity of Panamanian seaweeds, a DNA barcoding approach utilizing *tufA* and *rbcL* gene sequences, was adopted to characterize species richness amongst 43 specimens of *Codium* collected from Caribbean and Pacific Panama. Nine molecular clusters were identified in UPGMA trees based on comparisons of uncorrected p-distances for both molecular markers. Of the four Caribbean clusters identified, two represent species (*C. intertextum*, *C. isthmocladum*) previously reported for Panama, one matches a previously identified cryptic species of *C. isthmocladum* and one has no match to published sequences. Six Pacific clusters were also identified, two of which appear to represent species previously reported for Panama (*C. picturatum*, *C. isabelae*), three of which have no matches to published sequences and two of which match Caribbean *C. isthmocladum*. If

confirmed, the latter specimens would represent the first distributional records of *C. isthmocladum* in the Pacific Ocean, a range expansion that could be facilitated by ship-mediated transport through the Panama Canal or by migratory birds. In general, morphological variation within molecular clusters was minimal, and in some cases congruent with existing species concepts reported in prior floristic surveys.

Collectively these findings suggest an increase in species richness from seven to ten species, with six and four species reported for Pacific and Caribbean coasts, respectively.

(15 C) THE MARINE BENTHIC FLORA OF NORTHWESTERN AUSTRALIA: ADDITIONS TO THE PEYSSONNELIACEAE AND RHIZOPHYLLIDACEAE (RHODOPHYTA). Kyatt Dixon¹, Gary Saunders¹ & John Huisman^{2,3}. ¹Centre for Environmental & Molecular Algal Research, Biology, University of New Brunswick, Fredericton, NB, Canada; ²School of Veterinary and Life Sciences, Murdoch University, Murdoch, WA 6150, Australia; ³WA Herbarium, Science Division, Department of Environment and Conservation, WA 6983, Australia.

Northern Western Australia is home to an expansive and heterogeneous tropical marine environment but its organisms are largely unstudied primarily due to limited accessibility, much of the inshore and offshore coastline and reef systems being very remote and sometimes dangerous. To address this knowledge gap the Western Australian Museum, in conjunction with the Western Australian Herbarium, began an initiative to document the marine life of the Kimberley region, leading in part to the book “Marine Benthic Flora of Northwestern Australia” (Huisman in prep). DNA barcoding and morphological examination of samples from this region have revealed a diverse non-coralline crustose red algal flora. Prior to our sampling, the known Western Australian flora comprised two species of Peyssonneliaceae, *Peyssonnelia novae-hollandiae* Kützing and *Sonderophycus capensis* (Montagne) Wynne, and only one widespread species of Rhizophyllidaceae, the erect *Portieria hornemannii* (Lyngbye) P.C.Silva. We observed 26 species groups (none of which were previously reported from Australia) belonging to six genera of Peyssonneliaceae, *Peyssonnelia*, *Polystrata*, *Sonderophycus*, *Ramicrusta*, *Incendia* and one undescribed genus. Additionally, three species of crustose Rhizophyllidaceae were identified, *Contarinia pacifica* (Børgesen) Denizot, previously known only from its geographically isolated type locality of Easter Island in the eastern Pacific, and two undescribed species. Although these findings increase the known diversity of the region considerably, the presence of under-sampled groups and singletons suggests that the true richness of the area is probably not fully represented by the data at hand.

(16 C) FIRST REPORT OF THE GENUS *YAMADAELLA* (LIAGORACEAE, RHODOPHYTA) IN BERMUDA. Thea R. Popolizio¹, Craig W. Schneider² & Christopher E. Lane¹. ¹Department of Biological Sciences, University of Rhode Island, Kingston, RI 02881, U.S.A.; ²Department of Biology, Trinity College, Hartford, CT, 06106, U.S.A.

As is common with many red algal groups, liagoracean taxa are challenging to identify as they include numerous species and genera with remarkably similar gross morphologies. Almost universally among this family, algae possess a calcified thallus with a dichotomous or subdichotomous branching pattern. The genus *Yamadaella* (Liagoraceae, Nemaliales) was first described by Abbott (1970) and contained only the generitype, *Yamadaella caenomyce* (Descaisne) I.A. Abbott (type locality = Philippines). Originally thought to be restricted the Indo-Pacific, *Y. caenomyce* was later reported by Wynne and Huisman (1998)

from the Caribbean following a morphological investigation of specimens from the Dominican Republic. Using both molecular and traditional methods, we confirm that specimens newly discovered in the intertidal along the eastern south shore of Bermuda Island belong to the genus *Yamadaella*. Our collections represent a new report for the Bermuda Islands and warm temperate Atlantic. Preserved specimens exhibit the inflated, wedge-shaped terminal cortical cells that are archetypal for this genus and allow it to be easily distinguished from its siblings in the Liagoraceae. Phylogenetic sequence analysis clarifies the evolutionary relationship between Bermuda collections and *Yamadaella* from the Indo-Pacific.

Session IV

(17 C) THE *GRACILARIOPSIS ANDERSONII* PLASTID: CONSERVATION IN RED ALGAL PLASTID EVOLUTION. Nicolas A. Blouin, Elizabeth Sullivan & Christopher E. Lane. Department of Biological Sciences, University of Rhode Island, Kingston, RI 02881, U.S.A.

The *Gracilariopsis andersonii* plastid has a rare function in nature. In addition to performing its normal function within *G. andersonii*, it is the subject of serial transfer to reproductive spores of its obligate parasite, *Gracilariophila oryzoides*. The transferred plastid never performs photosynthesis. However, it is hypothesized that the plastid preforms vital functions during spore germination in the parasite. As part of an ongoing project to identify the complete plastid proteome for this host/parasite pair and the mechanism for organellar maintenance, we have sequenced and annotated the shared organelle's genome. The 181,581 bp long genome contains 226 genes that encode 193 proteins, 29 tRNAs, one RNA operon, and a single RNA predicted to have dual transfer and messenger function (tmRNA). Sequence alignments and RNA data from *G. andersonii* indicate that several of the potential open reading frames previously identified in the *Gracilaria tenuistipitata* plastid are not transcribed. Whole genome alignments with *Cyanidioschyzon*, *Cyanidium*, *Porphyra*, and *Gracilaria* demonstrate extensive genome remodeling among the red algae even though large clusters of genes maintain synteny and gene content is conserved. This suggests that there is strong selection within the red algae to maintain the largest gene repertoire among photosynthetic eukaryotes. The low number of nonsynonymous substitutions between the *G. andersonii* and *G. tenuistipitata* plastids in combination with conserved genome architecture suggest that the *G. andersonii* plastid is highly similar to the one that *G. oryzoides* lost during its evolution as a parasite. This high degree of interspecific similarity likely made it possible for *G. oryzoides* to lose its plastid entirely where formerly photosynthetic parasites in other lineages still maintain a reduced plastid in some form. Future analysis of relict nuclear encoded genes involved in plastid biochemical pathways will reveal the extent of parasitic control of the stolen plastid during spore germination.

(18 C) NUTRIENT BIOEXTRACTION VIA SEAWEED AQUACULTURE IN LONG ISLAND SOUND AND THE URBANIZED BRONX RIVER ESTUARIES. Jang K. Kim¹, George P. Kraemer², & Charles Yarish³. ¹Departments of Marine Sciences, University of Connecticut, CT, 06901, U.S.A.; ²Environmental Studies Program, Purchase College, Purchase, NY 10577, U.S.A.; ³Departments of Ecology & Evolutionary Biology, University of Connecticut, CT, 06901, U.S.A.

Nutrient bioextraction using *Gracilaria tikvahiae* and *Saccharina latissima* was tested at two sites: one off Fairfield, CT (LIS) and the other at the mouth of the Bronx River estuary (BRE), during the summer and fall of 2011 and 2012. In Aug. 2011 *Gracilaria* grew up to 11.8% d⁻¹ at BRE and 6.0% d⁻¹ at the LIS site. In July, 2012, the growth rate in BRE was as high as 16.5% d⁻¹. These results, plus tissue nutrient analyses, demonstrate rapid assimilation of nutrients fueling the growth of new *Gracilaria* tissue at the BRE site, while nutrients appeared to limit growth at the LIS site during the summer months. From a hypothetical nutrient bioextraction farm of one hectare with 3 m spacing between longlines, *Gracilaria* at the LIS site could remove 5.0 (Aug.) – 7.9 (Oct.) kg N mon⁻¹, and 9.96 (Oct.) – 41.9 (July) kg N mon⁻¹ at the BRE site. A winter crop, the sugar kelp (*Saccharina*) was farmed at the LIS site during winter 2012. Outplanted juvenile kelp (<1mm) grew as much as 3.0 m in length and yielded 18 kg m⁻¹ longline over five months (Dec.-May). Our hypothetical one hectare nutrient bioextraction sugar kelp farm at the LIS site with 5-10 m spacing between longlines could remove 46-87 kg N ha⁻¹ during that winter-spring growing season. These results suggest that year round seaweed aquaculture can be a useful technique for nutrient bioextraction in urbanized coastal waters, as well as for the production of valuable ancillary materials. Since N removal varies with site and season, seaweed bioextraction might be best applied at nutrient hot spots in LIS and New York estuaries.

(19 C) EXPRESSION OF POSITIVELY SELECTED GENES IN *THALASSIOSIRA PSEUDONANA* SUGGESTS A LINK BETWEEN GENOTYPE AND PHENOTYPE. Julie A Koester¹, Willie J. Swanson², & E. Virginia Armbrust³. ¹Geography and Environmental Science, Mount Allison University, Sackville, NB E4L 1A7, Canada; ²Genome Sciences and ³School of Oceanography, University of Washington, Seattle, WA 98105, U.S.A.

Positively selected genes evolve quickly and are maintained in a population because they confer adaptive advantage upon the individuals that carry them. Seven percent (809) of the genes of the marine planktonic diatom *Thalassiosira pseudonana* are under positive selection. This set is enriched for genes encoding proteins unique to *T. pseudonana*, transcriptional regulators, and protein-binding proteins. A group of genes upregulated under silicic acid and iron limitation is putatively associated with the cell wall and girdle band region of the diatom, which becomes elongated under these stressful conditions. The expressed proteins may function to protect and strengthen the weakened wall structure. The identification of positively selected genes provides the opportunity to test hypotheses in the lab and field to link adaptive phenotypes to the genes that drive them.

(20 C) COMPARATIVE GENOMICS OF FREE-LIVING AND PARASITIC RHODOPHYTE MITOCHONDRIA. Eric Salomaki & Christopher Lane. Dept. of Biological Sciences, University of Rhode Island, Kingston, RI, U.S.A.

Parasitism is a life strategy that has independently evolved countless times throughout the eukaryotic tree of life. Most parasitic lineages are distantly related from a free-living taxon making comparative studies difficult. Rhodophytes provide a unique framework with an evolutionary gradient of parasites and their free-living hosts. These relationships including adelphoparasites, which are only known to infect their closest relative, and alloparasites, which infect more distantly related hosts and are often capable of parasitizing multiple species. Furthermore, the red algal system is unique due to multiple independent origins of the parasitic lifestyle throughout the evolutionary history of the lineage. It is hypothesized that

as an organism becomes a parasite, non-essential genes/gene function will be lost as it begins to rely on a host for energy and nutrition. The mitochondrion (mt), often considered the cellular 'power-plant', produces most of the cellular ATP along with carrying out other cellular functions, making it an ideal location for functional gene loss in parasites. Previous research has shown the loss of the *sdhC* and *atp8* genes of a red algal adelphoparasite in comparison to its free-living sister taxon. Comparisons from four completed free-living mitochondrial genomes (*Chondrus crispus*, *Gracilariopsis andersonii*, *G. lemaneiformis*, and *Vertebrata lanosa*) with that of one completed parasite mt genome (*Gracilariaphila oryzoides*) and an incomplete mt genome (*Choreocolax polysiphoniae*) will be presented.

Session VI

(21 I) DEEP (PHYTO-) INVASION ECOLOGY AND THE ASSEMBLY OF MARINE COMMUNITIES IN HISTORICAL TIME. James T. Carlton. Department of Biology, Williams College, MA and Maritime Studies Program, Williams College - Mystic Seaport, CT. U.S.A.

Marine bioinvasions of coastal communities around the world have significantly altered patterns of plant and animal biodiversity and biogeography in the oceans over the past 150 years. The differential scales of recognition of invasions from the point of view of organism size and historical perspectives are explored, including the "small rule" of invasion ecology, cryptogenic species, and the application of shifting baseline theory to invasion biology. Finally, potential changes to invasion patterns of nearshore marine communities (using New England as a model system) are examined in the light (and heat) of climate change.

(22 I) EUTROPHICATION, RESTORATION, AND ALGAE IN GREAT LAKES COASTAL ECOSYSTEMS. Alan D. Steinman. Annis Water Resources Institute, Grand Valley State University, Muskegon, MI, 49441, U.S.A.

Great Lakes coastal ecosystems have suffered decades of environmental abuse, leaving a legacy of degraded habitat, contaminated sediments, and excessive nutrient loads. Restoration of these ecosystems requires a holistic, integrated approach. Algal communities can serve as excellent bioindicators of ecosystem health.

I review the status of several drowned-river mouth lakes in west Michigan, which connect to Lake Michigan. Spring Lake is a hypereutrophic system with summer total phosphorus and chlorophyll a concentrations averaging 92 µg/L and ~20 µg/L, respectively. An alum treatment has effectively reduced TP but not chl concentrations, indicating that external loads continue to impact this lake. Mona Lake is a eutrophic lake that suffers from both internal and external P loads. The invasive cyanobacterium *Cylindrospermopsis* has been observed in this system, but it does not produce the cyanotoxin cylindrospermopsin. Located just upstream of Mona Lake, former celery fields that have been flooded appear to be a major source of P to the lake; restoration of these fields will reduce P loads to the lake by ~30%. Muskegon Lake is a major commercial port in Lake Michigan, and is undergoing a \$10 million restoration project to re-soften the shoreline and restore wetlands. *Microcystis* dominates the phytoplankton community in most summer and fall months, and microcystin concentrations during bloom periods can exceed 150 µg/L. Similar to Mona Lake, *Cylindrospermopsis* has been observed but is not toxin-producing. Finally, Bear Lake drains into Muskegon Lake, and has very high TP and chl

concentrations, and also harbors non-toxin forming *Cylindrospermopsis*. Internal P loading is low in this shallow, polymictic lake, so external loads appear to be the major source of phosphorus.

A number of restoration activities are underway or planned for these west Michigan coastal lakes.

Success is dependent on a foundation of sound science, funding, community support, and adaptive management.

(23 I) SILICEOUS INVADERS: WHEN THE LEAST AMONG US GO BAD. Mark B. Edlund. St. Croix Watershed Research Station, Science Museum of Minnesota, Marine on St. Croix, MN 55047, U.S.A.

Despite increased awareness and control, invasive algae continue to threaten biodiversity and aquatic resources throughout the world. Among the algae, diatoms present some of the most insidious examples of invasives. Diatoms are readily transported along modified and natural drainages, within ballast, and through "bait bucket" transfer. In the Laurentian Great Lakes, over 15 diatom species have been documented as "introduced", adding to the growing burden of exotic species that have restructured the entire Great Lakes food web. Through analysis of sediment cores, the history of introduction and spread of exotic diatoms is revealed and provides retrospectives on historical periods of enhanced introduction, the pathways of transport and dynamics of colonization, and informs viewpoints on our inability to detect invasive introductions. One diatom that is native to the Great Lakes and oligotrophic high latitude and altitude streams is raising havoc in many regions of the world. *Didymosphenia geminata*, or "Didymo", is the poster child for invasive diatoms. Its appearance in Iceland in the 1990s, New Zealand rivers in the 2000s, and subsequent introduction to Europe, South America, and US streams have led to dramatic changes in high quality stream systems. *Didymosphenia* produces a thick, blanketing mat of periphyton on available substrates that degrades stream aesthetics and negatively impacts biodiversity and important sport fisheries. Linking these examples of diatom invasives are aspects of diatom biology, ecology, physiology, and biogeography that help us understand, predict, and hopefully control the spread of non-native diatoms throughout the world.

Session VII

(24 C) SOME IMPACTS OF AN INVASIVE ALGA (“*HETEROSIPHONIA*” *JAPONICA*) ON INDUSTRY IN LONG ISLAND SOUND. Jim Foertch¹, John Swenarton¹, Don Landers¹, & Deb Pacileo². ¹Millstone Environmental Lab, P.O. Box 128, Waterford, CT 06385, U.S.A.; ²CT DEEP Marine Fisheries, P.O. Box 719, Old Lyme, CT 06371, U.S.A.

Since the initial report of the presence of this alga in the western Atlantic (Rhode Island, 2009), the monitoring program at Millstone Power Station (MPS) in southeastern Connecticut had been anticipating its arrival to local waters. There is still some controversy regarding the generic epithet, but by any name, the alga appeared in January 2011 - attached, in the low intertidal and shallow subtidal at rocky shore sampling sites, and as drift, in our trawl monitoring program. Almost simultaneously, the CT DEEP received material from a commercial fisherman trawling off the Connecticut River (15 km west of MPS), and attached "*H.*" *japonica* was collected at Noank, CT (15 km east). The alga remained present and widely-distributed, but in apparently sparse populations, through 2011. In March 2012, "*H.*" *japonica* was more abundant; moderate quantities were collected in the MPS trawl monitoring program. However, in the 2012 CT DEEP Long Island Sound Spring Trawl Survey (Apr-Jun), very large amounts were collected (up to 170+ kg/tow), fouling nets and decreasing trawl efficiency. Despite the increased abundance (and reports of massive beach loading in CT, RI and MA), MPS experienced no operational challenges until January 2013, when "*H.*" *japonica* drawn into and carried through the power plant's

cooling water systems required extensive maintenance activities to remove material from intake and discharge structures. In the absence of an effective grazer or other control on this invasive alga, future developments will be awaited with interest.

(25 C) BIOTIC INTERACTIONS AND THE SUCCESS OF INVASIONS: BACTERIAL COMMUNITIES IN INVASIVE *VERSUS* NATIVE SPECIES OF ALGAE (*CAULERPA* SP.). Tania Aires¹, Ester Serrao¹, Carlos Duarte², & Sophie Arnaud-Haond³. ¹CCMAR - UAAlg, Gambelas, 8005, Faro, Portugal; ²Department of Global Change, IMEDEA (CSIC-UIB), Miquel Marqués 21, 07190 Esporles, Mallorca, Spain; ³IFREMER- Brest-Iroise BP 70 29280 Plouzane, France.

Biological invasions are one of the greatest threats of ecosystems. Worldwide shipping accelerated these processes in marine systems. Prevention and management involve the identification of sources and mechanisms of key elements facilitating settlement and spread. Interactions with antagonists showed to play a determinant role but interactions with symbionts have been neglected. The invasive algae *Caulerpa taxifolia* and *Caulerpa racemosa* exhibit diverse associated bacteria. We aim to test their stability/change along the invasion and explore their possible contribution to the success in the Mediterranean of these Australian species, while comparing results with the native *C. prolifera*. Bacterial communities from the coexisting *Caulerpa* sp., where characterized through 454 pyrosequencing of 16S rRNA. Highly diverse bacterial community was found, some of which could be obligate symbionts while others can be facultative and/or transient associates. Bacteria characterization in the three *Caulerpa* species in Mediterranean showed that communities are more structured according to species than to locality supporting the tight association between algae and their endophytes. Most representative OTUs were assigned to nitrogen-fixing bacteria capable to perform in anaerobic conditions fitting the sediment upheaval characteristic in locations invaded by *Caulerpa*. Characterization through genetic markers for the two invasive hosts (ITS sequencing and microsatellites) allowed us to compare host population structure with that from bacterial community. Endophytic bacteria emerged as a tool to trace introduction origin and reconstruct dispersal pathways and a possible key to understand mechanisms facilitating invasions. Based on our results we suggest and highlight the advantages of studying algal invaders as a meta-organism including bacterial communities, rather than the eukaryotic species alone, as a requisite for a comprehensive understanding and effective management of biological invasions.

(26 C) CULTURE-BASED STUDIES ON THE CARBONATE MICROBORING CHLOROPHYTE *OSTREOBIUM* (ULVOPHYCEAE, BRYOPSIDALES) REVEAL NOVEL DIVERSITY IN TEMPERATE MARINE WATERS. Charles J. O'Kelly¹, Geneva J. Mottet¹, Sylvain Santoni², & Aline Tribollet³. ¹Friday Harbor Laboratories, University of Washington, Friday Harbor, WA, 98250, U.S.A.; INRA, 2 place Viala, 34070 Montpellier Cedex 1, France; ³Centre IRD France Nord, 32 Avenue Henry Varagnat, 93143 Bondy Cedex, France.

Carbonate-boring algae are significant participants in global biogeochemical cycling; their remobilization of CO₂ from carbonates may contribute to ocean acidification and anthropogenic global warming. *Ostreobium* is common in both temperate and tropical marine waters, always in carbonate substrata and especially abundant in lower-light habitats. Until recently, most collections worldwide were assigned to a single species, *O. quekettii* Bornet & Flahault, 1889, but DNA sequencing studies of *Ostreobium*-containing corals in the Red Sea revealed evidence for several species. In this study, phylogenetic

analyses of *rbcL* gene sequences from 28 cultured *Ostreobium* strains from the temperate waters of Washington and Massachusetts, USA, placed the strains into eight clusters, none of which was closely related to any of the clusters documented from tropical locations. All strains grew in culture at 15°C, but strains from three of the clusters identified in the phylogenetic analyses failed to grow at 23°C. All strains tested bored into carbonate substrata at temperatures permitting growth, and the resulting morphology, as seen in cast preparations, closely resembled morphology in nature. Strains within a cluster shared subtle morphological traits. *Ostreobium* biodiversity in temperate zones, by this measure, is comparable to what has been recorded from tropical waters, and the overlap between temperate and tropical communities is small, despite the ability in culture of some temperate-zone strains to grow, and bore into carbonates, at warmer temperatures. The hypothesis that *Ostreobium quekettii* is a single, globally-distributed species is falsified for temperate as well as tropical waters. Analysis of specimens from western France, the type locality of *O. quekettii*, is required to establish the true identity of this species and facilitate revision of the genus.

(27 C) NEAS KEY V3 THROUGH THE LOOKING GLASS: AN ALTERNATIVE PERSPECTIVE ON SEAWEED DIVERSITY IN THE NORTHEAST AND HOW TO BEST MANAGE AND SHARE THAT KNOWLEDGE. Gary W. Saunders. Centre for Environmental & Molecular Algal Research, Department of Biology, University of New Brunswick, Fredericton, NB E3B 5A3, Canada.

Traditionally scientists have generated floristic lists for a region by examining the outward appearance of individuals. Although appropriate for a variety of organisms, this approach commonly fails for seaweeds. Using contemporary genetic tools researchers are developing a novel appreciation of seaweed diversity in our area, one that stands in stark contrast to the established literature. Such results are exciting during the initial discovery phase, but turn troublesome as researchers struggle to compare the decades of literature pertinent to the biota in an area to the realities of the actual biota present! The Churchill flora will be presented as an example of the conundrum, a small flora for which traditional floristic accounts and contemporary genetic studies realize only ~40% concordance! These results highlight the challenges we face in updating floristic guides for the Northeast. This task could take years to complete and must be produced in a more flexible format than earlier works to accommodate the inherent instability in summarizing biotas owing to ongoing species discovery, introductions and taxonomic corrections. The talk will close with a description of the state and the vision for the NEAS Keys V3.

Poster Presentations

(Board numbers in parentheses; C= Contributed; FTA= Francis R. Trainor Award Candidate; UP= Undergraduate President's Award Candidate)

(P1 FTA) NON-NATIVE *BRYOPSIS MAXIMA* (ULVOPHYCEAE, CHLOROPHYTA) INTRODUCTION TO LONG ISLAND SOUND. Simona Augyte, Louise A. Lewis, & Charles Yarish. University of Connecticut, Department of Ecology and Evolutionary Biology, 75 N. Eagleville Rd. Storrs, CT 06269-3043, U.S.A.

Introductions of non-indigenous marine species (NIS) have increased exponentially in marine ecosystems and pose significant threats to biodiversity by altering local community composition and ecosystem function. New England is particularly vulnerable to the introduction of exotic marine species as many species are at the limits of their distributional ranges. The region is also subjected to a high volume of ship traffic (both commercial and recreational) and shellfish aquaculture providing the mechanism to transport new species into the area. Furthermore, climate change may facilitate the establishment of NIS in New England. The chlorophyte *Bryopsis maxima* Okamura, is a large pseudo-perennial macroalga, native to the western Pacific. This weedy species blooms in the spring and forms great masses growing on solid substrate compared to the modest growth of *B. plumosa* and *B. hypnoides*, the two native species commonly found in LIS. A robust population of an unknown species of *Bryopsis* was found in Waterford, CT and Queens, NY. Our morphological and molecular analyses based on the *psb* gene of the unknown *Bryopsis* species have identified it as *B. maxima*, a native of Japan that has already been found in Virginia. From our initial observations, it appears to grow well under wide range of temperature, salinity and nutrient conditions. The thallus size (> 15 cm) and its occurrence in two very different habitats within the LIS estuary make this NIS of major concern. *Bryopsis maxima* has not yet expanded to inhabit all of LIS, and the rate and extent to which this will occur is unknown.

(P2 FTA) MONITORING THE DISTRIBUTION OF *DIDYMOSPHENIA GEMINATA* AND OTHER “ROCK SNOT” SPECIES IN THE FARMINGTON RIVER IN CONNECTICUT. Diba Khan-Bureau^{1,2}, Mike Beauchene³, Louise A. Lewis¹. ¹University of Connecticut, Storrs, Connecticut, 06269, U.S.A.; ²Three Rivers Community College, Norwich, Connecticut, 06360, U.S.A.; ³Department of Energy and Environmental Protection, Hartford, Connecticut 06106, U.S.A.

Didymosphenia geminata, often referred to as “rock snot” or “didymo” is described putatively as nuisance and invasive. This diatom species produces copious extracellular polymeric stalks that persist even after the cells have died, forming mats that can negatively impact the aquatic organisms within rivers. *Didymosphenia geminata*'s geographical range has expanded throughout the world. Over the past 5 years in the northeastern United States, *D. geminata* has been found in the main stem of The Connecticut River and several tributaries in Vermont, New Hampshire and Connecticut. *Didymosphenia geminata* was confirmed by the Connecticut Department of Energy and Environmental Protection (DEEP) in the West Branch Farmington River in 2011 after a fisherman collected and reported cotton-like tufts attached to rocks. In response the CT DEEP immediately conducted a longitudinal survey within the river system to define the most upstream extent. Additional surveys were conducted confirming the presence of four diatom taxa that produce copious stalks, creating confusion for future visual monitoring. One of the diatoms may be a new species of *Didymosphenia*. Monitoring of invasive species is essential but can be challenging for state agencies. Sharing monitoring efforts with state and local agencies, educational institutions, and NGOs can help alleviate costs and promote a consistent monitoring protocol. Also, shared monitoring efforts can contribute to an educated angler and boating community, provide real world job experience and launch an interest in science for college students, and reduce resource demands on resources management. Faculty from, Three Rivers Community College, the University of Connecticut,

and the CT DEEP have established the **Citizen's River Monitoring Program** to locate and identify these stalk forming nuisance and invasive diatoms in Connecticut.

(P3 FTA) A SYSTEMATIC INVESTIGATION OF THE RED ALGAL ORDER HALYMENIALES (FLORIDEOPHYCEAE, RHODOPHYTA) IN AUSTRALIA. Lesleigh Kraft & Gary W. Saunders. Centre for Environmental and Molecular Algal Research, Department of Biology, University of New Brunswick, Fredericton, NB, E3B 5A3, Canada.

Current taxonomic perspectives regarding the Australian benthic marine red algal flora suffer from a residual bias towards European species, as European references were used to identify most of the flora in the early days of Australian marine Botany. One substantial order of red algae, with an almost ubiquitous presence on Australian coasts, is the Halymeniales. Using the DNA barcode, molecular phylogenetics and traditional alpha taxonomy, the species diversity of this order is being investigated. Cluster analysis of barcode data indicates that our collections have already expanded the order past the known species diversity as represented in the literature. Molecular and preliminary morphological data indicate that both completely novel and overlooked species are contributing to this spike in observed biodiversity. Novel diversity has been found within the genus *Tsengia*, as well as for a species, '*Verona peltiformis*', of a potentially novel Tasmanian genus. Cryptic diversity is prevalent in the morphologically diverse genera *Cryptonemia*, *Grateloupia* and *Halymenia*, while *Carpopeltis*, *Gelinaria* and *Polyopes* also display some cryptic members. The work of accurately describing the morphology of this flora will be important for revising and understanding the unique taxonomic flavor of the region. While much of the enhanced biodiversity found in our study is not immediately assignable to an existing species, we have confirmed a new record for the Japanese *Grateloupia imbricata* in Western Australia. A further finding of our study, based on *rbcL*-derived phylogenies, is that species assigned to the genera *Cryptonemia*, *Grateloupia* and *Halymenia* in Australia do not form monophyletic groups and will require taxonomic revision. The present study will revise and improve appreciation of this complex and beautiful rhodophyte order in Australia.

(P4 UP) INVASION HISTORY AND POPULAR PRESS COVERAGE OF THE RED ALGA *HETEROSIPHONIA JAPONICA* IN THE WESTERN NORTH ATLANTIC OCEAN. Megan McConville¹, Katherine Rodrigue¹, Matthew Bracken², Christine Newton², & Carol Thornber¹.
¹University of Rhode Island, Kingston, RI, U.S.A.; ²Marine Science Center, Northeastern University, Nahant, MA, U.S.A.

A major threat to coastal environments is the introduction and successful invasion of nonnative species, which can drastically alter habitats by displacing or outcompeting native species and reducing biodiversity. A relatively new invader to the New England coast is the red alga *Heterosiphonia japonica*. Native to western North Pacific shorelines of Japan, China, Korea, and Russia, *Heterosiphonia* was first recorded in Brittany, France, in 1984 and has since become widespread along European coastlines, becoming established from Norway to Italy. It has also spread to the western North Atlantic where initial reports from 2007 and 2009 restricted its range to Rhode Island waters. However, we document the progression of *Heterosiphonia* from its initial location in Rhode Island to its current continuous distribution of nearly 700 km from Cape Elizabeth, Maine, through Long Island Sound. It has also been reported in Nova Scotia, Canada. This range expansion over 6 years in the western Atlantic is similar to *Heterosiphonia's* spread rate of approximately 3,000 km in 13 years in European waters. Data from its invaded habitats in Europe suggests that *Heterosiphonia* has the potential to thrive from Newfoundland to Florida in the western North Atlantic. This invasion has the potential to impact the structure and functioning of coastal ecosystems, as *Heterosiphonia* has already been accumulating on local beaches, where it subsequently decomposes causing a public nuisance. Consequently, there has been a substantial amount of recent press on and public interest in the invasion of *Heterosiphonia* and its progress along the coastline.

(P5 FTA) AMMONIUM UPTAKE BY *GRACILARIA* SPECIES FOR POTENTIAL USE IN INTEGRATED MULTI-TROPHIC AQUACULTURE. Katherine Hladki and Christopher D. Neefus. Department of Biological Sciences, University of New Hampshire, Durham, NH 03824, U.S.A.

Aquaculture produces nearly half the world's seafood. Most current aquaculture production comes from monoculture systems that are often associated with negative environmental impacts. Moving aquaculture onto land in recirculating aquaculture systems (RAS) can eliminate some of the negative impacts of aquaculture such as escapes and, but waste removal remains an issue. Integrated multi-trophic aquaculture (IMTA) systems utilize extractive crops such as seaweed to stabilize water quality, and increase economic viability. *Gracilaria* species have the potential to be used in IMTA systems because of their ability to take up waste products such as ammonium and their economic value as an agarophyte and for human food. In New Hampshire two species of *Gracilaria* are present, the native *Gracilaria tikvahiae* (McLachlan) and the introduced *Gracilaria vermiculophylla* (Ohmi) Papenfuss. This study is aimed at determining and comparing the short term ammonium uptake of *Gracilaria tikvahiae* (McLachlan) and *Gracilaria vermiculophylla* (Ohmi) Papenfuss *Gracilaria*. Plants were either collected from the wild or cultivated from wild reproductive material. Species were genetically identified and held in ten gallon aquaria with Von Stosh enriched natural seawater. Before each experiment plants were moved to tanks filled with un-enriched, filtered seawater to acclimate to experimental light levels and a low nitrogen environment. Plant material was measured (fresh weight) and placed in 250 ml flasks. Flasks were filled with filtered seawater spiked with 0, 50, 100, 150, 200, or 250 μM of ammonium using a concentrated stock solution of ammonium chloride. Experiments ran for four hours with samples taken at 0, 1, 2, and 4 hours. Salinity and temperature were maintained at 30ppt and 20° C respectively for all experiments. Initial results will be presented.

(P6 C) MOLECULAR AND MORPHOLOGICAL VARIATION IN SELECTED *PEDIASTRUM* STRAINS. Jacquelyn Schaub, Craig Frysinger & Hilary A. McManus. Department of Biology, LeMoyne College, Syracuse, NY, 13214, U.S.A.

The freshwater green algal genus, *Pediastrum*, is a member of the family Hydrodictyaceae (Chlorophyceae) and has recently been the focus of several molecular phylogenetic studies (Buchheim et al. 2005, McManus and Lewis 2005, 2011; McManus et al. 2011). As a result of these studies, *Pediastrum* was split into six genera: *Pediastrum*, *Pseudopediastrum*, *Parapediastrum*, *Stauridium*, *Monactinus*, and *Lacunastrum*. The molecular data have also revealed cryptic diversity, indicating the need to increase sampling to improve our understanding of the diversity and phylogenetic relationships within the family. Additional strains of *Pediastrum duplex* and *Pediastrum obtusum* were obtained and incorporated into the most recent molecular phylogenetic data set for analysis. The nuclear large subunit rDNA (28S) and chloroplast ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (*rbcL*) gene regions were targeted and analyzed using maximum likelihood phylogenetic inference; strains were characterized morphologically using scanning electron microscopy.

(P7 C) A NEW SPECIES OF *MEREDITHIA* (KALLYMENIACEAE, GIGARTINALES) FROM BERMUDA BASED UPON *KALLYMENIA LIMMINGHEI* MONT. *SENSU* W.R. TAYLOR. Craig W. Schneider¹, Gary W. Saunders² & Christopher E. Lane³. ¹Department of Biology, Trinity College, Hartford, CT, 06106, U.S.A.; ²Centre for Environmental & Molecular Algal Research, Biology, University of New Brunswick, Fredericton, NB E3B 5A3, Canada; ³Department of Biological Sciences, University of Rhode Island, Kingston, RI 02881, U.S.A.

In protected and shaded habitats of Bermuda, we have collected specimens referable to *Kallymenia limminghei* Mont. by W.R. Taylor. This species is illustrated by him in the literature from Bermuda, thus representing the standard for comparison in the western Atlantic by other floristic workers, but unfortunately Bermuda is distant to the type locality in Guadeloupe. Sequences of the COI-5P, LSU

rDNA and *rbcL* genetic markers show them to cluster with *Meredithia* and *Psaromenia* in the Kallymeniaceae (Gigartinales), not with the generitype of *Kallymenia*. Bermudian specimens are also shown to be morphologically distinct from the type of *K. limminghei* and are proposed as a new species, *Meredithia crenata*. Using these collections, as well as numerous undescribed genetic species from the Indo-Pacific, our analyses further show that *Psaromenia* is closely related to *Meredithia*.

(P8 UP) BROWN ALGAL DIVERSITY IN BERMUDA REVEALED USING DNA BARCODING. Alyssa Rogers¹, Thea Popilizio¹, Craig Schneider², Christopher Lane¹. ¹Department of Biological Sciences, University of Rhode Island, Kingston, RI 02881, U.S.A.; ²Department of Biology, Trinity College, Hartford, CT, 06106, U.S.A.

For nearly 60 years there has been very little investigation of the marine algal flora in Bermuda, which is an ideal location for a biodiversity assessment due to its size and location. Residing approximately 1000km off the coast of North Carolina, Bermuda is influenced by the cool water from the north during winter and by the warm water eddies that spin off the Gulf Stream for the much of the other seasons. The Bermuda Seaweed Project aims to extensively survey the marine algal flora in Bermuda and generate morphological and molecular data for all three major groups of macroalgae present. Whereas the focus of the project has thus far been on red algae, data presented here demonstrate similar trends for the brown algae of Bermuda. DNA barcode data were produced for the brown algal samples from the *cox1* and *rbcL* genes of the mitochondrion and plastid, respectively. Phylogenetic trees were produced from the molecular data produced thus far in order to assess the algal diversity, with emphasis on *Padina*, *Dictyota*, and *Lobophora*. Based on initial analyses, it appears that species diversity is considerable, with four separate clades of *Padina* and eight separate clades of *Dictyota*. Interestingly, two clades of *Lobophora* are resolved in our analysis despite a single species (*L. variegata*) being reported for Bermuda. Additional molecular studies as well as morphological examination of preserved samples will be undertaken to clarify the relationships between these and other genera within the brown algae in Bermuda and assign proper taxonomic names where necessary.

(P9 UP) GENETIC ANALYSIS OF A COMMON MARINE CYANOPHAGE STRAIN (RIM12) IN SOUTHERN NEW ENGLAND. Laura Dushkin & Marcie Marston. Department of Biology and Marine Biology, Roger Williams University, Bristol, RI, 02809, U.S.A.

Cyanophages are marine viruses that infect and lyse cyanobacteria, important and abundant primary producers in the marine environment. Cyanophages are extremely diverse and often difficult to classify; nevertheless, conserved marker genes such as DNA polymerase can be used to assign viral isolates to distinct strains. In a two-year study of the diversity of cyanophages in the waters of Southern New England, the dominant cyanophage strain was RIM12 (Rhode Island myovirus 12). It was found in high abundance in water samples from Cape Cod Bay, Vineyard Sound, Block Island Sound, and Narragansett Bay and was present in both winter and summer months. This study focuses on the genetic diversity of multiple genes in over 30 RIM12 isolates from different locations and collection dates. PCR followed by sequence analysis was used to characterize the genetic diversity of core viral genes, host-derived genes and hypothetical genes among the RIM12 isolates. Host range analysis was used in order to examine phenotypic diversity. Although all RIM12 isolates had nearly identical DNA polymerase gene sequences (<1% sequence divergence), RIM 12 isolates differed at other loci. Analyses of hypervariable genetic loci suggest that there may be three different subgroups within RIM12. In addition to nucleotide diversity within the genes, there were also differences in gene content in at least one region of the genome. Some of the isolates contained the host-derived *petE* gene, while other isolates do not appear to have this gene. Isolates also differed in the range of hosts that they could infect, suggesting that some of the genetic diversity among isolates may be ecologically significant. These results show that there can be significant allelic diversity, differences in gene content, and also phenotypic variability within a viral strain.

(P10 C) TESTING THE DIVERSITY OF THE GREEN ALGA *BOTRYOCOCCUS* (TREBOUXIOPHYCEAE). Dana Baltrusitis & Hilary A. McManus. Department of Biology, LeMoyne College, Syracuse, NY, 13214, U.S.A.

Botryococcus Kützing 1849 is a genus of colonial freshwater green microalgae that currently consists of 12 recognized species. The individual colonies are typically spherical, oval or irregularly shaped. *Botryococcus braunii* has been targeted in the biofuel industry because it produces liquid hydrocarbons within the colony extracellular matrix. Though *Botryococcus* is economically valuable, the classification remained dubious (Sayama et al. 1995, Senousy et al. 2004, Weiss et al. 2010) until a recent phylogenetic study supported its placement in the class Trebouxiophyceae (Kawachi et al. 2012). The genetic diversity of the genus, however, remains unclear. This study is focusing on analyzing genes from the nucleus (28S rDNA) and chloroplast (*rbcL*) to capture the diversity of *Botryococcus* species obtained both from culture collections and field samples. Phylogenetic analyses are used to assess the diversity within the genus, and scanning electron microscopy is utilized for morphological characterization.

(P11 FTA) VALVE SHAPE IN *EUNOTIA*: COMPARING MODERN AND FOSSIL FLORAS. Jordan Bishop, Peter Siver, & Anne Lizarralde, Department of Botany, Connecticut College, New London, CT, 06320, U.S.A.

Siliceous microfossils abound in lake sediments deposited in the Giraffe kimberlite diatreme, a Middle Eocene maar situated in the Northwest Territories of Canada. The lake persisted between the time of kimberlite emplacement at 48 Ma and final paludification at 40 Ma, as constrained by $^{87}\text{Rb}/^{87}\text{Sr}$ and fission-track ages. An exploration drill core taken from the crater in 1999 contains 113.1 m of organic sediment, including 44.8 m of peaty material underlain by 68.3 m of stratified lacustrine mudstone, in many places finely laminated, and rich in siliceous microfossils. The Giraffe core contains the oldest known fossil remains of the freshwater diatom genus *Eunotia*, a taxon characterized by lunate-shaped frustules that are asymmetrical in valve view and short raphe slits positioned on the ventral mantle. *Eunotia* is well represented within the core where the lake becomes shallow and acidic. The objective of this study is two-fold. First, to describe the different species of *Eunotia* within the core. Second, to characterize the range in valve shape of the fossil specimens relative to the modern flora. To date, we have uncovered at least ten different fossil species, the majority of which possess valves with simple curved dorsal and ventral margins. We used geometric morphometrics to identify variation in valve shape first among the fossil specimens, and then in relationship to modern species. For our initial analyses, we represented the modern flora by including all *Eunotia* species contained in Patrick & Reimer (1966), which included a wide range of valve shapes, including ones with highly modified dorsal and ventral margins. Based on initial findings, the fossils represent a very small component of the shape space represented by modern species in a relative warp analysis. It is likely that significant changes in valve shape in *Eunotia* have occurred since the Middle Eocene.

(P12 C) GENETIC DIVERSITY OF *SYNECHOCOCCUS* SPP. FOUND IN RHODE ISLAND COASTAL WATERS. Joseph Holbeche & Marcie Marston. Department of Biology and Marine Biology, Roger Williams University, Bristol, RI, 02809, U.S.A.

Synechococcus, a genus of unicellular cyanobacteria, is an important contributor to total primary production in marine environments. This study's main focus is to analyze temporal changes in the genetic diversity and community composition of *Synechococcus* spp. found in Rhode Island's coastal marine waters. Water samples from Narragansett Bay and Rhode Island Sound were collected in May 2012 and September 2012, and January 2013. Total DNA was extracted from the water samples and PCR was used to amplify the cyanobacterial 16S-23S rDNA internal transcribed spacer (ITS) region. PCR products were then cloned; between 30 and 70 clones were sequenced per sample. The phylogenetic relationships of the Rhode Island *Synechococcus* sequences were compared to known *Synechococcus* spp. and the Rhode

Island sequences were assigned to previously identified clades. Our preliminary results show that the genetic diversity of *Synechococcus* spp. in Narragansett Bay was lower in May than in September. In May, the community was dominated by members belonging to a single clade, while in September the sequences fell into at least five different clades. *Synechococcus* diversity in Rhode Island Sound was also high during the month of September with more than seven known clades represented. In addition, we observed differences in *Synechococcus* community composition between the Narragansett Bay and Rhode Island Sound sites. Although both locations contained sequences belonging to some of the same clades, unique clades were observed in Narragansett Bay and in Rhode Island Sound that were not found at the other location. We are continuing to analyze additional water samples to further assess temporal changes in *Synechococcus* diversity and community composition at these locations.

(P13 C) THE PLASTID GENOME SEQUENCE OF THE RED MACRO ALGA GRACILARIOPSIS ANDERSONII. Elizabeth Sullivan, Nicolas Blouin, & Christopher Lane, Department of Biological Sciences, University of Rhode Island, Kingston, RI, U.S.A.

The red algal plastid performs vital functions, like photosynthesis, that are necessary for survival in algae and other plants. Additionally, plastids can biosynthesize amino acids, lipids, and starch. The plastid genome contains a portion of the genes necessary for proper function, with the majority of the genes required having been transferred to the nucleus as part of endosymbiosis. To date, few red algal plastid genomes have been sequenced, resulting in a small reference library available to those who wish to make evolutionary comparison. Here, we have sequenced the plastid genome of *Gracilariopsis andersonii*. This genome is a critical piece of a larger project examining the role of plastid genes in red algal host/parasite interactions. Next-generation sequencing data from *G. andersonii* were mined for pieces of the plastid genome. The published genome *Gracilaria tenuistipitata* was used as a reference for initial assembly, resulting in thirty one assembled pieces (contigs) of the genome. A BLAST database of the remaining sequence reads was constructed to identify fragments that were not shared by the reference genome. After assembly, the genomic contigs were compared to the reference, allowing for a visual comparison with genes and relative placement and orientation. To close gaps between contigs, PCR primers were designed to walk the gaps to closure by sequencing missing data. The completed sequence was then annotated. Data from this genome will expand the understanding of which genes are conserved or under evolutionary selection within the red algae.

(P14 C) LIFE HISTORY, MOLECULAR PHYLOGENY AND TAXONOMIC REVISION OF PLATYSIPHON VERTICILLATUS (PHAEOPHYCEAE). Hiroshi Kawai¹, Takeaki Hanyuda¹, Atsushi Kai¹, Takahiro Yamagishi¹, Gary W. Saunders², Chris Lane², Dan McDevit², & Frithjof C. Küpper³.
¹Kobe Univ., Japan. ²Biology, UNB, Canada. ³Univ. Aberdeen, U.K.

Specimens morphologically referable to *Platysiphon verticillatus* and *Punctaria glacialis* (Ectocarpales *s.l.*) were collected at Baffin Island, Canada and used for molecular phylogenetic and morphological studies including crude culture experiments. All specimens identified for both species had virtually identical DNA sequences for *cox1-5P*, *cox3*, *rbcL* and rDNA ITS, as well as significant vegetative similarities. We therefore conclude that the two taxonomic entities are different developmental stages of a single species (i.e. the young stage of the thallus with flattened basal portion and terete distal portion, and the fully-developed stage losing the terete distal portion). Old foliose thalli had unilocular zoidangia-like structures with TEM confirming the production of flagellated zoids. However, the uni-zoids were not released in culture, but germinated *in situ* forming plurilocular zoidangia-like structures. Each of these walled cells formed several zoids, but their release was not been observed. From these results, we conclude that the species basically has a life history with a reduced generation developing within the unilocular zoidangia. Multigene molecular phylogeny using 8 chloroplast and mitochondrial genes showed that this species is genetically closest to *Halosiphon* and *Stschapovia*, the three genera sharing

many morphological features, and form a lineage sister to the Tilopteridales. We conclude that *Platysiphon verticillatus* is synonymous to *Punctaria glacialis*, and propose the establishment of a new family and order to accommodate this species.

(P15 UP) ELUCIDATION OF POLYMORPHIC MICROSATELLITE MARKERS IN *ULVA RIGIDA* AND *ULVA COMPRESSA*. Matthew Breseman¹, Shennel Gelin¹, Amy Battocletti², Carol Thornber², & JD Swanson¹. ¹Department of Biology and Biomedical Sciences, Salve Regina University, Newport, RI, 02840, U.S.A.; ²Department of Biological Sciences, University of Rhode Island, Kingston, RI 02881, U.S.A.

The macroalgal genus *Ulva* is present in shallow coastal systems worldwide. During the summer months, *Ulva* forms large macroalgal blooms which can have negative ecological and economic impacts on the coastal ecosystem. Of two common *Ulva* species, *U. rigida* and *U. compressa*, only 255 nucleotide sequences have been submitted to GenBank. The aim of our research is to utilize di- and tri- nucleotide repeats found in the genome, known as microsatellites, to create unique fingerprint profiles of *U. rigida* and *U. compressa*. Nine microsatellite primer pairs designed for *U. intestinalis* have been previously found to amplify microsatellite sequences in *U. rigida* and *U. compressa*; however, their polymorphic nature has not yet been determined. We have successfully optimized the annealing temperature for all nine primers by running successive 15 °C range PCR temperature gradients from 47 °C to 62 °C. The optimal temperature was found to be between 47.9 °C and 52.3 °C for seven of the nine primers. To further elucidate additional *Ulva* microsatellite markers, 100mg of extracted *U. rigida* DNA was sent to Washington State University to be sequenced using PacBio third-gen sequencing. We have obtained 5x coverage of the 134 Mbp genome and have completed a primary genome assembly. Currently we are scanning the 10 largest contiguous sequences from the assembled genome for potential microsatellite regions using Msatcomander. We initially intend to order 100 microsatellite primer sets and amplify them with 10 test samples collected during summer 2012 with the aim to identify many additional polymorphic microsatellite markers to fingerprint *U. rigida* and *U. compressa*.

(P16 UP) INVESTIGATING *ULVA RIGIDA* BLOOM FORMATION IN NARRAGANSETT BAY, RI. Amy Battocletti¹, Emily Bishop¹, Tanja Schollmeier¹, Shennel Gelin², Matthew Breseman², J.D. Swanson², Tania Aires¹, Carol Thornber¹. ¹Department of Biological Sciences, University of Rhode Island, Kingston, RI, U.S.A.; ²Department of Biology and Biomedical Sciences, Salve Regina University, Newport, RI, U.S.A.

During the summer months, blooms of the green macroalgal species *Ulva rigida* are a common occurrence in Narragansett Bay. *U. rigida* has a biphasic, isomorphic lifecycle that includes sexual reproduction via the syngamy of gametes, but may also reproduce clonally. It is unknown which form of reproduction plays a primary role in bloom formation. During the summer of 2012, we conducted repeated surveys to quantify algal density and the presence or absence of holdfasts on *U. rigida* at Chepiwanoxet Point, Warwick, Rhode Island. The mean biomass increased 465% from 32.74g/m² wet mass in early May, to 601.55g/m² in early June, followed by a decline of 98% to 13.21g/m² in early July. These data indicates a bloom event in early June; of the blades collected in June, 97% of them lacked a holdfast. These data indicate that during bloom formation, *U. rigida* likely reproduced clonally via vegetative fragmentation. Comparisons of genotypes will allow us to derive ploidy data and to compare the proportion of clones versus distinct individuals, indicating the reproductive strategies used. We stored samples for genotyping, and microsatellite marker analyses are currently being developed. Polymerase chain reaction using the successfully optimized marker U1 has produced fragments of the same base pair length in all samples tested. These results likely indicate that either U1 is monomorphic in this population or that the blades are genetically identical and either haploid or homozygous diploid. Our ongoing research is investigating these issues via additional microsatellite markers.

(P17 FTA) DEVELOPING A PROTOCOL FOR ANALYSIS OF ALGAL CELLS USING FLOW CYTOMETRY. E. Bishop¹, E. E. Potter¹, J.D. Swanson², & C. S. Thornber¹. ¹Department of Biological Sciences, University of Rhode Island, Kingston, RI 02881, U.S.A.; ²Department of Biology and Biomedical Sciences, Salve Regina University, Newport, RI 02840, U.S.A.

Narragansett Bay, RI experiences macroalgal blooms composed mostly of *Ulva compressa* and *Ulva rigida* in the summer months. The bloom-forming genus *Ulva* has an isomorphic, biphasic lifecycle and do not exhibit any morphological differences between ploidy levels. Data on the population structures of these species, in combination with temperature and salinity readings, are key to predicting pre-bloom conditions. By developing a protocol for analyzing algal cells with flow cytometry, we will examine the ploidy levels of *U. compressa* and *U. rigida* populations from three sites in Narragansett Bay, RI. By testing multiple methods of homogenizing blades, and using different types of nuclear buffer, we are working to refine a protocol for preparing tissue samples for flow cytometry. Our results show a varied quality of sample preparation, and more testing needs to be done to generate concrete results. By further refining our protocol and continuing to sample individuals from these sites, we will better understand community dynamics in Narragansett Bay and predict pre-bloom conditions in *Ulva* species.

(P18 FTA) EFFECTS OF AGRICULTURAL BMPs ON PERIPHYTON COMMUNITIES AND NUTRITIONAL QUALITY IN STREAM ECOSYSTEMS. Sarah B. Whorley & John D. Wehr. Louis Calder Center Biological Field Station - Fordham University 53 Whipoorwill Rd. Armonk, NY 10504, U.S.A.

Agricultural disturbances can negatively affect freshwater periphyton communities. Macroinvertebrates and fish depend on periphyton communities for essential fatty acids necessary for development and reproduction and are also be negatively affected by agricultural disturbances. Periphyton are the sole-source of fatty acids and are in limited supply in terrestrial-based leaf-litter. This study explores effects of agriculture and remediation by agricultural best management practices (BMPs) on algae and stream food web stability. We examine how the duration of BMP implementation may affect periphyton fatty acid profiles and community composition in streams within the upper Delaware River watershed, NY, and consider possible seasonal effects. We examined 19 streams in four categories: non-agricultural, agricultural +BMPs established <2 years, agricultural +BMPs established >3 years, and agricultural without BMPs present. Streams were sampled monthly (Jul-Nov 2011). Diatoms dominate periphyton communities; however, some have a significant (greater than 10% of counted diatoms) soft-bodied algal community present. Fatty acid proportions are largely driven by the diatom component of these communities. We expect to observe differences in the proportion of these communities comprised by soft-bodied algae based degree of agricultural mitigation as well as seasonal shifts in proportions. Groups of fatty acid compounds (>18C w3, w6, others) exhibited strong seasonal differences, as did the compound Docosahexaenoic acid (DHA 22:6w3). We also expect to observe differences in the proportion of total fatty acids and specific compounds such as α -Linolenic acid (ALA 18:3w3), Eicosapentaenoic acid (EPA 20:5w3), and DHA relative to the soft-body to diatom composition. Since different stream consumers prefer different types of algae, these results will provide information for how BMPs affect the stream food web base structure and quality.

(P19 C) INDUCIBILITY OF VOLATILE AND NON-VOLATILE COMPOUNDS IN BROWN MACROALGAE AND THEIR EFFECT ON HERBIVORE BEHAVIOR. Ursula S.R. Röse, Kyle Martin, & Janithri Wickramanayake. Department of Biology, University of New England, Biddeford, ME, 04005, U.S.A.

Brown macroalgae *Fucus vesiculosus* are very abundant in the intertidal zones of the coast of Maine despite considerable herbivore pressure. This implies that they may contain defense mechanisms that protect them against herbivore and microbial attack. We investigated the inducebility of compounds in

the alga *F. vesiculosus* in response to directly applied stressors like mechanical injury and plant signaling compounds under field conditions to determine how quickly these defense compounds are synthesized in the algae. We found that extracts of brown algae contained quantitatively and qualitatively different compounds in response to methyl jasmonate and mechanical injury. *F. vesiculosus* synthesized significant amounts of the compounds tocopherol and fucosterol which may have antimicrobial properties or play a role in tissue repair. In headspace collections, we found that *F. vesiculosus* released a significant amount of tribromomethane in response to all treatments. Further, hexadecane is emitted from *F. vesiculosus* and detectable after 1 day post mechanical injury or methyl jasmonate exposure but is not seen in control samples. These compounds may have antibacterial or antioxidant properties. Two-choice bioassays with the gastropod herbivore *Littorina littorea* showed a preference of the periwinkle snails for methyl jasmonate treated fronds. This preference of *L. littorea* is based on water born cues and perhaps additional volatile cues.

(P20 C) COMPETITION BETWEEN TWO BLOOM-FORMING *ULVA* SPECIES UNDER DIFFERENT NUTRIENT REGIMES. Michele Guidone^{1,2}, Tanja Schollmeier², & Carol S. Thornber². ¹Biology Department, Sacred Heart University, Fairfield, CT 06825, U.S.A.; ²Department of Biological Sciences, University of Rhode Island, Kingston, Rhode Island 02881, U.S.A.

In Narragansett Bay, RI, blooms composed of *U. compressa* and *U. rigida* are an annual occurrence. Previous studies determined that *U. compressa* was the superior competitor in environments enriched in both nitrate and ammonium. To further investigate competitive outcomes between these two species, we examined *Ulva* spp. growth across a range of blade densities and four nutrient enriched treatments: ammonium and phosphate; nitrate and phosphate; ammonium, nitrate, and phosphate; phosphate only. In all treatments we found that *U. compressa* grew significantly more than *U. rigida*. Additionally, *U. compressa* grew significantly more in the ammonium-phosphate treatment than in the treatments lacking ammonium. Moreover, the only instance in which *U. compressa* was more impacted by interspecific competition was in the nitrate-phosphate treatment. In contrast, *U. rigida* growth did not differ amongst the treatments containing nitrate and ammonium. These results support previous work that demonstrated *U. compressa*'s competitive superiority in the absence of herbivores. Furthermore, in conjunction with studies that have shown *U. compressa*, but not *U. rigida*, growth can be facilitated by snail nitrogenous wastes, this study supports the notion that this species specific response to snail wastes is due to *U. compressa* having a higher affinity for ammonium than *U. rigida*.

(P21 FTA) TURF WARS: HOW OCEAN ACIDIFICATION IS IMPACTING THE GROWTH AND DIVERSITY OF TROPICAL TURF ALGAL COMMUNITIES. Gordon Ober¹ & Guillermo Diaz-Pulido². ¹Department of Biological Sciences, University of Rhode Island, Kingston, RI, 02881, U.S.A.; ²Australian Rivers Institute, Griffith University, Nathan, QLD, 4111, Australia.

Turf algal communities provide a unique opportunity to study a community on a very small scale. These communities contain morphological and taxonomical diversity that is representative of larger macroalgal communities. As climate change continues to threaten ecosystems worldwide, it is becoming increasingly important to understand how organisms and communities respond. Here, we investigated how turf algal communities respond to stress from increased amounts of pCO₂, representing ocean acidification. Natural turf communities growing on coral rubble from the Great Barrier Reef, Australia were collected and exposed to low, medium, and high pCO₂ treatments in the laboratory. After exposure, we assessed communities for relative biomass and genus diversity. Differences in relative biomass of turf communities was insignificant over the pCO₂ treatments, indicating that turf algae are resilient to acidification stress in terms of density. However, turf community diversity, at the genus level, peaks under intermediate levels of acidification stress. This peak in diversity is also associated with a decrease in cover by the most common and ubiquitous genus, *Polysiphonia*. Our results are part of a larger study investigating pCO₂ impacts on macroalgae living in tropical coral reef habitats.

(P22 C) NATURAL HISTORY OF THE GREEN ALGAE - SPOTTED SALAMANDER SYMBIOSIS. Louise A. Lewis¹, Tobias Landberg², Chien Lo¹ & Andrew Fuller¹. ¹University of Connecticut, Department of Ecology and Evolutionary Biology, Storrs, CT 06269 U.S.A.; ²Murray State University, Watershed Studies Institute, Murray, KY 42071 U.S.A.

Green algae form symbioses with diverse organisms, including fungi, embryophytes, ciliates, invertebrates, and vertebrates. *Oophila amblystomatis* Lambert ex Wille was described in 1909 for green algae that colonize salamander eggs. The symbiotic algae have been shown to provide both oxygen and carbon to the developing salamanders. Recently, an even more intimate association of green algae and their salamander partners was described, where the algae occur inside tissues and even cells of embryonic salamanders. We investigated the natural history of the green algae by testing the hypothesis of their monophyly at three hierarchical levels. Green algae that colonize salamander eggs may vary among eggs of a single egg clutch, broadly across geographic regions in eastern U.S.A., and between different salamander species. Algae from eggs were placed into culture, followed by an examination of their phenotypes using light microscopy. We also obtained chloroplast *rbcL* and nuclear SSU rDNA data from the algae. Across the samples, several algal phenotypes were observed, including non-flagellate and flagellate cells. Our phylogenetic analyses of sequence data from algae isolated from multiple eggs of a single egg clutch show monophyly. However, we recovered six phylogenetic lineages of algae from salamander eggs across the eastern U.S.A., all in order Volvocales, Chlorophyceae. The phylogenetic groups do not correspond to salamander species, morphology, or to geography. In addition to demonstrating a need for taxonomic clarification, our results raise intriguing questions regarding the specificity and evolution of the algal-salamander symbiosis. The life history of these algae remains mysterious but our results suggest a great variety of symbiotic relationships between algae and salamanders have evolved independently.

(P23 C) COMPARISON OF LED AND FLUORESCENT LIGHTING IN THE CULTURE OF WILD AND GREEN MUTANT STRAINS OF *GRACILARIA TIKVAHIAE*. George P. Kraemer¹, G. Yunxiang Mao^{2,3}, Jang Kim³ & Charles Yarish³. ¹Environmental Studies Program, Purchase College, Purchase 10577, NY, U.S.A., ²College of Marine Life Sciences, Ocean University of China, Qingdao 266003, China, ³Ecology and Evolutionary Biology & Marine Sciences, University of Connecticut, Stamford 06901, CT, U.S.A.

As energy costs continue to rise, the financial incentive to conduct efficient research and commercial operations also increases. In support of our field aquaculture operations, we investigated the efficacy of energy efficient LED lighting in driving growth and determining pigment concentration of *Gracilaria tikvahiae*. We used two types of locally collected thalli; a wild strain and a green mutant. The wild strain grew faster under fluorescent lighting (17% d⁻¹) than under pure red, green, or blue LED lighting (14% d⁻¹, 13% d⁻¹, 6% d⁻¹, respectively). While chlorophyll and carotenoid contents were unaffected by light source, phycoerythrin and phycocyanin contents were elevated (50-113%) under blue light. Light source effects on growth rate and pigment content disappeared when primary LED colors were mixed. The growth rates of the wild strain and the green *G. tikvahiae* mutant under fluorescent lighting were statistically indistinguishable. The green mutant grew fastest under fluorescent light (15% d⁻¹) and slower under pure red (13% d⁻¹), green (13% d⁻¹), and blue LED lighting (3% d⁻¹). Chlorophyll concentrations were highest under green and blue LED, carotenoid content was unaffected, and both phycoerythrin and phycocyanin contents were 2-5 times higher under blue LED lighting than other light sources. By 2015, LED sources are predicted to consume 57% and 87% less energy than compact fluorescent and halogen sources over bulb lifetimes. Our results demonstrate that mixed LED lighting can function in support of seaweed growth.

(P24 C) OPPORTUNITIES AND CHALLENGES FOR THE DEVELOPING SEAWEED CULTURE INDUSTRY IN NEW ENGLAND. Sarah Redmond¹, Dana Morse², Charles Yarish³, Jang Kim⁴, George Kraemer⁵, Anoushka Concepcion⁶, ^{1,2}Maine Sea Grant & UMaine Cooperative Extension, University of Maine, Orono, ME 04469, U.S.A.; ^{3,4}Marine Biotechnology Laboratory, Department of Ecology & Evolutionary Biology and Department of Marine Sciences, University of Connecticut, Stamford, CT, 06901, U.S.A.; ⁵Department of Biology & Environmental Studies, Purchase College; ⁶Connecticut Sea Grant, University of Connecticut, Groton, CT, 06340, U.S.A.

A partnership of research, industry, and extension in the Northeast has resulted in successful commercial culture of native seaweed species in Maine and Long Island Sound. Development of nursery culture and grow-out technologies for sugar kelp (*Saccharina latissima*) and *Gracilaria* (*G. tikvahiae*) in the Seaweed Marine Biotechnology Laboratory at the University of Connecticut and the lab and farm of Ocean Approved, LLC, of Portland, ME, has allowed for the establishment of the first commercial kelp farms in the United States, as well as educational, research and commercial farms in Long Island Sound. Technology transfer through collaborative efforts have resulted in new experimental seaweed farms and projects in Maine, New Hampshire, Massachusetts, Rhode Island, Connecticut, and New York, and interest continues to grow as new and existing sea farmers consider the economic and ecological benefits of macroalgal culture. While the potential for a successful seaweed culture industry in the Northeast is substantial, the industry is only in its infancy, and there are still many questions and challenges ahead. The young industry could greatly benefit from the support of the Northeast algal scientific community as they carve a new market onto the American landscape.

(P25 C) A COMPARISON OF THE TANK-BASED AQUACULTURE POTENTIAL OF TWO LOCAL SPECIES OF NORI. Lindsay A. Green & Christopher D. Neefus. Department of Biological Sciences, University of New Hampshire, Durham, NH 03824, U.S.A.

In the Northwest Atlantic, there is growing interest in incorporating seaweed into tank-based recirculating aquaculture systems. *Porphyra umbilicalis* Kützinger is a local species of the economically important red seaweed nori that reproduces only asexually in the Northwest Atlantic making it an attractive candidate. *Pyropia leucosticta* (Thuret) Neefus & J. Brodie is another local species that reproduces asexually and sexually and is closely related to commercially produced nori species. This study aimed to determine the growth rate, photosynthetic efficiency and phycobolin content of *P. umbilicalis* and *P. leucosticta* under different temperatures, light levels, and photoperiods. Independently controlled water baths maintained temperature (10°, 15°, and 20°C), while neutral density filters controlled light levels (200, 100, 60, and 10 $\mu\text{mol photons m}^{-2} \text{s}^{-1}$), and separate growth chambers regulated photoperiods (8:16, 12:12, and 16:8 light:dark). Both species grew best at 10-15°C and above 100 $\mu\text{mol photons m}^{-2} \text{s}^{-1}$ light. *Pyropia leucosticta* had a higher growth rate than *P. umbilicalis* under all conditions (10.17% day^{-1} and 7.06% day^{-1} , respectively, at 10°C). Temperature had a significant effect on growth of *P. leucosticta* ($p=0.0004$) but that effect was dependent on photoperiod for *P. umbilicalis* ($p=0.0081$). Photosynthetic efficiency was negatively affected by increasing light level in both species although *P. leucosticta* had lower efficiency at all light levels. Temperature had a significant effect on phycobolin content in *P. umbilicalis* with R-phycoerythrin (R-PE; $p=0.003$) and R-phycoerythrin (R-PC; $p=0.0123$) content highest at 10°C (2.80 and 1.65 mg g^{-1} FW, respectively). Temperature also had an effect on the R-PE ($p=0.0034$) and R-PC ($p=0.0216$) content of *P. leucosticta* but content was higher at 20°C than all other temperatures (6.48 and 3.17 mg g^{-1} FW, respectively). Overall, *Pyropia leucosticta* performed better than *Porphyra umbilicalis*, exhibiting higher growth rates and phycobolin content despite lower photosynthetic efficiency.

(P26 FTA) IRON LIMITATION EFFECTS A MASSIVE SHIFT IN IRON AND FLAVIN BASED ANTIOXIDANT ENZYME SYSTEMS AND THEIR SUBSTRATES IN THE CHLOROPHYTE ALGA *DUNALIELLA TERTIOLECTA*. Hannah Traggis. Biological Sciences, University of New Hampshire, Durham NH 03824, U.S.A.

Ubiquitous in the neritic ocean, it is now believed that iron-limitation is the most important factor controlling primary production in oceanic phytoplankton. To investigate the effects of iron deficiency, *Dunaliella tertiolecta* was cultured under limiting (100 nM Fe) and replete (1 μM Fe) iron concentrations. The physiological status and the Water-Water antioxidant defense system were evaluated. Iron limitation effected a 21% drop in PSII efficiency (replete= 0.634± 0.012; limiting= 0.507± 0.012) concurrent with a 17.5% reduction in photosynthetic rates (replete= 265.8 μmol O₂/mg chl/hr ± 5.7; limiting= 219.3 μmol O₂/mg chl/hr ± 5.7). Both heme and non-heme based antioxidant enzyme activities were assessed. Heme-based Ascorbate peroxidase (APX), exhibits an 84% iron limited rate reduction (replete and limited = 36.23 and 5.72 μmol ascorbate mg prot⁻¹ hr⁻¹ ±2.96, respectively). Conversely, the flavin-based Monodehydroascorbate reductase (MDHAR), exhibits a significant rate increase, 2.16±0.19 (replete) to 3.86±0.19 μmol NADH mg prot⁻¹ hr⁻¹ under iron-limitation. Iron deficient cultures exhibit a 34% increase in total available ascorbate. These investigations suggest that *D. tertiolecta* is able to maintain a stable growth rate under iron limitation by re-allocating its subcellular usage of available iron and increasing the availability of total ascorbate. Further investigations will determine the presence of additional iron/flavin based molecules involved in the photosynthetic apparatus and anti-oxidant scavenging mechanisms.

(P27 FTA) POSTTRANSCRIPTIONAL REGULATION OF NITROGEN ASSIMILATION IN MARINE DIATOMS – THE ROLE OF RNA-BINDING PROTEINS. Minoli Perera, Jessica Alexander, Sohini Ghoshroy & Deborah Robertson. Department of Biology, Clark University, Worcester, MA 01610, U.S.A.

Posttranscriptional regulation of gene expression in eukaryotes is a complex and dynamic process that involves an extensive repertoire of RNA-binding proteins (RBPs). RBPs form dynamic associations with mRNAs, mediating maturation events in the nucleus and regulatory events in the cytoplasm, including mRNA localization, stability, decay, and translation. Diverse RBPs have been shown to interact with functionally related collections of mRNAs, indicating a multilayered and extensive regulatory system functioning at the RNA regulon level.

The regulation of nitrogen (N) assimilation in marine diatoms is under tight control. While regulation occurs at many levels, we propose that coordinated post-transcriptional regulation of genes encoding N transporters and assimilatory enzymes allows for rapid metabolic response to perturbations in nutrient source and supply and are mediated by changes in mRNA stability. We hypothesize that changes in transcript stability are brought about by RBPs that combinatorially regulate these functionally related mRNAs, consistent with the RNA operon and RNA regulon hypotheses. We identified and analyzed several well conserved RBP families in the genomes of *Thalassiosira pseudonana*, *Phaeodactylum tricorutum*, and *Fragilariopsis cylindrus*. We predict that RBPs will selectively bind to the 3'-untranslated regions (UTRs) of N assimilating mRNAs and that different RBPs will be present under nitrate-replete vs. nitrogen-starved conditions. We cloned and sequenced the 3'UTRs of transcripts for five N assimilating enzymes from *T. pseudonana*, synthesized biotinylated mRNA from the cloned 3'UTRs, and used these in *in vitro* binding assays with protein extracts obtained from *T. pseudonana* cells grown under different culture conditions, in order to pull down specifically bound proteins and examine the RBP profiles. We detected RBPs for all five transcripts. Interestingly, the binding profiles differed between transcripts as well as culture conditions. Future experiments are aimed at identifying the RBPs through protein sequencing and characterizing their functions.

(P28 C) PHAGOTROPHY IN THE SCALED CHRYSOPHYTE *CHRYSOLEPIDOMONAS DENDROLEPIDOTA*. Dale A. Holen. Penn State University, Worthington Scranton campus, Dunmore, PA, 18512, U.S.A.

With increasing frequency phytoplankton traditionally categorized as strict autotrophs are reclassified as mixotrophic because its discovered that they augment phototrophic growth with the uptake of particulate food and thereby contribute to both primary and secondary production.

Chrysolepidomonas dendrolepidota, a photosynthetic chrysophyte with unique scales that cover its flagella and cell body, was observed with ingested green algae while in laboratory culture. To determine the extent of its phototrophic and phagotrophic capabilities this alga was cultured under a variety of conditions of light and food availability. In illuminated cultures *C. dendrolepidota* exhibited a higher growth rate when bacteria were available as a food source regardless of conditions. Its fastest μ (0.65 d^{-1}) was observed when cultured on an inorganic growth medium (DY-V) at $240 \mu\text{E m}^{-2} \text{ s}^{-1}$ with added bacteria. Without added bacteria (although not axenic) the flagellate μ was 0.46 d^{-1} . When bacteria were the only source of N & P in a nutrient deplete medium μ was reduced to 0.41 d^{-1} , approximately 63% of the μ in nutrient replete medium with bacteria. Growth did not ensue in complete darkness or when fed a small green alga. Its estimated grazing rate based upon the uptake of fluorescently-labeled bacteria was $2.2 \text{ bacteria flagellate}^{-1} \text{ hr}^{-1}$. *C. dendrolepidota* is on the phototrophic end of a nutritional spectrum ranging from predominately photosynthetic to predominately phagotrophic mixotrophic algae. As the list of mixotrophic phytoplankton increases it becomes apparent that they may in fact represent a major functional group in pelagic environments and strongly impact trophic dynamics.

(P29 C) ALGAL BLOOMS AND THEIR MANAGEMENT IN NYC RESERVOIRS. Lorraine L. Janus, Gerry Marzec, Rich Van Dreason, Jim Mayfield, & Mark Zion. New York City Department of Environmental Protection. 465 Columbus Ave., Valhalla, NY 10560, U.S.A.

DEP manages the New York City's water supply, providing more than one billion gallons of water each day to more than nine million consumers. This water comes from the Catskill, Delaware, and Croton watersheds that covers approximately 2000 square miles and includes 19 reservoirs. When the reservoirs were newly formed, trophic upsurge and algal blooms led to frequent taste and odor problems that were treated with aeration, chlorination, and copper sulfate. Problematic genera included *Synura*, *Anabaena*, *Dinobryon*, *Tabellaria*, *Asterionella*, and *Chrysophaerella*. In the last 25 years, DEP has invested more than \$1.5 billion in watershed protection programs to maintain filtration avoidance status. Nutrient concentrations have been reduced and algal blooms are much less problematic.

Biography of James T. Carlton

Dr. Carlton is Professor of Marine Sciences and Professor of Biology at Williams College (Williamstown, Massachusetts USA) and Director (since 1989) of the Williams College - Mystic Seaport Maritime Studies Program at Mystic Seaport (Mystic, Connecticut USA). His research is focused on the environmental history of coastal marine ecosystems, including invasions of non-native species (which he began studying in 1962) and modern-day extinctions in the world's oceans. His research sites include the Atlantic and Pacific coasts of North America, the Hawaiian Islands, Argentina, and South Africa. He is founding editor-in-chief of the journal *Biological Invasions*, a Pew Fellow for Marine Conservation, a Fellow of the American Association for the Advancement of Science, a Fellow of the California Academy of Sciences, and has been the Paul Illg Distinguished Lecturer at Friday Harbor Laboratories (University of Washington). He is the only scientist to receive the Interagency Recognition Award from the U.S. Federal Government for his national and international work to reduce the impacts of exotic invasions in the sea. He was Co-Chair of the Marine Biodiversity Committee of the National Academy of Sciences, which produced *Understanding Marine Biodiversity: A Research Agenda for the Nation*. In 2010-2011 he was Chair of the National Academy of Sciences / National Research Council committee advising on setting discharge standards for ballast water to reduce non-native species invasions. Jim recently wrote and edited a monograph on the marine life of the Pacific Coast (*Intertidal invertebrates from Central California to Oregon*, University of California Press, 2007, 1001 pp.). Jim received his undergraduate degree (in paleontology) from the University of California-Berkeley, his Ph.D. (in ecology) from the University of California-Davis, and did his postdoctoral work at the Woods Hole Oceanographic Institution.

Biography of Mark Edlund

Mark Edlund is a Senior Scientist at the St. Croix Watershed Research Station, the environmental field station for the Science Museum of Minnesota. He received his Ph.D. from the University of Michigan studying Russia's Lake Baikal focusing on its diatom diversity, diatom life history strategies, and the environmental history of this ancient lake. His current research continues to focus on large lakes of the world including the North American Great Lakes and Mongolia's ancient and saline lake systems, as well as more typical lakes in the Upper Midwest and Arctic, where diatoms still play a key role in monitoring, documenting diversity, and determining ecological history through paleolimnological analysis. Mark co-teaches the annual *Ecology and Systematics of Diatoms* summer class at Iowa Lakeside Laboratory, which has been offered continuously for fifty years. When he is not playing scientist, Mark enjoys time with family, sharing his passion for the outdoors.

Biography of Alan Steinman

Alan (Al) Steinman has been Director of Grand Valley State University's Annis Water Resources Institute since 2001. Previously, he was Director of the Lake Okechobee Restoration Program at the South Florida Water Management District. Steinman has published over 120 scientific articles and book chapters, has been awarded over \$50 million in grants for scientific and engineering projects, has testified before Congress and the Michigan and Florida state legislatures, and has been invited to speak throughout the world. He serves on a number of scientific advisory boards, including those for the U.S. EPA, the

International Joint Commission, and the University of Notre Dame. Steinman's community service includes serving on the Board of Directors of the Michigan Chapter of The Nature Conservancy, Goodwill Industries of West Michigan, West Michigan Symphony, Community Foundation for Muskegon County, and Congregation B'Nai Israel. Al holds a Postdoctoral Research Fellowship from Oak Ridge National Laboratory, a Ph.D. in Botany/Aquatic Ecology from Oregon State University, an M.S. in Botany from the University of Rhode Island and a B.S. in Botany from the University of Vermont. He takes particular pride in receiving the Best Student Paper Award at the 1983 Northeast Algal Symposium.

