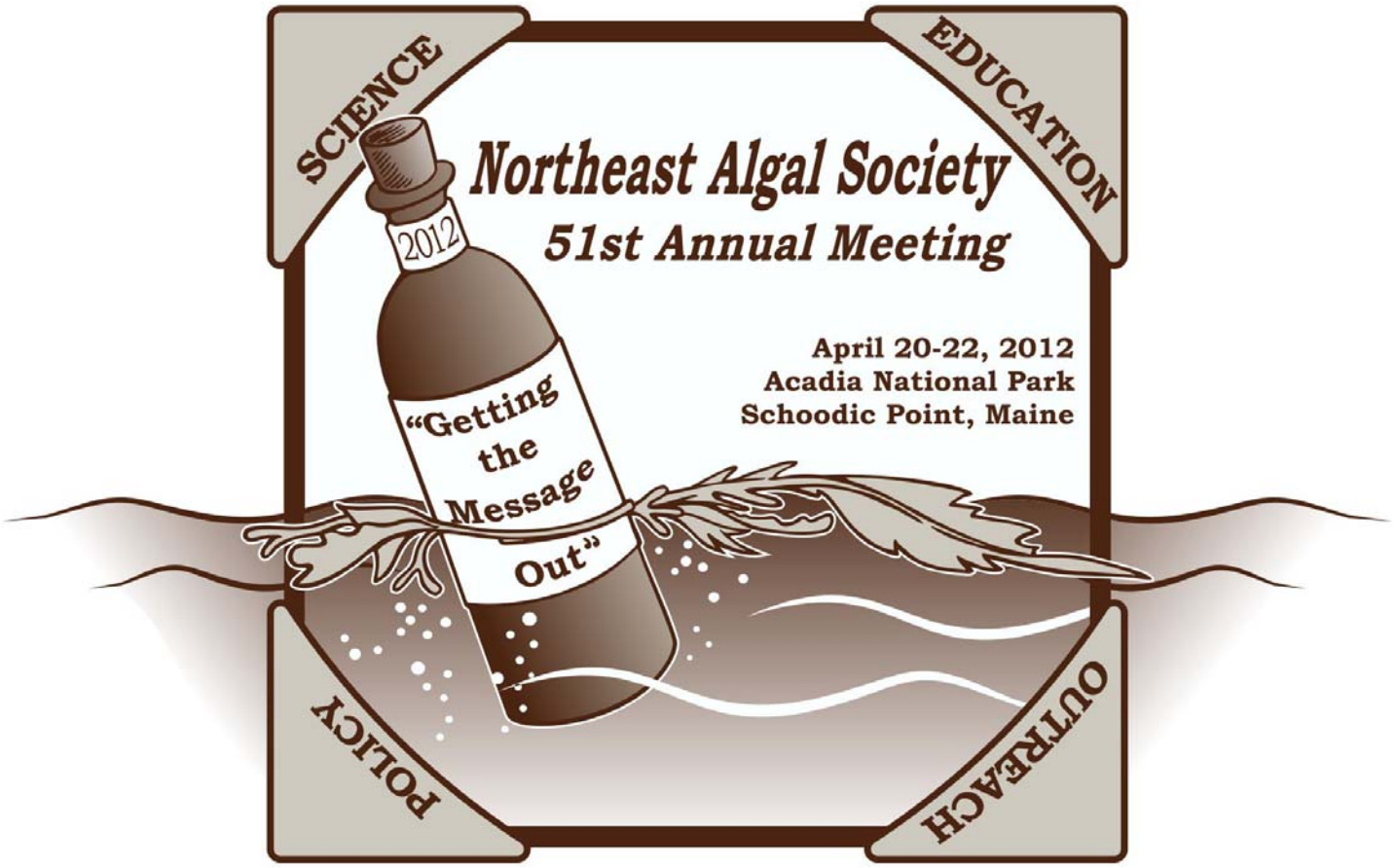
4-20-2012

Northeast Algal Society 51st Annual Meeting

Maine Sea Grant


SCIENCE
EDUCATION
Northeast Algal Society
51st Annual Meeting
April 20-22, 2012
Acadia National Park
Schoodic Point, Maine
2012
"Getting the Message Out"
POLICY
OUTREACH

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Sincere appreciation

The co-conveners acknowledge the generous support of our sponsors for this event, Maine Sea Grant (Paul Anderson) and Maine Coast Sea Vegetables (Shep Erhardt). In addition, Maine Coast Sea Vegetables has also donated sea vegetables to enrich our menu during this NEAS meeting. We thank two undergraduate student volunteers, Amy Smith (Maine Maritime Academy) and Jason Carley (University of Maine) 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), Charley O'Kelly, Naomi Phillips), Trainor Graduate Poster Award Committee (Hilary McManus (Chair), Kyatt Dixon, Steve Di Lonardo, Dan McDevit) and President's Undergraduate Presentation (oral & poster) Award Committee (Anita Klein (Chair), Nic Blouin, Meghann Bruce, Karolina Fučíková, Deb Robertson). We also thank the session moderators: Louise Lewis, David Garbary, Janet Kübler, John Wehr, Carol Thornber, and Thea Popolizio. We are grateful to our mini-symposium leaders: Catherine Schmitt, Abe Miller-Rushing, David Manski and panel participants: Thierry Chopin, Shep Erhardt, Larch Hanson, Sarah Redmond, and Charlie Yarish. We extend sincere gratitude to the staff at W.S. Emerson (Teresa and Rob) for beautifying our logo and SERC Institute, especially Kelley Bernier and Michelle Bierman, for providing logistical support for this meeting.

Welcome to the 51st Northeast Algal Symposium!

We are delighted to welcome everyone to SERC Institute and Acadia National Park. 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 Schoodic Point and take time exploring the trails along the newly-renovated campus. 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 70 combined talks and posters, along with a workshop and panel discussion, the schedule is packed with interesting presentations from locations near and far.

This year's theme is **"Getting the Message Out": gathering resources, exploring techniques, and practicing how to deliver messages to broader audiences.** We have a number of activities centered around this theme. On Saturday afternoon we have a communications workshop for scientists, allowing all to hone communication skills before we talk science with each other during the poster session. Our keynote speaker Sunday morning is **Dr. Nancy Knowlton**. Communications-centered activities following the keynote address include presentations focused on scientific messages to the general public via citizen science and a panel discussion examining the intersections between science and business.

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 before 7:30 am 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 following the poster session Saturday evening to allow the room to be reconfigured for oral presentations on Sunday.

The banquet will include 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! Following the banquet and auction, we invite you to stay and participate in a Maine party staple- a Contra Dance featuring live music provided by the Daub/Schubeck Family Band.

Our meeting will conclude with the annual Business Meeting on Sunday, followed by lunch before we meet again in 2013. Please take time to vote in society elections and consider serving NEAS in an elected role.

Best wishes for a wonderful weekend!

Jessie Muhlin and Karen Pelletreau (*2012 Co-conveners*)

General Program: 51st Northeast Algal Symposium
SERC Institute, Schoodic Point, Acadia National Park

Friday, April 20, 2012

5:00 – 9:00 pm **Evening Registration, Check-in & Auction Donation**
Schooner Commons
Speakers load presentations, Lounge, Schooner Commons
Poster setup, Moore Auditorium

7:00 – 9:00 pm **NEAS Welcome Mixer**
Schooner Commons
Bonfire and ball (weather-permitting)

Saturday, April 21, 2012

6:30 – 8:00 am **Continental Breakfast**
Schooner Commons
Poster setup, Moore Auditorium Breakout Room before 7:30 am

8:00 – 9:30 am **Morning Registration & Auction Donation**
Lobby, Moore Auditorium Breakout Room
Session I speakers load presentations

8:30 – 8:45 am **Welcome and Opening Remarks – Jessie Muhlin and Abe Miller-Rushing**
Moore Auditorium

SESSION I **STUDENT PRESENTATIONS, Moderator: Louise Lewis**
Moore Auditorium

8:45 – 9:00 am *Wilce Award Candidate*
Jennifer E. Dingman, James K. Roherty, Keizo Nagasaki & Janice E. Lawrence. CELL DEATH PROGRAMMES OF THE HARMFUL BLOOM-FORMING RAPHIDOPHYTE, *HETEROSIGMA AKASHIWO*, DURING VIRUS INFECTION WITH HARNAV, HANIV OR HAV.

9:00 – 9:15 am *Wilce Award Candidate*
Sarah Redmond & Charles Yarish. EXPLORING THE IMPACT OF OCEAN ACIDIFICATION AND WARMING ON THE MICROSCOPIC SURVIVAL STAGES OF THE KELP, *SACCHARINA LATISSIMA.*

9:15 – 9:30 am *Wilce Award Candidate*
Gina V. Filloramo & Gary W. Saunders. ASSESSMENT OF CRYPTIC *RHODYMENIA* SPP. (RHODYMENIACEAE, RHODOPHYTA) IN BRITISH COLUMBIA, CANADA: AN INTEGRATIVE TAXONOMIC APPROACH.

9:30 – 9:45 am *Wilce Award Candidate*
Michele Guidone, Shelby Rinehart & Carol Thornber. IMPACTS OF COMPETITION AND HERBIVORY ON THE GROWTH OF TWO BLOOM-FORMING *ULVA* SPECIES IN NARRAGANSETT BAY, RI.

9:45 – 10:00 am *Wilce Award Candidate*
Meghann Bruce & Gary W. Saunders. A COMPREHENSIVE TAXONOMIC REVIEW OF THE RED ALGAL GENUS *CERAMIUM* IN THE NORTHWEST ATLANTIC.

10:00 – 10:15 am *Wilce Award Candidate*
Katelyn White & David Garbary. POPULATION ECOLOGY OF *PALMARIA PALMATA* ON DIGBY NECK, NOVA SCOTIA CANADA.

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

SESSION II **STUDENT PRESENTATIONS, Moderator: David Garbary**
Moore Auditorium

10:45- 11:00 am *Wilce Award Candidate*
Jonathan Neilson & Dion Durnford. RESTRUCTURING OF THE PHOTOSYNTHETIC MACHINERY OF EUKARYOTES DURING PLASTID EVOLUTION.

11:00 – 11:15 am *Wilce Award Candidate*
Elizabeth Sargent, Alex Poulton, Mark Moore, Tom Bibby & Tracy Villareal. ASSESSING THE DIRECT CONTRIBUTION OF *TRICHODESMIUM* TO EXPORT.

11:15 – 11:30 am *Wilce Award Candidate*
Dylan W. Scott & Deborah L. Robertson. EXPLORATION OF THE ROLE OF 3' UTRs IN REGULATING mRNA STABILITY IN THE MARINE DIATOM *THALASSIOSIRA PSEUDONANA*.

11:30 – 11:45 am *Wilce Award Candidate*
Amanda Savoie & Gary W. Saunders INVESTIGATING SPECIES DIVERSITY AND BIOGEOGRAPHY OF *POLYSIPHONIA* (RHODOMELACEAE, RHODOPHYTA) IN BRITISH COLOMBIA USING MOLECULAR TOOLS.

11:45 – 12:00 pm *Wilce Award Candidate*
Caroline Longtin & Gary W. Saunders. OBSERVATIONS ON THE DISTRIBUTION AND PHENOTYPIC EXPRESSION OF THE KELP *SACCHARINA GROENLANDICA* ACROSS A WAVE EXPOSURE GRADIENT IN THE BAY OF FUNDY.

12:15 – 1:30 pm ***Lunch*** **(***Schooner Commons)*
Session III speakers load presentations

SESSION III **STUDENT & CONTRIBUTED PRESENTATIONS**
Moderator: Janet Kübler
Moore Auditorium

1:30 – 1:45 pm *President's Award Candidate*
Shampa A. Panda, Steve Di Lonardo & John D. Wehr. HOW DOES LAKE BIOMANIPULATION AFFECT NUTRITION LIMITATION OF FRESHWATER PHYTOPLANKTON?

1:45 – 2:00 pm *President's Award Candidate*
Ellen C. R. Snyder & Dion G. Durnford. ALTERING THE DURATION OF STATIONARY PHASE IN *CHLAMYDOMONAS REINHARDTII*.

2:00 – 2:15 pm *President's Award Candidate*
Pierre Muhoza, Orly Levitan, Tiago Guerra & Paul Falkowski. CHARACTERIZATION OF ACYL-COA:DIACYLGLYCEROL ACYLTRANSFERASE (DGAT) GENES AND PHYSIOLOGY IN THE DIATOM, *PHAEODACTYLUM TRICORNUTUM,* UNDER DIFFERENT NITRATE CONCENTRATIONS.

2:15 – 2:30 pm *Contributed paper*
Jennifer Burkhardt, Megan Tyrrell, Carol Thornber & Kelly Medeiros. DETERMINING THE ROLE OF SALT MARSH MACROALGAE (ECADS) IN CAPE COD SALT MARSHES.

2:30 – 2:45 pm *Contributed paper*
Thea R. Popolizio, Christopher E. Lane & Craig W. Schneider. EVOLUTION OF THE BERMUDA SEAWEED PROJECT: PROGRESS AND HIGHLIGHTS.

2:45 – 3:00 pm ***Coffee Break***

SESSION IV **COMMUNICATING SCIENCE WORKSHOP**
Workshop facilitator: Catherine Schmitt
Moore Auditorium

3:00 – 4:00 pm **Catherine Schmitt**. OUT OF THE PETRI DISH AND INTO THE PUBLIC SPHERE: A COMMUNICATIONS WORKSHOP FOR SCIENTISTS.

SESSION V	**POSTER SESSION & MIXER** *Moore Auditorium Breakout Room & Lobby*
4:00 – 6:00 pm	**Student and & Contributed Posters** ***Please take down posters by the end of the evening***
6:30 – 9:00 pm	**NEAS Banquet, Awards & Live Auction** *Schooner Commons*
9:00 – 11:00 pm	**Contra Dance and Music** *Schooner Commons*

Sunday, April 22, 2012

6:30 – 8:00 am	**Continental Breakfast** *Schooner Commons*
7:30 – 8:00 am	**Morning Registration** *Lobby*, *Moore Auditorium Breakout Room* ***Session VII A/B speakers load presentations***
8:00 – 8:15 am	**Announcements– Jessie Muhlin** *Moore Auditorium*
SESSION VI	**KEYNOTE SPEAKER, INVITED SPEAKERS & PANEL DISCUSSION** *Moore Auditorium*
8:15 – 9:15 am	**Nancy Knowlton.** GETTING THE MESSAGE OUT: MY 30+ YEAR JOURNEY FROM THE NATIONAL ENQUIRER TO TWITTER.
9:15 – 9:30 am	**Abe Miller-Rushing.** ENGAGING THE PUBLIC IN CLIMATE CHANGE SCIENCE.
9:30 – 9:45 am	**David Manski.** KNOWING WHAT LIVES IN YOUR NATIONAL PARK; EFFORTS TO SURVEY BIODIVERSITY IN ACADIA.
9:45 – 10:15 am	**PANEL DISCUSSION: THE INTERSECTION OF SCIENCE AND BUSINESS IN PHYCOLOGICAL-BASED INDUSTRIES** **Moderator: John Wehr** Panel: Thierry Chopin, Shep Erhardt, Larch Hanson, Sarah Redmond & Charlie Yarish
10:15 – 10:45 am	***Coffee Break,*** *Lobby, Moore Auditorium* ***Session VII A/B speakers load presentations***

SESSION VIIA **CONCURRENT SESSION, *Contributed Papers***
Moderator: Carol Thornber
Moore Auditorium

10:45 – 11:00 am **Brian Beal**, Raul Ugarte & Sean Stoddard. SHORT-TERM EFFECTS OF COMMERCIAL SEAWEED HARVESTING ON ALGAL BIOMASS AND SELECTED ROCKY INTERTIDAL ORGANISMS.

11:00 – 11:15 am **Jang. J. Kim**, George P. Kraemer, John Curtis & Charles Yarish. OPPORTUNITIES FOR SEAWEED CULTIVATION AS AN ESSENTIAL ELEMENT FOR NUTRENT BIOEXTRACTION IN LONG ISLAND SOUND AND BRONX RIVER ESTUARY.

11:15 – 11:30 am Anna J. Schliep, **Susan H. Brawley** & Charles T. Hess. EFFECT OF FUKUSHIMA NUCLEAR ACCIDENT ON MAINE MARINE ALGAE.

11:30 – 11:45 am **Janet E. Kübler**, Steven R. Dudgeon, Rebecca Rudy, P.A. Rudy & Stacy Krueger-Hadfield. TRADE-OFFS OF SEXUAL AND ASEXUAL LIFE CYCLES IN *MASTOCARPUS PAPILLATUS*: AN ECOLOGICALLY KEY SPECIES WITH A COMPLEX LIFE CYCLE.

11:45 – 12:00 pm **Ursula S.R. Röse** & Kyle Martin. MECHANISMS INVOLVED IN THE SYNTHESIS OF INDUCIBLE COMPOUNDS IN THE BROWN MACROALGAE *FUCUS VESICULOSUS.*

12:00 – 12:15 am Lindsay A. Green, **Arthur C. Mathieson,** Christopher D. Neefus, Hannah M. Traggis & Clinton J. Dawes. INTRODUCTION AND EXPANSION OF THE BROWN ALGA *COLPOMENIA PEREGRINA* SAUVAGEAU (SCYTOSIPHONALES) WITHIN THE GULF OF MAINE.

SESSION VIIB **CONCURRENT SESSION, *Contributed Papers***
Moderator: Thea Popolizio
Moore Auditorium Breakout Room

10:45 – 11:00 am **Nicolas A. Blouin** & Christopher E. Lane. RED ALGAL HOST/PARASITE DIFFERENCES IN NUCLEAR CONTRIBUTION TO THE ORGANELLAR PROTEOMES.

11:00 – 11:15 am **Kyatt R. Dixon** & Gary W. Saunders. USING DNA BARCODING TO INVESTIGATE BIOGEOGRAPHY AND EVOLUTIONARY HISTORY IN RED ALGAL CRUSTS.

11:15 – 11:30 am **Karolina Fučíková,** Valerie R. Flechtner & Louise A. Lewis. REVISION OF THE GENUS *BRACTEACOCCUS* TEREG (CHLOROPHYCEAE, CHLOROPHYTA) BASED ON A PHYLOGENETIC APPROACH.

11:30 – 11:45 am **John Wehr,** Kam Truhn, & Alissa Perrone. CHALLENGES AND REWARDS FOR FRESHWATER BIODIVERSITY RESEARCH IN RIVERS OF THE NORTHEAST.

11:45 – 12:00 pm **Brian Wysor**, D. Wilson Freshwater, Noemi Leon, Cindy Fernández-García, Paul Gabrielson, Valerie Charbonneau, Christopher Green, Jennifer Idol & Seth Parham. ALGAL DIVERSITY OF THE BURICA PENINSULA, PACIFIC PANAMA.

12:00 – 12:15 pm **Charles J. O'Kelly,** Geneva J. Mottet, Angela R. Little & Robin Kodner. CULTURE-BASED STUDIES ON THE BIODIVERSITY OF CARBONATE-BORING ALGAE AND CYANOBACTERIA: THE IDENTITY OF *PLECTONEMA TEREBRANS* (OSCILLATORIALES, CYANOBACTERIA).

12:15 – 12:45 pm ***Closing Remarks and General Business Meeting***
Moore Auditorium

12:45 – 1:30 pm ***Lunch***
Schooner Commons

Poster Presentation Summary (By Category)

(Poster No.) Authors/Title (Abstracts can be found on page 30)

Undergraduate Posters (President's Award)

(P4) Joseph Rankin, Lilibeth Miranda & Susan H. Brawley. EXPERIMENTAL ANALYSIS OF BACTERIAL ISOLATES FROM *PORPHYRA UMBILICALIS* KÜTZING (P.um.1) ON GROWTH AND MORPHOLOGY OF BLADE CALLUS.

(P8) Amanda Ziegler, Shelby Rinehart, Michele Guidone, Tanja Schollmeier & Carol Thornber. BLOOM-FORMING *ULVA* SPECIES OVERWINTER PRIMARILY AS FRAGMENTS IN NARRAGANSETT BAY, RI.

(P9) Tanja Schollmeier, Michele Guidone & Carol Thornber. POTENTIAL IMPACTS OF HERBIVOROUS FISH ON *ULVA* BLOOM BIOMASS.

(P10) Kyle Martin & Ursula S.R. Röse. INDUCIBLE DEFENSE COMPOUNDS IN BROWN MACROALGAE.

(P15) Jacob Torok & Kirk Shadle. PROTOCOL DEVELOPMENT FOR SMALL BATCH AGAR EXTRACTION FROM *GRACILARIA TIKVAHIAE.*

(P29) Amy K. Kivela, Craig W. Schneider, Thea R. Popolizio & Christopher E. Lane. A MOLECULAR–ASSISTED ALPHA TAXONOMIC STUDY OF A PUTATIVE *ETHELIA* SP. (PEYSSONNELIACEAE, RHODOPHYTA) FROM BERMUDA.

(P30) Grace Han, Latreasha Andersen, Lucky Niko, Ed Braun & Naomi Phillips. USING PHYLOGENOMICS FOR NUCLEAR LOCI DISCOVERY IN HETEROKONT LINEAGES.

(P31) Tayoot Chengsupanimit, Craig W. Schneider, Thea R. Popolizio, Thomas A. Shamp & Christopher E. Lane. IS *HELMINTHOCLADIA* IN THE WESTERN ATLANTIC REALLY THE SAME AS *H. CALVADOSII* FROM EUROPE?

Graduate Student Posters (Trainor Award)

(P2) Lindsay A. Green & Christopher D. Neefus. GROWTH AND PHOTOSYNTHETIC EFFICIENCY OF *PORPHYRA UMBILICALIS*: A CANDIDATE FOR RECIRCULATING INTEGRATED MULTI-TROPHIC AQUACULTURE.

(P3) Renée L. Eriksen & Anita S. Klein. COMPARISONS OF OPEN-COASTAL AND ESTUARINE POPULATIONS OF *PORPHYRA UMBILICALIS.*

(P12) Sheng Liu , **Zhi-Ling Guo**, Tao Li , Hui Huang & Senjie Lin. PHOTOSYNTHETIC DEPRESSION, CELL VOLUME ENLARGEMENT, AND STABLE ELEMENTAL RATIOS

IN *THALASSIROSIRA WEISSFLOGII* UNDER PHOSPHORUS LIMITATION: REVISIT OF THE UTILITY OF REDFIELD RATIO FOR ASSESSING NUTRIENT LIMITATION.

(P13) Christine Newton, Michele Guidone & Carol S. Thornber . INVASIVE *GRACILARIA VERMICULOPHYLLA* AS A NOVEL SUBSTRATE IN SOFT SEDIMENT BENTHIC COMMUNITIES.

(P14) Vanessa O'Donnell & Steven Zeeman. THE EFFECT OF OCEAN ACIDIFICATION ON THE BINDING CAPABILITIES OF EXOPOLYMERIC SUBSTANCES WITH METALS, OF A MARINE BENTHIC DIATOM, *CYLINDROTHECA CLOSTERIUM***.**

(P18) Sarah B. Whorley & John D. Wehr. EFFECTS OF BMP IMPLEMENTATION ON PERIPHYTON IN AGRICULTURAL STREAMS.

(P22) Lindsay A. Green, **Katherine R. Hladki** & Christopher D. Neefus. GROWTH AND AMMONIUM UPTAKE IN THE RED ALGA *CHONDRUS CRISPUS* (STACKHOUSE) AND ITS POTENTIAL USE IN RECIRCULATING INTEGRATED MULTI-TROPHIC AQUACULTURE SYSTEMS.

(P24) Chris Benton, Anita Klein, Kelley Thomas, Darren Bauer & Feseha Abebe-Akele. EVALUATING THE GENETIC DIVERSITY OF THE NON-MODEL ORGANISM, *CODIUM FRAGILE* IN THE NW ATLANTIC.

(P25) Lesleigh Kraft & Gary W. Saunders. CRYPTIC DIVERSITY WITHIN THE AUSTRALIAN HALYMENIACEAE (HALYMENIALES, RHODOPHYTA).

(P33) Yunyun Zhuang, Huan Zhang & Senjie Lin. POLYADENYLATION OF 18S RIBOSOMAL RNA IN ALGAE.

(P34) Xian Wang, John D. Wehr & Kenneth G. Karol. ORGANELLAR GENOME EVOLUTION OF THE FRESHWATER BROWN ALGA *PLEUROCLADIA LACUSTRIS* A. BRAUN.

(P35) Minoli Perera, Jessica Alexander, Sohini Ghoshroy & Deborah L. Robertson. CHARACTERIZATION OF 3'UTR SEQUENCES OF mRNA ENCODING NITROGEN ASSIMILATING ENZYMES FROM MARINE DIATOMS.

(P36) Jessica Alexander, Minoli Perera, Sohini Ghoshroy & Deborah L. Robertson. IDENTIFICATION AND CHARACTERIZATION OF PUF FAMILY RNA-BINDING PROTEINS IN MARINE DIATOMS.

Contributed Posters

(P1) Lilibeth N Miranda, Keith Hutchison, Arthur R Grossman & Susan Brawley. METAGENOMIC ANALYSIS OF THE BACTERIAL COMMUNITY ASSOCIATED WITH *PORPHYRA UMBILICALIS*.

(P5) Dale A. Holen. THE STOMATOCYST OF *OCHROMONAS* SP., (CHRYSOPHYCEAE) A SMALL MIXOTROPHIC ALGA.

(P6) Katherine Hubbard, Claire Ellis, Emlyn Resetarits, Inci Tüney, E. Virginia Armbrust & Donald Anderson. SEASONAL SUCCESSION IN GULF OF MAINE *PSEUDO-NITZSCHIA* COMMUNITIES.

(P7) Elizabeth Hanlon, Donald Cheney & John Logan. DIETARY CONNECTIONS BETWEEN *FUNDULUS HETEROCLITUS* AND A PCB-CONTAMINATED *ULVA* BLOOM IN NEW BEDFORD HARBOR.

(P11) Mary Cirino, Andrew Bramante, Jang K. Kim & Charles Yarish**.** MAKING FRIENDS WITH A LONG ISLAND SOUND INVASIVE: NOVEL EVALUATION OF KEY RESOURCES OF *GRACILARIA VERMICULOPHYLLA* RELATIVE TO NATIVE *GRACILARIA TIKVAHIAE.*

(P16) Raul A. Ugarte. LARGE SCALE OBSERVATIONS OF ROCKWEED (*Ascophyllum nodosum*) STANDS IN EASTERN CANADA: WHAT CAN WE GENERALIZE FROM SMALL SCALE STUDIES?

(P17) Charles J. O'Kelly & Geneva J. Mottet. CULTURE-BASED STUDIES ON THE BIODIVERSITY OF CARBONATE-BORING ALGAE AND CYANOBACTERIA: THE CULTURE COLLECTION.

(P19) Sarah Redmond, D. Morse, S. Brawley, N. Brown, P. Dobbins, S. Eddy, S. Erhart, P. Fischer, J. Larrabee, T. Levesque, M. Moretti, C. Newell, B. Olsen, V. Olsen, T. Olson & E. Young. DEVELOPMENT OF SEA VEGETABLE CULTURE TECHNOLOGIES IN MAINE.

(P20) Jang K. Kim, Kyle Kovtun, Richelle Stainton & Charles Yarish.EFFECTS OF HYPO-OSMOTIC STRESS AND TEMPERATURE ON THE GROWTH OF *GRACILARIA*.

(P21) Robin Hadlock Seeley & William H. Schlesinger. SUSTAINABLE SEAWEED CUTTING? THE ROCKWEED (*ASCOPHYLLUM NODOSUM*) INDUSTRY OF MAINE AND MARITIME CANADA.

(P23) Anne Marie Lott & Peter A. Siver. MORPHOLOGICAL VARIABILITY OF CHRYSOPHYTE CYSTS FROM AN EOCENE MAAR LAKE IN THE CANADIAN ARCTIC**.**

(P26) Inci Tüney, Katherine Hubbard & Atakan Sukatar. PHYLOGENETIC RELATIONSHIPS AND DISTRIBUTION PATTERNS OF *CYSTOSEIRA SPP.* IN THE AEGEAN SEA.

(P27) **Susan. L. Clayden** & Gary W. Saunders. A FIRST SURVEY OF THE GENUS *ACROCHAETIUM* IN CANADA WITH DESCRIPTION OF *ACROCHAETIUM BONNENSE* SP. NOV.

(P28) **Diba Khan-Bureau,** Louise Lewis & Gary Robbins. APPLICATION OF THE V4 REGION OF THE 18S RRNA GENE TO DNA BARCODE DIATOMS (BACILLARIOPHYTA) FROM ENVIRONMENTAL SAMPLES OF THE EIGHTMILE RIVER IN CONNECTICUT.

(P32) **Brian Wysor**, Charles J. O'Kelly, Juan Lopez-Bautista, Noel Sme & Valerie Charbonneau. ESTABLISHING ULVOPHYCEAN CONTEXT FOR THE UNIVERSAL PLASTID AMPLICON.

ABSTRACTS

Oral Presentations (In order of presentation)

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

Session I

(1 WA) CELL DEATH PROGRAMMES OF THE HARMFUL BLOOM-FORMING RAPHIDOPHYTE, *HETEROSIGMA AKASHIWO*, DURING VIRUS INFECTION WITH HARNAV, HANIV OR HAV**.** Jennifer E. Dingman[1], James K. Roherty[1], Keizo Nagasaki[2] & Janice E. Lawrence[1]. [1]Department of Biology, University of New Brunswick, Fredericton, NB E3B 5A3, Canada; [2] Harmful Algal Bloom Division, National Research Institute of Fisheries and Environment of Inland Sea, Hiroshima, 739-0452, Japan

Viruses play a key role in the ecology and physiology of marine microorganisms. However, little is known about the complex mechanisms that are involved in the host-virus relationship. Programmed cell death (PCD) may be involved in the arms race of some host-virus systems. We compared mortality in *Heterosigma akashiwo* (Y. Hada) Y. Hada ex Y. Hara & M. Chihara, a harmful bloom-forming raphidophyte, during infections with 3 unrelated lytic viruses (HaRNAV, HaNIV, and HaV). Our results demonstrate that some PCD hallmarks exhibited by *H. akashiwo* during infection (caspase-like enzyme activity) are common to all three lytic infections. However, DNA fragmentation was only seen during HaNIV and HaV infection, and the externalization of phosphatidylserine residues was only seen during HaV-infection. Combined with previously described changes in cellular-ultrastructure, our results show that *H. akashiwo* utilizes different cell death programmes during HaRNAV infection (paraptosis) compared to HaNIV and HaV infections (apoptosis-like cell death). Our study outlines the complexity of mortality of *H. akashiwo* and shows stress-dependant drivers of the cell death programs in *H. akashiwo.*

(2 WA) EXPLORING THE IMPACT OF OCEAN ACIDIFICATION AND WARMING ON THE MICROSCOPIC SURVIVAL STAGES OF THE KELP, *SACCHARINA LATISSIMA.* Sarah Redmond & Charles Yarish. Departments of Ecology & Evolutionary Biology & Marine Sciences, University of Connecticut, CT, 06901, U.S.A.

The kelps are large brown algae within the order Laminariales, and key components of cold temperate sublittoral regions worldwide. Highly productive kelp stands support coastal marine food webs by providing food and structurally complex habitats for other economically and ecologically important species. While highly adaptable to varying environments, it is unknown what the combined stressors of predicted ocean climate change, namely increased temperature and ocean acidification, may have on the critical microscopic gametophytic stages of the kelps. This study investigated impacts of projected increases in temperature and dissolved inorganic carbon on the gametophytic and early developmental sporophytic stages of *Saccharina latissima,* the most widely distributed kelp in the North Atlantic. Reproductive plants collected from the Gulf of Maine and Long Island Sound were collected in summer and fall of 2011 and released spores were cultivated through the gametophyte stage to the juvenile sporophyte stage on a

gradient table of increasing temperatures (16, 19, 22, 25, 28 °C) and pCO_2 values (1x, 2x, 3x, 4x ambient). All stages of the microscopic phases were investigated, from spore settlement and germination, gametophyte development, and production of juvenile sporophytes. Preliminary results indicate a strong temperature effect, with high mortality at 22°C, and complete mortality at 25 and 28°C for all trials. Successful gametophyte reproduction and sporophyte formation occurred only at 16°C for all trials, with vegetative gametophyte growth only occurring at 19°C. Further analysis is needed to determine effects of increased pCO_2 values. High mortality and reduced reproductive success at higher temperatures may result in loss of important kelp habitat at the Western North Atlantic southern boundary of *Saccharina latissima,* which occurs in Long Island Sound, if coastal water temperatures continue to rise.

(3 WA) ASSESSMENT OF CRYPTIC *RHODYMENIA* SPP. (RHODYMENIACEAE, RHODOPHYTA) IN BRITISH COLUMBIA, CANADA: AN INTEGRATIVE TAXONOMIC APPROACH. Gina V. Filloramo & Gary W. Saunders. Center for Environmental & Molecular Algal Research, Department of Biology, University of New Brunswick, Fredericton, NB, E3B 5A3, Canada

Accurate taxonomic assessments of red algae are complicated by convergent evolution, phenotypic plasticity and their simple morphologies. Using DNA barcoding it is possible to objectively establish genetic species groups, revealing overlooked or overestimated species diversity. Combined with morphological assessments, DNA barcoding has revolutionized our ability to delimit red algal species. A recent survey in British Columbia, Canada used the DNA barcode to reveal new and previously overlooked species within the cosmopolitan red algal genus *Rhodymenia.* Although two species of *Rhodymenia* were recognized in British Columbia (*R. pacifica* and *R. californica*), our molecular data resolved four distinct species groups. Analysis of vegetative and reproductive features confirmed the presence of *R. pacifica* and *R. californica.* Some samples that were initially field identified as *R. pacifica* were later resolved as a separate genetic species and determined to be *R. rhizoides,* resulting in the resurrection of this species. Additionally, some samples field identified as *R. californica* were found to be genetically distinct based on our barcode survey. These samples were determined to be *R. callophylloides*--representing a range extension of this species from its type locality in California to southern British Columbia. Morphological assessment of *R. callophylloides* uncovered a distinct pattern of tetrasporangial development that may be a novel pattern for the genus. Using an integrative taxonomic approach, we have thus doubled the number of species recognized for this genus in British Columbia and may have uncovered a novel pattern of tetrasporangial development for the genus.

(4 WA) IMPACTS OF COMPETITION AND HERBIVORY ON THE GROWTH OF TWO BLOOM-FORMING *ULVA* SPECIES IN NARRAGANSETT BAY, RI. Michele Guidone, Shelby Rinehart & Carol Thornber. University of Rhode Island, Kingston, RI, 02881, U.S.A.

In Narragansett Bay, Rhode Island, blooms composed of *U. compressa* and *U. rigida* are an annual occurrence. To determine whether intra- and interspecific competition occur within these blooms, we examined *Ulva* growth across a range of blade densities. Within mesocosms, we

varied light (sun/shade) and nutrient levels (enriched/ambient) in a fully factorial design. We also examined the influence of herbivory *in situ*; *Ulva* blades were placed in cages of two different mesh sizes (1mm and 10mm) that differentially excluded herbivores. For both species, we found that competition was absent under low nutrient conditions. For *U. compressa* in enriched treatments, interspecific competition dominated in full sun, while intraspecific competition dominated in shade. In contrast, *U. rigida* experienced greater inter- than intraspecific competition under all light levels. In the field, *U. compressa* showed decreased growth due to intraspecific competition in mud crab dominated large mesh cages; no competition was detected in amphipod dominated small mesh cages. *U. rigida* experienced greater interspecific competition in the large, but not small, mesh cages. We conclude that *U. compressa* is a superior competitor to *U. rigida*. However, within *Ulva* blooms this competition is mediated by amphipods that preferentially consume *U. compressa*, allowing *U. rigida* to proliferate.

(5 WA) A COMPREHENSIVE TAXONOMIC REVIEW OF THE RED ALGAL GENUS CERAMIUM IN THE NORTHWEST ATLANTIC. Meghann Bruce & Gary W. Saunders. Centre for Environmental and Molecular Algal Research, Department of Biology, University of New Brunswick, Fredericton, NB, E3B 5A3, Canada

Ceramium (Ceramiaceae, Rhodophyta) is a large cosmopolitan genus with approximately 180 species currently recognized, many of which have convoluted taxonomic histories. Traditionally, species identification and delimitation have relied on morphological characters such as thallus cortication and branching pattern, which are highly variable in relation to environmental conditions and developmental stage. Here we apply molecular taxonomic techniques (analyses of COI-5P & *rbc*L sequences) to investigate six species of *Ceramium* presently credited to the northwest Atlantic (*C. cimbricum*, *C. circinatum*, *C. deslongchampsii*, *C. diaphanum*, *C. tenuicorne* and *C. virgatum*). Our results contradict the current understanding of *Ceramium* in this region in three notable ways. Firstly, analyses of 156 specimens could not confirm the presence of three of the six currently reported species (*C. circinatum, C. diaphanum* or *C. tenuicorne).* Secondly, plants morphologically attributable to *C. virgatum* resolved as two distinct sister groups. Lastly, we discovered a potentially non-indigenous population of *C. secundatum* in Rhode Island. Our molecular analyses are further complemented with detailed morphological, biogeographical and ecological data, thus providing a holistic approach to species delimitation and facilitating a comprehensive taxonomic review of *Ceramium* in the northwest Atlantic.

(6 WA) POPULATION ECOLOGY OF *PALMARIA PALMATA* ON DIGBY NECK, NOVA SCOTIA CANADA. Katelyn White & David Garbary. St. Francis Xavier University, Antigonish, NS, B2G 2W5, Canada

Population ecology of *Palmaria palmata* (common name Dulse) was investigated from the low intertidal zone on Digby Neck, Nova Scotia. The primary objectives of this study were to determine: 1) the reproductive phenology of Dulse 2) the seasonality of vegetative development between distinct habitats, 3) the characterization of boulder size for epilithic thalli and 4) the role of disturbance in colonization. Eight beaches along Digby Neck, Nova Scotia that are currently used as harvesting sites were used in this study. These beaches are gently sloping rocky beaches that are unique from the typical basalt cliffs. Boulders on the Dulse beaches have a mean average

diameter of 48 cm and can be disturbed by extreme storm action. Each month, fifty representative fronds were collected along the Dulse beach reproductive state was determined. We found that reproductive maturity of the fronds peaks in the late fall with the majority of the frond being identified as male or tetrasporophytes. Fifteen of the largest fronds were collected from epiphytic and epilithic populations each month for 6 months. There was a significant difference between the fronds with different habits where the epilithic plants mean length was 20.1 cm and the epiphytic plants mean length was 15.5 cm. However, the proportion of fronds per size category was similar between the two habitats. All thalli had a high number of smaller fronds (between 1 cm and 5 cm) and a low number of larger fronds (25 to 30 cm or over 31 cm). We conclude that Dulse populations are subjected to high levels of disturbance and that there is a difference between epilithic and epiphytic populations.

Session II

(7 WA) RESTRUCTURING OF THE PHOTOSYNTHETIC MACHINERY OF EUKARYOTES DURING PLASTID EVOLUTION. Jonathan Neilson & Dion Durnford. Department of Biology, University of New Brunswick, Fredericton, NB, E3B 5A3, Canada

Photosynthesis was first acquired by eukaryotes through a primary endosymbiotic event between a cyanobacterium and a primitive eukaryote. This gave rise to three major lineages: the glaucophytes, red algae, and green plants. Since then, photosynthesis spread laterally through secondary endosymbiosis between a red or green alga and an unrelated, non-photosynthetic eukaryote. Much effort has been spent on understanding how endosymbiosis occurs and the evolutionary relationship between these organisms. What is perhaps less appreciated is the effect endosymbiosis can have on the structure, composition, and function of individual protein subunits and protein complexes. With the availability of recently completed genome sequences from both red and green algal derived secondary endosymbionts we can begin to address these questions using bioinformatics and proteomics. The purpose of this study is to examine how the composition, organization, and functionality of the photosynthetic machinery has changed during plastid evolution, with an emphasis on how endosymbiosis affects protein evolution. We are focusing on two components of the photosynthetic machinery: the photosystems and their associated antenna systems. We used a cluster network analysis to examine the origins of photosystem subunits in a taxonomically broad range of secondary endosymbionts. This analysis is primarily meant to identify putative horizontal gene transfers and/or cryptic endosymbiosis events that may alter the structure and functionality of the two photosystems. For the antenna complex analysis we began with a phylogenetic analysis of light-harvesting complex (LHC) proteins from primary endosymbionts and used this as a basis to identify characteristic domains for the different LHC types. This data was then used to classify LHCs from secondary endosymbionts. From this study we highlight the asymmetric nature of gene gain, loss and protein domain rearrangement as a result of endosymbiosis.

(8 WA) ASSESSING THE DIRECT CONTRIBUTION OF *TRICHODESMIUM* TO EXPORT. Elizabeth Sargent[1], Alex Poulton[2], Mark Moore[1], Tom Bibby[1] & Tracy Villareal[3].[1] Ocean and Earth Science, National Oceanography Centre Southampton, University of Southampton Waterfront Campus, European Way, Southampton SO14 3ZH; [2]National Oceanography Centre, European Way, Southampton SO14 3ZH;[3] Marine Science Institute, The University of Texas at Austin, 750 Channel View Dr., Port Aransas, TX, 78373, U.S.A.

Trichodesmium, a colonial marine cyanobacterium, is integrally involved in ocean biogeochemical cycling as it is a significant supplier of fixed nitrogen to the warm surface ocean. Recent reports have suggested that *Trichodesmium* is also important in the subsurface layer, and actively fixes nitrogen in the deep chlorophyll maximum (DCM); however, the role *Trichodesmium* plays in the biogeochemistry of deeper waters has yet to be described. This study focuses on *Trichodesmium*'s involvement in the direct export process. Contrary to previous expectations, results suggest that despite its buoyancy this organism is a constituent of sinking material. Sampling on research cruises in the eastern subtropical and tropical Atlantic, and in the Gulf of Mexico showed *Trichodesmium* was commonly present below 100 m in three forms: tufted colonies, free filaments, and free filaments included in aggregations with other organisms/faecal matter. The Marine Snow Catcher (MSC), a 100 L messenger-operated PVC closing water bottle, and *in situ* Stand Alone Pumping Systems (SAPS) were used to collect sinking particles, which were imaged and preserved for post-cruise assessment. All sub-DCM MSC collections between 80-250 m in areas where *Trichodesmium* was a significant counterpart of the surface population included negatively buoyant colonies sinking at 12 - 120 m d^{-1}, as well as free filaments; SAPS collections also revealed the presence of free filaments in low concentrations as deep as 500 m. Further microscopic analysis of these colonies will allow for the elucidation of the mechanism of sinking in *Trichodesmium*, such as gas vacuole collapse, as well as aiding in describing its involvement in the export flux of POC and PON.

(9 WA) EXPLORATION OF THE ROLE OF 3' UTRs IN REGULATING mRNA STABILITY IN THE MARINE DIATOM *THALASSIOSIRA PSEUDONANA*. Dylan W. Scott & Deborah L. Robertson. Biology Department, Clark University, Worcester, MA, 01610, U.S.A.

Nitrate reductase (NR) catalyzes the reduction of nitrate to ammonium, and is considered the rate-limiting step of nitrate assimilation. Within marine diatoms, NR expression is highly regulated. For example, in *Thalassiosira pseudonana, nia* transcripts, which encode NR, accumulate in the absence of nitrogen, are translated in the presence of nitrate, and are degraded in the presence of ammonium. More recently our lab showed that *nia* transcript levels were lower in the presence of ammonium and actinomycin D (inhibits RNA polymerase II) than in cells receiving actinomycin D alone. In contrast, actin mRNA levels were the same in the two treatments. These results suggest that *nia* transcripts are targeted specifically for degradation in the presence of ammonium. Regulatory sequences that influence mRNA stability are often observed in the 3'UTRs of eukaryotic mRNAs. Therefore, we tested the hypothesis that sequences in the 3'UTR of *T. pseudonana nia* transcripts are important in modulating mRNA stability. TpNR and Tpfcp/nat vectors were obtained from Nicole Poulsen (Dresden University). The TpNR vector uses approximately 1kb of *nia* DNA upstream of the start codon and 0.5kb of DNA downstream of the

stop codon to flank the reporter gene EGFP (*nia-egfp-nia*). We replaced the 3' *nia* sequence with 0.5kb of actin DNA downstream of the stop codon (*nia-egfp-actin*). Each vector was co-transformed pTpfcp/nat (provides antibiotic resistance) into cells. Transformed clones were grown in f/2-supplemented seawater to mid-log phase before the addition of ammonium. If sequences in *nia* 3'UTR regulate transcript stability in response to ammonium, we predict that *egfp* mRNA abundance in *nia-egfp-nia* transformed cells will decrease in response to ammonium while *egfp* mRNA levels in *nia-egfp-actin* transformed cells will not be effected. *efgp* transcript levels are currently being quantified using QRT-PCR and results from these experiments will be presented.

(10 WA) INVESTIGATING SPECIES DIVERSITY AND BIOGEOGRAPHY OF *POLYSIPHONIA* (RHODOMELACEAE, RHODOPHYTA) IN BRITISH COLOMBIA USING MOLECULAR TOOLS. Amanda Savoie & Gary W. Saunders. Center for Environmental & Molecular Algal Research, Department of Biology, University of New Brunswick, Fredericton, NB, E3B 5A3, Canada

Polysiphonia is currently the largest genus of red algae with its species widely distributed and ecologically diverse. The high number of species in the genus combined with the superficiality of many early descriptions has rendered *Polysiphonia* an especially difficult genus for taxonomic and phylogenetic research. There are nine species of *Polysiphonia* reported from the northwest Pacific coast of Canada with the current identification key for this area indicating that several of these species need taxonomic reassessment. In order to resolve these, and other uncertainties, a DNA barcode survey of *Polysiphonia sensu lato* (including *Neosiphonia* and *Pterochondria*) was initiated for coastal British Columbia. DNA barcoding, using the mitochondrial gene COI-5P as a species identification tool, has been shown to discriminate successfully among species of red algae and consequently can be used to assign specimens, as well as cryptic life stages, to known species. This tool is thus a powerful ally in ascertaining which, and how many, species of red algae are present in an area. To date, we have found 15 genetic species groups for *Polysiphonia* from the Northwest Pacific. Many of our genetic groups key out to the same morphological species, and, despite our thorough sampling, we have not collected three out of the nine species that are reported from British Colombia. We have recorded the presence of *Polysiphonia morrowii*, a known invasive species from Japan, in British Colombia. Finally, we have also uncovered interesting biogeographical patterns in this group, including a genetic species with a gap in distribution between one site in British Columbia (Tahsis) and California. These results indicate that species diversity in this group has been underestimated for this region, and that substantial taxonomic work remains.

(11 WA) OBSERVATIONS ON THE DISTRIBUTION AND PHENOTYPIC EXPRESSION OF THE KELP *SACCHARINA GROENLANDICA* ACROSS A WAVE EXPOSURE GRADIENT IN THE BAY OF FUNDY. Caroline Longtin & Gary W. Saunders. Centre for Environmental and 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 latissima* has a non-digitate blade and is abundant at wave-sheltered sites, while *L. digitata* has a digitate blade and is abundant at moderately exposed and wave-exposed sites. In the Pacific Ocean, *Saccharina groenlandica* displays either the non-digitate or digitate morphology, coincident with the wave exposures just discussed. As a result of its 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. The objective of our study was to determine whether *S. groenlandica* in the Maritime Provinces expresses the non-digitate and digitate phenotypes across a wave exposure gradient as observed in Pacific populations. We found that most individuals of *S. groenlandica* express the digitate phenotype at moderately exposed and exposed sites, while only a few non-digitate individuals (9% of total *S. groenlandica*) were found at all wave exposures and years collectively. Now that we have discovered how abundant *S. groenlandica* is in the Bay of Fundy our next objective is to determine 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 III

(12 UP) HOW DOES LAKE BIOMANIPULATION AFFECT NUTRITION LIMITATION OF FRESHWATER PHYTOPLANKTON? Shampa A. Panda [1,2], Steve Di Lonardo[1] & John D. Wehr[1]. [1]Louis Calder Center - Biological Field Station, Fordham University, Armonk, NY, 10504, U.S.A.; [2] Environmental Sciences and Engineering, University of North Carolina at Chapel Hill, Chapel Hill, NC, 27514, U.S.A.

A study was conducted in summer 2011 on North Lake, in suburban Armonk, NY, a lake managed to control aquatic vegetation and monitored for ten years for water clarity, nutrient chemistry, algal biomass, and phytoplankton community structure. North Lake receives nutrients from runoff, wildlife, and other human activities, and experiences episodes of dense aquatic vegetation and elevated phytoplankton biomass. Past data suggest that removal of aquatic vegetation by grass carp may have led to increases in internal nutrient loading and greater phytoplankton levels. To determine the factors driving algal productivity, a mesocosm experiment consisting of 12, 4-L cubitainers was conducted using a 2 x 2 factorial design: control, nitrogen, phosphorus, nitrogen + phosphorus. Three 4-day experiments quantified changes in chlorophyll-*a*, phytoplankton composition, and water chemistry under these treatments at 0-h, 3-h, and 4-d. In all three experiments the +N+P treatment resulted in the greatest algal biomass. Nutrient uptake (NH_4^+, NO_3^-, TDN, PO_4^{3-}, TDP) over 4 days was estimated and compared against algal biomass, with greatest rates of N and P uptake measured in +P treatments. The relationship was positive and significant for the uptake of all nutrient forms measured. Results indicate that algal biomass (as chlorophyll-*a*) was co-limited by the supply of N and P, and that nutrient uptake (both N and P) was limited by P availability. Managing phytoplankton blooms in North Lake in the future may require the identification and careful regulation of the sources of both nitrogen and phosphorus inputs into the lake.

(13 UP) ALTERING THE DURATION OF STATIONARY PHASE IN *CHLAMYDOMONAS REINHARDTII*. Ellen C. R. Snyder & Dion G. Durnford. Department of Biology, University of New Brunswick, Fredericton, NB, E3B 5A3, Canada

The potential use of microalgae as biofuels has generated considerable interest in their batch culture growth. In batch culture, microalgae grow exponentially and eventually reach a stationary phase of no growth, ultimately followed by a period of cell death. This is often referred to as conditional senescence, but the process is understudied. In order to investigate the physiology of aging in microalgal cultures, we used a cell wall-less strain of *Chlamydomonas reinhardtii* and focused on conditions that trigger a more rapid progression through stationary to the death phases. We examined the effect of atmospheric gases and light intensity on the duration of stationary phase and physiological characteristics. The duration of stationary phase was very dependent upon gas exchange with cells flushed continuously with air or 5% CO_2:N_2 mix showing no decrease in cell numbers over 2 weeks, compared to a gas-exchange limited culture whose numbers were reduced over 50%. However, a culture flushed with N_2 only, showed only a small decline, suggesting cell decline was not due to simply anaerobiosis, but oxidative damage. In support of this, no gas-exchange cultures showed a light dependent length of stationary phase, with high-light cells declining rapidly and dark/ very low light exposed cells experiencing only small declines. Abundance of the LHC-like photoprotective protein, LHCSR, also suggested that light-stress was a significant factor in determining the length of the stationary phase. Oxidative stress occurs when light capture exceeds the ability to utilize the reductant produced via photosynthesis. In *Chlamydomonas*, aging and culture longevity is intricately linked the magnitude of the oxidative stress.

(14 UP) CHARACTERIZATION OF ACYL-COA:DIACYLGLYCEROL ACYLTRANSFERASE (DGAT) GENES AND PHYSIOLOGY IN THE DIATOM, *PHAEODACTYLUM TRICORNUTUM,* UNDER DIFFERENT NITRATE CONCENTRATIONS. Pierre Muhoza[1], Orly Levitan[1], Tiago Guerra[2] & Paul Falkowski[1, 2]. [1]Institute of Marine and Coastal Sciences, Rutgers University, 71 Dudley Road, New Brunswick, NJ, 08901, U.S.A.; [2]Department of Chemistry and Chemical Biology, Rutgers, The State University of New Jersey, Piscataway, NJ, 08854, U.S.A.

Lipid biosynthesis in diatoms is typically upregulated under nutrient-deficient conditions. Additionally, the flux of carbon into lipids is highly controlled. One possible "control valve" is the flux of acetyl CoA into diacylglycerol to form triacylglycerols; an early step in the synthesis of storage lipids. The objective of this study is to follow the changes in mRNA expression of 5 orthologs related to type II DGAT genes in *Phaeodactylum tricornutum* during nitrogen (N) limitation and starvation, and the associated physiological responses. Preliminary results from qRT-PCR analyses suggest that DGAT 2B is upregulated 3 fold whereas no change in DGAT 2D gene expression was observed during nitrogen starvation. Cells grown in N-starved and N-limited conditions displayed various signs of physiological stress and reduced photosynthetic efficiency. Our results indicated that lipid content increased significantly with decreasing nitrate concentrations. Total protein per cell did not change between N-limited and N-replete acclimations, yet N-starved cultures exhibited a significant decrease in protein per cell. Cultures grown in low N concentrations exhibited a decrease in chlorophyll per cell. The results suggest

that DGATs are key enzymes in controlling the flux of carbon into storage lipids in *Phaeodactylum tricornutum.*

(15 C) DETERMINING THE ROLE OF SALT MARSH MACROALGAE (ECADS) IN CAPE COD SALT MARSHES. Jennifer Burkhardt[1,2], Megan Tyrrell[1], Carol Thornber[2] & Kelly Medeiros[1]. [1]Atlantic Research Center, Cape Cod National Seashore, Truro, MA, 02666, U.S.A.; [2]Department of Biological Sciences, University of Rhode Island, Kingston, RI, 02881, U.S.A.

Salt marsh macroalgae, commonly referred to as ecads, can be found in high abundance in the salt marshes of Cape Cod. These ecads, comprised of species of *Ascophyllum* and *Fucus* that are morphologically different than their rocky intertidal counterparts, form a dense mat (at times exceeding a canopy height of 15cm) along the edges of the marsh and within the *Spartina alterniflora* zone. However, the impacts of these ecads on salt marsh plants and sediments remain largely unknown. During the summer of 2011, we performed a series of experiments to assess the impact of ecads on a suite of salt marsh physical properties and *Spartina* survival rates. A control/ ecad removal experiment was set up in two salt marshes, Hatches Harbor and West End, in Provincetown, MA. We then assessed multiple metrics to determine how ecads affect sediment movement, composition of sediments, decomposition rate of *Spartina alterniflora*, and conductivity, light penetration, and soil temperature. We found significant differences in ecad impacts between the two marshes; however, at both marshes the presence of ecads reduced light, increased temperature at the sediment surface and increased the decomposition rate of *Spartina alterniflora*. In general, ecads presence resulted in reduced sediment movement, although these results were less straightforward. Our results present novel and surprising findings on the impacts of an understudied group of organisms on salt marsh structure. Based upon our results, ecads have the potential to greatly impact the future of northern temperate salt marshes.

(16 C) EVOLUTION OF THE BERMUDA SEAWEED PROJECT: PROGRESS AND HIGHLIGHTS. Thea R. Popolizio[1], Christopher E. Lane[1] & Craig W. Schneider.[2] [1]Department of Biological Sciences, University of Rhode Island, Kingston, RI, U.S.A; [2]Department of Biology, Trinity College, Hartford, CT, U.S.A.

Ideally located for marine biodiversity assessment studies, the isolated islands of the Bermudian archipelago are at the interface of tropical and warm temperate biogeographic zones, a climatic boundary that heavily influences the marine flora. Analysis of preliminary data collected for the Bermuda Seaweed Project has demonstrated that species diversity in the islands is greatly underestimated. A number of red algal species in Bermuda that were misidentified due to convergent morphology with other species (*e.g., Centroceras clavulatum* complex; *Helminthocladia calvadosii*; *Asteromenia peltata*) have been distinguished as novel cryptic species. Our molecular analysis shows that '*Halymenia bermudensis*' from the type locality in Bermuda clusters with the *Cryptonemia* rather than the *Halymenia* clade, and evidence suggests we have collected at least two other potentially novel *Cryptonemia* species. In some cases, taxa exhibit great phenotypic plasticity and can be misconstrued as separate species (*e.g.*, *Halymenia pseudofloresii* and *H. floresii sensu auct.).* Our data has confirmed that sequences from the alga known as *Platoma cyclocolpum* in Bermuda are phylogenetically distinct from those extracted from the type locality of this species (Canary Islands). Instead, *P. cyclocolpum* was discovered to

be the winter "morph" of *Nemastoma gelatinosum*, a species with a Bermuda type locality. Moreover, molecular sequencing has been paramount to identifying unknown collections, most recently *Archestenogramma profundum*, the novel proposed species *Halopeltis pellucida*, and an interesting *Meristotheca*. Large-scale collection and processing of marine algae reflecting seasonal changes in algal assemblages as well as habitat variation among the Bermuda flora is presently underway. We intend to integrate standard alpha-taxonomic morphological data with multi-gene molecular analysis to produce robust classifications of all marine red algae (Rhodophyta) in Bermuda, and expect that these methods will continue to expose misnamed taxa and numerous cryptic species.

Session IV

(17 C) OUT OF THE PETRI DISH AND INTO THE PUBLIC SPHERE: A COMMUNICATIONS WORKSHOP FOR SCIENTISTS. Catherine Schmitt. Maine Sea Grant, University of Maine, Orono, ME, 04469, U.S.A.

American scientists increasingly address questions that relate to an issue of public concern. For phycologists, such issues may include climate change, alternative energy sources, food supply, harmful algal blooms, or biomedical applications. Most scientists want their work to be valued and understood by their non-scientist colleagues and community. Yet many scientists are challenged by the prospect of communicating the meaning and importance of their research (the "So what?" question) to non-scientists. This challenge can be surmounted when scientists are aware of how the public understand the world of science, and how knowledge is facilitated (or not) by the news media. Participants in this workshop will draft important messages of their research, identify target audiences for various messages, and explore tools and resources for communicating to non-scientists.

Session VI

(18 C) GETTING THE MESSAGE OUT: MY 30+ YEAR JOURNEY FROM THE NATIONAL ENQUIRER TO TWITTER. Nancy Knowlton. National Museum of Natural History, Smithsonian Institution, U.S.A.

My first encounter with the press was not what you would call a resounding success, although it didn't do any lasting damage. Plus, back in the 1980s, getting the message out meant publishing in *Science* or *Nature*. But over the years, watching the coral reefs I used to study literally vanish before my eyes made me realize that people outside the Ivory Tower needed to know what was happening. Since then I have been media-trained as an Aldo Leopold fellow, passed on the lessons I learned to students, appeared in Vanity Fair, written a popular book, co-curated an community art project, become a fan of Twitter, and am now directing the Smithsonian's Ocean Portal. There are many platforms and styles for reaching out to broader audiences, and many resources to guide you. Practice with everything from message boxes to improvisation really helps, as do clear language, passion and a little humor (grant writing and teaching also benefit). Most importantly, you can be a citizen of the planet without jeopardizing your reputation as a scientist, and the planet needs more science-citizens.

(19 C) ENGAGING THE PUBLIC IN CLIMATE CHANGE SCIENCE. Abe Miller-Rushing. SERC Institute and Acadia National Park, ME, U.S.A.

(20 C) KNOWING WHAT LIVES IN YOUR NATIONAL PARK; EFFORTS TO SURVEY BIODIVERSITY IN ACADIA. David Manski. Acadia National Park, ME, U.S.A.

Concurrent Session VIIA

(21 C) SHORT-TERM EFFECTS OF COMMERCIAL SEAWEED HARVESTING ON ALGAL BIOMASS AND SELECTED ROCKY INTERTIDAL ORGANISMS. Brian Beal[1,2], Raul Ugarte[3] & Sean Stoddard[1]. [1]University of Maine at Machias, Machias, ME, 04654, U.S.A.; [2]Downeast Institute for Applied Marine Research & Education, Beals, ME, 04611, U.S.A.; [3]Acadian Seaplants Limited, Dartmouth, NS, B3B 1X8, Canada

We assessed short-term (first 40-days) effects of commercial harvesting of knotted wrackweed, *Ascophyllum nodosum*, on macroalgal and small invertebrate biomass at a protected and semi-protected intertidal site near Jonesport, Maine during the summer of 2011. A BACI (Before-After-Control-Impact) sampling design was used to examine harvesting effects. At each site, initial algal and invertebrate samples were taken on 6-7 June in two plots (30 x 35 m) using a generalized randomized complete block design at three tidal heights: Upper, Mid, and Lower. After sampling, the wrackweed in one plot at each site was randomly assigned to be cut by a commercial harvester. Harvesting occurred on 8 June at both sites by the same individual who used hand-held cutting gear to harvest each plot in a manner consistent with state of Maine regulations for cutting height (40.6 cm above the holdfast). Approximately 25% and 15% of the biomass was removed from the plot at the protected and semi-protected site, respectively. Sampling (as described above) occurred immediately after the harvest (9-10 June) and 40-days later (18-19 August). Initial mean algal biomass did not differ between sites ($P = 0.14$) or tidal heights ($P = 0.76$). Within two days after the harvest, there was a significant loss of algal biomass at the protected site (Control = 16.76 kg/m^2 vs. Cut = 10.56kg/m^2), but only at the mid and low tidal zones reflecting a harvesting bias likely due to the tidal cycle. No statistical difference was detected in algal biomass at the semi-protected site (Control = 11.38 kg/m^2 vs. Cut = 10.53 kg/m^2). After 40 days, however, no significant differences were detected in algal biomass between control and harvested plots at either site. A total of fourteen invertebrate species (four Phyla) was sampled over the three dates. The two most important species in terms of biomass were the periwinkles, *Littorina littorea* and *L. obtusata*. No significant effects on Littorinid biomass due to commercial harvesting were observed. *L. obtusata* biomass decreased significantly through time from 3.0 to 2.0 g/m^2; however, this 33% loss of biomass occurred equally across both sites and cutting/control treatments.

(22 C) OPPORTUNITIES FOR SEAWEED CULTIVATION AS AN ESSENTIAL ELEMENT FOR NUTRENT BIOEXTRACTION IN LONG ISLAND SOUND AND BRONX RIVER ESTUARY. Jang. J. Kim[1], George P. Kraemer[2], John Curtis[3] & Charles Yarish[1]. [1]Departments of Ecology & Evolutionary Biology and Marine Sciences, University of Connecticut, CT, 06901, U.S.A.; [2]Environmental Studies Program, Purchase College, Purchase, NY 10577, U.S.A.; [3]Bridgeport Regional Aquaculture Science and Technology Education Center, Bridgeport, CT 06604, U.S.A.

Our project is designed to demonstrate whether seaweed aquaculture is a useful biotextractive technology for the remediation of the water quality of Long Island Sound (LIS) and at the mouth of the Bronx River estuary. We cultivated and harvested the rhodophyte *Gracilaria tikvahiae* at two near shore farm sites in these coastal waters during the summer and fall of 2011. Due to circumstances beyond our control (permitting issues and post-Tropical Storm Irene repositioning of farm system), the deployment of the farm units in the Bronx River was delayed. Prior to Irene, the growth rates at Bronx River site were 11.8% and 10.0% d^{-1} at 0.5 and 1.0 m deep, respectively. The estimates of nitrogen (N) removal by *Gracilaria* during this period were approximately 343 and 275 g N ha^{-1} d^{-1}. During the same period, the growth rates and N removal at the LIS site were 5.9% and 6.0% $d^{-1}$and 48 and 50 g N ha^{-1} d^{-1} at 0.5 and 1.0 m deep, respectively. Interestingly, although *Gracilaria* at the LIS site grew ca. 10%, the seaweed removed no N from the water (it relied on stored N to enable biomass increase). In addition, *Gracilaria* harvested at the LIS site was light brown in color, indicating nutrient limitation, while *Gracilaria* from the Bronx River site presented almost black in color, indicating nutrient enrichment. These results suggest that nutrients were being rapidly assimilated and used to fuel the growth of new *Gracilaria* tissue grown at the Bronx River site while nutrients appear to be a limiting factor for the growth of *Gracilaria* at the LIS site during the summer months.

(23 C) EFFECT OF FUKUSHIMA NUCLEAR ACCIDENT ON MAINE MARINE ALGAE. Anna J. Schliep[1], Susan H. Brawley[2] & Charles T. Hess[1]. [1]Department of Physics and [2]School of Marine Sciences, University of Maine, Orono, ME 04469, U.S.A.

The Fukushima Daiichi accident (11 March 2011) released ^{137}Cs and ^{131}I into the air. It took approximately 11 days for radiation released in Fukushima to reach Maine, as determined from air samples above Bennett Hall (Orono, ME). The levels of ^{131}I reached a measured peak on 7 April 2011. Decay-corrected peak activity of ^{131}I was measured at 0.00075 +/- 0.00014 Bq/m^3, below EPA action limits. By 25 April 2011, activity returned to background in air samples (Schliep, 2011). Given the well-known concentration of iodine by some seaweeds, we sampled kelp and rockweeds following the Fukushima radiation release with a Canberra germanium semiconductor gamma ray detector at the University of Maine. A few early, student-collected samples of rockweeds (mixed *Ascophyllum nodosum* and *Fucus vesiculosus*) from the mid-intertidal zone at Rockport, ME, between 12 April and 26 April 2011 had low but detectable levels of ^{131}I. We then began a sampling program along transects in mid and lower areas of the intertidal zone. The earliest samples of kelp (*Saccharina longicruris*) and mid-zone *F. vesiculosus* were collected on 30 April 2011. At this time, samples were below the critical limit for detection. Monitoring continued throughout the Maine coast (Biddeford, Schoodic Point, Mahar Point) on a weekly basis through 9 June 2011, with all samples at baseline. The effective containment of

aerial release of radioactive material from Fukushima combined with the short half-life of ^{131}I resulted in undetectable levels of ^{131}I in Maine marine macrophytes soon after the initial explosion in Japan.

(24 C) TRADE-OFFS OF SEXUAL AND ASEXUAL LIFE CYCLES IN *MASTOCARPUS PAPILLATUS*: AN ECOLOGICALLY KEY SPECIES WITH A COMPLEX LIFE CYCLE. Janet E. Kübler, Steven R. Dudgeon, Rebecca Rudy, P.A. Rudy & Stacy Krueger-Hadfield. Department of Biology California State University, Northridge, CA, 91330, U.S.A.

Populations of asexual organisms inevitably accumulate mutations that could reduce performance and population growth rates, over time. Being clones, they often also lack genetic diversity relative to their sexual counterparts. These costs are hypothesized to relegate asexual organisms to peripheral, often marginal, habitats. We tested whether these expected patterns occurred in the common red seaweed, *Mastocarpus papillatus* in California. Patterns of distribution and abundance of asexual *Mastocarpus papillatus* conflict with those expectations. Asexual fronds are more abundant and distributed more widely than sexual fronds across tidal elevations in California, and are present in all habitats. Although reproductive effort of asexuals was less than that of sexuals during peak reproduction, asexuals reproduce throughout the year and asexual output was less sensitive to environmental variation. Surprisingly, genetic diversity in asexual lineages of *M. papillatus* is comparable to that in the sexually reproducing lineage at microsatellite loci tested, thus far. Moreover, asexual fronds of *M. papillatus* are diploid, not haploid as often assumed. The occurrence of greater than expected genetic diversity of asexual fronds (associated both with diploidy and multiple origins from sexual lineages) without incurring the cost of sex provides a basis to explain the ecological success of the asexual life cycle of *M. papillatus*.

(25 C) MECHANISMS INVOLVED IN THE SYNTHESIS OF INDUCIBLE COMPOUNDS IN THE BROWN MACROALGAE *FUCUS VESICULOSUS.* Ursula S.R. Röse & Kyle Martin. College of Arts and Sciences, Department of Biology, University of New England, Biddeford, ME, 04005, U.S.A.

The 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 inducibility of defense 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. Brown algae are only distantly related to vascular plants and green algae. In vascular plants, defenses against herbivores and microorganisms involve signaling via the jasmonic acid or the salicylic acid signaling pathway. In animals, fatty acid signaling occurs via arachidonic acid, but recent evidence indicates the possibility of shared signals between the animal and plant kingdom that allows some pathogens to successfully infest plants and animals. The induction of defense compounds in vascular plants by herbivore feeding can be partially mimicked by mechanical injury or by exposure to the vascular plant hormone methyl jasmonate. Our results show that mechanical injury to *F. vesiculosus* induced the synthesis of two major compounds that were

synthesized in the algae in larger amounts compared to control plants. Moreover, these two compounds were also found to be inducible in response to exposure to methyl jasmonate and amounts were comparable to those of mechanically injured algae. Analysis by GC-MS identified one compound as tocopherol. Tocopherol plays an important role in the arachidonic acid chain by inhibiting the formation of prostaglandins and thromboxan. In plants, tocopherol synthesis is regulated by jasmonic acid, salicylic acid, abscisic acid. In algae, the inducebility and regulation is unknown. A second compound was identified as fucosterol. Fucosterol has antioxidant properties like tocopherol and is an anticoagulant with reported health benefits to humans. It is possibly synthesized via the mevalonic acid pathway, but the isoprenoid production in brown algae is largely unknown.

(26 C) INTRODUCTION AND EXPANSION OF THE BROWN ALGA *COLPOMENIA PEREGRINA* SAUVAGEAU (SCYTOSIPHONALES) WITHIN THE GULF OF MAINE. Lindsay A. Green[1], Arthur C. Mathieson[1,2], Christopher D. Neefus[1], Hannah M. Traggis[1], & Clinton J. Dawes[3]. [1]Department of Biological Sciences, University of New Hampshire, Durham, NH, 03824, U.S.A.; [2]Jackson Estuarine Laboratory, University of New Hampshire, Durham, NH, 03824, U.S.A.; [3]Department of Biology, University of South Florida, Tampa, FL, 33620, U.S.A.

Recent floristic surveys (July 2011) have established the occurrence of *Colpomenia peregrina* in the southern Gulf of Maine. Blackler (1964) initially noted its presence in Nova Scotia, which was subsequently confirmed by Bird & Edelstein (1978). Recently *C. peregrina* was collected from 13 sites ranging from mid coastal Maine to New Hampshire and the Isles of Shoals. Newly designed primers were used to sequence the mitochondrial *cox3* gene from samples collected in southern Maine and New Hampshire and compare them to four Nova Scotian samples collected between 1967 and 1979. Although the *cox3* sequence of *C. peregrina* did not match a previously published sequence, they were all identical to four Nova Scotian specimens. Of the sequences of GenBank they were most closely related to an isolate from France, differing by 2 base pairs. Isolates on GenBank from Australia and Korea differed by 3 and 4 base pairs, respectively. Temporal and distributional records indicate its presence in mid coastal Maine at least during 2010. However, detailed historic records from Casco Bay indicate that it was not recorded in 2009, unless it was confused with *Leathesia difformis*. Therefore, *C. peregrina* has undergone a rapid and extensive expansion within the Gulf of Maine. It was most likely introduced via shellfish aquaculture that has been common within the "indented coastline of Maine". While the impacts of such a wide scale and rapid expansion of *C. peregrina* are not understood, it is likely that it will have a major impact on the lower intertidal and shallow subtidal seaweed communities that it epiphytizes by increasing drag and competing for space.

Concurrent Session VIIB

(27 C) RED ALGAL HOST/PARASITE DIFFERENCES IN NUCLEAR CONTRIBUTION TO THE ORGANELLAR PROTEOMES. Nicolas A. Blouin[1] & Christopher E. Lane[1]. [1]Department of Biological Sciences, University of Rhode Island, Kingston, RI, 02881, U.S.A.

Many virulent eukaryotic pathogens and parasites have either directly evolved from a photosynthetic ancestor or are hypothesized to have plastid containing ancestry. It is not clear why or how photosynthetic organisms so readily become parasites. The genomes of many of

these parasites have been sequenced, however, none have close free-living relatives from which fine-scale genetic comparisons can be made to elucidate the loss of photosynthesis, which is assumed to occur early in the evolutionary trajectory of parasite evolution. The primary barrier to understanding the early stages of evolution of these parasites has been the difficulty in finding parasites with closely related free-living lineages with which to make comparisons. Parasites found throughout the florideophyte red algal lineage, however, provide a unique and powerful model to investigate the genetic origins of a parasitic lifestyle. This is because they share a recent common ancestor with an extant free-living red algal (adelphoparasitism). Cytological studies have shown that the adelphoparasite *Gracilariophila oryzoides* contains a non-photosynthetic plastid (proplastid) that is derived from its host, *Gracilariopsis andersonii*. The presence of the proplastid in the parasite indicates that some plastid functions are required for normal growth even though photosynthesis appears to have been abandoned. Additionally, organellar genomes in green algal and apicomplexan parasites are highly conserved in their gene repertoire, gene arrangement suggesting that there are constraints to parasitic evolution in photosynthetic lineages. Aside from photosynthesis, plastids are required for amino acid metabolism, fatty acid biosynthesis and pyrimidine biosynthesis in a number of organisms. These functions, however, require the targeting of proteins to the plastid from the nuclear genome where they are encoded. We have identified candidate nuclear-encoded genes in the host-parasite pair through homology searches against known plastid proteomes and target signal prediction of transcriptome data. We present ongoing bioinformatics research to determine which nuclear encoded, plastid-targeted genes remain in the parasite's genome and are transcriptionally active. Further, we investigate how the proplastid is maintained in the heterokaryon cells of host/parasite associations.

(28 C) USING DNA BARCODING TO INVESTIGATE BIOGEOGRAPHY AND EVOLUTIONARY HISTORY IN RED ALGAL CRUSTS. Kyatt R. Dixon & Gary W. Saunders. Centre for Environmental & Molecular Algal Research, Biology, University of New Brunswick, Fredericton, NB E3B 5A3, Canada

DNA barcoding of algae has proved to be a powerful tool in resolving species-level issues in taxonomically difficult groups, including the elucidation of cryptic and closely related sister species. However, the utility of such datasets goes far beyond species-level taxonomy. Large DNA barcode datasets facilitate the realization of accurate species distributional information. This information, coupled with analyses of molecular and geophysical data, enables researchers to investigate biogeographical patterns and, in some cases, hypothesize the historical events leading to present day patterns. The marine biogeography of Canada, the region of focus in this study, is generally thought to reflect a history of anti-glacial dispersal followed by glacial vicariance and subsequent genetic divergence and speciation, although the contribution of different mechanisms (e.g. trans-Atlantic migration, recolonization from glacial refugia and various dispersal methods) to present day distributional patterns remains unclear. We analyzed COI-5P sequence data for an ancient and hyper-diverse asexual red algal lineage, the Hildenbrandiales (257 sequences from 53 species), from Canada and other parts of the world, to investigate distributional and phylogenetic patterns among species groups. These patterns were then considered in the context of contemporary marine biogeographic hypotheses in an attempt to retrace the complex evolutionary history of the order in Canada.

(29 C) REVISION OF THE GENUS *BRACTEACOCCUS* TEREG (CHLOROPHYCEAE, CHLOROPHYTA) BASED ON A PHYLOGENETIC APPROACH. Karolina Fučíková[1], Valerie R. Flechtner[2] & Louise A. Lewis[1]. [1]Ecology and Evolutionary Biology, University of Connecticut, Storrs, CT, 06269 , U.S.A. [2]Biology, John Carroll University, University Heights, OH, 44118, U.S.A.

The genus *Bracteacoccus* (Chlorophyceae) exemplifies the taxonomic challenges that are common in systematic studies of coccoid green algae. The original definition of the genus is extremely vague, which caused the genus name first to be synonymized with *Dictyococcus* and then segregated from it following emendments of the diagnoses of the two genera. Transfers of species in and out of *Bracteacoccus* followed, even prior to the advent of molecular phylogenetic methods. Since the 1990's, phylogenetic analyses have demonstrated monophyly of *Bracteacoccus*, but only after exclusion of morphologically similar but genetically distinct forms, such as the genera *Chromochloris* and *Pseudomuriella*. The present work reviews the taxonomic history of *Bracteacoccus*, confirms its monophyletic character using a multilocus phylogenetic analysis, and presents an assessment of the species-level diversity within the genus mainly using molecular sequence data to distinguish species. In addition, morphological and ultrastructural features were examined and evaluated for taxonomic use. After revision, thirteen species are recognized, including seven that are newly described, and two species for which molecular data are not obtainable because there is no live material available. Among the main contributions of this study are the designation of an epitype for the type species, ***B. aggregatus*** - a strain newly isolated from the type locality - and its morphological and molecular characterization. This is an important disambiguation of the original description of *Bracteacoccus*. Furthermore, by including many new *Bracteacoccus* strains (a total of 90 strains were examined), this study greatly expands the current knowledge about the among- and within-species diversity as well as the geographic distribution of the genus. This study's phylogenetic approach to species delimitation sets an example for future works on similarly challenging groups of microscopic organisms.

(30 C) CHALLENGES AND REWARDS FOR FRESHWATER BIODIVERSITY RESEARCH IN RIVERS OF THE NORTHEAST. John Wehr, Kam Truhn, & Alissa Perrone. Louis Calder Center – Biological Field Station, Fordham University, Armonk, NY, 10504, U.S.A.

Studies on the diversity of freshwater algae in North America has had a fairly long history, but studies of algal communities in rivers and streams within the northeastern U.S. lag behind those conducted in other regions of North America and Europe. This is particularly true of non-diatom taxa, so-called "soft-bodied" algae, by monitoring programs. An eco-region-based survey in NY State has been initiated to produce an account of algal species from a wide spectrum of streams and rivers across the state. In the first two years of sampling, 60 streams and rivers have been sampled for algae from benthic and transported ("planktonic") habitats during spring, summer, and autumn-winter, along with water quality and algal stoichiometry data. An accounting from these collections thus far has recorded more than 600 taxa, roughly half of which were ubiquitous diatom species. However, a number of non-diatom taxa have been rarely recorded (if ever) from the region, or may be new taxa that at present do not fit current identification keys. These include representatives from the cyanobacteria, green algae and chrysophytes. Discoveries of cyanobacteria include *Caposira brebissonii* Kützing, *Coleodesmium wrangelii* (C.Agardh) Borzì,

Heteroleibleinia fontana (Hansgirg ex Hansgirg) Anagnostidis & Komárek, *Stauromatonema viride* Frémy, and others that do not correspond well to descriptions in current European floras. Similarly, several eukaryotic algae, such as *Gongrosira fluminensis* F.E. Fritsch (Chlorophyceae) and *Chrysocapsa maxima* Lund (Chrysophyceae) apparently are not uncommon, but previously rarely reported in North American floras. A particular challenge is the common occurrence in streams of sterile forms of many filamentous chlorophytes and xanthophytes, which require culturing to observe reproductive structures. To understand the biodiversity of freshwater algae in North America, a coordinated and standardized effort is needed. Suggestions for future methods will be presented.

(31 C) ALGAL DIVERSITY OF THE BURICA PENINSULA, PACIFIC PANAMA. Brian Wysor[1], D. Wilson Freshwater[2], Noemi Leon[3], Cindy Fernández-García[4,5], Paul Gabrielson[6], Valerie Charbonneau[1], Christopher Green[1], Jennifer Idol[2] & Seth Parham[2,]. [1]Department of Biology, Marine Biology & Environmental Science, Roger Williams University, Bristol, RI, 02809, U.S.A.; [2] Center for Marine Sciences, University of North Carolina – Wilmington, 5600 Marvin Moss Lane , Wilmington, NC, 28409, U.S.A.; [3]Departmento de Botánica, Universidad de Panamá, Panamá. [4]Programa de Investigación en Botánica Marina, Departamento de Biología Marina, Universidad Autónoma de Baja California Sur, La Paz, C.P. 23080, México, [5]Centro de Investigación en Ciencias del Mar y Limnología (CIMAR) and Escuela de Biología, Universidad de Costa Rica, San Pedro, 11501-2060, San José, Costa Rica, [6]University of North Carolina Herbarium, CB#3280 Coker Hall, Chapel Hill, NC, 27599-3280, U.S.A.

The marine flora of Panama harbors a rich diversity of green, red and brown algae and, despite chronic understudy, it is reported as the second most diverse marine flora along the Pacific Central American coast with 174 macroalgal species. Here, we introduce the marine flora of the remote Burica Peninsula, which is characterized by an extensive and interesting intertidal environment composed of firm, sedimentary benthos known as mudrock, on which abundant algal communities thrive, even during extended periods of exposure. Our collection of nearly 200 specimens from January 2011 represents the first marine floristic inventory of this region and includes new distributions records, the diversity of which is elaborated with both molecular and morphological characterizations.

(32 C) CULTURE-BASED STUDIES ON THE BIODIVERSITY OF CARBONATE-BORING ALGAE AND CYANOBACTERIA: THE IDENTITY OF *PLECTONEMA TEREBRANS* (OSCILLATORIALES, CYANOBACTERIA). Charles J. O'Kelly, Geneva J. Mottet, Angela R. Little & Robin Kodner. Friday Harbor Laboratories, University of Washington, Friday Harbor, WA, 98250, U.S.A.

Carbonate-boring oscillatorioid cyanobacteria are common and ubiquitous in modern oceans, have a fossil history that dates at least to the early Paleozoic, and may play a significant role in global carbon cycling and related processes including ocean acidification. Nearly all reports have placed these cyanobacteria in a single species, *Plectonema terebrans* Bornet & Flahault ex Gomont, 1892. The boreholes of cyanobacteria assigned to *P. terebrans* bear the ichnospecies (trace fossil) name *Scolecia filosa* Radtke, 1991. However, recent results from molecular inventories of field-collected samples suggest that this "one" species may in fact be many. As

Scolecia filosa is one of the ichnospecies used to infer the bathymetry and climate of ancient carbonates, knowledge of the biodiversity responsible for this trace is significant. No culture-based studies exist on these organisms, and therefore results from molecular inventories are hard to interpret. The type locality for *P. terebrans* is Le Croisic, France, a temperate-zone harbor, and the type is pink. Consequently, we obtained pink oscillatorioid cyanobacteria from carbonates at two temperate-zone locations, the Salish Sea and Massachusetts Bay. Nine of the eleven cultures that we obtained bored into calcium carbonate in the laboratory. Casts of the boreholes from these cultures were identical with those in field-collected samples. Cell dimensions of cultured strains were slightly larger than those originally reported for *P. terebrans*, but otherwise the morphology of the strains was comparable with the protologue. In phylogenetic trees (partial 16s rRNA gene), the nine strains formed a clade, distinct both from sequences of cultures assigned to P. terebrans and from GenBank sequences obtained from field-collected samples. The two non-boring cultures differed from the rest both in morphology and in gene sequence. We think that our carbonate-boring cultures are representative of authentic *P. terebrans*. We predict that pink oscillatorioid cyanobacteria from subtidal carbonates elsewhere will belong to this clade.

Poster Presentations

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

(P1 C) METAGENOMIC ANALYSIS OF THE BACTERIAL COMMUNITY ASSOCIATED WITH *PORPHYRA UMBILICALIS*. Lilibeth N Miranda[1], Keith Hutchison[2], Arthur R Grossman[3] & Susan Brawley[1]. [1]School of Marine Sciences, University of Maine, Orono, ME,04469, U.S.A.; [2]Department of Molecular and Biomedical Sciences, University of Maine, Orono, ME, 04469, U.S.A.; [3]Carnegie Institution for Science, Stanford, CA, 94305, U.S.A.

Macroalgae harbor microbial communities but a comprehensive analysis of bacterial biodiversity within those communities is still lacking. In this study, we analyzed the bacterial population associated with *Porphyra umbilicalis* from Schoodic Point, ME using a metagenomic approach. Our primary goals are to determine whether there is a core group of bacteria associated with *P. umbilicalis*, and whether the populations on these blades show seasonal trends. Twelve *P. umbilicalis* blades were collected (n=5, fall 2010; n=5, winter2011; n=2, P.um.1 lab culture), and two sets of primers that amplify the V5-V7 (Primer A) and V8-V9 (Primer B) variable regions of the 16S rRNA were used for taxonomic determinations. A total of 24 DNA samples amplified from the rRNA (n=12 blades, Primer A, Primer B) were processed for 16S rRNA pyrosequencing, which yielded 131,371 reads. Sequences from all samples were classified at 99% confidence threshold into six phyla (Actinobacteria, Proteobacteria, Firmicutes, Bacteroidetes, Planctomycetes and candidate division TM7) and a total of 15 bacterial orders using the Ribosomal Database Project Pyrosequencing Pipeline (http://pyro.cme.msu.edu/). The relative proportions of the15 bacterial orders (and genera) were different in fall versus winter. The dominant bacterial group was Flavobacteriales, although the Caulobacterales and Sphingobacteriales were also abundant. All blades, either generated in laboratory cultures or

collected from the wild (whether collected in fall or winter) had Caulobacterales (Bacteroidetes), Flavobacteriales (Bacteroidetes) and Rhodobacterales (Proteobacteria) in their microbial assemblage. This taxonomic analysis is the first step toward deciphering the roles of bacteria in *Porphyra* biology.

(P2 FTA) GROWTH AND PHOTOSYNTHETIC EFFICIENCY OF *PORPHYRA UMBILICALIS*: A CANDIDATE FOR RECIRCULATING INTEGRATED MULTI-TROPHIC AQUACULTURE. Lindsay A. Green & Christopher D. Neefus. Department of Biological Sciences, University of New Hampshire, Durham, NH, 03824, U.S.A.

Intensive mariculture, typically finfish, has been criticized for causing environmental pollution leading to coastal eutrophication. The desire for environmental sustainability has been coupled with an increase in aquaculture-based activities world wide. Recirculating integrated multi-trophic aquaculture systems are tank based and reuse water, but require a significant amount of biological and mechanical filtration to maintain proper water quality. Integrated multi-trophic aquaculture (IMTA) represents an environmentally sustainable method of aquaculture by properly coupling the waste production of primary crops (finfish) with the extractive capabilities of secondary crops (seaweeds and/or shellfish). *Porphyra umbilicalis* is a local species of the economically important genus *Porphyra* that is suited for recirculating IMTAs due to its ability to asexually reproduce from blade to blade. This study aimed to determine the growth rate and photosynthetic efficiency of *P. umbilicalis* under a matrix of temperatures, light levels, and photoperiods. Independently controlled water baths were used to maintain temperature (10º, 15º, and 20ºC) and neutral density filters were used to achieve 200, 100, 60, and 10 µmol photons/m^2/s light. Photoperiods were controlled using separate growth chambers (8:16, 12:12, and 16:8 light:dark, respectively). The effects of temperature of growth (% growth/day) were dependent on photoperiod ($p=0.0274$) and light level ($p=0.005$) with the highest growth at 10ºC under 8:16 and 12:12 and 10º-15º C under 16:8 light dark. Growth at 10º and 15º was significantly higher than at 20ºC and increased with light level to 100 µmol photons/m^2/s. The effects of photoperiod on growth were dependent on light level ($p=0.0173$) and highest under 12:12 light:dark and above 100 µmol photons/m^2/s light. Photoperiod significantly effected photosynthetic efficiency (Fv/Fm), but was dependent on light level ($p<0.000$) and was highest under low light conditions, except for at 8:16 light:dark.

(P3 FTA) COMPARISONS OF OPEN-COASTAL AND ESTUARINE POPULATIONS OF *PORPHYRA UMBILICALIS*. Renée L. Eriksen & Anita S. Klein. Plant Biology, University of New Hampshire, 46 College Road, Durham, NH, 03824, U.S.A.

Local adaptation is one of the driving forces of evolution, but we are only beginning to understand which genes are responsible in non-model organisms. *Porphyra umbilicalis* is a stress-tolerant red alga that lives in the high inter-tidal region of the open-coast in the north Atlantic. An isolated population has also been identified in the Great Bay Estuary System in New Hampshire, USA, and previous research identified 0.1% divergence among these populations in the chloroplast gene *rbc*L. Individuals living in open-coastal or estuarine habitats experience differences in salinity, temperature, and nutrient levels, and local adaptation may enable these populations to persist. We identified five microsatellite loci from the *P. umbilicalis* EST library,

and screened individuals from an open-coastal population (Fort Stark, NH) and individuals from the estuarine population (Dover Point, NH). Microsatellite assays revealed two distinct haplotypes: the open-coastal population has both haplotypes, while the estuarine population has only one of those haplotypes. Future directions include the creation of a reduced representation genomic library to identify regions of the genome that may be under selection.

(P4 UP) EXPERIMENTAL ANALYSIS OF BACTERIAL ISOLATES FROM *PORPHYRA UMBILICALIS* KÜTZING (P.um.1) ON GROWTH AND MORPHOLOGY OF BLADE CALLUS. Joseph Rankin, Lilibeth Miranda, & Susan H. Brawley. University of Maine, Orono, ME, 04469, U.S.A.

The growth and morphology of some marine macroalgae are affected by associated bacteria. In this study, bacteria were isolated from laboratory P.um.1 (UTEX 2951) cultures on marine LB agar plates, and DNA was isolated from subcultures of bacterial isolates. PCR and sequencing to the genus level using both variable 16S and full 16S rDNA primers identified two species of *Pseudomonas* (Gammaproteobacteria, Pseudomonadales) and a single species of *Maribacter* (Bacteroidetes, Flavobacteriales). Bladeless callus tissue was grown in a common garden and treated with antibiotics (polymyxin B, 15 µg/ml and cefotaxime, 15 µg/ml) for 1 week. Bacterial isolates were inoculated ($1x10^7$cells/ml) onto P.um.1 callus (n=3 pieces/well; 2 replicate wells/treatment/plate; 4 plates [2/chamber]) at 12°C under white fluorescent lamps at 45 µmol photon/m^2/s irradiance with a 10:14 h (L:D) photoperiod on shakers (140 RPM) to assess the effect of bacterial isolates on growth and/or morphology of P.um.1. On each plate, we kept two positive controls (without antibiotics or bacteria) and two negative controls (without bacteria). By 4 weeks, spores were released from callus tissue across all treatments, and blades began to develop on cultures. It is unclear what proportion of blade development was from spores settling on callus surfaces versus direct differentiation from callus tissue. To date, bacterial addition does not appear to have produced differences in growth or morphology of P.um.1 compared to controls.

(P5 C) THE STOMATOCYST OF *OCHROMONAS* SP., (CHRYSOPHYCEAE) A SMALL MIXOTROPHIC ALGA. Dale A. Holen. Biology, Penn State University, Dunmore, PA, 18512, U.S.A.

Many chrysophyte algae produce species-specific siliceous resting cysts also called stomatocysts or statospores as part of the life-history cycle. As stomatocysts are preserved in lake sediments they leave an historical record of changes in chrysophyte flora which can be useful paleolimnological markers of past environmental conditions. However the biological affinity of most stomatocysts is unknown. In this paper I describe the morphological features of a stomatocyst produced, in laboratory culture, by a small (5.3 µm diameter) mixotrophic species of *Ochromonas* isolated from a eutrophic pond in Northeast Pennsylvania. During the early developmental stage of the stomatocyst the surface appears very convoluted with silica folds interwoven into a rugate reticulum. Continued silica deposition results in a developmentally-mature cyst with a smooth surface. The stomatocyst is primarily oval in shape with an average length and width of 7.5 x 6.2 µm respectively. Spherical-shaped cysts were also observed. Collar morphology, a feature regarded to be of taxonomic importance, is variable in this stomatocyst.

The collar is wide and conical with a rounded apex but some stomatocysts possess incomplete or false conical collars with breaks of variable length while others possess true conical collars. The pore is regular. To broaden the interpretative value of these microfossils there needs to be an increased emphasis towards linking stomatocyst morphotypes, including environmental requirements, to their vegetative counterparts.

(P6 C) SEASONAL SUCCESSION IN GULF OF MAINE *PSEUDO-NITZSCHIA* COMMUNITIES. Katherine Hubbard[1], Claire Ellis[2], Emlyn Resetarits[3], Inci Tüney[1,4], E. Virginia Armbrust[2] & Donald Anderson[1]. [1]Woods Hole Oceanographic Institution, Woods Hole, MA, U.S.A.; [2]University of Washington School of Oceanography, Seattle, WA, U.S.A.; [3]Columbia University, New York, NY, U.S.A; [4]Ege University, Biology, Bornova, Turkey.

Species in the toxic marine diatom genus *Pseudo-nitzschia* are commonly observed in the Gulf of Maine (GOM), but little is known about the spatial and temporal occurrence of toxic species and domoic acid toxicity there. A high-throughput DNA fingerprinting method, automated ribosomal intergenic spacer analysis (ARISA), was used to quantitatively describe *Pseudo-nitzschia* species distributions in field samples collected in the GOM, Georges Bank, and the Bay of Fundy during monthly hydrographic surveys (May to August) in 2008 and 2010. *Pseudo-nitzschia* species were detected on all cruises, in all 209 samples analyzed to date. Eight *Pseudo-nitzschia* species were identified, and three additional ARISA fragments were detected during both years and likely represent novel diversity. Nearshore GOM communities were primarily dominated by the minimally toxic, small-celled species *P. delicatissima*. Offshore at Georges Bank, more spatially and temporally diverse assemblages were observed. Six species demonstrated positive or negative associations with temperature and/or salinity ($p<0.05$ for Spearman's R), and similar patterns of community succession were observed at Georges Bank during both years. The toxic large-celled species *P. seriata* dominated May/June communities and was significantly, negatively correlated with temperature. A separate toxic species within the *P. pseudodelicatissima* species-complex was detected at only at a few stations south of Georges Bank in May and June. By July, this species dominated *Pseudo-nitzschia* communities in the flanking regions of Georges Bank, and by August, primarily occupied the shallow crest of the Bank. Preliminary analyses detected particulate DA in each of 26 Georges Bank stations tested. Ongoing and future research aims to further clarify the role of regional circulation and environmental processes in shaping local patterns of *Pseudo-nitzschia* species diversity and composition, as well as DA toxicity.

(P7 C) DIETARY CONNECTIONS BETWEEN *FUNDULUS HETEROCLITUS* AND A PCB-CONTAMINATED *ULVA* BLOOM IN NEW BEDFORD HARBOR. Elizabeth Hanlon[1], Donald Cheney[1] & John Logan[2]. [1]Biology Department and Marine Science Center, Northeastern University, Boston, MA, U.S.A.; [2]Massachusetts Division of Marine Fisheries, New Bedford, MA, U.S.A.

The frequency and distribution of algal blooms, particularly macroalgal blooms known as "green tides," appear to be increasing. New evidence collected regarding the polychlorinated biphenyl (PCB)-contaminated *Ulva* bloom located in the upper region of New Bedford Harbor (NBH), MA, Superfund site suggests that macroalgal blooms may be more harmful than previously thought. In the past, we have shown that the NBH *Ulva* bloom can concentrate total PCBs to

levels as high as 99 ppm. Here we present data collected from June to December, 2011, assessing the bloom's role as a major source of PCB entry into the NBH food web. We explored the dietary relationship between the bloom and one of NBH's two most abundant mid-trophic consumers, *Fundulus heteroclitus* (mummichogs). Monthly gut content analysis shows a consumption pattern that is highly correlated to the bloom's biomass. Gut contents were categorized as *Ulva,* detritus, or invertebrates and quantified for both total percent gut composition and relative quantity. *Ulva* was the dominant food item in the gut contents of *Fundulus* sampled from July-September (56-74%). This sampling period corresponds to the months of highest *Ulva* abundance and highest feeding activity of *Fundulus*. A dietary shift from *Ulva* to invertebrates was detected between September (55% *Ulva*, 44% inverts) and October (14% *Ulva*, 72% inverts), coinciding with a sharp decline in *Ulva* abundance from 657 g/m^2 to 10 g/m^2. Past ^{15}N stable isotope feeding studies using *Fundulus* have additionally shown that consumed *Ulva* is assimilated. Overall, these results imply that the contaminated bloom may be an important, newly reported method for the transfer of PCBs in the NBH food web to mid trophic species which could ultimately end up in the system's top-trophic predator, and popular recreational fish species, striped bass.

(P8 UP) BLOOM-FORMING *ULVA* SPECIES OVERWINTER PRIMARILY AS FRAGMENTS IN NARRAGANSETT BAY, RI. Amanda Ziegler, Shelby Rinehart, Michele Guidone, Tanja Schollmeier & Carol Thornber. University of Rhode Island, Department of Biological Sciences, Kingston, RI, 02881, U.S.A.

Anthropogenic pollution contributes to severe macroalgal blooms in Narragansett Bay, RI. These blooms are dominated by two distromatic *Ulva* species: *U. compressa* and *U. rigida*. Previously, we have demonstrated that bloom-forming distromatic *Ulva* species can overwinter as fragments in Narragansett Bay. However, field observations suggested that *Ulva* might also overwinter as germlings. As overwintering strategies can provide an avenue for bloom-forming species to quickly dominate in spring, the goal of this study was to determine the primary overwintering strategy of distromatic *Ulva* in Narragansett Bay. To accomplish this goal, we conducted a settlement tile experiment. Tiles were deployed at two bloom-impacted sites from October 2011-March 2012 and collected at monthly intervals to assess the total number of germlings of each algal species. In addition, we sampled available substrates from both field sites and inspected them for the presence and identity of germlings. We found significant differences in germling abundance and identity amongst all sites and months, while total germling abundance increased over time. We also observed a greater density of germlings at our protected cove site, while larger germlings were found at our more exposed site. Tiles collected in November and February were least similar in species composition, due to a shift in the algal community with the winter appearance of *Petalonia* spp. and *Punctaria* spp. In addition, distromatic *Ulva* decreased in abundance during winter months while tubular *Ulva* increased in abundance. The loss of distromatic *Ulva* during the winter suggests that the germlings of these species are competitively inferior to tubular *Ulva* and other winter species. This also indicates that, within Narragansett Bay, distromatic *Ulva* likely primarily overwinters as either fragments or as microscopic propagules below the size range examined during this study.

(P9 UP) POTENTIAL IMPACTS OF HERBIVOROUS FISH ON *ULVA* BLOOM BIOMASS. Tanja Schollmeier, Michele Guidone & Carol Thornber. University of Rhode Island, Department of Biological Sciences, Kingston, RI, 02881, U.S.A.

The addition of anthropogenically produced nitrogen and phosphorous to coastal habitats is a major problem that frequently results in the rapid growth, or bloom, of macroalgae. Within Narragansett Bay, RI, blooms are commonly formed by two species: *Ulva compressa* and *U. rigida*. These blooms co-occur with a number of invertebrates that have been previously studied for their impacts on bloom biomass. However, few studies have examined the abundance or potential grazing impacts of herbivorous fish. To address this information gap, we conducted surveys via seining from July 2011 to March 2012. In addition, we assessed gut contents of two suspected herbivores: *Fundulus heteroclitus* and *F. majalis*. We found that the most abundant fish species at bloom-impacted sites were *Fundulus heteroclitus* and *F. majalis*. *Fundulus heteroclitus* abundance peaked in September (mean 71.5 individuals per 216 m^3 of water) while *F. majalis* was most abundant in August (mean 108 individuals per 216 m^3 of water); no *Fundulus* were found in January and February. Preliminary results of gut content analysis suggest that *F. majalis* is carnivorous, as their winter diet consisted of copepods and ostracods. In contrast, *F. heteroclitus* appears to be herbivorous, as the majority of the gut contents were found to be phytoplankton of the genus *Prorocentrum*. If *F. heteroclitus* consumes *Ulva* as it becomes more abundant during the spring and summer, large populations of these fish could impact *Ulva* biomass, thereby influencing *Ulva* bloom severity. In future months, we intend to directly assess *F. heteroclitus* consumption of *Ulva* using paired-choice feeding assays to determine the rate of thallus consumption as well as whether they prefer *U. compressa* or *U. rigida*, as any feeding preference could influence the species composition of blooms.

(P10 UP) INDUCIBLE DEFENSE COMPOUNDS IN BROWN MACROALGAE. Kyle Martin & Ursula S.R. Röse. College of Arts and Sciences, Department of Biology, University of New England, Biddeford, ME, 04005, U.S.A.

The brown macroalgae *Fucus vesiculosus* remain abundant in the intertidal zones of the coast of Maine and the North Atlantic despite significant pressure from herbivores. This suggests that they may have defense mechanisms that protect them against herbivore and microbial attack. These defenses can be categorized into constitutive defenses that are always present in the algae and inducible defenses that are only produced by the algae when in the presence of an herbivore or injury. Phenolic compounds, particularly phlorotannins, have been suggested to act as antifeedants in brown algae *F. vesiculosus* in the intertidal zone at Biddeford Pool, Maine, U.S.A. were subjected to both mechanical injury and the signaling compound methyl jasmonate to investigate the inducibility of defense compounds and develop a time-course for their synthesis. Mechanical injury was achieved by using a razor blade to inflict small cuts along the algae thallus. At low tide, algae were also exposed to methyl jasmonate for 2 hours by dissolving the compound in ethanol to increase its volatility and releasing it into the headspace of the algae while enclosed in plastic bags. We found that both quantitative and qualitative differences in inducible compounds were observed within 6 days of mechanical injury or exposure to methyl jasmonate in comparison to control algae.

(P11 C) MAKING FRIENDS WITH A LONG ISLAND SOUND INVASIVE: NOVEL EVALUATION OF KEY RESOURCES OF *GRACILARIA VERMICULOPHYLLA* RELATIVE TO NATIVE *GRACILARIA TIKVAHIAE.* Mary Cirino[1], Andrew Bramante[1], Jang K. Kim[2] & Charles Yarish[2]. [1]Greenwich High School, Greenwich, CT, U.S.A. [2]Departments of Ecology & Evolutionary Biology and Marine Sciences, University of Connecticut, Stamford, CT, U.S.A.

Gracilaria vermiculophylla (*Gv*), a red alga native to northwest Pacific, invaded the Northeast U.S. coastal region nearly a decade ago. This invasive species appears well-adapted for its new environment replacing the native species *Gracilaria tikvahiae* (*Gt*). Both species represent a valuable ecological and economical resource, however, researchers require a better understanding of their composition, specifically the concentrations of lipids, proteins, and carbohydrates contained within its structure. This study is centered on the evaluation of these components of the invasive *Gv* and the native *Gt*, as well as on the development of quick and efficient methods for the determination of said components. *Gracilaria* samples were grown at the University of Connecticut's Marine Biotechnology Laboratory (Stamford, CT) and at the Bridgeport Regional Aquaculture Science and Technology Center aquaculture laboratory (Bridgeport, CT) during the summer of 2011. For total sterols analysis, 5g of dried, powdered seaweed was soaked with 50 ml of a 1:1 v/v MeOH:$CHCl_3$ mixture. Following separation and washing, the extracts were analyzed via ATR-FTIR and GC/FID. FTIR spectra support the successful separation of cholesterol, while GC-FID results indicate that the provided samples of *Gt* contain 0.4% cholesterol, the main sterol in red algae; that of *Gv* contain 0.2%. For total protein analysis, 0.5g of dried powdered algae was soaked in 40 ml water and incubated for 6 hours at 4°C. After the addition of 10ml of 0.1M NaOH, and separation via centrifugation, analysis of the crude extract via a Bradford Protein Assay indicate protein content of Gt is 5.6%, while that of *Gv* is 5.0%. Sugar content of both *Gt* and *Gv* was determined via HPLC, with RI Detection. *Gt* was found to contain 5.66% mannose, 8.7% galactose, and 1.06% xylose, while *Gv* contained 1.4% xylose and 22.1% galactose.

(P12 FTA) PHOTOSYNTHETIC DEPRESSION, CELL VOLUME ENLARGEMENT, AND STABLE ELEMENTAL RATIOS IN *THALASSIROSIRA WEISSFLOGII* UNDER PHOSPHORUS LIMITATION: REVISIT OF THE UTILITY OF REDFIELD RATIO FOR ASSESSING NUTRIENT LIMITATION. Sheng Liu [1,*], Zhi-Ling Guo[1,3], Tao Li [1,2], Hui Huang[1] & Senjie Lin[1,4]. [1] Key Laboratory of Marine Bio-resources Sustainable Utilization, South China Sea Institute of Oceanology, Chinese Academy of Sciences, Guangzhou, China, 510301; [2] Tropical Marine Biological Research Station in Hainan, Chinese Academy of Sciences, Sanya, China, 572000; [3] Graduate University of Chinese Academy of Sciences, Beijing, China, 100049; [4] Department of Marine Sciences, University of Connecticut, Groton, CT, 06340, U.S.A.

Phosphorus is one of the essential elements for the growth and metabolism of phytoplankton. In this study, physiological changes of *Thalassirosira weissflogii* were measured under different dissolved inorganic phosphate (DIP) addition treatment in semi-continuous cultures. The results showed that the cell size increased with decreasing DIP availability. In the P-deleted (f/2-P) treatment it was 1.48 times bigger than that in the P-limited (f/100) treatment and 2.67 times bigger than that in the P-saturated (f/2 and f/10) treatment. P content in P-saturated treatments (1.6 pg•$cell^{-1}$) was about 2.3 time higher than that in P-limited and P-deleted treatments (0.7 pg•$cell^{-1}$), however, N/P ratio of *T. weissflogii* was relatively stable among all treatments and fluctuated slightly around 25. The ratio of fucoxanthin to Chl *a* (Fuco/Chl *a*) kept stable in P-saturated cultures and decreased quickly in P-limited and P-deleted cultures. The photosynthetic

efficiency index $\Delta F/F_m$' was relatively stable at ~0.50 in the P-saturated cultures, and it dropped to 0.4 at P-limited treatment and quickly dropped to close to 0.1 at P-deleted treatment during the experimental period. In general, *T. weissflogii* exhibited photosynthetic depression, cell volume enlargement and relatively stable elemental ratios with DIP addition decreasing. Our results suggest that N/P ratio is not a universally useful parameter for evaluating algae nutrient dynamics, and $\Delta F/F_m$', Fuco/Chl *a* ratio and cell size may be better indicators of nutrient limitation.

(P13 FTA) INVASIVE *GRACILARIA VERMICULOPHYLLA* AS A NOVEL SUBSTRATE IN SOFT SEDIMENT BENTHIC COMMUNITIES. Christine Newton[1, 2]; Michele Guidone[1;] Carol S. Thornber[1].[1] University of Rhode Island, Kingston, RI, 02881, U.S.A.; [2] Marine Science Center, Northeastern University, Nahant, MA, 01908, U.S.A.

The recent invasion of the red alga, *Gracilaria vermiculophylla*, to the Atlantic and Eastern Pacific has the potential to significantly alter the soft sediment benthic habitat in which it invades. In particular, *G. vermiculophylla* provides a novel hard substrate, increasing the habitat complexity, and potentially facilitating the reproductive success of native organisms. *Illyanassa obsoleta*, the native mud snail, is extremely abundant in these soft sediment habitats and co-occurs over the entire invaded range of *G. vermiculophylla*. Following observations that *I. obsoleta* utilizes this novel substrate for egg deposition, we quantified the *in situ* abundance of eggs on *G. vermiculophylla*, along with other co-occurring macrophytes. Additionally, through mesocosm experiments we show *I. obsoleta* preferentially deposits eggs on the invasive *G. vermiculophylla* over native substrates. However, despite the thick layer of egg capsules found on *G. vermiculophylla,* no detrimental effects were seen on thalli growth, while growth of the native red alga, *Ceramium virgatum*, was significantly reduced when egg capsules were present, suggesting this invader will continue to out-compete native macrophytes while facilitating reproduction of the native mud snail. This novel interaction has the potential to significantly alter biological interactions in soft sediment communities through a variety of different mechanisms, including the alteration of trophic cascades via the increase in mud snail abundance, while increasing habitat complexity by introducing additional refuge habitat for benthic infaunal organisms. Furthermore, facilitation of the reproductive success of mud snails may lead to increases in the occurrence of cercarial dermatitis (commonly known as swimmer's itch), as *I. obsoleta* is a known intermediate host organism.

(P14 FTA) THE EFFECT OF OCEAN ACIDIFICATION ON THE BINDING CAPABILITIES OF EXOPOLYMERIC SUBSTANCES WITH METALS, OF A MARINE BENTHIC DIATOM, *CYLINDROTHECA CLOSTERIUM.* Vanessa O'Donnell & Steven Zeeman. Department of Marine Sciences, University of New England, Biddeford, ME, 04005, U.S.A.

Exopolymeric substances (EPS) are abundantly produced by marine diatoms and have strong absorptive and adhesive qualities, able to bind heavy metals from very dilute aqueous solutions. The binding properties of EPS are greatly impacted by shifts in ocean pH, changing the speciation of metals from complex to free, increasing their overall toxicity in marine environments. This work focuses on determining the effect of ocean acidification on metal binding within the EPS matrix created by the diatom *Cylindrotheca closterium.* This species was chosen because it is a

well-studied organism, that produces large quantities of EPS and is found in mudflats where toxic metals tend to accumulate. Preliminary data show lowering pH decreases the binding of EPS with copper. This study also aims at determining if metals are preferentially bound over one another. Diatom EPS was isolated by tangential flow filtration, exposed to various metals and analyzed using flame atomic absorption spectrometer. In summary, ocean acidification, caused by increased CO2 in the atmosphere is a growing concern and is directly correlated with anthropogenic activity. As oceans continue to acidify, changes in the binding capacity of EPS may decrease, increasing the mobility of toxic metals in marine environments.

(P15 UP) PROTOCOL DEVELOPMENT FOR SMALL BATCH AGAR EXTRACTION FROM *GRACILARIA TIKVAHIAE.* Jacob Torok & Kirk Shadle. Bridgeport Regional Aquaculture Science & Technology Education Center, 60 St Stephens Road, Bridgeport, CT, 06605, U.S.A.

Small batch agar extraction will allow labs to produce in house agar, giving them the ability to maintain quality control, ensure validity, and eliminate the need to purchase large batches of dehydrated agar. A small batch of agar will be extracted from *Gracilaria tikvahiae*, a red macro algae. The algae is dried in an oven at 65°C, and ground into a fine powder. Then the agar will be extracted from the seaweed via adding 2.5 g of the ground seaweed to 20 ml of the solvent (distilled water mixed with acetic acid) with a pH of 4. Let this sit for 10 minutes. The solution will be warmed on a hot plate at 99°C for 3 minutes. While the solvent is warming put 350 ml of distilled water in an Erlenmeyer flask, add a stir bar, and put it on the same hot plate. Put 50 ml of distilled water in a small beaker, this will be used to rinse the beaker with the solvent in it to ensure that all the seaweed particles are transferred into the Erlenmeyer flask. After the 3 minutes, pour the beaker with the solvent into the Erlenmeyer flask. Use the 50 ml of water to remove any remaining particles in the beaker and pour it into the Erlenmeyer flask. Turn the stirrer on, and set to 60 rpms. Keep the solution on the hot plate set to 99°C for another 6 hours. Place the flask in the drying oven overnight at 65°C. The solution is filtered and undergoes forced evaporation. After evaporation and once the extract gels, it will be placed in a freezer overnight and then lyophilized. The maximum percent yield of agar is 78.8%. The procedure has been altered to see if the same yield could be matched or increased. One yield of an altered procedure resulted in 74.8% of agar. The small batch of agar extraction is successful and is efficient. This procedure can be used in labs to obtain small batches of agar ensuring quality control of the product.

(P16 C) LARGE SCALE OBSERVATIONS OF ROCKWEED (*Ascophyllum nodosum*) STANDS IN EASTERN CANADA: WHAT CAN WE GENERALIZE FROM SMALL SCALE STUDIES? Raul A. Ugarte. Acadian Seaplants limited. 30 Brown Av. Dartmouth, NS, B3b 1X8, Canada.

Ascophyllum nodosum (rockweed) is an important economic resource for the seaweed industry in both Europe and the Atlantic Provinces of Canada and Maine, USA. Rockweed is used on both continents as a source of soil conditioner, animal feed and as a raw material for the extraction of alginate and biostimulant extracts. However, this brown macroalga is also an important habitat along the rocky intertidal as shoots and clumps of shoots add to the benthic structural complexity

of the intertidal environment, providing refuge and feeding grounds for invertebrates and vertebrates. For these reasons, *A. nodosum* is probably one of the most studied seaweed of the north Atlantic, with hundreds of papers published on its biology, ecology and population dynamics. As part of a management strategy, rockweed stands or "beds" have been studied / recorded and some population parameters measured annually for more than 15 years at a large scale by Acadian Seaplants Limited (ASL), the main user of this resource in eastern Canada. Some observations and information collected by ASL in this region on population dynamics do not necessarily match published information. This study analyses information on growth rates, productivity, regeneration capacity and recruitment and concludes that *A .nodosum* is highly flexible variable and resilient and caution should be exercised when extrapolating results from limited localized studies to all *Ascophyllum* populations.

(P17 C) CULTURE-BASED STUDIES ON THE BIODIVERSITY OF CARBONATE-BORING ALGAE AND CYANOBACTERIA: THE CULTURE COLLECTION. Charles J. O'Kelly & Geneva J. Mottet. Friday Harbor Laboratories, University of Washington, Friday Harbor, WA, 98250, U.S.A.

As the role of carbonate-boring algae and cyanobacteria in tropical reef ecosystems becomes both better understood and of greater concern in the contexts of anthropogenic global warming and ocean acidification, it becomes more important to understand the biodiversity of the algae and the contributions made by individual species to reef productivity and reef dissolution rates. Here, we report the current status of our library of carbonate-boring algal and cyanobacterial strains, isolated predominantly from the tropical waters of Hawai`i and the cold-temperate waters of Washington and Massachusetts. As of March 2012, the collection contains 355 strains, including 60 cyanobacteria (genera *Hyella*, *Mastigocoleus*, *Plectonema*), 208 chlorophytes (genera *Dilabifilum*, *Eugomontia, Gomontia, Monostroma, Ostreobium, Phaeophila, Ruthnielsenia, Ulvella*), and 87 rhodophytes ("*Porphyra*" assemblage: genera *Bangia*, *Pyropia*, *Wildemania*). We assess strains for their ability to bore into calcareous substrata and, to a limited degree, for their temperature tolerance, and we prepare casts for direct comparison of boreholes with ichnotaxa (trace fossil taxa) from the literature. We also obtain "barcode" DNA sequences from selected strains. From morphological, physiological, and molecular data, we infer that the global biodiversity of carbonate-boring algae and cyanobacteria is significantly greater than previously recognized, and that all species are not globally distributed as is commonly assumed for many taxa. Biodiversity appears to be particularly high among organisms assigned to the genera *Hyella*, *Ostreobium*, *Phaeophila*, and *Plectonema*, as well as the "*Porphyra*" assemblage. For some of these genera, the common practice of referring all or most collections to a single species has been falsified; the actual number of entities (putative species) documented may be in the tens or even (for *Ostreobium*) in the hundreds. Algae here assigned to *Dilabifilum*, collected from upper-intertidal barnacles at various Salish Sea and Vancouver Island locations, are seldom reported in either the phycological or geological literature, and may represent new taxa.

(P18 FTA) EFFECTS OF BMP IMPLEMENTATION ON PERIPHYTON IN AGRICULTURAL STREAMS. Sarah B. Whorley & John D. Wehr. Louis Calder Center Biological Field Station - Fordham University 53 Whipporwill Rd. Armonk, NY, 10504, U.S.A.

Anthropogenic disturbances often negatively impact stream ecosystems. This study explores effects of agriculture and remediation by agricultural best management practices (BMPs). We examine how the duration of BMP implementation may affect water quality and periphyton in streams within the upper Delaware River watershed, NY, and consider possible seasonal effects. We examined 20 streams in four categories: non-agricultural, agricultural +BMPs in place <2 years, agricultural +BMPs established >3 years, and agricultural without BMPs present. Streams were sampled monthly (July-Nov 2011) and analyzed for SRP, TDP, NO_3-, NH_4+, TDN, pH, and conductivity; periphyton assemblages were analyzed for species composition, biomass (*Chl-a*, , AFDM), C:N:P stoichiometry, and fatty acid composition. First year data indicate a trend in which non-agricultural streams had the lowest values of most metrics (but greater biodiversity), BMP streams had intermediate levels (BMP duration was NS), and agricultural streams with no BMPs had the greatest levels (but least biodiversity). While results are suggestive, these data support the need for continuation long-term studies to resolve the influence of established management plans on improving biological and chemical integrity of agriculturally influenced rivers.

(P19 C) DEVELOPMENT OF SEA VEGETABLE CULTURE TECHNOLOGIES IN MAINE. S. Redmond[1], D. Morse[2], S. Brawley[3], N. Brown[4], P. Dobbins[5], S. Eddy[6], S. Erhart[7], P. Fischer[8], J. Larrabee[9], T. Levesque[10], M. Moretti[11], C. Newell[12], B. Olsen[13], V. Olsen[14], T. Olson[15], E. Young[16]. [1,2] Maine Sea Grant, Orono, ME, 04469, U.S.A.; [3] Marine Sciences, University of Maine, Orono, ME, 04469, U.S.A.; [4,6] Center for Cooperative Aquaculture Research, Franklin, ME, 04634, U.S.A.; [5,15]OceanApproved, Portland, ME, 04103, U.S.A.; [7] Maine Coast Sea Vegetables, Franklin, ME, 04634, U.S.A.; [8,9,10,12] Pemaquid Mussel Company, Damariscotta, ME, 04543, U.S.A.; [11]WildOcean Aquaculture, Hampden, ME, 04444, U.S.A.; [13,14]LongCove Oyster Company, Stonington, ME, 04681, U.S.A.; [16]Blue Hill Bay Mussels, Hancock, ME, 04640, U.S.A.

Biological integration is important to achieve environmental sustainability and multiple crops in aquaculture. We are building infrastructure in Maine to encourage use of sea vegetables in integrated polytrophic aquaculture (IMTA or IPTA) with field trials of the kelp *Saccharina latissima* on shellfish lease sites and by establishing a spore seed-stock nursery for multiple species (e.g., laver, dulse, kelps) at the Center for Cooperative Aquaculture (University of Maine, Franklin, ME). A pilot project in integrated aquaculture was initiated in December 2011 by seeding seven different shellfish lease sites from Casco Bay to Lamoine with juvenile sugar kelp plants. Information on site characteristics, growth and yield will be collected throughout the growing period. Results from this pilot project will be used to inform further work in integrated systems, to build relationships between growers and potential buyers, and to encourage diversification. Our seed stock system for *Porphyra umbilicalis* was started in January 2012 from a unialgal culture from the Maine coast. Mature, spore-producing plants were produced from juveniles within 6 weeks. Net seeding with wild and laboratory raised seed stock is in progress. Seeded nets will be incubated in a recirculating fish aquaculture system, and preliminary trials

show blades retain their deep reddish-brown color without any other nutrient additions. These studies should expand interest among Maine aquaculturists in sea vegetable crops for the development of a sustainable seaweed aquaculture industry in Maine.

(P20 C) EFFECTS OF HYPO-OSMOTIC STRESS AND TEMPERATURE ON THE GROWTH OF *GRACILARIA*. Jang K. Kim, Kyle Kovtun, Richelle Stainton & Charles Yarish. Departments of Ecology & Evolutionary Biology and Marine Sciences, University of Connecticut, CT, 06901, U.S.A.

The salinity regime in the LIS habitats of *Gracilaria* is generally 15–30psu, however, *Gracilaria* is often found at much lower salinity conditions in embayments. Recent studies have demonstrated that the non-native *Gracilaria vermiculophylla*, is replacing the native species *G. tikvahiae* and has become the dominant species throughout southern New England and LIS. This study is focused on determining the effects of a hypo-osmotic stress in terms of growth and survival of both native and non-indigenous *Gracilaria* species to determine if tolerance to hypo-osmotic stress is important for the spread of the non-native species. Approximately one centimeter long apical segments from each *Gracilaria* species were cultivated over three weeks at five different salinities, 5, 15, 20, 25, and 30psu and at five different temperatures, 5, 10, 15, 20 and 25ºC. The length of apical segments was measured weekly to estimate growth rates. Both salinity and temperature affected the growth of both *Gracilaria* species. The native *G. tikvahiae* did not grow or even had negative growth rates at suboptimal conditions, < 20 psu and < 20ºC. However, the non-native *Gracilaria vermiculophylla* grew equally well in the salinity range of 15-30psu. The highest growth rates of *G. tikvahiae* were found at 30 psu and 20 and 25 ºC, 6.8 - 7.1% d-1. The highest growth rates of *G. vermiculophylla* were 7.6-9.5% d-1at 25 ºC and 15-30psu. The native *G. tikvahiae* did not survive over three weeks of culture at the suboptimal condition, < 10 ºC and < 20psu while the non-native *G. vermiculophylla* grew continuously at all conditions tested. This result suggests that tolerance to the environmental stresses, especially hypo-osmotic stress, may role as a key factor determining the growth and survival of the invasive *Gracilaria* species in embayments and estuaries.

(P21 C) SUSTAINABLE SEAWEED CUTTING? THE ROCKWEED (*ASCOPHYLLUM NODOSUM*) INDUSTRY OF MAINE AND MARITIME CANADA. Robin Hadlock Seeley[1] & William H. Schlesinger[2]. [1]Shoals Marine Laboratory and Department of Ecology and Evolutionary Biology, Cornell University, NY, U.S.A.; [2]Cary Institute of Ecosystem Studies, Millbrook, NY, U.S.A.

Burgeoning global demand for products derived from seaweeds is driving the increased removal of wild coastal seaweed biomass, an emerging low-trophic level industry. These products are marketed as organic and "sustainable." Brown macroalgae, such as kelps (Laminariales) and rockweeds (Fucales), are foundational species that form underwater forests and thus support a diverse vertebrate, invertebrate, and algal community—including important commercial species—and deliver organic matter to coastal ecosystems. The measure of sustainability used by the rockweed (*Ascophyllum nodosum* (L.) LeJolis) industry, maximum sustainable yield, accounts for neither rockweed's role as habitat for 150+ species, including species of commercial or conservation significance, nor its role in coastal and estuarine ecosystems. To determine whether

rockweed cutting is "sustainable" will require data on the long-term and ecosystem-wide impacts of cutting rockweed. Once a sustainable level of cutting is determined, strict regulation by resource managers will be required to protect rockweed habitat. Until sustainable levels of cutting and appropriate regulations are identified, commercial-scale rockweed cutting presents a risk to coastal ecosystems and the human communities that depend on those ecosystems.

(P22 FTA) GROWTH AND AMMONIUM UPTAKE IN THE RED ALGA *CHONDRUS CRISPUS* (STACKHOUSE) AND ITS POTENTIAL USE IN RECIRCULATING INTEGRATED MULTI-TROPHIC AQUACULTURE SYSTEMS. Lindsay A. Green, Katherine R. Hladki & 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; however, some types of aquaculture can have negative environmental impacts. Recirculating aquaculture systems (RAS) are closed systems that reduce environmental impacts by reusing water and eliminating potentially harmful interactions with wild species. Recirculating systems require significant mechanical and biological filtration to maintain appropriate water quality and fish health. Constant filtration has high energy costs and can decrease profitability of these systems. Integrated multi-trophic aquaculture (IMTA) systems utilize extractive crops such as seaweed to provide bio-filtration and stabilize water quality while increasing profitability by producing a secondary crop. *Chondrus crispus* (Stackhouse) is a good potential species for use in IMTA because of its ability to uptake compounds such as ammonium as well as it economic value as a carrageenophyte and a sea vegetable. This study looked at the effect of light level, temperature, and photoperiod on growth rates and ammonium uptake rates of *Chondrus crispus*. Blades were grown in individually controlled water baths at 10°, 15°, and 20° C. Neutral density filters were wrapped around each flask to obtain PAR levels of 200, 100, 60 and 20 μmol/m^2/s light. Photoperiod was controlled using separate growth chambers set at 16:8, 12:12, 8:16 light:dark, respectively. Fresh weights and ammonium uptake were measured weekly over a four week period. Preliminary results show that light level had a significant effect on growth rate ($p<0.001$). Growth (% growth/day) at 200 and 100 μmol/m^2/s were not significantly different from one another (8.1 and 6.8, respectively) but were significantly greater than growth at 60 and 20 μmol/m^2/s (3.7 and 1.2, respectively). Growth at 60 μmol/m^2/s was significantly greater than at 20 μmol/m^2/s.

(P23 C) MORPHOLOGICAL VARIABILITY OF CHRYSOPHYTE CYSTS FROM AN EOCENE MAAR LAKE IN THE CANADIAN ARCTIC**.** Anne Marie Lott & Peter A. Siver. Botany Department, Connecticut College, New London, CT, U.S.A.

Siliceous microfossils abound in lake sediments deposited in the Giraffe kimberlite diatreme, a Middle Eocene maar lake situated near the Arctic Circle in the Northwest Territories of Canada during the Cenozoic hot house. Overall, this extensive core contains an astonishing diversity of exquisitely preserved siliceous microfossils representing the Chrysophyceae, Synurophyceae and Bacillariophyceae, as well as sponge remains and scales from testate euglyphids and heliozoans. Of the vast array of microfossils, Chrysophyceae and Synurophyceae resting stages known as stomatocysts, or cysts, are by far the most abundant, often accounting for over 50% of all microfossils and dominating much of the 68.3 m of lacustrine facies. To date, we have

documented well over 100 different cysts that collectively represent a vast array of morphological structures. We will use remains of ten different cyst types to demonstrate the range in size, cyst wall ornamentation, pore structure and collar development. Although some of the cysts have smooth and unornamented walls as is commonly reported in modern waterbodies, many are highly ornamented with papillae, pores, ridges and spines, and it is clear that cyst development was well established by the Eocene. In modern lacustrine systems, we often do not know which organisms produce many of the cyst types that are observed. Interestingly, in the Giraffe core we can often uncover well developed cysts that still contain parts of the parent cell wall, allowing us to link some cyst types with specific organisms. In the future, we plan to publish an atlas of these Eocene resting stages and use their remains to piece together the history of the waterbody.

(P24 FTA) EVALUATING THE GENETIC DIVERSITY OF THE NON-MODEL ORGANISM, *CODIUM FRAGILE* IN THE NW ATLANTIC. Chris Benton[1], Anita Klein[2], Kelley Thomas[1], Darren Bauer[1]& Feseha Abebe-Akele[1]. [1]Molecular, Cellular and Biomedical Sciences, Rudman Hall, 46 College Road, University of New Hampshire, Durham, NH, 03824, U.S.A.; [2]Department of Biological Sciences, Rudman Hall, 46 College Road, University of New Hampshire, Durham, NH, 03824, U.S.A.

The invasive green alga *Codium fragile* subsp. *fragile* was first observed within the Northwest Atlantic during the 1950's. It has spread to the Gulf of Maine and the Canadian Maritime Provinces, as well as southward to the mid-Atlantic. We are investigating the phylogeography of *C. fragile* in the Northwest Atlantic and have observed haplotype variation among populations in Prince Edward Island (PEI), Canada. We detected 2 *rps3-rpl16* haplotypes, one of which was restricted to Malpeque Bay PEI. As chloroplast DNAs are too conserved for a population study, and there are no available nuclear sequences for *Codium,* 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 contaminating organisms, the contigs were examined by BLAST analysis against the NCBI non-redundant protein database. There were 1200 matches to other green algae, *Volvox carteri*, *Chlamydomonas reinhardtii*, and *Chlorella variabilis*. Among these contigs, there were a total of 180 microsatellites: 75.5% mononucleotide, 9% dinucleotide, 14.4% trinucleotide, and 1.1% tetranucleotide repeats. Fifty microsatellite containing contigs were analyzed for PCR primer design; currently we have constructed 10 primer pairs. We intend to use these markers to survey NW Atlantic populations of *Codium fragile* for genetic variation, which will allow us to describe population structure. Additional primers will be designed to survey putative single nucleotide polymorphisms observed in among the RNA seq reads. Further analysis of the metagenomes will also separate contigs based on GC content in order to assess endophyte and epiphyte diversity.

(P25 FTA) CRYPTIC DIVERSITY WITHIN THE AUSTRALIAN HALYMENIACEAE (HALYMENIALES, RHODOPHYTA). Lesleigh Kraft & Gary W. Saunders. Centre for Environmental and Molecular Algal Research, Department of Biology, University of New Brunswick, Fredericton, NB, E3B 5A3, Canada

The Halymeniaceae is a family of red algae that are unique in their possession of auxiliary cell ampullae. Globally the family encompasses roughly 270 species; in Australia, with its extremely

rich algal flora, records exist for 13 genera and 27 species – 22 with Australian type localities. Like almost all red algae, members of the Halymeniaceae have simple morphologies and are subject to high degrees of morphological plasticity and convergent evolution. In addition, Australia has long suffered from a Eurocentric bias with regards to marine macroalgal identification. As a result, traditional taxonomic approaches can be ineffective at resolving relationships among taxa and species richness can be under appreciated, with both novel and cryptic species overlooked. The DNA barcode (mitochondrial COI-5P) has demonstrated utility at identifying species diversity among red algae. Preliminary screening of Australian Halymeniaceae with COI-5P sequence data has revealed a two-fold increase in species richness compared to current morphological lists. These species are now being subjected to detailed alpha taxonomic and molecular phylogenetic studies. These combined approaches will identify novel/cryptic/overlooked Halymeniaceae in Australia, describe them in all of their anatomical detail, and include them in a wider halymeniacean classification.

(P26 C) PHYLOGENETIC RELATIONSHIPS AND DISTRIBUTION PATTERNS OF *CYSTOSEIRA SPP.* IN THE AEGEAN SEA. Inci Tüney[1,2], Katherine Hubbard[2] & Atakan Sukatar[1]. [1]Woods Hole Oceanographic Institution, Woods Hole, MA, U.S.A.; [2]Ege University, Biology, Bornova, Turkey

The brown macroalga genus *Cystoseira* is found mostly in temperate areas of the Northern Hemisphere. Up to 34 morphologically distinct variants of *Cystoseira spp.* have been previously recognized in the coastal regions of Turkey, however, definitive taxonomic identification can be difficult because there is widespread cryptic inter- and intraspecific morphological variability. We collected *Cystoseira* samples during February, June, and September of 2010 from the rocky infralittoral zone of the Aegean Sea along a 500 km section of the western coast of Turkey. Samples were collected at 20 stations. Northern stations were influenced by the colder, fresher Black Sea, in contrast with southern stations, influenced by the warmer, saltier Mediterranean Sea. Thirty-five *Cystoseira* thalli were collected. Microscopic identification took into account blade branching patterns and base and thallus structure. The variable internal transcribed spacer 1 (ITS1) region was sequenced for phylogenetic analyses. Previous studies informed the use of a DNA extraction methodology optimized for *Cystoseira*, and high quality sequence data was generated for 31 specimens. The presence of eleven previously described *Cystoseira* species along the Turkish coast was confirmed by both molecular and morphological taxonomic analyses. Three additional algal specimens exhibited unique morphological features that prevented definitive identification. Sequences for two of these were 19-30% differentiated from known *Cystoseira* species, suggestive of novel diversity. These and other sequences were grouped into three distinct ITS1 clades. During June and September, average water temperatures exceeded 20°C and taxa from two of the three clades were identified. During February, when the average temperature was 13°C, taxa within the same two clades and also a third clade were identified. The genus *Cystoseira* has been identified as a potential water quality indicator in European waters, and our preliminary results suggest that *Cystoseira* species may also be good bioindicators of ecological conditions.

(P27 C) A FIRST SURVEY OF THE GENUS *ACROCHAETIUM* IN CANADA WITH DESCRIPTION OF *ACROCHAETIUM BONNENSE* SP. NOV. Susan L. Clayden & Gary W. Saunders. Centre for Environmental & Molecular Algal Research, Biology, University of New Brunswick, Fredericton, NB E3B 5A3, Canada

Acrochaetium is a genus of diminutive marine filamentous red algae, world-wide in distribution. During routine sampling of macroalgae in Canada, we sampled *Acrochaetium* growing on other algae, seagrass, or invertebrates. Defining features of the genus include a stellate (star-shaped) plastid with central pyrenoid, and life history with gametophytes having a unicellular and sporophytes a multicellular base. Seven species were identified in the Atlantic, two in the Pacific and a single in the Arctic by mitochondrial COI-5P (cytochrome oxidase subunit I) analysis. Levels of intra (0-0.3%) and interspecific (7.9-19.3%) variation (including from a diverging species (0.9%)) were consistent with previous results from other florideophyte red algae. A collection from Newfoundland was unique in COI sequence (and interestingly a match to an isolate from Tasmania) and we describe *Acrochaetium bonnense* sp. nov. We also resolved and highlight relationships from analysis of the LSU (large subunit rDNA) among the Atlantic (*A. secundatum*/*A. virgatulum*/*A. luxurians*) and Pacific (*A. arcuatum*/*A. vagum*/*A. porphyrae*) complexes of species.

(P28 C) APPLICATION OF THE V4 REGION OF THE 18S RRNA GENE TO DNA BARCODE DIATOMS (BACILLARIOPHYTA) FROM ENVIRONMENTAL SAMPLES OF THE EIGHTMILE RIVER IN CONNECTICUT. Diba Khan-Bureau, Louise Lewis & Gary Robbins. University of Connecticut, Storrs, CT, 06269, U.S.A.

Diatoms are ubiquitous and ecologically important. Diatoms are accepted as biological indicators for monitoring and assessing watercourses but can be used additionally to evaluate other important ecological questions. Various approaches have been used to identify diatoms and more recently the use of molecular analysis has been employed. Using morphology alone to distinguish diatom species can be difficult, thus many researchers have proposed the use of DNA barcoding to provide consistent identification of diatoms and make the data from different studies directly comparable, even if taxonomy changes. In this investigation, we assess barcoding methods in a broad taxonomic array of diatoms from environmental samples from a river in Connecticut. We continue to contrast light microscopy (LM), scanning electron microscopy (SEM) and molecular approaches to estimate diatom diversity. Comparisons have been made previously but with limited taxonomic capacity and with the use of cultures. The use of molecular analysis in conjunction with LM and SEM could provide useful and new information about the diversity of diatoms found in a river sample. In this study we have extracted DNA and PCR amplified using the diatom specific 18S V4 marker region. We cloned the amplicon and sequenced with success. We continue to collect data to support and illustrate phylogenetic diversity. When we used the NCBI website we were able to BLAST our sequences to diatoms. We will continue to examine the practicability and efficacy of the 18S V4 marker for accurate identification of diatoms. If barcoding can consistently be applied effectively and economically, the use of this procedure may have a significant impact on the accurate classification of these important organisms as water quality biological indicators. Environmental sampling and DNA barcoding shows promise as one of the tools in the taxonomic and phylogenetic toolbox.

(P29 UP) A MOLECULAR–ASSISTED ALPHA TAXONOMIC STUDY OF A PUTATIVE *ETHELIA* SP. (PEYSSONNELIACEAE, RHODOPHYTA) FROM BERMUDA. Amy K. Kivela[1], Craig W. Schneider[1], Thea R. Popolizio[2] & Christopher E. Lane[2]. [1]Department of Biology, Trinity College, Hartford, CT, 06106, U.S.A.; [2]Department of Biological Sciences, University of Rhode Island, Kingston, RI, 02881, U.S.A.

Knowledge of the various red algal fleshy and calcareous crusts of Bermuda is limited, owing to little research in this Atlantic archipelago in the historical past. The present study investigates a common, deep water, rock conforming, fleshy red crust identified in the recent past as *Polystrata* species. Genetic barcoding of red algae using the conserved mitochondrial COI-5P sequence has recently been shown to be an effective tool to gain quick and reasonable results for species comparisons. By coupling COI-5P data with chloroplastic *rbc*L and LSU nuclear genes, more robust phylogenetic trees can be generated. After our recent samples were barcoded and compared, and species groupings among the Peyssonneliaceae were elucidated, we discovered that the "*Polystrata*" from Bermuda did not group with the type *P. dura*. Therefore, we conducted morphological studies to find unique characteristics to support the molecular distinctions. *Polystrata* is characterized by complete calcification, except for the nemathecia, and a single inferior perithallial layer generated from the mesothallial layer. The species from Bermuda lacks calcification entirely and has unequal, multi-layered superior and inferior perithallial layers. These characteristics are reminiscent of the genus *Ethelia*, a genus at present considered a junior synonym of *Polystrata*. Our data suggest the resurrection of *Ethelia* based molecular and morphological studies, and our species putatively represents a novel species.

(P30 UP) USING PHYLOGENOMICS FOR NUCLEAR LOCI DISCOVERY IN HETEROKONT LINEAGES. Grace Han[1], Latreasha Andersen[1], Lucky Niko[1], Ed Braun[2], & Naomi Phillips[1], [1]Biology Department, Arcadia University, Glenside, PA, U.S.A.; [2] Zoology Dept. University of Florida, Gainesville, FL, U.S.A.

The Brown algae are one of the most species rich and ecologically important groups of primary producers in marine environments. Despite their biological importance and recent advances, the evolutionary history of the brown algae remains poorly resolved. One drawback to evolutionary studies in brown algae is the lack of molecular markers, especially nuclear. To date there are about 10 KB of loci (mostly chloroplast and mitochondrial) for phylogenetic studies within brown algae, where power analyses estimate that ~ 20 Kb are needed to resolve the backbone of the brown algal tree. The goal of this project was to mine available genetic data for nuclear markers to use in phylogenetic studies within brown algae and related heterokonts. Two genetic databases were created, one with all available genetic data for brown algae and *Schizocladia* and the other with all available genetic data for brown algae and closely related Heterokonts. These two databases were searched for all loci shared among the groups. Resulting gene alignments and Maximum Likelihood trees were evaluated and candidate loci were selected for PCR evaluation using taxa from 7 brown algal orders. Resulting amplicons from positive loci were sequenced to further verify PCR products and evaluate primers. To date, ~100 loci have been screened with 14 positive loci developed. The last step in locus evaluation is to infer evolutionary relationships within brown algae using the locus. Thus far one locus has been evaluated and gives the correct

topology. In the future we will extend this last step to the other 13 loci along with screening additional loci.

(P31 UP) IS *HELMINTHOCLADIA* IN THE WESTERN ATLANTIC REALLY THE SAME AS *H. CALVADOSII* FROM EUROPE? Tayoot Chengsupanimit[1], Craig W. Schneider[1], Thea R. Popolizio,[2] Thomas A. Shamp[2] & Christopher E. Lane[2]. [1]Department of Biology, Trinity College, Hartford, CT, 06106, U.S.A.; [2]Department of Biological Sciences, University of Rhode Island, Kingston, RI, 02881, U.S.A.

Western Atlantic specimens of *Helminthocladia* from were initially identified as *Helminthora divaricata* J. Agardh when it was first collected and reported from the Florida Keys by Harvey in 1853 and from Bermuda by A.F. Kemp in 1857. When later workers studied these western Atlantic specimens [fide *Phycotheca Boreali-Americana* no. 2035 (1915)], they found them to be better identified as a second European species, *Helminthocladia calvadosii* (J.V. Lamour. ex Duby) Setch. (type locality: Calvados, France), thus even changing the original generic placement. Since the initial collections in the western Atlantic during the mid1800s, *H. calvadosii* has also been found in the Caribbean Sea and as far south as northern Brazil. Recent winter collections of *H. calvadosii* from Spanish Point in Bermuda have provided good comparative anatomical material and yielded COI-5P sequences for genetic barcoding and *rbc*L sequences for phylogenetic comparison. These specimens have gross morphologies that are somewhat reminiscent of eastern Atlantic plants of *H. calvadosii* and demonstrate anatomical features that greatly overlap European specimens. Our molecular results will begin to elucidate the relationships of the Bermuda isolates with *H. calvadosii* from near the type locality and their generic placement within the Liagoraceae.

(P32 C) ESTABLISHING ULVOPHYCEAN CONTEXT FOR THE UNIVERSAL PLASTID AMPLICON. Brian Wysor[1], Charles J. O'Kelly[2], Juan Lopez-Bautista[3], Noel Sme[1] & Valerie Charbonneau[1]. [1]Department of Biology, Marine Biology & Environmental Science, Roger Williams University, Bristol, RI, 02809, U.S.A.; [2]Friday Harbor Laboratories, University of Washington, 620 University Road, Friday Harbor, WA, 98250, U.S.A.; [3] Department of Biological Sciences, The University of Alabama, 500 Hackberry Lane, Mary Harmon Bryant Hall #309, Tuscaloosa, AL, 35487-0345, U.S.A.

The universal plastid amplicon (UPA) is an easy to amplify region of chloroplast DNA that has proven useful for delineating algal taxa with quasi species-level resolution. The ease of amplification across divergent algal phyla, and the short length of the UPA marker (~400 bp), make it ideally suited to DNA barcoding type applications. In particular, biodiversity surveys using environmental PCR of the UPA have uncovered novel elements of diversity where field-based collections techniques fail to detect the full range of species richness and where recovery of diversity from cultured specimens is low and/or prohibitively expensive. The challenge of such work lies in the elaboration of appropriate context against which unknown specimens can be compared, and while a rich database of sequences exists for the phylum Rhodophyta, and to a lesser extent the brown algal class Phaeophyceae, the phylogenetic context of green algae in the class Ulvophyceae is quite limited. Here, we attempt to establish the phylogenetic context of the UPA for green algae from each of the major orders of ulvophycean green algae.

(P33 FTA) POLYADENYLATION OF 18S RIBOSOMAL RNA IN ALGAE. Yunyun Zhuang[1,2], Huan Zhang[1] & Senjie Lin[1,2*]. [1]Department of Marine Sciences, University of Connecticut, 1080 Shennecossett Rd., Groton, CT, 06340, U.S.A.; [2]Marine Biodiversity and Global Change Laboratory, Xiamen University, Xiamen, Fujian 361005, China

Polyadenylation typically occurs to mRNA of eukaryotes transcribed by RNA polymerase II, stabilizing mRNA molecules and promoting their translation. Ribosomal RNAs (rRNAs) transcribed by RNA polymerase I or III are believed not to be polyadenylated. However, recent studies show that in humans, yeast and land plants, polyadenylation occurs to nucleus-encoded rRNAs as part of the RNA degradation pathway, prompting a question whether the same polyadenylation-assisted degradation machinery occurs in algae. We surveyed representative species of algae including diatoms, chlorophytes, cryptophytes and dinoflagellates using oligo(dT)-primed reversed transcriptase PCR (RT-PCR). In all the algal species examined, nucleus-encoded small subunit rRNA (18S rRNA) molecules with poly(A) tails were detected. Mining existing algal ESTs data revealed polyadenylated 18S rRNA in three additional phyla of algae. Sequence alignments showed that the rRNA polyadenylation occurred at various positions along the entire length of 18S rRNA sequence. Moreover, in some cases, the precursor molecules of 18S rRNA containing internal transcribed spacers were also found to bear poly (A) tails. Our detection of polyadenylated 18S rRNA in seven phyla of algae suggests that polyadenylation-assisted RNA degradation mechanism widely exists in algae, particularly for the nucleus-encoded rRNA and its precursors. This indicates that this mechanism emerged nearly 2 billion years ago. This finding explains why rRNAs (in the form of cDNAs) are often represented in oligo(dT)-based algal cDNA libraries and suggests that rDNA PCR amplification can serve as a convenient tool for quality check of cDNA libraries.

(P34 FTA) ORGANELLAR GENOME EVOLUTION OF THE FRESHWATER BROWN ALGA *PLEUROCLADIA LACUSTRIS* A. BRAUN. Xian Wang[1,2] John D. Wehr[1] & Kenneth G. Karol[2]. [1]Biology department, Fordham University, Bronx, NY, 10458, U.S.A.; [2]The Lewis B. and Dorothy Cullman Program for Molecular Systematics, The New York Botanical Garden, Bronx, NY, 10458, U.S.A.

Of an estimated 2000 brown algae species (Phaeophyceae), less than 1% occur in freshwater environments. Freshwater brown algae have been known for more than 150 years, but the phylogenetic placement of some species remains unclear. Currently, there are no comprehensive molecular phylogenetic studies of freshwater brown algae, which would provide more insight into evolution within this class. This study aims to better understand the phylogenetic position and organellar genome evolution of the freshwater brown alga *Pleurocladia lacustris* A. Braun (1855). Historically, *P. lacustris* has been classified with either Ectocarpaceae or Chordiariace. Complete mitochondrial and plastid genomes of *P. lacustris* have been successfully determined. These represent the third brown algal species for which both organellar genomes have been completely sequenced (i.e., *Fucus vesiculosu*s and *Ectocarpus siliculosus*). The physical map and gene organization of the complete mitochondrial and plastid genomes of *P. lacustris* is presented here. The mitochondrial genome is 37.8 kb, has a GC content of 32.9%, and includes genes for three rRNAs, 26 tRNAs and 34 protein-coding genes. The plastid genome is 138.8 kb, has a GC

content of 29.8%, and includes genes for three rRNAs, 30 tRNAs, 136 known protein-coding genes and 17 open reading frames of unknown function (e.g., orfs or ycfs). Selected mitochondrial and plastid-encoded genes were used to construct phylogenetic trees among Stramenopiles and Phaeophyceae, respectively. These phylogenetic trees supported the contention that *P. lacustris* is a member of the Ectocarpaceae, not the Chordiariace.

(P35 FTA) CHARACTERIZATION OF 3'UTR SEQUENCES OF mRNA ENCODING NITROGEN ASSIMILATING ENZYMES FROM MARINE DIATOMS. Minoli Perera, Jessica Alexander, Sohini Ghoshroy & Deborah L. Robertson. Department of Biology, Clark University, Worcester, MA, 01610, U.S.A.

Nitrogen availability is a key factor regulating marine primary productivity and diatoms exhibit rapid growth in response to increases in environmental nitrogen, which can vary over several spatial and temporal scales. The assimilation of nitrogen is tightly regulated and requires the coordinated expression and regulation of enzymes in the cytosol, chloroplast, and mitochondria. While there has been much focus on patterns of coordinated gene transcription, there is increasing evidence of coordinated post-transcriptional regulation of mRNA encoding functionally related proteins, such as enzymes in metabolic pathways. The goal of this project is to explore the general hypothesis that post-transcriptional regulation of genes involved in nitrogen assimilation in marine diatoms contributes to their rapid metabolic response to nitrogen fluctuations. RNA binding proteins (RBPs) regulate mRNA stability and translation in a variety of eukaryotic lineages. To test the hypothesis that RBPs bind and coordinate the post-transcriptional regulation of mRNA encoding nitrogen-assimilating enzymes, we cloned and sequenced the 3' untranslated regions (UTRs) of transcripts for five nitrogen assimilating enzymes from *Thalassiosira pseudonana* and two from *Skeletonema costatum*. The length of the UTRs ranged between 138-248 nucleotides and the AT content was greater in the 3' UTRs than the open reading frames, ranging between 57-62%. *In silico* analyses identified several putative RBP binding motifs that corresponded to the recognition sequences of PUF, KH-I and ELAVL1 RBP families. Conserved PUF binding domains were found in the 3'UTRs of transcripts encoding nitrate reductase (*nia*) in both *S. costatum* and *T. pseudonana*. Future experiments will examine RBP binding profiles in vitro using the PUF recognition motifs from *S. costatum* and *T. pseudonana nia* transcripts as well as binding sites for other RNA binding proteins.

(P36 FTA) IDENTIFICATION AND CHARACTERIZATION OF PUF FAMILY RNA-BINDING PROTEINS IN MARINE DIATOMS. Jessica Alexander, Minoli Perera, Sohini Ghoshroy & Deborah L. Robertson. Department of Biology, Clark University, Worcester, MA, 01610, U.S.A.

RNA-binding proteins (RBPs) form dynamic associations with mRNAs, mediating regulatory events in the nucleus and cytoplasm, including mRNA localization, stability, decay, and translation. We identified and analyzed several RBP families in the genomes of *Thalassiosira pseudonana*, *Phaeodactylum tricornutum,* and *Fragilariopsis cylindrus*, among them representatives of the PUF family proteins. The first members of this family, Pu*m*ilo and *F*BF (hence PUF), were described from *Drosophila melanogaster* and *Caenorhabditis elegans*, respectively. The PUF family appears structurally and functionally well conserved among

eukaryotes and members have been shown to mediate the post-transcriptional regulation of gene expression by promoting RNA decay and repressing translation. The goal of this study was to identify and characterize the distribution of PUF proteins in diatoms and examine their phylogenetic relationship among diatoms and other eukaryotes. Putative *puf* genes were identified based on a well-conserved RNA binding domain (PUM-HD). The number of *puf* genes in diatoms varied, ranging from nine in *T. pseudonana* to four in *P. tricornutum*. As observed in other eukaryotes, the PUM-HDs were well conserved while regions outside the homology domains were highly variable. EST data indicate that different PUF proteins are expressed under different environmental conditions, suggesting they may be important in post-transcriptional gene regulation in response to environmental stimuli. Future experiments are aimed at identifying the mRNA targets of the PUF proteins *in vitro*, and examining the expression and function of PUF proteins under different environmental conditions.

Biography of Catherine Schmitt

As the science writer for the Maine Sea Grant College Program at the University of Maine since 2004, Catherine Schmitt conveys research findings and information about the coasts and oceans to Maine residents and visitors. She has a background in science, including field experience in lakes, streams, wetlands, and beaches across the Northeast. This background informs and inspires her writing, which appears in newspapers, magazines, and literary journals. Schmitt is the author of A Coastal Companion: A Year in the Gulf of Maine from Cape Cod to Canada, and she teaches a course on science and the news media in the Department of Communication and Journalism at the University of Maine. Find her online at www.catherineschmitt.com and reportingscience.wordpress.com.

Biography of Abe Miller-Rushing

Abe Miller-Rushing is the Science Coordinator for the Schoodic Education and Research Center (SERC) and Acadia National Park. He received his PhD in Biology from Boston University. His research focuses on long-term changes in the environment, particularly those caused by climate change. He involves the public in many aspects of his research, and is helping to expand citizen science programs at SERC and Acadia. He has also contributed to the development of a national citizen science program and is co-organizing a national conference on citizen science and the development of a new professional association for citizen science.

Biography of David Manski

David Manski is Chief of Resource Management at Acadia National Park. He supervises the park's natural and cultural resources management and lands programs. David has 33+ years science experience with the National Park Service (NPS) in a diversity of settings; besides his 18+ years at Acadia, he was research wildlife biologist at the NPS Center for Urban Ecology in Washington, D.C., biologist in two Alaska national park areas, and Chief of Natural Resource Programs at Cape Cod National Seashore. He also has had a number of conservation assignments in England, China, and the Middle East. He has undergraduate and graduate degrees in wildlife ecology from the University of Arizona and Texas A&M University. Outside of work, David stays busy gardening, breeding rare chickens, and playing music as a bluegrass radio host on WERU-FM and as a member of the acoustic and bluegrass Blue Northern band.

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Biography of Nancy Knowlton

Dr. Nancy Knowlton holds the Sant Chair in Marine Science at the Smithsonian's National Museum of Natural History, where her research focuses on the diversity and conservation of life in the ocean. She received her BA at Harvard University *summa cum laude*, her PhD at the University of California at Berkeley, and was a NATO postdoctoral fellow. Later, she was a professor at Yale University, a scientist at the Smithsonian Tropical Research Institute in Panama, and Professor and founding Director of the Center for Marine Biodiversity and Conservation at the Scripps Institution of Oceanography. Past service included advisory positions with the National Geographic Society, the World Bank, the Cosmos Prize, and the Census of Marine Life. She was a past member of the editorial board of the Annual Review of Marine Science and the National Board of the American Association for the Advancement of Science. She currently serves on the Pew Marine Fellows Advisory Committee, the Sloan Research Fellowship in Ocean Sciences committee, The Savannah Ocean Exchange Board of Governors, and the national board the Coral Reef Alliance. She is an Aldo Leopold Leadership Fellow, winner of the Peter Benchley Prize and the Heinz Award, and author of *Citizens of the Sea.*

History of SERC Institute

The Schoodic Peninsula, containing the only portion of Acadia National Park on the mainland, boasts granite headlands, rocky beaches, and spruce-fir forests. Although similar in scenery to Mount Desert Island, the coast of the Schoodic Peninsula is more intimate and secluded.

Much of the Schoodic Peninsula was once owned by John G. Moore, a Maine native and Wall Street financier. In the 1920s, Moore's heirs donated the land to the Hancock County Trustees of Public Reservations with the stipulation that the land be used as a public park and for other uses, including the "promotion of biological and other scientific research." In 1929, legislation authorized the National Park Service to accept land on the Schoodic Peninsula as an addition to the park and changed the name of the park to Acadia. Soon after the law's enactment, the Hancock County Trustees of Public Reservations donated the former Moore property (2,050 acres) to the National Park Service "for the public good and for the extension or improvement of said park, forever."

In the 1930s and 1940s, some of this land was transferred to the U.S. Navy for use as a radio communication station. The U.S. Navy operated the base until the land was transferred back to the National Park Service in 2002.

The former base has become the Schoodic Education and Research Center - SERC Institute is one of 17 National Park Service research learning centers across the country. The center facilitates research projects throughout Acadia National Park and provides opportunities for learners of all ages to discover the park's natural and cultural resources.

Schoodic Education and Research Center