Table of Contents

General Program: 46th Northeast Algal Symposium

Friday, April 20, 2007

5:00 – 7:00pm **Registration**

Saturday, April 21, 2007

7:00 – 8:30am **Continental Breakfast & Registration**
8:30 – 8:45am **Welcome and Opening Remarks – Morgan Vis**

SESSION 1 Student Presentations Moderator: Don Cheney

8:45 – 9:00am Wilce Award Candidate
FUSION, DUPLICATION, AND DELETION: EVOLUTION OF *EUGLENA GRACILIS* LHC POLYPROTEIN-CODING GENES. **Adam G. Koziol** and Dion G. Durnford. (Abstract p. 9)

9:00 – 9:15am Wilce Award Candidate
UTILIZING AN INTEGRATIVE TAXONOMIC APPROACH OF MOLECULAR AND MORPHOLOGICAL CHARACTERS TO DELIMIT SPECIES IN THE RED ALGAL FAMILY KALLYMENIACEAE (RHODOPHYTA). **Bridgette Clarkston** and Gary W. Saunders. (Abstract p. 9)

9:15 – 9:30am Wilce Award Candidate
AFFINITIES OF SOME ANOMALOUS MEMBERS OF THE ACROCHAETIALES. **Susan Clayden** and Gary W. Saunders. (Abstract p. 10)

9:30 – 9:45am Wilce Award Candidate
BARCODING BROWN ALGAE: HOW DNA BARCODING IS CHANGING OUR VIEW OF THE PHAEOPHYCEAE IN CANADA. **Daniel McDevit** and Gary W. Saunders. (Abstract p. 10)

9:45 – 10:00am Wilce Award Candidate
CCMP622 *UNID. SP*.—A CHLORARACHNIOPHTYE ALGA WITH A ‘LARGE’ NUCLEOMORPH GENOME. **Tia D. Silver** and John M. Archibald. (Abstract p. 11)

10:00 – 10:15am Wilce Award Candidate
PRELIMINARY INVESTIGATION OF THE NUCLEOMORPH GENOME OF THE SECONDARILY NON-PHOTOSYNTHETIC CRYPTOMONAD *CRYPTOMONAS PARAMECIUM* CCAP977/2A. **Natalie Donaher**, Christopher Lane and John Archibald. (Abstract p. 11)

10:15 – 10:45am **Break**

SESSION 2 Student Presentations Moderator: Hilary McManus

10:45 – 11:00am
Wilce Award Candidate
IMPACTS OF HABITAT-MODIFYING INVASIVE MACROALGAE ON EPIPHYTIC ALGAL COMMUNTIES. **Emily Jones** and Carol Thornber. (Abstract p. 12)

11:00 – 11:15am
Wilce Award Candidate
THE SPATIAL HETEROGENEITY OF PERIPHYTON IN EIGHT SOUTHEASTERN OHIO STREAMS: HOW FAR CAN ONE SAMPLE TAKE YOU? **Emily K. Hollingsworth** and Morgan L. Vis. (Abstract p. 12)

11:15 – 11:30am
Wilce Award Candidate
MONITORING OF THE SPREAD OF THE INVASIVE RED ALGA *GRATELOUPIA TURUTURU* YAMADA ALONG THE CONNECTICUT COASTLINE, LONG ISLAND SOUND, USA. **Rebecca Gladych**, Charles Yarish, and George Kraemer. (Abstract p. 13)

11:30 – 11:45am
Wilce Award Candidate
EARTH, WIND, AND ?: PROCESSES AFFECTING GENETIC STRUCTURE IN AN INTERTIDAL ALGA. **Jessica F. Muhlin** and Susan H. Brawley. School of Marine Sciences, University of Maine, Orono, Maine 04469, USA. (Abstract p. 13)

11:45 – 12:00
Wilce Award Candidate
DESMID FLORA OF THE GREAT SMOKY MOUNTAINS NATIONAL PARK. **Karolina Fučíková**, John D. Hall, Jeffrey R. Johansen, and Rex L. Lowe. (Abstract p. 14)

12:00 – 1:20pm Lunch

SESSION 3 Student & Contributed Papers Moderator: Susanne Menden-Deuer

1:30 – 1:45pm
President's Award Candidate
STUDY OF NUISANCE DRIFT ALGAE ON CAPE COD'S NATIONAL SEASHORE. **Patrick Lyons**, Carol Thornber, John Portnoy, and Evan Gwilliam. (Abstract p. 14)

1:45 – 2:00pm
President's Award Candidate
GROWTH RESPONSES TO NUTRIENTS, DISTURBANCE, AND GRAZING IN THE FILAMENTOUS CYANOBACTERIUM *LYNGBYA WOLLEI*. **Melissa Vaccarino**, Kam Truhn, and John D. Wehr. (Abstract p. 15)

2:00 – 2:15pm
Contributed Paper
THE ZOOCHLORELLA SYMBIONT OF *ANTHOPLEURA* FORM A DISTINCT MONOPHYLETIC TAXON IN TREBOUXIOPHYCEAE. **Molly R. Letsch**, Louise A. Lewis and Gisele T. Muller-Parker. (Abstract p. 15)

2:15 – 2:30pm Contributed Paper
USING MOLECULAR PHYLOGENETICS AND MORPHOMETRICS TO DETERMINE SPECIES BOUNDARIES WITHIN THE FRESHWATER GREEN ALGAL FAMILY HYDRODICTYACEAE (SPHAEROPLEALES, CHLOROPHYCEAE). **Hilary A. McManus**[1] and Louise A. Lewis[2]. (Abstract p. 16)

2:30 – 2:45pm Contributed Paper
NEW USES FOR SEAWEEDS IN THE 21ST CENTURY. **Don Cheney**, T. Hogan, T. Cruz-Uribe, G. Rorrer, D. Aulisio, and K. Gardner. (Abstract p. 17)

2:45 – 3:00pm Break

3:00 – 4:00pm Distinguished Speaker Presentation:

HEROES IN THE SEAWEED: JOHN H. RYTHER. Dennis Hanisak

4:00 – 5:00pm Break

SESSION 4 Poster Presentations

5:00 – 7:00pm Posters & Social

7:00 – 10:00pm Banquet, Awards and Auction

Sunday, April 22, 2007

7:00 – 8:30am Continental Breakfast
8:30 – 8:45am Announcements

SESSION 5 Contributed Papers Moderator: Dion Dunford

8:45 – 9:00am Contributed Paper
TURNING ALGAE ON: INDUCIBLE DEFENSES AND ECOLOGICAL CONSEQUENCES. **Jeremy D. Long**. (Abstract p. 17)

9:00 – 9:15am Contributed Paper
ENIGMATIC REPRODUCTIVE STRUCTURES IN *PLATYSIPHON VERTICELLATUS* WILCE (1962): AN ARCTIC ENDEMIC. **Robert T. Wilce** and Peter M. Bradley. (Abstract p. 18)

9:15 – 9:30am Contributed Paper
RE-ASSESSING SPECIES BOUNDARIES IN THE CRYPTOMONAD GENUS *HEMISELMIS*. **Christopher E. Lane** and John M. Archibald. (Abstract p. 18)

9:30 – 9:45am Contributed Paper
MACROALGAL BLOOMS IN NARRAGANSETT BAY: IMPACTS OF SEWAGE-DERIVED NITROGEN. **Carol Thornber**, Peter DiMilla, and Scott Nixon. (Abstract p. 19)

9:45 – 10:00am Contributed Paper
PSEUDO-NITZSCHIA BLOOMS AND DOMOIC ACID IN FLORIDA COASTAL WATERS. **Sheila N. O Dea**, Leanne J. Flewelling and Jennifer L. Wolny. (Abstract p. 19)

10:00 – 10:15am Contributed Paper
GEOMETIC DIFFERENCES BETWEEN GREEN ALGAE RELATED TO THE ORIGIN OF LAND PLANTS. **Larry M. Lewis**. (Abstract p. 20)

10:15am – 10:45am Break

SESSION 6 Contributed Papers Moderator: Susan Brawley

10:45 – 11:00am Contributed Paper
UTILITY OF 16S-23S ITS SEQUENCE AND SECONDARY STRUCTURE FOR RECOGNITION OF INTRAGENERIC AND INTERGENERIC LIMITS WITHIN CYANOBACTERIAL TAXA: *LEPTOLYNGBYA CORTICOLA* SP. NOV. (PSEUDANABAENACEAE, CYANOBACTERIA). **Jeff Johansen**, Lubomír Kovácik Dale Casamatta, Karolina Fučíková and Jan Kaštovský. (Abstract p. 20)

11:00 – 11:15am Contributed Paper
ECOLOGY OF DOMINANT SPECIES IN CYANOBACTERIAL BLOOMS IN THE CZECH REPUBLIC. **Klára Řeháková**, Eliška Zapomělová, and Petr Znachor. (Abstract p. 21)

11:15 – 11:30am Contributed Paper
USING ECOSYSTEM SERVICES TO MEASURE THE VALUE OF FRESHWATER ALGAL BIODIVERSITY. **John D. Wehr**, Alissa A. Perrone, Monica Torres-Ruíz, and Kam Truhn. (Abstract p. 21)

11:30 –11:45am Contributed Paper
INTEGRATING MODELS, EXPERIMENTS AND FIELD OBSERVATIONS TO EXAMINE PREDATOR PREY INTERACTIONS IN THE PLANKTON. **Susanne Menden-Deuer**. (Abstract p. 22)

11:45 – 12:00 Contributed Paper
METAPOPULATION STRUCTURE IN THE PLANKTONIC DIATOM *DITYLUM BRIGHTWELLII:* INSIGHTS INTO DIATOM ECOLOGY AND EVOLUTION. **Tatiana A. Rynearson.** (Abstract p. 22)

12:00 – 1:00pm Box Lunch, Student Awards and General Business Meeting

Poster # **Title (Abstracts begin on p. 23)**

Undergraduate Posters (President's Award)

1 A BASELINE STUDY USING BIOFILM COMMUNITIES IN SHAMOKIN CREEK, AN AMD STREAM IN NORTHUMBERLAND COUNTY, PENNSYLVANIA. **Christopher J. Gehman** and Jack R. Holt. (Abstract p. 23)

2 DIFFERENCES IN STREAM DIATOM COMMUNITY STRUCTURE INFERRED FROM SAMPLING ROCK AND BRYOPHYTE SUBSTRATA. **Jamie Deppen**, Kam Truhn, and John D. Wehr. (Abstract p. 24)

3 CALCIUM DYNAMICS AND POLAR GROWTH IN THE DESMID, *PENIUM MARGARITACEUM*. **Daniel K. Washko** and David S. Domozych. (Abstract p. 24)

4 SCANNING ELECTRON MICROSCOPY OF THE UNUSUAL CELL WALLS OF *ECTOCARPUS SILICULOSUS*. **Bolajoko Fayoda**, Paul Kelly, and Larry Lewis. (Abstract p. 25)

5 WOUND HEALING IN *CLADOPHORA CATENATA*. **Michael J. Costello, Matthew Favazza**, and Larry Lewis. (Abstract p. 25)

6 DIURNAL OSCILLATIONS IN NITRATE REDUCTASE TRANSCRIPT ABUNDANCE IN THE MARINE DIATOM *THALASSIOSIRA PSUEDONANA* (BACILLARIOPHYCEAE): INFLUENCE OF NITRATE, LIGHT, AND THE CIRCADIAN OSCILLATOR. **Katrina Twing**, Katherine Brown, and Deborah L. Robertson. (Abstract p. 25)

7 CHARACTERIZATION OF GSIII AND GSII FROM THE MARINE HAPTOPHYTE *EMILIANIA HUXLEYI* (PRYMNESIOPHYCEAE): EVIDENCE FOR SHARED EVOLUTIONARY HISTORY AMONG HETEROKONTS AND HAPTOPHYTES? Aurélien Tartar, Sohini Ghoshroy, **Kevin Brown**, and Deborah L. Robertson. (Abstract p. 26)

8 ADIRONDACK WETLAND BIOFILM ALGAE: COMMUNITY DYNAMICS, SEDIMENTATION EFFICACY AND NITRATE/PHOSPHATE ENRICHMENT IN A MICROCOSM STUDY. **Katie Scheu** and David S. Domozych. (Abstract p. 27)

9 POLAR CELL GROWTH AND CELL WALL DEVELOPMENT IN THE DESMID *PENIUM MARGARITACEUM*: PECTIN DYNAMICS. **Laura Lambiase** and David S. Domozych. (Abstract p. 27)

10 RIBOSOMAL RNA LEADER SEQUENCE PERMITS SECONDARY STRUCTURE DETERMINATION OF THE ITS REGION IN HETEROCYSTOUS CYANOBACTERIA. **Mary Bridget Bowen**, Jeff Johansen, Mike Martin, and Chris Sheil. (Abstract p. 28)

11 DETERMINATION OF THE OPTIMUM HARVESTING TIME OF UNIALGAL FOOD STOCKS IN SHELLFISH AQUACULTURE. **Alexandra Lawlor**, Karin A. Tammi, Kari Pohl, Jessie Alden and Timothy Scott. (Abstract p. 28)

Graduate Posters (Wilce Award)

12 EFFECT OF LIGHT AND NITRATE ON NITRATE REDUCTASE GENE EXPRESSION IN *THALASSIOSIRA PSEUDONANA* (BACILLARIOPHYCEAE). **Kathryn Brown** and Deborah Robertson. (Abstract p. 29)

13 A FLORISTIC SURVEY OF MARINE TUBE-FORMING DIATOMS AND THEIR COHABITANTS IN CANADIAN WATERS USING DNA BARCODING. **Sarah E. Hamsher** and Gary W. Saunders. (Abstract p. 29)

14 DNA BARCODING: AN EFFICIENT TOOL TO DISTINGUISH TAXONOMICALLY DIFFICULT ALGAL SPECIES OF *PORPHYRA* (RHODOPHYTA), *ULVA* (CHLOROPHYTA) AND *FUCUS* (PHAEOPHYCEAE). **Hana Kucera** and Gary Saunders. (Abstract p. 30)

15 THE G:T RATIO OF INTERTIDAL CHONDRUS CRISPUS IN THE LONG ISLAND SOUND, CONNECTICUT. **Michele Guidone**. (Abstract p. 31)

16 SEDIMENT CHLOROPHYLL CONCENTRATIONS IN A HEADWATER STREAM UPSTREAM AND DOWNSTREAM FROM A MICHIGAN FISH HATCHERY. **Gwen Kloosterman** and Donna K. King. (Abstract p. 31)

17 BACTERIAL ATTACHMENT TO PHYTOPLANKTON IN MONTEREY BAY. **Jason R. Graff**, Jan Rines, and David C. Smith. (Abstract p. 31)

18 AUTOMATED IMAGE ANALYSIS OF AUTOTROPHIC PICOPLANKTON. **Malcolm McFarland** and Jan Rines. (Abstract p. 32)

19 DIATOMS OF THE HOLOCENE FROM POUTWATER POND BOG, HOLDEN, MA. **Adrienne P. Smyth** and Peter M. Bradley. (Abstract p. 32)

20 TEMPORAL COMPARISONS OF PHYTOPLANKTON SPECIES COMPOSITION AMONG HABITAT TYPES IN POOL 8 IN THE UPPER MISSISSIPPI RIVER. **Jillian Smith** and John D. Wehr. (Abstract p. 33)

21 A SURVEY OF MACROALGAL DISTRIBUTION AND ABUNDANCE IN NINIGRET POND, A RHODE ISLAND COASTAL LAGOON. **Heather M. Shannon** and Carol S. Thornber. (Abstract p. 33)

22 BIOGEOGRAPHY OF MICROBIOTIC CRUSTS IN JOSHUA TREE NATIONAL PARK. **Nicole Pietrasiak**, Jeffrey R. Johansen and Tasha La Doux. (Abstract p. 34)

23 EXAMINATION OF THE *THALASSIOSIRA LACUSTRIS* (BACILLARIOPHYCEAE) SPECIES COMPLEX. **Nicole Miller** and Jeff Johansen. (Abstract p. 34)

24 CYANOBACTERIA OF WET WALLS AND SEEPS AT GRAND STAIRCASE-ESCALANTE NATIONAL MONUMENT. **Markéta Krautová** and Jeff Johansen. (Abstract p. 35)

25 COMPARISON OF THREE ORGANELLE MARKERS FOR PHYLOGEOGRAPHIC INFERENCE IN *BATRACHOSPERMUM HELMINTHOSUM* (BATRACHOSPERMALES, RHODOPHYTA) FROM NORTH AMERICA. **Denise L. House**, Alison R. Sherwood and Morgan L. Vis. (Abstract p. 35)

26 MECHANISM OF DESICCATION TOLERANCE IN *PORPHYRA* SPECIES **Yen-Chun Liu** and Donald Cheney. (Abstract p. 36)

27 REGULATION OF POLYUNSATURATED FATTY ACID SYNTHESIS IN THE MARINE RED ALGA *PORPHYRA YEZOENSIS*. **Angela Silvestro**, Yen-Chun Liu, and Donald Cheney. (Abstract p. 36)

28 CHARACTERIZATION OF A ROCKY INTERTIDAL SHORELINE WITHIN ACADIA NATIONAL PARK: IMPACT OF SHORT-TERM TRAMPLING IMPLICATIONS FOR MANAGEMENT. **David Olson**, Susan Brawley, and James Wilson. (Abstract p. 37)

29 IMITATING SOLAR UV-B RADIATION IN THE LABORATORY: PROBLEMS AND SOLUTIONS. **Priya Sampath-Wiley** and Leland S. Jahnke. (Abstract p. 37)

*30 THE ROLE OF PHYTOPLANKTON PRODUCTIVITY AS A POSSIBLE MECHANISM FOR PLANKTON LAYER FORMATION. **Heather Anne Wright** and Susanne Menden-Deuer. (Abstract p. 38)

*31 REPRODUCTIVE ECOLOGY OF *CODIUM FRAGILE* SSP. *TOMENTOSOIDES* IN MASSACHUSETTS. **Chris McHan**, Donald P. Cheney, Geoffrey C. Trussell, and Sal Genovese. (Abstract p. 38)

32 THE USE OF cDNA LIBRARIES TO INVESTIGATE ASEXUAL REPRODUCTION IN *PORPHYRA UMBILICALIS* (L.) Kützing. **Nicolas A. Blouin**, Arthur Grossman, Susan H. Brawley. (Abstract p. 39)

* Not participating in the Wilce Poster Award

Contributed Posters

33 CELLULOSE SYNTHASE (*CesA*) GENES IN THE RED ALGA *PORPHYRA YEZOENSIS* UEDA **Eric Roberts** and Alison W. Roberts. (Abstract p. 39)

34 *ASCOPHYLLUM NODOSUM*: EARLY ZYGOTE SURVIVAL FOLLOWING CANOPY REDUCTION. **Jill C. Fegley**, Robert L. Vadas, and Wesley A. Wright. (Abstract p. 40)

35 THE EVOLUTION OF CELL WALL MATRIX POLYMERS IN CHAROPHYCEAN GREEN ALGAE. Simon T. Gunner, Catherine E. Domozych and **David S. Domozych**. (Abstract p. 40)

36 KF_C: KARLODINIUM-AMPHIDINIUM (DINOPHYCEAE) FULL-LENGTH cDNA SEQUENCING. **Senjie Lin**, Huan Zhang, Allen Place, Terry Gaasterland and Yu-Hui Rogers. (Abstract p. 41)

ABSTRACTS

ORAL PRESENTATIONS (In order of presentation)

FUSION, DUPLICATION, AND DELETION: EVOLUTION OF *EUGLENA GRACILIS* LHC POLYPROTEIN-CODING GENES.

Adam G. Koziol and Dion G. Durnford. Department of Biology, University of New Brunswick, Fredericton, NB, E3B 6E1, Canada

Light-harvesting complexes (LHCs) are a superfamily of chlorophyll and carotenoid-binding proteins, present in nearly all photosynthetic eukaryotes, which are responsible for the capture of light energy and its transfer to the photosynthetic reaction centres. The antenna system is composed of distinct LHC types that are associated either with photosystem I (LHCI) or with photosystem II (LHCII plus the minor LHCs). Unlike in most other eukaryotes, the LHCs of *Euglena gracilis* are translated from large polycistronic mRNAs, producing polyprotein precursors consisting of multiple (5-10) concatenated LHC subunits that are separated by conserved decapeptide linkers. These precursors are post-translationally targeted to the chloroplast, and cleaved into individual proteins. As a part of the Protist EST Program, over 25 000 expressed sequence tags from *Euglena* have been sequenced, clustered, and analysed in an effort further characterize the structural features of the Lhc polyprotein-coding genes and to examine the evolution of this multigene family. This family is composed primarily of numerous polyprotein-coding genes, though we did detect a few that were monocistronic, one of which evolved from the truncation of a polyprotein-coding gene. In total, we identified 17 LHC transcriptional units, of which we have evidence for 15 as being organized into polycistronic mRNAs. Many of these apparently evolved from the duplication of entire multi-subunit polyprotein-coding genes. The organization of the polyproteins themselves was complex, involving tandem and non-tandem repeats of LHC subunits, some of which appeared to be evolving in concert. The presence of variable numbers of distinct LHCs in polyproteins indicates that they may have originated in order to ensure the proper stoichiometry of the different antenna proteins within the thylakoid membrane.

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UTILIZING AN INTEGRATIVE TAXONOMIC APPROACH OF MOLECULAR AND MORPHOLOGICAL CHARACTERS TO DELIMIT SPECIES IN THE RED ALGAL FAMILY KALLYMENIACEAE (RHODOPHYTA).

Bridgette Clarkston and Gary W. Saunders. Center for Environmental & Molecular Algal Research, Department of Biology, University of New Brunswick, Fredericton, N.B., E3B 6E1, Canada.

Along the coast of British Columbia, Canada, the majority of species in the red algal family Kallymeniaceae (Rhodophyta) are taxonomically challenging. The morphological and anatomical traits traditionally used for identification are often subject to variability, making species discrimination difficult. As such, there are potentially many cryptic species in the flora that have been overlooked. We utilize a taxonomic approach that involves both molecular and morphological characters to delimit species. While various molecular markers have been shown to resolve algal taxonomy effectively, we use the DNA barcode (*coxI*-5') because: 1) it is sufficiently variable to discriminate between even closely related species of red algae; 2) it is a rapid and inexpensive molecular tool; and 3) our data will contribute to the growth of a Canada-wide database for all eukaryotic life. Here, we present a combination of molecular, morphological and anatomical results for members of the genera *Pugetia* and *Euthora*. Currently,

two species of *Pugetia* (*P. firma* & *P. fragilissima*) are recognized in B.C, however, our molecular results indicate *Pugetia* may have up to four taxa. As well, we have a group of samples field-identified as *Pugetia* for which molecular data, and subsequent anatomical examination, indicate no affiliation to the genera of the family Kallymeniaceae currently reported from B.C. We have resolved two species of the genus *Euthora* in B.C., where currently only one is recognized. The use an integrated molecular, morphological, and anatomical approach to resolving taxonomic confusion within members of the family Kallymeniaceae in B.C. will be discussed.

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AFFINITIES OF SOME ANOMALOUS MEMBERS OF THE ACROCHAETIALES. Susan Clayden and Gary W. Saunders. Centre for Environmental & Molecular Algal Research, Biology, University of New Brunswick, Fredericton, N.B., Canada, E3B 6E1.

The red algal Acrochaetiales, Colaconematales, and Palmariales form a complex united by similarities including pit plug (proteinaceous cores that close incomplete wall deposition between cells) ultrastructure, and relatively simple reproductive features. An eventful taxonomic history has seen some former anomalous members of the Acrochaetiales, specifically *Meiodiscus spetsbergensis* (formerly *Rhodochorton spetsbergense*) and *Rhodothamniella floridula*, transferred to the Palmariales based on morphological, biochemical (phycoerythrin-type), and life history (monosporangia and carposporophyte stage absent) attributes. These transfers were confirmed by the addition of subsequent molecular data. *Meiodiscus spetsbergensis* was initially allied to the family Rhodophysemataceae within the Palmariales, a key feature being the presence of B phycoerythrin, however, molecular analyses were equivocal on the familial affiliations of this taxon. Here we discuss other rogue members of the Acrochaetiales – *Meiodiscus concrescens*, of questionable synonymy with *M. spetsbergensis*, and two species of *Rhodochorton*: *R. membranaceum*, an endozoic acrochaete; and *R. subimmersum*, an epi/endophytic species – and the nature of their morphological, biochemical, life history, and molecular affinities to the Palmariales. Molecular analyses employed the nuclear large-subunit ribosomal DNA (LSU), a suitable region for distinguishing red algal phylogeny at the ordinal level and below, and the more variable mitochondrial 5’*cox1* DNA barcode, as a species identifier. Preliminary LSU results support the transfer of all these taxa to the Palmariales. The resulting reorganization and changes necessitated in taxonomy at the species, generic, and familial levels are discussed.

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BARCODING BROWN ALGAE: HOW DNA BARCODING IS CHANGING OUR VIEW OF THE PHAEOPHYCEAE IN CANADA. Daniel McDevit and Gary W. Saunders. University of New Brunswick, Fredericton, NB, Canada.

Historically, the process of discovering new species involved finding a unique specimen in the field, taking it back to the lab for further examination and determining if it was significantly different that other known species. However, by screening only a small number of obviously unique collections there is a high probability of overlooking cryptic diversity. For the past year and a half we have been scaling up our field collections as part of the Canadian Barcode of Life Network initiative, which aims to identify every eukaryotic species in the country and their corresponding distribution. In order to screen this large number of collections we are utilizing the DNA barcode (the 5’ end of the cytochrome oxidase 1 gene) to quickly assign the collections to a species. The barcode has been successful in differentiating between the majority of brown algal species, however, in cases where the barcode fails to clearly separate species we are given the opportunity to explore some very exciting science. By screening a large number of samples from across Canada we are learning about species biogeography, incipient speciation, as well as cryptic (and not so cryptic) diversity. Here we present several of the stories we are currently working on in the Phaeophyceae, including: the importance of sequencing sufficient isolates, competitive exclusion of species and hybridization and the common occurrence of cryptic species from the smallest filaments to the grand kelps. We consider that, far from being the ruin of taxonomy envisioned by critics, the barcode is uncovering a plethora of fascinating stories that will keep taxonomists busy for years to come.

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CCMP622 *UNID. SP*.—A CHLORARACHNIOPHTYE ALGA WITH A ‘LARGE’ NUCLEOMORPH GENOME. Tia D. Silver and John M. Archibald. Canadian Institute for Advanced Research, Program in Evolutionary Biology, Department of Biochemistry and Molecular Biology, Dalhousie University, Halifax, Nova Scotia, Canada.

The chlorarachniophytes are a group of unicellular amoeboflagellate algae with a plastid (chloroplast) derived from the secondary endosymbiotic uptake of a green alga. The chlorarachniophytes still retain the nuclear genome of the green algal endosymbiont in a miniaturized form called a nucleomorph, a feature that is only found is these and the cryptomonad algae. Studies of the nucleomorph genomes in a wide range of previously unstudied chlorarachniophyte species indicate that, although all appear to have three chromosomes, there is great diversity in size and structure between different species. In the course of this work, we discovered that the nucleomorph genome of unidentified chlorarachniophyte species CCMP622 is significantly larger than those of all other chlorarachniophytes examined thus far. Using a combination of pulsed-field gel electrophoresis and Southern hybridizations, we estimate the CCMP622 nucleomorph genome to be ~610 kilobases (Kb), more than 200 Kb larger than the completely sequenced genome of the model chlorarachniophyte *Bigelowiella natans* CCMP621, and larger than any other known chlorarachniophyte nucleomorph. To obtain purified nucleomorph DNA, total genomic DNA from Unid. sp. CCMP622 was applied to a cesium chloride density gradient. The resulting fractions were subjected to Southern hybridization to determine which fraction contained nucleomorph DNA, which will be used for molecular analysis. The possible evolutionary significance of this observation is discussed.

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PRELIMINARY INVESTIGATION OF THE NUCLEOMORPH GENOME OF THE SECONDARILY NON-PHOTOSYNTHETIC CRYPTOMONAD *CRYPTOMONAS PARAMECIUM* CCAP977/2A. Natalie Donaher, Christopher Lane and John Archibald. Canadian Institute for Advanced Research, Program in Evolutionary Biology, Department of Biochemistry and Molecular Biology, Dalhousie University, Halifax, NS, Canada.

The cryptomonads are an enigmatic group of unicellular algae that have acquired photosynthesis through a process called secondary endosymbiosis. This occurs when a phagotrophic eukaryote engulfs a photosynthetic eukaryote and retains its plastid (chloroplast). Together with the chlorarachniophytes, cryptomonads are unusual in that the nucleus of the eukaryotic endosymbiont persists in a highly reduced form, called a nucleomorph. The Archibald

Laboratory is using a comparative genomics approach to study the diversity and evolution of nucleomorph genomes in a wide range of cryptomonad species. Here I present preliminary genome sequence data from the ~450 kilobase pair nucleomorph genome of the secondarily non-photosynthetic cryptomonad *Cryptomonas paramecium* CCAP977/2A. Comparison with the previously sequenced nucleomorph genomes of *Guillardia theta* and *Hemiselmis rufescens* provides insight into changes in the structure and coding capacity of nucleomorphs in distantly related cryptomonad species.

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IMPACTS OF HABITAT-MODIFYING INVASIVE MACROALGAE ON EPIPHYTIC ALGAL COMMUNTIES.

Emily Jones and Carol Thornber. Department of Biological Sciences, University of Rhode Island, Kingston, RI, 022881, USA.

Although invasive species can negatively impact communities by competing for limiting resources, they may also add new resources that facilitate the presence or abundance of other species. In rocky intertidal systems, many benthic macroalgae compete for primary substrate, while providing secondary substrata that sessile organisms, such as epiphytic algae, can attach to. From June 2005 to September 2006, we conducted monthly intertidal surveys at Brenton Point in Newport, RI. We compared epiphyte richness, and diversity on two invasive macroalgal species, *Codium fragile* ssp. *tomentosoides* and *Grateloupia turuturu*, to two native macroalgal species, *Chondrus crispus* and *Fucus vesiculosus*. We found significant seasonal differences in epiphyte composition, both within and among host species. While epiphyte richness and diversity was generally low on *Fucus* and *Grateloupia* over time, summer increases occurred on *Chondrus.* Epiphyte richness and diversity on *Codium* remained high over the course of the year, including during the winter months when the richness and diversity on the other hosts remained low or showed large declines. In addition, we also examined seasonal patterns of the herbivorous snail, *Lacuna vincta.* We found a significant peak in *Lacuna* abundance during the summer months, as well as correlations between the snails and the two most abundant epiphyte species, *Neosiphonia harveyi* and *Ceramium virgatum*. Choice feeding assays showed a significant preference for *Ceramium* over *Neosiphonia.* These results suggest that epiphyte facilitation by these invasive algal species is not only seasonally important for maintaining species richness and diversity, but may also provide both food and habitat for higher trophic levels.

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THE SPATIAL HETEROGENEITY OF PERIPHYTON IN EIGHT SOUTHEASTERN OHIO STREAMS: HOW FAR CAN ONE SAMPLE TAKE YOU?

Emily K. Hollingsworth and Morgan L. Vis. Department of Environmental and Plant Biology, Ohio University, Athens OH 45701.

Periphyton is commonly used as a biomonitoring tool for stream research. Often only one or few sites are sampled and assumed to be representative of an entire stream reach. Current literature focuses on periphyton heterogeneity at a smaller scale, on individual rocks within a riffle, and larger scales, within a watershed or ecoregion. For the purpose of this research, the understudied intermediate scales, within a single riffle and among riffles, were sampled. Periphyton was collected at four nested spatial scales: eight reaches (each nested within a different stream), ten riffles (nested within a reach), five samples (nested within a riffle), and ten rock scrapings (nested within a sample). The eight streams included three highly impacted, three moderately impacted, and two unimpacted by acid mine drainage. Scores from a diatom index of biotic integrity and species composition data was analyzed using UPGMA cluster analysis and ordination techniques to determine heterogeneity of periphyton communities within and among riffles. As expected, these data show little variation within riffles and among riffles of highly impacted streams. The length of a stream represented by the biological monitoring of a single point and whether the represented length is dependent upon the health of the stream is discussed.

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MONITORING OF THE SPREAD OF THE INVASIVE RED ALGA *GRATELOUPIA TURUTURU* YAMADA ALONG THE CONNECTICUT COASTLINE, LONG ISLAND SOUND, USA.

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The non-native red alga *Grateloupia turuturu* Yamada was first found in Narragansett Bay, Rhode Island, USA in 1994. In 2004, it was discovered in Waterford, Connecticut, and in December 2006, in Groton, Connecticut. *Grateloupia turuturu* appears to prefer the rocky intertidal and subtidal habitats, and appears to be competing with the native red alga, *Chondrus crispus* Stackhouse. To monitor the impact of the spread of *G. turuturu* on the native flora, we initiated a monitoring effort at Waterford, CT, in July of 2006. Our studies were initially along a cobble beach where *G. turuturu* was discovered. Twenty-four randomly placed quadrats have been used to estimate the change of percent cover over the past 8 months. In addition to percent cover, the monitoring operation has been expanded (January, 2007) to permanent quadrats on rocky intertidal platforms adjacent to the cobble field. This is expected to provide a basis for the comparison of population dynamics between the *G. turuturu* invasion on a cobble field versus a rocky, low-intertidal platform in Long Island Sound. Changes in the composition of the macroalgal assemblages and the associated faunal communities are being observed. The population in Waterford is located adjacent to a nuclear power plant, which uses once-through cooling water systems. Seawater that is released back into Long Island Sound is approximately 2°C above ambient temperature at the study site. This thermally impacted site provides an additional basis for comparison to the ambient temperature site at the recently discovered Groton site. We are also looking at the reproductive phenology of *Grateloupia turuturu* and are quantifying spore output for both tetrasporophytic and carposporophytic blades. We expect to determine the spore output of each phase of the life history and its contribution to its spread to other areas in Long Island Sound.

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EARTH, WIND, AND ?: PROCESSES AFFECTING GENETIC STRUCTURE IN AN INTERTIDAL ALGA.

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Reproduction in the brown alga *Fucus vesiculosus* L. is confined to calm, sunny conditions. We examined genetic structure using 6 microsatellite loci in *F. vesiculosus* and predicted that genetic structure would correlate with coastal topography. For example, weather frequently varies on the Maine shore when *F. vesiculosus* is reproductive so that one side of a coastal point experiences high levels of water motion (=no gamete release) while the other side is calm (=gamete release).

Furthermore, low dispersal capacities of gametes and zygotes suggest strong spatial genetic structuring at relatively short distances. Using surface drifters, we characterized near-shore circulation patterns around the study sites to investigate whether directionality of gene flow was correlated with directionality of currents. In addition, we examined the longevity of *F. vesiculosus* eggs and sperm and viability of zygotes produced from crosses with aged gametes in order to evaluate how these life history stages contribute to gene flow. We revealed significant genetic differentiation among the sites sampled at two different promontories, but patterns of differentiation were complex and unrelated to coastal topography or to among or within-site spatial structuring. *Fucus vesiculosus* eggs had greater longevity than sperm. Sperm were competent for several hours, while eggs were still fertile after 7 days. However, as eggs aged, polyspermy increased (*t*-test, $p < 0.001$). From our genetic and near-shore circulation data, as well as our examination of gamete longevity, we conclude that gene flow at a regional scale is dependent upon storm-detached, rafting, reproductive adults. This study highlights the significance of rafting as a mechanism for structuring established populations of macroalgae and associated biota. (Supported by NSF OCE-99043 and a PSA Grant-In-Aid of Research).

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DESMID FLORA OF THE GREAT SMOKY MOUNTAINS NATIONAL PARK. Karolina Fučíková[1], John D. Hall[2], Jeffrey R. Johansen[1], and Rex L. Lowe[3]. [1]Department of Biology, John Carroll University, University Heights, OH 44118, USA; [2]Department of Cell Biology and Molecular Genetics, University of Maryland, College Park, MD 20742, USA; [3]Department of Biological Sciences, Bowling Green State University, Bowling Green, OH 43403, USA. (Karolina Fučíková currently at: Department of Ecology and Evolutionary Biology, University of Connecticut, Storrs, CT 06269, USA.)

The Great Smoky Mountains National Park (GSMNP) generally is considered to harbor an extraordinarily diverse flora and fauna. Since 1997, a large number of biologists have been investigating biodiversity in the park as part of the All Taxa Biodiversity Inventory (ATBI). Within the ATBI, algae of the GSMNP have been studied since 1999. Many desmid species occur in various habitats throughout the park and their diversity is summarized in the present study. A total of 125 desmid taxa have been found in the park since the first study published in 1944. The present study enhanced the most recent published species list (JOHANSEN et al. 2004) by 106 additional taxa. This study provides an updated list of desmids of the GSMNP, adds several species to the known regional flora, and extends the ranges of 25 taxa. In addition, a new species of conjugating green algae, *Mesotaenium testaceovaginatum*, is described.

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STUDY OF NUISANCE DRIFT ALGAE ON CAPE COD'S NATIONAL SEASHORE. Patrick Lyons[1], Carol Thornber[1], John Portnoy[2], Evan Gwilliam[2]. [1]Department of Biological Sciences, 100 Flagg Rd., University of Rhode Island, Kingston, RI 02874, USA; [2] Cape Cod National Seashore, 99 Marconi Site Rd., Wellfleet, MA 02667, USA.

Nuisance drift algae, which many locals and tourists refer to as "mung", have been present along beaches at the Cape Cod National Seashore (Cape Cod, MA) for over fifty years. The presence of macroalgae in the water and on the shoreline can detract from human aesthetics and use of beaches. In this study, we obtained quantitative data on the identity, abundance and distribution of drift macroalgae throughout the summer of 2006 at the Cape Cod National Seashore. We found a mix species dominated by *Ulva lactuca* (Chlorophyta) and several species in the *Polysiphonia* and *Neosiphonia* genera (Rhodophyta). Macroalgal biomass varied significantly on both spatial and temporal scales. Algae were present throughout the study period, from late June through September 2006. However, a distinct peak in algal abundance occurred during the second week of August 2006. Algae were spatially variable, with peaks in abundance at two areas of the shore. Analyses of dissolved nutrients in water samples revealed that, dissolved inorganic nitrogen was depleted in areas of higher algal abundance. Temperature loggers and wind data revealed that several upwelling events occurred during the summer; however, upwelling was not significantly correlated with algal abundance. Gulf of Maine circulation would seemingly be responsible for transport to Cape Cod, and our results indicate that predictable peaks in temporal and spatial patterns occur.

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GROWTH RESPONSES TO NUTRIENTS, DISTURBANCE, AND GRAZING IN THE FILAMENTOUS CYANOBACTERIUM *LYNGBYA WOLLEI*.

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The cyanobacterium *Lyngbya wollei* is a benthic, invasive alga occurring in many southeastern US lakes and reservoirs, with some populations producing cyanobacterial toxins. It has now been observed in Lake Mahopac, a eutrophic lake in NY State, which also experiences extensive hypolimnetic anoxia. Lab and field studies were conducted to assess factors affecting its growth in this northeastern population. Short filaments (1-2 mm) were grown in Allen's blue-green medium, with varying amounts of nitrogen (0, 1, 100 mg N/L) and phosphorus (0.69; 6.9 mg P/L), and under shaken (75 rpm) or still conditions. Shaking resulted in a six-fold increase in growth ($P < 0.001$; ANOVA), but no clear effects were demonstrated with either nitrogen or phosphorus additions ($P = 0.37$, 0.87 respectively), although a strong but variable negative trend with the nitrogen treatments was observed. A second experiment varied N (0, 1, 100 mg N/L) and Ca (9.8 and 49.0 mg Ca/L) and demonstrated a significant Ca x N effect ($P = 0.0134$); the nitrogen trend was again inconsistent. A field experiment examined the potential effects of herbivory by benthic invertebrates (mainly amphipods), using bags of contrasting mesh size (5 mm = macroinvertebrates excluded; 250 μm = macroinvertebrate access). Five grams (FW) of *L. wollei* were placed in each bag and deployed in pairs for two weeks at 12 sites around the littoral zone of Lake Mahopac. There was a significant mesh-size effect ($P = 0.0178$), with increased growth (mean = 1.0 g) of *Lyngbya* in smaller mesh bags, but an average decrease of 0.2 g in larger mesh bags. Future experiments are planned to examine effects of nitrogen uptake and/or N-fixation as well as other water quality variables on growth and toxicity production.

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THE ZOOCHLORELLA SYMBIONT OF *ANTHOPLEURA* FORM A DISTINCT MONOPHYLETIC TAXON IN TREBOUXIOPHYCEAE.

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The sea anemones *Anthopleura xanthogrammica* and *A. elegantissima* from the North Pacific intertidal can each form an intracellular symbiosis with a unicellular green alga (Chlorophyta). A recent phylogenetic analysis of single sequences from the nuclear 18S rDNA and the plastid encoded rbcL gene region placed this symbiont in the Trebouxiophyceae. Though commonly called “zoochlorellae,” this symbiont is not a true *Chlorella* (*sensu* Huss et al. 1999) but is more closely related to *Trebouxia* and *Coccomyxa* (Lewis and Muller-Parker 2004). In order to determine if this symbiont is a new taxon, we have gathered morphological and molecular data from samples of *A. xanthogrammica* and *A. elegantissima* tissue containing green symbionts from their known range along the North Pacific coast, including Alaska, Oregon and Washington. The symbiont cells we observed using TEM were small, between 7 - 10 microns in diameter, non-motile, and reproduced by dividing into two daughter cells. The morphology visible in TEM was not sufficient to classify zoochlorellae as a distinct taxonomic group. Our molecular analysis of 18S rDNA shows monophyly of all zoochlorellae isolated directly from these anemone samples regardless of the host species or geographic location. A close relationship to *Hemichloris* and *Elliptochloris* is also indicated. The 18S sequences of the zoochlorellae, however, all share a short (4 bp) insertion at position1659 that is absent from all other aligned sequences. Phylogenetic analysis of the *rbcL* data supports that zoochlorellae are a monophyletic group. Therefore, we propose that the zoochlorellae of *A. xanthogrammica* and *A. elegantissima* are a distinct taxon and should be named as a new species.

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USING MOLECULAR PHYLOGENETICS AND MORPHOMETRICS TO DETERMINE SPECIES BOUNDARIES WITHIN THE FRESHWATER GREEN ALGAL FAMILY HYDRODICTYACEAE (SPHAEROPLEALES, CHLOROPHYCEAE).

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Accurate recognition of green algal species is essential for ecological studies, estimates of biodiversity, reconstructing past climates, and biotechnology. This study combined molecular and morphological data to resolve evolutionary relationships among the genera of the freshwater family Hydrodictyaceae (Chlorophyta), and tested species boundaries within historic *Pediastrum* Meyen 1829. Molecular phylogenetic analyses using nuclear large subunit (26S rDNA) and chloroplast RuBisCo (*rbc*L) sequence data were performed on 103 ingroup isolates, 44 of which were from culture collections representing North America and Europe, and the remaining 59 were wild isolates unique to this study from North America, Europe and Australia. The results revealed the *P. duplex* morphotype is polyphyletic, recovering the morphotype in three distinct lineages. A landmark-based morphometric analysis was performed to determine if the three lineages possessing *Pediastrum duplex* morphology were morphologically distinguishable. Only one of the groups was shown to be morphologically distinct, and this supported its phylogenetic placement separate from the other two *P. duplex* groups. The erection of a new genus is recommended to recognize this group as its own taxonomic unit. In addition to the polyphyly of the *P. duplex* morphotype, the morphologically distinct *P. angulosum* morphotype was nested among *P. duplex*-type isolates. This study supports the conclusions of other recently published investigations of microscopic eukaryotes, that the morphospecies concept is inadequate for accurately recognizing species lineages of eukaryotic microorganisms because the diversity of these organisms is poorly captured and vastly underestimated by phenotype alone. The inclusion of additional forms of data is therefore integral for accurate assessments of species boundaries and biodiversity.

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NEW USES FOR SEAWEEDS IN THE 21^{ST} CENTURY. Don Cheney[1], T. Hogan[1], T. Cruz-Uribe[2], G. Rorrer[2], D. Aulisio[3], and K. Gardner[3]. [1]Biology Dept., Northeastern University, Boston, MA; [2]Dept. Chem. Engineering, Oregon State University, Corvalis, OR;[3] Dept. Chem. Engineering, University of New Hampshire, Durham, NH.

Our lab has been working for the past couple of years on the development of new uses for seaweeds with potentially significant environmental applications. So far, the results look most promising in two new areas: 1) the use of seaweed as a supplemental feed ingredient for salmon and trout aquaculture, and 2) the use of seaweed as bioremediation agents of the organic pollutants TNT, PCBs and PAHs. In the first study, we determined the palatability and digestibility of using *Porphyra yezoensis* in a rainbow trout diet. The experimental diet contained 30% seaweed and showed similar palatability, specific growth rate and feed conversion ratios to that of a reference diet. Additionally, manually stripped fecal samples revealed that nutrient ADCs (Apparent Digestibility Coefficients) of protein, lipid and phosphorous were high in the experimental diet, while those of nitrogen-free extracts (NFE) and total energy were low. Overall, the results of this study were promising and suggest that *Porphyra* would be a good candidate for further investigation into the use of seaweed as a fish meal supplement. In the second study, we have been investigating the innate ability of native seaweeds to take up and metabolize (bioremediate) the two most common organic pollutants found in sediments of the Northeast's estuaries, PCBs and PAHs, as well as one less common, TNT. Preliminary experiments conducted with a model PAH (phenanthrene) and PCB (3-chlorobiphenyl) are very promising. In both cases, we see a very rapid uptake and removal of the pollutant from spiked media by our best seaweed candidate to date, a strain of the green seaweed *Ulva lactuca* collected from an oil-contaminated site in greater Boston Harbor. In phenanthrene experiments, approximately 73-90% of a 10 ppm spike was removed from the media by 1 g of tissue after only 2 hrs. The amount of phenanthrene that was recovered in the plant tissue after 2 hrs was approximately 40-49% of that spiked in; this amount declined significantly after 4 hrs (eg. from 49% to 19%), possibly suggesting its metabolism and conjugation to a form we could not detect. Interestingly, we recently described a similar uptake pattern and clear evidence of metabolism for TNT by three other seaweed (Cruz-Uribe et al, 2007, Chemosphere, in press).

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TURNING ALGAE ON: INDUCIBLE DEFENSES AND ECOLOGICAL CONSEQUENCES. Jeremy D. Long. Marine Science Center, Northeastern University, Nahant, MA, 01908.

Macro- and microalgae can respond to changing environments in surprising ways such as inducing chemical and morphological defenses when the threat of attack is high. Although marine algae may use such inducible defenses to deter grazers, few examples exist and the broader-scale consequences of these defenses on communities and ecosystems are largely unknown. This talk will use recent examples of inducible defenses as a platform for discussing the major gaps in our understanding. These examples will include the phytoplankton *Phaeocystis globosa* that shapeshifts after detecting chemical signals from grazers and fucoid algae that increase production of defensive metabolites after attack. These defenses may regulate energy flow in pelagic ecosystems and competitive interactions between herbivores in rocky shore communities. Future challenges for the study of algal inducible defenses include 1) moving beyond the laboratory and into the field, 2) testing for indirect effects of herbivores mediated by inducible defenses, 3) isolating and identifying mechanisms of defense such as secondary metabolites, and 4) assessing geographic variation within individual algal species. As these challenges are met, we will enhance our understanding of the ecological and evolutionary importance of these surprising defensive strategies.

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ENIGMATIC REPRODUCTIVE STRUCTURES IN *PLATYSIPHON VERTICELLATUS* WILCE (1962): AN ARCTIC ENDEMIC.

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Platysiphon verticellatus is a rare thalloid brown alga. We describe its known occurrence from northeast and northwest Greenland and northern Baffin Island, its distinctive annual seasonality, mode of thallus development, and portions of its life history. Descriptions are based on seven years of *in situ* studies in northern Baffin Island, Nunavik, Canada, and culture observations. Despite collections from the entire light season, unilocular and plurilocular sporangia remain unknown. In culture, expanded thalli become reproductive after varying periods of darkness at temperature from 4.º-8.oº C. Vegetative cells with numerous discoidal plastids and photosynthetic reserves change dramatically as the protoplast shrinks away from the cell wall to become spherical, ultimately irregular in outline. Cytoplasmic change occurs in cells of the median portion of the blade. Protoplasts attach to the inner face of the parent cell walls where a discharge pores are formed on either side of the thallus, probably by enzymatic wall digestion. Protoplasts emerge and attach to the surface of the thallus. A pad of “cement” is then apparent between the protoplast and parent cell wall. Protoplasts then form a cell wall, resulting in a novel, rigid, lightly sculptured, cyst-like resting stage. Cysts contain a single protoplast that becomes a biflagellate zoospore, which is released under low light through an irregularly ruptured aperture. Zoospores have a single parietal plastid, one long anterior flagellum and one short posterior flagellum, and lack an eyespot. They attach to solid substrata and initiate branched filaments. Cells of the filaments contain non-pyrenoidal plastids. Ordinal status of *Platysiphon* remains questionable. Novel morphological and reproductive features suggest a new family Platysiphonaceae, alternatively, genome sequence analysis likely points to a second genus in the Halosiphonaceae.

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RE-ASSESSING SPECIES BOUNDARIES IN THE CRYPTOMONAD GENUS *HEMISELMIS.*

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Cryptomonads are a ubiquitous and diverse assemblage of aquatic flagellated phototrophs. The relatively obscure genus, *Hemiselmis*, includes some of the smallest of these cells. This genus contained only two species until 1967, when Butcher added seven new species from the coastline of the British Isles based mainly on observations with the light microscope, but failed to designate types for his species. The validity of the features Butcher used to distinguish species has since been questioned and the taxonomy within *Hemiselmis* has remained clouded due to the difficulty in unambiguously applying his classification and validating his species. As a result, marine strains are often placed into one of three species, *H. rufescens* Parke, *H. virescens* Droop or the invalid *H. brunnescens* Butcher, based on pigmentation alone. We applied microscopic and molecular tools to 13 publicly available *Hemiselmis* strains in an effort to clarify species boundaries. Scanning electron microscopy failed to provide sufficient morphological variation to distinguish species of *Hemiselmis* and results from light microscopy did not correlate with clades found using both molecular phylogenetic and nucleomorph genome karyotype analysis, indicating a high degree of morphological plasticity within species. This plasticity suggests that Butcher's seven species should not be validated, but only his culture of *H. brunnescens* still exists for examination. Based on molecular characters, geography and growth physiology, we recognize *H. rufescens, H. virescens* and four new species of *Hemiselmis* from the waters around North America.

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MACROALGAL BLOOMS IN NARRAGANSETT BAY: IMPACTS OF SEWAGE-DERIVED NITROGEN. Carol Thornber[1], Peter DiMilla[2], and Scott Nixon[2]. [1]Department of Biological Sciences, University of Rhode Island, Kingston, RI 02881 USA. [2]Graduate School of Oceanography, University of Rhode Island, Narragansett, RI 02882 USA.

Macroalgal blooms are becoming increasingly common in shallow bays and estuaries worldwide. Nitrogen is a primary limiting nutrient for macroalgae; formations of these blooms are frequently attributed to increases in anthropogenic sources of nitrogen. In this study, we investigated the relative contributions of natural vs. anthropogenic (from sewage) nitrogen to macroalgal growth via stable nitrogen isotope ratios in bloom-forming species from Narragansett Bay, RI. The northern end of this bay has a high population density (including the city of Providence) and large inputs of nitrogen from sewage treatment plants; the southern end of the bay is more lightly populated and opens to the Atlantic Ocean. We: 1) conducted a bay-wide survey of *Ulva* species, and 2) cultured *Ulva* and *Gracilaria* in water collected from four locations in Narragansett Bay along a latitudinal gradient of anthropogenic nitrogen inputs. For both, we then examined the nitrogen isotopic signature (as d15N) and the percent nitrogen content to determine the relative impacts of different nitrogen sources on algal species. We found a range of responses in the d15N signatures of cultured and collected algae from different water sources. These data, when coupled with models of circulation patterns, will permit the rapid estimation of the relative contribution of the major nitrogen sources to this bay, and their impacts on macroalgae.

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PSEUDO-NITZSCHIA BLOOMS AND DOMOIC ACID IN FLORIDA COASTAL WATERS. Sheila N. O Dea, Leanne J. Flewelling and Jennifer L. Wolny. Florida Fish and Wildlife Conservation Commission, Fish and Wildlife Research Institute, St Petersburg, Florida, 33701.

Domoic acid (DA), a potent neurotoxin that has the potential to cause Amnesic Shellfish Poisoning (ASP), is produced by members of the marine diatom genus *Pseudo-nitzschia*. Outbreaks of ASP in humans, and of domoic acid poisoning in birds and marine mammals have been reported across the United States and Canada since the late 1980's. *Pseudo-nitzschia spp.* are often extremely abundant in Florida waters, with densities sometimes exceeding 10^6 cells/Liter. Nine species of *Pseudo-nitzschia* have been described from Florida. At least six of these species are known to produce DA in other parts of the world. However, despite the strong presence of *Pseudo-nitzschia*, there has never been a report of ASP or a DA-related animal mortality event recorded from Florida. To assess the potential that such events might occur, we examined samples from three locations to determine relative abundances of *Pseudo-nitzschia* as well as DA levels in water and shellfish. Samples were collected from the Florida panhandle, southwest Florida, and the Indian River Lagoon (IRL) system on Florida's east coast between 2004 and 2006. Maximum abundances exceeded 12 x 10^6cells/L in the Florida panhandle, 5 x

10^6cells/L in southwest Florida and 49 x 10^6cells/L in the IRL. Low levels of DA were detected in Florida panhandle and southwest Florida water samples. However no DA was detected in any IRL samples. The regulatory limit for DA in bivalves is 20.0 µg/g. Concentrations measured in shellfish from our study sites never exceeded 2.1 µg/g, suggesting that *Pseudo-nitzschia* poses little threat to human health in Florida. However, DA production in *Pseudo-nitzschia spp*. has been shown to be variable, in that production increases under conditions of nutrient stress or low iron or copper availability. Although our data does not indicate that a significant threat currently exists, the potential for domoic acid-related events in Florida should be investigated further.

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GEOMETIC DIFFERENCES BETWEEN GREEN ALGAE RELATED TO THE ORIGIN OF LAND PLANTS.

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Uniseriate filaments occur in green, red, and brown divisions of algae and in early forms of bryophytes and ferns. Previous molecular studies point to a limited number of green algal orders closely related to the ancestors of land plants: includes Charales, Zynematales, and Klebsormidiales. As suggested long ago by D'Arcy Thompson, we applied Plateau's Law of fluid cylinders to analyze cells of *Spirogyra communis*, *S. pratensis*, and *Klebsormidium flaccidum*. Thus given, $L = (K)2(\pi)r$, or $K = L/\text{cell width}^* \pi$, when K is a constant that considers algal cells have a cell wall as a boundary, then *S. communis* has a mean K of 1.23, *S. pratensis* has a mean K of 2.11, while *K. flaccidum* has a mean K of 0.53. These data are consistent with the hypothesis that an increase in cell length relative to cell width reflects the evolutionary trend to land plants. This change implies an increase in the tensile strength of the cell walls. Consistent with this hypothesis, cells in the genus *Spirogyra* display a high degree of birefringence with plane-polarized light, while cells of the genus *Klebsormidium* do not display birefringence when the polarizer and analyzer are at extinction. In conclusion, the data suggest evolution proceeded with an increase in the length/width ratio of cells and an increase in the structural order of the cell wall as evidenced by significant birefringence in *Spirogyra* relative to *Klebsormidium*.

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UTILITY OF 16S-23S ITS SEQUENCE AND SECONDARY STRUCTURE FOR RECOGNITION OF INTRAGENERIC AND INTERGENERIC LIMITS WITHIN CYANOBACTERIAL TAXA: *LEPTOLYNGBYA CORTICOLA* SP. NOV. (PSEUDANABAENACEAE, CYANOBACTERIA).

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An unusual species of *Leptolyngbya* was isolated from tree bark by Marie Takačová in 1983. It has resided in the Culture Collection of the Czech Academy of Sciences since that time, under the tentative designation of *L. foveolarum* TAKACOVA 1983/4. We have studied the morphology, ultrastructure, and ribosomal 16S rDNA sequence data for this strain and found it to be unique among all previously described species. An analysis of 16S rDNA sequence data for many *Leptolyngbya* taxa indicate close affinity with *L. boryana*, *L. tenerrima* and *L. angustata*, which is consistent with the morphological similarity we have seen among the three taxa as well. The 16S-23S ITS regions of 14 strains in the polyphyletic taxon *Leptolyngbya* were sequenced and folded, and the structure and sequence of the ITS regions were highly congruent with phylogeny determined from 16S rRNA sequence data, and provide an easy means for recognition of intrageneric and possibly intergeneric taxonomic diversity. This taxon has distinct 16S-23S ITS sequences, which together with the morphological autapomorphies it possesses are sufficient to clearly differentiate it from the three sister taxa sequenced thus far. We propose the name *L. corticola* for this strain.

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ECOLOGY OF DOMINANT SPECIES IN CYANOBACTERIAL BLOOMS IN THE CZECH REPUBLIC. Klára Řeháková, Eliška Zapomělová, Petr Znachor**.** Centre of Biology, Institute of Hydrobiology AS CR, České Budějovice

Suitable light and temperature conditions coupled with high nutrient concentrations in water lead to a mass development of cyanobacterial blooms in the reservoirs in the Czech Republic. Cyanobacterial blooms cause serious problems and their presence impairs water quality e.g. many produce toxins, which pose a health risk in recreational and drinking water reservoirs. Although increased attention has been paid to this problem recently, the definitive mechanisms affecting species composition of a particular bloom still remain unclear. Our knowledge about the competition and competitiveness of cyanobacterial and algal dominants is still unsatisfactory. Our team studied the ecological demands of bloom dominants, mainly of the genera *Anabaena*, *Aphanizomenon* and *Microcystis* and their growth optima. We tested 15 selected strains. Strains were chosen according their differing phenotypical features (coiled and straight trichomes, toxic and nontoxic, bundles and single trichomes). The ecological demands of strains are used for finding the competition mechanisms among single dominants of phytoplankton, and particular factors, which favor the development of certain species forming summer phytoplankton blooms. *In situ* experiments with mesocosms (Plexiglas cylinder, volume 14 l) were conducted in the Římov Reservoir to find out the competitive ability of *Microcystis*. Different biomass ratios of *Microcystis aeruginosa* and *Fragilaria crotonensis,* collected from natural populations during the summer 2006, were grown together at these different ratios (1:1, 4:1, 1:4) for 21 days. At regular intervals changes in their biomass and abundance were observed. The experimental part of our work preceded the long- term observation of natural population in ponds and reservoirs and their seasonal changes in species diversity. The discovery of the interesting invasive cyanobacteria *Aphanizomenon aphanizomenoides* was additionally.

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USING ECOSYSTEM SERVICES TO MEASURE THE VALUE OF FRESHWATER ALGAL BIODIVERSITY. John D. Wehr, Alissa A. Perrone, Monica Torres-Ruíz, and Kam Truhn. Louis Calder Center – Biological Field Station, Fordham University, Armonk, NY 10504

Preserving biodiversity is one of the key objectives of global conservation efforts, yet little attention has been paid to the diversity of freshwater algae, despite their enormous species richness and vital roles in ecosystem processes. To resolve this issue, greater research effort should be paid to developing metrics that directly quantify the value of algal diversity. Conceptual models exist and can be tested, provided adequate biodiversity datasets and appropriate measures of ecosystem integrity. These measures should represent robust ecological properties and/or quantify ecosystem services that may have economic value. A long-term study of algal diversity in streams and rivers has been initiated in New York State, combined with a range of potential metrics such as biomass, primary production, carbon, nitrogen and phosphorus content, nutrient stoichiometry, and essential fatty acids (EFAs). A number of studies, including the present study, suggest that the most common yardstick used in studies of other ecosystems, primary production, is negatively correlated with algal biodiversity, and may be a poor index of ecosystem integrity. Other nutritional measures that have been proposed more recently, such as P content or C:N ratios, also correlate weakly or negatively with greater algal species richness. One measure, the supply of EFAs available to lotic consumers appears to be greater in streams with more macroalgal species. Despite a general agreement among phycologists that algal biodiversity is of value, there presently are not enough data to link this attribute with ecosystem integrity or economic measures, and which may lead to protection of algal species and their habitats.

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INTEGRATING MODELS, EXPERIMENTS AND FIELD OBSERVATIONS TO EXAMINE PREDATOR PREY INTERACTIONS IN THE PLANKTON. Susanne Menden-Deuer, University of Rhode Island, Graduate School of Oceanography, Narragansett, Rhode Island, 02882, USA

The distribution of resources in the ocean (e.g. nutrients, prey) is highly variable and spatially structured, which can have consequences for the biological dynamics of the system. To quantify the significance of spatial structure and predator foraging behaviors, 3-D movement behaviors and population distributions of single-celled zooplankton were quantified using video-based observation and computer analysis techniques. In laboratory experiments, predators rapidly aggregated to remote phytoplankton patches. Resulting estimates of growth and grazing rates were over ten-fold higher when predator foraging behaviors were accounted for. Based on the observed behaviors, predictions were made as to how accessible phytoplankton patches would be in the coastal ocean. These predictions were tested within the San Juan Archipelago, Washington, where layers of high plankton concentrations (plankton-rich layers, PRLs), form naturally. Analysis of the plankton community composition over the course of several weeks showed that different processes drove phytoplankton and heterotrophic protist distributions: phytoplankton species were found throughout the water column (although in different concentrations), whereas heterotrophic protists were aggregated by and large within PRLs when present. Phytoplankton prey within PRLs uniformly exceeded dominant predator's survival threshold, whereas prey concentrations outside PRLs were insufficient to support growth in any but three samples. Therefore, prey distribution and more importantly predator foraging behaviors have important ramifications for ecosystem productivity and the transfer of organic matter and energy to higher order food chain components.

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METAPOPULATION STRUCTURE IN THE PLANKTONIC DIATOM *DITYLUM BRIGHTWELLII:* INSIGHTS INTO DIATOM ECOLOGY AND EVOLUTION. Tatiana A. Rynearson, Graduate School of Oceanography, University of Rhode Island, Narragansett, RI 02882.

Diatoms are ubiquitous, unicellular, eukaryotes that generate about 40% of the organic carbon fixed annually in the sea. Interpretation of diatom species distributions and abundances in relation to environmental conditions has relied on two assumptions: (1) cells with identical morphologies represent the same species and (2) high potentials for dispersal and gene flow in passively drifting diatoms prevent local adaptation. Here, both genomic and morphological variation were examined in field isolates of the planktonic diatom *Ditylum brightwellii* to examine spatial and temporal patterns of gene flow and population structure. Single-cell isolates were collected between 1997 and 2004 from Puget Sound and the Strait of Juan de Fuca, WA and analyzed using microsatellite markers, 18S rDNA sequences, internal transcribed spacer region I (ITSI) sequences and scanning electron microscopy (SEM). Microsatellites, the most variable set of markers analyzed here, revealed four significantly different populations that were each composed of thousands of genetically distinct clonal lineages. One population was sampled repeatedly over seven years. Isolates from each population contained identical 18S rDNA sequences, the most conserved region we analyzed. Furthermore, SEM revealed no morphological variation among isolates from different populations. Both 18S and SEM methods indicated that the different populations represent a single species. The ITS1, a moderately conserved region, contained two sequence types with a nucleotide divergence of 1.1 %. One sequence type was predominant in isolates of two populations. The remaining two populations contained isolates with a second sequence type. The clustering of ITS1 sequence types indicated long-term differential gene flow among populations. These results suggest that planktonic diatoms can be structured into metapopulations, with gene flow occurring more readily among some populations than others. By examining metapopulation dynamics, we are beginning to unravel factors that affect the adaptive potential of planktonic organisms and their ability to respond to environmental change.

POSTER PRESENTATIONS (Poster Board locations in parentheses)

(1) A BASELINE STUDY USING BIOFILM COMMUNITIES IN SHAMOKIN CREEK, AN AMD STREAM IN NORTHUMBERLAND COUNTY, PENNSYLVANIA

Christopher J. Gehman and Jack R. Holt. Department of Biology, Susquehanna University, Selinsgrove, PA.

Acid mine drainage has a significant impact on the aquatic ecosystems of Shamokin Creek, a tributary of the Susquehanna River in Northumberland County, Pennsylvania. Major portions of the creek have been declared dead, and are devoid of fish and benthic macroinvertebrates. However, a biofilm that includes periphyton dominated by diatoms does occur. Because the benthic diatom community structure is modulated by environmental conditions, it can integrate temporal and spatial variability as well as collective influences of multiple environmental factors. Also, periphyton communities have short lifespans, and they respond rapidly and predictably to pollutants. Therefore, we used diatom community structure, and biofilm composition as integrative biomonitors, in addition to standard water chemistry parameters of 4 sites on the main creek and upper tributaries for a six month period at 3-week intervals. Relative abundance of diatom taxa was assessed as an ongoing biomonitoring program of the stream and completion of a baseline survey on diatom community composition. Water chemistry parameters measured such as metal ion loads, buffering capacity, pH, and oxidation reduction potential varied significantly between sampling sites and sampling intervals. The most prevalent diatom taxa, *Eunotia exigua*, *Eunotia fallax, Pinnularia subcapita,* and *Frustulia rhomboides* are all species commonly found in highly acidic environments and collectively accounted for 89 percent of the diatom population. A two-way ANOVA analysis indicated that there is no significant difference in diatom community structure between sampling sites at the 0.05 significance level, which suggests that Shamokin Creek is uniformly impaired from the headwaters to the confluence with the Susquehanna River. We plan to use our baseline survey of diatom community composition as a reference to evaluate the efficacy of passive limestone drain mitigation treatment implemented in September 2006.

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(2) DIFFERENCES IN STREAM DIATOM COMMUNITY STRUCTURE INFERRED FROM SAMPLING ROCK AND BRYOPHYTE SUBSTRATA.

Jamie Deppen[1,2], Kam Truhn[1], and John D. Wehr[1]. [1]Louis Calder Center – Biological Station, Fordham University, Armonk, NY 10504; [2]Department of Biology, SUNY New Paltz, New Paltz, NY 12561.

Diatoms are an important part of stream food webs and are widely used as indicators of water quality in streams. Most ecological studies examining these communities focus almost entirely on epilithic (rock) habitats, even though some studies have also shown that the type of substrate can affect the biomass and species composition of diatom assemblages, and that at least some diatom species prefer to colonize lotic bryophytes. This study examined the species composition, richness and diversity of diatom assemblages from seven, 1st to 3rd-order streams in Harriman State Park, New York (same date, similar land cover and geology), using pairwise contrasts of assemblages from rock and bryophyte habitats. A total of 101 different taxa were identified from these streams, of these 39 taxa were unique to one stream, but diatom richness (ANOVA, $p = 0.091$) and diversity did not differ significantly among streams (Shannon H': $P = 0.73$; Simpson S: $P = 0.79$). Diatom species richness tended to be greater on bryophytes than on rocks, but differences were non-significant ($P = 0.189$). However, diatom diversity was significantly greater on bryophytes (H': 2-fold greater, $P = 0.0003$; S: 1.9-fold; $P < 0.0001$) than on rocks. Although rock and bryophytes communities differed, a comparison of diatom assemblages among different species of aquatic bryophytes revealed no significant differences in diatom richness or diversity. These data suggest that stream community analyses may differ according to habitats sampled, and that biodiversity surveys may need to consider algae that are epiphytic on aquatic bryophytes, in addition to standard epilithic samples.

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(3) CALCIUM DYNAMICS AND POLAR GROWTH IN THE DESMID, *PENIUM MARGARITACEUM*.

Daniel K. Washko and David S. Domozych, Department of Biology, Skidmore College, Saratoga Springs, NY 12866, USA.

Polar growth in green plant cells represents the manifestation of precisely coordinated events entailing various subcellular systems, the extracellular matrix and complex signal transduction mechanisms. In higher plants, polar growth is exemplified by pollen tubes, root hairs, rhizoids and protonemata. In charophycean green algae, tip-based expansion and associated development is found in rhizoids and protonema stages of *Chara*/*Nitella*, hair development in some *Coleochaete* species and in semicell development in desmids. In most desmids, polar growth occurs after cytokinesis when a small, daughter semicell undergoes morphogenesis and ultimately yields the same size/shape as the parent semicell. However, in the simple placoderm desmid, *Penium margaritaceum*, polar growth is expressed prior to cell division. Cell expansion and cell wall growth occurs in the central isthmus zone and displaces the older “parent” semicells outward. After a certain size is attained, rapid mitosis and cytokinesis occurs to yield “complete” daughter cell products. This type of growth pattern represents a transition from polar growth to a more “intercalary growth” mechanism. Calcium and associated signal transduction cascades play a significant role in regulating this type of growth. Fluorescence imaging with

Calcium Crimson reveals increased calcium levels in the isthmus zone during cell expansion. Wall and cell morphogenesis are altered under treatments with nifedipine, caffeine, verapmil and the calmodulin antagonist, W7. Cell wall deposition was also altered under low calcium conditions and when strontium was substituted. These results indicate that calcium dynamics both external and internal availability as well as transport mechanisms across the plasma membrane are critical to morphogenesis in this desmid.

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(4) SCANNING ELECTRON MICROSCOPY OF THE UNUSUAL CELL WALLS OF *ECTOCARPUS SILICULOSUS*. Bolajoko Fayoda, Paul Kelly, and Larry Lewis. Department of Biology, Salem State College, Salem, MA 01970, USA.

In cylindrical plant cells, at least one layer of cellulose microfibrils (approximately 5 nm in diameter) are observed at right angles to the long axis of the cells. It is believed that this arrangement is caused by the orientation of cortical microtubules. Commonly, multiple layers are found at 90^{o} angles with respect to each other. Others have found brown algal cells lack cortical microtubules. Some brown algal walls have been observed to have a multilayered and fibrillar nature as seen by transmission electron microscopy. In our study of *Ectocarpus siliculosus* using scanning electron microscopy and freeze fracture, we find the walls to consist of an outer amorphous layer and an inner layer of thick cables approximately 0.4-2.5 µm in diameter. At times, 0.3 µm extensions of the cables extend out from the wall. The large cables lie parallel to the long axis of the cells and appear embedded in an extension of the amorphous matrix. Thus, the cell walls of *E. siliculosus* appear unique and the expression of cellulose is unclear.

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(5) WOUND HEALING IN *CLADOPHORA CATENATA.* Michael J. Costello, Matthew Favazza, and Larry Lewis. Department of Biology, Salem State College, Salem, MA 01970, USA.

Wound healing is well established in the coenocytic members of the order Caulerpales. *Cladophora catenata* (UTEX #2888) has large multinucleated cells. After we cut through the cell wall and plasma membrane of a *C. catenata* cell, cytoplasm burst out of the wound and then quickly appeared to stop moving. The cell was placed in enriched seawater, and a week later the cell had not only recovered but had divided. Following this observation, individual apical and non-branching main axis cells were isolated by excision from healthy filaments. Cuts were made through the cell wall and plasma membrane, perpendicular to the long axis, approximately one-third of the way around the circumference of the cell. Expulsion of cytoplasm out of the cell through these wounds ceased rapidly as the expelled cytoplasm coagulated. Seven days subsequent to wounding, the cytoplasm in the recovering cell was restricted to a limited region of the cell. Recovering regions of punctured cells grew into irregular shapes in the second week of recovery. These observations of wound healing in a member of the Cladophorales are consistent with the hypothesis that this order is closely related the Caulerpales.

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(6) DIURNAL OSCILLATIONS IN NITRATE REDUCTASE TRANSCRIPT ABUNDANCE IN THE MARINE DIATOM *THALASSIOSIRA PSUEDONANA* (BACILLARIOPHYCEAE):

INFLUENCE OF NITRATE, LIGHT, AND THE CIRCADIAN OSCILLATOR. Katrina Twing, Katherine Brown, and Deborah L. Robertson. Clark University, Department of Biology, Worcester, MA 01610

Primary nitrogen assimilation is the process by which photosynthetic eukaryotes convert inorganic nitrogen, such as nitrate or ammonium, into organic nitrogen for use within the cell. Nitrate reductase (NR), which reduces nitrate to nitrite, is the first and rate limiting step in the assimilation of nitrate. Previous studies have shown that NR expression is highly regulated in marine diatoms with diurnal oscillations in enzyme activity and protein abundance. More recently, we documented diurnal oscillations in NR mRNA (*nia*) levels in the marine diatom *Thalassiosira pseudonana* (Hustedt) Hasle et Heimdal. In this study, we used quantitative real-time PCR to examine whether there was a correlation between the amount of nitrate available to cultures of *T. pseudonana* and *nia* abundance. Although all cultures exhibited diurnal oscillations in *nia* abundance, *nia* transcript abundance was greatest in *T. pseudonana* cultures grown on high levels of nitrate (880 μM), lowest in cultures grown on ammonium (60 μM), and intermediate levels were observed in cultures grown on lower concentrations nitrate (60 μM). These results indicate the importance of the environmental and/or intracellular concentration of nitrate in the regulation of *nia* abundance. We further examined whether *nia* abundance was under the control of a circadian oscillator and results from these experiments will be discussed. These results contribute to our understanding of the regulation of nitrate assimilation, a critical process regulating the growth and productivity of marine diatoms.

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(7) CHARACTERIZATION OF GSIII AND GSII FROM THE MARINE HAPTOPHYTE *EMILIANIA HUXLEYI* (PRYMNESIOPHYCEAE): EVIDENCE FOR SHARED EVOLUTIONARY HISTORY AMONG HETEROKONTS AND HAPTOPHYTES? Aurélien Tartar, Sohini Ghoshroy, Kevin Brown, and Deborah L. Robertson. Clark University, Department of Biology, Worcester, MA 01610.

Glutamine synthetase (GS) is an essential enzyme for ammonium assimilation and glutamine biosynthesis. Three distinct gene families (GSI, GSII, and GSIII) have been identified and are distributed among the major lineages of prokaryotes and eukaryotes. Although most photosynthetic eukaryotes express isoenzymes that function in either the cytosol or chloroplast, the evolutionary events that gave rise to the isoenzymes vary among lineages. For example, GS isoenzymes in vascular plants arose by relatively recent GSII gene duplications while in contrast, members of the GSII and GSIII gene families encode the chloroplast- and cytosolic-localized isoenzymes in diatoms, respectively. Here we report a similar pattern of GS isoenzymes expression in the haptophyte *Emiliania huxleyi* Hay et Mohler. The complete GSIII sequence was obtained from *E. huxleyi* using RT-PCR and a partial GSIII sequence was retrieved for *Prymnesium parvum* from an EST project. GSIII sequences of diatoms, *E. huxleyi*, and *P. parvum* were found in a well-supported clade in phylogenetic analyses of prokaryotic and eukaryotic GSIII sequences. GSIII sequences were retrieved for *Dictyostelium discoideum* and *Entamoeba histolytica*. Although there was only weak support for the monophyly of eukaryotic GSIII sequences, the presence of GSIII genes in diverse eukaryotic lineages suggests this gene family was present in nuclear genomes of early eukaryotes. GSII was also amplified from *E. huxleyi* and phylogenetic analyses revealed strong support among members of photosynthetic lineages (Plants + Chlorophytes + Rhodophytes + Heterokonts + Haptophytes). GSII from diatoms and *E. huxleyi* formed a well-supported clade; however, GSII sequences from heterokonts (diatoms and oomycetes) were not monophyletic. We propose that the evolution of

GS isoenzymes in diatoms and haptophytes reflects the endosymbiotic history of these lineages and indicates a clear link between host and symbiont genomes of heterokonts and haptophytes.

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(8) ADIRONDACK WETLAND BIOFILM ALGAE: COMMUNITY DYNAMICS, SEDIMENTATION EFFICACY AND NITRATE/PHOSPHATE ENRICHMENT IN A MICROCOSM STUDY. Katie Scheu and David S. Domozych, Department of Biology, Skidmore College, Saratoga Springs, NY 12866, USA.

Biofilm communities growing upon soft substrates within the photic zones of Adirondack wetlands contain a rich assortment of eukaryotic algae. The extracellular polymeric substances (EPS) secreted by these organisms are important to many biofilm-based activities and may also play key roles in the removal of particulate matter that enters the wetland. In this study, field and experimental microcosm analyses were employed in order to determine the changing biofilm algal populations over time, the ability of eukaryotic algae to remove particulates from the surrounding water column and to ascertain community make-up of eukaryotic algae under nitrate (N) and phosphate (P) enrichment. In the study of native biofilms, desmid population numbers were greatest during the mid-summer months while during September and October, diatoms and cyanobacteria dominated. In a corresponding laboratory-based microcosm experiment, we monitored the development of biofilms under controlled nutrient enrichment conditions, i.e., increased levels of N, P and N+P together. Subsequent Variable Pressure Scanning Electron Microscopic, confocal laser scanning microscopic and biochemical protocols showed that in pre-enrichment microcosm conditions, diatoms and the green alga, *Scenedesmus,* constituted much of the biofilm algal population. In the initial 3-week period after enrichment, diatoms, cyanobacteria and *Scenedesmus* characterized most of the biofilms except that the desmid, *Micrasterias*, and various filamentous and colonial green algae became prominent in N- or P-enrichment conditions. After 8 weeks, diatoms and cyanobacteria were common in all biofilms and several desmid species were found under N- and P- enrichment. In our microscopic analyses, the EPS of the biofilms was almost universally found to be rich in particulate materials. In order to assess the particulate uptake capabilities of the EPS of biofilm desmids, fluoresbrite beads were used in incubation studies. This work showed that different desmid taxa have distinct sedimentation efficacy capacities. Additionally, in a two-day competitive adhesion analysis, the adhesion efficacy of desmids was, in descending order, *Cosmarium, Pleurotaenium, Penium, and Closterium*. This introductory study indicates that biofilm algal populations are adaptable to nutrient changes and that algal EPS may also serve as an important sedimentation conduit in wetland biofilms.

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(9) POLAR CELL GROWTH AND CELL WALL DEVELOPMENT IN THE DESMID *PENIUM MARGARITACEUM*: PECTIN DYNAMICS. Laura Lambiase and David S. Domozych, Department of Biology, Skidmore College, Saratoga Springs, NY 12866, USA.

Penium margaritaceum is a simple placoderm desmid that possesses a cell wall rich in calcium-complexed, homogalacturonan (HGA). This desmid also displays an atypical form of cell morphogenesis in that semicell expansion and cell wall growth occurs prior to, rather than after, cytokinesis. The focal point of this cell expansion is a thin band found in the isthmus zone where relatively highly esterified HGAs are secreted. As these pectins are displaced outward from the isthmus, de-esterification occurs and is followed by the complexing of calcium. In this study, we performed a live cell labeling analysis of *P. margaritaceum* using monoclonal antibodies raised against various epitopes of higher plant HGAs including JIM5, JIM7, LM7 and 2F4. JIM7 was the marker used to identify the isthmus-based cell wall expansion band and was nearly always associated with the nucleus. During post-cytokinetic displacement of the nucleus to the center of the new daughter cell, the JIM7 band remained at the polar zone of the daughter semicell before ultimately fading. However, a new expansion band redeveloped quickly near the displaced nucleus and often yielded intercalary zones of new cell wall growth. This led to an asymmetrical pattern of pectin deposition in this desmid's cell wall. TEM analysis of this expansion zone revealed that the band, 2.5µm in width, possessed a cell wall that was devoid of the outer calcified projections common throughout most of the cell wall. On either side of this band, the projections were apparent. These observations suggest that highly esterified HGAs are secreted in the expansion band and as they are displaced in a polar fashion, they complex calcium to create a rigid wall. This distinct type of cell wall development was not affected by microtubule poisons but was reversibly inhibited by the Golgi Apparatus-affecting agent, brefeldin A. Cytochalasin E treatment inhibited cytokinesis which resulted in the formation of "filament-like" cell division products. Phalloidin and latrunculine treatment reduced cell wall growth significantly. Cell wall growth also appeared to be pH- and light- dependent. Finally, substitution of exogenous calcium with barium resulted in distinct oscillations in the cell wall morphogenesis.

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(10) RIBOSOMAL RNA LEADER SEQUENCE PERMITS SECONDARY STRUCTURE DETERMINATION OF THE ITS REGION IN HETEROCYSTOUS CYANOBACTERIA.

Mary Bridget Bowen, Jeff Johansen, Mike Martin, and Chris Sheil. Department of Biology, John Carroll University, University Heights, OH 44118.

Cyanobacteria have very few morphological characteristics that allow for differentiating between taxonomic classes. The paucity of phenotypes necessitates the use of molecular characters. Typically, researchers compare the 16S rRNA gene sequence and 16S-23S Internal Transcribed Spacer (ITS) sequence to determine evolutionary relationships among species. However, exclusively examining the linear DNA sequences ignores the functionally relevant secondary structures. We sequenced the entire 16S rRNA sequence for *Nostoc commune* from Wyoming. The secondary structure of the 16S rRNA molecule was determined and is reported for the first time for this genus. We also cloned and sequenced the promoter/leader/16S rRNA/16S-23S ITS region from several hetercytous cyanobacterial species in the genera *Nostoc* and *Tolypothrix*. The leader sequence and proximal 16S-23S ITS region interact in producing the secondary structure. The sequences we determined have permitted us to determine the secondary structure of the ITS, particularly the poorly studied structure at the 5' end of the ITS that binds to the leader. All ITS structures we determined vary markedly from each other and from published ITS structures in other genera.

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(11) DETERMINATION OF THE OPTIMUM HARVESTING TIME OF UNIALGAL FOOD STOCKS IN SHELLFISH AQUACULTURE.

Alexandra Lawlor, Karin A. Tammi, Kari Pohl, Jessie Alden and Timothy Scott. Center for Economic and Environmental Development, Roger Williams University, One Old Ferry Road, Bristol, Rhode Island 02809-2921.

Algal production can account for as much as 50% of the cost for rearing shellfish seed in a hatchery operation. For optimal shellfish production, there must be efficient algae production. Roger Williams University's shellfish hatchery maintains a variety of flagellate and diatom unicellular marine microalgal strains that are used as a food source for adult and larval shellfish. To feed the shellfish, the hatchery cultures eleven algal varieties, *Chaetoceros muelleri*, *Chaetoceros neogracile*, *Isochrysis galbana*, *Isochrysis* sp. (CISO), *Isochrysis* sp. (TISO), *Pavlova pinguis*, *Pavlova lutheri*, and *Tetraselmis* sp. (PLAT P, PLY 429, MC2). Beginning in January 2006, we monitored these strains for two months to determine the specific growth rate of each strain and to document our algal production. Batch cultures were transferred through volumes beginning at 125 ml and scaled up to 240 L. Growth rates for each strain were calculated repeatedly for two months based on direct haemocytometer counts. The results of this study indicated that logarithmic growth was achieved in the 240L calwall tubes, approximately 6 to 10 days after inoculation from a 20 L bath culture. Both *Pavlova* and *Isochriyisis* strains achieved maximum cell densities between 6 and 9 days respectively, followed by *Chaetoceros* and *Tetraselmis* strains, at 8 and 10 days respectively. This investigation determined the best time to harvest the algae before it crashes, thus optimizing algal production for the shellfish hatchery.

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(12) EFFECT OF LIGHT AND NITRATE ON NITRATE REDUCTASE GENE EXPRESSION IN *THALASSIOSIRA PSEUDONANA* (BACILLARIOPHYCEAE). Kathryn Brown and Deborah Robertson. Clark University, Department of Biology, Worcester, MA, 01610.

Diatoms contribute significantly to global primary productivity and nitrogen availability is a key factor regulating their productivity. Nitrate (NO_3^-), which enters marine ecosystems through physical processes such as upwelling and riverine inputs, is readily assimilated by diatoms. Reduction of NO_3^- to nitrite (NO_2^-) by nitrate reductase (NR) is the first and rate-limiting step in NO_3^- assimilation. Previous work demonstrated that in marine diatoms, NR activity and protein abundance exhibit a diurnal oscillation with maximal levels occurring mid-light period and lowest levels occurring during the dark phase. Both light and NO_3^- availability appear important in establishing and maintaining the diurnal pattern. Although the regulation of NR activity and protein abundance has been investigated, little is known regarding the role of transcriptional regulation. We examined the influence of NO_3^- and light on NR mRNA (*nia*) levels in the marine diatom *Thalassiosira pseudonana* (Hustedt) Hasle et Heimdal. The presence of NO_3^- in the culture medium was important in maintaining *nia* levels regardless of whether cells had light. Following a nutrient 'shift-up' (to NO_3^- or NH_4^+), a diurnal oscillation in *nia* abundance was observed, similar to the pattern of NR abundance and activity. Levels of *nia* in both treatments increased over the first 24 h following the shift, reached maximum transcript levels 2 h after the dark:light transition period, and then declined over the light period. There was a greater amplitude in *nia* abundance in NH_4^+- than NO_3^- -grown cells; *nia* decreased rapidly after the addition of NH_4^+ and the onset of light. Further experiments are underway to distinguish whether the rapid decrease in *nia* abundance is a direct effect NH_4^+ addition or due to the absence of nitrate. Our results indicate that either transcriptional or post-transcriptional processes are important in regulating *nia* abundance and are important in the regulation of NR expression.

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(13) A FLORISTIC SURVEY OF MARINE TUBE-FORMING DIATOMS AND THEIR COHABITANTS IN CANADIAN WATERS USING DNA BARCODING. Sarah E. Hamsher

and Gary W. Saunders. Department of Biology, University of New Brunswick, Fredericton, N.B., Canada, E3B 6E1.

Diatoms are ubiquitous single-celled algae that are commonly identified by the fine structure of their silica valves. Unfortunately, many of the morphological characters used to identify diatoms including valve shape, pore occlusion, and hollow versus solid spines are qualitative and identification for similar species can differ between analysts and laboratories. This can be especially a problem when compiling data across large geographical regions or between various authors. DNA barcoding is a molecular technique that uses sequence comparisons of the *coxI*-5' region of the mitochondrial genome to distinguish species and has been used successfully to identify species of Rhodophyta. My project will use DNA barcoding to identify species of marine tube-forming diatoms and document their distribution and biogeography in Canada. Clonal cultures of these diatoms will be established and used to develop a protocol for single cell extraction, which will facilitate analyses of environmental samples and determine the presence/absence of tube-forming diatoms collected from a variety of habitats in the Bay of Fundy. In addition, we will examine evolutionary relationships among species of the genera *Berkeleya*, *Parlibellus*, and *Navicula* (specifically the tube-forming species) using small subunit ribosomal DNA. Preliminary results for this research program will be presented.

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(14) DNA BARCODING: AN EFFICIENT TOOL TO DISTINGUISH TAXONOMICALLY DIFFICULT ALGAL SPECIES OF *PORPHYRA* (RHODOPHYTA), *ULVA* (CHLOROPHYTA) AND *FUCUS* (PHAEOPHYCEAE). Hana Kucera and Gary Saunders. Department of Biology, University of New Brunswick, Fredericton, N.B., Canada, E3B 6E1

A consortium of researchers is undertaking a large-scale project to discover and identify all eukaryotes in Canada using the DNA barcode. DNA barcoding (*cox1*-5' = DNA barcode) has been used to distinguish species, and identify new species. A major advantage of this undertaking is that DNA barcoding will become a standardized, rapid species identification tool, with a relatively low cost. The DNA barcode is an ideal method to assess species diversity in taxonomically difficult genera because it provides an objective approach to species identification. In this study we develop, test and apply the DNA barcode technique to taxonomically difficult genera within three dominant marine macro-algal genera: *Porphyra* (Rhodophyta), *Ulva* (Chlorophyta), and *Fucus* (Phaeophyceae). Species within these genera are often difficult to identify in the field because they have simple morphologies that lack substantial characters for taxonomic work and display phenotypic plasticity such that there is morphological overlap between some species. The DNA barcode distinguishes three of the four currently recognized species of *Fucus* in Canada (it fails only in the case of the close sister species *F. vesiculosus* and *F. spiralis*), and has uncovered substantial phenotypic plasticity in Pacific *F. distichus*. Preliminary testing in the genus *Porphyra* shows that the DNA barcode is an effective tool for species identification and the recognition of cryptic species. Within the genus *Ulva*, the existence of previously published species-level molecular phylogenetic data provides a solid framework against which to evaluate the effectiveness of the DNA barcode in delimiting species. To this end we are designing barcode primers specific to the green algae in order to assess the utility of this marker for discriminating among species in this group. We will present our results in evaluating the DNA barcode as a tool for distinguishing among these species taxonomically difficult algal genera.

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(15) THE G:T RATIO OF INTERTIDAL CHONDRUS CRISPUS IN THE LONG ISLAND SOUND, CONNECTICUT.

Michele Guidone. Biology Department, Southern Connecticut State University, 501 Crescent St., New Haven, CT 06515, USA.

Describing the distribution of a species life history stages is an essential step towards revealing patterns in population structure and understanding the forces that cause such patterns. Studies of intertidal populations of the alga *Chondrus crispus* Stackhouse have reported a wide range of life history ratios, but no consistent pattern has emerged. The purpose of this study was to measure the ratio of gametophytes to tetrasporophytes (G:T ratio) of intertidal populations of *Chondrus crispus* in the Long Island Sound, Connecticut. Sampling was conducted at three sites in the Long Island Sound and one from the Rhode Island Sound for comparison. Sites sampled within the Sound were 62, 78, and 90% gametophytic, with gametophyte abundance increasing from west to east. Several environmental factors have a west to east gradient in the Long Island Sound, including flow speed and salinity. More studies will be needed to verify the consistency of the observed west to east pattern in G:T ratio and to determine which environmental factors play a role in *C. crispus* life history stage distribution.

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(16) SEDIMENT CHLOROPHYLL CONCENTRATIONS IN A HEADWATER STREAM UPSTREAM AND DOWNSTREAM FROM A MICHIGAN FISH HATCHERY.

Gwen Kloosterman and Donna K. King. Central Michigan University, Mount Pleasant, MI 48858.

A comparison of water quality parameters was performed on Slagle Creek in Wexford County, Michigan to determine the effects of hatchery effluent on the stream. Two sampling sites were chosen, one upstream and one downstream from Harrietta State Fish Hatchery. Sampling was conducted monthly from May through September 2005 at both sites. Stream water was sampled for temperature, pH, dissolved oxygen, conductivity and nutrients (PO_4, NO_3, NH_4). Sediment core samples (75cm diameter) were collected for trichromatic chlorophyll analysis to estimate algal abundance. Nutrients were generally higher at the downstream site. Soluble reactive phosphorus, the form readily available to organisms, ranged from 2.20 to 6.46 μg/l at the upstream site and from 4.28 to 9.61 μg/l at the downstream site. Ammonia concentrations ranged from 0.02 to 3.34 μg/l at the upstream site and 1.21 to 5.56 μg/l at the downstream site. Phaeophyton corrected chlorophyll a concentrations were higher at the downstream site (15.21 $\mu g/cm^2$, standard error 1.38) than at the upstream site (10.24 $\mu g/cm^2$, standard error 1.17). Despite the lower chlorophyll a concentrations, chlorophyll b and c concentrations were consistently higher at the upstream site than at the downstream site. At the upstream site the average chlorophyll b concentration was 3.28 $\mu g/cm^2$ (standard error 0.77) and the average chlorophyll c concentration was 16.25 $\mu g/cm^2$ (standard error 2.4). At the downstream site, average chlorophyll b and c concentrations were 1.72 $\mu g/cm^2$ (standard error 0.77) and 11.34 $\mu g/cm^2$ (standard error 1.11), respectively. The trichromatic analysis suggests that the increased algal abundance at the downstream site consists primarily of cyanobacteria while the upstream site has a community dominated by diatoms and chlorophyta.

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(17) BACTERIAL ATTACHMENT TO PHYTOPLANKTON IN MONTEREY BAY.

Jason R. Graff, Jan Rines, and David C. Smith. The Graduate School of Oceanography, University of Rhode Island, South Ferry Road, Narragansett, RI 02906, USA.

Interactions between phytoplankton and bacteria are important in microbial loop processes and may be important in phytoplankton bloom dynamics and species succession. In 1966, as knowledge regarding the ecological roles of marine bacteria was growing, the rate of bacterial attachment to the marine diatom *Skeletonema costatum* was quantified by Droop and Elson. Since then, many studies have confirmed the attachment of bacteria to phytoplankton cells with few quantifying specific rates of attachment. In July 2006, the attachment of bacteria to phytoplankton was studied in Monterey Bay, California. Phytoplankton and free-living and attached bacteria were visualized and enumerated with the fluorescent nucleic acid stain SYBR Green I and fluorescence microscopy techniques. An analysis of two of the dominant diatoms in the ecosystem, *Chaetoceros sp.* and *Pseudo-nitzschia sp.*, indicates that these diatoms harbored low numbers of attached bacteria. More than 80% of cells and 58% of diatom chains were bacteria free in all samples. Cells or chains with bacteria harbored as few as 1 and as many as 4 bacteria.

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(18) AUTOMATED IMAGE ANALYSIS OF AUTOTROPHIC PICOPLANKTON, Malcolm McFarland and Jan Rines, Graduate School of Oceanography, University of Rhode Island, South Ferry Rd., Narragansett, RI 02882, USA.

Small autotrophic picoplankton, such as *Synechococcus* and *Prochlorococcus*, are important components of marine phytoplankton communities. Their distribution, abundance, and physiology can influence ecosystem structure and function. Traditional manual cell counts of these organisms are labor intensive, limiting the type of data and total number of samples that can be analyzed. Flow cytometry is an efficient technique that can quantify picoplankton cell density, fluorescence and light scatter, but instrument cost is often prohibitive. Epifluorescence microscopy combined with digital photomicrography and automated image analysis represent an alternative methodology that can quantify cell density, cross sectional area, shape and relative fluorescence with high efficiency. Size and shape, in particular, are biologically important characteristics of cells that are not easily measured by traditional microscopy or flow cytometry. Autofluorescent picoplankton are well suited to automated image analysis techniques because of their high abundance, small size and simple shapes. We have used image analysis to characterize picoplankton populations in water samples collected from Monterey Bay, CA during a large collaborative oceanographic research project (Layered Organization in the Coastal Ocean). The resulting data reveals patterns in the vertical distributions of cell density, fluorescence, and morphology.

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(19) DIATOMS OF THE HOLOCENE FROM POUTWATER POND BOG, HOLDEN, MA. Adrienne P. Smyth and Peter M. Bradley. Department of Biology, Worcester State College, 486 Chandler St., Worcester, MA 01602, USA.

Diatoms isolated from a 495 cm core from the *Sphagnum* peatland surrounding Poutwater Pond, Holden, Massachusetts, were examined by scanning electron microscopy to evaluate their historical colonization of the site and their presence as environmental indicators over the last 8,500 years. Both freshwater centric and pennate diatom species were found. The presence of the centric *Aulacoseira* and *Cyclotella* diatom species at the earliest time suggests a planktonic deep-water oligotrophic lake environment of low acid neutralizing capacity indicative of peatland initiation. Acidophilic pennate diatom species characteristic of bogs, *Eunotia*, *Pinnularia* and *Tabellaria* were present, in addition to *Stauroneis*, and *Neidium* species types. The diatom taxa at this site were similar to other peatlands, but differences in diatom species distribution worldwide may be observable by high-resolution picture documentation and identification.

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(20) TEMPORAL COMPARISONS OF PHYTOPLANKTON SPECIES COMPOSITION AMONG HABITAT TYPES IN POOL 8 IN THE UPPER MISSISSIPPI RIVER.

Smith, J.K and Wehr, J.D. Louis Calder Center- Biological Station, Fordham University, Armonk, USA

The Upper Mississippi River is one of the largest and most spatially heterogeneous river floodplain ecosystems in the world. This study focused on two aquatic habitat types, main channel and backwaters, each varying in degree of discharge, sediment type, and macrophytes densities. Our work is focused in Pool 8 (near La Crosse, Wisconsin) of the Upper Mississippi and aimed to (a) produce both a quantitative assessment of spatial and temporal patterns in phytoplankton composition and (b) to identify functional algal groups. Samples used for this study were a subset of archived samples collected between 1994 and 2006. We found clear differences in algal species composition among habitats; the most pronounced differences were associated with reduced discharge (low connectivity) and backwater habitats. Whereas centric diatoms, particularly *Aulacoseira granulata*, *Cyclotella meneghiniana*, and other diatoms dominate main channel habitats, cyanobacteria (*Microcystis* spp., *Aphanizomenon flos-aquae)* and cryptophytes predominate in backwater habitats. Additionally, species composition was found to vary among years, which could be the result of long-term anthropogenic impacts such as channel alternation and nutrient loading, as well as impacts caused by invasive grazer introductions over this 12-year period. Annual variation is most likely the result of climate and discharge.

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(21) A SURVEY OF MACROALGAL DISTRIBUTION AND ABUNDANCE IN NINIGRET POND, A RHODE ISLAND COASTAL LAGOON.

Heather M. Shannon and Carol S. Thornber. Department of Biological Sciences, University of Rhode Island, Kingston, RI 02874.

Coastal lagoons form the southern boundary of much of Rhode Island; one of the largest lagoons in this system is Ninigret Pond. Many ecological studies of the distribution and abundance of marine organisms have been performed here over the past several decades, as it is home to both ecologically and economically important species. However, the last formal investigation of the macrophyte communities was conducted in 1980, when extensive eelgrass beds (*Zostera marina*) and associated macroalgal communities dominated the western end of the lagoon; since that time, anecdotal reports had suggested a large decrease in algal and eelgrass abundance. During the summer of 2005, we monitored six stations located throughout the pond for algal and plant cover on a biweekly basis, and the data were analyzed to determine shifts in the seasonal and temporal abundance of macroalgae, as well as describe the changes that have occurred over the past two decades. We found that eelgrass had completely disappeared from the western end of the pond, and the majority of the pond was devoid of any vascular plant life. Macroalgae that are dominant in this area of the pond are mainly unattached and filamentous species (i.e. *Polysiphonia spp.*, *Chaetomorpha linum*). The highest diversity of macroalgae occurred nearest the one ocean breachway, and consisted mainly of unattached algae of a variety of functional forms and taxonomic groups. These results are sharply different from previous surveys, indicating the need for repeated, long-term monitoring of ecologically sensitive habitats.

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(22) BIOGEOGRAPHY OF MICROBIOTIC CRUSTS IN JOSHUA TREE NATIONAL PARK.

Nicole Pietrasiak[1], Jeffrey R. Johansen[1] and Tasha La Doux[2], [1]Biology, John Carroll University, 20700 North Park Blvd., University Heights, OH 44118, [2]Joshua Tree National Park, National Park Service, 74485 National Park Drive, Twentynine Palms, CA 92277, USA.

All wilderness segments within the boundaries of Joshua Tree National Park were surveyed for frequency and cover of microbiotic soil crusts. Areas within both the Mojave Desert and Colorado Desert were examined. A total of eight vegetation community types were sampled. In order of greatest sample representation, these community types were: Sonoran Creosote Bush Scrub, Mojave Creosote Bush Scrub, Blackbrush Scrub, Mojave Pinyon-Juniper Woodland, Mojave Mixed Woody Scrub, Mojave Mixed Steppe, Stabilized Sand Dunes, Sonoran Mixed Woody and Succulent Scrub. A total of 75 research sites were established in the summer of 2006. At all sites, 100 1.0 m^2 frequency plots and 250 cover points were scored for shrub vegetation (by species), perennial grass and forbs, cacti, annuals (cover only), rock, and several crust categories (algal, lichen, moss, mixed crust). Crust cover was generally low in most areas of the park in comparison to crust cover in other arid lands of the western United States. Cover for total microbiotic crust was on average only 13.1%, with most of that cover attributable to algal crust (11.4%). The remaining cover was due to lichens. Only one site of the 75 had any detectable moss cover. The vegetation zones with highest crust cover were Mojave Creosote Bush Scrub (18.7%), Sonoran Creosote Bush Scrub (14.4%), and Mojave Mixed Woody Scrub (9.9%). All other vegetation zones had less than 6% average crust cover. There was a weak correlation between the soil stability index and crust cover (R^2=0.41).

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(23) EXAMINATION OF THE *THALASSIOSIRA LACUSTRIS* (BACILLARIOPHYCEAE) SPECIES COMPLEX.

Nicole Miller and Jeff Johansen. Department of Biology, John Carroll University, University Heights, OH 44118.

An unusual centric diatom taxon in the genus *Thalassiosira* (Thalassiosiraceae, Bacillariophyceae) was collected in a small lotic system in a city park in Northeastern Ohio. The species closely resembles a species reported from brackish waters of the Baltic Sea, *Thalassiosira lacustris*. Our species was smaller, more finely striated, and less tangentially undulate than *T. lacustris*, and we concluded it was a species separate from that taxon. Upon examination of type material of *T. lacustris*, it was clear that our taxon represented a taxon separate from *T. lacustris*. However, a freshwater species known as *Cyclotella punctata*, was very similar to our material. *C. punctata* has long been considered a synonym of *T. lacustris*, but examination of type materials showed it to be much smaller and less tangentially undulate, similar to our strains. *T. kilarskii*, a recently described taxon from fossil material, is similar to our taxon, but differs in the absence of spines. It appears to us that we have either two taxa, *T. lacustris* and T. *punctata*, or four taxa, *T. lacustris*, *T. punctata*, *T. kilarskii* and a new species from Ohio. It is difficult to draw a clear conclusion due to the variability in expression of spines on the valves. At present we can certainly conclude that the brackish water taxon *T. lacustris* is definitely not the same as the freshwater species *T. punctata*. The fate of the other two undecided freshwater populations is uncertain at this time, although we suspect they are distinct taxa.

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(24) CYANOBACTERIA OF WET WALLS AND SEEPS AT GRAND STAIRCASE-ESCALANTE NATIONAL MONUMENT.

Markéta Krautová and Jeff Johansen. Department of Biology, John Carroll University, University Heights, OH 44118, USA.

Grand Staircase-Escalante National Monument was established as a park by President Clinton in 1997 under authority of the Antiquities Act. This park is one of the largest national parklands set aside in the western United States, yet because of the recentness of its establishment, relatively little biological research has been done in the park. In August 2006 we sampled many of the wet seeps and springs located in the monument and have undertaken study of the algae of these seeps. At present we have about 200 cultures of cyanobacteria isolated from these habitats, and have found at least 50 taxa within these cultures. The most commonly isolated genus is *Leptolyngbya*, and we have many species in this problematic character-poor group. Putative new species have been found in the genera *Chamaesiphon, Rivularia, Lyngbya, Microchaete, Tapinothrix* and *Cyanosarcina.* Species unambiguously identified include: *Pleurocapsa minor, Calothrix parietina, Geitlerinema amphibium, Aphanocapsa musicola, Chroococcus cohaerens, Chroococcus spelaeus, Leptolyngbya subtillissima, Leptolyngbya compacta*, and *Leptolyngbya carnea*.

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(25) COMPARISON OF THREE ORGANELLE MARKERS FOR PHYLOGEOGRAPHIC INFERENCE IN *BATRACHOSPERMUM HELMINTHOSUM* (BATRACHOSPERMALES, RHODOPHYTA) FROM NORTH AMERICA.

Denise L. House[1], Alison R. Sherwood[2] and Morgan L. Vis[1]. [1]Department of Environmental and Plant Biology, Ohio University, Athens, OH 45701; [2]Botany Department, University of Hawaii, Honolulu, HI 96822

Phylogeographic signal provided by the newly proposed 23S plastid rRNA marker (UPA) and the cytochrome oxidase subunit 1 marker (COI) for intraspecific variation in the freshwater red alga *Batrachospermum helminthosum* throughout its range in North America was investigated. These markers were compared in individuals from a previous study of the cytochrome oxidase 2-3 spacer region (*cox*2-3), which has yielded the most useful data to date with thirteen haplotypes among geographic locations. Five haplotypes were resolved for the UPA, differing by only 1-2 base pairs (bp), and we conclude that this marker may be more appropriate for studying interspecific variation among closely related taxa. In contrast, the COI gene revealed 14 haplotypes, differing from 1-46 base pairs or up to 6.9% sequence variation. The intraspecific variation of COI in this taxon is much greater than that reported thus far for marine red algae (generally <5 bp), but is in accord with levels shown *B. macrosporum* with up to 48 bp within distant locations in Brazil. The COI gene is comparable to the *cox*2-3 spacer for phylogeographic studies as the haplotype networks were similar and showed the same geographic patterns. To our knowledge, this is the first comparison of these two regions for phylogeographic research in the red algae.

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(26) MECHANISM OF DESICCATION TOLERANCE IN *PORPHYRA* SPECIES

Yen-Chun Liu, and Donald Cheney. Biology Department, Northeastern University, Boston, MA 02115.

Intertidal seaweeds provide a unique model system for studying desiccation tolerance because of their large and rapid change in water content twice a day. We are studying the mechanism of desiccation tolerance in *Porphyra* because these plants can be easily grown in the lab, which removes other environmental stresses such as high light and extreme temperatures, and allows us to study solely desiccation tolerance. In addition, because *Porphyra* has a simple construction, the results will not be confounded by structural protection. *Porphyra umbilicalis* and *P. yezoensis* exhibit significant differences in their tolerance to desiccation. While both species lose more than 95% of their water in the first two hours of desiccation and their final relative water content is virtually the same, *P. umbilicalis* survives up to three weeks whereas *P. yezoensis* dies after three hours of desiccation. Thus, the resistance in *P. umbilicalis* is not due to acclimation or avoidance of water loss, which is a common approach in terrestrial plants. Massive membrane leakage, reduced respiration and reduced oxygen evolution was observed in the susceptible species, *P.* yezoensis, after three hour desiccation, but not in *P. umbilicalis*. Similarly, TEM investigation has showed extensive membrane disruption only in desiccated *P. yezoensis.* Reactive oxygen species (ROS) defense does not appear to be a key factor, because neither species show an increase in membrane peroxidation after desiccation. We are using FTIR to investigate whether differential membrane fluidity plays a role in desiccation tolerance in *P. umbilicalis.*

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(27) REGULATION OF POLYUNSATURATED FATTY ACID SYNTHESIS IN THE MARINE RED ALGA *PORPHYRA YEZOENSIS.*

Angela Silvestro, Yen-Chun Liu, and Donald Cheney. Biology Department, Northeastern University, Boston, MA 02115.

The marine red macroalga *Porphyra yezoensis* is rich in long-chain polyunsaturated fatty acids (PUFAs). In particular, the omega-3 fatty acid eicosapentaenoic acid (EPA; C20:5) comprises about 50% of the total fatty acids of the blade life phase. The conchocelis phase is high in the omega-6 fatty acid arachidonic acid (AA; C20:4). Because of their health benefits, these PUFAs are essential in the human diet and in the diet of aquacultured fish. Despite the prevalence of PUFAs in *P. yezoensis,* the exact function and biosynthesis pathway of these fatty acids in this species or in any other seaweed is unknown. Since *P. yezoensis* is cold and freezing tolerant, it was hypothesized that this species can acclimate to low temperature by increasing membrane lipid unsaturation. To understand the regulation of fatty acid synthesis at different temperatures, *P. yezoensis* was grown at 0°C, 8°C, and at 15°C for 1-6 days. An increase in the percentage of unsaturated fatty acids was observed in *P. yezoensis* only after 6 days of culture at 0°C. Currently, investigations are underway to determine if this increase in unsaturation confers greater membrane fluidity and to determine the transition temperature (T_m) of *P. yezoensis* membranes using Fourier Transform Infrared (FTIR) spectroscopy analysis. An inverse relationship between AA and EPA production was also observed, as would be expected if *P. yezoensis* uses a PUFA biosynthesis pathway similar to that of other species in which both EPA and AA are synthesized from one common precursor. In addition, to better understand PUFA biosynthesis in *P. yezoensis,* a putative fatty acid desaturase was identified. This 1957 bp gene codes for an ORF of 566 amino acids that shows highest sequence similarity to the delta-5 fatty acid desaturase from *Pythium irregulare,* an oomycete fungus. The source of this gene was determined to be the *P. yezoensis* genome by confirming that cultures are free of *Pythium* contaminants.

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(28) CHARACTERIZATION OF A ROCKY INTERTIDAL SHORELINE WITHIN ACADIA NATIONAL PARK: IMPACT OF SHORT-TERM TRAMPLING IMPLICATIONS FOR MANAGEMENT.

David Olson, Susan Brawley, and James Wilson. School of Marine Sciences, University of Maine, Orono, ME, 04469, USA.

Millions of people visit Acadia National Park (ANP) in Maine each year. For example, over six million people visited ANP between 2004 and 2006, with the peak period being July - September. In July 2002, ANP staff received management responsibilities from the National Park Service (NPS) for a 2 km section of shoreline and approximately 100 acres of land located on Schoodic Point, Winter Harbor, Maine. Prior to July 2002, this land and shoreline were a U.S. Naval Base. Due to its military status, there was no public access to this shore from the mid-1930s until its transfer to the NPS in 2002. The restricted access protected the shore, which appears to be unusually pristine. Studies elsewhere have found an inverse relationship between the intensity of foot traffic on rocky intertidal shores and the abundance of large, sessile organisms and percent cover of macroalgae. In summer 2006, we conducted an observational pilot study to determine what visitors to ANP do in the intertidal zone and how much time they spend in the intertidal zone. We observed higher numbers of visitors at sites with designated pull-out areas and easy access to the shoreline. We will conduct a full study of visitor intensity and activities in summers 2007 and 2008. In addition, we will characterize the biota on the shoreline and conduct an experimental trampling study. Characterization of the shoreline will provide the NPS with a baseline on the assemblage structure at five study sites with similar exposures in ANP, and results of the trampling study will provide data on potential impact from visitor use. The Park Service will use these data in management of the shores. (Funded by the NPS).

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(29) IMITATING SOLAR UV-B RADIATION IN THE LABORATORY: PROBLEMS AND SOLUTIONS.

Priya Sampath-Wiley and Leland S. Jahnke. Department of Plant Biology, University of New Hampshire, Durham, NH.

One design limitation in laboratory UV-B experiments results from the spectral composition of radiation emitted by UV-B lamps. Commonly used lamps generate shorter wavelengths not present in natural solar flux reaching ground level (i.e. UV-C) plus excessive short wavelength UV-B. We have developed a liquid urate (UA) filter that has proven to be more effective than cellulose acetate (CA) at removing UV-C and short wave UV-B radiation from UV-B lamp emissions. Liquid filters containing an aqueous solution of uric acid were shown to generate a sharp transmission cutoff in the middle of the UV-B range. By altering the concentration of the urate solution within the filter, we are able to reshape the UV-B spectrum emitted by UV-B lamps, rendering it nearly identical to that of sunlight. Initial comparisons between CA and UA filtration have suggested that seemingly minute differences in the shortwave UV-B spectrum facilitate dramatic physiological responses. Cultures of the unicellular green alga *Dunaliella tertiolecta* were exposed for 12hrs to UV-B radiation (6mmol m^{-2} s^{-1}) filtered by either CA or UA. Cultures exposed to UV-B radiation filtered by CA exhibited 50% higher ascorbate peroxidase activities, 36% lower catalase activities and 30% lower photosynthetic activities compared to cultures exposed to UV-B radiation through UA filters. The effect of shortwave UV-B on the physiology of *Dunaliella* will be discussed in relation to its antioxidant and photosynthetic metabolisms.

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(30) THE ROLE OF PHYTOPLANKTON PRODUCTIVITY AS A POSSIBLE MECHANISM FOR PLANKTON LAYER FORMATION.

Heather Anne Wright and Susanne Menden-Deuer. Graduate School of Oceanography, University of Rhode Island, Narragansett, R.I., 02882, USA.

East Sound, Washington is a shallow fjord where concentrated patches of phytoplankton form in layers, here termed plankton-rich layers (PRLs). To investigate the role of phytoplankton growth contribution to PRL formation, productivity rates were measured at a total of four stations along a longitudinal transect through the fjord. At each station, vertical fluorescence profiles were used to identify two sampling depths: one within a PRL (when present) and one below. Net productivity rates were measured using the ^{14}C incubation method for 2 hours at six light intensities ranging from 0 to 100%, for size fractionated plankton < and > 20μm respectively. Higher rates of productivity were measured for phytoplankton <20μm irrespective of layer association. Generally, the smaller size fraction reached higher maximum photosynthetic rates (P_{max}) and utilized light more efficiently (higher α) at low light levels. Despite the higher productivity rates of smaller phytoplankton, larger cells dominated the phytoplankton biomass, suggesting that growth is balanced by loss processes for the smaller size class. This summer, zooplankton grazing rates will be measured to examine if differential grazing pressure on the two size classes can explain the difference in production and accumulation. Quantifying both growth and removal rates will establish mechanisms for layer formation and maintenance and provide insight into how changes in composition affect trophic dynamics in a coastal marine ecosystem.

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(31) REPRODUCTIVE ECOLOGY OF *CODIUM FRAGILE* SSP. *TOMENTOSOIDES* IN MASSACHUSETTS.

Chris McHan[1], Donald P. Cheney[1], Geoffrey C. Trussell[1,2], and Sal Genovese[2]. [1]Department of Biology, Northeastern University, Boston, MA 02115, USA; [2]Northeastern University Marine Science Center, 430 Nahant Road, Nahant, MA 01908, USA.

Since its initial introduction into Long Island Sound, NY reported in 1957, the green marine alga *Codium fragile* ssp. *tomentosoides* has invaded, and often dominated, subtidal communities from Nova Scotia to North Carolina. The rapid dispersal and unusual success of this alga has prompted numerous studies on the physiological and ecological characteristics of this introduced subspecies. Emerging from these studies is a picture of an introduced species highly plastic in its physiological tolerances, reproductively versatile, and, for the most part, ecologically freed from herbivory and competition. Building on the findings of these past studies, this work concentrates on two areas of the reproductive ecology of *Codium*: 1) the role of fragmentation in the dispersal of parthenogenic reproductive cells and, 2) the mechanisms allowing this alga to persist in sandy habitats not typically suited for marine algae requiring hard substrate. For the first objective I am testing the ability of fragments to remain non reproductive over various time intervals before being stimulated to develop reproductive structures and release parthenogenic gametes, examining differences in reproductive output and viability of the gametes released. For the second objective I am examining the role of the benthic mollusk *Crepidula fornicata* as a form of living substrate. Preliminary data taken from Harwichport, MA in the spring of 2006 has shown that 98% of the *Codium* sampled was found attached to *Crepidula*. Based on these findings field studies are being used to examine both selective settlement on and subsequent survival of *Codium* on *Crepidula* versus non-living substrates.

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(32) THE USE OF cDNA LIBRARIES TO INVESTIGATE ASEXUAL REPRODUCTION IN *PORPHYRA UMBILICALIS* (L.) Kützing.

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Gene expression varies across different cell types within organisms. We are investigating gene expression during asexual versus sexual differentiation in *Porphyra umbilicalis*. This red alga is a model organism for studying differences in gene expression during reproduction because of its reproductive biology. *Porphyra umbilicalis* reproduces sexually in the northeastern Atlantic while it appears to have lost this ability in at least part of the northwestern Atlantic. An exclusively asexual population appears to exist within this species in the Gulf of Maine. We constructed lambda phage cDNA libraries from poly(A)$^+$ RNA extracted from vegetative tissue and tissue of either differentiating or fully mature asexual reproductive structures from northwest Atlantic *P. umbilicalis*. We will also generate libraries from sexually reproductive tissue and construct subtracted libraries to identify genes specific for both sexually and asexually differentiating tissue. Preliminary screening of clones derived from our library of asexually differentiating tissue has revealed genes encoding proteins involved in photosynthesis, translation, signaling, and nutrient transport. Further screening of the libraries should allow us to identify specific genes that may be involved in sexual/asexual differentiation. Differences in expression levels will be confirmed using quantitative RT-PCR and Northern blot analysis of targeted genes. This study could lead to new information concerning regulatory control of biochemical pathways during reproduction and of the advent and persistence of asexuality within sexual lineages. (Supported by Maine Sea Grant College Program, Grant #NA06-OAR-4170108)

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(33) CELLULOSE SYNTHASE (*CesA*) GENES IN THE RED ALGA *PORPHYRA YEZOENSIS* UEDA

Eric Roberts[1] and Alison W. Roberts[2]. [1]Department of Biology, Rhode Island College, Providence, RI 02908, USA; [2]Department of Biological Sciences, University of Rhode Island, Kingston, RI 02892, USA.

The cell walls of the conchocelis phase of *Porphyra* species contain cellulose microfibrils. As in green plants, these microfibrils are synthesized by clusters of cellulose synthase enzymes (“terminal complexes”) that move in the plasma membrane. However, the morphologies of the *Porphyra* terminal complexes and the cellulose microfibrils they produce differ from those of green plants (J. Phycol. 30:300). To characterize the genetic basis for these differences, we are identifying and sequencing cellulose synthase (*CesA*) genes from *Porphyra yezoensis* Ueda strain TU-1. A single sequence with similarity to land plant *CesA* genes was identified by searching a database of 20,779 *P. yezoensis* EST sequences (DNA Res. 7:223). The conceptual translation of the corresponding 1093 bp cDNA clone (provided the Kazusa Plant Research Institute) includes two of the four catalytic domains that characterize CesA proteins. Using TAIL PCR with primers based on the cDNA sequence, we amplified four *CesA* fragments from *P. yezoensis* TU-1 genomic DNA. These fragments assembled with the cDNA sequence to form a contig that hypothetically encodes all four CesA catalytic domains and the expected N- and C-terminal transmembrane domains. The sequence is most similar to cyanobacterial *CesA* genes and a class of *CesA-like* genes present in the genomes of *Physcomitrella patens* and *Selaginella moellendorfii* but not spermatophytes. Slight differences in the overlapping sequences show that the contig represents at least two different *CesA* genes, a finding consistent with the presence of multiple *CesA* genes in land plant genomes. We are currently attempting to generate full length genomic and cDNA clones of *P. yezoensis CesA*s and preparing Southern blots to estimate the number *CesA* genes in the genome. Comparing the *CesA* genes of *P. yezoensis* and land plants may lead to the identification and ultimately the ability to manipulate the sequences that control terminal complex and cellulose microfibril morphology.

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(34) *ASCOPHYLLUM NODOSUM*: EARLY ZYGOTE SURVIVAL FOLLOWING CANOPY REDUCTION Jill C. Fegley[1], Robert L. Vadas[2], and Wesley A. Wright[2]. [1]Marine Science Department, Corning School of Ocean Studies, Maine Maritime Academy, Castine, ME 04420, USA; [2]Department of Biological Sciences, University of Maine, Orono, ME 04469, USA.

Here we examine the effect of disturbances to the understory of a canopy-forming species. Specifically, we test the survival of newly settled zygotes under different canopy reductions, which mimic natural and harvested canopy removal processes. Three different cutting height treatments (uncut, cut to18cm, cut to 36cm) were randomly imposed on twelve 5m x 5m plots on Cape Cove, Great Wass Island, Beals Island, ME. Within each plot additional experimental factors included proximity of zygotes to a holdfast (near/away), protection from disturbance (open/cover/cage), and type of microhabitat (flat surface, vertical or horizontal grooves). *Ascophyllum* gametes were released in buckets, combined in shallow pans, and then allowed to fertilize for 40 min. During fertilization zygotes were stained with Tinopal (a fluorescent optical brightener). Zygotes were seeded onto pottery chips containing three microhabitats and allowed to settle for 2 h prior to placement. Zygotes in protected microhabitats (vertical and horizontal grooves) consistently had higher percent survival than those on flat surfaces. Survival increased in cage and cover treatments compared to chips in the open due to protection from whiplash of fronds. The importance of whiplash is also shown by the relatively higher percent survival of zygotes on flat surfaces in plots cut to 18cm compared to the treatments with longer fronds (36cm and uncut). Whiplash has a greater negative impact on zygote survival in plants with longer, more highly branched fronds. The increased survival of greater than 100% in the protected microhabitats may have been the result of disturbance (whiplash/water motion) to zygotes causing dislodgement from the flat surfaces and settlement into the nearby grooves. Herbivory and desiccation were not factors in these treatments as the duration of the experiment was only 12 h overnight.

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(35) THE EVOLUTION OF CELL WALL MATRIX POLYMERS IN CHAROPHYCEAN GREEN ALGAE. Simon T. Gunner, Catherine E. Domozych and David S. Domozych. Department of Biology, Skidmore College, Saratoga Springs, NY 12866, USA.

The emergence of green plants onto land represents one the more profound evolutionary events in modern earth history. The cell wall of these green plants was critical to adaptation to terrestrial life. Charophycean green algae are the most closely-related organisms to land plants and have a remarkable diversity of extracellular coverings, including cellulose-based cell walls. However, very little is currently known about the matrix polysaccharides and proteins found in charophycean cell walls. In this study, we performed a comparative screening for matrix polysaccharides/proteins of a) representatives of the five major groups of charophycean algae, the Chlorokybales, Klebsormidiales, Conjugales, Charales and Coleochaetales, b) the primitive sister clade, the Mesostigmales, and c) the protonemata of the moss, *Polytrichum*. An immunocytochemical study using monoclonal antibodies raised against various pectin, arabinoglalactan protein and extensin epitopes was performed. Homogalacturonic acid polymers were found in the primary cell walls or cross walls of recently-divided cells of all major groups. JIM5, LM7 and 2F4 labeling was also found in the extracellular fibrillar matrix surrounding the scales of *Mesostigma.* Extensin and arabinogalactan epitopes were recognized in the outer pore complexes of the cell walls of many placoderm desmids and in *Coleochaete scutata*. In *Polytrichum* protonemata, a diverse assortment of pectin and arabinogalactan protein epitopes was found. However, no immunocytochemical evidence could be determined for the presence of xylogalacturonans in either *Polytrichum* or any of the charophycean algae. This data suggests that the origin of the homopolymeric galacturonic acid pectins and arabinogalactan proteins occurred very early on in the charophycean line of green algal evolution. Also, this study shows the remarkable similarities between the cell walls of moss protonemata and the charophycean algae.

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(36) *KF$_C$*: KARLODINIUM-AMPHIDINIUM (DINOPHYCEAE) FULL-LENGTH cDNA SEQUENCING.

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Dinoflagellates (Dinoflagellata, Dinozoa) are a prominent group of unicellular eukaryotes closely related to malaria parasites, which live in the aquatic ecosystem and contribute significantly to carbon cycling, coral growth, red tides and marine toxins. Recent EST studies of dinoflagellates have provided key insights into plastid evolution and genome remolding. However, our knowledge of composition and function of their enormous genomes is very limited yet critical for understanding how these organisms grow and impact the environment. Previous studies suggest that 1) *the dinoflagellate nuclear genome contains vastly more genes than other eukaryotes when multiple variants of each gene are taken into account*; and 2) *the dinoflagellate genome is rich in noncoding functional RNA genes*. To gain evidence verifying these conjectures and to provide a genome-wide, well-annotated expressed gene dataset, we propose to sequence 60,000 full-length cDNA clones for *K. micrum* and 30,000 clones for *A. carterae*. Bioinformatic analysis will be conducted to annotate genes, predict gene functions, estimate gene content, and characterize genomic features. Results will provide insights into genome composition, evolution, and gene regulation in dinoflagellates. The dataset will facilitate understanding on molecular mechanisms of cell division, toxin production, and feeding of dinoflagellates. An exhibit of “Red Tides and Their Genomes” featuring hands-on “feet-on” activities will be developed and displayed at Connecticut’s Maritime Aquarium to promote public awareness and youth education on environmental impacts of red tides and how genomes work to regulate dinoflagellate growth, bioluminescence, and toxin production.