

## *Table of Contents*

§

|   |       |
|---|-------|
| Honorary chairperson.....                             | 2-4   |
| General program .....                                 | 5-9   |
| Poster presentation summary .....                     | 10-12 |
| Oral abstracts (in order of presentation) .....       | 13-24 |
| Poster abstracts (numbered presentation boards) ..... | 24-39 |
| Notes .....   | 40    |

§

*48<sup>th</sup> Northeast Algal Symposium Honorary Chairperson*

Francis R. Trainor



*F.R. Trainor*

*On the occasion of his 80<sup>th</sup> birthday.  
This year, his poster reads, “50 years of desiccation,”  
for NEAS, his record would read, “Nearly 50 years of service”!*

Amherst, Massachusetts

17 April 2009

We are pleased to designate **Francis (Frank) R. Trainor** as the Honorary Chair of the 48<sup>th</sup> NEAS symposium. Our choice of candidates could not have been better. Ironically, Frank initiated the idea of having honorary chairs for our symposia. Bill Johansen has in his archival NEAS files a letter Frank wrote to Bob Wilce in 1983 [when Bob was NEAS president] in which he made a motion to the effect that NEAS should “have an honorary chairperson... whenever the occasion is right. This should be a ‘senior phycologist’.” Well, it seems to us that the time is right, and on the occasion of his 80<sup>th</sup> birthday, we conclude he qualifies as a senior phycologist! Frank has long been a prolific and important contributor in Phycology, specifically in the area of unicellular green algal studies. After his Master’s and Ph.D. from Vanderbilt, Frank began his career as an Instructor at the University of Connecticut in 1956, retired as Professor (1997), and still contributes to the field as an Emeritus Professor—that’s 53 years of professional work on the algae! For example, take a look at the poster he is presenting at our meeting this year. He is long in the field, and he is solid—he has the great respect and friendship of his peers and his many former students and friends.

Know this well—Frank has been involved with NEAS since it was first proposed in the fall of 1968 as the Metropolitan (NY) Area Algal Discussion Group (later to become the Northeast Algal Discussion Group, and eventually NEAS). He has been a continuous contributor to the development of the Society, as executive committee member and co-convenor of the three symposia (1969, 1973, 1977). Frank was the recipient of our prestigious Frank Shipley Collins Award (2002), and he has already once presided as Honorary Chair of the annual symposium (1992). Twice Frank was our distinguished speaker (1978, 1992). Frank has brought a great deal to our society—his service, his science, his many graduate students, his counsel and his friendship. Yes, and also his dry humor. We will never forget Frank’s love of his research ‘tools’, most notably *Scenedesmus*, that he fondly refers to, using his favorite phycological distortion, as his “*Skinny-dead-mice*” in presentations to the Society with a slide of four side-to-side mice with alternating heads and tails! And for some time now, we remember Frank as that distinguished fella’ who sits in the back of the lecture room, and brings to the symposium his beautifully carved water birds as auction items unexcelled (see the following letter).

Thank you, Frank, for all you have done for NEAS, and for all you continue to do.

Bob Wilce

Bill Johansen  
Co-convenors

Craig Schneider



Trinity College  
HARTFORD CONNECTICUT

17 April 2009

Dear Fellow Members of NEAS,

In 1997, the last time that the Northeast Algal Society met at the Marine Biological Laboratory in Woods Hole, Massachusetts after a run of 22 straight years, Frank Trainor brought along a beautiful hand-carved, stylized loon of cacao and pecan woods glued together. On the bottom was his signature and a drawn *Scenedesmus*! He donated this loon to NEAS's Student Development Committee to see if there would be any interest in it from the attending phycologists. Would his carvings help raise funds for students to attend future meetings and purchase books needed for their research? Actually, this was the first that many of us at NEAS knew that Frank was a prolific and extremely talented wood-carver. Frank wanted this first donated bird to be a silent auction so he could watch the "bid card" and gauge interest. He was pleased to discover that his very first loon sold for \$85 after spirited bidding and was encouraged to come back the next year with more. So, beginning in 1998, and every NEAS since, Frank arrived at our annual symposium with several carvings of ducks, ducklings, teal, loons, puffins and the like, all wrapped in their transport packing, his old socks!

Well, it turns out that I "won" that prized first loon for a bargain price, as many of his larger carvings over the years have reached prices close to, and even exceeding, \$200. Even his small pintails less than 4" long often command near \$100 at our auctions. With a handful or more carvings every year since 1998, these wonderful artworks have raised thousands of dollars for students of algae over the past 12 years. Many of us have several of Frank's birds, with large collections held by Peter Bradley, Susan Brawley, Morgan Vis and Pete Siver that I know of. We all enjoy their buzz of seeing what Frank brings each April, and all enjoy the competition of bidding for a great cause. The winning bidder successfully brings another prized bird home to join the flock! And the Society raises lots of money.

The autographed picture of Frank on a previous page shows a goose made of sumac that was carved in 2004. The next year, this terrific picture "appeared" at the NEAS auction, and the auctioneer, Glen Thursby, announced that it would be a "wonderful complimentary piece" to the person who purchased the sumac goose the previous year. You see, Glen took the picture of Frank and the goose at the 2004 Avery Point meeting knowing there was still money in this carving after it sold at the auction. And of course he was right, as I walked away from the auction for the second straight year with the "same" goose! When you come to the 48<sup>th</sup> meeting this year, you will see the spectacle of Frank's carvings bidding higher and higher—money committed to the dedicated students in our Society. Bring your checkbook, be impressed by Frank's creativity, and support the students!

Sincerely,

Craig W. Schneider  
Co-convenor 48<sup>th</sup> NEAS Symposium, Amherst, Massachusetts

DEPARTMENT OF BIOLOGY

300 SUMMIT STREET, HARTFORD, CT 06106-3100  
TEL (860) 297-2539 FAX (860) 297-2538 www.trincoll.edu

**General Program: 48<sup>th</sup> Northeast Algal Symposium, Amherst**

.....

**Friday, April 17, 2008**

- 6:00 — 7:00 pm**      **Evening Registration/Poster Setup**  
Lower Lobby concourse, University Conference Center  
*Poster setup, Lower Lobby concourse & Room 165*
- 7:00 — 10:00 pm**    **NEAS Friday Mixer**  
1003 Bar area, 10<sup>th</sup> floor, University Conference Center

**Saturday, April 18, 2009**

- 7:00 — 8:30 am**      **Continental Breakfast**  
Room 163, University Conference Center  
*Poster setup, lower lobby concourse and Room 165*  
*Session I speakers load presentations on Rm. 163 computer*
- 8:00 — 9:30 am**      **Morning Registration**  
Lower Lobby concourse, University Conference Center
- 8:30 — 8:45 am**      **Welcome and Opening Remarks — Bob Wilce**  
Room 163, University Conference Center
- SESSION I**            **Student Presentations, Moderator Ron Hoham**  
Room 163, University Conference Center
- 8:45 — 9:00 am**      *Wilce Award Candidate*  
**Katharine Hind** & Gary W. Saunders—Identification of the genus  
*Corallina* (Corallinales, Rhodophyta) in Canada. (**Abstract 1, p. 13**)
- 9:00 — 9:15**            *Wilce Award Candidate*  
**Nathan J. Smucker** & Morgan L. Vis—Using diatom data from  
different sampling protocols in stream biomonitoring: Potential for  
integration. (**Abstract 2, p. 13**)
- 9:15 — 9:30**            *Wilce Award Candidate*  
**Bridgette Clarkston** & Gary W. Saunders—A comparison of  
DNA barcode markers for species discrimination in marine red  
algae. (**Abstract 3, p. 13**)
- 9:30 — 9:45**            *Wilce Award Candidate*  
**Daniel McDevit** & Gary W. Saunders—DNA Barcoding reveals  
cryptic diversity among Phaeophyceean taxa with simple and plastic  
morphologies in Canada. (**Abstract 4, p. 14**)
- 9:45 — 10:00**        *Wilce Award Candidate*  
**Ian Misner**, Kristi Sommer, J. Craig Bailey & Christopher E.  
Lane—Is there a relict plastid in Oomycetes? (**Abstract 5, p. 14**)

- 10:00 – 10:15** *Wilce Award Candidate*  
**Lillian Hancock** & Christopher E. Lane—Mitochondria in red algal parasite evolution. (**Abstract 6, p. 15**)
- 10:15 – 10:45** *Coffee Break*
- SESSION II** *Student Presentations, Moderator Chris Lane*  
Room 163, University Conference Center
- 10:45 – 11:00 am** *Wilce Award Candidate*  
**Margaret M. Pavlac**, Travis T. Smith, Sean P. Thomas, Gregory L. Boyer, Joseph C. Makarewicz, Theodore W. Lewis, William J. Edwards, Christopher M. Pennuto, Caleb P. Basiliko & Joseph F. Atkinson—Application of continuous monitoring in the Lake Ontario nearshore nutrient survey. (**Abstract 7, p. 15**)
- 11:00 – 11:15** *Wilce Award Candidate*  
**Sohini Ghoshroy**, Aurelien Tartar & Deborah L. Robertson—Glutamine synthetase II: A case of lateral gene transfer in basal Viridiplantae? (**Abstract 8, p. 15**)
- 11:15 – 11:30** *Wilce Award Candidate*  
**Bethann Balazsi** & Sean Grace—Attachment strength in numbers of the northern kelp, *Saccharina latissima*. (**Abstract 9, p. 16**)
- 11:30 – 11:45** *Wilce Award Candidate*  
**David E. Olson** & Susan H. Brawley—Characterization of a rocky intertidal shoreline within Acadia National Park: Impact of short-term trampling and implications for management. (**Abstract 10, p. 16**)
- 11:45 – 12:00 pm** *Wilce Award Candidate*  
**Yunyun Zhuang** & Senjie Lin—Regulatory network of cell cycle in marine phytoplankton. (**Abstract 11, p. 16**)
- 12:00 – 1:30 pm** *Lunch*  
Amherst Room, University Conference Center  
*Executive Committee Meeting*  
Room 1001, University Conference Center
- SESSION III** *Student & Contributed Presentations, Moderator Dan McDevit*  
Room 163, University Conference Center
- 1:30 – 1:45 pm** *Wilce Award Candidate*  
**Ralph B. Perkerson**, Emilie A. Stringfellow & Dale A. Casamatta—Comparison of the commonly confused cyanobacterial genera *Geitlerinema* and *Limnothrix* (Pseudanabaenaceae) using a polyphasic approach. (**Abstract 12, p. 17**)

- 1:45 – 2:00** *Wilce Award Candidate*  
**Nicolas A. Blouin** & Susan H. Brawley—Reproduction in *Porphyra umbilicalis* Kützing: Insights from amplified fragment length polymorphisms (AFLP). (**Abstract 13, p. 17**)
- 2:00 – 2:15** *Wilce Award Candidate*  
**Agnes Mols Mortensen**, Juliet Brodie, Christopher D. Neefus, Ruth Nielsen & Karl Gunnarsson—*Porphyra* (Bangiales, Rhodophyta) diversity in Iceland: a larger perspective. (**Abstract 14, p. 18**)
- 2:15 – 2:30** *Wilce Award Candidate*  
**Laurie C. Hofmann**, Christopher D. Neefus, and Arthur C. Mathieson—Biodiversity and bioremediation potential of *Ulva* spp. populations in the Great Bay Estuarine System. (**Abstract 15, p. 18**)
- 2:30 – 2:45** *President’s Award Candidate*  
**Elizabeth Sargent**, Jessie Alden & Brian Wysor—Assessing the species richness of *Dictyota* from Caribbean Panama using a DNA barcoding approach. (**Abstract 16, p. 19**)
- 2:45 – 3:00** *Contributed paper*  
**Elliot Shubert**—Phenotypic plasticity in *Desmodesmus*: A never ending story. (**Abstract 17, p. 19**)
- 3:00 – 3:30** *Coffee Break*
- SESSION IV** *Contributed Presentations, Moderator—Carl Grobe*  
Room 163, University Conference Center
- 3:30 – 3:45** *Contributed paper*  
**H. Dail Laughinghouse IV**, Walter H. Adey, Patrick C. Kangas, John Miller & Jamie A. Hestekin—Algal Turf Scrubber (ATS<sup>TM</sup>) potential for water quality control and biomass production for biofuels. (**Abstract 18, p. 19**)
- 3:45 – 4:00** *Contributed paper*  
**Dennis Hanisak**—A green look at the red algae: Cultivating *Gracilaria* for biofuel production and biomediation. (**Abstract 19, p. 20**)
- 4:00 – 5:00** *Speaker Introduction—Bob Wilce*  
*Distinguished Speaker Presentation*  
**Scott Gordon**—Small scale biodiesel production (including some do’s & don’t’s for making biodiesel from algae). (**Abstract 20, p. 20**)

**SESSION V** *Poster Session & Social*

**5:00 – 6:00**            **Student & Contributed Posters**  
Lower Level concourse/Room 165, University Conference Center

.....  
**6:00 – 7:00**            **NEAS Social & Silent Auction**  
Amherst Room, University Conference Center

**7:00 – 10:00 pm**    **Banquet, Awards, “Phyco” Quiz & Live Auction**  
Amherst Room, University Conference Center

.....  
*Sunday, April 19, 2009*

**7:00 – 8:20 am**        **Continental Breakfast**  
Room 163, University Conference Center

**8:25 – 8:30 am**        **Announcements – Craig Schneider**  
Room 163, University Conference Center

**SESSION VI**            **Contributed Papers, Moderator Bridgette Clarkston**  
Room 163, University Conference Center

**8:30 – 8:45 am**        *Contributed paper*  
**Jim Foertch**, John Swenarton & Milan Keser—Multivariate analyses of 30 years of rocky shore community data. (**Abstract 21, p. 21**)

**8:45 – 9:00 am**        *Contributed paper*  
**John D. Hall** & Kenneth G. Karol—A preliminary report on the freshwater algae of eastern New York. (**Abstract 22, p. 21**)

**9:00 – 9:15**            *Contributed paper*  
**Paulette Peckol**, Katherine Morrice & H. Allen Curran—Herbivorous fish abundance and grazing rates: Reef rugosity as a control in Belize and the Bahamas. (**Abstract 23, p. 21**)

**9:15 – 9:30**            *Contributed paper*  
**Ronald W. Hoham**, Frank M. Frey, Jesse D. Berman, Jeffrey B. Ryba, Jared E. Duncan, Andrew A. Forbes, Blair M. Goodridge & Paris R. Miller—The effects of irradiance level, photoperiod, and cell density on sexual reproduction in the green snow alga, *Chloromonas chenangoensis* (Chlorophyta, Volvocales), from Upstate New York. (**Abstract 24, p. 22**)

**9:30 – 9:45**            *Contributed paper*  
**Brian Wysor**—Molecular delimitation of Narragansett Bay sea lettuce. (**Abstract 25, p. 22**)



- 9:45 – 10:00**      *Contributed paper*  
                          **Daniela Milstein** & Gary W. Saunders— A molecular floristic survey in Canadian waters reveals cryptic diversity in the order Ahnfeltiales. (**Abstract 26, p. 22**)
- 10:00 – 10:15**      *Contributed paper*  
                          **Max H. Hommersand** & Showe-Mei Lin— Phylogeny and systematics of species of *Phycodrys* and *Membranoptera* (Delesseriaceae, Rhodophyta) that exhibit trans-Arctic distributions between the North Pacific and North Atlantic Oceans. (**Abstract 27, p. 23**)
- 10:15 – 10:45**      *Coffee Break*
- SESSION VII**      *Special Papers & Phyco-Speed Dating, Moderator C. Schneider*  
                          Room 163, University Conference Center
- 10:45 – 11:15 am**      *Special invited paper*  
                          **Michael J. Wynne**— Marine algae and early explorations in the upper North Pacific and Bering Sea. (**Abstract 28, p. 23**)
- 11:15 – 11:45**      *Phyco-Speed Dating, Coordinator Hilary McManus*
- 11:45 – 12:15 pm**      *Special invited paper*  
                          **Gary W. Saunders**— The promises and pitfalls of molecular-assisted alpha taxonomy. (**Abstract 29, p. 24**)
- 12:15 – 1:30**      *NEAS Annual Business Meeting & Lunch*  
                          Room 163, University Conference Center  
                          Attend the annual meeting & your boxed-lunch will come in a **UMass tote bag**

**Poster No. Authors/Title (Abstracts begin on p. 24)**

*Undergraduate Posters (President's Award)*

- P1** — **Samuel A. Drerup**, Kam Truhn, Alissa Perrone & John Wehr—Relationships between diatom community composition, periphyton stoichiometry and primary consumers (Abstract p. 24)
- P2** — **Alexander M. VandenBroek** & Morgan L. Vis—Desiccation tolerance of various types of cells in the freshwater red alga, *Batrachospermum gelatinosum*. (Abstract p. 25)
- P3** — **Chien Lo & Louise A. Lewis**—Molecular phylogenetic characterization of desert green algae from South African biotic soil crusts. (Abstract p. 25)
- P4** — **Jared Rada**, Karolina Fučíková & Louise A. Lewis—Confusion caused by limited morphology: Two case studies in green coccoids. (Abstract p. 26)
- P5** — **Portia A. Osborne**, Sean P. Thomas & Gregory L. Boyer—Effects of variable growth conditions on algal lipid production. (Abstract p. 26)
- P6** — **Yusuff Abdu**, Kim, J.K., Kraemer, G.P. & Yarish, C.—Mapping ecologically significant inorganic nitrogen in the nearshore environments of Long Island Sound, USA using macroalgal tissue samples. (Abstract p. 26)
- P7** — **Heather Meyer** & Kenneth G. Karol—Are you the real *Nitella flexilis*? (Abstract p. 27)
- P8** — **Rachel Rock-Blake**, James T. Carlton & Paulette Peckol—Documenting 150 years of coastal change: Revisiting the work of amateur phycologist Eliza M. French. (Abstract p. 27)

*Graduate Student Posters (Wilce Award)*

- P9** — **Michele Guidone** & Carol Thornber—Herbivore impact on macroalgal blooms in Narragansett Bay, RI. (Abstract p. 27)
- P10** — **Aditi Rambani** & Morgan L. Vis—Phylogeographic study of *Tuomeya americana* (Rhodophyta) in eastern North America. (Abstract p. 28)
- P11** — **Justin R. Pool**, Morgan L. Vis, Bob Verb, Jason Zalack, Melissa Verb & Nate Smucker—Phenology of *Batrachospermum helminthosum* (Rhodophyta). (Abstract p. 28)
- P12** — **Lucy E. Pleticha**, Christopher S. Benton, Anita S. Klein & Arthur C. Mathieson—Molecular and morphological variation in *Codium fragile* in the NW Atlantic. (Abstract p. 29)

- P13** — **Sarah E. Hamsher** & Gary W. Saunders—Barcoding marine tube-forming diatoms from Canadian waters: Investigating alternative markers to COI. (**Abstract p. 29**)
- P14** — **Susan L. Clayden** & Gary W. Saunders—“Birds of a feather”: Molecular phylogenetic analyses and novel life history interpretations ally *Colaconema subimmersum* and *Halosacciocolax kjellmanii* with the Rhodophysemataceae (Palmariales, Rhodophyta). (**Abstract p. 30**)
- P15** — **Molly R. Letsch**, Gisèle Muller-Parker & Louise A. Lewis—A chloroplast genome rearrangement in the symbiotic green alga, *Elliptochloris marina* (Trebouxiophyceae, Chlorophyta). (**Abstract p. 30**)
- P16** — **Bernadette Clabeaux** & Mary A. Bisson—Cd uptake by charophytes: The potential for phycoremediation. (**Abstract p. 31**)
- P17** — **Chiu-Yen Kuo** & Senjie Lin—Characterization of a Long Island Sound *Eutreptiella* sp. for its potential as biofuel feedstock and excess nutrient biofilter. (**Abstract p. 31**)
- P18** — **Meghann Bruce** & Gary W. Saunders—Investigating species diversity within the genera *Scagelia*, *Neoptilota* & *Ptilota* in Canada using an integrated taxonomic approach. (**Abstract p. 31**)
- P19** — **Rebecca Gladych**, Charles Yarish & George Kraemer—Tracking and predicting a path of invasion along the southern New England coast: *Grateloupia turuturu* Yamada. (**Abstract p. 32**)
- P20** — **Jeremy C. Nettleton**, Christopher D. Neefus & Arthur C. Mathieson—Using macroalgae to track environmental trends in the Great Bay Estuarine System. (**Abstract p. 32**)
- P21** — **Xin Yuan**, Sarina J. Ergas & Amit Kumar—Wastewater treatment and CO<sub>2</sub> sequestration using an airlift photo-bioreactor. (**Abstract p. 33**)
- P22** — **Jennifer Dingman** & Janice Lawrence—Examining for markers of programmed cell death in *Heterosigma akashiwo*. (**Abstract p. 33**)
- P23** — **Anil Patel** & Mark Lefsrud—Coupling phycoremediation and biodiesel production using microalgae. (**Abstract p. 34**)

#### *Contributed Posters*

- P24** — **Margaret Van Patten** & John Doody—A new use for the algae: A Connecticut seaweed survey safari using algae to determine tidal elevations. (**Abstract p. 34**)
- P25** — **Francis R. Trainor** & Louise A. Lewis—Fifty years of desiccation. (**Abstract p. 34**)

- P26** — **Patrick M. Eggleston** — Are the rivers in New England, USA getting more acidic? (Abstract p. 35)
- P27** — Hilary A. McManus, Louise A. Lewis, **Karolina Fučíková** & Peik Haugen — Occurrence of group I introns in Chlorophyceae. (Abstract p. 35)
- P28** — **Amy Snyder**, Matthew Weiss, Michelle Bossler & David S. Domozych — Rapid remodeling of the extracellular matrix of *Spirogyra* during its wound response mechanism: Rhizoid formation, gliding and AGPS. (Abstract p. 35)
- P29** — **Jessica F. Muhlin**, Amanda Brinkman, Michael Iannone, Karin Knudson, Robin Parker & Capt. Richard Miller — “A little science on the side”: Incorporating phycolgical research aboard the Arctic schooner *Bowdoin*. (Abstract p. 36)
- P30** — **Brian Wysor** — Development of a Filemaker Pro database for studying patterns of algal diversity. (Abstract p. 36)
- P31** — **Kam Truhn**, Michael Bell, Mark Burnham, Alissa Perrone & John Wehr — Observations and field studies examining the spread of the invasive Cyanobacterium *Lyngbya wollei* in a northeastern US lake. (Abstract p. 36)
- P32** — **Carol S. Thornber**, Michele Guidone & Christopher Deacutis — Community analyses of macroalgal blooms. (Abstract p. 37)
- P33** — **Dale Casamatta**, Michael Lentz, Jennifer Wilson, Jason Teman & Tessa Davenport — An exploration of the role and specificity of two freshwater cyanophages from eutrophic lakes in northeast Florida. (Abstract p. 37)
- P34** — **Emilie Perkerson**, R. Perkerson & D. Casamatta — Is *Geitlerinema* really involved in Black Band Disease? An investigation of the ubiquitous, commonly confused genus *Geitlerinema* (Pseudanabaenaceae, Cyanobacteria). (Abstract p. 38)
- P35** — **Donald Cheney**, Anna Meador & Kevin Gardner — An *Ulva* bloom in New Bedford Harbor may have beneficial function because of its removal of PCBs. (Abstract p. 38)
- P36** — **Robert Vadas**, B. Beal, D. Anderson, Shannon Alexa, Milan Keser & B. Larson — Growth of *Ascophyllum*: An indicator of ocean warming? (Abstract p. 39)
- P37** — **Manuela Parente**, Filipe Costa & Gary W. Saunders — DNA barcoding reveals incipient speciation in the northwestern Atlantic *Colpomenia sinuosa*. (Abstract p. 39)

## ABSTRACTS

### *Oral Presentations (In order of presentation)*

**1 — IDENTIFICATION OF THE GENUS *CORALLINA* (CORALLINALES, RHODOPHYTA) IN CANADA.** Katharine Hind & Gary W. Saunders. Centre for Environmental and Molecular Algal Research, Department of Biology, University of New Brunswick, Fredericton, NB, Canada.

The process of identifying and classifying seaweed has largely been restricted to the study of morphological and anatomical traits. Species identification of seaweeds is problematic for many groups due to a high level of phenotypic plasticity and cryptic diversity. In the last decade, the use of genetic characters in the identification of red algal species has become an established tool for such challenging groups. This study examines the species diversity of the genus *Corallina* in Canada using an integrative taxonomic approach. The approach involves establishing genetic species groups using the mitochondrial gene cytochrome C oxidase subunit 1 (CO1) and then assessing the morphological characters that are ubiquitous within these groups. Current taxonomic classifications recognize five species in the genus *Corallina* in Canada, however my preliminary results suggest nine unique genetic species groups. This finding indicates that cryptic diversity may be present for this genus. My future research will be directed towards using molecular data in combination with a rigorous morphological examination to elucidate species diversity in this taxonomically challenging algal group.

**2 — USING DIATOM DATA FROM DIFFERENT SAMPLING PROTOCOLS IN STREAM BIOMONITORING: POTENTIAL FOR INTEGRATION.** Nathan J. Smucker & Morgan L. Vis, Department of Environmental and Plant Biology, Ohio University, Athens, OH.

Diatoms are excellent indicators of human impacts on stream ecosystems and are very useful for management, restoration, and conservation plans. Various sampling protocols have been used in the scientific literature and controversy has existed pertaining to inter-study comparability and reliability of conclusions with data generated from different methods. To address this concern, we sampled 58 streams with two common protocols: (1) epilithic habitat samples (EHS) from riffles and (2) multi-habitat samples (MHS). Multiple regressions of environmental and taxonomic variables were conducted on Bray-Curtis and Jaccard similarities calculated between each pair of sites to investigate potential causes contributing to dissimilarity between the two protocols. Nonmetric multidimensional scaling was used to ordinate sites from each data set. Procrustes analysis indicated no significant difference between ordinations created from the two datasets ( $m_{12} = 0.36, p = 0.001$ ). The main axis of variation from each dataset was highly correlated with conductivity, cations,  $PO_4$ , and forested land use ( $p < 0.05$ ). Pearson correlation coefficients were greater for the MHS dataset. Canonical correspondence analyses for each dataset using one constraining variable at a time indicated similarly strong relationships of diatom assemblages with conductivity, cations,  $PO_4$ , and land use between the two protocols. Metrics indicating nutrient status were highly concordant between the two methods. Morphological guilds were similar with the exception of motile taxa, which were significantly greater in MHS ( $p < 0.01$ ). Taxonomic metrics differed significantly between the two methods, especially evenness and diversity, which were significantly greater in MHS than EHS ( $p < 0.01$ ). Diatom data produced by MHS and EHS generally responded similarly to environmental conditions, which makes ecological inferences and assessments of human impacts from different protocols reliable. However, taxonomic composition was not concordant, which has implications for understanding diversity patterns and species distributions.

**3 — A COMPARISON OF DNA BARCODE MARKERS FOR SPECIES DISCRIMINATION IN MARINE RED ALGAE.** Bridgette Clarkston & Gary W. Saunders. Center for Environmental & Molecular Algal Research, Department of Biology, University of New Brunswick, Fredericton, NB, Canada.

The accurate identification of many red algae to the species level using traditional morphological characters can be frustrating and overwhelming. For example, members of the red algal family Kallymeniaceae (Rhodophyta) are often challenging to identify due to high plasticity of morphological and anatomical traits typically used to delimit species. This difficulty in identification can be alleviated greatly by an emerging method known as “molecular-assisted alpha taxonomy.” In this method, a large number of specimens are sequenced for a standard DNA barcode marker as a first step to “species” assignment, followed by detailed morphological observations. Regions of the mitochondrial cytochrome c oxidase I gene (COI-5’) and the plastid 23S rRNA gene (UPA) have both been proposed as DNA barcode markers for rapid species identification in red algae. COI-5’ is a more variable marker and has higher resolution for delimiting closely related species but can be difficult to sequence for some taxa requiring specific primers. UPA primers are universal and work in diverse lineages (*e.g.* red algae, brown algae, green algae) but low interspecific sequence variation in this marker may result in underestimates of species diversity. Here a comparison of COI-5’ and UPA for resolving species of the Kallymeniaceae from British Columbia, Canada will be discussed.

**4 — DNA BARCODING REVEALS CRYPTIC DIVERSITY AMONG PHAEOPHYCEAN TAXA WITH SIMPLE AND PLASTIC MORPHOLOGIES IN CANADA.** Daniel McDevit & Gary W. Saunders. Center for Environmental & Molecular Algal Research, Department of Biology, University of New Brunswick, Fredericton, NB, Canada.

A number of genera found in Canada, such as *Chorda*, *Chordaria*, *Delamarea*, *Dictyosiphon*, *Halosiphon*, *Melanosiphon*, *Papenfussiella*, *Petalonia* and *Scytosiphon*, have simple and highly plastic morphologies making it very difficult to tell species apart, or even to assign some collections to the correct genus at the morphological level. For the past four years our lab has been using a molecular marker, the DNA barcode (5’ end of the cytochrome c oxidase I gene) as a tool to assign quickly our collections to genetic species groups. As an example of the problem, we have uncovered substantial genetic diversity among collections that were field identified as *Scytosiphon* spp. Further molecular work using additional markers, such as the nuclear internal transcribed spacer region (ITS) and the plastid photosystem I gene (*PsaA*), in combination with morphological observations, has revealed that many of these collections do not match known species and likely fall within several brown algal genera (including several of those listed above). Similar results were obtained for collections with branched thalli of the *Chordaria*-type morphology. In this presentation, we highlight some of our findings and preliminary evidence for a number of new brown algal species from Canada.

**5 — IS THERE A RELIC PLASTID IN OOMYCETES?** Ian Misner<sup>1</sup>, Kristi Sommer<sup>2</sup>, J. Craig Bailey<sup>2</sup>, & Christopher E. Lane<sup>1</sup>. <sup>1</sup>Department of Biological Sciences, University of Rhode Island, Kingston, RI; <sup>2</sup>Center for Marine Science, Department of Biology, University of North Carolina Wilmington, Wilmington, NC.

The sequencing of five oomycete nuclear genomes has discovered genomic evidence to support a photosynthetic past of the group. Analysis of the *Phytophthora ramorum* and *P. sojae* genomes has revealed genes with phylogenetic affinities for algal and cyanobacterial homologs, likely transferred to the nucleus from a red algal-derived “secondary” plastid. These genes suggest that the ancestor of oomycetes was at one point photosynthetic, supporting the chromalveolate hypothesis, which proposes a photosynthetic common ancestor for a variety of photosynthetic and non-photosynthetic taxa. Our current investigation has uncovered definitive *psbA* genes in a variety of oomycete species, further strengthening the argument that oomycetes evolved from a photosynthetic ancestor. Interestingly, *psbA* is an essential protein involved in photosystem II, performs its only known function in the plastid, and the transfer of *psbA* to the nucleus has never been documented in any lineage. The oomycete copies of *psbA* we have recovered appear to be functional or have only recently begun accumulating mutations resulting

in premature stop codons. These data raise the possibility that some oomycetes still contain a vestigial plastid with a genome, both of which have yet to be characterized.

**6 — MITOCHONDRIA IN RED ALGAL PARASITE EVOLUTION.** Lillian Hancock & Christopher E. Lane, Department of Biological Sciences, University of Rhode Island, Kingston, RI.

Parasitism is a common life history strategy that has arisen independently numerous times in the course of evolution and in some instances these parasites have evolved directly from their hosts. This occurrence of host/parasite sister species pairs, termed adelphoparasitism, has been observed in multiple groups of organisms including the derived red algae (Florideophyceae). Red algal parasitism is unique in that infection of the host occurs through the transfer of parasite DNA-containing organelles rather than the whole organism. Interestingly, a parasite cell retains its mitochondrion but has abandoned its own plastid in favor of co-opting the host version, suggesting that there is something about the native mitochondrion that cannot be lost. This study aims to compare the mitochondrial genomes of adelphoparasite *Gracilariophila oryzoides* and host *Gracilariopsis lemaneiformis* in effort to determine the effect of a parasitic life style on genome architecture and sequence. Since the red algae host and parasite are closely related taxa, direct comparisons can be made between the mitochondrial genomes of the two species. By elucidating differences, we can then start to understand the evolutionary process by which a species adopts its parasitic lifestyle.

**7 — APPLICATION OF CONTINUOUS MONITORING IN THE LAKE ONTARIO NEARSHORE NUTRIENT SURVEY.** Margaret M. Pavlac<sup>1</sup>, Travis T. Smith<sup>1</sup>, Sean P. Thomas<sup>1</sup>, Gregory L. Boyer<sup>1</sup>, Joseph C. Makarewicz<sup>2</sup>, Theodore W. Lewis<sup>2</sup>, William J. Edwards<sup>3</sup>, Christopher M. Pennuto<sup>4</sup>, Caleb P. Basiliko<sup>4</sup>, and Joseph F. Atkinson<sup>5</sup>. <sup>1</sup>Department of Chemistry, SUNY-College of Environmental Science and Forestry, Syracuse, NY; <sup>2</sup>SUNY-Brockport, Brockport, NY; <sup>3</sup>Niagara University, Lewiston, NY; <sup>4</sup>Buffalo State University, Buffalo, NY; <sup>5</sup>University at Buffalo, Buffalo, NY.

The Lake Ontario Nearshore Nutrient Survey (LONNS) conducted in the summer of 2008 was designed to assess the effect of *Cladophora*, dreissenid mussels, and physical forces on the movement of nutrients entering the lake. As part of that survey, continuous real-time monitoring was employed in the nearshore areas of Oak Orchard, Rochester, and Mexico Bay in New York. The ferry box was equipped with sensors for chlorophyll, phycocyanin, CDOM, temperature, conductivity, turbidity, dissolved oxygen, and pH. Phytoplankton class abundance was estimated using the BBE FluoroProbe operated in continuous-flow mode. These data streams were geo-referenced and used to examine the spatial and temporal change of the different parameters relative to the riverine inputs. Initial results showing the variations in the distribution and composition of algal growth, as well as the physical data, will be presented.

**8 — GLUTAMINE SYNTHETASE II: A CASE OF LATERAL GENE TRANSFER IN BASAL VIRIDIPLANTAE?** Sohini Ghoshroy<sup>1</sup>, Aurelien Tartar<sup>2</sup> & Deborah L. Robertson<sup>1</sup>. <sup>1</sup>Clark University, Worcester, MA; <sup>2</sup>Nova Southeastern University, Fort Lauderdale, FL.

Lateral gene transfer (LGT) is rampant among prokaryotic organisms, whereas strong evidence of LGT from prokaryotes to eukaryotes or among eukaryotes is rare. In this study, we test the hypothesis that one gene encoding Glutamine Synthetase II (GSII<sub>B</sub>) in Viridiplantae arose via LGT from a eubacterial lineage. GS is an essential enzyme involved in nitrogen assimilation. In the majority of photosynthetic eukaryotes, cytosolic and chloroplastic isoenzymes are expressed. Phylogenetic analysis of GSII amino acid sequences from taxa representing Eubacteria, Plantae (Glaucophytes, Rhodophytes and Viridiplantae), stramenopiles and opisthokonts, uncovered a well supported GSII clade containing chlorophytes and basal streptophytes (GSII<sub>B</sub>; *Chlamydomonas reinhardtii*, *C. incerta*, *Volvox carteri*, *Chlorella* sp. NC64A, *C. ellipsoidea*, *C. vulgaris*, *Scherffelia dubia*, *Closterium peracerosum-strigosum-littorale* complex, *Marchantia polymorpha* and *Physcomitrella patens*) that grouped with GSII of eubacteria. The closest

extant relatives of the putative prokaryotic donor are  $\gamma$ -proteobacteria (*Francisella tularensis*, *F. philomiragia* and *Coxiella burnetii*). The eukaryotic GSII<sub>B</sub> functions in the chloroplast as evidenced by presence of chloroplast transit peptide found in a few taxa among chlorophytes and lower streptophytes. We propose that GSII<sub>B</sub> evolved via LGT rather than endosymbiotic gene transfer because: a) GSII genes are not observed in extant cyanobacteria (plastid progenitor) and b)  $\alpha$ -proteobacteria (mitochondria progenitor) are not sister to the eukaryotic GSII<sub>B</sub> clade. We propose a recent LGT event, after the divergence of Plantae (Glaucophytes, Rhodophytes and Viridiplantae), as homologs of GSII<sub>B</sub> are not observed in other eukaryotic lineages and thus would require numerous independent losses of GSII<sub>B</sub> within the eukaryotes. While we cannot formally exclude these alternative hypotheses, we are currently using tests of topology and rates of evolution to further evaluate the LGT origin of GSII<sub>B</sub> in Viridiplantae.

**9 — ATTACHMENT STRENGTH IN NUMBERS OF THE NORTHERN KELP, *SACCHARINA LATISSIMA*.** Bethann Balazsi & Sean Grace, Department of Biology, Southern Connecticut State University, New Haven, CT.

The attachment strength of the northern kelp, *Saccharina latissima*, was examined for individuals and groups. Measurements *in situ* of individuals and groups were taken at a depth of 3-7 meters in Fort Wetherill State Park, Jamestown, Rhode Island. In addition to attachment strength, morphological measurements of total length, greatest width, and stipe width were taken for both individuals and groups of *S. latissima* consisting of between three and five individuals. There was a significant difference in holding strength of groups compared to individuals while only a ratio of length:width (“squatness”) of the morphological characteristics measured showed significant differences between randomly selected individuals within groups and individuals. However, significant differences exist in total length, greatest width, stipe width and “squatness” when all individuals within a group were compared to individuals.

**10 — CHARACTERIZATION OF A ROCKY INTERTIDAL SHORELINE WITHIN ACADIA NATIONAL PARK: IMPACT OF SHORT-TERM TRAMPLING AND IMPLICATIONS FOR MANAGEMENT.** David E. Olson & Susan H. Brawley, School of Marine Sciences, University of Maine, Orono, ME.

Acadia National Park, Maine, is visited by more than two-million people annually. A percentage of these people visit rocky intertidal locations within the Park. The Park Service is concerned about potential visitor impact to a recently acquired shoreline near the new Schoodic Education and Research Centers (SERC), Schoodic Peninsula. Studies worldwide show that rocky intertidal vegetation is sensitive to human foot traffic and that damage to intertidal fauna and flora increases with the number of footsteps. Using a randomized block design, eighteen 0.25m<sup>2</sup> plots were randomly placed and distributed between three blocks, six plots per block, within the mid-intertidal zone of the SERC shoreline. Two plots in each block were randomly assigned to one of three treatment levels: control, high, and low. Treatments were applied once per month for six months, June – October, 2007 using a Before and After Control Impact experimental design. No significant differences were observed in percent fucoid canopy cover between trampling treatments ( $p > 0.05$ ). This result likely is due to using realistic levels of foot traffic determined during a pilot study conducted in summer 2006. A detailed observational study of visitation levels was conducted at five rocky intertidal sites during the months of June – October in 2007 and 2008. Management recommendations were provided to the Park Service on future monitoring and levels of access to the SERC shoreline. (This project funded by the NPS, Department of the Interior).

**11 — REGULATORY NETWORK OF CELL CYCLE IN MARINE PHYTOPLANKTON.** Yunyun Zhuang & Senjie Lin, Department of Marine Sciences, University of Connecticut, Groton, CT.

Cell cycle regulation is the key to growth, development, and differentiation of an organism, and is of particularly relevance to phytoplankton population dynamics since cell division in these unicellular



organisms directly lead to population growth. Knowledge on the molecular regulatory network of the cell cycle of marine phytoplankton will be important in order for us to understand how they adapt to the environment and respond to its changes. While the network is well studied in model systems such as yeast and humans, there has been no systematic analysis of such network for marine phytoplankton. In this study, we analyzed currently available phytoplankton genomic and EST data, searched and annotated cell cycle related genes in these algae. Core regulatory genes, including CDC2 and other CDKs, cyclins, and proliferating cell nuclear antigen, were identified and mapped to KEGG cell cycle pathway. Similarity and uniqueness in the cell cycle engine among marine phytoplankton species is being characterized and compared to counterparts in other eukaryotes to look for an evolutionary trend of this critical cellular machinery.

**12 — COMPARISON OF THE COMMONLY CONFUSED CYANOBACTERIAL GENERA *GEITLERINEMA* AND *LIMNOTHRIX* (PSEUDANABAENACEAE) USING A POLYPHASIC APPROACH.** Ralph B. Perkinson, Emilie A. Stringfellow & Dale A. Casamatta, Department of Biology, University of North Florida, Jacksonville, FL.

*Geitlerinema* is a widely distributed genus of the Pseudanabaenaceae (Cyanobacteria), commonly found in a variety of aquatic habitats. Characterized by highly motile, gliding trichomes under 4  $\mu\text{m}$  and an obligate absence of a sheath, the monophyly of this genus has not been evaluated via molecular methods. A sister genus, *Limnothrix*, is characterized by solitary, unsheathed trichomes with obligate gas vacuoles and a planktic life cycle. However, these two genera are often confused in the literature. To evaluate the phylogenetic relationships between these genera, we employed seven strains from culture and field collections, combined with those sequences available through GenBank, using 16S rRNA gene sequence data. Sequence analysis revealed the presence of four distinct clades, whose members were not clearly discernable by microscopic investigation. Two of these highly supported clades correspond to *Limnothrix* and *Geitlerinema* and contain strains that morphologically correspond to the types. The third clade contains a mixture of strains matching the morphology of *Limnothrix* and *Geitlerinema*, while the fourth clade contains *Geitlerinema* strains isolated solely from marine habitats, and both may be new genera. Further, we found that folding patterns and presence of a single tRNA transcript in the 16S-23S ITS region may be useful as a phylogenetic marker. Combined with cell ultra-structural (type of cell division, thylakoid arrangements) data, 16S gene sequences, and ecological data, we propose that *Geitlerinema* and *Limnothrix* as currently circumscribed are polyphyletic.

**13 — REPRODUCTION IN *PORPHYRA UMBILICALIS* KÜTZING: INSIGHTS FROM AMPLIFIED FRAGMENT LENGTH POLYMORPHISMS (AFLP).** Nicolas A. Blouin & Susan H. Brawley, University of Maine, Orono, ME.

The red alga *Porphyra umbilicalis* is described as being mostly sexual in Europe; however, >4000 individuals that represent collections made each month over multiple years, reproduce exclusively through asexual (neutral) spores on the Maine coast. Molecular data confirm that these trans-Atlantic populations belong to the same species. Although *P. umbilicalis* appears to be obligately asexual on the Maine coast, it is possible that there is a low level of sexual reproduction that was not detected in earlier field studies or that obligate asexuality is restricted to a portion of the western Atlantic range. To determine whether or not sexual reproduction exists, we investigated genetic differences among individuals of *P. umbilicalis* in locations where asexual or sexual reproduction is known to occur using amplified fragment length polymorphisms (AFLPs). This method offers a relatively easy, inexpensive way to look at genetic differences between individuals. If individuals were clones of each other, then their AFLP profiles would be expected to be identical. Alternatively, if multiple clones exist, we predicted that genetic differentiation would increase with distance (between site variability). Seventy-five *Porphyra umbilicalis* individuals were collected from 3 locations (n=25 per site). The sites selected included two locations in Maine that were previously well characterized as locations where asexual

reproduction occurs, and a third location in the UK where a sexual population occurs. Four *MseI* and fluorescent-labeled *EcoRI* primer pairs were determined to be informative for use in this investigation. Genetic profiles were determined for all individuals. Genetic profiles for individuals from the Maine collections were not identical; thus we conclude that Maine populations are not clonal. Cluster analysis shows that individuals within sites are more closely related than individuals between sites.

**14 — PORPHYRA (BANGIALES, RHODOPHYTA) DIVERSITY IN ICELAND: A LARGER PERSPECTIVE.** Agnes Mols Mortensen<sup>1</sup>, Juliet Brodie<sup>2</sup>, Christopher D. Neefus<sup>1</sup>, Ruth Nielsen<sup>3</sup> & Karl Gunnarsson<sup>4</sup>. <sup>1</sup>Department of Biological Sciences, University of New Hampshire, Durham, NH 03824; <sup>2</sup>Natural History Museum, Department of Botany, London, SW7 5BD, United Kingdom; <sup>3</sup>The Natural History Museum of Denmark, Botanical Museum, Gothersgade 130, DK-1123 Copenhagen K, Denmark; <sup>4</sup>Marine Research Institute, Skulagata 4, 121 Reykjavík, Iceland.

The taxonomy of *Porphyra* is not well resolved due to the simple and plastic morphology that varies within species and overlaps between species. Molecular methods are, with great success, used to overcome identification challenges, but there are still geographical regions, such as the northern parts of the North Atlantic, that are poorly investigated. The taxonomy and phylogeny of *Porphyra* cannot be fully resolved until a clearer understanding of species diversity on a global scale has been reached. As a step towards this goal, the current work addresses the *Porphyra* diversity in Iceland. Comprehensive collections were made around Iceland in 1999 and between 2005-2007 and this together with historic and contemporary collections held at the Natural History Museum, London (BM) and the Botanical Museum, Copenhagen (C) provided the basis for the Icelandic work. Species identifications were based on morphology and *rbcL* sequence data and a phylogenetic analysis was carried out including available *rbcL* data from the Pacific and the Atlantic. *Porphyra amplissima*, *P. dioica*, *P. "leucosticta"*, *P. linearis*, *P. miniata*, *P. purpurea* and *P. umbilicalis* which were recorded in Iceland prior to this work are now molecularly verified and *P. birdiae* together with two unidentified taxa are new records for the area. One of the unidentified taxa might be an undescribed North Atlantic sister taxon to *P. brumalis* from the Northeast Pacific and the other is a sublittoral taxon that might represent what Kjellman described as *P. abyssicola*. With the inclusion of *Porphyra thulaea*, that was previously molecularly verified, eleven *Porphyra* species are currently known from Iceland.

**15 — BIODIVERSITY AND BIOREMEDIATION POTENTIAL OF ULVA SPP. POPULATIONS IN THE GREAT BAY ESTUARINE SYSTEM.** Laurie C. Hofmann, Christopher D. Neefus & Arthur C. Mathieson, Department of Biological Sciences, University of New Hampshire, Durham, NH.

Eutrophication of coastal ecosystems is an issue at the forefront of scientific research. Algae have become an important potential resource for bioremediation, particularly as a biofilter for eutrophic coastal environments and aquaculture effluents. The goals of this study were (1) to assess the biodiversity of *Ulva* spp. in the Great Bay Estuary of New Hampshire and Maine, and (2) to assess which *Ulva* populations are most appropriate for bioremediation by determining if environmental nutrient history and/or taxonomic differences affect ammonium uptake kinetics. Molecular analysis of the internal transcribed spacer nrDNA regions (ITS1 and ITS2 regions), including the 5.8S gene, from field collected *Ulva* spp. revealed four distinct taxa with distromatic blade morphology: *Ulva lactuca* Linnaeus, *Ulva rigida* C. Agardh, *Ulva compressa* Linnaeus, and *U. pertusa* Kjellman. *Ulva lactuca* is a well documented species for Great Bay Estuary. *Ulva rigida* is common in the western Atlantic, but this report extends its range into New Hampshire. Although *U. compressa* is common in Great Bay Estuary, its distromatic morphotype is reported here for the first time. *Ulva pertusa* is a species of Asian origin. To our knowledge this represents the first report of *U. pertusa* on the east coast of North America. Hence, there is a clear need for reassessment of global *Ulva* populations using molecular tools to distinguish between morphologically similar species. Intra- and interspecific comparisons between *Ulva* populations revealed that both nutrient history and taxonomic differences influence ammonium uptake kinetics. Nutrient

history influences substrate affinity, whereas taxonomy influences uptake rate. *Ulva lactuca* and *U. pertusa* from low ammonium sites proved to be the most appropriate populations for bioremediation based on their ammonium uptake kinetics. Consequently, nutrient history along with taxonomic differences should be considered when using *Ulva* for bioremediation.

**16 — ASSESSING THE SPECIES RICHNESS OF *DICTYOTA* FROM CARIBBEAN PANAMA USING A DNA BARCODING APPROACH.** Elizabeth Sargent, Jessie Alden & Brian Wysor. Department of Biology, Roger Williams University, 1 Old Ferry Road, Bristol, RI.

Genus and species distinctions are problematic in the brown algal class Phaeophyceae for two reasons; 1) the difficulty in detecting cryptic diversity in morphologically convergent (but phylogenetically distinct) individuals, and 2) a poor understanding of the range of phenotypic plasticity within a species. The first issue can lead to an underestimate of species richness, while the second issue can lead to an overestimate. As part of a larger project to elucidate patterns of algal biodiversity for the Republic of Panama, we are interested in assessing diversity within the brown algal genus *Dictyota*. Approximately 80 species are attributed to the genus, 11 of which have been reported for Caribbean Panama. In order to facilitate species identifications, we initiated a DNA barcoding study using the 650-base pair region of the mitochondrial cytochrome oxidase I (*cox1*) gene. Sequence analysis of 28 specimens identified to 7 different morphological species from the Bocas del Toro region of Panama, revealed 6 clades of putative, *cox1*-defined species. Intraclade sequence difference ranged from 0-3 base pairs, while interclade sequence differences ranged from 67-98 base pairs within the order Dictyotales. Thus, it appears that the *cox1* barcode is useful for delineating species of *Dictyota*; continuing studies that include the remainder of Caribbean Panama species as well as Pacific Panama species will allow further testing of this idea.

**17 — PHENOTYPIC PLASTICITY IN *DESMODESMUS*: A NEVER ENDING STORY.** Elliot Shubert, Department of Botany, The Natural History Museum, London, U.K.

*Desmodesmus* exhibits phenotypic plasticity in nature and in the laboratory. Yet, many species are narrowly circumscribed and do not take into account morphological variability as viewed with the LM. The outer wall of *Desmodesmus* is ornamented and has features that may be of taxonomic value. However, one must determine if these ultrastructural characters are stable, if they are to be used to delimit the species. Two different clones of *Desmodesmus subspicatus* were cultured in a dilute inorganic medium and examined with LM and SEM. Clones produced spiny and spineless unicells, and spiny and spineless colonies. SEM analysis of wall ultrastructure produced a catalogue of characters that varied between clones cultured in a variety of nutrient conditions. When spiny unicells were compared to colonies and spiny colonies to spineless colonies, wart density was statistically different. Also, spine length varied within and between morphs. These results raise numerous taxonomic questions. How do we describe a plastic species whose characters are environmentally controlled, when environments change with time? How do we identify different morphological stages of the same organism from field collections?

**18 — ALGAL TURF SCRUBBER (ATS™) POTENTIAL FOR WATER QUALITY CONTROL AND BIOMASS PRODUCTION FOR BIOFUELS.** Haywood Dail Laughinghouse IV<sup>1</sup>, Walter H. Adey<sup>1</sup>, Patrick C. Kangas<sup>2</sup>, John Miller<sup>3</sup> & Jamie A. Hestekin<sup>4</sup>. <sup>1</sup>Department of Botany, National Museum of Natural History, Smithsonian Institution, Washington, DC; <sup>2</sup>Natural Resources Management Program, Department of Environmental Science and Technology, University of Maryland, College Park, MD; <sup>3</sup>Department of Chemistry, Western Michigan University, Kalamazoo, MI; <sup>4</sup>Ralph E. Martin Department of Chemical Engineering, University of Arkansas, Fayetteville, AR.

Algal Turf Scrubbers (ATS) are mini-ecosystems dominated by periphytic algal mats (algal turfs) and have been in constant operation as dozens of systems for over 150 ecosystem-years. Ranging from 0.1m<sup>2</sup>

to 3ha in size, the systems provide multiple benefits to the environment by improving water quality in addition to their capability of producing biomass for biofuels and other algal co-products. The algal turf production rate varies among systems, producing yearly means between 20-40g dry weight per m<sup>2</sup> per day, absorbing 2.3-3(7)% TN and 0.4-2% TP. Typically, the periphytic mat contains more than a hundred species within the major groups of Cyanobacteria, Chlorophyceae, Zygnemaphyceae, Oedogoniophyceae, Euglenophyceae, and Bacillariophyta. Occasionally, species within Chlamydomonadales, Dinophyceae, and Xanthophyceae are encountered. Diatoms (mainly *Diatoma* sp., *Gomphonema* spp., *Melosira* spp., *Navicula* spp., *Synedra* spp., and *Ulnaria ulna*) tend to colonize first, followed by cyanobacteria (primarily *Leptolyngbya* spp., *Lynbya* spp., and *Phormidium* spp.), chlorophytes (principally *Cladophora* spp., *Rhizoclonium* sp., and *Microspora* spp.), and the other groups. During mid to late summer months, *Spirogyra* spp. can become abundant on the ATSs of some temperate regions and may be a nuisance for overall production rate, probably due to its mucilaginous structure. Analyses of carbohydrate and lipid content of overall algal biomass are currently being conducted. Typically gravity-drained to moderate moisture content for processing, we have found the dry algal mass to be composed of approximately 23% soluble carbohydrates, 16% insoluble carbohydrates, 5% lipids, 10% protein, 44% ash, and 2% of other substances. Research is underway to refine the ATS biomass to liquid fuels; butanol/ethanol from carbohydrates, biodiesel from lipids, and co-products, like fertilizer, from ash and protein.

**19 — A GREEN LOOK AT RED ALGAE: CULTIVATING *GRACILARIA* FOR BIOFUEL PRODUCTION AND BIOREMEDIATION.** M. Dennis Hanisak, Harbor Branch Oceanographic Institute at Florida Atlantic University, 5600 U.S. 1 North, Fort Pierce, FL.

The recent unstable prices of fossil fuels and the growing awareness that their consumption has contributed significantly to global climate change, there is renewed interest in alternative energy sources. Algae are potential sources of renewable energy, and macroalgae, with their relative ease of harvest compared to microalgae, merit scrutiny as part of a much needed alternative to fossil fuels. Such a concept is not new, as the oil embargos and resulting shortages in the United States during the 1970s led to a substantial body of research on the cultivation of macroalgae for bioconversion. Early success with rapidly growing strains of the red alga *Gracilaria* in Florida, as well as the existing commercial harvesting of the brown alga *Macrocystis* in California, lead to the development of research programs (ca. 1975-1985) on the feasibility of using marine biomass (macroalgae or seaweeds) as an alternative energy source. While neither the economics nor the political climate for raising seaweeds for bioconversion were then favorable, this period of time was productive in terms of advances in macroalgal cultivation. Can lessons learned thirty years ago contribute to environmental and energy solutions clearly needed by society now? In particular, can the cultivation of red algae such as *Gracilaria* at the local level throughout the world contribute to global solutions? Can cultivating macroalgae for the purpose of bioconversion and bioremediation become feasible if Acarbon taxes@ become a reality?

**20 — SMALL SCALE BIODIESEL PRODUCTION (INCLUDING SOME DO'S & DON'T'S FOR MAKING BIODIESEL FROM ALGAE).** Scott Gordon, Green Technologies, LLC, 150 West Canal St., #1, Winooski, VT, 05404, <[sgordon@greentechvt.com](mailto:sgordon@greentechvt.com), [www.greentechvt.com](http://www.greentechvt.com)>

GreenTech has designed, constructed and operates a small scale biodiesel manufacturing plant located in Winooski, VT. Feedstocks are from a wide variety of waste oils primarily palm and soy but also including canola, sunflower, coconut, chicken, tallow, and fish oil. Fish oil biodiesel is notable because fish oil is chemically very similar to algae oil. Although GreenTech has only limited experience with the growth and harvesting of algae, we do have a lot of hands on experience with making biodiesel from just about every kind of oil. What does not seem to have entered the algae field yet are the very real constraints that making biodiesel provides. For example: cost, iodine number, crop density, water content and so on. Our limited engine and boiler field trials for fish oil (*i.e.* “algae oil”) biodiesel and some of the challenges and opportunities intrinsic to “algae oil” biodiesel will be discussed.

**21 — MULTIVARIATE ANALYSES OF 30 YEARS OF ROCKY SHORE COMMUNITY DATA.** Jim Foertch, John Swenarton & Milan Keser, Millstone Environmental Lab, P.O. Box 128, Waterford, CT.

As part of a monitoring program for an electric generating power station in southeastern Connecticut, rocky intertidal communities have been studied for over 30 years. Sites in close proximity to the station's cooling-water discharge are exposed to elevated water temperatures. All sites are subject to direct and indirect effects of, *e.g.*, climate change (including increased ambient water temperatures) and introduced species, as well as to the variability inherent to biological systems. One facet of the rocky shore program estimates abundance (as percent cover) of algae and sessile or slow-moving invertebrates in permanently marked 0.5m-wide transects, perpendicular to the shore-line, from MHW to MLW levels. Each of four sites has five transects, each divided into as many as 17 quadrats, each sampled six times per year. The program generates a lot of numbers; this presentation will describe results from a number of analysis techniques that have been adopted and adapted over the years to summarize the data, and to permit comparisons among seasons, years and sites. For example, simply plotting abundance of a taxon over time can illustrate short- and long-term cycles or trends; this is particularly appropriate for species that are consistently abundant, or show clear seasonal patterns. However, comparisons among stations, or among years at a given station, may be made using multivariate techniques, using abundance of all taxa found in the transects, even those that are rare or unpredictable in their occurrence. For example, multiple pair-wise comparisons of annual collections at each site may be illustrated as clustering dendrograms of Bray-Curtiss similarity, allowing differentiation among groups of years. More recently, multi-dimensional scaling has been used to produce an easily-visualized representation of relationships among stations and years. Complementary analyses have permitted determination of spatial and temporal differences among communities, some of which are related to power station operation.

**22 — A PRELIMINARY REPORT ON THE FRESHWATER ALGAE OF EASTERN NEW YORK.** John D. Hall & Kenneth G. Karol, The Cullman Program for Molecular Systematics, The New York Botanical Garden, Bronx, NY.

In the summer of 2008, samples of freshwater algae were collected in eastern New York particularly Harriman State Park. This area was among the first regions studied in North America by J. W. Bailey (beginning in 1841). Plankton in the lakes in the then newly formed Palisades Interstate Park was later studied by G. M. Smith in 1924. Over the intervening decades, there have been many changes in land use in the region. Despite these changes, many of the species originally described from the region were found during the 2008 field season including many of the species first described by Bailey and Smith. A total of 185 species were identified, 143 of these were Zygnematophyceae. Many of these species were not previously recorded for the region. Some of the more interesting species will be discussed.

**23 — HERBIVOROUS FISH ABUNDANCE AND GRAZING RATES: REEF RUGOSITY AS A CONTROL IN BELIZE AND THE BAHAMAS.** Paulette Peckol<sup>1</sup>, Katherine Morrice<sup>1</sup> & H. Allen Curran<sup>2</sup>. <sup>1</sup>Biological Sciences, Smith College, Northampton, MA 01063; <sup>2</sup>Geology Department, Smith College, Northampton, MA.

Human activities and natural disturbances (*e.g.*, thermal anomalies, hurricanes) have resulted in coral reef decline at a global scale, sometimes with a consequent phase shift from live coral cover to macroalgal dominance. On highly degraded reefs, bioerosion can exceed rates of reef accretion, resulting in reductions in topographic complexity, or rugosity. Reef fish prefer more rugose habitats because they offer protection from predators and shelter from physical stress. We examined the relationships between coral reef rugosity, herbivore abundance, and grazing rates on reefs off San Salvador Island, Bahamas and Belize. Surveyed reefs showed no significant change in rugosity over eight years despite near or direct hits by several hurricanes. Herbivore abundances (parrotfish and surgeonfish) were significantly related to rugosity, while other parameters, including live coral cover, displayed no clear association to fish

abundance. Sites with higher herbivore abundances were characterized by elevated grazing rates and lower macroalgal cover. Off the coast of Belize, Hol Chan Marine Reserve had highest total fish abundances of surveyed areas; however, this site showed the lowest herbivorous fish densities and highest macroalgal cover (nearly 40%) during recent (2007 and 2008) surveys of reef sites in northern Belize near San Pedro, an increase in nearly 50% over a 1999 census. In contrast, a site outside the reserve, Coral Gardens near Caye Caulker, had high herbivore densities and low macroalgal cover (~10%). Similarly, lower algal cover was coupled with higher herbivorous fish density and grazing rates off San Salvador Island, Bahamas. Maintenance of high levels of reef rugosity has a positive effect on herbivorous fish populations and is a major factor contributing to the resilience and balance of coral reefs in the face of chronic disturbances.

**24 — THE EFFECTS OF IRRADIANCE LEVEL, PHOTOPERIOD, AND CELL DENSITY ON SEXUAL REPRODUCTION IN THE GREEN SNOW ALGA, *CHLOROMONAS CHENANGOENSIS* (CHLOROPHYTA, VOLVOCALES), FROM UPSTATE NEW YORK.** Ronald W. Hoham, Frank M. Frey, Jesse D. Berman, Jeffrey B. Ryba, Jared E. Duncan, Andrew A. Forbes, Blair M. Goodridge, and Paris R. Miller, Department of Biology, Colgate University, Hamilton, NY.

The effects of strain differences, irradiance level, photoperiod, and cell density on sexual reproduction were studied in the snow alga, *Chloromonas chenangoensis*, from Upstate New York. Mating experiments were conducted over an 8-hour period and normal, abnormal, and total matings were tabulated. Significantly more total matings were observed in strain CU 725B than in CU 721A, and consequently strain CU 725B was used in the remaining experiments. There were no significant differences in total matings among irradiance levels of 70, 85, 100, 115, 130, and 145  $\mu\text{mol photons m}^{-2} \text{ s}^{-1}$  or cell densities of  $0.5 \times 10^6$ ,  $1.0 \times 10^6$ , and  $1.5 \times 10^6$  cells  $\text{mL}^{-1}$ . When comparing photoperiods of 12:12, 14:10, 17:7, 20:4, and 24:0 hour (light:dark), there were significantly more total matings in photoperiod 24:0 than in 12:12, but other differences were not observed. There were no significant differences in abnormal matings in any experiments and the percent of abnormal matings varied between 7-19%. Comparisons are made between this taxon and its close relative, *Chloromonas tughillensis*, with respect to optimal conditions for sexual reproduction.

**25 — MOLECULAR DELIMITATION OF NARRAGANSETT BAY SEA LETTUCE.** Brian Wysor, Department of Biology, Roger Williams University, 1 Old Ferry Road, Bristol, RI.

Sequences of the plastid encoded *rbcL* gene and the nuclear encoded internal transcribed spacer regions were compared from over 75 specimens of *Ulva* spp. from Narragansett Bay, RI. The phylogenetic position of specimens within putative species clades was largely congruent in *rbcL* and rDNA ITS-inferred trees. Preliminary analyses suggest that at least 9 species of sea lettuce are present throughout Narragansett Bay, but a morphological concept for this clade structure remains elusive. In all but a few cases, sequences generated in this study are already represented in public databases, suggesting that Narragansett Bay sea lettuce species are widespread in distribution. Understanding exactly which species are present in Narragansett Bay is critical to environmental management of *Ulva* blooms, which have become a persistent feature of shallow areas of Narragansett Bay during summer months.

**26 — A MOLECULAR FLORISTIC SURVEY IN CANADIAN WATERS REVEALS CRYPTIC DIVERSITY IN THE ORDER AHNFELTIALES.** Daniela Milstein & Gary W. Saunders, Centre for Environmental & Molecular Algal Research, Department of Biology, University of New Brunswick, Fredericton, NB, Canada.

Identification of red algae based only on morphological characters can be imprecise due to their simple morphologies, phenotypic plasticity, convergent evolution and the occurrence of cryptic species. More accurate identification can be performed when molecular markers are applied to augment morphological

observations. There are a number of molecular markers available that have been used to this end, which is problematic for floristic surveys in which investigators want a standard system for the identification of unknown specimens. To overcome this issue, partial sequences of both the mitochondrial cytochrome oxidase I (COI) and the plastid 23S rRNA (UPA) genes have been promoted as potential DNA barcodes (candidate markers for rapid specimen identification). The objectives of this work are to compare the applicability and variability of COI and UPA within the context of the first large-scale survey of species diversity for the order Ahnfeltiales in Canada, and secondly, to use these data to assess species richness. Two ahnfeltialean species are currently recognized along the coasts of Canada, *Ahnfeltia fastigiata* and *A. plicata*. However, as many as five versus four genetic species groups were resolved for COI and UPA, respectively. Based on these results we can conclude that COI is a more sensitive (variable) marker than UPA; and there is cryptic species diversity within the genus *Ahnfeltia* in Canada. Morphological observations in combination with further molecular analyses are being completed to assess species diversity for this order in Canadian waters and preliminary results will be presented.

**27 — PHYLOGENY AND SYSTEMATICS OF SPECIES OF *PHYCODRYS* AND *MEMBRANOPTERA* (DELESSERIACEAE, RHODOPHYTA) THAT EXHIBIT TRANS-ARCTIC DISTRIBUTIONS BETWEEN THE NORTH PACIFIC AND NORTH ATLANTIC OCEANS.** Max H. Hommersand<sup>1</sup> & Showe-Mei Lin<sup>2</sup>, <sup>1</sup>Department of Biology, University of North Carolina, Chapel Hill, NC 27599-3280; <sup>2</sup>Institute of Marine Biology, National Taiwan Ocean University, Keelung City 202-24, Taiwan, R.O.C.

*Phycodrys rubens* and *Membranoptera alata* are species that have traditionally been thought to exhibit trans-Atlantic distributions between Europe and North America. This opinion was challenged by van Open *et al.* (1995, *Marine Biology* 23:179-188) who observed that nuclear rDNA ITS sequences of *Phycodrys* samples from Newfoundland and Nova Scotia corresponded to sequences of *P. riggii* from the North Pacific rather than to *P. rubens* from Europe. A phylogenetic analysis of *rbcL* sequences from species belonging to the two genera indicated that both *Phycodrys* and *Membranoptera* originated in the North Pacific and reached Atlantic North America only recently, whereas similar-appearing species reached the European North Atlantic earlier. Our observations yielded the following: Most specimens of *Phycodrys* from Atlantic North America are referable to *P. fimbriata* (Kuntze) Kylin 1924 (Lectotype locality: Newfoundland). These have base pair sequences that are nearly identical to those of samples from the North Pacific that have been widely referred to as *P. riggii* N.L. Gardner 1927. *Membranoptera alata* (Hudson) Stackhouse appears to be restricted to Europe. Our *Membranoptera* samples from Atlantic North America are separated by only six base pairs from samples of *M. spinulosa* (Ruprecht) Kuntze 1891 from the North Pacific. A sample of *Pantoneura fabriciana* (Lyngbye) M.J. Wynne 1997 [formerly *P. baerii*] from Spitsbergen is sister to *Membranoptera alata* from Europe and is unrelated to the type species of *Pantoneura*, *P. plocamioides*, from Antarctica. Questions regarding the taxonomy, nomenclature, biogeography, biosystematics and ecophysiology of trans-Arctic *Phycodrys* and *Membranoptera* species will be addressed.

**28 — MARINE ALGAE AND EARLY EXPLORATIONS IN THE UPPER NORTH PACIFIC AND BERING SEA.** Michael J. Wynne, University of Michigan Herbarium, Ann Arbor, Michigan.

A synthesis of early exploration and the discovery of marine algae in the upper North Pacific and Bering Sea is presented covering the period from the late 1730s to around 1900. Information is provided about these early efforts to gather natural objects, including seaweeds. The first collections of marine algae in this broad region were those made by Steller and Krasheninnikov from the Kamchatka Peninsula, Russia, during the Second Kamchatkan Expedition (1735-1742) and were described by Gmelin (1768). The first known algal collections in Alaska were those made by Merck in his 1790-1791 visits to Unalaska Island during the Billings expedition (1785-1794). British-sponsored expeditions for commercial purposes and for exploration and discovery allowed surgeon-naturalist Menzies to gather seaweeds that Turner and others worked up back in Europe. Several of the Russian expeditions during the first half of the 18<sup>th</sup>

century had naturalists aboard. The first Russian circumnavigation of the globe (1803-1806), with the ships 'Nadeshda' and 'Neva', under the command of von Krusenstern had naturalists Tilesius, Langsdorff, and Horner, all of whom collected seaweeds. The naturalist Chamisso accompanied the Romanzof Expedition (1815-1818) on the Russian vessel 'Rurik' under the command of von Kotzebue and made collections of algae in the Aleutians as well as in the Kurils and Kamchatka. The Lütke expedition of 1826-1829 consisted of two ships. Lütke was in command of the 'Seniavin' with K. Mertens aboard as physician-naturalist, and the 'Moller' was under the command of Staniukovich accompanied by the naturalist Kastalsky. The first American-sponsored scientific expedition (1838-1842) was that commanded by Wilkes. The algal collections were worked up by Bailey and Harvey. The Russian naturalist Voznesenskii spent 1839-1849 in Russian America traveling and making numerous collections of natural objects. His algae were described by Ruprecht in St. Petersburg. The 'Vega', a Swedish scientific vessel (1878-1880), was under the command of Nordenskiöld. The naturalist Kjellman collected algae at Port Clarence, Alaska, and also from Bering Island and St. Lawrence Island in the Bering Sea. The Harriman Alaskan Expedition in the summer of 1899, with the ship 'George W. Elder', was sponsored by railroad magnate E. H. Harriman of New York City and had several scientific personnel aboard, including the phycologist Saunders. During the same summer of 1899 an expedition, organized by the University of California and including Jepson, Hunt, Lawson, and Setchell as participants, also visited Alaska and made algal collections from various locations.

**29 — THE PROMISES AND PITFALLS OF MOLECULAR-ASSISTED ALPHA TAXONOMY.** Gary W. Saunders, Centre for Environmental & Molecular Algal Research, Department of Biology, University of New Brunswick, Fredericton, NB, Canada.

To contend that molecular tools have dramatically changed algal systematics is to grossly understate what has been a remarkable revolution. Initially emphases were placed on resolving evolutionary relationships and their corresponding taxonomic changes. More recently, under the banner DNA barcoding, molecular tools are being applied to floristic studies challenging our traditional concepts on species diversity and distribution, indeed even our definition of a species. In our work on the Canadian flora, we have made significant advances in our understanding of algal diversity through an approach termed molecular-assisted alpha taxonomy – collect, sequence, cluster specimens based on genetic species groups, go back and review the ecological, biogeographical, morphological and anatomical attributes and bring all of the information together in a holistic or integrative species concept. This approach shows substantial promise to revolutionize our understanding of algal diversity and I will highlight some of our successes. However, these methods are not without their pitfalls. Powerful tools can lead to equally powerful errors if not used with due caution, and reconciliation of the new data and conclusions with the traditional type-based system of taxonomy (as outlined in our various nomenclatural codes) can be difficult. These issues will be explored in the context of advancing algal floristics and taxonomy.

### ***Poster Presentations (Board numbers in parentheses)***

**(P1) RELATIONSHIPS BETWEEN DIATOM COMMUNITY COMPOSITION, PERIPHYTON STOICHIOMETRY, AND PRIMARY CONSUMERS.** Samuel A. Drerup<sup>1</sup>, Kam Truhn<sup>2</sup>, Alissa Perrone<sup>2</sup> & John Wehr<sup>2</sup>. <sup>1</sup>Department of Environmental and Plant Biology, Ohio University, Athens, OH; <sup>2</sup>Department of Biology, Fordham University, Bronx, NY.

The purpose of this study is to investigate relationships between periphyton stoichiometry and the benthic community of small order rivers in eastern New York State. The work done was divided into two related studies, a pilot study using data collected in 2001 and a second study using data collected in 2008. The pilot study was conducted using historical chemical, stoichiometric, and physical data collected May-July 2001 as part of a larger study investigating changes in periphyton stoichiometry due to increased distance



from New York City. Nine stream locations were chosen based on historical data and available preserved periphyton samples. Preserved periphyton samples (2001) were digested using standard cold/hot nitric acid digest methods and mounted as permanent slides. Diatom frustules were identified to species level using Patrick and Reimer's *The Diatoms of the United States* (1966). Counts were then used to calculate Shannon's and Simpson's diversity index scores in addition to Trophic Diatom Index (TDI) and Generic Diatom Index (GDI) scores. In the current study, eight of the original nine study sites were used (ninth stream not able to be sampled) as well as three additional southern streams. Three rocks within the sample area were selected and measured for surface area calculations. Periphyton was removed from rocks and the total volume was recorded. Invertebrates (grazers only) were collected by hand from rocks within the sample area. Periphyton was processed for diatom identification as above. Collected material, periphyton and invertebrate, were prepared for C, N, and P analysis. Index scores then were compared to nutrients (C, N, and P) per surface area. Trends observed in both studies but only GDI scores (pilot) and nutrients per surface area resulted in significant statistical results.

**(P2) DESICCATION TOLERANCE OF VARIOUS TYPES OF CELLS IN THE FRESHWATER RED ALGA, *BATRACHOSPERMUM GELATINOSUM*. Alexander M. VandenBroek & Morgan L. Vis.** Department of Environmental and Plant Biology, Ohio University, Athens, OH.

Freshwater red algae are unusual in that they have no desiccation tolerant propagule like many other algae. Although they do not possess this structure, they have dispersed widely and are found in streams throughout the world. The goal of this project was to evaluate various sized tufts of gametophyte thalli to document if a microenvironment is created, within which cells might remain viable for some period of time. If so, dispersal of freshwater red algae might be possible via birds. Gametophytes of *Batrachospermum gelatinosum* were collected from the field and immediately after transport to the laboratory, put into three size treatment classes (clumps). These treatments were desiccated in an incubator at 15°C 12:12 day length for 24 hrs, three days, ten days, and 17 days (five replicates each). These clumps were analyzed in a microscope using a viability stain, methyl blue, to determine the number of living fascicle cells, carpogonia, and carposporangia. The results indicated a tolerance to desiccation after the first day (24 hrs) in all three tuft sizes. The larger two tufts had > 40% viability for all cell types and the smallest tuft had <35%. At day ten, the smallest tuft showed no viability for any cell type while the larger two tufts had between 5-30% viability for all three cell types. In the future, other red algal taxa will be tested to compare desiccation tolerance among taxa that produce varying amounts of mucilage.

**(P3) MOLECULAR PHYLOGENETIC CHARACTERIZATION OF DESERT GREEN ALGAE FROM SOUTH AFRICAN BIOTIC SOIL CRUSTS. Chien Lo & Louise A. Lewis,** University of Connecticut, Biology of Ecology and Evolutionary Biology, Storrs, CT.

Biological or biotic soil crusts include diverse communities of microorganisms such as cyanobacteria, diatoms, fungi, protists, invertebrates, and green algae. The microorganisms inhabiting the biotic crusts aggregate the soil particles, contributing to soil stability, and add carbon and nitrogen to the soil. This project investigates the distribution and phylogenetic relationships of seventeen isolates of South African desert green microalgae. Sequence data from three gene regions were utilized during this study: the chloroplast large subunit of the ribulose-bisphosphate carboxylase (*rbcL*), the nuclear small subunit (18S) rDNA, and the nuclear internal transcribed spacer (ITS) rDNA. The data were aligned with data from North American biotic crust algae previously collected in our lab, plus published data from aquatic algae, and then analyzed using maximum likelihood and Bayesian methods. Both the *rbcL* and 18S genes are fairly evolutionarily conserved and were used to determine relationships at more inclusive taxonomic levels, whereas the ITS data are more variable and were used to resolve relationships among more closely related taxa. We will show that South African green algal isolates have close relationships to previously described desert species of *Scenedesmus*, and other desert chlorophycean and trebouxiphycean taxa.

Focusing on examples from Chlorophyceae our data support an interpretation of diversification in the desert habitat.

**(P4) CONFUSION CAUSED BY LIMITED MORPHOLOGY: TWO CASE STUDIES IN GREEN COCCOIDS.** Jared Rada, Karolina Fučíková & Louise A. Lewis, Department of Ecology and Evolutionary Biology, University of Connecticut, Storrs, CT.

Cocoid green algae are difficult to categorize due to the relatively low number of morphological characters. Traditionally, the classification of these algae depended on subtle morphological differences, without much information about the potential variation or plasticity of these traits. The use of molecular sequence data provides a high number of characters that are not subject to phenotypic plasticity and therefore are assumed to provide a more direct measure of phylogenetic relationships. Molecular phylogenetic studies of coccoids often yield unexpected results, uncovering cryptic diversity as well as placing taxa in dramatically different positions from those expected under the morphological paradigm. As part of a monographic study of the chlorophycean genus *Bracteacoccus*, several strains deposited in culture collections under this generic name were found to belong to other green algal genera. Although morphologically similar to young cells of *Bracteacoccus*, these algae were demonstrated to belong to the genera *Myrmecia* and *Pseudomuriella* based on 18S and *rbcL* sequence data. A contrasting case was found in the genus *Dictyococcus*, which was examined as putative sister taxon to *Bracteacoccus*. Only two type cultures of *Dictyococcus* are available worldwide: *D. schumacherensis* and *D. varians*. Analysis of the 18S and *rbcL* sequences showed *D. schumacherensis* to be nested in *Bracteacoccus* and therefore in need of a formal transfer to *Bracteacoccus*. Determination of the phylogenetic position of *D. varians* requires further analysis. These cases may represent two of potentially many discrepancies of morphological and sequence data. Morphology of these algae is limited and may be homoplasious. Therefore, sequence data appears more useful for resolving phylogenetic relationships between taxa. As more sequence data are collected for cocoid algae, more taxa are likely to be revised.

**(P5) EFFECTS OF VARIABLE GROWTH CONDITIONS ON ALGAL LIPID PRODUCTION.** Portia A. Osborne, Sean P. Thomas & Gregory L. Boyer, Department of Chemistry, State University of New York College of Environmental Science and Forestry, 1 Forestry Dr., Syracuse, NY.

Algal cultures are increasingly being seen as viable economic resources for biodiesel production. However, the great amount of space and light required for growing algal cultures continues to limit the feasibility of this idea, especially on the small-scale. If ideal growing conditions to maximize lipid production can be determined, the ease at which algal biodiesel can be produced would increase. Cultures of *Chlorella vulgaris* were grown under a range of conditions with varying amounts of available nitrogen and in varying temperatures. Results on the overall biomass and lipid content for each growing condition will be presented.

**(P6) MAPPING ECOLOGICALLY SIGNIFICANT INORGANIC NITROGEN IN THE NEARSHORE ENVIRONMENTS OF LONG ISLAND SOUND, USA USING MACROALGAL TISSUE SAMPLES.** Abdu, Y.<sup>1</sup>, Kim, J.K.<sup>2</sup>, Kraemer, G.P.<sup>3</sup> & Yarish, C.<sup>1,2</sup>. <sup>1</sup>Department of Ecology & Evolutionary Biology, University of Connecticut, Stamford, CT; <sup>2</sup>Department of Marine Sciences, University of Connecticut, Groton, CT; <sup>3</sup>Environmental Studies Program, Purchase College (SUNY), Purchase, NY.

As a consequence of cultural eutrophication from point and nonpoint sources of inorganic nitrogen (N), Long Island Sound (LIS) faces hypoxia and harmful algal blooms. Monitoring and managing the effects of anthropogenic N entering marine ecosystems is a major environmental priority of the EPA Long Island Sound Study (LISS). LISS's water quality monitoring program measures the concentration of inorganic N at fixed off-shore stations along an east–west gradient; however, it fails to define the N available to near-shore primary producers. In an attempt to establish baseline information, we are measuring the nitrogen

content in the perennial macroalgae, *Chondrus crispus* and *Fucus vesiculosus*, and the opportunistic macroalga *Ulva lactuca* throughout the year along an east-west gradient in LIS. Tissue carbon (C) and N contents will quantify the temporal and spatial variability to ascertain if there is a N gradient reflected through algal tissues across the northern shore of LIS. Tissue samples of *Chondrus crispus* collected in early January had significantly higher tissue N contents (4.69%) in western LIS than in middle and eastern LIS (4.19% and 4.29%, respectively), reflecting the decreasing west-east N gradient. Based on these preliminary results, *Chondrus crispus* and other benthic marine algae maybe useful as monitors of the availability of ecologically significant N in LIS.

**(P7) ARE YOU THE REAL *NITELLA FLEXILIS*?** Heather Meyer<sup>1,2</sup> & Kenneth G. Karol<sup>2</sup>. <sup>1</sup>Department of Biology, Sarah Lawrence College, Bronxville, NY; <sup>2</sup>The Cullman Program for Molecular Systematics, The New York Botanical Garden, Bronx, NY.

In 1965, R.D. Wood and K. Imahori published *A Revision of the Characeae*, a global monograph of the fresh water green algal family Characeae. In this monograph, a broad morphological species concept was used to reduce more than 500 named species to approximately eighty loosely defined species, each with numerous subspecies, varieties and forms. Currently, we are using molecular phylogenetic methods in combination with vegetative morphology and oospore membrane architecture to test and revise this classification. For this study we present finding for *Nitella flexilis*, which includes more than thirteen previously recognized species either as synonyms or subspecific taxa. Chloroplast sequence data (*rbcL* and *atpB*) reveal that *N. californica*, *N. capitata*, *N. mexicana*, *N. mirabilis*, *N. missouriensis* and *N. opaca* each form distinct clades separate from *N. flexilis sensu stricto*. Gross morphological characters and oospore membrane architecture are consistent with these findings. Taken together, the taxa examined here appear to warrant species status separate from, but closely related to, *N. flexilis*.

**(P8) DOCUMENTING 150 YEARS OF COASTAL CHANGE: REVISITING THE WORK OF AMATEUR PHYCOLOGIST ELIZA M. FRENCH.** Rachel Rock-Blake<sup>1</sup>, James T. Carlton<sup>2</sup> & Paulette Peckol<sup>1</sup>. <sup>1</sup>Department of Biological Sciences, Smith College, Northampton, MA; <sup>2</sup>Williams-Mystic Program, Mystic, CT.

Any effort to understand ecological change in coastal habitats must begin with a record of what has previously existed in that given location. Macroalgal diversity and abundance patterns were documented by the amateur phycologist Eliza M. French along the coast of New London, Connecticut during the 1850s and 1880s. As revealed in her books of annotated pressed algal specimens, French highlighted changes in the algal assemblage during her thirty years of work at several sites. For example, she noted during the 1880s that species such as *Polysiphonia variegata* (now *Polysiphonia denudata*) and *Dasya elegans* (now *Dasya baillouviana*) were “not so common as formerly here,” a trend that might be a reflection of the industrialization of New London during her lifetime. In this study, French’s collecting sites are revisited to reveal patterns of change in this assemblage in the intervening 150 years. While the perennial brown (e.g. *Fucus vesiculosus*, *Ascophyllum nodosum*) and red (*Chondrus crispus*) species remain the dominants at her collecting sites, we noted some differences in late winter (March) and early spring collections. For example, *Neosiphonia harveyi*, only noted in French’s summer collections, was collected during March. In contrast, *Callithamnion corymbosum* was absent from our winter survey but listed among French’s records as a common drift specimen. Summer collecting trips to French’s sites are planned. Such careful records of collections in the mid- and late-1800s offer a unique baseline to highlight long-term changes in coastal algal assemblages, some that might be linked to human-induced effects.

**(P9) HERBIVORE IMPACT ON MACROALGAL BLOOMS IN NARRAGANSETT BAY, RI.** Michele Guidone & Carol Thornber, Department of Biological Sciences, University of Rhode Island, Kingston, RI.

In Narragansett Bay, RI, macroalgal blooms consisting of *Ulva* sp. and *Gracilaria* sp. have become an annual occurrence. This study examined the effect of invertebrate herbivores on the most abundant of these bloom species, *U. lactuca*, in order to determine which herbivore species are consuming it and how large an impact their grazing has on *U. lactuca* biomass. During July, August, and September 2008 we deployed herbivore exclusion cages at three locations within Narragansett Bay. Cages were constructed of three different mesh sizes to differentially exclude herbivores. Within each cage we placed a pre-weighed piece of *U. lactuca*. After 10 days, cages were retrieved with all of their contents, *U. lactuca* was reweighed, and herbivores inside the cages were counted and identified. Co-occurring herbivore densities outside of the exclusion cages and dissolved inorganic nitrogen (DIN) levels were also measured monthly. We found that the change in *U. lactuca* mass differed significantly among month, with losses to herbivory in July and net growth in August and September. Our results do not identify which herbivores are consuming *U. lactuca*, as cage mesh size did not have a significant impact on *U. lactuca* biomass; however, mud crab abundance was negatively correlated to the change in *U. lactuca* biomass. In addition, DIN values were positively correlated with the change in *U. lactuca* biomass. Our results indicate that the growth of macroalgal blooms in this system may be dependent on both herbivore abundance and nutrient availability.

**(P10) PHYLOGEOGRAPHIC STUDY OF *TUOMEYA AMERICANA* (RHODOPHYTA) IN EASTERN NORTH AMERICA.** Aditi Rambani & Morgan L. Vis. Department of Environmental and Plant Biology, Ohio University, Athens, OH.

The freshwater red alga, *Tuomeya americana*, is the only species in the genus and its distribution is restricted to eastern North America. The mitochondrial DNA region consisting of the intergenic spacer between the cytochrome oxidase subunit 2 and cytochrome oxidase subunit 3 genes with the flanking gene regions (*cox2-3*) was used to conduct a preliminary study investigating the phylogeographic trends throughout its range. A total of nine stream sites were sampled, Georgia (GA), Kentucky (KY), New Brunswick (NB), North Carolina (NC), Nova Scotia (NS1, NS2), Ontario (ON) and Rhode Island (RI1, RI2). A single individual per site was analyzed except for Kentucky and New Brunswick for which 14 thalli and 2 thalli were available, respectively. Three haplotypes were revealed from the 23 individuals. One haplotype represented all specimens from KY, and the individuals from NS1 and RI1. The individuals from NS2, NC and RI2 were second haplotype, which differed from first haplotype by a single pair transition. The third haplotype was from GA differing from the other haplotypes by 7-8 bp. Although limited morphological plasticity has been recorded in *Tuomeya americana*, preliminary analyses show that there is intraspecific variation across its range and further investigation could offer useful insights about phylogeographic trends of this species. Comparison of these data with those previously collected for other freshwater reds can provide a better understanding of general dispersal patterns for these organisms in eastern North America.

**(P11) PHENOLOGY OF *BATRACHOSPERMUM HELMINTHOSUM* (RHODOPHYTA).** Justin R. Pool<sup>1</sup>, Morgan L. Vis<sup>1</sup>, Robert Verb<sup>2</sup>, Jason Zalack<sup>3</sup>, Melissa Verb<sup>2</sup> & Nate Smucker<sup>1</sup>. <sup>1</sup>Department of Plant and Environmental Biology, Ohio University, Athens, OH; <sup>2</sup>Department of Biological & Allied Health Sciences, Ohio Northern University, Ada, OH; <sup>3</sup>Department of Zoology, Michigan State University, Lansing, MI.

Many freshwater red algae in temperate streams exhibit maximum biomass, growth, and reproduction during early spring before a dense leaf canopy forms above the stream. *Batrachospermum helminthosum* is widespread throughout temperate eastern North America. During 1999, 2005, and 2006, a population of *B. helminthosum* was monitored in a southeastern Ohio stream. The site was visited from late March until late June, which corresponded to the period that macroscopic gametophytes were present. Each sampling date, the water depth, current velocity, and percent algal cover were recorded in each of 160 quadrats.

Individual thalli were collected for morphological analysis during the 2006 sampling season. The growth and reproduction of *B. helminthosum* appeared to be correlated with water temperature and day length. Spermatangia were observed in early spring and absent by May. Immature carpogonia were abundant in early spring and by May only mature carpogonia were observed. The onset of reproduction was accompanied by reduced vegetative growth and a lower number of whorls per plant. As the number of spermatangia decreased throughout the season, the number of carposporophytes increased. The greatest percent cover of *B. helminthosum* was observed in mid to late May before thalli senescence in mid to late June. This taxon appears to follow a typical growth pattern for spring ephemeral freshwater red algal taxa in temperate regions.

**(P12) MOLECULAR AND MORPHOLOGICAL VARIATION IN *CODIUM FRAGILE* IN THE NW ATLANTIC.** Lucy E. Pleticha<sup>1</sup>, Christopher S. Benton<sup>2</sup>, Anita S. Klein<sup>1</sup> & Arthur C. Mathieson<sup>1</sup>. <sup>1</sup>Department of Biological Sciences, University of New Hampshire, Durham, NH; <sup>2</sup>Department of Molecular, Cellular and Biomedical Sciences, University of New Hampshire, Durham, NH.

*Codium fragile* (Suringar) Hariot is an invasive Asiatic green alga that has colonized areas in Long Island Sound, the Gulf of Maine, and the Canadian Maritime Provinces within the past fifty years. The plant has a dichotomously branched cylindrical thallus. The thallus is made up of tangled filaments surrounded by a densely packed outer covering of swollen filament tips, or utricles. Each utricle ends with a pointed tip, the mucron. The goals of this study were to investigate the morphological and genetic differences in NW Atlantic *C. fragile* populations to determine which subspecies are present. In the summer of 2008, we surveyed 19 sites from the Canadian Maritimes to Long Island Sound. For each population collected, we measured size variation in the utricles and mucrons, two morphological characters commonly used to differentiate subspecies in *C. fragile*. Haplotype variation was investigated by sequencing the *C. fragile* chloroplast *rps3-rpl16* region from field-collected material. We observed the distribution of *C. fragile* to be changing; there was a decrease in Prince Edward Island material and an increase in material found in Nova Scotia. Morphological investigations revealed a two-fold difference in both utricle length and mucron length between different populations. Although utricle length variation was within the given range for *C. fragile* subsp. *fragile*, some mucron lengths were in the range of *C. fragile* subsp. *atlanticum*, which could be due to genetic variation or habitat differences. Thus far, we have sequenced samples from the complete geographic range but have not observed DNA polymorphisms for this locus and the haplotypes match *C. fragile* subsp. *fragile*. These results suggest that only *C. fragile* subsp. *fragile* may be present in the NW Atlantic.

**(P13) BARCODING MARINE TUBE-FORMING DIATOMS FROM CANADIAN WATERS: INVESTIGATING ALTERNATIVE MARKERS TO COI.** Sarah E. Hamsher & Gary W. Saunders. Department of Biology, University of New Brunswick, Fredericton, NB, Canada.

Diatoms are ubiquitous single-celled algae that are commonly identified by the fine structure of their silica valves. Many of the morphological characters used to identify diatoms, such as valve shape, are qualitative. DNA barcoding is a molecular technique that uses sequence comparisons of a short region of DNA, often the 5' region of the mitochondrial COI gene, to distinguish species. This marker has been used successfully to identify species of *Sellaphora*, but has not displayed wide utility in diatom taxa. Our objective was to use DNA barcoding to identify species of marine tube-forming diatoms in Canada - these species were not previously investigated using molecular tools. Despite testing many primer combinations (25), amplification of the COI from many collections failed, possibly due to the presence of introns. Therefore, our study has focused on sequencing alternative barcoding markers including: the internal transcribed spacer 2 region (ITS-2); the variable D2 region of the 28S rDNA (LSU); the large subunit of RUBISCO (*rbcL*); and the Universal Plastid Amplicon (UPA). The ITS-2, LSU, and *rbcL* regions are often used to investigate relationships among species of diatoms. The UPA is a short region (ca. 330 bp) of the 23S plastid rDNA and is being promoted as a universal species identification tool for algae. Each

marker will be assessed for ease of developing universal primers, ease in amplification, and utility in discriminating among sister pairs of species. Preliminary results for this research will be presented.

**(P14) “BIRDS OF A FEATHER”: MOLECULAR PHYLOGENETIC ANALYSES AND NOVEL LIFE HISTORY INTERPRETATIONS ALLY *COLACONEMA SUBIMMERSUM* AND *HALOSACCIOCOLAX KJELLMANII* WITH THE RHODOPHYSEMATACEAE (PALMARI-ALES, RHODOPHYTA).** Susan L. Clayden & Gary W. Saunders, Centre for Environmental & Molecular Algal Research, Biology, University of New Brunswick, Fredericton, NB, Canada.

*Colaconema subimmersum*, currently, but incongruously a member of the Colaconematales, and *Halosaccicolax kjellmanii*, tenuously allied with the Rhodophysemataceae, Palmariales, were assessed with respect to their molecular phylogenetic placement, and associated life history patterns. Anomalous features *Colaconema subimmersum* displays relative to other Colaconematales include lack of monosporangia and a reportedly diphasic life history consisting of gametophytic and carpotetrasporophytic generations. *Halosaccicolax kjellmanii* is tentatively assigned to the Rhodophysemataceae based on vegetative structure and reproduction. In the description of the type, Lund documented tetrasporangia and spermatangia (the sole record), but carpogonia were not observed and the life history remains unknown. We addressed the uncertainty surrounding these taxonomic placements by sequencing large subunit ribosomal DNA (LSU) and the mitochondrial barcode (5' – COI) in the context of broader representation for members of the Colaconematales, Palmariales, and related Acrochaetiales. *Colaconema subimmersum* resolved as sister to *Rhodophysema* spp. in separate and combined analyses of these gene regions, consistent with inclusion in the Rhodophysemataceae. Our interpretation of direct development of a tetrasporophyte, rather than carpotetrasporophyte, from the fertilized carpogonium indicates a life history that is intermediate between the *Rhodophysema* and *Palmaria* types in support of generic status for *C. subimmersum* within this family. *Halosaccicolax kjellmanii* resolved within the genus *Rhodophysema* and, despite its parasitic nature, we assign it to the genus *Rhodophysema*. Tetrasporangia, spermatangia, and carpogonia, previously unreported, on the same thallus, suggest a *Rhodophysema* type life history in support of the molecular data.

**(P15) A CHLOROPLAST GENOME REARRANGEMENT IN THE SYMBIOTIC GREEN ALGA, *ELLIPTOCHLORIS MARINA* (TREBOUXIOPHYCEAE, CHLOROPHYTA).** Molly R. Letsch<sup>1</sup>, Gisèle Muller-Parker<sup>2</sup> & Louise A. Lewis<sup>1</sup>, <sup>1</sup>Department of Ecology and Evolutionary Biology, University of Connecticut, Storrs, CT; <sup>2</sup>Department of Biology and Shannon Point Marine Center, Western Washington University, Bellingham, WA.

Until now there has been limited work on the taxonomy, variability and distribution of the green algae symbionts of the Pacific sea anemones, *Anthopleura elegantissima* and *Anthopleura xanthogrammica*. We collected and phylogenetically analyzed data from the nuclear SSU rDNA and the plastid encoded *rbcL* gene and showed that the *Anthopleura* green algae are a distinct monophyletic lineage nested in the genus *Elliptochloris*, regardless of host species or geographic range. Given their ecological and molecular distinction from other named species of *Elliptochloris* we recently designated these green symbionts as a new species, *Elliptochloris marina* (Trebouxiophyceae, Chlorophyta). To investigate population level variability within *Elliptochloris marina* we began collecting data from more variable regions of the genome, including ITS rDNA and several chloroplast spacer regions. During this investigation we discovered a chloroplast genome rearrangement in *E. marina* that is unique from the published chloroplast genomes of other photosynthetic trebouxiophytes, *Leptosira* and *Chlorella*. The rearrangement in *E. marina* was detected when examining the spacer region beyond the 3' end of the *rbcL* gene. The gene order in *E. marina* is *rbcL*-trnM-trnV, whereas in *Leptosira*, *E. marina*'s closest relative with a published chloroplast genome sequence, the gene order is *rbcL*-trnW-trnP. In *Chlorella*, which is even more distantly related, the gene order is *rbcL*-rps14-trnM. The *E. marina* arrangement is also found in *Elliptochloris subsphaerica*. On going work will determine if this gene order is found in the genomes

of other species of *Elliptochloris*, thereby indicating a genus-level marker, or if it also occurs in phylogenetically close relatives such as *Coccomyxa*.

**(P16) Cd UPTAKE BY CHAROPHYTES: THE POTENTIAL FOR PHYCOREMEDIATION.** **Bernadette Clabeaux** & Mary A. Bisson, Department of Biological Sciences, University at Buffalo, Buffalo NY.

The potential for *Chara australis* (R.Br.) to be used as a model plant for the phycoremediation of cadmium-contaminated sediments has been investigated. Phycoremediation involves the accumulation of Cd from the sediment by *Chara* rhizoids and subsequent translocation of the contaminant to aboveground shoot tissues. Our preliminary results show that *Chara* is capable of accumulating Cd in its rhizoids and translocating it to shoot tissues. As added Cd concentration in the sediment increased from 0 to 20 ppm Cd, the amount of Cd taken up by *Chara* rhizoids and shoots also increased to levels above those present in the soil. Additionally, *Chara* showed a significant increase in Cd tolerance over time, indicating the development of resistance mechanisms. To visualize Cd localization, staining of live *Chara* shoots and rhizoids with dithizone reagent was performed. Cd was shown to be localized within the cytoplasm of shoots and rhizoids, along the cell wall of shoots and rhizoids, and within the apoplast of the nodal complex. The effects of Cd and Zn on *Chara* growth and tolerance are also being investigated. Overall, our results show that *Chara* spp. are candidates for the remediation of sediments in contaminated aquatic environments.

**(P17) CHARACTERIZATION OF A LONG ISLAND SOUND *EUTREPTIELLA* SP. FOR ITS POTENTIAL AS BIOFUEL FEEDSTOCK AND EXCESS NUTRIENT BIOFILTER.** **Chiu-Yen Kuo** & Senjie Lin, Department of Marine Sciences, University of Connecticut, Groton, CT.

Energy shortage and global warming have become urgent and challenging issues. Microalgae, which can grow fast and are lipid-rich, have high potential as alternatives for renewable biofuel, and through photosynthesis are able to remove the green-house gas CO<sub>2</sub> and excessive inorganic nitrogen and phosphorus that pollute (eutrophicate) our aquatic environment. In an effort to screen microalgae to identify promising species for both biofuel and environmental cleanup, we set out to characterize a euglenophyte, *Eutreptiella* sp., which was isolated from an effluent area in Long Island Sound. Morphological and molecular analysis indicated that this strain is closely related to an *E. gymnastica* strain (CCMP1594) whose species designation has recently been changed to *E. braarudii*. Effects of temperature on growth rate, growth capacity, and lipid content were investigated. The preliminary results showed that temperature had a vital effect on the growth pattern of *Eutreptiella* sp. Nile Red Staining method was developed for this species to provide an efficient way to evaluate its neutral lipid content. Preliminary results on lipid content under different temperatures will be presented. A plan to examine other growth conditions and to investigate genetic pathways regulating lipid synthesis in this species will be discussed.

**(P18) INVESTIGATING SPECIES DIVERSITY WITHIN THE GENERA *SCAGELIA*, *NEOPTILOTA* & *PTILOTA* IN CANADA USING AN INTEGRATED TAXONOMIC APPROACH.** **Meghann Bruce** & Gary W. Saunders, Center for Environmental & Molecular Algal Research, Department of Biology, University of New Brunswick, Fredericton, NB, Canada.

Identification of red algae (Rhodophyta) using traditional methods can be challenging due to the prevalence of phenotypic plasticity, evolutionary convergence, presence of cryptic species and a reliance on ephemeral reproductive structures for species-level delimitation. DNA barcoding provides a solution to these challenges because it frees taxonomists from a total reliance on morphological and anatomical characters. This study will investigate species diversity in Canadian waters for three red algal genera in the Ceramiaceae: *Scagelia*, *Neoptilota* and *Ptilota*. An integrative taxonomic approach will be used

combining molecular data with traditional morphological identification. Current literature presents contradictions as to the number of species recognized in the genus *Scagelia* (Athanasiadis, 1996; Hansen, 1997). According to Sears (2002) and Gabrielson *et al.* (2000), two species of *Scagelia* are present in Canada, and our preliminary barcode data support this finding. However, their respective biogeography differs from current views. In the case of *Neoptilota* and *Ptilota* there are six species recognized in Canada (four *Neoptilota* and two *Ptilota*). However, preliminary barcode data have revealed seven genetic species groups suggesting that there is cryptic diversity within the *Ptilota-Neoptilota* complex in Canada. The genetic data further indicate that the two genera may not be monophyletic. Additional studies investigating the evolutionary history of these genera will involve constructing a multiple gene phylogeny, including large-subunit nuclear ribosomal DNA (LSU), ribulose-bisphosphate carboxylase (*rbcL*) and elongation factor 2 (EF2) sequence data, to elucidate the diversity and relationships within this species complex.

**(P19) TRACKING AND PREDICTING A PATH OF INVASION ALONG THE SOUTHERN NEW ENGLAND COAST: *GRATELOUPIA TURUTURU* YAMADA.** Rebecca Gladych<sup>1</sup>, Charles Yarish<sup>1,2</sup> & George Kraemer<sup>3</sup>. <sup>1</sup>Department of Marine Science, University of Connecticut, Groton, CT; <sup>2</sup>Department of Ecology and Evolutionary Biology, University of Connecticut, Stamford, CT; <sup>3</sup>Departments of Environmental Studies and Biology, Purchase College (SUNY), Purchase, NY.

*Grateloupia turuturu* Yamada, a non-native red alga, was found in Narragansett Bay, Rhode Island, USA, in 1994. This was the first recorded presence of this species on the eastern coast of North America. Its spread has been tracked since its arrival in Rhode Island, and its current known distribution extends from Boston Harbor, Massachusetts, to Waterford, Connecticut, a range consistent with environmental conditions present in its native habitat, Japan. To predict the habitats into which it may spread, growth experiments have commenced on newly released tetraspores. Once *G. turuturu* spores settle on a suitable substrate, they germinate and form a germ tube which leads to the development of a crustose stage, before upright blades are produced. The tetraspores were grown under varying temperatures (5 – 30°C) and light intensities (25 – 100  $\mu\text{mol photons m}^{-2} \text{s}^{-1}$ ) and monitored regularly for a period of 16 days. Preliminary results indicate a clear thermal optimum of 25°C, although crusts also developed satisfactorily at 15 and 20°C. There was no clear light effect, as growth at different photon fluence rates at the same temperatures was similar. Prior field observations of *G. turuturu* populations have determined that tetrasporophyte production is continuous throughout the year, and exhibits maximum release during February and March. Using the data gathered from these laboratory experiments and prior field observations, the optimal physical conditions of *G. turuturu* can be determined, and potential areas of introduction along the east coast of North America may be identified.

**(P20) USING MACROALGAE TO TRACK ENVIRONMENTAL TRENDS IN THE GREAT BAY ESTUARINE SYSTEM.** Jeremy C. Nettleton, Christopher D. Neefus, Arthur C. Mathieson, University of New Hampshire, Department of Biological Sciences, G28 Spaulding Life Science Center, Durham, NH.

In recent years, international studies have shown that monitoring macroalgae populations is an effective way to detect water quality changes. The Great Bay National Estuarine Research Reserve has identified the need to monitor water quality parameters through the use of indicator organisms. To illuminate environmental trends in New Hampshire's Great Bay Estuarine System, this study compares historical and present-day green algal nutrient content and community structure data. The objectives of the two-year study are to assess the abundance and distribution of macrophytes, particularly *Gracilaria tikvahiae* McLachlan and *Ulva* spp. relative to major patterns of eutrophication within this system; to compare historical (1980s) and current biomass and percent cover measurements for algal populations at several sites where multi-year floristic and ecological studies were previously conducted; to compare the levels of nitrogen and phosphorus in *Ulva* spp. and *G. tikvahiae* tissues to those in the surrounding water; to



evaluate historical and current water quality measurements for each study site. The results of this study will facilitate the assessment of anthropogenic influences of the past two decades on water quality and species composition. Compared to historical records, algal population data gathered in year one suggest significant increases in biomass and cover by *Ulva* spp. and *G. tikvahiae*. Due to recent molecular work on local *Ulva* populations, herbarium collections, from the 1950s to present, are being screened, using ITS2 and rbcL genes, to clarify the history of several *Ulva* species in Great Bay.

**(P21) WASTEWATER TREATMENT AND CO<sub>2</sub> SEQUESTRATION USING AN AIRLIFT PHOTO-BIOREACTOR.** **Xin Yuan**<sup>1</sup>, Sarina J. Ergas<sup>1</sup> & Amit Kumar<sup>2</sup>. <sup>1</sup>Dept. Civil & Environmental Engineering, Univ. Massachusetts, Amherst; <sup>2</sup>EnVOC Research Group, Faculty of Bioscience Engineering, Ghent University, Belgium.

In the presence of light, micro-algae convert CO<sub>2</sub> and nutrients to biomass that can be used as a fuel source. Wastewater treatment by micro-algae has been used world-wide to remove organic matter and nutrients (N and P) from wastewater. There is a lack of information; however, on the performance of engineered photo-bioreactors, which can offer much higher areal production rates than conventional open pond processes. This research investigates an airlift photo-bioreactor for: (1) treatment of high nutrient strength wastewaters, (2) production of micro-algae as a biofuel for methane, ethanol and/or H<sub>2</sub> production, and (3) CO<sub>2</sub> sequestration from combustion gases. *Spirulina platensis* was used in these experiments, due to their high tolerance for ammonia and easy harvesting by sedimentation. Batch culture experiments were carried out at 20°C and constant light intensity (8,000 lux) in modified Zarouk medium with varying ammonia concentrations. *S. platensis* inhibition was not observed at ammonia concentrations below 1.2 mM, but was significant at ammonia concentrations above 2.4 mM. Airlift photo-bioreactor experiments were conducted in a 1.5 L bench-scale system with a inner/outer loop ratio of 2:1. Synthetic high strength wastewater with varying nitrate:ammonia ratios was fed to the reactor at a hydraulic residence time of 5 days. Growth rates of *S. platensis* were in the range of 200 - 550 g m<sup>-3</sup> d<sup>-1</sup> and increased with increasing algal biomass concentrations. No inhibition was observed at a nitrate:ammonia ratio of 1:1. Data collected so far shows that this approach has great potential for treatment of high strength wastewaters and production of biomass for biofuel production. Future research will focus on investigating the effect of ammonia concentration on the growth of *S. platensis*, the performance of other algal strains and the performance of other types of photobioreactors.

**(P22) EXAMINING FOR MARKERS OF PROGRAMMED CELL DEATH IN *HETEROSIGMA AKASHIWO*.** **Jennifer Dingman** & Janice Lawrence, Department of Biology, University of New Brunswick, Fredericton, NB, Canada.

Despite their enormous production and turnover rates, the life and death strategies of phytoplankton are poorly understood. It was previously thought that, because of on-going cell division, single-celled phytoplankton do not die unless effected by external factors such as predator grazing or sedimentation. However, researchers have observed cell lysis, viral infection, autocatalytic cell death and caspase activation in phytoplankton, which suggests necrotic and programmed cell death (PCD) pathways may exist. This also suggests there may be additional factors controlling primary productivity, although we still know very little about these other processes. In this study, the bloom forming raphidophyte *Heterosigma aksashiwo* was examined for the PCD hallmarks of DNA laddering and caspase activation. Lytic viral infection and heat stress were examined as possible inducers of PCD. Viral infection was achieved by inoculating *H. aksashiwo* with 10% vol/vol HaNIV lysate. Heat stressed cultures were subjected to 35°C, 36°C and 37°C for 1 hour and returned to control conditions following stress. These temperatures were found to be the minimum threshold for inducing death in this alga. DNA laddering assays indicated DNA degradation increased from 0 to 24 hours after heat stress, but the characteristic laddering was not present. The presence of active caspase-8 significantly increased in response to 37°C heat stress (p = 0.0004). Active caspase-8 was also significantly higher in HaNIV infected cultures (p < 0.0001), peaking 168h post

inoculation, after which the cultures completely lysed. The presence of active caspase-8 and controlled DNA degradation suggests a PCD pathway is present in *H. akashiwo*. Further studies will be conducted to confirm the existence of such a pathway in *H. akashiwo*, and elucidate the implications on the physiology and ecology of phytoplankton.

**(P23) COUPLING PHYCOREMEDIATION AND BIODIESEL PRODUCTION USING MICRO-ALGAE.** Anil Patel & Mark Lefsrud. Department of Bioresource Engineering, Macdonald Campus, McGill University, Ste. Anne de Bellevue, Quebec, Canada.

Global change and energy security have renewed interest in using microalgae to make biofuel. Certain strains of microalgae are optimized by evolution for high lipid productivity, with higher yields of algal oil, a precursor to biodiesel, than crop based feedstocks. Despite five decades of research this technology is not mature or commercially viable due in large part to the cost of biomass production. Nutrient removal using microalgae (phycoremediation) can potentially offset biomass production costs, increase Net Energy Ratio (NER) and mitigate the impacts of phosphorus (P) additions to the environment. Coupling phycoremediation and biodiesel production systems will require significant R&D focused on combining bioreactor and pond processes, nutrient dynamics, algal suspension, genetic engineering and culturing and harvesting techniques. Preliminary data from freshwater culture screens show the importance of strain selection and P load concentration on growth and nutrient removal.

**(P24) A NEW USE FOR THE ALGAE: A CONNECTICUT SEAWEED SURVEY SAFARI USING ALGAE TO DETERMINE TIDAL ELEVATIONS.** Margaret Van Patten<sup>1</sup> & John Doody<sup>2</sup>, <sup>1</sup>Connecticut Sea Grant/University of Connecticut at Avery Point, Groton, CT; <sup>2</sup>Connecticut Dept. of Transportation, Hartford, CT.

Over the years, surveyors, engineers, environmental regulators, and shoreline homeowners along the Connecticut coast of Long Island Sound have made presumptions and judgments as to the location of the mean high water (ownership boundary) and other coastal regulatory lines based on the physical evidence that they have seen, such as seaweed lines, wrack lines, beach grass, and other vegetation. Do these natural phenomena represent an actual line of elevation in relation to important tidal boundary and regulatory lines? Do they represent the actual tidal boundary or regulatory line? These questions had been addressed only anecdotally. Surveyors from the Connecticut Department of Transportation and Connecticut Association of Land Surveyors led by Jay Doody teamed up with Peg Van Patten, Connecticut Sea Grant, and Kevin Zavoy, Connecticut DEP, to scientifically assess these questions. Six tidal sites in New London with established Mean High Water (MHL) benchmarks were examined for elevation and orientation of wrack lines, and species of abundant intralittoral and supralittoral algae as well as salt marsh plants were identified and measured for elevation in relation to MHW. Statistical comparisons showed that *Blidingia minima* and bands of blue-green algae could be used reliably to determine tidal boundaries, while others such as *Fucus* and *Spartina* were not reliable indicators. Wave action and other means of determining the tidal elevations were less reliable in comparison. Sites in Greenwich CT were subsequently added. This work applies to Connecticut coast at present but has potential for study elsewhere. Future work is looking into seasonal and geographic effects on results. The work has implications for surveyors, state regulators, coastal developers, and homeowners.

**(P25) 50 YEARS OF DESICCATION.** Francis R. Trainor & Louise A. Lewis, University of Connecticut, Department of Ecology and Evolutionary Biology, Storrs, CT.

In 1958, soil was collected from a Connecticut cornfield and dried for one year before isolating algae. Later Hilton and Trainor (1963) reported the recovery of 23 algae, including cyanobacteria and green algae. Further probing by Trainor and collaborators stimulated growth of additional taxa, finally totaling 31. Subsequent studies reported that 11 of these taxa survived 10 years' desiccation, just seven

for 25 years and five in a 35 year study. The latter included: *Chlamydomonas* sp., *Chlorella* sp., *Protosiphon* sp., *Tetracystis isobilateralis* and *Chlorococcum perforatum*. There appear to be no survivors after 50 years. In this report, we note that a *Protosiphon* has survived desiccation for 43 years. We characterized the Storrs soil isolate using microscopy and analysis of DNA sequence data from the nuclear small subunit rDNA, ribosomal internal transcribed spacer regions, and the plastid encoded *rbcL* gene. Phylogenetic analyses place this isolate with published data from *Protosiphon botryoides* (UTEX 99). *Protosiphon* is a multinucleate soil alga that forms large tubular cells, which can cleave to produce aplanospores or swimming gametes. This might be the longest documented period of recovery after desiccation for a green alga.

**(P26) ARE THE RIVERS IN NEW ENGLAND, USA GETTING MORE ACIDIC? Patrick M. Eggleston, Biology Department, Keene State College, Keene, NH.**

A team of people has been monitoring 10 locations on the Ashuelot River in southwestern New Hampshire from 2001 to 2008. Several locations on this river have been getting steadily more acidic. Some locations have dropped over one pH unit in this time. Parts of the river are low conductivity, and they are showing a greater decline in pH. The implications for many species seem dire. The author hopes others will check data from their local rivers to see if this is a general trend.

**(P27) OCCURRENCE OF GROUP I INTRONS IN CHLOROPHYCEAE.** Hilary A. McManus<sup>1</sup>, Louise A. Lewis<sup>1</sup>, **Karolina Fučíková<sup>1</sup>** & Peik Haugen<sup>2</sup>. <sup>1</sup>Department of Ecology and Evolutionary Biology, University of Connecticut, Storrs, CT; <sup>2</sup>Department of Biological Sciences and Center for Comparative Genomics, University of Iowa, Iowa City, IA.

Group IA introns are found in a wide range of eukaryotes, but their distribution is not well reported in chloroplast genes of green algae except for the order Volvocales. As part of phylogenetic studies of the family Hydrodictyaceae and genus *Bracteacoccus*, group IA introns were found in the *rbcL* (large subunit ribulose-1,5-bisphosphate carboxylase/oxygenase) gene of several independent lineages: 14 members of Hydrodictyaceae and 9 members of the genus *Bracteacoccus*. These introns are inserted in either or both of two positions in the gene, 462 and 699, range from 6 to 15 kbp, and often contain an open reading frame which in some cases encodes a putative homing endonuclease. A phylogenetic distribution of these mobile elements in the chlorophycean algae, along with their secondary structure, are reported here.

**(P28) RAPID REMODELING OF THE EXTRACELLULAR MATRIX OF SPIROGYRA DURING ITS WOUND RESPONSE MECHANISM: RHIZOID FORMATION, GLIDING AND AGPS.** Amy Snyder, Matthew Weiss, Michelle Bossler & David S. Domozych, Department of Biology and Skidmore Microscopy Imaging Center, Skidmore College, Saratoga Springs, NY.

*Spirogyra* is a filamentous green alga (Zygnematales, Streptophyta) that commonly forms ephemeral metaphyton blooms in freshwater wetlands. When a filament is wounded, cells immediately adjacent to the wound site rapidly produce multi-branched rhizoids that attach the filament to a substrate. The development of rhizoids requires both remodeling of existing cell wall material and the production of new polymers. In this study, we analyzed the behavioral characteristics of rhizoid formation and the associated alteration of cell wall macromolecule constituencies using various microscopy-based methodologies. Thallus adhesion and rhizoid wall synthesis are closely associated with a transparent material that affixes the rhizoid to a variety of substrates. The monoclonal antibodies, JIM13 and JIM8, specifically label a sheath found on the outside of the cell wall. Treatment of experimentally wounded filaments with  $\beta$ -glucosyl Yariv reagent reversibly inhibits adhesion and production of rhizoids. These results demonstrate that arabinogalactan proteins (AGPs) are integral components of the rhizoid extracellular matrix and are necessary for adhesion. Dynamic time-lapse imaging also demonstrates that unattached filaments glide in a phototactic mechanism through the water column and may be responsible for positioning wounded

filaments near substrates. Time-lapse imaging also reveals that rhizoids form in an anisotropic, bifurcating manner dividing into successive finger-like projections at each tip as it grows. Cytoplasmic streaming delivers both wall material and portions of the chloroplast to the growing tips chloroplast into the new rhizoid as it is forming. Treatment with brefeldin A and cytochalasin E reversibly inhibit rhizoid growth and suggest that both the endomembrane system and actin cytoskeleton are necessary for the anisotropic growth mechanism. All of these results suggest that the wound response mechanism in *Spirogyra* requires the rapid expression of specific extracellular matrix components.

**(P29)** “A LITTLE SCIENCE ON THE SIDE”: INCORPORATING PHYCOLOGICAL RESEARCH ABOARD THE ARCTIC SCHOONER *BOWDOIN*. **Jessica F. Muhlin**<sup>1</sup>, Amanda Brinkman<sup>1</sup>, Michael Iannone<sup>1</sup>, Karin Knudson<sup>1</sup>, Robin Parker<sup>1</sup> & Captain Richard Miller<sup>2</sup>. <sup>1</sup>Corning School of Ocean Studies, Maine Maritime Academy, Castine, ME.; <sup>2</sup>School of Marine Transportation, Maine Maritime Academy, Castine, ME.

As oceans conditions shift due to climate change, there are predicted changes in high latitude environments. Some ecological alterations may include range expansions and contractions of intertidal organisms, shifts in the reproductive ecology for organisms that are cued by specific weather conditions and temperature, and changing phytoplankton abundance and composition. Maine Maritime Academy (MMA) has a unique opportunity to study the changing ecology of the Arctic aboard the Arctic Schooner *Bowdoin*. Following in the tradition of the Macmillan Arctic voyages in which student crew members participated in scientific activities, four MMA students conducted pilot studies during the 2008 summer Arctic voyage. Students gathered preliminary data on the distribution, abundance, and sex ratio of *Fucus vesiculosus* L. as well as collected tissue samples to be used for genetic analyses. These *F. vesiculosus* genetic specimens can provide resolution on how populations are structured at the upper latitude range limits of the species. In addition, students observed the floral and faunal communities associated with algal rafts and collected some plankton samples to examine the abundance and diversity of organisms. There is a tremendous potential to integrate scientific research into future voyages of the Arctic Schooner *Bowdoin*.

**(P30)** DEVELOPMENT OF A FILEMAKER PRO DATABASE FOR STUDYING PATTERNS OF ALGAL DIVERSITY. **Brian Wysor**, Department of Biology, Roger Williams University, 1 Old Ferry Road, Bristol, RI.

In an effort to both streamline data management and identify region-specific patterns of algal biodiversity, a relational database was designed using FileMaker Pro software. The database consists of a main specimen data entry page that records taxonomy, collection site information, methods of sample preservation and associated image data. These related records are used to generate sample labels and run reports, organized by user-defined search criteria. Reports include species lists as well as a taxonomy summary that will report the number of unique taxa at different levels of taxonomic hierarchy. The design incorporates practical features such as autofilling higher level taxonomy when lower level taxonomy is known, and an automatic link to AlgaeBase, for quickly accessing distribution records and species descriptions when connected to the internet. In addition, a related literature table, when accurately populated with published distribution records, will report if a species represents a new record for a defined area (*i.e.*, country). While designed specifically for questions related to the biodiversity of Panamanian marine algae, the database template should be useful for surveys of marine macroalgae in general by facilitating the rapid identification of interesting species records in addition to providing a means of organizing preserved specimens.

**(P31)** OBSERVATIONS AND FIELD STUDIES EXAMINING THE SPREAD OF THE INVASIVE CYANOBACTERIA *LYNGBYA WOLLEI* IN A NORTHEASTERN LAKE. **Kam Truhn**<sup>1</sup>, Michael

Bell<sup>1,2</sup>, Mark Burnham<sup>1,3</sup>, Alissa Perrone<sup>1</sup> & John Wehr<sup>1</sup>. <sup>1</sup>Louis Calder Center Biological Field Station, Fordham University, Armonk, NY; <sup>2</sup>Texas A&M University, Galveston, TX; <sup>3</sup>St. Lawrence University, Canton, NY.

The invasive benthic cyanobacterium *Lyngbya wollei* has colonized a mesoeutrophic lake in southeastern New York. Lake Mahopac is 240 hectares, 20m deep, and hypoxic below 7-10 m for 6 months / year. The lake occupies a suburban landscape with heavy summertime recreation use. Grass carp introduced in 1994 reduced aquatic macrophytes, with *L. wollei* the new dominant benthic autotroph. Annual surveys and experiments have investigated its spatial distribution and links with nutrient inputs: benthic biomass increased more than 3-fold since 1993, and is now recorded in 14 of 30 littoral monitoring sites lake-wide, and which correlate with 2 to 3x greater available sediment-N (as  $\text{NH}_4^+$ ). Adjacent riparian soils contain elevated  $\text{NO}_3^-$ , which is thought to contribute DIN, which is then reduced in hypoxic sediments to ammonium. Total sediment-P (but not available-P) was also 2x greater in *Lyngbya* sites. We propose that the combination of elevated  $\text{NH}_4^+$  and P contributes to the growth and spread of this invasive alga. Field studies also examined the role of macroinvertebrates (potential grazers) on *Lyngbya*, as compared with other algal species. *Hyaella sp.*, *Asellus sp.*, and various gastropods were the most common taxa associated with algal mats. Also, greater macroinvertebrate densities were associated with *L. wollei* than with *Spirogyra*, and were least in non-algal sites. Laboratory grazing experiments further demonstrated that isopods exerted the greatest negative effect on *Lyngbya* growth (declined by 40%), while consumption by amphipods kept paces with algal growth (no net increase), relative to controls. A combination of elevated nutrients and possible preferential use by invertebrates may have led to the rapid increase of this cyanobacterium in Lake Mahopac.

**(P32) COMMUNITY ANALYSES OF MACROALGAL BLOOMS. Carol S. Thornber<sup>1</sup>, Michele Guidone<sup>1</sup> & Christopher Deacutis<sup>2</sup>.** <sup>1</sup>Department of Biological Sciences, University of Rhode Island, Kingston, RI 02881; <sup>2</sup>Narragansett Bay Estuary Program, University of Rhode Island Coastal Institute, URI Bay Campus, Box 27, Narragansett, RI.

Macroalgal blooms are frequent occurrences in estuarine systems worldwide. These blooms typically consist of a suite of rapidly growing species drifting in the water column, including genera such as *Ulva*, *Cladophora*, and many others. In Narragansett Bay, RI, USA, blooms have been recorded since the early 1900s, but have rapidly increased in duration and frequency over the past few decades. Through a combination of repeated intertidal and subtidal quantitative surveys over 4 years, as well as larger-scale aerial photography, we assessed the distribution, density, and composition of blooms in this bay through univariate and multivariate statistical techniques. The most common bloom species included flat bistromatic blades of *Ulva*, numerous tubular, branched *Ulva* species, the red algae *Gracilaria tikvahiae* and *G. vermiculophylla*, and *Agardhiella subulata*. However, more than 30 other species also occurred in bloom formations. The highest biomass density recorded was 149g/ 0.25m<sup>2</sup> (wet weight) for intertidal habitats, and 47g/m<sup>3</sup> (for subtidal habitats). We found significant spatial and temporal (both seasonal and yearly) variation in bloom composition and abundance, with strong local variation (<2km) in bloom density. Our data indicate the likelihood of rapid shifts in bloom location and composition in estuarine systems.

**(P33) AN EXPLORATION OF THE ROLE AND SPECIFICITY OF TWO FRESHWATER CYANOPHAGES FROM EUTROPHIC LAKES IN NORTHEAST FLORIDA. Dale Casamatta, Michael Lentz, Jennifer Wilson, Jason Teman & Tessa Davenport,** Department of Biology, University of North Florida, Jacksonville, FL.

Cyanobacterial blooms have increased in frequency and severity over the last several years in northeast Florida and other regions due to anthropogenic influences and changes in local climate.

These blooms impact not only the macroscopic community, but may trigger a significant change in the microbial community. The purpose of this study is to examine the cyanobacterial-specific component (cyanophages) of typical eutrophic lakes with copious, persistent cyanobacterial populations in order to determine if cyanophages play a role in bloom dynamics. We have isolated two cyanophages thus far, and preliminary infection studies show specificity for one phage to infect only coccid cyanobacteria (Chroococcales) and the other only the filamentous Oscillatorialean clade. Genetic analyses indicate that the former phage is a double-stranded DNA virus with a genome in the 25-30kB in length. Initial genomic library analyses have revealed not only genes for viral replication and establishment, but also a number of sequences whose closest BLAST matches are from photosynthetic organisms. Thus, it appears that these phages may play a role in lateral gene transfer in freshwater ecosystems. We have also begun culture work, and thus far each phage has shown a very narrow range of infectivity. While phage specificity was examined and subsequently discarded as a phylogenetically useful tool in the 1970s, we believe this deserves a reexamination in light of recent molecular (e.g., 16S rDNA gene sequencing) and morphological (e.g., the whole-scale rearrangement of the Oscillatoriales) revisions over the last several years.

**(P34) IS *GEITLERINEMA* REALLY INVOLVED IN BLACK BAND DISEASE? AN INVESTIGATION OF THE UBIQUITOUS, COMMONLY CONFUSED GENUS *GEITLERINEMA* (PSEUDANABAENACEAE, CYANOBACTERIA).** Emilie Perkerson, R. Perkerson & D. Casamatta, Department of Biology, University of North Florida, Jacksonville, FL.

Black Band Disease (BBD) is an emerging problem in coastal coral reefs. Recently, one of the chief members of the complex microbial consortium responsible for coral fouling has been identified as *Geitlerinema*. *Geitlerinema* is a widely distributed, freshwater member of the Pseudanabaenaceae (Cyanobacteria), commonly found in a variety of aquatic habitats. This genus is characterized by usually having an elongated apical cell, prominent cyanophycin granules or local carotenoid bodies, and lack aerotopes (gas vesicles). Five cultures from the University of Toronto Culture Collection (UTCC) that have been previously described as belonging to the genus *Geitlerinema* were obtained and compared with strains isolated from BBD corals. 16S rRNA sequences were obtained for each of the cultures and combined with all available *Geitlerinema* data from GenBank to create a phylogenetic tree. From our preliminary molecular and morphological analyses it appears that the BBD organisms are not *Geitlerinema*, but represent a genus new to science.

**(P35) AN ULVA BLOOM IN NEW BEDFRORD HARBOR MAY HAVE BENEFICIAL FUNCTION BECAUSE OF ITS REMOVAL OF PCBs.** Donald Cheney<sup>1</sup>, Anna Meador<sup>1</sup> & Kevin Gardner<sup>2</sup>. <sup>1</sup>Department of Biology and Marine Science Center, Northeastern University, Boston, MA; <sup>2</sup>Department of Civil Engineering, University of New Hampshire, Durham, NH.

In the summer of 2007, we discovered a bloom of the green macroalga *Ulva lactuca* growing in the upper portion of New Bedford Harbor (NBH); an area designated a Superfund Site since 1982 because of its extremely high levels of PCBs. Based upon quadrat data collected in July, 2008, we estimated there was over 18 tons of *Ulva* just in shallow depths along the western shoreline of the Upper Harbor and as much as 50-100 tons in the whole Upper Harbor. The concentration of (total) PCBs in *Ulva* samples ranged from a high of 98 ppm to a low of 2 ppm. PCB concentrations were correlated with distance from the Aerovox plant, where PCBs were used in the manufacture of electrical transformers and capacitors from ca. 1940 to 1977. Our highest PCB conc. (98 ppm) is almost 800 times greater than the highest conc. previously reported for macroalgae. We also measured PCB uptake by uncontaminated *Ulva* plants placed in intertidal cages above Aerovox and found rates as high as 4 ppm in just 24 hrs. In laboratory grazing experiments on NBH *Ulva* by the most common herbivore we saw, mysid shrimp, we found a very low rate of herbivory. Because of the huge amount of PCBs taken up by *Ulva* in the Superfund Site and what appears to be a low herbivory rate, we believe the *Ulva* bloom in NBH reduces the amount of PCBs taken

up by phytoplankton and transferred up the food chain, and thus, it is having a previously unknown, beneficial effect on the transport and bioaccumulation of PCBs in the system. It may in fact be the first reported case of a “beneficial” seaweed bloom.

**(P36) GROWTH OF ASCOPHYLLUM: AN INDICATOR OF OCEAN WARMING?** Robert Vadas<sup>1</sup>, B. Beal<sup>2</sup>, D. Anderson<sup>1</sup> Shannon Alexa<sup>1</sup> Milan Keser<sup>3</sup> & B. Larson<sup>4</sup>. <sup>1</sup>University of Maine, Orono, ME; <sup>2</sup>University of Maine, Machias, ME; <sup>3</sup>Northeast Utilities, Niantic, CT; <sup>4</sup>Marine Colloids, Rockland, ME.

Temperature has long been important in explaining algal distributions, growth and gamete release. We followed growth of mature, random and tagged *A. nodosum* plants at six sites over a broad temporal and spatial scale. Three sites were located in areas used to assess thermal discharge from a power plant in the 1970s. This provides a comparative database with present-day growth to determine if this alga could serve as an index of ocean warming. We followed growth for two years and used regression to determine the pattern of module (shoot segments) size. Generally, modules examined over the past two years are growing at higher rates (by 10-50%) than modules were in the 1970s. We correlated present-day growth and phenology with habitat variables such as nutrients, salinity, turbidity and temperature. The data suggest that *A. nodosum* could serve as an accurate index of ocean warming.

**(P37) DNA BARCODING REVEALS INCIPIENT SPECIATION IN THE NORTHWESTERN ATLANTIC COLPOMENIA SINUOSA.** Manuela Parente<sup>1,2</sup>, Filipe Costa<sup>2</sup> & Gary W. Saunders<sup>1</sup>. <sup>1</sup>Centre for Environmental & Molecular Algal Research, Biology, University of New Brunswick, Fredericton, NB, Canada; <sup>2</sup> Departamento de Ciências e Engenharia do Ambiente Instituto do Mar – IMAR, Faculdade de Ciências e Tecnologia, Universidade Nova de Lisboa, Quinta da Torre - 2829-516 Caparica, Portugal.

*Colpomenia sinuosa* (Mertens ex Roth) Derbès & Solier is characterized by a spherical saccate thallus, plurilocular sporangial in punctuate sori with a cuticle, and commonly four to six layers of medullary cells. This species is generally reported to be widely distributed in tropical to warm temperate seas throughout the world. Morphological and molecular examinations were performed using isolates from different regions including the Macaronesian archipelagos, the Azores, Madeira and the Canary Islands, as well as the central coast of mainland Portugal. Cytochrome *c* oxidase 1 sequences, which are reported to resolve species-level diversity among brown algae, displayed 1.23 % divergence (7 bp out of the 566 positions) between isolates from the Macaronesian archipelagos and mainland Portugal. These results suggest a period of genetic isolation for two incipient species in the Northwest Atlantic, but, owing to the low divergence between these populations in this genetic marker, confirmation with a variable nuclear region is necessary to confirm the mitochondrial result and test for possible hybridization. Our preliminary results will be presented.

## NOTES