

49th Annual Northeast Algal Symposium
April 16 - 18, 2010



Northeast Algal Society

Algal Biodiversity: Shifts in Algal Distribution

Roger Williams University
Bristol, RI

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Welcome to the 49th Northeast Algal Symposium!

We are pleased this year to be bringing NEAS back to Rhode Island, where the society has met in several locations over the years, from Whispering Pines to Narragansett. This year we will be convening for the first time at Roger Williams University for what promises to be an excellent meeting. As usual, the schedule is packed with interesting presentations – we have nearly 70 combined talks and posters to take in from all over the region and the world.

The theme for this year’s plenary symposium is “*Algal Biodiversity: Shifts in Algal Distribution*” and we have a slate of talks from local experts on Sunday, as well as a keynote lecture by Dr. Olivier De Clerck on Saturday. These talks and others will be in room 157 of the Feinstein College of Arts & Sciences building (#16 on map). The poster session will be in Global Heritage Hall (#10 on map), followed by the banquet* in the same building.

If you are giving an oral presentation, please be sure to have your talk loaded onto the computer in FCAS157 well before your session. Someone will be available to assist you during breaks and before the start of talks on each day. When transferring your presentation, please include your last name in the document title to make locating your talk easier. Poster can be set up any time on Saturday in the GHH. Look for the poster board that corresponds to the number next to your title in the following schedule.

Finally, we would like to acknowledge the generous support of our sponsors for this event. Both the Feinstein College of Arts and Sciences at Roger Williams University and the College of the Environment and Life Sciences at the University of Rhode Island are providing financial and logistical support for the conference this year. Additional financial contributions have been donated by FMC BioPolymer and Rhode Island Sea Grant, for which we are grateful.

Best wishes for a productive and relaxed conference.

Brian Wysor
Chris Lane
2010 Co-conveners



* Only individuals aged 21 and older will be served alcohol at this event.

General Program: 49th Northeast Algal Symposium, Amherst

Friday, April 16, 2010

- 6:00 — 7:00 pm** **Evening Registration, NEAS Sales & Auction Donations**
Bristol Harbor Room, Bristol Harbor Inn
- 7:00 — 10:00 pm** **NEAS Welcome Mixer**
Bristol Harbor Room, Bristol Harbor Inn

Saturday, April 17, 2010

- 7:00 — 8:30 am** **Continental Breakfast**
Feinstein College of Arts & Sciences (FCAS), rm 157
Poster setup, Global Heritage Hall
Session I speakers load presentations FCAS 157
- 8:00 — 9:30 am** **Morning Registration, NEAS Sales & Auction Donations**
Feinstein College of Arts & Sciences, rm 152
- 8:30 — 8:45 am** **Welcome and Opening Remarks — Brian Wysor**
Feinstein College of Arts & Sciences, rm 157
- SESSION I** ***Student Presentations, Moderator: John Hall***
Feinstein College of Arts & Sciences, rm 157
- 8:45 — 9:00** *Wilce Award Candidate*
Meghann Bruce & Gary W. Saunders - Investigating species diversity, biogeography and taxonomy within the red algal genus *Scagelia* (Ceramiales, Rhodophyta)
- 9:00 — 9:15** *Wilce Award Candidate*
Bridgette Clarkston & Gary W. Saunders - Systematics of select members of the Kallymeniaceae (Rhodophyta) in Canada
- 9:15 — 9:30** *Wilce Award Candidate*
Karolina Fučíková, Jared C. Rada, Alena Lukešová & Louise A. Lewis - Cryptic Species of the Genus *Pseudomuriella*: To Barcode or Not to Barcode?
- 9:30 — 9:45** *Wilce Award Candidate*
Sarah E. Hamsher, Katharine M. Evans, David G. Mann, Aloisie Pouličková, & Gary W. Saunders - Barcoding diatoms: exploring alternative markers

- 9:45 —10:00** *Wilce Award Candidate*
Daniel McDevit & Gary W. Saunders - A molecular investigation of the Scytosiphonaceae in Canada
- 10:00 —10:15** *Wilce Award Candidate*
Hana Kucera & Gary W. Saunders - A pilot-study evaluation of *rbcL*, UPA, LSU and ITS as DNA barcode markers for the marine green macroalgae
- 10:15 —10:45** *Coffee Break, Session I speakers load presentations FCAS 157*
- SESSION II** *Student Presentations, Moderator: Bridgette Clarkston*
 Feinstein College of Arts & Sciences, rm 157
- 10:45 —11:00 am** *Wilce Award Candidate*
Ian Misner, Lindsey Haus, J. Craig Bailey, & Christopher E. Lane - Photosynthetic ancestry of the oomycetes: The hunt for a vestigial organelle
- 11:00 —11:15** *Wilce Award Candidate*
Lillian Hancock & Christopher E. Lane - Unraveling the role of mitochondria in red algae parasite evolution
- 11:15 —11:30** *Wilce Award Candidate*
Molly R. Letsch, & Louise A. Lewis - Four chloroplast gene arrangements in a closely related group of Trebouxiophyceae (Chlorophyta)
- 11:30 —11:45** *Wilce Award Candidate*
Michele Guidone & Carol Thornber - Examination of the abundance and relative palatability of select *Ulva* species in Narragansett Bay, Rhode Island
- 11:45 —12:00 pm** *President's Award Candidate*
Matthew Cashman, John Wehr, & Kam Truhn - Land-use and nutrient effects on benthic algal biomass, nutrient stoichiometry, and species composition in an urbanized watershed
- 12:00 —1:30 pm** *Lunch*
 2nd floor, The Commons
Executive Committee Meeting
 East Private Dining Room, 2nd floor, The Commons
- SESSION III** *Student & Contributed Presentations, Moderator: Hilary McManus*
 Feinstein College of Arts & Sciences, rm 157
- 1:10 —1:30** *Session III speakers load presentations, FCAS 157*

- 1:30 —1:45 pm** *President's Award Candidate*
Heather M. Meyer & Kenneth G. Karol - A systematic investigation of the *Nitella flexilis* (L.) Ag. Species complex
- 1:45 —2:00** *President's Award Candidate*
Ryan T. Higgins, Brian Wysor & Charles J. O'Kelly - Molecular Assessment of Panamanian *Ulva* (Ulvales, Chlorophyta) using *rbcL* and ITS rDNA
- 2:00 —2:15** *President's Award Candidate*
Elisabeth Cianciola, Thea Popolizio, Christopher E. Lane & Craig W. Schneider — Molecular-assisted alpha taxonomy of the 'Centrocercas clavulatum complex' (Ceramiales, Ceramiaceae) in Bermuda, western Atlantic
- 2:15 —2:30** *Contributed paper*
Elizabeth Rodríguez-Salinas, Li Zhong-Kui, Karolina Fučíková, Louise A. Lewis, Jerry J. Brand, & Diego González-Halphen - What does the mitochondrial *cox2* gene tell us about chlorophycean algae evolution?
- 2:30 —2:45** *Contributed paper*
Manuela I. Parente, Florence Rousseau, Bruno de Reviere, Robert L. Fletcher, Filipe Costa & Gary W. Saunders - Molecular divergence within *Ralfsia verrucosa* (Ralfsiales, Phaeophyceae) indicates cryptic species
- 2:45 —3:00** *Contributed paper*
John D. Hall & Kenneth G. Karol - A comparison of algal community composition between 1924 and 2010 in Harriman State Park, New York
- 3:00 —3:30** *Coffee Break*
Session IV speakers load presentations, FCAS 157
- SESSION IV** *Phyco-Speed Dating & Distinguished Presentation*
 Feinstein College of Arts & Sciences, rm 157
- 3:30 —4:00** *Phyco-Speed Dating, Coordinator: Hilary McManus*
- 4:00 —5:00** *Speaker Introduction—Brian Wysor*
Distinguished Speaker Presentation
Olivier De Clerck - Species, Patterns & Algae: a phylogenetic perspective.

SESSION V *Poster Session & Social*

5:00 — 6:00 **Student & Contributed Posters**
1st & 2nd floor, Global Heritage Hall

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6:00 — 7:00 **NEAS Social & Silent Auction**
Atrium, Global Heritage Hall

7:00 — 10:00 pm **Banquet, Awards & Live Auction**
Atrium, Global Heritage Hall

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Sunday, April 18, 2010

7:00 — 8:20 am **Continental Breakfast**
Feinstein College of Arts & Sciences, rm 157

8:00 — 8:20 am ***Session VI speakers load presentations, FCAS 157***

8:25 — 8:30 am ***Announcements — Chris Lane***
Feinstein College of Arts & Sciences, rm 157

SESSION VI ***Contributed Papers, Moderator: Chris Lane***
Feinstein College of Arts & Sciences, rm 157

8:30 — 8:45 *Contributed paper*
Raul Ugarte - Production and productivity of the brown algae
Ascophyllum nodosum after 20 years of consecutive harvesting in
the Canadian Maritimes

8:45 — 9:00 *Contributed paper*
Raul A. Ugarte, **Alan T. Critchley**, A. R. Serdyska & J. P.
Deveau - Changes in *Ascophyllum nodosum* beds due to possible
recent increase in sea temperature in eastern Canada

9:00 — 9:15 *Contributed paper*
Milan Keser, Jim Foertch & John Swenarton - Rocky shore
community changes noted over 30+ years of monitoring

9:15 — 9:30 *Contributed paper*
Dale A. Holen - The stomatocyst of *Ochromonas pinguis*
Conrad (Chrysophyceae)

- 9:30 —9:45** *Contributed paper*
 John D. Wehr, Kurt Gabel, & Kam Truhn - Diatom biodiversity to assess best management practices in agricultural streams
- 9:45 —10:15** *Coffee Break*
- SESSION VII** ***Contributed papers, Moderator: Molly R. Letsch***
 Feinstein College of Arts & Sciences, rm 157
- 10:00 —10:15** *Contributed paper*
 Arthur C. Mathieson & Clinton J. Dawes - A new seaweed flora for the northwest Atlantic- a progress report
- 10:15 —10:30** *Contributed paper*
 Viviana Reyes, Hernan Velasquez, **Brigitte Gavio** & Michael Wynne - Biodiversity of marine macroalgae in the archipelago of San Andres, Old Providence and Saint Catalina island, Caribbean Colombia
- 10:30 —11:00 am** *Special invited paper*
 Peter A. Siver & Anne-Marie Lott - Everything is everywhere or maybe not: the biogeography of scaled chrysophytes along the east coast of North America.
- 11:00 —11:30 am** *Special invited paper*
 Craig W. Schneider – An assessment of the island biogeography theory using a century of floristics in Bermuda—immigration and extirpation or simply systematics?
- 11:30 —12:00 am** *Special invited paper*
 Marcie Marston – Population dynamics and biogeography of marine viruses in Southern New England.
- 12:00 —12:30 am** *Special invited paper*
 Tatiana Rynearson, Chris Piecuch, Dayna Rignanese & Kerry Whittaker – Just go with the flow: plankton connectivity in a high dispersal world.
- 12:30 —1:30** ***NEAS Annual Business Meeting & Lunch***
 Feinstein College of Arts & Sciences, rm 157

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

UNDERGRADUATE POSTERS (PRESIDENT'S AWARD)

- P1** — **Emily T. Johnston**, Sarah A. Stewart, Timothy J. Entwisle & Morgan L. Vis — Phylogeny of Australasian endemic taxa in the Batrachospermales (Rhodophyta) using the *rbcL* and LSU genes.
- P2** — **Edrenkin Victor** — Ecological monitoring of snow and soil of Asha using microscopic algae and cyanobacteria.
- P3** — **Ashley Heinze**, Michele Guidone, & Carol Thornber — Morphological characteristics of *Ulva* species occurring in Narragansett Bay, RI.
- P4** — **Andrew Barber**, Anne-Marie Lott, William Karis & Peter Siver — Unraveling the paleolimnology of the Giraffe Pipe kimberlite maar lake using siliceous microfossils.
- P5** — **Alexander M. VandenBroek** & Morgan L. Vis — Desiccation tolerance in three freshwater red algae (Rhodophyta).
- P6** — **Zoe Madden**, Anne-Marie Lott & Peter Siver — The Giraffe Pipe database project: a web-based database for siliceous microfossils from freshwater arctic maar lakes during the Cenozoic hot house.
- P7** — **Nolon Ciemniecki**, Dana Price, Debashish Bhattacharya, Ed Braun, Don Kapraun, & Naomi Phillips — Insights into the evolution of multicellularity and the greening of the heterokont genome through 454 sequencing of *Schizocladia ischiensis*.
- P8** — **Noel Sme** & Marcie Marston — Comparison of southern New England and Long Island coastal cyanophage communities.
- P9** — **Samantha Taylor** & Marcia Marston — Temporal patterns of cyanophage diversity in Bermuda's coastal waters.
- P10** — **Jack Tuchman**, Jocelyn Nadeau & Ray Kepner — Quest for antibiotics produced by an arctic cyanobacterium

GRADUATE STUDENT POSTERS (TRAINOR AWARD)

- P11** — **Melissa A. Vaccarino**, Emily G. Tillmaand, Michael P. Martin & Jeffrey R. Johansen — Phylogenetic placement of the Microchaetaceae (Cyanobacteria).
- P12** — **Gulshat Bakieva** — Cyanobacteria and soil algae of the Bashkir State Natural Reserve (South Urals, Russia).

- P13** — **Christine Newton** & Carol Thornber — Can algae save our salt marshes? Impacts of macroalgal blooms on salt marsh community structure.
- P14** — **Amanda Savoie** & Gary W. Saunders — Establishing species limits and phylogenetic relationships for Canadian Rhodomelaceae using molecular tools.
- P15** — **Susan L. Clayden** & Gary W. Saunders — Drew's *Acrochaetium porphyrae*: a diminutive acrochaete but not an *Acrochaetium*, with description as *Rhododrewia porphyrae* gen. nov. (Acrochaetiales).
- P16** — **Karina Osorio-Santos** & Johansen, Jeffrey — Cyanobacterial flora from soil of the Atacama desert, Chile.
- P17** — **Katharine Hind** & Gary W. Saunders — Identification of cryptic species in the genus *Bossiella* (Corallinales, Rhodophyta) in Canada.
- P18** — **Jeremy C Nettleton**, Christopher D Neefus, Arthur C Mathieson & Larry G Harris — Using macroalgae to track environmental changes in the Great Bay estuarine system.
- P19** — **Lindsay A. Green**, Salvatore J. Genovese & Geoffrey C. Trussell — The effects of habitat availability on trait-mediated indirect interactions in a kelp forest food chain.
- P20** — **Hannah Traggis** & Dr. Leland Jahnke — Recovery of the photosynthetic mechanism under oxidative stress induced by iron deficiency.
- P21** — **Agnes Mols Mortensen**, Christopher D. Neefus & Juliet Brodie — *Porphyra njordii* sp. nov. (Bangiales, Rhodophyta) and further insights into the *P. linearis* complex in the North Atlantic.
- P22** — **Jillian Decker**, Kam Truhn, & John Wehr — Phytoplankton and nutrient dynamics following a spring flood event in a backwater lake of the upper Mississippi River.
- P23** — **William Pérez** & Kenneth G. Karol — A systematic revision of *Tolypella* a. Br.: preliminary investigations.
- P24** — **Justin R Pool** & Morgan L Vis — Diatom community composition and biofilm enzyme activity for water quality assessment of acid mine remediated streams.
- P25** — **Nicole E. Rohr**, Carol S. Thornber, & Emily Jones — Biotic influences on epiphyte and herbivore recruitment in a marine subtidal system.
- P26** — **Cindy Fernández-García**, Rafael Riosmena-Rodríguez, Brian Wysor, Olga Lidia Tejada & Jorge Cortés — Checklist of the Pacific marine macroalgae of Central America

P27 — **Caroline Longtin** & Gary Saunders — Does the distribution of macroscopic kelp (*Nereocystis luetkeana*, *Laminaria ephemera*) sporophytes reflect the distribution of microscopic gametophytes?

CONTRIBUTED POSTERS

P28 — **Jang K. Kim**, Balakrishnan Prithiviraj, David J. Garbary & Jim Duston — *Chondrus crispus* stocking density affects nutrient removal efficiency in high water flux effluent from a land-based Atlantic halibut farm.

P29 — **Jang K. Kim**, George P Kraemer & Charles Yarish — Desiccation of the genus *Porphyra* cause release of nitrogen.

P30 — Benjamin Parmentier, Adrienne P. Smyth and **Peter M. Bradley** — Identification of diatoms from the peat bog at Poutwater Pond suggests pH changes occurred during the Holocene.

P31 — **Elizabeth V. Garlo** & Paul Geoghegan — The decline of *Laminaria digitata* in the southwestern Gulf of Maine in relation to summer water temperatures.

P32 — **Raul A. Ugarte**, James S. Craigie & Alan T. Critchley — Furoid flora of the rocky intertidal of the Canadian Maritimes: implications for the future with rapid climate change.

P33 — Krautová, Markéta, **Jeffrey R. Johansen**, Karolina Fučíková, Michael P. Martin — *Tapinothrix clintonii* sp. nov. (Pseudanabaenaceae, Cyanobacteria), a new species at the nexus of five genera.

P34 — Margarita Albis & **Brigitte Gavio** — Distribution of macroalgal epiphytes associated to *Thalassia testudinum* in San Andres Island, Caribbean Colombia

P35 — **Rui Pereira**, Luisa Valente, Isabel Sousa-Pinto and Paulo Rema — Digestibility coefficients of IMTA produced seaweeds, by rainbow trout (*Oncorhynchus mykiss*) and Nile tilapia (*Oreochromis niloticus*).

ABSTRACTS

Oral Presentations (In order of presentation)

Session I

1 - INVESTIGATING SPECIES DIVERSITY, BIOGEOGRAPHY AND TAXONOMY WITHIN THE RED ALGAL GENUS *SCAGELIA* (CERAMIALES, RHODOPHYTA). Meghann Bruce & Gary W. Saunders. Center for Environmental & Molecular Algal Research, Department of Biology, University of New Brunswick, Fredericton, NB E3B 5A3, Canada

Like many members of the Rhodophyta, identification of *Scagelia spp.* (Ceramiales, Rhodophyta) using traditional taxonomic techniques can be overwhelmingly complicated. In the case of *Scagelia*, this is due to phenotypic plasticity, as well as the lack of diagnostic species-level characters among members of the genus, making it difficult to determine how many species exist. Consequently, previous studies of *Scagelia* have generated a complex taxonomic history for the genus. In this study, we use DNA barcoding and ITS sequence data in order to identify how many genetic species groups are present within the genus *Scagelia* in Canada where two species are currently recognized (viz. Pacific *Scagelia occidentale* and Arctic and Atlantic *Scagelia pylaisaei*). DNA barcoding has shown support for two genetic species groups, which are closely related. However, the biogeography for the genetic species groups contradicts that of the morphological species currently recognized – *Scagelia occidentale* occurs in the Arctic rather than *Scagelia pylaisaei*. Contrary to the DNA barcode results, however, the ITS sequence data does not delineate two species of *Scagelia* indicating the possibility of a past incipient speciation event, but with the two populations again interbreeding. My future research will use a third marker in combination with the mitochondrial and nuclear data to help resolve further this discrepancy.

2 - SYSTEMATICS OF SELECT MEMBERS OF THE KALLYMENIACEAE (RHODOPHYTA) IN CANADA. Bridgette Clarkston & Gary W. Saunders. Center for Environmental & Molecular Algal Research, Department of Biology, University of New Brunswick, Fredericton, N.B., E3B 6E1, Canada.

The Kallymeniaceae is a large red algal family with eight genera and 18 species reported currently from Canada. A recent survey along the coast of British Columbia using the DNA barcode (COI-5P - the 5' region of the mitochondrial cytochrome c oxidase I gene) as a species identification tool reported species from *Callophyllis*, *Pugetia*, *Euthora*, *Kallymeniopsis*, *Erythrophyllum* and *Beringia* and revealed new records and overlooked diversity in *Callophyllis*, *Pugetia*, *Euthora* and *Beringia*. Phylogenetic relationships among these genera were investigated using combined large-subunit nuclear ribosomal DNA (LSU) and combined LSU and COI-5P data that were subjected to maximum likelihood and Bayesian analyses. Subsequent morphological examination of each species was also conducted. These analyses revealed the following: the currently reported species of *Pugetia* in Canada (*P. fragilissima* and *P. firma*) were in fact two pairs of cryptic species, and the “*P. fragilissima*” group and “*P. firma*” group were morphologically and molecularly divergent enough to suggest a generic level distinction should be made; *Kallymeniopsis oblongifruca*, *Erythrophyllum delesserioides*

and a new record for Canada (*Beringia* sp.) were closely allied and had low sequence divergences in all analyses, suggesting these morphologically distinct species belong in a single genus; and the fourteen species of *Callophyllis* reported in the survey (nine are currently reported in the literature) resolved as a monophyletic group that also included several species from California, Chile and Australia. Additionally, our morphological and molecular analyses to date supported a proposal by Norris and Abbott (1966) that the presence of a single carpogonial branch per supporting cell in female gametophytes (monocarpogony) vs. multiple branches per supporting cell (polycarpogony) can be used to distinguish two evolutionary lineages within *Callophyllis*.

3 - CRYPTIC SPECIES OF THE GENUS *PSEUDOMURIELLA*: TO BARCODE OR NOT TO BARCODE? Karolina Fučíková¹, Jared C. Rada¹, Alena Lukešová² & Louise A. Lewis¹.

¹ University of Connecticut Department of Ecology and Evolutionary Biology, University of Connecticut, 75 North Eagleville Road, Storrs, 06269-3043 (USA).

² Institute of Soil Biology AS CR, Na Sádkách 7, 370 05 České Budějovice, Czech Republic.

The taxonomy of green coccoid algae traditionally has been limited by their character-poor morphology observable by light microscopy. Alternative methods, especially the use of molecular sequence data, often reveal cryptic diversity and help clarify phylogenetic affiliations of green coccoids. The present study focuses on the genus *Pseudomuriella* Hanagata and its phylogenetic relationships to morphologically similar genera.

Morphologically cryptic diversity of the genus *Pseudomuriella* was revealed using the traditionally utilized nuclear ribosomal marker ITS2. Suitability of two other markers, the plastid *rbcL* gene and the mitochondrial *cox1* gene, for species recognition (barcoding) was assessed. The utility of the three markers is discussed using a comparison of their performance in species-level resolution within the *Pseudomuriella* clade, while also considering the ease of their use. All three genes examined were found to contain variation usable for species-level resolution, and provided largely consistent phylogenies. A joint use of the three markers may be the ideal tool for barcoding cryptic green algal species, but *rbcL* appears to be the most practical combination of good phylogenetic signal and ease of use.

4 - BARCODING DIATOMS: EXPLORING ALTERNATIVE MARKERS. Sarah E. Hamsher¹, Katharine M. Evans², David G. Mann², Aloisie Pouličková³ & Gary W. Saunders¹.

¹Biology Department, University of New Brunswick, Fredericton, NB E3B 5A3, Canada.

²Royal Botanical Garden Edinburgh, 20A Inverleith Row, Edinburgh EH3 5LR, UK.

³Department of Botany, Faculty of Science, Palacký University, Šlechtitelů 11, Olomouc, CZ-783 71, Czech Republic

Diatoms are a diverse lineage with cryptic species that can be difficult to identify, but DNA barcoding, a new molecular technique, can assist identification and facilitate studies of speciation and biogeography. The most common region used for DNA barcoding, COI-5P, can distinguish diatom species, but has not displayed universality (i.e., successful PCR amplification of the region from diverse taxa). Therefore, we have assessed the following alternative markers: ~1400 bp of *rbcL*; 748 bp at the 3' end of *rbcL* (*rbcL*-3P); the LSU D2/D3; and the UPA. *Sellaphora* isolates were used to determine each marker's ability to discriminate among closely related species and culture collection material was utilized to

further explore the universality of each marker. Both full and partial (3P) *rbcL* regions had the power to discriminate between all species, but the *rbcL*-3P can be sequenced more easily. The LSU D2/D3 and UPA were easily amplified and sequenced and distinguished 96% and only 20% of species pairs, respectively. In light of our observations, we propose that the *rbcL*-3P should be used as the primary marker for diatom barcoding, while the LSU D2/D3 should be sequenced as a secondary marker to facilitate the identification of diatoms in environmental surveys.

5 - A MOLECULAR INVESTIGATION OF THE SCYTOSIPHONACEAE IN CANADA.
Daniel McDevit & Gary W. Saunders. University of New Brunswick, Fredericton, NB, Canada.

Marine macroalgae, with their plastic features, convergent morphologies and simple constructions, can be a challenge to identify, even for the experienced taxonomist. For the past few years we have been using molecular tools (including the DNA barcode – COI-5P = 5' end of cytochrome c oxidase 1) to aid us in species identification. In addition to redefining our concept of many species this method has uncovered massive amounts of cryptic diversity. One example of this is in the Scytosiphonaceae, a group that has long been a source of taxonomic confusion. Although only two species of *Scytosiphon* are reported from North America molecular evidence suggests the presence of seven *Scytosiphon* species. Continued molecular examination, using nuclear (ITS) and plastid (*psaA* and *rbcL*) markers, have supported our barcode findings, but have additionally highlighted the need for a complete taxonomic reassessment of the Scytosiphonaceae. In this presentation we present some of our findings, including the descriptions of two new species.

6 - A PILOT-STUDY EVALUATION OF *RBCL*, UPA, LSU AND ITS AS DNA BARCODE MARKERS FOR THE MARINE GREEN MACROALGAE. Hana Kucera & Gary W. Saunders. Centre for Environmental & Molecular Algal Research, Department of Biology, University of New Brunswick, PO Box 4400, Fredericton, NB, E3B 5A3, Canada.

Marine green macroalgae are the last group of seaweeds for which a DNA barcode marker remains to be developed. The aim of this study was to evaluate the universality and species discriminatory power of the rubisco large subunit (*rbcL*) (considering the 5' and 3' fragments independently), the universal amplicon (UPA), the D2/D3 region of the large ribosomal subunit (LSU) and the internal transcribed spacer of the ribosomal cistron (ITS) for green macroalgae. Each marker was assessed for 99 samples representing a variety of seaweed species. Of the markers tested, the 3' region of the *rbcL* had the highest universality and genetic variation at the species level, and thus showed the most promise as a DNA barcode. Unfortunately, the presence of introns within the *rbcL* for some taxa reduces the utility of this marker as a universal barcode system and more research is required before a DNA barcoding marker can be recommended for the green macroalgae. Despite the drawbacks, our *rbcL* analyses revealed putative cryptic species in the genera *Acrosiphonia*, *Monostroma*, and *Ulva* in Canadian waters.

Session II

7 – PHOTOSYNTHETIC ANCESTRY OF THE OOMYCETES: THE HUNT FOR A VESTIGIAL ORGANELLE. Ian Misner¹, Lindsey Haus², J. Craig Bailey², & Christopher E. Lane¹. ¹Department of Biological Sciences, University of Rhode Island, Kingston, RI 02881, U.S.A.; ²Center for Marine Science, Department of Biology, University of North Carolina Wilmington, Wilmington, NC, 28409, U.S.A.

Long thought to be related to fungi, more recent data have shown that oomycetes are nested within the stramenopiles – a diverse assemblage of organisms containing photosynthetic and non-photosynthetic members. Though hotly debated, the ancestor of the stramenopiles is thought to be photosynthetic (Chromalveolate hypothesis). Analysis of the *Phytophthora infestans*, *P. 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. We have discovered two core photosynthetic genes (*psbA* & *rbcL*) from the saprolegnialean oomycetes. The oomycete copies of *psbA* & *rbcL* we have recovered appear to be functional or have only recently begun accumulating mutations resulting in premature stop codons. We have also attempted to isolate the potential vestigial plastid genome using CsCl fractionation and obtain size estimates using pulse-field gel electrophoresis. Moreover, analysis of existing ESTs from the saprolegnian oomycete *Aphanomyces euteiches* identified genes that are homologs to plastid-targeted genes from the diatom *Thalassiosira pseudonana*. These data raise the possibility that some oomycetes still contain a vestigial plastid with a genome.

8 - UNRAVELING THE ROLE OF MITOCHONDRIA IN RED ALGAE PARASITE EVOLUTION. Lillian Hancock, Christopher E. Lane. Department of Biological Sciences, University of Rhode Island, Kingston, RI 02881, U.S.A.

Red algal parasitism is unique in that the host and parasite evolved from a recent common ancestor and that infection of the host occurs through the transfer of parasite DNA-containing organelles rather than the whole organism. During host cellular transformation, the parasite abandons its own plastid in favor of co-opting the host version, while maintaining its own genetically unique mitochondrion. To understand why the mitochondrion cannot be lost, we sequenced the mitochondrial genomes of adelphoparasite *Gracilariophila oryzoides* (25,180bp) and host *Gracilariopsis andersonii* (~27,500bp). Genome comparisons indicate that the *G. oryzoides* mitochondrion is undergoing both reduction and compaction with the loss of intergenic spaces, the development of pseudogenes, and gene loss. Interestingly, the evolutionary trends observed in *G. oryzoides* are conserved in the mitochondrial genome of the more divergent alloparasite *Plocamiocholax pulvinata* (25,894bp). Parasite mitochondrial genomes have a higher A/T content and maintain additional tRNAs in comparison to host mtDNA. Trends, such as the acquisition and retention of additional tRNAs and loss of essential genes involved in respiration, are being explored more fully in attempts to understand why the parasite maintains its own mitochondrial genome.

9 - FOUR CHLOROPLAST GENE ARRANGEMENTS IN A CLOSELY RELATED

GROUP OF TREBOUXIOPHYCEAE (CHLOROPHYTA). Molly R. Letsch¹, & Louise A. Lewis¹. ¹Department of Ecology and Evolutionary Biology, University of Connecticut, Storrs, CT, 06269, USA.

Chloroplast gene order data are available for a limited number green algal species; the 24 species that have published chloroplast genomes are fairly widely distributed across the Chlorophyta. Using single directional amplification and sequencing we have determined the identity and relative position of the two genes adjacent to the 5' end of the *rbcL* locus for 11 species within close phylogenetic space including several isolates of *Elliptochloris* and their close relatives *Hemichloris* and *Coccomyxa* (Trebouxiophyceae). We detected four different gene arrangements that are all distinct from the gene orders in the four Trebouxiophyceae with published chloroplast genomes. Within the isolates of *Elliptochloris* we sampled three different gene arrangements were detected. All three *Hemichloris* isolates examined shared one of these gene arrangements with *Elliptochloris*. The two *Coccomyxa* isolates sequenced had a fourth unique gene order. The amount of gene order rearrangement found within this closely related group of green algae is in stark contrast with the conserved gene order seen in Embryophytes.

10 - EXAMINATION OF THE ABUNDANCE AND RELATIVE PALATABILITY OF SELECT *ULVA* SPECIES IN NARRAGANSETT BAY, RHODE ISLAND. Michele Guidone & Carol Thornber. Department of Biology, University of Rhode Island, Kingston, RI, 02881, USA.

In Narragansett Bay, RI, green macroalgal blooms are an annual occurrence. Previously thought to be composed of the blade-forming *Ulva lactuca* and four tube-forming *Ulva* species, genetic analyses have identified two cryptic blade-forming bloom species: *U. rigida* and *U. 'compressa'*. In order to determine which blade forming *Ulva* species is most abundant in Narragansett Bay blooms, we conducted monthly intertidal surveys (May-September, 2009) using quadrat methodology at four RI sites. Warwick City Park and Chepiwanoxet are located within Greenwich Bay (Warwick, RI), an area of Narragansett Bay that is impacted by annual macroalgal blooms. These sites were contrasted to two sites located near the mouth of Narragansett Bay (GSO Beach and Pier 5, Narragansett, RI), which do not experience *Ulva* blooms. As expected, bloom impacted sites had the greatest *Ulva* biomass each month, with a maximum total *Ulva* biomass at Warwick City Park in July (mean 883.08 g/m²). Throughout the summer, *Ulva* found at the bloom-impacted sites was a mix of *U. rigida* and *U. 'compressa'*, with a greater percentage of *U. 'compressa'* every month except July. In contrast, the non-impacted sites were dominated by *U. lactuca*. These results indicate that *Ulva* blooms in Narragansett Bay are composed of *U. rigida* and *U. 'compressa'*, not *U. lactuca* as previously thought. In addition, image analysis indicates there may be differences in herbivore usage of these three species.

11 - LAND-USE AND NUTRIENT EFFECTS ON BENTHIC ALGAL BIOMASS, NUTRIENT STOICHIOMETRY, AND SPECIES COMPOSITION IN AN URBANIZED WATERSHED. Matthew Cashman,¹ John Wehr,¹ & Kam Truhn.¹ ¹Louis Calder Center - Biological Field Station, Fordham University, Armonk, NY, 10504, USA.

We compared the degree of urbanization based on % impervious surfaces (IS%) in the watershed and local riparian zone of streams in Westchester County, NY, to determine the scale of watershed influence on water quality, periphyton biomass, and nutrient content. A comparative survey was conducted among 10 streams with varying IS% and complemented by an experimental study using nutrient-diffusing substrata at varying pulse rates. Specific conductance strongly varied with watershed impervious surfaces (91%; $P < 0.0001$) and less strongly with buffer IS% (70%; $P=0.0026$). [Mg] and [NO₃⁻] were also more closely predicted by %IS in riparian buffer zones, but the relationship was also significant at the watershed scale. Periphyton biomass (as Chl-*a* and AFDM) varied significantly only with buffer IS% (47%, $P = 0.028$; 65%, $P = 0.005$). Periphyton C (71%, $P = 0.002$) and N (76%, $P = 0.001$) increased with urbanization, but only vs. buffer IS%; periphyton-P was NS at both scales. The experimental study placed tiles in rural, suburban, and urban streams for 41 days for algal colonization with different nutrient-pulse treatments. At day 41, periphyton biomass did not vary significantly among nutrient treatments, but varied significantly among watersheds ($F = 6.127$, $P = 0.005$).

Session III

12 - A SYSTEMATIC INVESTIGATION OF THE *NITELLA FLEXILIS* (L.) AG. SPECIES COMPLEX. Heather M. Meyer^{1,2} & Kenneth G. Karol¹ Lewis B. & Dorothy Cullman Program for Molecular Systematics Studies, The New York Botanical Garden, Bronx, NY 10458, USA. ²Biology Department, Sarah Lawrence College, 1 Mead Way, Bronxville, NY 10708, USA.

Wood and Imahori (1965) published a *Revision of the Characeae*, a global monograph of the fresh water algal family *Characeae*. In this monograph, a broad morphological species concept was used to reduce more than 400 named species to 81 loosely defined species, each with various 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 findings for *Nitella flexilis* (L.) Ag., which includes more than thirteen previously recognized species either as synonyms or subspecific taxa. Using chloroplast sequence data (*rbcL* and *atpB*) at least 12 distinct clades separate from *N. flexilis sensu stricto* have been identified. 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*.

13 - MOLECULAR ASSESSMENT OF PANAMANIAN *ULVA* (ULVALES, CHLOROPHYTA) USING *RBCL* AND ITS RDNA. Ryan T. Higgins, Brian Wysor & Charles J. O'Kelly. Roger Williams University. One Old Ferry Rd, Bristol, RI, 02809, USA.

The sea lettuces of genus *Ulva* are common fouling organisms in marine environments worldwide and can form extensive blooms known as green tides. Species within this genus exhibit both morphological plasticity and convergence, making species identification problematic. Thus, molecular analysis has become commonplace for assessing species diversity within the genus. The plastid encoded *rbcL* gene and the nuclear encoded internal transcribed spacer regions (ITS nrDNA) have been used to document the diversity of *Ulva* from cold, temperate waters, but few studies have addressed the diversity of tropical *Ulva*.

This study used *rbcL* and ITS sequences to examine the diversity of species of *Ulva* from Panama. Preliminary assessment of approximately 250 *rbcL* sequences reveals close matches of Panamanian specimens to *U. reticulata* and *U. ohnoi*, but the majority of individuals form a distinct Panamanian clade, representing 4-5 species. Phylogenetic patterns inferred from ITS data are largely congruent with the *rbcL* phylogeny. These results suggest that sea lettuce diversity has been underestimated for Panama and are consistent with other recent studies revealing novel diversity for tropical *Ulva*.

14 - MOLECULAR-ASSISTED ALPHA TAXONOMY OF THE ‘CENTROCERAS CLAVULATUM COMPLEX’ (CERAMIALES, CERAMIACEAE) IN BERMUDA, WESTERN ATLANTIC. Elisabeth Cianciola¹, Thea Popolizio², Christopher E. Lane² & Craig W. Schneider¹, ¹Department of Biology, Trinity College, Hartford, CT 06106-3100, USA; ²Department of Biological Sciences, University of Rhode Island, Kingston, RI, 02881, USA.

The variable morphology of red algae (Rhodophyta) has historically made species-level identification quite challenging. For this reason, the use of molecular-assisted alpha taxonomy is becoming increasingly widespread for these algae. Molecular-assisted taxonomy combines DNA analysis of specimens with subsequent analysis of the vouchers’ morphological features so that only morphological features which are taxonomically significant are used in the identification process. *Centroceras clavulatum* (C. Agardh) Mont. (Ceramiales, Ceramiaceae) was a cosmopolitan complex of cool temperate to tropical red algae until molecular sequencing of a number of isolates worldwide greatly restricted its biogeography to the Pacific Ocean. Thus, analysis of specimens from other locations in the Atlantic, Pacific and Indian Oceans not presently sequenced, such as the Caribbean, Bahamas and Bermuda, to name a few, is necessary. In this study, we perform molecular and morphological analyses of collections previously identified as *C. clavulatum* from various locations in the Bermuda islands. Performing *rbcL* analysis for eight Bermuda isolates and the morphological analysis of 52 collections, two potentially undescribed species have been identified and the distributions of three taxa recently segregated from the ‘complex’ in western Atlantic, *Centroceras gasparinii* (Menegh.) Kütz., *C. hyalacanthum* Kütz., and *C. micracanthum* Kütz., have been expanded to include Bermuda.

15 - WHAT DOES THE MITOCHONDRIAL COX2 GENE TELL US ABOUT CHLOROPHYCEAN ALGAE EVOLUTION? Elizabeth Rodríguez-Salinas¹, Li Zhong-Kui², Karolina Fučíková³, Louise A. Lewis³, Jerry J. Brand² & Diego González-Halphen¹. ¹Instituto de Fisiología Celular, Universidad Nacional Autónoma de México, México D.F., México; ²The University of Texas at Austin, Department of Molecular Cell and Developmental Biology and Culture Collection of Algae, Austin, TX 78712, USA; ³Department of Ecology and Evolutionary Biology, University of Connecticut, 75 North Eagleville Road, Storrs, CT, 06269-3043, USA.

Gene fragmentation is a relatively rare molecular event with significant consequences and implications at the molecular, cellular and evolutionary level. Previously, our lab described the fragmentation of the mitochondrial *cox2* gene into two genes, *cox2a* and *cox2b*, in the chlorophycean algae *Chlamydomonas reinhardtii*, *Polytomella* sp. and *Scenedesmus obliquus*. Moreover, in *C. reinhardtii* and *Polytomella* sp. *cox2a* and *cox2b* genes are located in different

nuclear chromosomes, are independently transcribed, and translated into separate polypeptides. These two proteins assemble to form a heterodimeric subunit COX2, that interacts with other cytochrome *c* oxidase subunits embedded in the inner mitochondrial membrane. Here, we sought to determine if the fragmentation of the *cox2* gene is a molecular feature characteristic of the entire lineage *Chlorophyceae*. Our data suggest that different forms of *cox2* genes are found in chlorophycean algae: some lineages have orthodox, intact, mitochondrial *cox2* genes; others exhibit fragmented *cox2a* and *cox2b* genes, with *cox2a* in the mitochondrial genome and *cox2b* in the nucleus; yet other lineages show nucleus-encoded *cox2a* and *cox2b* genes. Also, different degrees of splicesomal intron invasion have modified the genes that migrated to the nucleus. We describe how reconstruction of the evolutionary history of *cox2* gene fragmentation and migration provides new insights to our understanding of green algal phylogenetic relationships.

16 - MOLECULAR DIVERGENCE WITHIN *RALFSIA VERRUCOSA* (RALFSIALES, PHAEOPHYCEAE) INDICATES CRYPTIC SPECIES. Manuela I. Parente^{1,2}, Florence Rousseau³, Bruno de Reviere³, Robert L. Fletcher⁴, Filipe Costa² & Gary W. Saunders¹.

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Morphology and molecular phylogeny of a crustose brown algal species, *Ralfsia verrucosa* (J. E. Areschoug) J. E. Areschoug, were investigated based on isolates from different regions including the Azores, the northern and central coasts of mainland Portugal, the Atlantic and Mediterranean coasts of France, as well as isolates from Helgoland and England. *Ralfsia verrucosa* is characterized by a crustose and orbicular thallus, verrucose and relatively easy to raise from the substratum, with upwardly directed erect filaments, punctuate sori obvious in surface view and plurilocular sporangia with only one sterile terminal cell. In order to study DNA divergence and phylogenetic relationships of the species, analyses of mitochondrial (cytochrome *c* oxidase 1) and nuclear (internal transcribed spacer 1 and 2) genomic DNA sequence data were performed and revealed the presence of clearly divergent lineages. These results indicate cryptic species within the concept of *Ralfsia verrucosa*.

17 - A COMPARISON OF ALGAL COMMUNITY COMPOSITION BETWEEN 1924 AND 2010 IN HARRIMAN STATE PARK, NEW YORK. John D. Hall¹ & Kenneth G. Karol¹.

¹Lewis B. & Dorothy Cullman Program for Molecular Systematics Studies, The New York Botanical Garden, Bronx, NY, 10458, USA.

Harriman State Park is the largest contiguous tract of land under the supervision of the Palisades Interstate Park Commission. The plankton algae in the Palisades Interstate Park were surveyed by G. M. Smith (1924) soon after many of the lakes were created. Floristic surveys of the plankton and periphyton communities performed in 2008 and 2009 revealed a diverse algal flora. To date, 340 species have been identified from the park including many desmids.

Many of the species encountered and described by Smith (1924) were encountered in our 2008-2009 surveys, but some conspicuous species were not. In addition, we report many species not previously known from the park or the region. Changes in the regional algal flora will be discussed including the apparent increase in the number of desmid species and shifts in species composition of other groups. We hypothesize that these changes may have been caused by various factors including normal succession in newly constructed lakes and changes in land use. We cannot eliminate the possibility that large-scale factors such as regional climate change may have also contributed to changes in algal community.

Session IV

18 – SPECIES, PATTERNS & ALGAE: A PHYLOGENETIC PERSPECTIVE. Olivier De Clerck. Research Group Phycology & Centre for Molecular Phylogenetics and Evolution, Ghent University, Krijgslaan 281, S8, 9000 Gent, Belgium.

The advent of DNA sequencing two decades ago has considerably altered our ideas about algal species level diversity. A plethora of studies have revealed cryptic or sibling species within morphologically defined species, falsifying the assumption that speciation events always coincide with any noticeable morphological differentiation. Although novel and exciting at first, the widespread nature of cryptic diversity and the failure of morphological data to address algal species level diversity adequately, presents an impediment to address evolutionary questions related to algal diversification. To date morphological differentiation, or the lack thereof, has been the focus of the vast majority of phylogenetically oriented algal studies. Phylogenies, however, can be used for a lot more than assessing species identity and discovering potential cryptic diversity. Coupled with data on the characteristic and lifestyles of species, phylogenies can be used to infer the historical evolutionary processes of the past. I will outline a methodology which combines ecological niche modeling (ENM) with comparative phylogenetic methods (CPM's) to study diversification and distribution patterns of marine macroalgae, using a number of genera which are under study at the Ghent Phycology lab (*Halimeda*, *Codium* and *Dictyota*) as examples. Most efforts have concentrated on macroevolutionary patterns. In addition, I will explain how ENM and coalescent modeling can be integrated in studies at the population level to study speciation and phylogeographic patterns in the marine environment.

Session VI

19 - PRODUCTION AND PRODUCTIVITY OF THE BROWN ALGAE *ASCOPHYLLUM NODOSUM* AFTER 20 YEARS OF CONSECUTIVE HARVESTING IN THE CANADIAN MARITIMES. Raul Ugarte. Acadian Seaplants Limited, 30 Brown Avenue, Dartmouth, Nova Scotia, B3B 1X8, Canada.

Commercial exploitation of rockweed (*Ascophyllum nodosum*) along the coastal areas of Nova Scotia began in the late 1950's when it was used as a raw material for manufacturing sodium alginate and "kelp" meal. Today this seaweed resource is used as a source of a fertilizer extract and as an animal feed supplement. Rockweed is the main economic resource of the seaweed industry in the Maritimes Provinces and indeed of Canada as a whole. Acadian Seaplants

Limited (ASL) currently holds leases to approximately 90% of the commercial resource in the region and has harvested the resource consecutively for 20 years. The company has carried out extensive annual surveys of the resource since 1995. The current summer (July – August) standing crop for this region has been calculated at 353,395 wet tonnes, covering an area of close to 4,960 ha, with an average biomass density of 71.3 tonnes ha⁻¹. The rockweed harvest in the region reached peak landings in 2008 with just over 36,500 tonnes. Although the total landings represent only 10.3% of the standing biomass, the harvest in the region (with the exception of NB) is considered to be in a fully exploited condition because only 2118 ha or 42.7% of the resource is actually accessible to current methods of hand harvest. Thus, the harvest yield varies between 13.6 and 20.5 tonnes ha⁻² a⁻¹. The total annual *Ascophyllum* production for the region is 54,055 dry tonnes, equivalent to 20,000 tonnes of carbon annually. This production provides additional environmental services of the net absorption of 73,284 tonnes of CO₂ from the environment each year. In this presentation, these figures are compared to previous estimates calculated by the industry and independent scientists working with the resource in the region. We conclude that the resource has maintained and, in some cases, increased its production in the region. Some explanations for this increase will be provided.

20 - CHANGES IN *ASCOPHYLLUM NODOSUM* BEDS DUE TO POSSIBLE RECENT INCREASE IN SEA TEMPERATURE IN EASTERN CANADA. Raul A. Ugarte, Alan T. Critchley, A. R. Serdynska & J. P. Deveau. Acadian Seaplants Limited, 30 Brown Avenue, Dartmouth, NS, Canada.

Ascophyllum nodosum is the main economic seaweed resource in the Atlantic Provinces of Canada. The annual harvest reaching a historic peak of 37,000 tonnes in 2007.

Due to a high demand for fertilizers and animal supplements derived from rockweed, this trend will continue. The current management plan for the sustainable harvest of the *A. nodosum* resource is considered conservative. The resource has been managed with a precautionary approach since 1995 to protect the integrity of the habitat. Acadian Seaplants Limited (ASL) has been granted approximately 90% of the government-issued licenses to harvest *A. nodosum* resources in the Maritimes. The Canadian approach is based on an annual harvest from a given bed and not strip-and-return after several years. Since 1995, ASL has proactively undertaken extensive annual surveys and research on biomass productivity of this renewable resource to establish acceptable annual exploitation rates. Historically, the rockweed beds of southwestern Nova Scotia (NS) have been almost 99% pure *A. nodosum*, with a minor component of *Fucus vesiculosus*. However, since 2004, a steady increase in *F. vesiculosus*, with a peak of 4.6% of the total biomass in 2008, was recorded. This coincided with one of the mildest winters on record for the Maritimes. This increase in temperature seemed to be also responsible for an unusual recruitment of the blue mussel *Mytilus edulis* in rockweed beds in some areas of southern New Brunswick (NB) in 2006, causing the detachment of up to 30% of the seaweed biomass in some harvesting sectors. Another phenomenon observed in southwestern NS during 2003 and 2004 was extensive ice damage on rockweed beds produced by an early melting of the ice, with losses of up to 90% of the rockweed biomass in some areas.

21 - ROCKY SHORE COMMUNITY CHANGES NOTED OVER 30+ YEARS OF MONITORING. Milan Keser, Jim Foertch & John Swenarton. Millstone Environmental Lab, P.O. Box 128, Waterford, CT, USA.

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. In addition to changes at sites near the power station, clearly related to construction and operation, we have observed patterns and trends in community composition at sites unimpacted by the station. Some of these changes involve introduction or range extension of intertidal organisms or, more subtly, by altered season of occurrence or reproduction for local species. Some, in turn, may be related to on-going environmental modifications in, *e.g.*, water temperature or pH, which may affect the resident algae directly, or indirectly, via changes to the behavior or structure of grazers and predators. Fortunately, we have over 30 years of measurements of these physical parameters, as well. Clearly, our rocky shore community is complex, with many interactions within and among species and trophic groupings, and between the organisms and their physical environment. We have developed a suite of uni- and multivariate analysis techniques to illustrate various components of the community, and their inter-relationships, and their changes over time. We hope to use this forum to discuss and explore some possible correlations among the biotic and abiotic variables.

22 - THE STOMATOCYST OF *OCHROMONAS PINGUIS* CONRAD (CHRYSOPHYCEAE). Dale A. Holen. Pennsylvania State University, Worthington Scranton campus, 120 Ridge View Dr., Dunmore, PA, 18512-1699 USA.

The stomatocyst of *Ochromonas pinguis* Conrad is described from observations of laboratory cultures using a combination of light and scanning electron microscopy. The cyst is spherical (16-20 μm in diameter) with a cylindrical, complex collar. The surface of the cyst is heavily ornamented with thick, prominent, lunate ridges that are non-uniform in length and height and occasionally bifurcate giving it a spiny appearance. Light microscopy images of H_2O_2 treated samples reveal an inner smooth primary cyst wall with conical collar surrounded by the ornamented secondary cyst wall with the thick secondary cylindrical collar. Immature and mature stages of the statospore in laboratory cultures are typically embedded within a circular, mucilaginous sheath with vegetative cells attached peripherally.

23 - DIATOM BIODIVERSITY TO ASSESS BEST MANAGEMENT PRACTICES IN AGRICULTURAL STREAMS. John D. Wehr¹, Kurt Gabel² & Kam Truhn¹. ¹Louis Calder Center – Biological Field Station, Fordham University, Armonk, NY 10504, U.S.A.; ²NYC Department of Environmental Protection, Bureau of Water Supply, Watershed Water Quality Operations, Valhalla, NY, USA.

Agricultural practices (farming, cattle grazing) are widely recognized as having severe negative impacts on water quality in rural watersheds. The NYC Department of Environmental Protection, the Watershed Agricultural Council and local farmers have implemented Best Management Practices (BMPs) to reduce potential negative impacts on stream water quality in Delaware and Sullivan Counties of NY. BMPs include riparian buffers, manure management, and barnyard improvements in affected watersheds. To assess BMP effectiveness, we examined diatom communities in similar 1st-2nd order streams within the region, comparing reference (non-agricultural), non-BMP and BMP streams during spring and autumn. Diatom species richness, % eutraphenic species, diatom model affinity, trophic diatom index and

generic diatom index all indicated greater water quality in BMP streams than unimproved agricultural streams, although diatom data suggested that reference streams had significantly greater water quality than either stream class. Biological diversity measures (species richness, Simpson's, Shannon-Weiner H') were less sensitive to water quality shifts among stream types than were water quality indexes based on diatoms. Several indexes also correlated significantly with turbidity, conductance, and dissolved P and N. In contrast, macroinvertebrate data and indexes (richness, % EPT, HBI, DMA) showed similar trends, but none were statistically significant among stream classes. Data suggest that diatoms may be more sensitive indicators of BMP effectiveness in first order agricultural streams in NY state than are macroinvertebrates.

Session VII

24 – A NEW SEAWEED FLORA FOR THE NORTHWEST ATLANTIC- A PROGRESS REPORT. Arthur C. Mathieson¹ & Clinton J. Dawes². ¹Department of Biological Sciences, University of New Hampshire, Durham, NH, 03824; ²Integrative Biology, University of South Florida, Tampa, FL, 33620 USA.

As Taylor's second revised printing of the "Marine Algae of the Northeastern Coast of North America" was published almost five decades ago (i.e. 1962) it is out of date and in need of revision/replacement. Recently (1998 & 2002) several individuals associated with NEAS (i.e. J. R. Sears and others) have published two revised sets of keys to the seaweeds from Long Island Sound to the Strait of Belle Isle, attempting to include additions and changes to the flora, plus nomenclatural updates. One of the obvious goals of this NEAS project was to encourage one or more individuals to write a comprehensive modern flora, including recent records, molecular evaluations, taxonomic changes, documentations of introduced species, etc. Having recently finalized a joint text on the "The Seaweeds of Florida" (i.e. C. J. Dawes and A. C. Mathieson, 2008) that took us ~8 years, we felt that our cooperative efforts could be extended to the Northwest Atlantic as several taxa were in common and perhaps it would not take such an extended period to complete. During the past two years we have been documenting detailed seaweed records from Ellesmere Island (Canada) to Maryland, the synonymy of various taxa (>450), their name derivations, recent taxonomic changes, morphological features, molecular affinities, ecologies, and distributional patterns. Some checklists and other resources have been particularly helpful, including those of Cardinal (1968), South and Tittley (1986), Bird and McLachlan (1992), Silva et al. (1996), Colt (1999), Sears (2002), Brodie et al. (2007), and Guiry and Guiry (2009). Examples of specific progress and a request for future help with recent records and some taxonomic clarifications are summarized.

25 - BIODIVERSITY OF MARINE MACROALGAE IN THE ARCHIPELAGO OF SAN ANDRES, OLD PROVIDENCE AND SAINT CATALINA ISLAND, CARIBBEAN COLOMBIA. Viviana Reyes¹, Hernan Velasquez², Brigitte Gavio^{1,3} & Michael Wynne⁴
¹ Universidad Nacional de Colombia, Sede Bogotá, Colombia, ² Universidad Nacional de Colombia, Sede Medellín, Colombia, ³ Universidad Nacional de Colombia, Sede Caribe, Colombia, ⁴ University of Michigan Herbarium, MI, USA

The Archipelago of San Andrés, Old Providence and Saint Catalina, off the coast of Nicaragua, has been declared an International Biosphere Reserve for the conservation state of its marine ecosystems. However, despite the great extension of its waters (300.000 Km²), only 201 species of macroalgae have been registered so far. Of these, 37.5% corresponds to red, 18.2% to brown and 44.8% to green algae. For other islands of the Caribbean (e.g. Puerto Rico, Cuba, Hispaniola) the marine flora is composed of an average 55.2% of red, 13.1% of brown and 31.7% of green algae. The apparent anomaly in the San Andrés archipelago flora may be explained by a large component of its red algal flora being overlooked, which, traditionally, is the less conspicuous (often small and epiphyte) and the most difficult to identify. In a recent survey of the marine flora of the archipelago, we found 151 taxa, 9 Cyanophyta, 56 Rhodophyta, 23 Phaeophyceae and 63 Chlorophyta. Of these, 34 species are new additions for the archipelago, and another 31 species are new records for Colombia, for a total of 65 new taxa. With this contribution, we have increased the seaweed biodiversity of the archipelago by 16.9%, and the marine flora of Caribbean Colombia by 5.4%. With these findings, the flora of the archipelago at present shows a composition of 42.2% of red, 16.3% of brown, and 41.4% of green algae. Although we are still far from the average floristic composition of other islands in the Caribbean, we may state that the anomaly is indeed correlated more with a lack of studies than with a different floristic assemblage.

26 - EVERYTHING IS EVERYWHERE OR MAYBE NOT: THE BIOGEOGRAPHY OF SCALED CHRYSOPHYTES ALONG THE EAST COAST OF NORTH AMERICA. Peter A. Siver & Anne-Marie Lott. Botany Department, Connecticut College, New London, CT, 06320, USA.

We described and quantified the scaled chrysophyte floras from 300 waterbodies representing nine regions and 20 subregions spread over 2,200 km from Florida to Newfoundland. Sites included ones from central Florida, coastal North Carolina, the Delmarva Peninsula, the New Jersey Pine Barrens, Connecticut, Cape Cod, coastal Maine, Nova Scotia and Newfoundland. A suite of physical and chemical parameters, including lake transparency, water color, pH, alkalinity, specific conductivity, chlorophyll content, total phosphorus and total nitrogen concentrations, chloride, sulfate and base cations, were developed for each study site, and each site was also characterized for climate variables. Scaled chrysophytes were quantified using surface sediments from the middle or deepest basin from each waterbody, and all identifications were verified using SEM. We are interested in understanding the distribution patterns along this east coast gradient, and evaluating the relative proportions of variation independently described by physical, chemical and climate related variables. The Baas-Becking ubiquity hypothesis, “everything is everywhere and the environment selects”, would predict that species the size of scaled chrysophytes would be found along the entire gradient, and if habitat variables were similar throughout the range that the flora along this gradient would also be similar. Although data is very limited, if birds and major wind events, including hurricanes, serve as successful dispersal mechanisms for scaled chrysophytes, these mechanisms should facilitate dispersal along our latitudinal gradient since this part of North America represents a major bird fly zone and the track that many tropical storms follow. We found significant differences in the scaled chrysophyte floras between all nine regions, as well as between over 80% of the subregion comparisons, confirming that these organisms indeed have distinct biogeographical patterns along the east coast of North America. Different sets of

species dominated the floras in each region, and some of the more abundant taxa had very restricted distributions. *Chrysohaerella longispina* and *Mallomonas galeiformis*, two species often found in abundance in all glaciated regions, were not found south of Connecticut. *Mallomonas wujekii* was only present, and often abundant, throughout the non-glacial regions. We next tested if these differences could be explained solely by chemical and physical features of the sites, or if other factors, including climate variables also described significant portions of the variance. When the dataset was divided into groups of waterbodies with statistically similar chemical characteristics, the floras in each group remained distinct. The pH variable was the most important factor explaining the distributional patterns, however, July temperature described the next largest portion of variability in the data set. Our results either call into question the ability of birds and wind to disperse scaled chrysophytes, indicate that these organisms have a poor transportability, or both.

27 - AN ASSESSMENT OF THE ISLAND BIOGEOGRAPHY THEORY USING A CENTURY OF FLORISTICS IN BERMUDA—IMMIGRATION AND EXTIRPATION OR SIMPLY SYSTEMATICS? Craig W. Schneider. Department of Biology, Trinity College, Hartford, CT, 06106, USA.

In over a hundred years of assessment of the marine algae of Bermuda (western Atlantic), the content and size of the known flora has changed dramatically. Some of the changes were made during decades of study of archival specimens left by early collectors, the rest by sustained diving/collecting in both inshore and deepwater habitats around the islands. Well over a hundred binomials of red, green and brown algae have been added to the list of species in Bermuda since the time of F.S. Collins and A.B. Hervey at the turn of the 20th century. Conversely, a great number of reported names in the flora have been removed, often replaced with another taxon, or at times, with more than one cryptic species, due to anatomical and molecular studies. Several species that have been found in just the past 25 years were either overlooked by early workers or have recently immigrated from distant shores. Many species from the distant past with vouched archival specimens have not been collected in the islands recently, and being large and obvious seaweeds would not be expected to have been overlooked. Have these been extirpated locally? Examples of all of these floristic changes will be illustrated, and the implications to the balance of algal species in the islands will be examined.

28 – POPULATION DYNAMICS AND BIOGEOGRAPHY OF MARINE VIRUSES IN SOUTHERN NEW ENGLAND. Marcie Marston. Department of Biology, Roger Williams University, Bristol, RI, 02809, U.S.A

Viruses infecting cyanobacteria are abundant and genetically diverse in coastal environments. Viral-induced mortality of host cells can influence the abundance and genetic diversity of cyanobacterial communities. In addition, these viruses carry numerous cyanobacteria-derived genes and may facilitate the exchange of these genes among their hosts. To assess the impact of viruses on marine *Synechococcus* communities, we have been tracking changes in the genetic diversity and relative abundance of cyanophages in Narragansett Bay, Rhode Island for ten years. The cyanophage community in this location is dynamic; however, there are predictable temporal changes in genotypic composition. In 2009, we extended our study to

include seven additional sites along the coast of Southern New England, ranging from Cape Cod Bay to Long Island Sound. Following viral isolation, PCR was used to amplify segments of the *g43* DNA polymerase gene from each viral isolate. At present, over 700 cyanophage isolates have been characterized. These isolates can be grouped into over 80 distinct DNA polymerase genotypes. Both spatial and temporal variations in community composition were observed. In addition of the DNA polymerase gene, the *psbA* gene, encoding a cyanobacteria-derived photosystem II reaction center protein, was also amplified from a subset of the isolates. While many isolates have identical DNA polymerase gene sequences, host-derived photosystem II *psbA* genes are very variable. Multiple *psbA* alleles (differing from one another by up to 10% in nucleotide sequence) were observed among isolates with the same DNA polymerase sequence. Some of this variability is due to intragenic recombination events among viruses and perhaps between viruses and their hosts. We are continuing to analyze additional isolates and also are examining the biotic and abiotic factors that may influence the composition of cyanophages at different locations.

29 - JUST GO WITH THE FLOW: PLANKTON CONNECTIVITY IN A HIGH DISPERSAL WORLD. Tatiana Rynearson, Chris Piecuch, Dayna Rignanese & Kerry Whittaker. University of Rhode Island, Graduate School of Oceanography, Coastal Institute Rm 236, Narragansett, RI, 02882, USA

Connectivity among populations can influence a species' ecology, adaptive potential, evolutionary longevity and ultimately, speciation potential. It is commonly assumed that marine phytoplankton, organisms that drift with tides and currents, have such high potentials for dispersal and gene flow that local adaptation does not occur. In this talk, I will examine this assumption using diatoms as a model organism. Diatoms are ubiquitous, unicellular, eukaryotes that generate about 40% of the organic carbon fixed annually in the sea. Although there is emerging evidence of intra-specific population differentiation on local scales (~100km), it is commonly assumed that planktonic microbes are homogeneously distributed on global scales. In this talk, I will describe how my research lab is examining if and how populations of planktonic diatoms are connected from local to global scales. I will also discuss how our results serve to generate many new hypotheses about mechanisms that regulate ecological processes such as bloom formation over space and time and evolutionary processes such as the development of reproductive isolation and eventual speciation in planktonic organisms.

POSTER PRESENTATIONS (BOARD NUMBERS IN PARENTHESES)

UNDERGRADUATE POSTERS (PRESIDENT'S AWARD)

(P1) – PHYLOGENY OF AUSTRALASIAN ENDEMIC TAXA IN THE BATRACHOSPERMALES (RHODOPHYTA) USING THE *rbcL* AND LSU GENES. Emily T. Johnston¹, Sarah A. Stewart¹, Timothy J. Entwisle² & Morgan L. Vis¹. ¹Department of Environmental and Plant Biology, Ohio University, Athens, OH 45701. ²Royal Botanic Gardens Sydney, Mrs Macquaries Road, Sydney, NSW 2000, Australia.

In previous research using the *rbcL* gene alone, the majority of the Australasian endemic taxa have grouped together within the Batrachospermales phylogeny, but with little intermediate node support. More specimens were collected from Australia, New Zealand, and New Caledonia, representing ten currently recognized endemic species as follows:

Batrachospermum antipodites, *B. bourrellyi*, *B. camplyoclonum*, *B. diatyches*, *B. discorum*, *B. kraftii*, *B. pseudogelatinosum*, *B. ranuliferum*, *B. theaquum*, *B. watsii*, and *Nothocladus nodosus*. In addition, New Zealand specimens of *B. atrum*, a cosmopolitan species, were included. Data from the large subunit or 26S rDNA (LSU; ~1350bp; nuclear) gene and the ribulose-1,5-bisphosphate carboxylase/oxygenase (*rbcL*; 1282bp; chloroplast) gene were used to augment the previously published *rbcL* sequence data. Phylogenetic analyses using maximum parsimony, maximum likelihood and Bayesian analyses were conducted for both genes separately and in combination. The tree topologies for both genes were similar. Unfortunately, the addition of LSU data did not provide additional support, especially to the intermediate nodes. Nevertheless, new insights were gained for a number of taxa. One new species added to the dataset, *B. diatyches*, did not clade with the other species of section *Setacea*, rendering that section paraphyletic. The addition of new specimens of *B. theaquum* showed it to be paraphyletic with the need for a new species to be described. Although the clade is primarily composed of Australasian endemics, two taxa from South America (*B. puiggarianum* and *Petrohvia bernabei*) and one cosmopolitan species (*B. atrum*) are present leading to interesting biogeographic questions for future exploration.

(P2) - ECOLOGICAL MONITORING OF SNOW AND SOIL OF ASHA WITH USING MICROSCOPIC ALGAE AND CYANOBACTERIA. Edrenkin Victor. Department of Botany, Bioecology and Landscape designing, Bashkir State Pedagogical University named after M.Akmullah, Ufa, Bashkortostan, Russia.

Today's global environmental crisis calls for greater use of environmental monitoring. The effectiveness of such evaluation depends on the diagnostic system chosen. Recently, great emphasis has been placed on the value of biological testing and bioindication for assessing environmental condition of ecosystems. Asha is a city in the Chelyabinsk region of Russia that is subject to heavy metal pollution from a smelting factory in the town. The aim of this study was to evaluate the toxicity of snow and soil in the city Asha testing several taxonomic groups used in biomonitoring (plants, fungi, green algae, cyanobacteria). Of the species tested, I found two species to be very effective bioindicators of heavy pollution: *Chlorella vulgaris* and *Trichormus variabilis*. A map was made of Asha showing degree of toxicity of snow and soil based on the abundance and condition of these two taxa. Comparison of toxicity of snow for the town of Asha for 2003 and 2006 showed that the snow in Ashe became less toxic over time. Soil also became less toxic over the study period 2003-2007. Comparison of toxicity of soil and snow in 2006-2007 showed that the snow was more toxic than the soil. These algae proved effective at monitoring soils in a polluted urban area.

(P3) – MORPHOLOGICAL CHARACTERISTICS OF ULVA SPECIES OCCURRING IN NARRAGANSETT BAY, RI. Ashley Heinze, Michele Guidone & Carol Thornber. Department of Biological Sciences, University of Rhode Island, Kingston, RI, 02881, U.S.A.

Macroalgal blooms are a major problem in coastal ecosystems around the world, posing a serious threat to coastal biological communities, as well as coastal commercial and recreational activities. Numerous studies have been conducted to determine the abiotic causes of macroalgal blooms, as well as the negative impacts of macroalgal blooms. However, many questions remain concerning the biodiversity of the algae in these blooms and the relative environmental impact of each species in the bloom. This is particularly true of *Ulva* blooms, because the morphological plasticity of these species makes it impossible to identify them in the field. Proper identification of these species is crucial, as some may be toxic while other more palatable species provide food for numerous fish and invertebrates. In this study, we utilized the results of recent molecular analyses of Rhode Island *Ulva* species to determine a suite of morphological characters that can be used to distinguish between the ten *Ulva* species that occur along the RI shoreline. Morphological features were determined using both microscope pictures (taken of specimens prior to herbarium preservation) and rehydrated portions of previously sequenced specimens. For each sample we examined cell shape, cell arrangement, cell size, chloroplast shape, and pyrenoid number. Consistent morphological differences were found between the three blade forming *Ulva* species (*U. 'compressa'*, *U. lactuca*, and *U. rigida*). In contrast, the morphological features of the tube forming *Ulva* species were found to overlap, making the identification of these species difficult without genetic sequencing of individual specimens.

(P4) - UNRAVELING THE PALEOLIMNOLOGY OF THE GIRAFFE PIPE KIMBERLITE MAAR LAKE USING SILICEOUS MICROFOSSILS. Andrew Barber, Anne-Marie Lott, William Karis & Peter Siver. Botany Department, Connecticut College, New London, CT, 06320, USA.

We are investigating siliceous microfossil remains from an ancient Eocene maar lake that was situated in the Giraffe Pipe kimberlite crater that existed near the Arctic Circle in the Northwest Territories, Canada. A drilled core into the crater uncovered 60 meters of lacustrine sediments deposited over 40 Ma ago. We are using siliceous microfossils, including chrysophyte scales, cysts, diatoms, testate amoebae, sponges and heliozoans to reconstruct past conditions. The maar lake existed during the Cenozoic Hot House and could serve as an important analog for better understanding future climate change. We have examined 100 sections of the core and are beginning to piece together major events concerning the paleoecology and biodiversity of Giraffe Pipe. Contrary to our initial hypothesis that the crater began as a deep maar lake and slowly infilled to become a bog, our results indicate that initially the lake was quite shallow and that this condition lasted for a significant time. These sediments are dominated with chrysophyte cysts and testate amoebae, with moderate sponge concentrations. Based on sudden appearances of massive numbers of planktonic centric diatoms, the crater apparently filled and indeed became a deep waterbody. This phase, dominated by *Aulacoseira*, covers approximately 15 meters and transitions to a phase where colonial chrysophytes eventually replace them. Over time, periphytic diatoms, most notably acidic species of *Eunotia*, *Actinella* and *Oxyneis*, become integral components of the assemblages indicating a shallowing and acidification of the waterbody. Eventually, the concentrations of testate amoebae and sponges increased, along with some acidic scaled chrysophytes, characteristic of a bog habitat. The landscape then became terrestrialized and dominated by *Metasequoia*. Massive numbers of microfossils dominate virtually the entire

core, however, the overall biodiversity of diatoms often is exceptionally low compared to modern habitats, and overwhelmed by the chrysophytes.

(P5) - DESICCATION TOLERANCE IN THREE FRESHWATER RED ALGAE (RHODOPHYTA). Alexander M. VandenBroek & Morgan L. Vis. Department of Environmental and Plant Biology, Ohio University, Athens OH 45701.

Freshwater red algae are unusual, having no desiccation tolerant propagule, like many other algae. Although they don't possess these structures, they have dispersed widely and are found in streams throughout the world. This project's goal was to evaluate various sized tufts of gametophyte thalli for three taxa to document cell viability potentially allowing for dispersal via birds or other means. Gametophytes of *Batrachospermum gelatinosum*, *B. helminthosum*, and *Tuomeya americana* were put into three different sized tufts. These tufts (five replicates each) were desiccated in an incubator for one, three, ten, and 17 days. The tufts were analyzed using the viability stain, methyl blue, to determine living fascicle cells, carpogonia, and carposporangia. Fifty fascicle cells, ten carpogonia and 50 carposporangia were counted to determine the percent living cells for the two *Batrachospermum* species. Only fascicle cells were enumerated for *Tuomeya americana* because no reproductive cells were present. After 24 hours, the two larger tuft sizes had > 40% viability for all cell types, while the smallest had <35% viability. At day ten, the smallest tuft size showed no viability for any cell type, while the larger two tufts had 5-30% viability for all cell types in the *Batrachospermum* species. For *Tuomeya* there was <1.6 % viability for fascicle cells in the largest tuft size and no viability for the smaller. None of the three taxa had viable cells after 17 days. Based on these results, we conclude that there is the possibility for vegetative and reproductive cells to be dispersed via clumps of gametophytic thalli over a short time period. In addition, we hypothesize that *Tuomeya* had lower viability than the *Batrachospermum* species due to the lack of mucilage. In turn, this lower viability may affect dispersal capabilities as *Tuomeya* has a much smaller geographic range than the *Batrachospermum* species.

(P6) - THE GIRAFFE PIPE DATABASE PROJECT: A WEB-BASED DATABASE FOR SILICEOUS MICROFOSSILS FROM FRESHWATER ARCTIC MAAR LAKES DURING THE CENOZOIC HOT HOUSE. Zoe Madden, Anne-Marie Lott & Peter Siver. Botany Department, Connecticut College, New London, CT, 06320, USA.

We are investigating the siliceous microfossil remains from ancient Paleocene and Eocene maar lakes situated in kimberlite craters near the Arctic Circle in the Northwest Territories, Canada. To date, our primary focus has been on examination of material from two cores, Giraffe Pipe and Wombat, with emplacement dates representing the Middle Eocene and Paleocene, respectively. Drilled cores from each site have yielded over 150 meters of lacustrine sediments containing exquisitely preserved microfossils. As part of this project, we plan to survey and inventory all siliceous microfossils found in these cores and make the results available through both publications and the Web. The Web portion of the project has been developed using FileMaker Pro, a versatile relational database software package. The goals of the Web component of the project will include a searchable image database for use in 1) dissemination of information and findings from the cores; 2) fostering the development of ideas on the biodiversity, paleoecology and evolution of siliceous organisms, 3) aiding in the

identification of specimens and, 4) distributing information among members of our research team. Currently, the database includes information and images of chrysophyte scales, bristles, cysts, diatoms, testate amoebae, sponges, heliozoans and several unknowns. The database currently contains over 2500 records, including thumbnail and larger-sized images of each specimen. Users can view all records or conduct custom searches in order to extract specific information. An example search could be to find all chrysophyte cysts over 10 microns in diameter with secondary structures that were uncovered from shallow portions of the waterbody. Our initial focus has been on the Giraffe Pipe core, but we will soon expand the site to include several hundred microfossil images from Wombat and link each record to specific core images.

(P7) – INSIGHTS INTO THE EVOLUTION OF MULTICELLULARITY AND THE GREENING OF THE HETEROKONT GENOME THROUGH 454 SEQUENCING OF *SCHIZOCLADIA ISCHIENSIS*. Nolon Ciemniecki¹, Dana Price², Debashish Bhattacharya², Ed Braun³, Don Kapraun⁴ & Naomi Phillips¹. ¹Biology Department Arcadia University; ²Department of Ecology, Evolution and Natural Resources, Institute of Marine and Coastal Sciences, Rutgers University; ³Zoology Department, University of Florida. ⁴University of North Carolina.

Schizocladia ischiensis is a recently defined monotypic class of marine algae and the closest sister group to the brown algae. It is part of a large, heterogeneous, primarily unicellular, group of protists unified by the biflagellate condition. It has a weakly filamentous habit and represents a transitional group to the more complex multicellular brown algae. The heterokonts are considered part of the eukaryotic supergroup Chromalveolata along the red algal plastid endosymbiotic line. The heterokonts contain an enormous amount of biodiversity, with species potentially numbering into the millions in ~14 different major lineages. Despite the diversity of the heterokonts and their fascinating evolutionary history, only a small number of heterokont genome sequences are currently available. We have initiated genome sequencing efforts of *Schizocladia* to gain insights into shift to multicellularity and endosymbiotic or lateral gene transfer events in the heterokonts. Today we report on preliminary 454 and EST sequencing efforts. Using 454 pyrophosphate technology we sequenced a 1/8 th of plate generating ~1.9 Mbp of data. Using the Celera Assembler ~64,000 reads were assembled into contigs/singletons which were subsequently blasted in BLASTX generating 5601 Celera contigs/singletons hits. Phylogenomic analyses discovered 53 red and 238 green genes representing potential lateral or endosymbiotic transfer events consistent with trends seen in the Diatom. We blasted our assembled EST data against the Celera assembly resulting in 40 hits representing ~5.7% of the genome. We used this data to estimate the total genome size of ~330 Mbp consistent with our DAPI sizing data. These data provide some of the first insights into the genome of this heterokont and a represent an important foundation for future work.

(P8) - COMPARISON OF SOUTHERN NEW ENGLAND AND LONG ISLAND COASTAL CYANOPHAGE COMMUNITIES. Noel Sme & Marcie Marston. Department of Biology and Marine Biology, Roger Williams University, Bristol, RI 02809, U.S.A.

Cyanophages are viruses that infect cyanobacteria including *Synechococcus* spp. These viruses are abundant and genetically diverse in coastal environments. Although the cyanophage

community in Rhode Island's coastal waters has been extensively studied, little is known about the cyanophages in the Atlantic waters south of Long Island. In this study, we compared the genetic diversity of viruses from Long Island with the diversity of viruses isolated in Southern New England. Seawater samples were collected from one site on Long Island (Long Beach) and ten sites in Southern New England. Viral abundance was determined using the most probable number assay with *Synechococcus* strain WH7803. Individual viral genotypes were isolated using extinction dilution enrichment. For each viral isolate, the DNA polymerase gene was amplified via PCR and then sequenced. The abundance of cyanophages in seawater samples from Long Island varied each month and ranged from 65 to 349 virus/mL. To date, six distinct DNA polymerase genotypes have been detected. Of these genotypes, four had not been detected in the previous ten years of sampling in Rhode Island. The most abundant type of virus in Rhode Island during the fall months matched one of the twelve isolates from Long Island. We are continuing to analyze additional isolates from Long Island to assess the extent to which the Long Island cyanophage community differs from cyanophage communities in Southern New England.

(P9) - TEMPORAL PATTERNS OF CYANOPHAGE DIVERSITY IN BERMUDA'S COASTAL WATERS. Samantha Taylor & Marcia Marston. Department of Biology, Roger Williams University, Bristol, RI, 02809, U.S.A

Marine viruses are one of the most abundant and genetically diverse entities in coastal waters. Cyanophages, viruses that infect cyanobacteria, are an important component of the marine food web. In this study, we characterized the cyanophage community in Bermuda's coastal water at four different time points: July 2008, August 2009, September 2009, and January 2010. At each sampling date, viruses were isolated from ten sites in Bermuda using three *Synechococcus* strains (WH7803, WH8101, and WH8012). Two different methods were used to isolate cyanophages: plaque purification and extinction dilution enrichment. PCR was used to amplify segments of the *g43* DNA polymerase gene from each viral isolate. The *psbA* gene, encoding a cyanobacteria-derived photosystem II reaction center protein, was also amplified from a subset of the isolates. Currently, over 250 viral isolates have been characterized from Bermuda and these belong to 29 distinct *g43* genotypes. Multiple isolates with the same DNA polymerase genotype were found at different sites and in samples collected in different years. The number of different *g43* genotypes detected at each time point ranged from 8 to 16 and over 50% of the *g43* genotypes detected at one sampling time matched genotypes found in Bermuda samples from other time points. In contrast, only one of the 29 Bermuda DNA polymerase genotypes has ever been detected in Rhode Island waters in 10 years of monthly sampling. Our preliminary results suggest that there are temporal variations in Bermuda cyanophage communities, both in the abundance of cyanophages and in the genotypic composition of the communities. These temporal patterns resemble the seasonal patterns that have been observed in Rhode Island coastal waters. Further characterization of Bermuda cyanophage communities and those found elsewhere will help to establish if global patterns exist.

(P10) - QUEST FOR ANTIBIOTICS PRODUCED BY AN ARCTIC CYANOBACTERIUM. Jack Tuchman¹, Jocelyn Nadeau² & Ray Kepner¹. Departments of ¹Biology, and ²Chemistry, Biochemistry & Physics, Marist College, Poughkeepsie, NY, 12601, U.S.A.

The public health threat posed by antibiotic resistant bacteria is widely recognized. The search for, and development of, new and effective antimicrobials is a high priority. We have begun a search for antibiotics potentially produced by a cyanobacterium, tentatively identified by morphology as *Leptolyngbya sp.*, isolated from an extreme polar environment. A methanolic extract of the cyanobacterium was separated by thin layer chromatography (TLC) and extracts from four individual bands were assayed for activity against four species of bacteria known to be related to potential pathogens (*i.e.*, *Enterococcus faecalis*, *Escherichia coli*, *Klebsiella pneumoniae* and *Salmonella cholerae-suis*) using the Kirby-Bauer disk-diffusion technique. One of the four extracts showed a very slight inhibitory action against *K. pneumoniae*, while all four extracts inhibited growth of *E. faecalis* to varying degrees. A future assay is planned utilizing extract fractions at higher concentration and also testing against additional bacterial species.

GRADUATE STUDENT POSTERS (TRAINOR AWARD)

(P11) - PHYLOGENETIC PLACEMENT OF THE MICROCHAETACEAE (CYANOBACTERIA). Melissa A. Vaccarino, Emily G. Tillmaand, Michael P. Martin & Jeffrey R. Johansen Department of Biology, John Carroll University, 20700 North Park Blvd University Heights, OH, 44118

The heterocytous cyanobacteria which demonstrate false branching were long considered to be in one family, the Scytonemataceae. In revisions of the Cyanobacteria, Komárek and Anagnostidis separated the false-branching Nostocales into two families based upon polarity of the filaments. The Scytonemataceae is isopolar, while the Microchaetaceae is heteropolar. This proposed dichotomy has not been tested with molecular data because of the paucity of strains available. We sequenced the 16S rRNA gene together with the 16S-23S ITS region for 12 strains. A phylogeny based on sequence data from 285 OTU's was constructed, and secondary structure of conserved domains was determined. Both molecular approaches demonstrated that Scytonemataceae and Microchaetaceae belong to separate clades, and should be recognized at an equal hierarchy as other major heterocystous clades. *Tolypothrix* is the most problematic taxon, as species of this genus are dispersed among Microchaetacean genera. *Scytonema* forms a paraphyletic grade at the base of the Nostocales.

(P12) — CYANOBACTERIA AND SOIL ALGAE OF THE BASHKIR STATE NATURAL RESERVE (SOUTH URALS, RUSSIA). Gulshat Bakieva, Department of Botany, Bioecology and Landscape Design, Bashkir State Pedagogical University named after M.Akmullah, Ufa, Bashkortostan, Russia.

The aim of the present work is investigating the species diversity, ecological structure and distribution of cyanobacteria and soil algae of the Bashkir State Natural Reserve (BSNR). BSNR is situated in the Burzyan District of the Republic of Bashkortostan, on the slopes of the Southern Urals. In June-October 2007-2009, samples of soils were collected in different forest ecosystem plots. The taxonomic composition includes a total of 95 species and infraspecific taxa of cyanobacteria and algae from 5 divisions: Chlorophyta (with Streptophyta) - 36 taxa, Bacillariophyta - 33 taxa, Cyanobacteria - 22 taxa, Xanthophyta - 3 taxa, Eustigmatophyta - 1

taxon. Algal communities of all investigated places have low to moderate similarity of species structure (from 21 % up to 76 %). The samples fall into three clusters in cluster analysis based on Sorenson's Similarity Index.

(P13) - CAN ALGAE SAVE OUR SALT MARSHES? IMPACTS OF MACROALGAL BLOOMS ON SALT MARSH COMMUNITY STRUCTURE. Christine Newton & Carol Thornber. Department of Biology, University of Rhode Island, Kingston, RI, 02881, USA.

Despite excessive growth of macroalgae in estuarine systems, relatively little research has been conducted on the increased algal biomass that drifts into salt marshes and accumulates on tidal flats. Many opportunistic algal species store excess nitrogen for future growth and, upon decomposition, release these nutrients. Since lower marsh plants can be nitrogen limited, algal decomposition has the potential to significantly alter marsh communities by pulsing excess nutrients into the system, resulting in increased growth of *Spartina alterniflora* as well as impacts on higher trophic levels. We conducted monthly surveys in nine fringing salt marshes around Narragansett Bay, RI, documenting the species composition and biomass of macroalgal blooms in these habitats. We also conducted *in situ* cage experiments to determine the bottom-up impacts from blooms on the dominant salt marsh plant (*S. alterniflora*) and herbivores. Neither herbivore densities nor the growth rate of *S. alterniflora* were significantly affected by algal biomass. Additionally, the organic content of *S. alterniflora* was not significantly different in cages that received and those that did not receive algal additions, suggesting no short-term community impacts from increased macroalgal biomass. Future research will explore the possibility that uptake rates of *S. alterniflora* rhizome mats may delay the effects of nutrient additions until subsequent growing seasons. The possibility that most of the excess nutrients from the decomposition of macroalgae are removed from the system during tidal cycles will also be explored.

(P14) - ESTABLISHING SPECIES LIMITS AND PHYLOGENETIC RELATIONSHIPS FOR CANADIAN RHODOMELACEAE USING MOLECULAR TOOLS. Amanda Savoie & Gary W. Saunders. Centre for Environmental and Molecular Algal Research, Department of Biology, University of New Brunswick, Fredericton, NB E3B 5A3, Canada.

The identification and classification of red algae (Rhodophyta) can be a very difficult task due to their phenotypic plasticity, convergent evolution and simple morphology. DNA barcoding, however, has been shown to discriminate successfully among species of red algae and thus can be used to assign specimens, as well as cryptic life stages, to known species. This tool is thus a highly efficient way to resolve the difficulties in identifying and studying red algae. The red algal family Rhodomelaceae is currently the largest with 927 species recognized worldwide. The extraordinary diversity in vegetative structure and high number of species makes the Rhodomelaceae an especially difficult family to work with taxonomically. Despite considerable taxonomic study, there remain a number of uncertainties with regards to species diversity and respective biogeography in the Canadian flora. This study will investigate the species diversity of the Rhodomelaceae in Canada using an integrative taxonomic approach. In addition, phylogenetic relationships will be determined for Canadian species within a broader familial context using COI-5P in combination with other genes such as the *LSU*, *rbcl*, etc. To date, we have focused mainly on the genus *Polysiphonia*. We have identified 25 unique

genetic species groups for *Polysiphonia* (including members of the genus *Neosiphonia*) through preliminary barcode data from Canada and the northern U.S., however, there are only 18 species recognized. These results suggest that there is hidden species diversity within the genus *Polysiphonia* in Canada.

(P15) - DREW'S *ACROCHAETIUM PORPHYRAE*: A DIMINUTIVE ACROCHAETE BUT NOT AN *ACROCHAETIUM*, WITH DESCRIPTION AS *RHODODREWIA PORPHYRAE* GEN. NOV. (ACROCHAETIALES). Susan L. Clayden & Gary W. Saunders. Biology, University of New Brunswick, Fredericton, NB E3B 5A3, Canada.

An outcome of a floristic survey of the diminutive and epi/endobiontic species of *Acrochaetium* along Canada's coast was discovery of more than one Pacific acrochaete associated with host *Porphyra*. Molecular analysis of the barcode region of the cytochrome oxidase subunit I gene (COI-5P) uncovered a divergent sequence from *Porphyra* collections consistent in morphological and anatomical features with *Acrochaetium porphyrae* Drew. In phylogenetic analyses of COI-5P, LSU (large subunit ribosomal) and a combined alignment this taxon did not group with other species of *Acrochaetium* or with other genera of the order. This molecular divergence was paired with substantial anatomical variation in cell shape, from thin elliptical to thicker, more nearly isodiametric cells, commonly tapering at cell ends, and length. Some irregular cells and associations of cells defied identification as vegetative or reproductive in development. Internal structures (typically 1-3) visible in most cells and 'pyrenoid-like', require ultrastructural study to characterize them. *Rhododrewia* is currently monospecific and its relation to and among other genera in the Acrochaetiales, including *Grania* (also monospecific), *Rhodochorton* and *Audouinella* (both species poor genera) and *Acrochaetium* (species rich), remain largely unresolved and requires further phylogenetic investigation.

(P16) - Karina Osorio-Santos & Jeffrey R. Johansen. CYANOBACTERIAL FLORA FROM SOIL OF THE ATACAMA DESERT, CHILE. Department of Biology, John Carroll University, University Heights, OH, 44118, USA.

The Atacama Desert, Chile is considered the driest desert on earth, although it has an unusually temperate climate due to the moderating influence of the Humboldt Current. We report preliminary results of a floristic survey of the cyanobacteria of the soils of the Atacama Desert collected from a 1000 km north-south transect from La Serena to Iquique. Soil samples were collected in May-June, 2009. Cyanobacteria were isolated into culture from enrichment cultures of the soils, characterized in light microscope, and photographed. Common taxa include *Leptolyngbya* cf. *hansgirgiana*, *L. foveolarum*, *L. voronichiniana*, *Nostoc commune*, *N. punctiforme*, *N. verrucosum*, *N. sphaericum*, *Tolypothrix boutellei*, *Microcoleus vaginatus*, *M. steenstrupii*, *Pseudanabaena* sp., *Chroococciopsis* sp., and *Trichocoleus* sp. The most frequently encountered taxa are *Leptolyngbya* cf. *hansgirgiana*, *L. foveolarum*, *Nostoc commune*, *N. punctiforme* and *Microcoleus steenstrupii*. While these taxa have been found in more mesic desert soils, it was interesting to note that the dominance pattern is different. *Microcoleus vaginatus* is typically the dominant cyanobacterial taxon in North American desert soils, but it was not dominant in our samples. The near-absence of *Scytonema* (we had only one isolate from 88 samples) was also very unusual.

(P17) - IDENTIFICATION OF CRYPTIC SPECIES IN THE GENUS *BOSSIELLA* (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 E3B 5A3, 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 *Bossiella* 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 taxa in the genus *Bossiella* in Canada, however my preliminary results suggest 17 unique genetic groups. This finding indicates that there are cryptic species present in this genus. My future research will use this molecular data in combination with a rigorous morphological examination to elucidate species diversity in this taxonomically challenging algal group.

(P18) - USING MACROALGAE TO TRACK ENVIRONMENTAL CHANGES IN THE GREAT BAY ESTUARINE SYSTEM. Jeremy C Nettleton, Christopher D Neefus, Arthur C Mathieson & Larry G Harris. University of New Hampshire, Department of Biological Sciences, G28 Spaulding Life Science Center, 38 College Road Durham, NH 03824, USA

Monitoring macroalgae populations can be an effective means of detecting long term water quality changes in estuarine systems. New Hampshire's Great Bay National Estuarine Research Reserve has identified the need to monitor water quality parameters through the use of indicator organisms. To investigate the environmental status of the system, this study aimed to: assess the abundance and distribution of macrophytes, particularly *Gracilaria* and *Ulva* species, relative to major patterns of eutrophication within this system; compare historical (1970s-1990s) and current biomass/percent cover measurements for algal populations at several sites; compare the levels of nitrogen and phosphorus in *Ulva* and *Gracilaria* tissues to those in the surrounding water; evaluate current water quality measurements for each study site. Compared with historical records, algal population data gathered in years one and two showed significant increases in biomass and cover by *Ulva* and *Gracilaria* species at several sites. Cover by *Ulva* species, at seasonal maxima, was over 90 times the value recorded in the 1970s at Lubberland Creek, and exceeded 50% at all sites in the upper estuary. *Gracilaria* cover was greater than 25% at Depot Road in the upper estuary, whereas historical maxima for the area reached only 1%. Sequencing of ITS2, *rbcL* and CO1 revealed the presence of previously undetected *Ulva* and *Gracilaria* species, including *Gracilaria vermiculophylla* (Ohmi) Papenfuss, an invasive species of Asian origin. Molecular screening revealed that *G. vermiculophylla* has exceeded *G. tikvahiae* as the dominant *Gracilaria* species in Great Bay, and examination of historical voucher specimens suggests that *G. vermiculophylla* was recently introduced.

(P19) - THE EFFECTS OF HABITAT AVAILABILITY ON TRAIT-MEDIATED INDIRECT INTERACTIONS IN A KELP FOREST FOOD CHAIN. Lindsay A. Green¹, Salvatore J. Genovese² & Geoffrey C. Trussell². ¹ Department of Biological Sciences, University of New Hampshire, Durham, NH 03824, U.S.A. ²Marine Science Center, Northeastern University, Nahant, MA, 01908, U.S.A..

Classic population ecology perspectives have emphasized the importance of predation on driving trophic cascade interactions [density-mediated interaction (DMIs)] while evolutionary ecological perspectives focus on trait-mediated interactions (TMIs). TMIs involve a change in prey traits such as behavior, development, and growth in response to predator cue and can have an effect on a prey's resource by reducing foraging [trait-mediated indirect interactions (TMIs)]. Growing evidence has suggested that TMIs may be more important than density-mediated indirect interactions (DMIs). In addition, studies have shown that the effects of TMIs can vary depending on habitat type and domain. Therefore, habitat availability may be an important factor affecting TMIs. A laboratory mesocosm experiment on the tri-trophic food chain consisting of the predatory California spiny lobster, *Panulirus interruptus*, the herbivorous purple sea urchin, *Strongylocentrotus purpuratus*, and the giant forest-forming kelp, *Macrocystis pyrifera*, was performed over a period of eleven days on Catalina Island, CA. Habitat availability and predator cue were manipulated in a replicated fully orthogonal design. The results suggest that both predator cue and habitat availability have a significant effect on the consumption of kelp by purple sea urchins although the effects were additive. This study provides further evidence supporting the effects of trait-mediated indirect interactions in kelp forest communities. Furthermore, these results suggest that habitat availability plays an important role in the trade-off decisions that consumers make between foraging and mortality and may also affect trophic cascades, food web interactions, and community dynamics.

(P20) - RECOVERY OF THE PHOTOSYNTHETIC MECHANISM UNDER OXIDATIVE STRESS INDUCED BY IRON DEFICIENCY. Hannah Traggis & Leland Jahnke. College of Life Sciences and Agriculture, University of New Hampshire Department of Biological Sciences, Spaulding Life Sciences Building, Room 117 46 College Road Durham, NH 03824

In the current reality of global climate change one of the biggest challenges we, as scientists, face is understanding both the physical and biological processes related to the earth's carbon cycling. Oceanic primary productivity, accounting for nearly 50% of the photosynthetic CO₂ drawdown, is arguably one of the most important pieces of this puzzle. It has been determined that iron deficiency, in otherwise nutrient rich waters, leads to unexpectedly low chlorophyll concentrations (areas referred to as 'HNLC', i.e. High Nutrient, Low Chlorophyll), thus being one of the major limitations of photosynthesis in the oceans. We have endeavored to investigate the physiological effects of iron limitation on the photosynthetic and photo-protective apparatus of *Dunaliella tertiolecta*. *D. tertiolecta* cultured in 100nM Fe growth medium, exhibit reductions in growth and photosynthetic rates accompanied by reductions in FV/FM ratios compared to those cultured in Iron-replete medium (10μM Fe). Preliminary investigation of the iron-dependent antioxidant enzyme, ascorbate peroxidase, demonstrates a rate reduction. Future investigations will include further investigation of various iron-

dependent enzymatic rates and their genetic expression, as well as low molecular weight antioxidant molecules such as α -tocopherol.

(P21) - PORPHYRA NJORDII SP. NOV. (BANGIALES, RHODOPHYTA) AND FURTHER INSIGHTS INTO THE *P. LINEARIS* COMPLEX IN THE NORTH ATLANTIC. Agnes Mols Mortensen¹, Christopher D. Neefus¹ & Juliet Brodie². ¹Department of Biological Sciences, University of New Hampshire, Durham, NH 03824, USA. ²Natural History Museum, Department of Botany, London, SW7 5BD, United Kingdom.

Comparing floras from different areas requires correct species identification, and this has been a central problem in understanding the distribution of *Porphyra* species. Detailed studies of *Porphyra* floras have been carried out in several areas of the world and shifting to a molecular approach *Porphyra* research has moved into an era of global investigation. By using molecular tools it has become clear that multiple species have been confused with *P. linearis* Greville both in herbaria and culture collections, and sequences based on specimens misidentified as *P. linearis* have been published on GenBank. An *rbcL* sequence for an unidentified species collected from the Faroe Islands and Iceland matched a sequence from GenBank identified as *P. linearis* that came from a culture specimen collected at Sandy Cove, Nova Scotia. However, *rbcL* sequences from species identified as *P. linearis* from the Faroes and Iceland did not match the specimen from Nova Scotia but matched *P. linearis* topotype material from Sidmouth, England. Based on these observations, the *P. 'linearis'* sequence from the culture collection is not *P. linearis* sensu stricto, and represents a new species. Annotations of *Porphyra* collections from Nova Scotia show that researchers were already aware of an 'abnormal' type of *P. 'linearis'* in the 1960s, and detailed publications on the life history and ecology of *P. linearis* in Nova Scotia, indicate that more than one species were involved in this research. The aim of this work is to describe *Porphyra njordii* sp. nov., using *rbcL* sequences, gross morphology and available ecological and seasonal information, and to make comparisons with the 'abnormal' *P. 'linearis'* from Nova Scotia and *P. linearis* sensu stricto.

(P22) — PHYTOPLANKTON AND NUTRIENT DYNAMICS FOLLOWING A SPRING FLOOD EVENT IN A BACKWATER LAKE OF THE UPPER MISSISSIPPI RIVER. Jillian Decker¹, Kam Truhn¹ & John Wehr¹. ¹Louis Calder Center – Biological Field Station, Fordham University, Armonk, NY 10504, U.S.A.

Phosphorus has long been recognized to be the limiting nutrient of phytoplankton production in most freshwater systems, especially lakes. Less is known about limitation in large river ecosystems, given the dynamic spatial and temporal variations that occur especially in systems with intact floodplain networks. In this study, we quantified phytoplankton dynamics on the receding end of a spring flood event in a backwater of the Upper Mississippi River. We identified nutrient limitation using three linked, simultaneous approaches: (1) conducting nutrient bioassay experiments in which N, P, N+ P, Fe, and Si (4x ambient) were added to 4 L mesocosms, (2) measuring net nutrient uptake (NO_3^- , NH_4^+ , and SRP), and (3) characterizing shifts in algal species composition associated with changes in the nutrient environment. On the falling limb of the flood-cycle in this habitat, initial N concentrations were greater than the annual average for this site. Initial phytoplankton composition was diverse, although small

single-celled (*Chlamydomonas* spp. and *Chlorella*-like spp.) and colonial (*Tetrastrum glabrum*/*Gonium sociale*-like) chlorophytes had the greatest initial cell density. After a 4 day incubation period, biomass (as Chl-*a*) in the bioassays was greatest in treatments where P and N+P were added, suggesting P limitation since biomass in the N+P treatment was not greater than that in the P-added treatment. Net uptake of NO₃⁻ on day 4 was greatest in the P-added treatment. The combination of data on net phytoplankton assemblage nutrient uptake, phytoplankton composition, and biomass change under different nutrient regimes, will be used to explain the community and ecosystem dynamics associated with nutrient limitation following a spring flood in floodplain-river systems.

(P23) — A SYSTEMATIC REVISION OF *TOLYPELLA* A. BR.: PRELIMINARY INVESTIGATIONS. William Pérez^{1,2} & Kenneth G. Karol¹. ¹Lewis B. & Dorothy Cullman Program for Molecular Systematics Studies, New York Botanical Garden, Bronx, NY, 10458, U.S.A.; ²Plant Sciences Ph.D. Subprogram in Biology, City University of New York, New York, NY, 10016, U.S.A.

The Characeae contain two tribes with six genera: the tribe Chareae, which includes *Chara*, *Lamprothamnium*, *Lychnothamnus* and *Nitellopsis*; and the tribe Nitelleae, which includes *Tolypella* and *Nitella*. The Characeae exhibit a broad range of morphological diversity and in the most recent and comprehensive taxonomic treatment (Wood & Imahori, 1965) more than 400 species were reduced to 81 broadly defined species, including 16 *Tolypella* species subsumed under 2 species (*T. nidifica* and *T. intricata*) representing two sections, *Tolypella* and *Rothia*. Wood & Imahori (1965) further suggested that *Tolypella* may be a derived species of *Nitella*. Currently, there are no comprehensive molecular phylogenetic studies of *Tolypella* that address relationships within the genus or to the rest of Characeae. Instead, phylogenetic studies of Characeae and closely related taxa have sampled between one and three *Tolypella* species to serve as placeholders or outgroup taxa. In a preliminary investigation into species diversity and evolution in *Tolypella*, chloroplast DNA sequence data for *rbcL* and *atpB* and nuclear DNA sequence data for enolase were assembled for several field collected and herbarium specimens. Phylogenetic analyses of plastid sequence data support monophyly of *Tolypella* and the sections within but a relationship to the rest of Characeae was unspecified. Nuclear sequence data for two species supports monophyly of the genus and suggests a utility for enolase in phylogenetic studies.

(P24) - DIATOM COMMUNITY COMPOSITION AND BIOFILM ENZYME ACTIVITY FOR WATER QUALITY ASSESSMENT OF ACID MINE REMEDIATED STREAMS. Justin R Pool & Morgan L Vis. Department of Environmental and Plant Biology, Ohio University, Athens, OH 45701 USA.

Coal is the primary energy source for the United States and is obtained through either surface or underground mining. Prior to the 1970s, few regulations were in place regarding the operation and subsequent reclamation of mines, which would prevent acid mine drainage (AMD) from leaching into streams. AMD is characterized by low pH, sulfate-rich water, and high levels of dissolved metal cations. Southeast Ohio has many mines that were abandoned prior to the 1970s regulations; thus many waterways are impacted by AMD. Two alkaline doser remediation projects, Monday Creek and Hewitt Fork, were assessed for effectiveness by

examining the diatom community, biofilm extra-cellular enzyme activity, and water chemistry. Diatoms were sampled at 9 locations on Hewitt Fork and 14 locations on Monday Creek, beginning above the remediation site and continuing downstream for several kilometers. Biofilm enzyme activities, water chemistry, and total chlorophyll a were measured at 6 locations along each stream on three dates. Based on the diatom community composition, water quality improved greatly in Hewitt Fork 16.5 kilometers downstream from the remediation site, while Monday Creek remained fairly impacted over most of the length sampled (41.5 km). Total chlorophyll a increased in Hewitt Fork along the entire stream length sampled. In Monday Creek, however, total chlorophyll a tended to increase from the remediation project to the midstream locations, but then decreased in the locations furthest downstream. Monday Creek has multiple sources of AMD and only one is being treated by the remediation project; thus the effectiveness of the remediation upstream is counteracted by the other inputs. Hewitt Fork does not have as many other sources of AMD downstream as Monday Creek does, thus the remediation project seems to be effective, but yet far downstream of the remediation project.

(P25) - BIOTIC INFLUENCES ON EPIPHYTE AND HERBIVORE RECRUITMENT IN A MARINE SUBTIDAL SYSTEM Nicole E. Rohr¹, Carol S. Thornber¹ & Emily Jones^{1,2}

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Marine assemblages are influenced by the rate and timing of species settlement and recruitment. Both abiotic factors and biotic interactions can impact recruitment rates of marine species in a variety of systems. However, the impacts of species which recruit at the same time upon each other are less well understood. We investigated the relationship between the recruitment of *Lacuna vincta*, a small (< 6 mm shell length) marine snail, and two species of algal epiphytes, the native *Ceramium virgatum* and the invasive *Neosiphonia harveyi*, in the shallow subtidal zone of Narragansett Bay, Rhode Island. All three species exhibit peak recruitment densities during two summer months. We found that the presence of algal epiphytes facilitates the recruitment rate of *L. vincta*, regardless of the epiphyte species composition. We also found a positive relationship between the number of *L. vincta* present and epiphyte recruitment, which is disproportionately driven by higher recruitment of *N. harveyi* than *C. virgatum*. Understanding recruitment dynamics and interactions is vital to effectively mitigate the effects of, and adaptations to, ecological changes due to the establishment of non-native species.

(P26) - CHECKLIST OF THE PACIFIC MARINE MACROALGAE OF CENTRAL AMERICA. Cindy Fernández-García^{1,2}, Rafael Riosmena-Rodríguez¹, Brian Wysor³, Olga Lidia Tejada⁴ & Jorge Cortés². ¹Programa de Investigación en Botánica Marina, Departamento de Biología Marina, Universidad Autónoma de Baja California Sur, México; ²Centro de Investigación en Ciencias del Mar y Limnología (CIMAR) and Escuela de Biología, Universidad de Costa Rica, San Pedro, 11501-2060 San José, Costa Rica; ³Roger Williams University, Rhode Island; ⁴Laboratorio de Ficología, Escuela de Biología, Universidad de El Salvador, El Salvador

Our present knowledge of marine macroalgae diversity for the Pacific coast of Central America (PCA) is limited due to a short history of investigations (ca. 100 years) and few algal specialists throughout a large geographical area. While recent checklists have emerged for other regions of the Eastern Pacific, there have been virtually no attempts to inventory macroalgae diversity for the PCA. The checklist of the marine macroalgae of the PCA was developed based on published scientific literature and unpublished records in student theses. A total of 493 species records are documented of which 410 are regarded as current valid names of marine macroalgae. The red algae (Rhodophyta) exhibit the highest diversity (275 species), followed by green algae (Chlorophyta: 85 species) and brown algae (Phaeophyceae: 50 species). The country with the greatest diversity of marine macroalgae is Costa Rica with 231 species, followed by Panama with 182, El Salvador with 153, Nicaragua with 26, and Guatemala with 15. At present there are no published records for the Pacific coast of Honduras. Variation in species richness throughout PCA is likely due to unbalanced research efforts, and differences in geomorphology and habitat heterogeneity of each country's coastal-marine zone.

(P27) - DOES THE DISTRIBUTION OF MACROSCOPIC KELP (*NEREOCYSTIS LUETKEANA*, *LAMINARIA EPHEMERA*) SPOROPHYTES REFLECT THE DISTRIBUTION OF MICROSCOPIC GAMETOPHYTES? Caroline Longtin¹ & Gary Saunders¹. ¹Centre for Environmental & Molecular Algal Research, Department of Biology, University of New Brunswick, Fredericton, NB, E3B 5A3, Canada.

North Pacific kelp forests are highly productive, and provide food and habitat for numerous organisms, which in turn promotes increased species diversity. However, kelp forests are threatened by climate change, overfishing and increased sea urchin presence. In order to conserve kelp forests we must develop a better understanding of their biodiversity and ecology. Whereas many studies have focused on the diversity and ecology of kelp sporophytes (macroscopic stage), few have considered the cryptic gametophyte (microscopic stage) due to sampling difficulty in the field. This lack of a cohesive understanding of kelp species in all phases impacts negatively on any attempts to manage and conserve these species and the forests that they support. It has been hypothesized that gametophytes act similarly to terrestrial seedbanks by enhancing recruitment, persistence and recovery following disturbance. Gametophytes may extend across a greater range than sporophytes and remain dormant until environmental conditions become favorable or competition is lessened. I will focus my research on the distribution of the canopy forming species *Nereocystis luetkeana* and the rare intertidal species *Laminaria ephemera*. The designation of *L. ephemera* as a rare species is based solely on the distribution of its sporophyte form. I will sample *N. luetkeana* beds and urchin barrens in Barkley Sound, BC by SCUBA and perform species-specific PCR on samples to determine whether or not gametophytes are present. I will also perform intertidal sampling of *L. ephemera* by collecting rock scrapings from intertidal sites for species-specific PCR to determine whether or not *L. ephemera* is more widely distributed in its gametophyte form than the sporophyte form. These observations are crucial for proper conservation practices. If seedbank analogues exist then kelp forest regeneration may be possible following urchin removal or regulation.

Contributed Posters

(P28) - *CHONDRUS CRISPUS* STOCKING DENSITY AFFECTS NUTRIENT REMOVAL EFFICIENCY IN HIGH WATER FLUX EFFLUENT FROM A LAND-BASED ATLANTIC HALIBUT FARM. Jang K. Kim¹, Balakrishnan Prithiviraj¹, David J. Garbary² & Jim Duston¹. ¹Department of Plant & Animal Sciences, Nova Scotia Agricultural College, Truro, NS, B2N 5E3, Canada; ²Department of Biology, St. Francis Xavier University, Antigonish, NS, B2G 1C0, Canada

Stocking density and water flux are important factors affecting the growth and nutrient uptake of seaweeds. Most land based fish aquaculture farms maintain the water flux at higher rates to maintain good water quality in the fish tanks. Therefore, it is critical to determine optimal stocking density of seaweed at a fast water flux to maximize nutrient removal and plant growth in integrated land-based aquaculture systems. To determine an optimal stocking density, *Chondrus crispus* was reared at 0.2, 2, 4, 6, 10 and 20 kg m⁻², at 6 ± 2 °C in 50 L tanks. Light intensity and photoperiod were 140 ± 10 μmol photons m⁻²s⁻¹ and 16:8 L:D, respectively. The growth rate was the highest (4 % d⁻¹) at the lowest stocking density, 0.2 kg m⁻² and decreased as the stocking density increased. The growth rate at the highest stocking density, 20 kg m⁻², was only 0.31 % d⁻¹. However, the productivity was significantly higher at 2 kg m⁻² or higher densities than at the lowest density. Approximately, 420 mmol d⁻¹ of nitrogen and 50 mmol d⁻¹ of phosphorus were introduced to each 50 L seaweed tank, and 26 and 29 % of total nitrogen and phosphorus, respectively, were removed by 2.5 kg (10 kg m⁻²) of *C. crispus*. Higher stocking density may require a higher light intensity for optimum growth. Therefore, higher light intensity (e.g. > 150 μmol photons m⁻²s⁻¹) may improve the growth rate of *C. crispus* which subsequently can increase the nutrient removal in fish effluent at a high water flux condition.

(P29) - DESICCATION OF THE GENUS *PORPHYRA* CAUSE RELEASE OF NITROGEN. Jang K. Kim^{1,2}, George P Kraemer³ & Charles Yarish¹. ¹Departments of Ecology & Evolutionary Biology and Marine Sciences, University of Connecticut, CT, 06901, U.S.A.; ²Dept. Plant & Animal Sciences, Nova Scotia Agricultural College, Truro, NS, B2N 5E3, Canada; ³Environmental Studies Program, Purchase College, Purchase, NY 10577, U.S.A.

We examined an upper littoral cosmopolitan species, *Porphyra umbilicalis* (Linnaeus) Kützinger, to investigate the desiccation-induced nitrogen (N) loss from this seaweed. Both tissue N and soluble protein contents decreased during desiccation, and were positively correlated. With no evidence that growth of *Porphyra* simply diluted the tissue N concentration, we conclude that tissue N was lost during desiccation. Our results support the hypothesis that desiccation-induced N release occurs when N-containing organic compounds are catabolized. Glutamine synthetase (GS) activity was significantly affected by emersion but, interestingly, desiccation enhanced GS activity in *Porphyra*. The high level of GS activity when *P. umbilicalis* experienced periodic desiccation stress suggests the possible increase of photorespiration during desiccation. Tissue δ¹⁵N values did not change during desiccation. The constant N isotopic fractionation suggests that N release from *Porphyra* during desiccation does not occur by denitrification, but may have occurred via other process including photorespiration. As a consequence, it is likely that eulittoral *Porphyra* emits N into the

atmosphere during emersion, suggesting a novel role of eulittoral seaweeds such as *Porphyra* in the global N cycle.

(P30) - IDENTIFICATION OF DIATOMS FROM THE PEAT BOG AT POUTWATER POND SUGGESTS pH CHANGES OCCURRED DURING THE HOLOCENE. Benjamin Parmentier, Adrienne P. Smyth & Peter M. Bradley. Department of Biology, Worcester State College, 486 Chandler Street, Worcester MA 01602-2597.

Peatlands provide a record of environmental history through centuries of preserved sediments containing microfossils such as diatom frustules, pollen grains and sponge spicules. A 5m core of peat was collected from Poutwater Pond in Holden, Massachusetts. This location is a National Natural Landmark and Massachusetts' first Nature Preserve. The basal date was 8,500 years before present as shown by radiocarbon dating. The contents of the core were examined with a scanning electron microscope at nine different depths that represent different ages about 1,000 years apart. A large number of pollen grains and 250 diatoms were counted and identified for each time point. The diatom data are presented here as abundance diagrams and the changes in the assemblage suggest fluctuations in pH and climate at the site during the last 8,500 years. *Cyclotella* species that are characteristic of an open pond environment were later replaced with *Tabellaria* and *Eunotia* species as the acid bog conditions developed. Other fluctuations in climate and acidity during the Holocene are also suggested by the diatom data. These include a progression from circumneutral to more acid conditions from 8,500 to 7,000 years before present, followed by a dryer mid-Holocene period with little change in acidity and then increased acidification in the late-Holocene as conditions also became wetter and cooler. The results correlate well with other studies done at other locations in the Northeastern United States.

(P31) - THE DECLINE OF *LAMINARIA DIGITATA* IN THE SOUTHWESTERN GULF OF MAINE IN RELATION TO SUMMER WATER TEMPERATURES. Elizabeth V. Garlo & Paul Geoghegan, Normandeau Associates Inc., Bedford, NH.

Temperature is an important factor in determining the distribution and reproductive success of seaweeds. In the western North Atlantic, the southern boundary of *Laminaria digitata* corresponds with the 19 °C surface isotherm that represents the August mean temperature and it occurs in the Long Island Sound region. During two exceptionally warm summers when water temperatures were >17 °C and up to 19 °C, field populations of *L. digitata* from the North Sea had reduce numbers of sori and did not release meiospores. Therefore water temperatures which range between 17 and 19° C may represent critical temperatures for reproductive success. Seasonal counts of *L. digitata* holdfasts as well as other macrobenthic species have been made off the New Hampshire coast since 1978 at two shallow subtidal stations (5-6 m depth) and two mid-depth subtidal stations (9-12 m depth). The density of *L. digitata* declined more than 50% during the time series. Other species such as *Agarum clathratum* at mid-depth stations and *Chondrus crispus* at shallow stations have remained stable. A positive warming trend in annual mean summer surface temperature occurred during the study period. The number of days when the surface water temperature was ≥ 18 °C increased significantly during the study period, and may be contributing to the decrease in *L. digitata*. Other factors that may also contribute to the decline of *L digitata* in the region

include an increase of the encrusting bryozoan, *Membranipora membranacea*, an increase in sea urchin abundance to a maximum of 8/sq. meter from 1992-1994, wave action from storms and a decline in water quality.

(P32) - FUCOID FLORA OF THE ROCKY INTERTIDAL OF THE CANADIAN MARITIMES: IMPLICATIONS FOR THE FUTURE WITH RAPID CLIMATE CHANGE. Raul A. Ugarte, James S. Craigie & Alan T. Critchley. Acadian Seaplants Limited, 30 Brown Avenue, Dartmouth, B3B1X8, Nova Scotia, Canada.

Few reports on the effects of current climate change on macroalgae have been found in the literature, but these describe significant changes in distribution and abundance of algae. If such changes are now being detected when the global climate has warmed by an estimated average of 0.65°C in the last half-century, the effects on species and ecosystems will be obviously more drastic in response to a change in temperature as high as 6 C° by 2100 as predicted by the IPCC (2007). Furoid species, particularly the brown seaweed *Ascophyllum nodosum* (rockweed), are key habitat formers and energy producers, and their responses to climate change can have significant population, community and even ecosystem consequences in the Canadian Maritime Provinces. From the economic point of view, these changes could seriously affect a 50-year old seaweed industry that currently provides hundreds of jobs and injects millions of dollars into the local economy. The objective of this paper is to outline the potential changes in the furoid flora of the Maritime Provinces that could result from the predicted increases in air and SST due to future climate change. The predictions take into consideration the current biological and ecological information of these species in the region.

(P33) - *TAPINOTHRIX CLINTONII* SP. NOV. (PSEUDANABAENACEAE, CYANOBACTERIA), A NEW SPECIES AT THE NEXUS OF FIVE GENERA. Krautová, Markéta¹, Jeffrey R. Johansen¹, Karolina Fučíková², Michael P. Martin¹. ¹Department of Biology, John Carroll University, University Heights, OH 44118 and ²Department of Ecology and Evolutionary Biology, University of Connecticut, Storrs, CT 06269.

In the course of study of the algal flora of Grand Staircase-Escalante National Monument, we isolated a distinctive non-heterocytous, filamentous strain of cyanobacteria. This strain is characterized by having isopolar filaments which taper at the apices and fragment in the center to form heteropolar tapering trichomes. Within the Pseudanabaenaceae, there is only one genus that is attached at the base and tapers to a hair: *Tapinothrix*. However, there are a number of taxa with species that are highly similar to *Tapinothrix*, including *Ammatoidea*, *Homoeothrix*, *Leptolyngbya*, and *Phormidiochaete*. Phylogenies based on 16S rRNA gene sequence data indicate that our *Tapinothrix* is sister to *Leptolyngbya sensu stricto*. The relationship of *Tapinothrix* to *Ammatoidea*, *Homoeothrix* and *Phormidiochaete* is uncertain at this time due to lack of sequence data for species in these genera.

(P34) — Margarita Albis¹ & Brigitte Gavio^{1,2} — DISTRIBUTION OF MACROALGAL EPIPHYTES ASSOCIATED TO *THALASSIA TESTUDINUM* IN SAN ANDRES ISLAND, CARIBBEAN COLOMBIA. ¹Universidad Nacional de Colombia, Departamento de Biología, Bogotá, Colombia. ²Universidad Nacional de Colombia, Sede Caribe, San Luis Free Town #52-44, San Andrés Isla, Colombia

Epiphytic macroalgae have been used as bioindicator species of the water quality, as well as an indirect indicator of the health of seagrass bed ecosystems. We evaluated the epiphytic richness and cover of macroalgal epiphytes on leaves of *Thalassia testudinum*, in 6 beds around the San Andrés island. Three sites (Bahía Hooker, Bahía Honda and the Harbor) were considered nutrient-enriched, while the other three (Rocky Cay, La Mansión and North End) were less impacted, according to the historical data of the coastal water monitoring program of the island. The leaves were collected in dry and wet season, epiphyte cover was measured and macroalgae were identified to species. We encountered a total of 49 species, 16 of which are new records for the island, and an additional 13 are new records for Colombia. No clear relation was evident among epiphyte cover and richness and nutrient load in the water. However, the Harbor disclosed the greatest cover (83%) and species richness (31 species). Although in Bahía Honda we recorded a low number of species, the genera found (*Chaetomorpha* spp. *Cladophora* spp., *Gracilaria* spp. *Acantophora* spp.) have been identified by previous studies as the most noxious for the seagrass, for their turf-forming growth form.

(P35) - DIGESTIBILITY COEFICIENTS OF IMTA PRODUCED SEAWEEDES, BY RAINBOW TROUT (*ONCORHYNCHUS MYKISS*) AND NILE TILAPIA (*OREOCHROMIS NILOTICUS*). Rui Pereira, Luisa Valente, Isabel Sousa-Pinto and Paulo Rema. CIIMAR/CIMAR – Centre for Marine and Environmental Research Rua dos Bragas, 289. 4050-123. Porto. Portugal.

The apparent digestibility coefficients of three species of seaweed by rainbow trout (*Oncorhynchus mykiss*) and nile tilapia (*Oreochromis niloticus*) were assessed after incorporation of 1% chromic oxide in each test diet, and compared with a reference diet. The seaweeds *Gracilaria vermiculophylla*, *Porphyra dioica* and *Ulva* spp. were incorporated, at a 30% level, in reference diets for each fish species. The seaweeds were produced in integrated multitrophic aquaculture systems (IMTA). As a result, their protein contents increased when compared to wild harvested material. In trout, the apparent digestibility coefficients (ADC) of the seaweed diets varied between 71.2 and 79.3% for dry matter (DM), 87.5 and 91.8% for protein, 89.0 and 98.1% for lipid and between 76.9 and 86.7% for energy. For this fish species, the ADC of the reference diet was, in the same order, 85.8%, 91.6%, 98.0% and 91.5%. In tilapia, the ADC of the seaweed diets varied between, 64.9 and 83.0% for DM, 75.6 and 86.3% for protein, 91.7 and 96.6% for lipid and between 69.4 and 84.7% for energy. Also in tilapia, the ADC of the reference diets was, in the same order, 65.6%, 65.9%, 84.9% and 66.9%. The results indicate that some seaweed are well digested by the fish and are interesting ingredients for fish-feed. In fact, in tilapia, the diets containing *Porphyra*, *Gracilaria* and *Ulva* had higher ADCs than the reference diet. Furthermore, this work also shows that seaweeds produced in IMTA can have high protein content, which is necessary for any novel ingredient intended for animal protein replacement in fish-feed.

NOTES

Parking Instructions

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Academic Year 2009-2010

Enclosed is your parking permit and a map indicating designated parking areas.

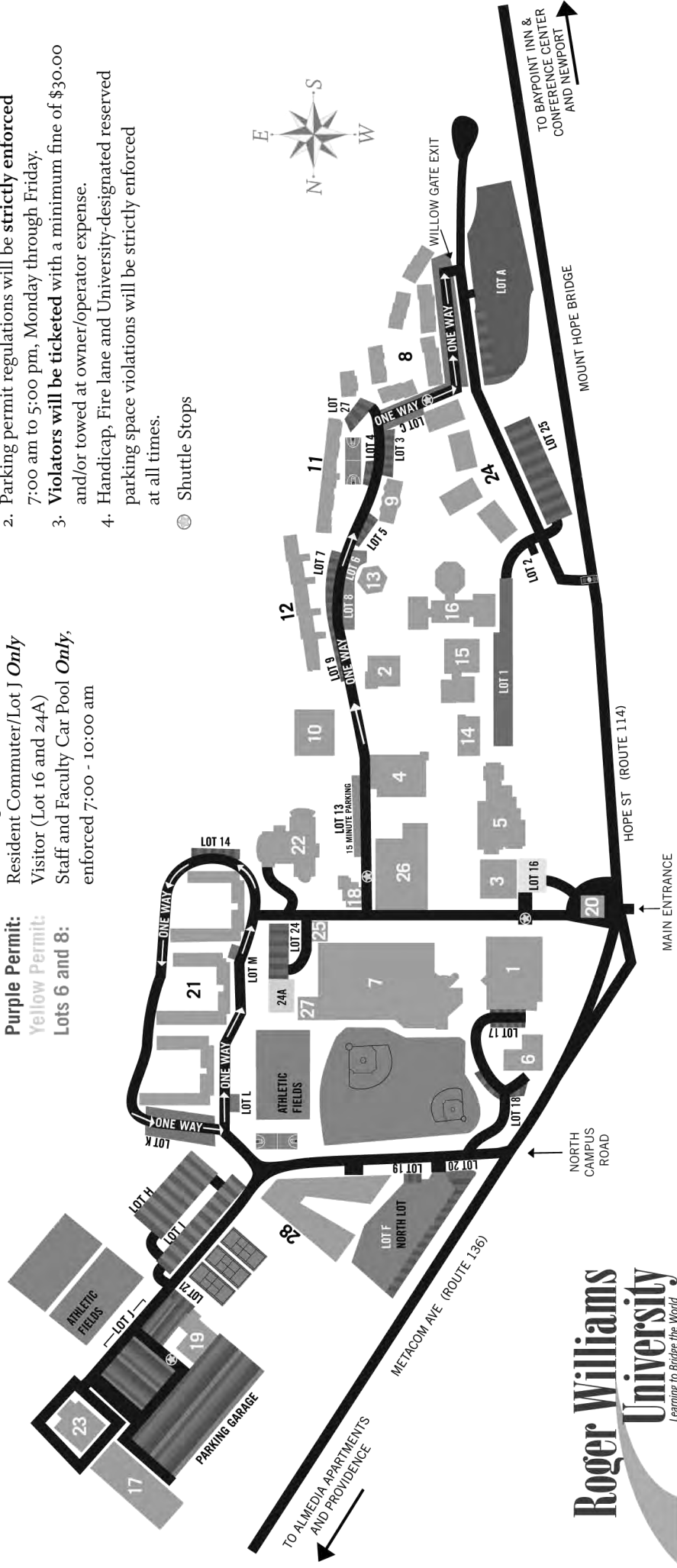
- Blue Permit:** Administration and Professional Staff
- Red Permit:** Staff and Part-Time Faculty
- Green Permit:** Commuter, Graduate
- Silver Permit:** Law
- Orange Permit:** On-Campus Resident
- Purple Permit:** Resident Commuter/Lot J *Only*
- Yellow Permit:** Visitor (Lot 16 and 24A)
- Lots 6 and 8:** Staff and Faculty Car Pool *Only*, enforced 7:00 - 10:00 am

For more detailed information on issues such as winter parking bans, please refer to your Student Handbook on the web at <http://publicsafety.rwu.edu/parking/rules.htm>

Please note the following instructions:

1. Your parking permit must be permanently affixed to the outside of the windshield, driver's side lower corner.
2. Parking permit regulations will be **strictly enforced** 7:00 am to 5:00 pm, Monday through Friday.
3. **Violators will be ticketed** with a minimum fine of \$30.00 and/or towed at owner/operator expense.
4. Handicap, Fire lane and University-designated reserved parking space violations will be strictly enforced at all times.

⊙ Shuttle Stops



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|---------------------------------------------------------|-----------------------------------------------------------------------------------------|-----------------------------------------|
| 1 School of Law | 16 Feinstein College of Arts and Sciences and School of Justice Studies | 20 Public Safety & Information |
| 2 Gabelli School of Business | 17 Facilities Management, Public Safety, Human Resources, Purchasing & Capital Projects | 21 Bayside Residence Complex |
| 3 Alumni & Admissions Center | 18 Feinstein Service Learning / Career Center | 22 Marine and Natural Sciences Building |
| 4 Main Library | 19 North Hall Classroom Building | 23 Maher Center (privately owned) |
| 5 School of Architecture, Art and Historic Preservation | | 24 Stonewall Terrace Residence Complex |
| 6 Performing Arts Center | | 25 Mail Room |
| 7 Campus Recreation Center | | 26 The Commons |
| | | 27 ELS Language Centers |
| | | 28 North Campus Residence Hall |