



NEAS

THE PAST, PRESENT AND FUTURE
OF PHYCOLOGY IN THE NORTHEAST

Northeast Algal Society
50th Anniversary Symposium
Woods Hole, MA. 15-17 April, 2011

Logo credit: Bridgette Clarkston (CEMAR) and Mike Weger – incorporating a *Licmorpha* sketch from Ernst Haeckel (1904, plate 84) *Kunstformen der Natur* ("Artforms of nature").

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Special thanks!!!

The Co-conveners wish to thank the many student volunteers who contributed to this meeting including those in the Lewis lab for assisting with registrations and the Saunders lab for organizing the logo design and t-shirt orders. We wish to thank the student award judges including the Wilce Graduate Oral Award Committee (Craig Schneider (Chair), Paul Gabrielson, Pete Siver), Trainor Graduate Poster Award Committee (Susan Brawley (Chair), Ken Karol, Charlene Mayes) and President's Undergraduate Presentation (oral & poster) Award Committee (John Wehr (Chair), Bridgette Clarkston, Chris Lane). We also wish to thank the session moderators: Bridgette Clarkston, Curt Pueschel, Craig Schenider, John Wehr and Charlie Yarish.

Our 50th celebration would not have been as successful without the generous support of our sponsors. We would like to acknowledge and thank sincerely FMC/Erick Ask, MBL Sea Grant and PP Systems.

Welcome to the 50th Northeast Algal Symposium – The past, present & future of phycology in the northeast!!!

Welcome back to Woods Hole and to the 50th anniversary meeting of our Society. This is truly an exciting year for our society! For many of our members this marks a long overdue return to the roots of our society. As Co-conveners we have spared no energy on your behalf to make certain that both our return and the 50th celebrations are memorable. NEAS is first and foremost about the science, and for many of us this is best recognized and celebrated through the next generation of Phycology. Student-first policies have always been at the heart of our society and this year is no different. We also have a fairly set agenda that we adhere to in our annual meetings, a winning formula that keeps us all returning, and we have resisted the temptation to stray too far from the recipe that we have all come to know and cherish.

Attendees are reminded that there will be a society mixer on Friday evening from 7-9 PM during which registration can be completed. This mixer – Ghosts of NEAS Past – will provide an opportunity for everyone to bring his/her favorite photo from past meetings and post it, with or without a caption, to share with your colleagues (remember to be nice, big brother is watching☺). The registration and mixer will be set up in Swope. Saturday morning from 6:45 to 8:00 AM attendees will be able to enjoy breakfast in Swope, and complete registration for late arrivals. A buffet lunch will also be offered as part of the conference registration and will follow the student talks on Saturday morning. After the Saturday afternoon talks there will be a generous allotment of time to view posters at Swope. Take this opportunity to talk science with the many presenters and peers, and please take time to welcome and chat with the student members. Following our poster session we are truly fortunate to share in the life-lessons, wisdom and phycological experiences of this year's distinguished speaker – Dr Michael Graham. The Banquet will provide the evening meal on Saturday, and the breakfast on Sunday will be served from 6:45 to 8:00 AM in Swope. The banquet will be preceded by a mixer (also in Swope) to loosen the pocketbooks for the post-banquet auction. The auction is a major source of revenue for all of the student activities that NEAS funds to foster the next generation of phycologists – please consider this and participate liberally! Sunday will explore the future of Phycology. World-leaders in various aspects of Phycological research will be asked to describe their vision of how emerging technologies and novel paradigms will shape our science in the decades to come. The meeting will end with the Annual Business Meeting on Sunday to be completed in the Lillie Auditorium followed by lunch in Swope.

Please take time to vote in the society elections and to attend the business meeting on Sunday. NEAS is your society and it is up to you to direct its future.

Best wishes for a productive and relaxed conference,

Louise Lewis
Gary W. Saunders
2011 Co-Conveners

General Program: 50th Northeast Algal Symposium

Friday, April 15, 2011 – NEAS Past

5:00 – 7:00 pm Registration and check-in (Swope Lobby).

7:00 – 9:00 pm Ghosts of NEAS past mixer (Swope Meigs Room) and registration (Swope Lobby). Bring a picture with caption to post Friday night.

Saturday, April 16, 2011 – NEAS Present

6:45 – 8:00 am. Registration and breakfast (Swope Dining Hall)

---Note: #1: At this time, Saturday speakers should take their presentations to the Lillie Auditorium.

---Note #2: Posters can be put up in the display area in Swope Upper Lobby.

---Note #3: A room (TBA) will be available throughout the meeting to preview oral presentations.

Opening remarks (Lillie Auditorium)

8:00 – 8:10 am. Welcome and Opening Remarks.

8:10 – 8:30 am. Craig W. Schneider. THE NORTHEAST ALGAL SOCIETY: A BRIEF HISTORY OF THE FIRST HALF CENTURY. (p. 49)

SESSION 1 Student presentations (Lillie Auditorium; G = graduate, U = undergraduate). Moderator: Craig Schneider

8:30 – 8:45 am (G). Matthew Cashman, John Wehr & Kam Truhn. BIOCHEMICAL COMPOSITION OF PERIPHYTON FOOD QUALITY AS AFFECTED BY LIGHT AND NUTRIENT AVAILABILITY. (p. 19)

8:45 – 9:00 am (G). Jillian Decker, Kam Truhn, John Wehr, Lynn Bartsch, William Richardson & Jeff Houser. CYANOBACTERIAL NITROGEN-FIXATION IN THE UPPER MISSISSIPPI RIVER. (p. 22)

9:00 – 9:15 am (G). Hannah Traggis & Leland Jahnke. IRON LIMITATION EFFECTS ON THE ASCORBATE-GLUTATHIONE CYCLE OF THE CHLOROPHYTE ALGAL DUNALIELLA TERTIOLECTA. (p. 52)

9:15 – 9:30 am (G). Carolina C. Aguila & Matthew E.S. Bracken. EFFECTS OF MULTIPLE NUTRIENT ENRICHMENT ON THE GROWTH OF SEAWEEDS ON WAVE-SWEPT ROCKY SHORES. (p. 14)

9:30 – 9:45 am (G). Michele Guidone & Carol Thornber. IMPACT OF INVERTEBRATE HERBIVORES ON *ULVA* BLOOM BIOMASS IN NARRAGANSETT BAY, RHODE ISLAND. (p. 30)

9:45 – 10:00 am (G). Christine Newton & Carol Thornber. MACROALGAL BLOOMS IN NEW ENGLAND SALT MARSHES: DISTRIBUTION SURVEYS AND POTENTIAL ECOLOGICAL IMPACTS. (p. 43)

10:00 – 10:30 am. Coffee break (Lillie Lobby)

SESSION 2 Student presentations (Lillie Auditorium; G = graduate, U = undergraduate). Moderator: John Wehr

10:30 – 10:45 am (G). Rita Kuo & Senjie Lin. ECTOSYMBIOTIC AND ENDOBIOTIC BACTERIA ASSOCIATED WITH *EUTREPTIELLA* SP. FROM LONG ISLAND SOUND. (p. 35)

10:45 – 11:00 am (G). Yunyun Zhuang, Huan Zhang & Senjie Lin. 454 PYROSEQUENCING FOR EUKARYOTIC MICROBES: DINOFLAGELLATES AS A FOCUS. (p. 55)

11:00 – 11:15 am (U). Valerie Charbonneau & Brian Wysor. ASSESSING TURF ALGAL DIVERSITY OF PANAMA: A COMPARISON OF CULTURE BASED & ENVIRONMENTAL PCR APPROACHES. (p. 20)

11:15 – 11:30 am (G). Sarah E. Hamsher & Gary W. Saunders. A FLORISTIC SURVEY OF MARINE TUBE-FORMING DIATOMS IN CANADA. (p. 31)

11:30 – 11:45 am (G). Karolina Fučíková & Louise A. Lewis. UNRAVELING THE TAXONOMIC KNOT OF *BRACTEACOCCLUS*, *DICTYOCOCCLUS*, *PSEUDOMURIELLA*, AND *CHROMOCHLORIS* (CHLOROPHYCEAE, CHLOROPHYTA): A CASE OF CRYPTIC GENERA. (p. 27)

11:45 – 12:00 am/pm (G). William Pérez, Richard M. McCourt, Michelle T. Casanova & Kenneth G. Karol. A SYSTEMATIC STUDY OF *TOLYPELLA* A. BR. (CHARALES, CHAROPHYTA): RECENT ANALYSES BASED ON PLASTID SEQUENCE DATA. (p. 44)

12:00 – 12:15 pm (U). Heather M. Meyer & Kenneth G. Karol. A SYSTEMATIC INVESTIGATION OF THE *NITELLA FLEXILIS* (CHARALES, CHAROPHYTA) SPECIES COMPLEX. (p. 41)

LUNCH Buffet 12:15 – 1:30 pm (Swope Dining Hall) (Exec Comm meeting, Location TBA)

SESSION 3 Student presentations (Lillie Auditorium; G = graduate, U = undergraduate). Moderator: Curt Pueschel

1:30 – 1:45 pm (U). Julia M. Maritz & Kenneth G. Karol. MOLECULAR PHYLOGENETICS OF *CHARA* L. (CHARALES, CHAROPHYTA) WITH EMPHASIS ON *CHARA VULGARIS* SENSU LATO. (p. 40)

1:45 – 2:00 pm (U). Tabetha M. Peavey, John D. Hall & Kenneth G. Karol. IDENTIFYING LATIN AMERICAN *CHARA* (CHARALES: CHAROPHYTA) USING DNA SEQUENCES. (p. 44)

- 2:00 – 2:15 pm (G).** Amanda Savoie & Gary W. Saunders. IDENTIFICATION AND DELIMITATION OF SPECIES WITHIN *POLYSIPHONIA* (RHODOPHYTA) IN THE NORTHWEST ATLANTIC USING MOLECULAR TOOLS. (p. 48)
- 2:15 – 2:30 pm (G).** Thea R. Popolizio, Christopher E. Lane, Craig W. Schneider & Daniel C. McDevit. MOLECULAR TOOLS EXPOSE MISIDENTIFIED AND NOVEL TAXA AMONG BERMUDIAN RHODOPHYTA. (p. 45)
- 2:30 – 2:45 pm (G).** Katy Hind & Gary Saunders. A MOLECULAR PHYLOGENETIC STUDY OF THE TRIBE CORALLINEAE (CORALLINALES, RHODOPHYTA) WITH AN ASSESSMENT OF GENUS-LEVEL TAXONOMIC FEATURES. (p. 32)

Contributed presentation.

- 2:45 – 3:00 pm.** Peter A. Siver, Alex P. Wolfe & Anne Marie Lizarralde. THE GIRAFFE PIPE: USING ALGAL MICROFOSSILS TO RECONSTRUCT THE PAST AND INFORM THE FUTURE. (p. 50)

3:00 – 3:10 pm. Picture on the front steps of Lillie

SESSION 4 Poster session & coffee (Swope Upper Lobby & Meigs Room)

3:10 – 5:10 pm. (For list see p. 9 – 13)

5:15 – 6:15 pm. Distinguished speaker (Lillie Auditorium): Dr. Michael Graham, Moss Landing Marine Labs (Abs. p. 29; CV p. 56-61). Effects of climate change on distribution and productivity potential of global kelp systems (introduction by Gary W. Saunders).

6:45 – 7:30 pm. Pre-banquet Mixer (Swope Meigs Room)

7:30 – ODT. Retro Banquet and auction (dress to the past or future of Phycology) (Swope Meigs Room)

Sunday, April 17, 2011 – NEAS Future

6:45 – 8:00 am. Breakfast (Swope Dining Hall)

---Note: #4: At this time, Sunday speakers should take their presentations to the Meigs Rm (Swope; Session 5a) and the Lillie Auditorium (Session 5b).

CONCURRENT SESSION 5A (Meigs Rm, Swope) Contributed talks (ecological & utilization). Moderator: Charlie Yarish

8:00 – 8:15 am. Jeff T. Hafting, Alan T. Critchley and M. Lynn Cornish. SUCCESSFUL INDUSTRIALIZATION OF FUNCTIONAL SEAWEED PRODUCTS FOR HUMAN USAGE REQUIRES ON-LAND CULTIVATION. (p. 31)

- 8:15 – 8:30 am.** Steve Di Lonardo, John Wehr, Gregory Boyer, Alissa Perrone & Kam Truhn. CYANOBACTERIA BLOOM AND NITROGEN IMBALANCE LINKED TO STOCKED STERILE CARP IN A EUTROPHIC LAKE. (p. 24)
- 8:30 – 8:45 am.** Donald Cheney, Kevin Gardner & John Logan. A NEW TYPE OF HARMFUL ALGAL BLOOM: THE PCB-CONCENTRATING ULVA BLOOM OF NEW BEDFORD HARBOR. (p. 20)
- 8:45 – 9:00 am.** Euan D. Reavie. WHAT IS THE ROLE OF ALGAE IN THE RECENT COLLAPSE OF THE GREAT LAKES FOOD WEB? (p. 46)
- 9:00 – 9:15 am.** Matthew E. S. Bracken & Susan L. Williams. REALISTIC BIODIVERSITY CHANGES ALTER NITRATE UPTAKE AND PHOTOSYNTHESIS RATES OF INTERTIDAL SEAWEED ASSEMBLAGES. (p. 18)
- 9:15 – 9:30 am.** Valerie Perini & Matthew E.S. Bracken. EFFECTS OF SEASONAL NUTRIENT VARIATION AND TIDAL ELEVATION ON PRIMARY AND SECONDARY PRODUCTION IN A ROCKY INTERTIDAL ECOSYSTEM. (p. 45)
- 9:30 – 9:45 am.** Félix L. Figueroa, Nathalie Korbee, Eugenia Márquez, Cristina de Miguel, Isabel Díez, Nahia Muguerza, Alberto Santolaria & J.M. Gorostiaga. CHANGES IN SUBTIDAL MACROALGAE AT THE BAY OF BISCAY: ECOLOGICAL AND PHYSIOLOGICAL INDICATORS OF THE EFFECTS OF GLOBAL WARMING. (p. 26)
- 9:45 – 10:00 am.** Susan Brawley, Ladd Johnson & Walter Adey. *FUCUS SERRATUS* IN EASTERN NORTH AMERICA: HISTORY, RATES, AND FACTORS AFFECTING CONTINUED SPREAD. (p. 18)

**CONCURRENT SESSION 5B (Lillie Auditorium) Contributed talks
(phylogenetic & biogeography). Moderator: Bridgette Clarkston**

- 8:00 – 8:15 am.** Lilibeth N. Miranda, Huan Zhang & Senjie Lin. PHYLOGENETIC ANALYSIS FOR *A. TAMARENSE*/*FUNDYENSE*/*CATENELLA* COMPLEX GUIDED BY INTRAGENOMIC 18S rDNA POLYMORPHISM SUGGESTING SEPARATION OF THE COMPLEX INTO TWO SPECIES. (p. 41)
- 8:15 – 8:30 am.** Molly R. Letsch, Gisele Muller-Parker & Louise A. Lewis. GEOGRAPHIC DISTRIBUTION AND INTRASPECIFIC VARIATION IN *ELLIPTOCHLORIS MARINA* (TREBOUXIOPHYCEAE, CHLOROPHYTA) THE GREEN SYMBIONT OF *ANTHOPLEURA* SPP. (p. 38)
- 8:30 – 8:45 am.** John Wehr, Kam Truhn & Alissa Perrone. ENCRUSTING EPILITHIC ALGAE: AN UNDERSTUDIED FRESHWATER ASSOCIATION? (p. 53)
- 8:45 – 9:00 am.** Kyatt Dixon & Gary W. Saunders. SOUTHERN BIODIVERSITY BLOWOUT: CRYPTIC CRUSTS IN AUSTRALIA. (p. 24)
- 9:00 – 9:15 am.** Daryl W. Lam, Timothy J. Entwisle, Pertti Eloranta, Janina Kwandrans & Morgan L. Vis. MOLECULAR PHYLOGENY OF THE FRESHWATER MACROPHYTE *SIRODOTIA* (BATRACHOSPERMALES, RHODOPHYTA). (p. 36)
- 9:15 – 9:30 am.** Paul W. Gabrielson. MOLECULAR SEQUENCING OF FIELD-COLLECTED AND TYPE SPECIMENS REVISES NORTHEAST PACIFIC CORALLINALES (RHODOPHYTA). (p. 27)

9:30 – 9:45 am. Walter H. Adey & Lee-Ann C. Hayek. QUANTITATIVE ANALYSIS OF NORTH ATLANTIC MACROPHYTES DEMONSTRATES A DISTINCT SUBARCTIC REGION. (p. 14)

9:45 – 10:00 am. Max H. Hommersand, Chang-Jun Lee & Lee G. Pedersen. MUTATIONAL CHANGES IN THE AMINO ACIDS OF RUBISCO BETWEEN TEN ANTARCTIC AND TEMPERATE SISTER SPECIES OF MARINE RED ALGAE DISTRIBUTED BETWEEN THE ANTARCTIC PENINSULA AND CHILE OR THE FALKLAND ISLANDS MAY HAVE BIOGEOGRAPHICAL AND ECOLOGICAL SIGNIFICANCE. (p. 33)

10:00 – 10:30 am. Coffee break (Lillie Lobby)

**SESSION 6 Special symposium (Lillie Auditorium): Phycology of the Future.
Moderator: Louise Lewis**

10:30 – 11:00 am. Christopher Lane, Ian Misner, Cedric Bicep, Sebastien Halary, Philippe Lopez, Eric Bapteste, Scott Grandpre. USING EVOLUTIONARY GENE NETWORKS TO HARNESS THE NEXT GENERATION ERA DATA DELUGE. University of Rhode Island (p. 36)

11:00 – 11:30 am. Heroen Verbruggen. ALGAL PHYLOGENETICS AND BIOGEOGRAPHY IN THE HIGH-THROUGHPUT AGE. Phycology Research Group, Ghent University, Belgium. (p. 52)

11:30 – 12:00 am/pm. Don Anderson. BLOOM DYNAMICS OF THE RED TIDE DINOFLAGELLATE *ALEXANDRIUM FUNDYENSE* IN THE GULF OF MAINE: A SYNTHESIS AND PROGRESS TOWARDS A FORECASTING CAPABILITY. Woods Hole Oceanographic Institution. (p. 15)

12:00 – 12:30 pm. Closing remarks & General Business meeting (Lillie Auditorium).

12:30 – 1:30 pm Lunch (Swope Dining Hall)

POSTER PRESENTATION SUMMARY

Undergraduate (President's Award; alphabetical by first author)

Poster #23) RANGE EXPANSION OF THE NEWLY INVASIVE "*HETEROSIPHONIA*" *JAPONICA* IN NEW ENGLAND AND MECHANISMS FOR ITS SUCCESS. Natalie H. N. Low^{1,2}, Christopher J. Marks² and Matthew E. S. Bracken². ¹Department of Ecology and Evolutionary Biology, Brown University, Providence, RI 02912; ²Marine Science Center, Northeastern University, Nahant, MA 01908. (p. 39)

Poster #22) CHARACTERIZATION OF LONG ISLAND COASTAL CYANOPHAGE COMMUNITIES. Sme, N. A., and Marston, M. F. Department of Biology and Marine Biology, College of Arts and Sciences, Roger Williams University, Bristol, RI. (p. 50)

Graduate (Francis R. Trainor Award; alphabetical by first author)

Poster #7) LOCAL ADAPTATION IN *FUCUS VESICULOSUS* AND ITS CONSEQUENCES FOR INTERTIDAL COMMUNITY STRUCTURE AND DYNAMICS. Kylla M. Benes & M.E.S. Bracken. Northeastern University - Marine Science Center, 430 Nahant Road, Nahant, MA 01908 U.S.A. (p. 16)

Poster #8) A COMPARISON OF TIDE POOL POPULATIONS OF *CODIUM FRAGILE* SSP. *FRAGILE* WITHIN THE BRAVE BOAT HARBOR ESTUARY, YORK-KITTERY, ME. Chris Benton, Stephen McKernan, Arthur Mathieson and Anita Klein. University of New Hampshire, Durham, NH. (p. 16)

Poster #31) INVESTIGATING NORTHWEST ATLANTIC SPECIES OF *CERAMIUM* USING AN INTEGRATIVE TAXONOMIC APPROACH. Meghann Bruce and Gary W. Saunders. Centre for Environmental and Molecular Algal Research, Department of Biology, University of New Brunswick, Fredericton, NB E3B 5A3, Canada. (p. 19)

Poster #32) A ROSE BY ANY OTHER NAME: TAXONOMIC REVISIONS IN CANADIAN 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. (p. 21)

Poster #20) CHARACTERIZATION OF BACTERIA ASSOCIATED WITH THE SEA SLUG *ELYSIA CHLOROTICA* AND ITS ALGAL PREY *VAUCHERIA LITOREA*. Susan Devine, Karen Pelletreau, and Mary Rumpho. Dept. of Molecular & Biomedical Sciences, University of Maine, Orono, ME 04469. (p. 23)

Poster #25) EST-SSRS IN *PORPHYRA UMBILICALIS* AND *PORPHYRA PURPUREA*. Renée L. Eriksen and Anita S. Klein. Department of Biological Sciences, University of New Hampshire, Durham, NH 03824, USA. (p. 25)

Poster #33) ESTABLISHMENT OF SPECIES DIVERSITY OF THE RHODYMENIALES (RHODOPHYTA) IN BRITISH COLUMBIA USING MOLECULAR AND MORPHOLOGICAL TECHNIQUES. Gina V. Filloramo & Gary W. Saunders. Center for Environmental & Molecular Algal Research, Department of Biology, University of New Brunswick, Fredericton, NB E3B 5A3, Canada. (p. 26)

Poster #17) THE EFFECTS OF BIODIVERSITY ON THE RESISTANCE AND RESILIENCE OF MARINE COMMUNITIES TO OCEAN ACIDIFICATION. Brendan C. Gillis & Matthew E.S. Bracken. Marine Science Center, Northeastern University, 430 Nahant Road, Nahant, MA 01908, USA. (p. 28)

Poster #26) CAPTURING NEW CONSERVED GENES USING EVOLUTIONARY GENE NETWORKS. Scott Grandpre¹, Ian Misner¹, Philippe Lopez², Eric Bapteste² & Christopher Lane¹. ¹Department of Biological Sciences, University of Rhode Island, Kingston, RI, 02881, U.S.A.; ²UMR CNRS 7138 Systematique, Adaptation, Evolution, University Pierre et Marie Curie, Paris, France. (p. 29)

Poster #3) PHYSIOLOGICAL STUDIES OF CULTURED NEW ENGLAND *PORPHYRA* SPP. AND IMPLICATIONS FOR USE IN INTEGRATED MULTI-TROPHIC AQUACULTURE SYSTEMS. Lindsay A. Green & Christopher D. Neefus. Department of Biological Sciences, University of New Hampshire, Durham, NH 03824, U.S.A. (p. 30)

Poster #34) MOLECULAR DATA REVEALS PARAPHYLLY AND UNDESCRIBED DIVERSITY IN THE GENUS *THOREA*. Emily Johnston, Daryl Lam, & Morgan Vis., Department of Environmental and Plant Biology, Ohio University, Athens, OH 45701, USA. (p. 33)

Poster #37) AUSTRALIAN HALYMENIALES (FLORIDEOPHYCEAE, RHODOPHYTA), PAST, PRESENT AND FUTURE: USING THE DNA BARCODE TO ASSESS SPECIES DIVERSITY IN AN AUSTRALIAN RHODOPHYTE ORDER. Lesleigh G. K. Kraft & Gary W. Saunders, Centre for Environmental & Molecular Algal Research, Department of Biology, University of New Brunswick, Fredericton, NB, E3B 5A3 Canada. (p. 35)

Poster #18) ALGAL TURF SCRUBBER (ATSTM) PRODUCTION ON THE GREAT WICOMICO RIVER, VIRGINIA, USA: A LOOK AT DIVERSITY AND BIOCHEMISTRY WHILE CLEANING THE RIVER. H. Dail Laughinghouse IV^{1,2}, Walter H. Adey¹, John Miller³. ¹Department of Botany, National Museum of Natural History, Smithsonian Institution, Washington, DC, USA; ²MEES Program, College of Computer, Mathematical and Natural Sciences, University of Maryland, College Park, MD, USA; ³Department of Chemistry, Western Michigan University, Kalamazoo, MI, USA. (p. 37)

Poster #9) DOES THE DISTRIBUTION OF MACROSCOPIC KELP (*LAMINARIA EPHEMERA*) SPOROPHYTES REFLECT THE DISTRIBUTION OF MICROSCOPIC GAMETOPHYTES? Caroline Longtin & Gary W. Saunders. Centre for Environmental &

Molecular Algal Research, Department of Biology, University of New Brunswick, Fredericton, NB, E3B 5A3, Canada. (p. 39)

Poster #35) FOLIOSE BANGIALES (RHODOPHYTA) SPECIES DIVERSITY IN GREENLAND. Agnes Mols-Mortensen¹, ¹Chris D. Neefus, ²Poul M. Pedersen and ³Juliet Brodie. ¹University of New Hampshire, Department of Biological Sciences, G32 Spaulding Life Science Center, 38 College Road, Durham, NH 03824, USA; ²Institute of Biology, Phycology Section, Øster Farimagsgade 2D, DK-1353 Copenhagen K, Denmark; ³Natural History Museum, Department of Botany, London, SW7 5BD, United Kingdom. (p. 42)

Poster #6) NUTRIENT STATUS ASSESSMENT OF THE GREAT BAY ESTUARINE SYSTEM USING ANALYSES OF ALGAL TISSUES AND WATER. Jeremy C Nettleton, Christopher D Neefus, Arthur C Mathieson. University of New Hampshire, Department of Biological Sciences, G28 Spaulding Life Science Center, 38 Academic Way Durham, NH 03824, USA. (p. 42)

Poster #4) DEVELOPMENT OF SEAWEED CULTURE SYSTEM TECHNOLOGIES TO SUPPORT INTEGRATED MULTI-TROPHIC AQUACULTURE AND SEA VEGETABLE AQUACULTURE IN NEW ENGLAND COASTAL WATERS. Sarah Redmond & Charles Yarish. Departments of Ecology & Evolutionary Biology & Marine Sciences, University of Connecticut, CT, 06901, U.S.A. (p. 46)

Poster #36) A PRELIMINARY INVESTIGATION OF THE *BATRACHOSPERMUM BORYANUM* SPECIES COMPLEX (BATRACHOSPERMALES, RHODOPHYTA) IN NORTH AMERICA AND EUROPE. Eric D. Salomaki & Morgan L. Vis. Environmental and Plant Biology, Ohio University, Athens, OH, 45701, U.S.A. (p. 48)

Poster #10) DIATOM COLONIZATION PATTERNS IN A SUBURBAN STREAM AFFECTED BY GRAZING PRESSURE. Sarah B. Whorley & John D. Wehr. Louis Calder Center – Biological Field Station, Fordham University. Armonk, NY, 10504, USA. (p. 54)

Professional (alphabetical by first author)

Poster #16) ASSESSING BALLAST WATER TREATMENTS: VIABILITY ASSESSMENT FOR AMBIENT MICROPLANKTON ASSEMBLAGES. Lisa E. Allinger¹, Euan D. Reavie¹ & Allegra A. Cangelosi². ¹Natural Resources Research Institute, University of Minnesota Duluth, Ely, MN 55731 U.S.A.; ²Northeast-Midwest Institute, Washington, DC 20001 U.S.A. (p. 15)

Poster #24) HAVE RED ALGAL PARASITES LOST THEIR NUCLEAR-ENCODED PLASTID GENES? Nicolas A. Blouin & Christopher E. Lane. Department of Biological Sciences, University of Rhode Island, Kingston, RI 02881, U.S.A. (p. 17)

Poster #1) NEW YORK'S GREAT LAKES RESEARCH CONSORTIUM: A MULTIDISCIPLINARY APPROACH TO LOOKING AT MULTIDISCIPLINARY ISSUES.

Gregory Boyer, Director, Great Lakes Research Consortium, SUNY-ESF, Syracuse NY 13210. (p. 17)

Poster #5) MARINE PLANT PRODUCTION FOR HIGH VALUE APPLICATIONS IN FUNCTIONAL FOOD AND COSMECEUTICAL APPLICATIONS: SECURITY OF SUPPLY AND TRACEABILITY. M. L. Cornish, J. Hafting, A. T. Critchley. Acadian Seaplants Limited, 30 Brown Avenue, Dartmouth, NS B3B 1X8, Canada. (p. 21)

Poster #2) ARIZONA CENTER FOR ALGAE TECHNOLOGY AND INNOVATION (AZCATI): A NEW OPEN TEST BED SPANNING THE ALGAE VALUE CHAIN. Thomas Dempster, Milton Sommerfeld, Qiang Hu & Gary Dirks. Applied Sciences and Mathematics, Arizona State University, Mesa, AZ, 85212, U.S.A. (p. 23)

Poster #11) SAME ACTORS, DIFFERENT PLAYS: QUANTIFYING HOW ECOSYSTEM EFFECTS OF INTERTIDAL ALGAL DIVERSITY VARY ALONG A 500 KM LATITUDINAL GRADIENT. James G. Douglass¹, Matthew Bracken¹, & Geoffrey C. Trussell¹. ¹Marine Science Center, Northeastern University, Nahant, MA, 01908, U.S.A. (p. 25)

Poster #28) MOLECULAR EVOLUTION OF GLUTAMINE SYNTHETASE II AND III IN SELECT CHROMALVEOLATE LINEAGES. Sohini Ghoshroy and Deborah L. Robertson. Clark University, 950 Main Street, Worcester, MA 01610. (p. 28)

Poster #15) ENCYSTMENT BY THE MIXOTROPHIC FLAGELLATE *OCHROMONAS PINGUIS* CONRAD (CHRYSOPHYCEAE) IN LABORATORY CULTURE. Dale A. Holen. Penn State University, Worthington Scranton Campus, Dunmore, PA, 18512. (p. 32)

Poster #30) TESTING DNA BARCODING METHODS OF DIATOMS IN AN ENVIRONMENTAL SAMPLE. Diba Khan-Bureau, Louise Lewis & Gary Robbins. University of Connecticut, Storrs, CT 06269. (p. 34)

Poster #19) BIOEXTRACTION OF NUTRIENTS FROM THE BRONX RIVER WATERSHED (NYC) AND LONG ISLAND SOUND. Jang. J. Kim¹, George P. Kraemer², John Curtis³ & Charles Yarish¹. ¹Departments of Ecology & Evolutionary Biology and Marine Sciences, University of Connecticut, CT, 06901, U.S.A.; ²Environmental Studies Program, Purchase College, Purchase, NY 10577, U.S.A. ³Bridgeport Regional Aquaculture Science and Technology Center, Bridgeport (BRASTECC), CT 06604, U.S.A. (p. 34)

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ABSTRACTS (Alphabetical by first author)

QUANTITATIVE ANALYSIS OF NORTH ATLANTIC MACROPHYTES DEMONSTRATES A DISTINCT SUBARCTIC REGION. Walter H. Adey^a and Lee-Ann C. Hayek^b. Museum of Natural History, ^aDepartment of Botany and ^bStatistics and Mathematics, Smithsonian Institution, Washington D.C.

Quantitative analyses of North Atlantic seaweeds were used to test the Thermogeographic Model (TM), a construct based on coastal area, seawater temperature and Pleistocene time. The TM reveals climate/area clusters that predict biogeographic regions; a northwestern Atlantic Subarctic, a subset of the North Pacific Region, is centered on the Strait of Belle Isle, between Newfoundland and Labrador. Nova Scotia and Gulf of Maine shores are mixed Boreal/Subarctic, transitional with western Europe.

Seaweed assemblages were studied at 51 depth-zoned SCUBA stations from southern Labrador to Cape Elizabeth, Maine. Meter-square quadrats, at-sea sorting, identification, and weighing gave biomass by species. The 3000 km of coasts radiating from the Strait of Belle Isle have a unique assemblage of seaweeds: 62% by biomass, of its top ten species, have their origins in the North Pacific. The same species on Gulf of Maine and southern Nova Scotia coasts occupy 13% and 5 % of the flora respectively. Of top ten species on the Nova Scotia Coast, seven occur widely in Europe, providing 94% of the biomass, but only 4% of the biomass of the top ten in the Atlantic Subarctic..

Bray-Curtis similarities, with multi-dimensional scaling, show this Subarctic Region as very distinct from Nova Scotia and the Gulf of Maine in shallow and mid-depths. A wide variety of statistical tests provide a very high level of significance. In deeper, colder water, the flora is more similar to that of the Subarctic.

In the early Holocene, western Atlantic rocky shores were likely occupied by Subarctic relict seaweeds. The mid-Holocene's pre-rebound hypsithermal, with a warmer and deeper Northwest Passage, likely supplemented North Pacific Subarctic additions. Eastern North Atlantic Boreal seaweeds entered the northwestern Atlantic more recently, likely representing a major anthropogenic bridging of an oceanographic barrier.

EFFECTS OF MULTIPLE NUTRIENT ENRICHMENT ON THE GROWTH OF SEAWEEDS ON WAVE-SWEPT ROCKY SHORES. Carolina C. Aguila, Matthew E.S. Bracken. Northeastern University, Marine Science Center, Nahant, Massachusetts 01908 USA.

Anthropogenic nutrient inputs into the environment have been steadily increasing, often as a result of direct additions (e.g., from agriculture, industry, and wastewater) and/or habitat modification. Increased nutrient levels in marine systems can alter community structure and dynamics. We have developed a technique to effectively deliver specific nutrients to experimental plots on wave-swept New England rocky shores. Plots at three sites in the southern Gulf of Maine were enriched with nitrate, phosphate, both nitrate and phosphate, or no additional nutrients to examine the potential for nutrient co-limitation of seaweed growth. Experiments were maintained from June through August 2010. We monitored ambient water nutrient levels and growth of individual *Fucus* thalli in each plot. When plots were enriched with both nitrate and phosphate, *Fucus* growth was higher than when either nitrate or phosphate was added alone. Our finding of co-limitation by both nitrogen and phosphorus has implications for management of nutrient inputs into coastal habitats.

ASSESSING BALLAST WATER TREATMENTS: VIABILITY ASSESSMENT FOR AMBIENT MICROPLANKTON ASSEMBLAGES. Lisa E. Allinger¹, Euan D. Reavie¹ & Allegra A. Cangelosi².

¹Natural Resources Research Institute, University of Minnesota Duluth, Ely, MN 55731 U.S.A.;

²Northeast-Midwest Institute, Washington, DC 20001 U.S.A.

For decades aquatic invasive species, including many algal taxa, have been confirmed as introduced and established through the discharge of commercial ships' ballast water. These organisms threaten ecological stability, diversity and abundance of native taxa as well as maritime commerce. Using a land-based test facility, the Great Ships Initiative (GSI – www.greatshipsinitiative.org), is evaluating candidate shipboard treatment systems for their ability to prevent the introduction of freshwater nuisance species. The facility meets International Maritime Organization guidelines and is the only system dedicated to testing ballast water treatment applications on freshwater organisms. Assessing the efficacy of these technologies involves estimating the number of viable propagules in treated discharge relative to untreated controls. To date estimates of ballast treatment effectiveness on microorganisms in the 10-50 μm size range (largely algae) have been absent or based on responses of standard test organisms in the laboratory or bulk algal biomass evaluations. We present a process of ambient assemblage concentration, staining with fluorescein diacetate (FDA), and microscopic observation as a reliable and efficient method to assess densities of viable freshwater algae. The selected method provides a strong foundation for live/dead algal enumeration of ambient assemblages in ballast water treatment assessments.

BLOOM DYNAMICS OF THE RED TIDE DINOFLAGELLATE *ALEXANDRIUM FUNDYENSE* IN THE GULF OF MAINE: A SYNTHESIS AND PROGRESS TOWARDS A FORECASTING CAPABILITY. Donald M. Anderson. Woods Hole Oceanographic Institution, Woods Hole, MA, 02543, USA.

Blooms of the toxic dinoflagellate *Alexandrium fundyense*, commonly called “red tides” have been a serious problem in the Gulf of Maine since 1972. The blooms are associated with the accumulation of potent neurotoxins in shellfish and some fish species, leading to paralytic shellfish poisoning (PSP) in human consumers – a potentially fatal poisoning syndrome. This talk will summarize more than a decade of large-scale field and modeling activities in the nearshore waters of the region, leading to a conceptual model of bloom dynamics that is consistent with cruise observations and with patterns of shellfish toxicity, and to numerical models that are being used for weekly and seasonal forecasts. The long-term implications of the blooms and their deposition of dormant cysts will also be discussed, as we hypothesize that the western Gulf of Maine region will experience more frequent and more intense PSP outbreaks in the coming years, compared to the last decade. The challenges and potential for an operational red tide forecasting system in the Gulf of Maine will also be discussed, summarizing successes and failures in the 2008, 2009, and 2010 seasonal forecasts, lessons learned, and plans for improved forecasts in the future.

LOCAL ADAPTATION IN *FUCUS VESICULOSUS* AND ITS CONSEQUENCES FOR INTERTIDAL COMMUNITY STRUCTURE AND DYNAMICS. Kylla M. Benes & M.E.S. Bracken. Northeastern University - Marine Science Center, 430 Nahant Road, Nahant, MA 01908 U.S.A.

Seaweeds shape the community in which they live by providing habitat and food resources. Therefore, variation in genetic diversity, phenotypic variation, and population demography of seaweeds may lead to changes in the abundance and distribution of associated organisms. Environmental differences may cause variation in seaweed traits via adaptation (i.e., genetic differentiation) or acclimation (i.e., phenotypic plasticity) to local conditions. On rocky shores, a steep gradient in environmental conditions over a short distance (meters) can generate differences between seaweeds from high and low intertidal zones, which may have cascading effects on associated organisms. The proposed study will use common garden and reciprocal transplant experiments to determine if local adaptation is occurring in an intertidal seaweed (*Fucus vesiculosus*). The results from these experiments will be corroborated with studies of population demographics and genetic structure of *Fucus* species in the Gulf of Maine. Furthermore, the effects of local adaptation in *Fucus vesiculosus* on herbivores will be determined using a laboratory feeding assay. Results from this study will enhance our understanding of how foundation species alter community structure by examining the connections between evolutionary processes in a foundation species and the ecology of the community associated with that foundation species.

A COMPARISON OF TIDE POOL POPULATIONS OF *CODIUM FRAGILE* SSP. *FRAGILE* WITHIN THE BRAVE BOAT HARBOR ESTUARY, YORK-KITTERY, ME. Chris Benton, Stephen McKernan, Arthur Mathieson and Anita Klein. University of New Hampshire, Durham, NH.

Codium fragile is an invasive green algae that was first observed in the Northwest Atlantic in Long Island Sound in the 1950's. From here it spread northward to the Gulf of Maine. This study was undertaken in the Brave Boat Harbor Estuary in Southern Maine. This area is exposed to occasional strong wave action that causes erosion and creates tidal panes in the outer marsh. Our major objectives were to study the *C. fragile* populations in these panes to compare their growth as a function of major hydrographic properties and to determine whether reproductive patterns influence population demographics. We chose four *Codium*-containing tidal panes and recorded pool perimeter, depth, and elevation to mean low water. From October 2009 to November 2010 we made monthly measurements of pool temperature (thermometer) and salinity (refractometer), as well as measured the height of each plant. Free-floating *Codium* was observed microscopically for gametangia. In the warmer summer months we observed a high number of juvenile plants in one pool, which suggests some type of motile reproduction. We only observed a single gametangia among 385 utricles surveyed. We found a correlation between pane distance and elevation from major channels with increased plant reproduction and growth. Hydrographic findings are consistent with other studies in regards to the optimal temperature and salinity for *Codium* growth (>16°C and > 27 ppt).

HAVE RED ALGAL PARASITES LOST THEIR NUCLEAR-ENCODED PLASTID GENES? Nicolas A. Blouin & Christopher E. Lane. Department of Biological Sciences, University of Rhode Island, Kingston, RI 02881, U.S.A.

Parasitism within red algae is common (~8% of described genera), and has evolved independently numerous times within the Florideophyceae. The majority of red algal parasites form adelphoparasitic ("kin", "brother") relationships where these parasites share a recent common ancestor with their free-living host species. Additionally, other parasites form relationships with more distantly related taxa that can extend across ordinal barriers (alloparasites). It is known that typical anciently derived eukaryotic parasites have lost large numbers of canonical genes in either modified or abandoned metabolic pathways, but it is unclear which pathways are early casualties. Because of the close relationship in adelphoparasitic associations, a single pair of organisms can provide direct comparative data on the cellular and genomic changes occurring early in the evolution of a parasite, as well as information on host/parasite co-evolutionary dynamics. Although adelphoparasite *Gracilariophila oryzoides* does not maintain photosynthetically competent plastids, their nuclear-encoded plastid genes may still be active to affect host-derived plastids when they form heterokaryon associations. We will present ongoing comparative genomics analysis of the nuclear-encoded, plastid-targeted genes of the non-photosynthetic adelphoparasite *G. oryzoides* and host its *Gracilariopsis andersonii* to investigate the possible loss of their function in *G. oryzoides*.

NEW YORK'S GREAT LAKES RESEARCH CONSORTIUM: A MULTIDISCIPLINARY APPROACH TO LOOKING AT MULTIDISCIPLINARY ISSUES. Gregory Boyer, Director, Great Lakes Research Consortium, SUNY-ESF, Syracuse NY 13210.

The Great Lakes Research Consortium (GLRC) is an organization of eighteen colleges and universities in New York, with nine affiliate campuses in Ontario, dedicated to collaborative research and education on the Great Lakes. Formed with the expressed goal of increasing New York's competitiveness for federal research grants, the GLRC has nearly 400 member faculty, who are conducting research in every facet of Great Lakes science. Communication between campuses is fostered by a cross campus seminar series given by GLRC members, support for workshops, multi-campus internships, a student conference very similar to NEAS and, in association with New York's Department of Environmental Conservation, support for a small seed grants program. Recent research activities of the GLRC include involvement with the Great Lakes Observing System (GLOS), nutrient fluxes in the Lake Ontario nearshore environment, monitoring for harmful algal blooms and the occurrence of viral hemorrhagic septicemia (VHS) in fish. The GLRC also encourages interactions with Universities and students outside of the Great Lakes basin.

REALISTIC BIODIVERSITY CHANGES ALTER NITRATE UPTAKE AND PHOTOSYNTHESIS RATES OF INTERTIDAL SEAWEED ASSEMBLAGES. Matthew E. S. Bracken¹ & Susan L. Williams². ¹Northeastern University, Marine Science Center, Nahant, Massachusetts 01908 USA; ²University of California-Davis, Bodega Marine Laboratory, Bodega Bay, California 94923 USA.

Declining biodiversity has prompted research into how diversity affects community and ecosystem processes. However, most experiments evaluating the consequences of biodiversity change have focused on random diversity changes, so it is difficult to predict the consequences of realistic changes. We compared the functional consequences (nitrate uptake and photosynthesis) of realistic and random biodiversity changes and found that the effects of realistic diversity changes—those based on patterns of community structure found in nature—can be very different from the effects of random changes. Realistic increases in intertidal seaweed richness did not alter nitrate use at low nitrate concentrations but resulted in declines in nitrate uptake when nitrate concentrations were high. However, random diversity increases had no effect on nitrate uptake, regardless of ambient nitrate concentrations. Photosynthesis rates—oxygen production by seaweed assemblages measured as a function of light intensity—were also affected by realistic, but not random, changes in seaweed diversity, but results were opposite to those for nitrate uptake. Realistic increases in seaweed richness had no effect on photosynthesis rates at high light intensities but were associated with declines in the photosynthesis rates at low light intensities. There was no effect of random diversity increases on photosynthesis, regardless of light intensity. Changes in these key physiological processes were associated with shifts in both species composition and species interactions as diversity changed. Our results highlight the need to consider realistic diversity gradients and to measure multiple response variables in order to understand the functional consequences of biodiversity changes.

FUCUS SERRATUS IN EASTERN NORTH AMERICA: HISTORY, RATES, AND FACTORS AFFECTING CONTINUED SPREAD. Susan Brawley¹, Ladd Johnson² & Walter Adey³. ¹School of Marine Sciences, University of Maine, Orono, ME 04469, U.S.A.; ²Département de biologie and Québec-Océan, Université Laval, Québec, QC G1V 0A6, Canada; ³Botany, Smithsonian Institution, Washington, DC 20013, USA.

Records of the spread of *Fucus serratus* (Phaeophyceae) in the Canadian Maritimes exist from 1887, 1903, 1933, 1952, and 1971-73; these records are updated (2007-2009) here. Following the seaweed's introduction from Scotland and Ireland in the early 1800s, at least five discrete primary and secondary introductions occurred. Rates of spread vary from 6.0 km year⁻¹ (early) to 0.9 km year⁻¹ (recently), and intra-North American shipping may have created secondary sites of spread that were not distinguished from linear expansion from Pictou and Inverness in the Gulf of St. Lawrence. Hybridization between *F. serratus* and the native *F. distichus* occurs at a recent contact zone (Capelin Cove, Nova Scotia), as detected with microsatellite markers, but we did not find evidence for introgression of *F. serratus* as it migrated through native *F. distichus* on the SE shore of Cape Breton. Historical hybridization studies of M. A. Howe and information from other founder populations suggest the importance of the size of founder populations/propagule pressure to successful invasion.

INVESTIGATING NORTHWEST ATLANTIC SPECIES OF *CERAMIUM* USING AN INTEGRATIVE TAXONOMIC APPROACH. Meghann Bruce and Gary W. Saunders. Centre for Environmental and Molecular Algal Research, Department of Biology, University of New Brunswick, Fredericton, NB E3B 5A3, Canada.

Ceramium (Ceramiaceae, Rhodophyta) is a large genus with over 180 species recognized worldwide, six of which are presently credited to the northwest Atlantic (Guiry and Guiry 2011). However, disclaimers in the current taxonomic key for this region acknowledge that there is considerable uncertainty surrounding the identity of the reported species (Sears 2002). In this investigation, we apply molecular taxonomic techniques to assist in resolving the taxonomy of *Ceramium* species in the northwest Atlantic. Preliminary analyses of COI-5P DNA barcode sequence data have indicated that the number of genetic groups is equivalent to the number of morphological species currently recognized (six), however, *rbcL* sequence data confirm the presence of two *Ceramium* species that are currently not recognized for this region: *C. secundatum* and *C. sincola*. We are investigating whether these two species are synonymous with currently recognized species for this region. Detailed morphological examinations will supplement molecular assisted species identifications and identify characters that are diagnostic of the genetic species groups. Biogeographical and ecological data (collection metadata) will also be incorporated into analyses, providing a holistic approach to species discrimination, which will facilitate a comprehensive taxonomic review of *Ceramium* in the northwest Atlantic.

BIOCHEMICAL COMPOSITION OF PERIPHYTON FOOD QUALITY AS AFFECTED BY LIGHT AND NUTRIENT AVAILABILITY. Matthew Cashman, John Wehr, and Kam Truhn. Louis Calder Center - Biological Field Station, Fordham University, Armonk, 10504, U.S.A.

The biochemical composition of algae can be an important driver of aquatic food web dynamics and may limit growth, reproduction, and other physiological responses in secondary consumers. Understanding algal communities from the perspective of food quality is necessary to quantify consumer energy assimilation and stream ecosystem function. We measured the factors that may regulate algal chemical composition, particularly nutrient content (C:P, C:N ratios) and polyunsaturated fatty acid (PUFA) concentrations. We conducted a manipulative *in situ* experiment to examine the effect of light and nutrient availability on the biomass, nutrient stoichiometry, and fatty acid composition of stream periphyton. Periphyton assemblages were colonized *in situ* in three streams in Westchester County, New York on terracotta tiles. Tiles were relocated to create a factorial nutrient x shade treatment experiment and sampled over time for chlorophyll, ash-free dry mass, algal stoichiometry, and fatty acid composition. These data were also compared with fatty profiles of algal material of single-species collections to assess the effects of species succession on the tiles over time. Tiles in high light conditions had higher levels of chlorophyll-*a*, -*b*, -*c*, and AFDM. There was no observed response under nutrient enrichment. We will also discuss the change in tissue C:P and C:N stoichiometry and the change in PUFA concentrations as both an individual percentage of the total and as a ratio of $\omega 3/\omega 6$ PUFAs.

ASSESSING TURF ALGAL DIVERSITY OF PANAMA: A COMPARISON OF CULTURE BASED & ENVIRONMENTAL PCR APPROACHES. Valerie Charbonneau & Brian Wysor. Biology, Roger Williams University, Bristol, RI 02809, U.S.A.

Turf algae play a variety of important ecological roles in tropical marine systems, but their diversity is often poorly known due to their diminutive stature, and problems of morphological convergence and plasticity. As part of a larger survey of the Panamanian marine flora, we have begun isolating micro-filamentous turf algae into uni-algal culture. Field samples (usually a fouled surface) were also preserved in silica gel to facilitate a molecular assessment of turf algal diversity using an environmental PCR approach. PCR products of the 400-bp Universal Plastid Amplicon derived from community DNA extracts were cloned and sequenced and compared to sequences of isolated uni-algal cultures from the same source material. Results show that culturing and the environmental PCR approaches reveal different diversity, although greater diversity was uncovered through the environmental PCR method.

A NEW TYPE OF HARMFUL ALGAL BLOOM: THE PCB-CONCENTRATING ULVA BLOOM OF NEW BEDFORD HARBOR. Donald Cheney¹, Kevin Gardner² and John Logan³. ¹Mar. Sci. Center, Northeastern University; ²Civil Engineering, UNH; ³Mass. Div. Mar. Fisheries.

Macroalgal (seaweed) blooms are generally thought of as a nuisance or as causing limited localized ecological harm, but not as a threat to human health. While this may be true for most seaweed blooms, we discovered a bloom that does pose a threat to human health. In the summer of 2007, we discovered a large bloom of the common green alga *Ulva lactuca* in the estuarine upper harbor of New Bedford Harbor, an area designated a Superfund Site in 1982 because of the extremely high levels of PCB contamination in its sediments. More importantly, we discovered the *Ulva* plants growing in the Superfund site are loaded with PCBs. The maximum (total) PCB conc. we measured was 99 ppm. This is ca 100,000X the PCB conc. in the water and 800X higher than the previously highest report of PCBs in any macroalga. Last year, we discovered that the *Ulva* in the Superfund site is being consumed by the principal intermediate-level food chain species in the Superfund site: grass shrimp and mummichogs (*Fundulus*). Based upon our gut analyses, *Ulva* was the principal food item of the mummichogs that we caught during the summer. In addition, SIA studies show that *Ulva* is being assimilated by *Fundulus*. These findings suggest for the first time that a macroalgal bloom may be a major conduit for PCB transfer up an estuary's food chain. In addition, because of *Ulva*'s consumption by *Fundulus*, our findings suggest that PCBs taken up by *Ulva* may be getting into recreationally-caught fish species at the top of the Superfund site's food chain, namely striped bass, and ultimately to humans that consume them. Interestingly, the highest levels of PCBs ever reported for striped bass from Mass. were caught in Buzzards Bay, not far from New Bedford Harbor.

A ROSE BY ANY OTHER NAME: TAXONOMIC REVISIONS IN CANADIAN KALLYMENIACEAE (RHODOPHYTA). Bridgette Clarkston and Gary W. Saunders. CEMAR, Biology, University of New Brunswick, Fredericton, N.B., E3B 6E1, Canada.

For the last six years, members of the red algal family Kallymeniaceae have been collected intensely from locations throughout Canada and screened molecularly using the DNA barcode (COI-5P – the 5' region of the mitochondrial cytochrome c oxidase I gene) as a species identification tool. Prior to this survey, there were eight kallymeniacean genera and 18 species reported in the Canadian flora. Following our survey, those numbers have increased to ten genera and 25 species, with new records and overlooked diversity in *Callophyllis*, *Pugetia*, *Euthora* and *Beringia*. Interestingly, the genera *Hommersandia*, *Cirrulicarpus* and *Kallymenia* were not encountered, despite intensive collecting from locations where species have been reported. Subsequent morphological examination of each species was also conducted, however, in most cases, they failed to determine unequivocal diagnostic features for the new species. Phylogenetic relationships among the Kallymeniaceae were investigated subsequently using large-subunit nuclear ribosomal DNA (LSU), combined LSU and COI-5P data, and, for some genera, nuclear elongation factor 2 sequences (EF2) as well. All datasets were subjected to maximum likelihood and Bayesian analyses, which supported the increased kallymeniacean diversity revealed by the DNA barcode. Following the molecular, morphological and phylogenetic assessments, all potential matches to the new species were investigated in the literature. Here we discuss the highlights of the taxonomic revisions made following the investigation, including descriptions of *Callophyllis schneideri* sp. nov. and *Beringia wynnei* sp. nov.

MARINE PLANT PRODUCTION FOR HIGH VALUE APPLICATIONS IN FUNCTIONAL FOOD AND COSMECEUTICAL APPLICATIONS: SECURITY OF SUPPLY AND TRACEABILITY. M.L. Cornish, J. Hafting, and A. T. Critchley. Acadian Seaplants Limited, 30 Brown Avenue, Dartmouth, NS B3B 1X8, Canada.

As a pioneer in land-based cultivation technology and possessing the largest, on-land commercial macroalgal production facility in the world, Acadian Seaplants Limited (ASL) ensures its cultivated marine plants have an established chain of custody. Wild harvested seaweeds are derived from marine environments exposed to a variety of human influences, making them unreliable and inconsistent sources of high quality compounds. Acadian Seaplants' global leadership in generating pure cultures of premium marine plant biomass necessitates the integration of a reliable traceability system together with world-class management of operations and processes. To accomplish these commercial goals, production protocols have been optimized to batch sizes and critical control points correlated throughout the tightly-managed growth systems. Extensive documentation is maintained from beginning to end of each production cycle, ensuring security of supply through a safe and traceable system. This information accompanies the product throughout its life span up to and including the finished product format, as required by the customer. The nature of ASL's traceability system inspires commercial confidence and its cultivation system provides flexibility in addressing customer's unique product requirements while maintaining safety, quality, sustainability and environmental stewardship.

CYANOBACTERIAL NITROGEN-FIXATION IN THE UPPER MISSISSIPPI RIVER. Jillian Decker¹, Kam Truhn¹, John Wehr¹, Lynn Bartsch², William Richardson², and Jeff Houser². ¹Louis Calder Center – Biological Field Station, Fordham University, Armonk, NY USA; ²USGS Upper Midwest Environmental Sciences Center, La Crosse, WI, USA.

Densities of N-fixing cyanobacteria (*Anabaena*, *Aphanizomenon*) have increased in the Upper Mississippi River in recent years. Although elevated nutrient conditions resulting from agricultural runoff occur in the main channel, nitrogen depletion occurs in less connected (minimal exchange) backwater habitats via transformations (e.g. denitrification), which favor N-fixing species. We hypothesized: (1) under non-flood flow, nitrogenase activity will be greatest in less-connected backwaters and least in the main channel; (2) under low-flow summer conditions, activity will increase across all sites; and (3) P would be a major influence on activity in summer. We conducted *in situ* bioassays using river water enriched with N, P, or NP, during three seasons at three sites along a hydrological connectivity gradient for two years. Nitrogenase activity was estimated via acetylene reduction assays in ambient water samples and nutrient-amended bioassays. Nitrogenase activity was relatively low across sites during spring and fall, but varied strongly among sites in summer. Greatest activity was measured at the least-connected site in summer 2008 and in the main channel in summer 2009. Both periods corresponded with high N: P ratios (32:1 and 51:1, respectively), indicating P limitation versus Redfield values. Our data support the hypothesis that P was a major driver of nitrogenase activity both years. In summer 2008, nitrogenase activity was 8 times greater in P-amended than N-amended assays in the main channel. In the least-connected backwater in summer 2009, N-fixation in +P and +N+P-amended treatments was ~4 times greater than in controls, while N-fixation in N-amended treatments was half that of controls. Our results indicate that the main channel of the Upper Mississippi is more important source of ecosystem N inputs via N-fixation than originally hypothesized, with several factors regulating riverine N-fixation.

ARIZONA CENTER FOR ALGAE TECHNOLOGY AND INNOVATION (AZCATI): A NEW OPEN TEST BED SPANNING THE ALGAE VALUE CHAIN. Thomas Dempster, Milton Sommerfeld, Qiang Hu & Gary Dirks. Applied Sciences and Mathematics, Arizona State University, Mesa, AZ, 85212, U.S.A.

The Arizona Center for Algae Technology and Innovation (AzCATI) was founded in fall 2010 with funding from the Science Foundation of Arizona. AzCATI is located at Arizona State University-Polytechnic Campus and is designed as an open test bed facility for academic institutions and industry partners. AzCATI provides test and evaluation facilities to assess the performance of individual and combined unit operations across the algal value chain. The test bed facilities of AzCATI provide access to baseline technologies and best practices allowing for the development and objective assessment of current and proposed technologies. AzCATI offers services to test performance of bioreactors or strains over appropriate periods to validate production volumes. Strain selection facilities are capable of rapidly growing inoculum from partner-provided strains or AzCATI strains to test equipment or side-by-side comparisons. AzCATI has the capability of monitoring strains and providing differing conditions for evaluation. Evaluation of genetically modified organisms (GMOs) may be conducted in the AzCATI Biosafety Level 2 greenhouse facilities. AzCATI has a variety of cultivation systems available for use in evaluations, including a variety of vertical photobioreactors ranging in size from 55 – 1,400 liters and raceways ranging in size from 1,500 – 150,000 liters. AzCATI also provides services to test downstream equipment. The facility is capable of growing biomass at pilot scale from either raceways or PBRs. AzCATI can provide biomass and fractional biomass in paste, freeze-dried, dried or pellet form dependent upon the needs of the client, as well as biochemical analyses to determine the quality of biomass including proteins, carbohydrates and lipids. In addition, some capacity for systems integration (multiple units) is possible. Standard harvesting and dewatering techniques are also available including dissolved air flotation, flocculation, filtration, centrifugation, and sedimentation.

CHARACTERIZATION OF BACTERIA ASSOCIATED WITH THE SEA SLUG *ELYSIA CHLOROTICA* AND ITS ALGAL PREY *VAUCHERIA LITOREA*. Susan Devine, Karen Pelletreau, and Mary Rumpho. Dept. of Molecular & Biomedical Sciences, University of Maine, Orono, ME 04469.

The sea slug *Elysia chlorotica* is best known for its ability to sustain itself photoautotrophically with chloroplasts from its algal prey *Vaucheria litorea*. However, both the mollusc and alga also form associations with multiple bacterial species that may contribute to the symbiosis. The production of kahalalide F, a secondary metabolite with anti-cancer properties, by tropical *Elysia* spp. has been linked to a resident *Vibrio* sp., believed to be acquired from the algal prey. Our study focused on identifying symbiotic bacteria associated with the alga *V. litorea* and comparing this to the bacterial population of two populations of *E. chlorotica* from Martha's Vineyard, MA (MV) and Halifax, Nova Scotia (NS). The objective was to identify bacteria linked to the production of secondary metabolites of pharmaceutical importance and those that may provide essential nutrients (e.g., nitrogen or vitamins), and to determine commonalities between the sea slugs' and algal bacterial profiles. Bacterial 16S rDNA was amplified from lab-cultured *V. litorea* DNA, along with animal DNA from both populations under varied conditions (e.g., wild, lab-maintained, lab-bred, and digestive tissue). DNA was sequenced using clone sequencing and/or 454 amplicon sequencing, and analyzed using the Ribosomal Database Project and BLAST. Generally, bacterial profiles varied greatly between all conditions, between populations, and between animal and algae. Of interest, bacteria capable of nitrogen fixation, cellulose digestion, and possible kahalalide F production were identified in various *E. chlorotica* samples. Photosynthetic bacteria and bacteria potentially capable of vitamin B₁₂ production were found in common between the animal and algae although further sequencing of *V. litorea* 16S rDNA is needed for a more complete comparison of sea slug- and algal-associated bacteria.

CYANOBACTERIA BLOOM AND NITROGEN IMBALANCE LINKED TO STOCKED STERILE CARP IN A EUTROPHIC LAKE. Steve Di Lonardo¹, John Wehr¹, Gregory Boyer², Alissa Perrone¹, and Kam Truhn¹. ¹Louis Calder Center – Biological Station, Fordham University, Armonk, NY 10504; ²SUNY ESF, 1 Forestry Drive, Syracuse, NY 13210.

A small, shallow eutrophic lake (ca. 20 acres) in a suburban environment has been monitored 10 years to assess the growth of phytoplankton and submerged aquatic vegetation (SAV). The lake's eutrophic state and dense SAV growth is attributed to human activity in the watershed, in particular increased impervious surface and lawn fertilizer use. In 2008, the lake was stocked with triploid grass carp (*Ctenopharyngodon idella*) to control SAV, which had affected recreational uses by residents (swimming, non-motorized boating). Carp were chosen as the management method to avoid using chemical treatment or mechanical harvesting. A vegetation survey and New York State Department of Environmental Conservation guidelines suggested 10 carp per vegetated acre, with a final total of 120 carp. The first two growing seasons (2008, 2009) were characterized by reduced SAV growth, as desired. In the third growing season (2010), almost no SAV was present, presumably due to feeding by growing carp. In addition, a dense cyanobacteria bloom (not common in prior years) developed in mid-summer, and has persisted throughout winter under the ice. As a precaution, Microcystin levels were tested (summer, winter) and found to be below WHO guidelines for drinking water ($< 1 \mu\text{g L}^{-1}$). The dominant cyanobacteria taxa changed over the course of the bloom with *Woronichinia naegeliana* and *Planktothrix* spp. dominating in mid-summer, to almost exclusively *Aphanizomenon flos-aquae* in autumn-winter. Over this period, dissolved nitrogen levels varied strongly from low N:P ratios in the summer, to very high N:P in the winter. This was accompanied by very low frequencies of heterocysts in *Aphanizomenon* trichomes. Future studies will test whether nutrient release from non-vegetated sediments may have affected water quality and caused the dramatic changes in the phytoplankton community.

SOUTHERN BIODIVERSITY BLOWOUT: CRYPTIC CRUSTS IN AUSTRALIA. Kyatt Dixon & Gary W. Saunders. Centre for Environmental & Molecular Algal Research, Biology, University of New Brunswick, Fredericton, NB E3B 5A3, Canada.

Australia is widely regarded as an area of considerable marine macrophyte biodiversity, particularly along the algal-dominated temperate southern coasts. Regional surveys of the Australian marine flora have, until recently, been restricted to anatomy-based, alpha taxonomic studies. While the value of good alpha taxonomy is undeniable, the incorporation of molecular data into floristic surveys is rapidly highlighting the limitations inherent in traditional methods for recognising fully the diversity of many algal groups. This is exemplified in the primarily crustose red algal family Peyssonneliaceae for which a combination of cryptic diversity and lack of rigorous study has resulted in a gross ignorance of the true species richness. For instance, in Western Australia only two species of Peyssonneliaceae are recorded, although COI-5P DNA barcoding results reveal the presence of at least an additional 72 species. *Sonderopelta capensis* provides a good example of cryptic diversity, represented in Australia by at least six distinct genetic groups, the identities of which are discussed with regard to current synonyms of *S. capensis* and their type localities. Integrative taxonomy, combining the traditional and molecular approaches, has provided numerous benefits including new ways to investigate and understand species boundaries, which enables better estimates of species diversity and distribution. In many cases the integrative approach has also presented fresh challenges, particularly in crustose red algae where we are only now beginning to understand how little we know.

SAME ACTORS, DIFFERENT PLAYS: QUANTIFYING HOW ECOSYSTEM EFFECTS OF INTERTIDAL ALGAL DIVERSITY VARY ALONG A 500 KM LATITUDINAL GRADIENT. James G. Douglass¹, Matthew Bracken¹, & Geoffrey C. Trussell¹. ¹Marine Science Center, Northeastern University, Nahant, MA, 01908, U.S.A.

Increasing plant diversity has been shown to increase primary and secondary productivity, nutrient cycling rates, and resistance to disturbance, among other important ecosystem functions. However, the effects of plant diversity depend on context, which for rocky intertidal algal communities includes physical conditions, nutrient availability, herbivory, and competition with sessile invertebrates. To determine the magnitude and context-dependence of algal diversity effects on New England rocky shores, we are manipulating algal diversity and measuring community responses at three sites within each of three latitudinal regions from Nahant, Massachusetts, to Lubec, Maine. Whereas all sites include the same dominant algal taxa--*Ascophyllum nodosum*, *Fucus* spp., and *Mastocarpus stellatus*--they differ with respect to physical conditions and the relative abundances of algae, sessile invertebrates, and herbivores. These differences are indicated in our multivariate analyses of community composition from site surveys performed prior to algal diversity manipulation, which show moderate distinction among sites within regions but significant distinction among regions. Bivariate correlations from the site surveys indicate that while algal cover and biomass are highest at northern sites, cover is positively related to algal species richness in all regions. Algal cover also varies inversely with sessile invertebrate density, and algal cover is lower in plots with higher herbivore abundances. Analysis of community responses following our algal diversity manipulations should help to determine the processes underlying these correlations, in particular, whether high algal diversity is a cause or consequence of other community characteristics. Our work will be important in identifying how environmental context mediates the relationship between seaweed biodiversity and intertidal community structure and ecosystem functioning.

EST-SSRS IN *PORPHYRA UMBILICALIS* AND *PORPHYRA PURPUREA*. Renée L. Eriksen and Anita S. Klein. Department of Biological Sciences, University of New Hampshire, Durham, NH 03824, USA.

Databases of expressed sequence tags (ESTs) have been called the “poor person’s genome” for their high utility for acquiring genomic data but their relatively low cost. They have been used extensively for data mining of genomic markers, and have dramatically reduced the time and money necessary to develop population markers such as microsatellites or simple sequence repeats (SSRs). EST-SSRs have the advantage over conventionally described microsatellites of increased cross-species utility, because at least one of the primers is anchored in a coding region which can be conserved across taxa. We used the EST databases recently made available for *Porphyra umbilicalis* and *P. purpurea* from the *Porphyra* Research Coordination Network to develop EST-SSR markers for population studies of these species and related taxa. About 24% of the sequences available for *P. umbilicalis* contain SSRs, compared to about 10% of the larger *P. purpurea* database. Both databases contain roughly 1 SSR for every 2 kilobases of sequence data, and both databases contain comparable numbers of single nucleotide, di-, tri-, 4-, 5-, and 6-nucleotide motifs. Single nucleotide and tri-nucleotide motifs were the most common SSRs. Of the single nucleotide motif SSRs, the majority of short SSRs (between 10-20 repeats) were G or C motifs, though longer SSRs (greater than 20 repeats) are either strings of A or T. The most common tri-nucleotide motif in the EST databases was GGC, and the number of repeats varies from 5-14 in *P. umbilicalis* and from 5-15 in *P. purpurea*. We have evaluated some of these tri-nucleotide markers for polymorphisms among populations, and we have also evaluated some for cross-species utility.

CHANGES IN SUBTIDAL MACROALGAE AT THE BAY OF BISCAY: ECOLOGICAL AND PHYSIOLOGICAL INDICATORS OF THE EFFECTS OF GLOBAL WARMING. Félix L. Figueroa¹, Nathalie Korbee¹, Eugenia Márquez¹, Cristina de Miguel¹, Isabel Díez² Nahiara Mugerza², Alberto Santolaria² & J.M. Gorostiaga². ¹Department of Ecology, Faculty of Sciences, Málaga University, 29071-Málaga, Spain. ²Department of Botany and Ecology, Faculty of Sciences and Technology, University of Basque Country, 49480-Leioa, Spain.

Changes in macroalgal species abundance and distribution coincident with global warming have been detected at the Basque coast (Northern Spain). An increasing of surface seawater temperature (0.26°C per decade since 1980) and frequency of days with water temperatures above 22°C have been produced. The most relevant changes in the subtidal vegetation in the last two decades have been: i) changes in the distribution pattern of the canopy species *Gelidium corneum* and *Cystoseira baccata*, ii) disappearance of *Laminaria ochroleuca* populations, iii) increases of photophilous coralline algae: *Corallina elongata*, *Jania rubens*, *Lithophyllum incrustans*, iv) increases of morphologically simple filamentous forms of meridional affinity: *Aglaothamnion tenuissimum*, *Gayliella flaccida*, *Aphanocladia stichidiosa*, *Acrosorium ciliolatum*, v) introduction and expansion of non-indigenous species, and vi) increases in species richness and diversity. These results suggest that changes in water transparency and nutrients availability may be also acting synergically with increased temperatures. Multifactorial experiments were conducted to examine the effects of the interaction between temperature, PAR and UVR irradiance, and nutrient availability on the capacity of acclimation of key species in order to identify ecophysiological indicators of the impact of the Climate Change for monitoring purposes. The indicators have been applied both in-door and out-door and in different coastal zones i.e. maximal quantum yields (Fv/Fm), electron transport rates (ETR) and non-photochemical quenching (NPQ) using the measurement of *in vivo* Chla fluorescence of Photosystem II and (2) oxidative stress and antioxidant activities. In general, those macroalgae that have experienced over the last three decades an increase in abundance had higher acclimation capacity to simulated stress conditions according to climate change variables (increased temperature and PAR-UVR irradiance, and low nutrient availability) than species with decreased abundances.

ESTABLISHMENT OF SPECIES DIVERSITY OF THE RHODYMENIALES (RHODOPHYTA) IN BRITISH COLUMBIA USING MOLECULAR AND MORPHOLOGICAL TECHNIQUES. Gina V. Filloramo & Gary W. Saunders. Center for Environmental & Molecular Algal Research, Department of Biology, University of New Brunswick, Fredericton, NB E3B 5A3, Canada.

The Rhodymeniales includes six diverse families and over 300 species. Like many algal groups, accurate taxonomic assessment for representative Rhodymeniales at the species level has been complicated by convergent features, phenotypic plasticity and poorly understood life histories. As a result of the challenges associated with traditional morphology-based identification, molecular tools have become increasingly relied upon to redefine species with inaccurate or inadequate descriptions. A recent survey in British Columbia, Canada used the DNA barcode (COI-5P – the 5' region of the mitochondrial cytochrome c oxidase I gene) to reveal new and previously overlooked species within the Rhodymeniales. Barcode data resulted in novel discoveries for three genera: *Rhodymenia*, *Botryocladia* and *Gloiocladia*. This study focused on assessing species diversity for the genus *Rhodymenia*. Although there are currently two species of *Rhodymenia* recognized in British Columbia (*R. californica* and *R. pacifica*), molecular data resolved four distinct species groups. Morphological analysis of vegetative, anatomical and reproductive features confirmed the presence of *R. californica* and *R. pacifica* while extending the northern range of *R. callophyloides* from the type locality in California into southern British Columbia. Morphological analysis also supported the resurrection of *R. rhizoides* as a distinct species from *R. pacifica* and again extended the known range of this species into southern British Columbia. Future studies will include morphological examination of novel British Columbian *Botryocladia* and *Gloiocladia* species to assess their respective status with the Rhodymeniales.

UNRAVELING THE TAXONOMIC KNOT OF *BRACTEACOCCLUS*, *DICTYOCOCCLUS*, *PSEUDOMURIELLA*, AND *CHROMOCHLORIS* (CHLOROPHYCEAE, CHLOROPHYTA): A CASE OF CRYPTIC GENERA. Karolina Fučíková & Louise A. Lewis. Ecology and Evolutionary Biology, University of Connecticut, 75 North Eagleville Rd., Storrs, CT, 06269-3043, U.S.A.

Bracteacoccus, one of the most common soil algae, is taxonomically interwoven with several other genera. In particular, its relationship with the morphologically similar *Dictyococcus*, *Muriella* and *Pseudomuriella* is quite tangled because these share a similar overall morphology with *Bracteacoccus*. This has raised questions about the validity of these genera and the proper taxonomic disposition for their species. Phylogenetic relationships for a number of these taxa can be addressed using molecular sequence data obtained from live type strains. Using analyses of the 18S and *rbcL* genes, we determined that monophyly of *Bracteacoccus* can be achieved only by excluding four unrelated lineages that historically have been included under this name. Firstly, *B. engadinensis* belongs in the genus *Pseudomuriella*, along with *Dictyococcus schumacherensis*. Secondly, *B. cinnabarinus* and *B. minutus* group with *Muriella zofingiensis*, a species with its own obscure taxonomic history. These three species are distinct from the true *Muriella* lineage (Trebouxiophyceae) and we propose to assign them to the resurrected genus *Chromochloris* (Chlorophyceae). Thirdly, our results corroborate the 1995 transfer of *B. irregularis* into *Myrmecia*. Three other strains deposited in the UTEX collection as *Bracteacoccus* also likely belong to *Myrmecia*. Lastly, *Dictyococcus* was shown to be an unrelated lineage that can be reliably distinguished from *Bracteacoccus* based on chloroplast morphology. Our results indicate that *Pseudomuriella*, *Chromochloris* and *Bracteacoccus* are morphologically cryptic genera, representing closely related yet divergent lineages.

MOLECULAR SEQUENCING OF FIELD-COLLECTED AND TYPE SPECIMENS REVISES NORTHEAST PACIFIC CORALLINALES (RHODOPHYTA). Paul W. Gabrielson. Herbarium, University of North Carolina at Chapel Hill, Chapel Hill, NC 27599-3280 USA.

Molecular sequencing of type and historically important specimens along with field-collected material is rapidly changing our understanding of northeast Pacific coralline species. Because of uncertainty about which morphological characters are phylogenetically useful in characterizing both articulated and non-articulated genera, it is essential that generitype species be included in molecular analyses. Some examples that will be discussed and that call into question our historical reliance on morphological characters are: 1) *Calliarthron* is a northeast Pacific endemic--northwest Pacific species belong in *Alatocladia*, 2) *Chiharaea* is not monotypic and may not be endemic to the northeast Pacific, 3) *Yamadaia melobesioides* the generitype species from Japan and *Yamadaia americana* from Washington are unrelated, 4) *Arthrocardia silvae*, the only species in that genus reported from the northern hemisphere, does not belong in *Arthrocardia*, and 5) three species are reported in the genus *Pseudolithophyllum* in the northeast Pacific, and all are unrelated. Biogeography and molecular data are more reliable indicators of evolutionary relationships at the generic rank than are many morphological characters currently in use.

MOLECULAR EVOLUTION OF GLUTAMINE SYNTHETASE II AND III IN SELECT CHROMALVEOLATE LINEAGES. Sohini Ghoshroy and Deborah L. Robertson. Clark University, 950 Main Street, Worcester, MA 01610.

Glutamine synthetase (GS), essential for nitrogen assimilation and glutamine biosynthesis, is encoded by three distinct gene families (GSI, GSII and GSIII). Previous studies established that GSII and GSIII were present in diatoms, however little was known regarding the evolution of the gene families in other algal lineages. Hence, we examined the molecular evolution of GSII and GSIII in select lineages of chromalveolates.

GSII cDNA sequences were isolated from three cryptophytes (*Guillardia theta*, *Cryptomonas phaseolus*, and *Pyrenomonas helgolandii*) and GSIII was sequenced from *G. theta*. In Bayesian and maximum likelihood analyses, chromalveolate GSII sequences formed a weakly supported clade that nested among glaucophyte, red algal and plant sequences. Within the chromalveolates, cryptophytes, oomycetes, and haptophytes + stramenopiles formed three well-resolved clades. However, stramenopiles were paraphyletic within the chromalveolates, suggesting the presence of orthologous and paralogous sequences. The placement of haptophyte sequences within the heterokont clade is suggestive of a lateral gene transfer (LGT) event.

Chromalveolate GSIII sequences (stramenopiles+haptophytes+cryptophytes) formed a well-supported clade in both Bayesian and maximum likelihood phylogenies, in which cryptophyte sequence diverged from the deepest node. The topology was similar to those of plastid genes and is one of the first nuclear gene phylogenies to support the monophyly of heterokonts, haptophytes, and cryptophytes. Placement of a single GSIII sequence from *Aureococcus anophagefferens* within the dinoflagellates suggests an LGT event or gene losses in multiple chromalveolate lineages

An understanding of the evolutionary history of nitrogen assimilating enzymes within chromalveolates provides an important framework for physiological studies of nitrogen assimilation in marine and freshwater phytoplankton. These studies may provide insights into the selective advantages of obtaining and retaining genes encoding essential enzymes via LGT events.

THE EFFECTS OF BIODIVERSITY ON THE RESISTANCE AND RESILIENCE OF MARINE COMMUNITIES TO OCEAN ACIDIFICATION. Brendan C. Gillis & Matthew E.S. Bracken. Marine Science Center, Northeastern University, 430 Nahant Road, Nahant, MA 01908, USA.

The pH in the world's oceans has decreased by 0.1 units since 1850, and pH is expected to decline by another 0.3-0.4 units by 2100 due to anthropogenic emission of CO₂. This increase in ocean acidity is likely to have major effects on calcification, metabolic stability and larval development for a wide variety of organisms. Not all organisms are expected to be adversely affected, however, and it is predicted that some algal species may even thrive in an acidified ocean environment due to higher CO₂ concentrations. Tide pool pH levels are naturally more variable than oceanic levels due to photosynthesis (consuming CO₂) and respiration (producing CO₂) by plants and animals during isolation at low tide. Despite large natural variation in tide pool pH, severe negative effects have been demonstrated for two species of periwinkles (*Littorina littorea* and *L. obtusata*) due to relatively small changes in pH. While physiological changes may have an effect on individual species and community structure, biodiversity could buffer and mediate the impact of acidic conditions. By crossing a CO₂-mediated acidification treatment with a biodiversity treatment, we are examining how tide pool species diversity mediates community resistance and resilience in response to acidification. We have developed a technique for delivering CO₂ to tide pools *in situ* in the field, and have been able to successfully reduce tide pool pH by XX units relative to control tide pools. Experiments will involve a factorial manipulation of tide pool diversity (reduced vs. ambient) and acidification (CO₂-enriched versus control) in tide pools to evaluate the effects of biodiversity loss on the response of tide pool communities to CO₂-mediated pH declines. This research will increase our understanding of how two major anthropogenic threats—biodiversity loss and ocean acidification—may interact to impact marine communities.

EFFECTS OF CLIMATE CHANGE ON DISTRIBUTION AND PRODUCTIVITY POTENTIAL OF GLOBAL KELP SYSTEMS. Michael H. Graham. Moss Landing Marine Labs, 8272 Moss Landing Road, Moss Landing, CA, 93933, USA.

Debate on the causes of kelp deforestation-forestation cycles in global kelp systems has focused on differences in top down (kelp-sea urchin-top predator trophic cascades) versus bottom-up (variability in oceanographic climate) forcing. Although top-down/bottom-up processes are not mutually exclusive, little effort has been made to study the structure of kelp systems using energetic approaches that address the balance between kelp productivity and consumer pressure. Data from 25 kelp systems were used to study kelp productivity potential at a global scale. We found that the productivity potential of global kelp systems can be well explained by spatial variability in ocean climate (temperature, nutrients, light, etc), with regional differences in ocean climate explaining why some kelp systems are more productive than others. Temperate zones had the most productive kelp systems, with productivity potential generally decreasing with increasing latitude. Consequently, future ocean warming may have positive effects on kelp systems in low productivity regions as productive kelp taxa expand their range or conditions become more temperate, whereas high productivity systems may be negatively impacted if ocean warming exceeds kelp tolerances, depending on associated changes in nutrient supply. Our understanding of current and future kelp deforestation-forestation events at a global scale will benefit from studies that address the causes of imbalance in kelp productivity, especially as it relates to herbivore consumption pressure.

CAPTURING NEW CONSERVED GENES USING EVOLUTIONARY GENE NETWORKS. Scott Grandpre¹, Ian Misner¹, Philippe Lopez², Eric Baptiste² & Christopher Lane¹. ¹Department of Biological Sciences, University of Rhode Island, Kingston, RI, 02881, U.S.A.; ²UMR CNRS 7138 Systematique, Adaptation, Evolution, University Pierre et Marie Curie, Paris, France.

The field of deep eukaryotic phylogenetics is increasingly using large multi-gene datasets, but many of the same genes are used in different analyses. These analyses would benefit from including novel genes. This is especially relevant for a large number of algal lineages, particularly ‘chromalveolate’ groups, whose phylogenetic position remains contentious. We devised a fast approach for finding highly homologous sets of sequences in the wealth of data continuously produced by the sequencing projects. In our analysis we built networks out of a wide range of eukaryotic proteomes. Networks are built with genes as their nodes, and nodes are connected to each other with edges if they return a blast value lower than what was specified by the user. One of the many network parameters that can be measured is the clustering coefficient of individual connected components. The clustering coefficient is a measure of how related genes in a component are to each other, with highly conserved genes approaching a value of 1. We used the software program R to capture components that are both tightly clustered (score close to 1) and include all or most taxa in the analysis. We have utilized this technique to identify new genes useful for deep eukaryotic phylogenies.

PHYSIOLOGICAL STUDIES OF CULTURED NEW ENGLAND *PORPHYRA* SPP. AND IMPLICATIONS FOR USE IN INTEGRATED MULTI-TROPHIC AQUACULTURE SYSTEMS. Lindsay A. Green & Christopher D. Neefus. Department of Biological Sciences, University of New Hampshire, Durham, NH 03824, U.S.A.

The desire to create more environmentally sustainable aquaculture has increased significantly in recent years. Integrated multi-trophic aquaculture (IMTA) systems are recirculating systems with primary crops that release effluent and extractive crops that acquire their nutrients from that effluent. IMTAs can represent an environmentally sustainable method of aquaculture when waste production and extraction are properly coupled. Extractive crops used in IMTA systems can also become a secondary crop, used for fish meal, fertilizer, or marketed as a human food product. *Porphyra* is the most economically valuable maricultured seaweed in the world and serves as a major source of food for humans. *Porphyra* is a candidate for IMTAs due to its ability to uptake nutrients and successful substitution of fish meal. While many physiological studies have been performed on *Porphyra* there are still gaps in our knowledge for the local species as it pertains to integrated aquaculture. This study aimed to determine growth rate, photosynthetic efficiency, and pigment concentrations of local *Porphyra* spp. (including *P. umbilicalis*, *P. leucosticta*, and *P. purpurea*) under a matrix of temperature, light intensity, and photoperiod. Independently controlled water baths were used to maintain temperature (10°, 15°, and 20° C) and neutral density filters were used to achieve 100%, 50%, 30%, 10% light intensities using cool white fluorescent bulbs. Photoperiod was controlled using separate growth chambers (8:16, 12:12, and 16:8 L:D, respectively). Preliminary results will be discussed. This study will help determine the optimal conditions and best candidate of local *Porphyra* for integration into IMTA systems and determine the suitability of each species as secondary crops.

IMPACT OF INVERTEBRATE HERBIVORES ON *ULVA* BLOOM BIOMASS IN NARRAGANSETT BAY, RHODE ISLAND. Michele Guidone and Carol Thornber. Department of Biology, University of Rhode Island, Kingston, RI, 02881, U.S.A.

In Narragansett Bay, Rhode Island, blooms of *Ulva compressa* and *U. rigida* are an annual occurrence. We examined whether invertebrate herbivores exert top-down control on bloom biomass by conducting monthly (June-August) herbivore exclusion experiments during 2010. Experiments were conducted at three field sites, representing a range of macroalgal bloom intensities. At each site, we placed a known biomass of *U. compressa* and *U. rigida* inside cages constructed from one of three mesh sizes. The large mesh (100 mm²) permitted the entrance of all invertebrate organisms commonly found at the field sites, the medium mesh (24 mm²) excluded large mud crabs, and the small mesh (1 mm²) excluded all invertebrates except amphipods, polychaetes, and juvenile crabs < 1 mm in carapace width. After a period of ten days, the cages were retrieved, macroalgal biomass was measured, and organisms found within the cages were counted and identified. For both *Ulva* species, changes in biomass differed significantly amongst months, sites, and cage types. The greatest increases in biomass were observed during June. Large decreases in biomass were observed during July at the two high intensity bloom sites; this decrease was more pronounced in *U. rigida*. Interestingly, for both species across all months, thalli in the medium mesh cages lost the most biomass, indicating medium sized mud crabs and/or grass shrimp are the main *Ulva* consumers in this system. Overall, our results demonstrate that herbivores exert top-down control on both *U. compressa* and *U. rigida* biomass. Additionally, we hypothesize that *U. rigida* is preferred by herbivores in this system.

SUCCESSFUL INDUSTRIALIZATION OF FUNCTIONAL SEAWEED PRODUCTS FOR HUMAN USAGE REQUIRES ON-LAND CULTIVATION. Jeff T. Hafting, Alan T. Critchley and M. Lynn Cornish. Acadian Seaplants Limited, 30 Brown Avenue, Dartmouth, Nova Scotia, Canada, B3B 1X8.

Worldwide, there has been much interest in the development and commercialization of human functional products from seaweeds. Novel seaweed compounds with potential applications as bioactive ingredients in natural health products are being isolated in a number of active research programs on this topic. The majority of these research programs do not include cultivation as a critically important component in scaling the discoveries up to industrialization (i.e., economies of scale realized). Many of these seaweeds of interest with potential as functional human products are diminutive in size, sparse in density, and seasonal in occurrence and bioactive efficacy, making industrialization by resource management and harvesting economically challenging, and the application of traditional ocean-based production methods risky. Human functional products will require sustainable production coupled with quality assurance and standardized, consistent efficacy. Since humans are the consumers of these types of functional seaweed products, traceability and security of supply are of the utmost importance to successful industrialization. On-land cultivation is essential for commercial success in the development of human functional products from seaweeds at industrial scales. On-land cultivation allows the highest levels of control over quality, efficacy, traceability, and security. On-land cultivation represents the most environmentally acceptable method for the production of biomass from natural resources that could not be economically or sustainably developed any other way. However, on-land cultivation has many associated barriers to development, including high costs associated with capital, operations, maintenance, and cultivar development, and these demands limit industrial scale development of seaweed functional products for human consumption.

A FLORISTIC SURVEY OF MARINE TUBE-FORMING DIATOMS IN CANADA.

Sarah E. Hamsher and Gary W. Saunders. Biology Department, University of New Brunswick, Fredericton, NB E3B 5A3, Canada.

Marine tube-forming diatoms along the rocky intertidal form macroscopic colonies that are often mistaken for filamentous brown algae. These diatoms have been understudied with only a few floristic surveys completed and those available are based purely on morphological features. Many of the morphological features used to identify these diatoms, such as valve shape, are qualitative, making species difficult to identify. Molecular techniques can be used to distinguish species more objectively. Our study focuses on using the *rbcL*-3P and LSU D2/D3 regions to identify marine tube-forming diatoms in Canadian waters. No molecular data for this group of diatoms are available currently. This study will provide the first molecular survey of these taxa. Preliminary results will be discussed.

A MOLECULAR PHYLOGENETIC STUDY OF THE TRIBE CORALLINEAE (CORALLINALES, RHODOPHYTA) WITH AN ASSESSMENT OF GENUS-LEVEL TAXONOMIC FEATURES. Katy Hind & Gary Saunders. Centre for Environmental & Molecular Algal Research, Biology, University of New Brunswick, Fredericton, NB E3B 5A3, Canada.

A multi-gene phylogeny using CO1-5P (cytochrome oxidase subunit 1), psbA (photosystem 1) and EF2 (nuclear elongation factor) sequence data for members of the tribe Corallineae (Corallinaceae, Corallinales, Rhodophyta) was constructed to assess generic boundaries. We determined that traditional reliance on conceptacle position as an indicator of generic affinities in the Corallineae is not supported and taxonomic changes are required. Notably, the genus *Serraticardia* was polyphyletic; we propose synonymy of *Serraticardia* with *Corallina*, effecting transfer of the type species *S. maxima* to *Corallina* (*C. maxima* (Yendo) comb. nov.). We propose the new genus *Johansia* for *S. macmillanii* (*J. macmillanii* (Yendo) comb. nov.), which does not have affinities with *Corallina*. Our molecular data also indicate that *Arthrocardia* and *Marginisporum* have evolutionary affinities among species of *Corallina* and these genera should be synonymized, *Corallina* having nomenclatural priority. Thus, we propose the new combinations *Corallina corymbosa* (Lamarck) comb. nov., *Corallina aberrans* (Yendo) comb. nov., *Corallina crassissimum* (Yendo) comb. nov., and *Corallina declinata* (Yendo) comb. nov. *Corallina elongata* was divergent from all other members of the *Corallina* clade and is also transferred to a new genus.

ENCYSTMENT BY THE MIXOTROPHIC FLAGELLATE *OCHROMONAS PINGUIS* CONRAD (CHRYSOPHYCEAE) IN LABORATORY CULTURE. Dale A. Holen. Penn State University, Worthington Scranton Campus, Dunmore, PA, 18512

Although the presence of Chrysophyte stomatocysts are well documented in lake sediment cores little is known relative to the physical or chemical cues responsible for stomatocyst formation in these algae.

Ochromonas pinguis, a mixotrophic Chrysophyte isolated from oligotrophic Lake Giles, was incubated in batch cultures under a variety of nutritional and environmental conditions to assess their affect on encystment. The treatments included N and P limitation, light limitation, low pH and low temperature. Except for growth in continuous darkness, all treatments resulted in positive growth of the flagellate. Stomatocyst formation occurred in all treatments excluding those where flagellates were cultured in the dark or at a temperature of 10° C. In cultures that produced cysts, it was a decline in flagellate growth rate, rather than the treatment effect, that appeared to initiate stomatocyst formation. Stomatocysts were observed in all cultures approximately 10 -12 days after the beginning of each treatment, corresponding with the onset of the stationary phase of flagellate growth. However, the encystment frequency was minimal in all cases with on average 0.002 – 0.01% of the population undergoing cyst formation.

MUTATIONAL CHANGES IN THE AMINO ACIDS OF RUBISCO BETWEEN TEN ANTARCTIC AND TEMPERATE SISTER SPECIES OF MARINE RED ALGAE DISTRIBUTED BETWEEN THE ANTARCTIC PENINSULA AND CHILE OR THE FALKLAND ISLANDS MAY HAVE BIOGEOGRAPHICAL AND ECOLOGICAL SIGNIFICANCE. Max H. Hommersand¹, Chang-Jun Lee² & Lee G. Pedersen², ¹Department of Biology, University of North Carolina, Chapel Hill, NC 27599-3280, U.S.A.; ²Department of Chemistry, University of North Carolina, Chapel Hill, NC 27599-3280, U.S.A.

Our unpublished studies indicate that rates of both synonymous and nonsynonymous *rbcL* base pair changes are not significantly different among sister red algal species distributed in temperate regions of the Southern Hemisphere in New Zealand, western South Africa and southern South America. On the other hand, both synonymous and nonsynonymous base pair differences were significantly greater among sister species distributed between the Antarctic Peninsula and any of the other three regions. When ten pairs of sister species distributed between Antarctica and either Chile or the Falkland Islands were compared, the number of amino acid changes in the large subunit of RuBisCo varied from 7 to 16. The positions of the amino acid changes between species pairs were investigated as a function of their impact on the tertiary structure of the large subunit of RuBisCo expressed in the X-ray structure of *Galdieria partita*. Few changes were encountered in the highly conserved core region of the enzyme, and none in sites that are regarded as being particularly sensitive for conformational changes during catalysis, or the region of the active site for CO₂ carboxylase/O₂ oxygenase activity compared to the corresponding positions in spinach. With one exception, the net difference in the charge of proteins that underwent a change was either zero or slightly negative in the direction from Antarctica to southern South America. Amino acid changes between sister species were seen in the most variable regions of RuBisCo, but also as isolated pairs in regions that are not especially variable. The implications of these observations for our understanding of the phylogeny, biogeography and ecology of red algae distributed between Antarctica and the temperate waters of southern South America will be discussed.

MOLECULAR DATA REVEALS PARAPHYLLY AND UNDESCRIBED DIVERSITY IN THE GENUS *THOREA*. Emily Johnston, Daryl Lam, & Morgan Vis. Department of Environmental and Plant Biology, Ohio University, Athens, OH 45701, USA.

In the past two decades, the number of recognized species within the genus *Thorea* has ranged from as few as four to as many as 14. In addition to these species, two new species have been described from Thailand and Australia and potentially undescribed species have been collected from Micronesia and Vanuatu. The *rbcL* gene was sequenced for *Thorea* samples from Europe, Guam, Micronesia, North America, and South Pacific islands. This data set was combined with published sequences originating from Brazil and Japan. All data were analyzed using Maximum Parsimony, Bayesian Inference and Maximum Likelihood. Results showed both paraphyly in the morphologically circumscribed *T. violacea* and support the description of at least one new species from Micronesia and Vanuatu. The *rbcL* data gathered to date suggest at least nine species are present within *Thorea*. However, this number may increase as specimens from other areas of the world are added. Preliminary data for other gene regions, such as the *cox1* marker, will be discussed. This study is the most comprehensive molecular analysis of the genus *Thorea* to date. However, further work and the inclusion of type material for a number of species is needed to fully understand species boundaries and evolutionary relationships within this group.

TESTING DNA BARCODING METHODS OF DIATOMS IN AN ENVIRONMENTAL SAMPLE.
Diba Khan-Bureau, Louise Lewis & Gary Robbins. University of Connecticut, Storrs, CT 06269.

Diatoms are accepted as biological indicators for assessing watercourses, since many diatom taxa have been shown to be linked to particular environmental and water chemistry conditions and have ranges and tolerances for environmental fluctuations. In order to address issues such as water quality using diatoms, accurate taxonomic identification of the diatoms in question is essential. Various approaches have been used to identify diatoms and more recently the use of molecular analysis has been employed. Using morphology alone to distinguish diatom species can be difficult because morphology of a species can be influenced by the life cycle stage and phenotypic plasticity in response to environmental conditions. Many researchers believe that DNA barcoding would be a valuable tool to provide a consistent identification of diatoms and make the data from different studies directly comparable, even if taxonomy changes. In this study, we will assess barcoding methods in a broad taxonomic spectrum of diatoms from environmental samples from the Eightmile River in Connecticut. The results will be contrasted with light microscopy (LM) and scanning electron microscopy (SEM). Such comparisons have been made previously but with limited taxon sampling and with the use of cultures rather than environmental samples. The use of molecular analysis in conjunction with LM and SEM could provide useful and new information about the diversity and the identity of diatoms found in a river sample. In our initial investigation we were able to extract DNA and amplify the *rbcL* and *rbcS* markers. We cloned the amplicon and sequenced with some success. The NCBI BLAST tool identified our sequences as diatoms. We will continue to examine the utility of *rbcL* and 18S markers to identify diatoms. If this method can be consistently applied and optimized, it may have a significant impact on the accurate identification of these important organisms and their use as water quality bioindicators.

BIOEXTRACTION OF NUTRIENTS FROM THE BRONX RIVER WATERSHED (NYC) AND LONG ISLAND SOUND. Jang, J. Kim¹, George P. Kraemer², John Curtis³ & Charles Yarish¹.

¹Departments of Ecology & Evolutionary Biology and Marine Sciences, University of Connecticut, CT, 06901, U.S.A.; ²Environmental Studies Program, Purchase College, Purchase, NY 10577, U.S.A.

³Bridgeport Regional Aquaculture Science and Technology Center, Bridgeport (BRASSTEC), CT 06604, U.S.A.

Anthropogenic flux of nutrients into coastal waters leads to coastal eutrophication, which can lead to hypoxia, a condition which threatens ecosystem health. Attempts to control or reverse coastal eutrophication have centered on the reduction of point- and nonpoint-sources, such as waste water treatment effluent and fertilizer run-off, respectively. However, these mitigation strategies have had mixed success managing nutrient influxes into Long Island Sound and the Bronx River Watershed. Resource managers may be able to harvest cultured seaweed (such as *Gracilaria* and kelp species) to extract inorganic nutrients. The overall goal of this study is to demonstrate that seaweed aquaculture and natural assemblages of seaweeds are valuable bioextractive technologies for Long Island Sound and the Bronx River watershed. Cultures of *Gracilaria tikvahiae* were initiated from plants collected from Long Island Sound. Strains of *Gracilaria* were isolated and mass cultured at the University of Connecticut and BRASSTEC, and will be used as “seed stock” for field deployment. This “seed stock” will be outplanted in June 2011 using long-line culture units at near-shore sites in Long Island Sound (Fairfield, CT) and at the mouth of the Bronx River Estuary, at two depths (0.6 and 1.2m) and two stocking densities (0.1 and 0.2kg m⁻²). It will demonstrate the applicability of growing the warm temperate rhodophyte, *G. tikvahiae* and harvesting natural assemblages of seaweeds for bioextraction of inorganic nutrients from these coastal waters during the summer and fall growing seasons. We expect that this study will provide critical information to the suite of potential nutrient reduction approaches to increase water quality through bioextraction of aquacultured and natural assemblages of seaweeds.

AUSTRALIAN HALYMENIALES (FLORIDEOPHYCEAE, RHODOPHYTA), PAST, PRESENT AND FUTURE: USING THE DNA BARCODE TO ASSESS SPECIES DIVERSITY IN AN AUSTRALIAN RHODOPHYTE ORDER. Lesleigh G. K. Kraft & Gary W. Saunders, CEMAR, Department of Biology, University of New Brunswick, Fredericton, NB, E3B 5A3 Canada.

The Halymeniales is a red algal order comprised of two families (the Halymeniaceae and the Tsengiaceae) that encompass some 270 species worldwide. Australia has an extremely rich algal flora, currently comprising 14 Halymeniales genera and 30 species –24 having type localities within the country. Like most red algae, members of the Halymeniales have simple morphologies and are subject to high degrees of morphological plasticity and convergent evolution. As a result, traditional taxonomic approaches can be ineffective at resolving relationships among taxa and species richness can be underappreciated with cryptic species overlooked. Molecular tools are an effective means to explore species relationships and richness. The DNA barcode is a short, standardized DNA sequence amplified from the 5' end of the mitochondrial marker cytochrome oxidase subunit I. The DNA barcode is highly effective at identifying species and species groups among algae where morphological traits are varied or uninformative. In a highly successful approach termed molecular-assisted alpha taxonomy, the DNA barcode is used in conjunction with traditional alpha taxonomy and molecular phylogenetics to identify novel/cryptic species and infer relationships within higher-order taxonomic groups. Currently, 94 Australian Halymeniales have been barcoded and 246 collected specimens are pending analysis. Preliminary examination of barcode data indicates the genera *Cryptonemia*, *Grateloupia* and *Halymenia* are polyphyletic. Additionally, there appears to be a high level of cryptic diversity within the genera *Gelinaria*, *Polyopes*, *Tsengia* and *Zymurgia*. Further anatomical examination and additional molecular work will elucidate the species richness and phylogenetic relationships among the Australian Halymeniales.

ECTOSYMBIOTIC AND ENDOBIOTIC BACTERIA ASSOCIATED WITH *EUTREPTIELLA* SP. FROM LONG ISLAND SOUND. Rita Kuo & Senjie Lin. Marine Sciences, University of Connecticut, Groton, CT, 06340, U.S.A.

Eutreptiella sp. isolated from Long Island Sound was used to study the type of bacteria associated with the alga and how the bacteria affect algal growth. By analyzing 16S rDNAs for the culture filtrate, we found species of *Marinobacteria*, *Roseobacteria*, *Maritimibacteria*, and *Alphaproteobacteria*, and unknown species. To investigate the effect of bacteria on the growth of *Eutreptiella* sp., we treated the culture with a cocktail of antibiotics and achieved an axenic culture. When the bacteria were added to the axenic culture, *Eutreptiella* sp. growth was promoted. The bacteria-supported algal growth was comparable to that when vitamin B₁₂ was supplied to the axenic culture, indicating that the bacteria-*Eutreptiella* association might be related to the vitamin B₁₂ supply. The results from DAPI (4',6-diamidino-2-phenylindole) staining showed intracellular presence of some bacteria. Analysis 16S rDNA from broken *Eutreptiella* sp. cells in the axenic cultures revealed two sequences 98 % identical to *Rickettsiales* sp., NCBI, EF667892.1 in addition to *Eutreptiella* plastid 16S rDNA (142 clones). This suggests that *Eutreptiella* sp. has an endosymbiont bacterium. Further study is required to understand the relationship between *Eutreptiella* sp. and the endosymbiotic bacterium.

MOLECULAR PHYLOGENY OF THE FRESHWATER MACROPHYTE *SIRODOTIA* (BATRACHOSPERMALES, RHODOPHYTA). Daryl W. Lam¹, Timothy J. Entwisle², Pertti Eloranta, Janina Kwandrans³ & Morgan L. Vis¹. ¹Department of Environmental and Plant Biology, Ohio University, Porter Hall 315, Athens, OH 45701 USA ²Royal Botanic Gardens Sydney, Mrs Macquaries Road, Sydney, NSW 2000, Australia ³Institute of Nature Conservation PAS, Department of Freshwater Biology Al. A. Mickiewicza 33, 31-120, Kraków, Poland.

Species level assessments within the genus *Sirodotia* Kylin have been debated. Previous studies inferred *Sirodotia tenuissima* (Collins) Skuja *ex* Flint as a synonym of *S. suecica* Kylin, while *S. huillensis* (Welwitsch *ex* West et G.S. West) Skuja and *S. delicatula* Skuja were inferred as closely related, but distinct species. However, these molecular phylogenies were taxon limited and based on solely New World collections. As a result, the name *S. tenuissima* remains in use. Our study has a much broader sampling range which includes collections from Australia, Brazil, Costa Rica, Canada, Finland, Mexico, New Zealand, South Africa, and the United States. Species level taxonomy and phylogeographic distribution patterns in *Sirodotia* were elucidated based on phylogenetic inferences of *rbcL* and *cox2-3* DNA sequences. Both *rbcL* and *cox2-3* phylogenies inferred *S. suecica*, *S. tenuissima*, and another species *S. goebelii* Entwisle et Foard as a monophyletic group with little sequence divergence in either molecular marker. Our results support the synonymy of *S. tenuissima* and *S. goebelii* to *S. suecica* (the species name with priority). Within this clade, samples collected from Australia and New Zealand formed a monophyletic group. However, no other phylogeographic patterns were evident. *S. huillensis* and *S. delicatula* are maintained as separate species. Lastly, a single specimen from South Africa may represent a potentially new species of *Sirodotia* based on carpogonium length and the aforementioned molecular phylogenies.

USING EVOLUTIONARY GENE NETWORKS TO HARNESS THE NEXT GENERATION ERA DATA DELUGE. Christopher Lane¹, Ian Misner¹, Cedric Bicep², Sebastien Halary², Philippe Lopez², Eric Bapteste², Scott Grandpre¹. ¹Department of Biological Sciences, University of Rhode Island, Kingston, RI, 02881; ²UMR CNRS 7138 'Systématique, Adaptation, Evolution' Equipe 'Modélisation Dynamique des Systèmes Intégrés' Université Pierre et Marie Curie, Case Postale 05 – 75005 Paris.

Over the last 5 years, the cost of sequencing DNA has plummeted while the output of a new wave of "next generation" sequencers has increased on a nearly logarithmic scale. The confluence of these factors has made large-scale sequencing projects, including metagenomics and full eukaryotic genome sequencing, available to individual labs on reasonable budget. As a result, there has been an explosion of sequence data in public databases and genomes are being sequenced at an ever increasing rate. Where there was once a single, or no, genomes to represent large lineages of organisms, available genomes are rapidly dotting the eukaryotic landscape. With the infusion of data, however, it is critical to devise strategies to effectively utilize the large number of sequences while keeping the computational burden manageable. Evolutionary Gene Networks (EGNs) are a fast and efficient tool for the comparative analysis of genomic data that enable the user to visualize data on a broad scale. These networks can be employed at the sequence assembly stage to verify quality, or serve to compare genes and gene families across a wide range of taxa. We have used EGNs to assemble and analyze the genome of the facultative pathogenic oomycete *Achlya hypogyna* and the proteome of the free-living oomycete *Thraustotheca clavata*. In comparison with several obligate oomycete pathogens, our data indicate that gene family evolution is highly correlated with life style.

ALGAL TURF SCRUBBER (ATS™) PRODUCTION ON THE GREAT WICOMICO RIVER, VIRGINIA, USA: A LOOK AT DIVERSITY AND BIOCHEMISTRY WHILE CLEANING THE RIVER. H. Dail Laughinghouse IV^{1,2}, Walter H. Adey¹, John Miller³. ¹Department of Botany, National Museum of Natural History, Smithsonian Institution, Washington, DC, USA; ²MEES Program, College of Computer, Mathematical and Natural Sciences, University of Maryland, College Park, MD, USA; ³Department of Chemistry, Western Michigan University, Kalamazoo, MI, USA.

Algal Turf Scrubbers (ATS) are mini-ecosystems dominated by periphytic algal mats (algal turfs) and have been in constant operation as dozens of systems over decades, ranging from 0.1 hectares to 3 hectares in size. Systems provide multiple benefits to the environment by improving water quality in addition to their capability of producing biomass for biofuels and other algal co-products. Two systems were implemented on the Great Wicomico River, a small tributary on the northwestern shore of the Chesapeake Bay, to assess periphytic diversity, nutrient uptake/removal, biochemical co-products, and any relation among these. Furthermore, experiments were conducted on one of these systems, with the addition of CO₂ and oxamate to verify its effect on the community structure as well as biochemical outputs. The algal turf production rate varied, producing yearly means between 10-70g (35g avg.) dry weight per m² per day. Diatoms (Bacillariophyta) dominated the system, but there were seasonal changes within the community, where *Berkeleya rutilans* (Trent.) Grun., *Melosira nummuloides* Agardh, and *Melosira moniliformis* (Muller) Agardh dominated during the warmer months and several species of *Grammatophora* dominated during the colder months. Cyanobacteria, Chlorophyta, Rhodophyceae, and Chrysophyceae were the following most abundant groups in relative order. In one experiment with CO₂, there was a significant drop in pH which increased cyanobacterial biomass. This *Lyngbya* sp. is currently being cultured for phylogenetic analysis. Omega-3 fatty acid tends to increase during colder months. Data from these systems are being analyzed and preliminary results from these two systems will be presented.

GEOGRAPHIC DISTRIBUTION AND INTRASPECIFIC VARIATION IN *ELLIPTOCHLORIS MARINA* (TREBOUXIOPHYCEAE, CHLOROPHYTA) THE GREEN SYMBIONT OF *ANTHOPLEURA* SPP. Molly R. Letsch¹, Gisele Muller-Parker² & Louise A. Lewis¹. ¹University of Connecticut, Department Ecology & Evolutionary Biology, Storrs, CT; ²National Science Foundation, Division of Graduate Education, Arlington, VA.

The Pacific sea anemones *Anthopleura xanthogrammica* and *Anthopleura elegantissima* can host symbionts of two phyla; two dinoflagellate species in the genus *Symbiodinium* (Dinophyta), and a green alga, *Elliptochloris marina* (Chlorophyta). The *Symbiodinium* species, defined using ITS rDNA sequences, have different latitudinal ranges likely corresponding to different environmental preferences. We use analyses of sequence data to examine the genetic variation of the green symbiont across its known range from Alaska to California, USA. The plastid-encoded *rbcL* gene was used as a species-level marker. Data from the nuclear internal transcribed spacer region (ITS) were used to examine intraspecific variation in the green symbiont across its geographic range, and among seasons, and host species in Washington. The *rbcL* sequences showed no variation within samples and very low variation among samples; which is consistent with a single species of green algae. A single variable nucleotide site in the *rbcL* gene was recovered from six of the ten Oregon samples. In contrast, numerous diverse heterologous ITS sequences were obtained. Analyzing the ITS2 secondary structure, we identified putative pseudogenes and sequences that were interpreted as functional ITS copies. Among the functional copies we used the 5.8S sequences to define orthologs, a method that has been used for other species of vascular plants and green algae. The largest set of ITS haplotypes with identical 5.8S sequences were interpreted as orthologs, and used in population analyses. Haplotype trees demonstrated three main clusters, each represented by samples spanning the geographic range. Analysis of molecular variance (AMOVA) indicated that most ITS variation is apportioned within anemones (algal populations) rather than among geographic regions, host species, or seasons. This suggests that the *E. marina* symbiont is a single geographically widespread population.

MORPHOLOGICAL VARIABILITY OF CHRYSOPHYTE CYSTS FROM AN EOCENE MAAR LAKE IN THE CANADIAN ARCTIC. Anne-Marie Lizarralde & Peter A. Siver. Botany Department, Connecticut College, New London, CT, U.S.A.

Siliceous microfossils abound in lake sediments deposited in the Giraffe kimberlite diatreme, a Middle Eocene maar lake situated near the Arctic Circle in the Northwest Territories of Canada during the Cenozoic hot house. Overall, this extensive core contains an astonishing diversity of exquisitely preserved siliceous microfossils representing the Chrysophyceae, Synurophyceae and Bacillariophyceae, as well as sponge remains and scales from testate euglyphids and heliozoans. Of the vast array of microfossils, Chrysophyceae and Synurophyceae resting stages known as stomatocysts, or cysts, are by far the most abundant, often accounting for over 50% of all microfossils and dominating much of the 68.3 m of lacustrine facies. To date, we have documented well over 100 different cysts that collectively represent a vast array of morphological structures. We will use remains of ten different cyst types to demonstrate the range in size, cyst wall ornamentation, pore structure and collar development. Although some of the cysts have smooth and unornamented walls as is commonly reported in modern waterbodies, many are highly ornamented with papillae, pores, ridges and spines, and it is clear that cyst development was well established by the Eocene. In modern lacustrine systems, we often do not know which organisms produce many of the cyst types that are observed. Interestingly, in the Giraffe core we can often uncover well developed cysts that still contain parts of the parent cell wall, allowing us to link some cyst types with specific organisms. In the future, we plan to publish an atlas of these Eocene resting stages and use their remains to piece together the history of the waterbody.

DOES THE DISTRIBUTION OF MACROSCOPIC KELP (*LAMINARIA EPHEMERA*) SPOROPHYTES REFLECT THE DISTRIBUTION OF MICROSCOPIC GAMETOPHYTES? Caroline Longtin & Gary W. Saunders. Centre for Environmental & Molecular Algal Research, Department of Biology, University of New Brunswick, Fredericton, NB, E3B 5A3, Canada.

Kelp forests are extremely productive and diverse ecosystems; however, they are threatened by climate change, overfishing and increased sea urchin presence. To conserve kelp forests we must develop a better understanding of their biodiversity and ecology. Whereas many studies have focused on the diversity and ecology of kelp sporophytes (macroscopic stage), few have considered the cryptic gametophyte (microscopic stage) due to sampling difficulty in the field. This lack of a cohesive understanding of kelp species in all phases impacts negatively on any attempts to manage and conserve these species and the life that they support. It has been hypothesized that gametophytes act similarly to terrestrial seedbanks by enhancing sporophyte recruitment, persistence and recovery following disturbance. Gametophytes may extend across a greater range than sporophytes and remain dormant until environmental conditions become favorable or competition is lessened. If seedbank analogues exist then kelp forest regeneration may be possible following urchin removal or regulation. My research focuses on the distribution of the rare intertidal species *Laminaria ephemera* in Barkley Sound, B.C. The designation of *L. ephemera* as a rare species is based solely on the distribution of its sporophyte form. I am sampling three sites where *L. ephemera* has been previously recorded and three sites where *L. ephemera* has not been recorded to determine the distribution of sporophytes compared with gametophytes. In the low intertidal zone of each site I am recording the presence of both life history stages separately. To detect gametophytes I am performing species-specific PCR on rock scrapings collected from each site. I am comparing the distributions of sporophytes with gametophytes to determine if *L. ephemera* is more widely distributed in its gametophyte form than the sporophyte form.

RANGE EXPANSION OF THE NEWLY INVASIVE “*HETEROSIPHONIA*” *JAPONICA* IN NEW ENGLAND AND MECHANISMS FOR ITS SUCCESS. Natalie H. N. Low^{1,2}, Christopher J. Marks² and Matthew E. S. Bracken². ¹Department of Ecology and Evolutionary Biology, Brown University, Providence, RI 02912; ²Marine Science Center, Northeastern University, Nahant, MA 01908.

Marine species invasions have increased exponentially, and invasive species can present a major threat to their new communities. It is therefore essential to understand the characteristics of both invasive species and communities that allow an invader to become established. In 2009, the invasive red seaweed “*Heterosiphonia*” *japonica* was discovered for the first time on the northwest Atlantic coast. Here, we report a 200-km northward extension of the invader's known range to Cape Ann, Massachusetts, USA, *in situ* observations and surveys of its abundance on New England subtidal reefs, and evidence for rapid growth and reduced herbivory relative to native seaweeds as likely mechanisms for its successful establishment. Our subtidal surveys found “*H.*” *japonica* growing abundantly at six sites along the New England coast, from Fort Wetherill, Rhode Island to Rockport, Massachusetts. Field assessments of herbivore densities and a multiple choice feeding preference experiment in the laboratory showed that “*H.*” *japonica* grew more rapidly, harbored fewer native grazers, and was consumed less by native grazers than the native red seaweeds *Polysiphonia stricta* and *Polysiphonia fucoides*. Our study provides evidence for the combined effects of rapid growth and reduced grazing by native herbivores in promoting the successful establishment and growth of “*H.*” *japonica* on New England subtidal reefs and its spread into the Gulf of Maine.

MOLECULAR PHYLOGENETICS OF *CHARA* L. (CHARALES, CHAROPHYTA) WITH EMPHASIS ON *CHARA VULGARIS* SENSU LATO. Julia M. Maritz^{1,2} & Kenneth G. Karol². ¹The Cullman Program for Molecular Systematics, The New York Botanical Garden, Bronx, NY 10458, USA; ²Department of Biology, Sarah Lawrence College, Bronxville, NY 10798, USA.

The extant Charales contain one family (Characeae), which is composed of six genera, two of which are species rich, *Chara* and *Nitella*. The species of *Chara* exhibit tremendous morphological variability, not only between closely related taxa but also within a single taxon. Identification of *Chara* species is based on morphological characters that include cortication patterns, stipulode number and arrangement as well as gametangial position; none alone are indicative of a particular species. Morphological plasticity associated with these characters has made identification challenging and has impeded a classification that accurately reflects evolutionary history. The most recent monograph of Characeae (Wood & Imahori 1965) used a broad morphological species concept to reduce the number of *Chara* species from 120 to 19, each with numerous subspecies, varieties and forma. *Chara vulgaris sensu* Wood & Imahori (including *C. contraria*, *C. imperfecta* and others), and closely allied taxa (*C. hispida*, *C. polyacantha*, *C. tomentosa*) were the focus of this study. This complex was chosen because it represents morphologically variable taxa, where many previously recognized species were reduced to a few macrospecies with broad biogeographic distributions. We sequenced four plastid-encoded genes (*atpB*, *ndhD*, *psbC* and *rbcL*) to test and revise this classification. Phylogenetic analyses recovered *C. vulgaris* and *C. contraria* as distantly related phylogenetic units, contrary to their classification as varieties of a single species. *Chara aspera*, originally included as part of the outgroup, was found to be closely related to *C. contraria*, not to *C. globularis* where it is currently classified. Additionally, intraspecific variation was detected that could represent cryptic species or variation associated with biogeographic patterns. Many of the taxa examined here form distinct clades suggesting greater species diversity than is currently recognized.

CRYPTIC BROWN ALGAL COMPLEXES IN THE CANADIAN FLORA AS REVEALED THROUGH DNA BARCODING. Daniel McDevit and Gary W. Saunders. University of New Brunswick, Fredericton, NB, Canada.

The use of molecular tools (including the DNA barcode – COI-5P = 5' end of cytochrome c oxidase 1) to aid species identification has dramatically changed our understanding of algal taxonomy. In Canada, the process we now refer to as 'molecular assisted alpha taxonomy' – where collections are clustered based on genetic species groups prior to morphological, anatomical and ecological analysis – has revolutionized our approach to studying algal diversity. Over the past six years our understanding of the Canadian brown algal flora has improved vastly allowing us to uncover overlooked species (such as *Saccharina groenlandica* in the Atlantic) and to explore cryptic diversity (such as our work on the Scytosiphonaceae). However, the use of molecular tools has uncovered numerous cryptic species complexes that have yet to be explored thoroughly. This poster highlights several known Canadian brown algal cryptic species complexes (including: *Desmarestia*, *Ectocarpus*, *Punctaria* and arctic collections of *Chorda*, *Chordaria* and *Halosiphon*) and our current efforts towards resolving their respective taxonomy.

A SYSTEMATIC INVESTIGATION OF THE *NITELLA FLEXILIS* (CHARALES, CHAROPHYTA) SPECIES COMPLEX. Heather M. Meyer^{1,2} & Kenneth G. Karol¹. ¹The Cullman Program for Molecular Systematics, The New York Botanical Garden, Bronx, NY 10458, USA; ²Department of Biology, Sarah Lawrence College, Bronxville, NY 10708, USA.

Wood and Imahori (1965) published a *Revision of the Characeae*, a global monograph of the fresh water algal family Characeae. In this monograph, a broad morphological species concept was used to reduce more than 400 named species to 81 loosely defined species, each with various subspecies, varieties, and forma. Currently, we are using molecular phylogenetic methods in combination with vegetative morphology and oospore membrane architecture to test and revise the classification of *Nitella flexilis* (L.) Ag. along with allied members of this species. *Nitella flexilis* was chosen for this study because it is a highly variable taxon that includes many heterotypic synonyms and 13 previously distinct species reduced into infraspecific taxa or synonymy. We sequenced two plastid-encoded genes (*atpB* and *rbcL*) from a broad range of taxa allied to the *N. flexilis* complex (i.e., *N. californica*, *N. capitata*, *N. missouriensis*, *N. montana*, *N. obtusa*, *N. syncarpa*) and performed phylogenetic analyses. Many of the samples were taken from type specimens often dating more than 100 years old. When possible, SEM was used to examine the exterior layer of the oospore membrane, known as the fossa, to complement phylogenetic analysis and to test the utility of this characteristic in identifying species. Phylogenetic analyses of the DNA data resulted in at least 12 distinct clades separate from *N. flexilis sensu stricto*. Nine of these clades are consistent with previously described species and three may represent new species. Gross morphological characters and oospore membrane architecture were generally consistent with most clades, however surprising variation was recovered for *N. flexilis sensu stricto*. Taken together, many of the taxa examined here appear to warrant species status separate from, but closely related to, *N. flexilis sensu stricto*.

PHYLOGENETIC ANALYSIS FOR *A. TAMARENSE/FUNDYENSE/CATENELLA* COMPLEX GUIDED BY INTRAGENOMIC 18S rDNA POLYMORPHISM SUGGESTING SEPARATION OF THE COMPLEX INTO TWO SPECIES. Lilibeth N. Miranda^{1,2}, Huan Zhang¹, & Senjie Lin¹.

¹Department of Marine Sciences, University of Connecticut, Groton, CT 06340; ²School of Marine Sciences, University of Maine, Orono, ME 04469.

We analyzed 18S rRNA gene (rDNA) in monoclonal strains of *Alexandrium fundyense* and *A. catenella* by both direct and clone-based sequencing, and found 42-50 polymorphic sites from the 1.7kb sequence we obtained, including three insertions/deletions in all but one *A. fundyense* strain and some *A. catenella* strains. Clone sequencing for ten of the polymorphic amplicon libraries revealed various intragenomic 18S rDNA variants, with nucleotide differences ranging 0-3.5%, some of which exceeded commonly used species boundary (2%). Phylogenetic analyses including all reported and new *A. tamarense/fundyense/catenella* 18S rDNA data indicated that sequences from this complex formed two major clades well separated from each other. Clade I comprised *A. tamarense/fundyense* from Northeast America as well as the *A. catenella* from American coast of the Pacific, all with IRP, mixed with reported *A. tamarense/fundyense* from Asia. In Clade I, *A. catenella* formed a separate subclade from *A. tamarense/fundyense* and the IRP sequences dispersed across strains from each species forming “polyphyletic” clusters. Clade II has no evidence of IRP, contained a subclade exclusively of *A. catenella* from various geographic locations and several other subclades predominantly of *A. tamarense*. While the several subclades in Clade II remain to be resolved with more taxon sampling, Clade I is a clearly resolved taxon, likely a distinct species. Our result suggests that IRP should be examined when using rDNA to study species/population diversity in this species complex and perhaps other dinoflagellates as well. Analysis based on a single 18S rDNA clone sequence could lead to incorrect grouping of the intragenomic 18S rDNA variants as distinct geographic populations or even species.

FOLIOSE BANGIALES (RHODOPHYTA) SPECIES DIVERSITY IN GREENLAND. Agnes Mols-Mortensen¹, ¹Chris D. Neefus, ²Poul M. Pedersen and ³Juliet Brodie. ¹University of New Hampshire, Department of Biological Sciences, G32 Spaulding Life Science Center, 38 College Road, Durham, NH 03824, USA; ²Institute of Biology, Phycology Section, Øster Farimagsgade 2D, DK-1353 Copenhagen K, Denmark; ³Natural History Museum, Department of Botany, London, SW7 5BD, United Kingdom.

The red algal order Bangiales has undergone major revisions, and the foliose members of the order, previously placed in *Porphyra*, are now represented in eight different genera: *Boreophyllum*, *Clymene*, *Fuscifolium*, *Lysithea*, *Miuraea*, *Porphyra*, *Pyropia* and *Wildemanina*. Recent taxonomic work on the foliose Bangiales flora in the North Atlantic has reported eleven species in Iceland, eleven species in the Faroe Islands and eighteen species in the North West Atlantic, from Maine to Long Island. *Boreophyllum*, *Porphyra*, *Pyropia* and *Wildemanina* species are represented in the studied North Atlantic floras. Previous work in Greenland reports *Porphyra miniata*, *P. thulaea* and *P. umbilicalis* but preliminary molecular work on collections from Greenland suggest a more diverse flora. Here we hypothesize that the foliose Bangiales flora in Greenland is more diverse than previously thought and we ask i) How many species are there? ii) Which species are found in the flora? iii) How does the flora compare to other areas in the North Atlantic? Collections were made on the west coast of Greenland from Ilulissat in the north to Nanortalik in the south from May to October. The collections were from the intertidal and shallow subtidal. The collected material was dried to herbarium sheets, species identification was based on *rbcL* sequences and gross morphology, and a phylogenetic analysis was undertaken. *Porphyra umbilicalis*, *Pyropia thulaea* and *Wildemanina miniata* were molecularly verified in the flora and *Boreophyllum birdiae*, *Porphyra purpurea* and *Pyropia njordii* sp. nov. were new reports for Greenland.

NUTRIENT STATUS ASSESSMENT OF THE GREAT BAY ESTUARINE SYSTEM USING ANALYSES OF ALGAL TISSUES AND WATER. Jeremy C Nettleton, Christopher D Neefus, and Arthur C Mathieson. University of New Hampshire, Department of Biological Sciences, G28 Spaulding Life Science Center, 38 Academic Way Durham, NH 03824, USA.

Algal tissue nutrient analyses have been proposed as superior alternatives to water analyses for tracking long-term nutrient regimes for given locations due to their resistance to rapid fluctuations related to storm and tidal events, and for their ability to exclusively measure biologically usable forms of nutrients such as nitrogen and phosphorus. To examine the nutrient status of the Great Bay Estuarine System, NH, USA, *Ulva* and *Gracilaria* tissues and water were collected from five study sites from September 2008 to July 2010. Total nitrogen, total phosphorus, and atomic N:P ratios of site water and algal tissues were determined bimonthly, and the results of both methods were compared to one another and to historical values for Great Bay. Water analyses revealed more between-site differences in nutrient availability and gave lower overall estimates of nitrogen concentrations than did the tissue analyses. Water analyses were possible at every site and time throughout the study, whereas the tissue analyses could not always be done due to inadequate amounts of available algae. The water analyses results agreed with other recent findings that nitrogen levels have risen markedly in Great Bay in the last decade. However, *Gracilaria* tissue analyses revealed that tissue nitrogen and phosphorus have remained relatively unchanged since the early 1980s. *Ulva* tissue nitrogen levels remained above the proposed 2.2% minimum threshold for unlimited growth throughout the study period, even during the unprecedented *Ulva* bloom events (over 90% cover) observed during the study. Water mean atomic N:P ratios were greater than 30:1 for every study site, far above the expected 16:1 Redfield ratio. In *Ulva* tissues, the mean N:P ratios were between 35:1 and 75:1 for each site, which is further evidence that the Great Bay Estuarine System is nutrient enriched to the point that regular large algal blooms should be expected for the foreseeable future.

MACROALGAL BLOOMS IN NEW ENGLAND SALT MARSHES: DISTRIBUTION SURVEYS AND POTENTIAL ECOLOGICAL IMPACTS. Christine Newton & Carol Thornber. University of Rhode Island, Kingston, Rhode Island, USA.

Observations of macroalgae growing or deposited among the stems of lower marsh plants have been made throughout the United States, particularly along the East coast; however, no reports have been made regarding the abundance or species composition of these macroalgal blooms. Without this critical information, the extent to which these senescing blooms may impact salt marshes is unknown. Therefore, the purpose of this study was to document the abundance and species composition of macroalgae in a New England salt marsh, as well as to determine any potential impacts of drifting macroalgal blooms. Monthly surveys were conducted throughout Narragansett Bay, R.I. between May 2009 and August 2010. The percent cover of each macroalgal species, along with living and dead *Spartina alterniflora* was recorded using 0.25 m² quadrats placed at 1 m intervals along three 10 m transects. We also collected all macroalgae and assessed their wet mass, by species, in the lab. Macroalgae were most commonly found along the lower edge of the regularly flooded *S. alterniflora* zone; dominant species of macroalgae included *Ascophyllum nodosum* and *Fucus* spp. but varied greatly among sites. To determine the impacts of drifting macroalgae on salt marsh communities, we conducted a combination of *in situ* cage and laboratory mesocosm experiments during the summers of 2009 and 2010. Results from the mesocosm experiments suggest that the nutrients being released from the senescing blooms positively impact *S. alterniflora* growth. However, in the field, we found that nutrients from macroalgae are removed by tidal cycles before they can be absorbed by *S. alterniflora* and later transferred to higher trophic levels.

DNA BARCODING REPRESENTATIVE SCYTOSIPHONACEAE (PHAEOPHYCEAE) FROM THE NORTHEAST ATLANTIC EMPHASIZING THE AZORES. Manuela I. Parente^{1,2}, Filipe O. Costa³ & Gary W. Saunders². ¹Departamento de Ciências e Engenharia do Ambiente Instituto do Mar – IMAR, Faculdade de Ciências e Tecnologia, Universidade Nova de Lisboa, Quinta da Torre - 2829-516 Caparica, Portugal.; ²Centre for Environmental & Molecular Algal Research, Biology, University of New Brunswick, Fredericton, NB, Canada, E3B 5A3.; ³Centre of Molecular and Environmental Biology (CBMA), Department of Biology, University of Minho, Campus de Gualtar, 4710-057 Braga, Portugal.

The Scytosiphonaceae is a brown algal family characterized by a heteromorphic life history with crustose or tufted sporophytic phases and erect gametophytes. The taxonomic identity of Macaronesian specimens assigned to this family was investigated using the cytochrome c oxidase I (COI-5P) DNA barcode, which revealed overlooked diversity and provided new insights into the life history of some of its members. *Colpomenia sinuosa* resolved as three closely related genetic groups each with a unique biogeographical pattern, while a *Chilionema*-like microthallus was uncovered as its prostrate phase. Although only one species of *Scytosiphon* is presently recognized in the Azores, two significantly divergent genetic groups (4.5-5.0%) were uncovered. One of these is genetically similar (0.6%) to specimens from Nova Scotia, Bermuda and Australia, while the other is most closely allied (1.4-1.7%) to specimens from the British Isles. Our data confirm previous life history studies establishing that *Microspongium gelatinosum* is the sporophytic phase of a *Scytosiphon*. Collections of *Petalonia fascia* from the Canary Islands are genetically divergent from all other Scytosiphonaceae sequenced to date. Similarly, *Compsomena saxicola* from the Azores, possibly the prostrate phase of a *Scytosiphon/Petalonia*, was not closely allied to any other species. *Endarachne binghamiae* from the Azores is relatively divergent (1.9%) from a possible Southern Korea specimen assigned to this species and slightly less divergent (1.4%) from an Australian specimen.

IDENTIFYING LATIN AMERICAN *CHARA* (CHARALES: CHAROPHYTA) USING DNA SEQUENCES. Tabetha M. Peavey^{1,2}, John D. Hall^{1,3} & Kenneth G. Karol¹. ¹The Cullman Program for Molecular Systematics, The New York Botanical Garden, Bronx, NY, 10458, USA; ²Department of Natural Sciences, Fordham College at Lincoln Center, New York, NY 10036, USA; ³Department of Botany, Academy of Natural Sciences, Philadelphia, PA, 19103, USA.

The Characeae are macroscopic green algae closely related to terrestrial plants. Traditionally, in the genus *Chara*, species identification has been based on morphological characteristics such as cortication, gametangial position as well as stipulode number and placement. A common problem with the identification of *Chara* based on morphological features is the disagreement over which characters and character states are indicative of distinct species. The New York Botanical Garden Herbarium (NY) houses approximately 500 *Chara* specimens collected from Latin America. These specimens were catalogued and made available through the NYBG's virtual herbarium (sciweb.nybg.org/science2/hcol/chara/index.asp). DNA was extracted from 339 of the ~500 Latin American *Chara* specimens. Attempts were made to amplify and sequence plastid genes *atpB* and *rbcL*. The resulting sequences were incorporated into a larger data set that included many species of *Chara* from around the world, and phylogenetic relationships were determined. One hundred and thirteen (~33%) of the specimens were successfully sequenced to some extent, and of those specimens 56 (~49%) were fully sequenced for *atpB* and/or *rbcL*. Of those specimens sequenced the molecular data were consistent with the original determinations for 48 (~42%) specimens and inconsistent with the original determinations for 23 (~20%). Additionally, seven previously unidentified specimens were determined. By using phylogenetic methods we were unable to identify 57 (~50%) of the specimens to species due to partial sequence data. However, we were able to place these individuals into distinct clades thus narrowing possible determinations. Many of the specimens sampled here were collected in the late 1800's to early 1900's; these techniques prove powerful in identification even for relatively old specimens.

A SYSTEMATIC STUDY OF *TOLYPELLA* A. BR. (CHARALES, CHAROPHYTA): RECENT ANALYSES BASED ON PLASTID SEQUENCE DATA. William Pérez^{1,2}, Richard M. McCourt³, Michelle T. Casanova⁴ & Kenneth G. Karol¹. ¹The Cullman Program for Molecular Systematics, The New York Botanical Garden, Bronx, NY, 10458, USA; ²The Graduate Center, City University of New York, New York, NY, 10016, USA; ³Academy of Natural Sciences, Philadelphia, PA, 19103, USA; ⁴Royal Botanic Gardens, Melbourne, Vic. 3141, Australia.

The Characeae contain two tribes with six genera: the tribe Chareae, which includes *Chara*, *Lamprothamnium*, *Lychnothamnus* and *Nitellopsis*; and the tribe Nitelleae, which includes *Tolypella* and *Nitella*. The Characeae exhibit a broad range of morphological diversity and in the most comprehensive taxonomic treatment more than 400 species were consolidated into 81 broadly defined species. Within this treatment, 16 *Tolypella* species were subsumed under two species (*T. intricata* and *T. nidifica*) in two sections, *Rothia* and *Tolypella*, respectively. It was further suggested that *Tolypella* might be a derived group within *Nitella*. Currently, there are no comprehensive molecular phylogenetic studies of *Tolypella*. Instead, phylogenetic studies of Characeae and closely related taxa have sampled between one and three of the 16 described *Tolypella* species to serve as placeholders or outgroup taxa. In our ongoing investigation of species diversity in *Tolypella*, chloroplast DNA sequence data for *atpB* and *rbcL* were assembled from field-collected and herbarium specimens. Phylogenetic analyses of plastid sequence data supported monophyly of *Tolypella* and of sections *Rothia* and *Tolypella*. Furthermore, several clades were identified which suggests greater species diversity than currently recognized.

EFFECTS OF SEASONAL NUTRIENT VARIATION AND TIDAL ELEVATION ON PRIMARY AND SECONDARY PRODUCTION IN A ROCKY INTERTIDAL ECOSYSTEM. Valerie Perini & Matthew E.S. Bracken. Northeastern University Marine Science Center, Nahant MA, 01908, U.S.A.

Nutrient availability is an important factor determining the health and functioning of intertidal ecosystems. In near-shore New England waters, seasonal fluctuations can produce pronounced variation in levels of ambient nutrients. Primary producers, including seaweeds, are essential in capturing these nutrients and making them available to the rest of the community and can exhibit variable nutrient uptake and storage strategies in response to seasonal nutrient fluctuations. Studies have shown that individuals of the same species can also exhibit phenotypic plasticity in nutrient uptake physiology in response to stress induced by environmental differences across tidal elevation. An important question remains. How do these factors mediate nutrient transfer to the rest of community? To address this question I evaluated the importance of nutrient variation in mediating herbivore-algae interactions with a feeding assay assessing grazer preference for algal individuals of varying tissue quality (i.e. nutrient content), as well as the algal response to nutrient inputs from these grazers. Results illustrated a positive non-consumptive effect of the herbivorous snail *Littorina obtusata* on the growth of *Fucus vesiculosus* individuals living low on the shore. Additionally, a negative consumptive effect on individuals living high on the shore indicated that variable algal tissue nutrient levels associated with different tidal elevation influenced herbivore preference. These results illustrate that nutrient availability and interactions between primary and secondary production are influenced by both the top down effects of herbivory and the bottom up processes of ambient nutrient fluctuations. These habitat-based modifications of seaweed-grazer relationships emphasize the importance of studying community interactions in an environmental context.

MOLECULAR TOOLS EXPOSE MISIDENTIFIED AND NOVEL TAXA AMONG BERMUDIAN RHODOPHYTA Thea R. Popolizio, ¹Christopher E. Lane, ²Craig W. Schneider & ³Daniel C. McDevit. ¹Department of Biological Sciences, University of Rhode Island, Kingston, RI 02881, USA; ²Department of Biology, Trinity College, Hartford, CT, 06106, USA; ³Department of Biology, University of New Brunswick, Fredericton, NB E3B 5A3 Canada.

The use of molecular-assisted alpha taxonomy (MAAT), which combines molecular tools with subsequent analysis of morphological features, has become increasingly widespread for red algae (Rhodophyta). The application of this technique has proven useful for exposing cryptic relationships within the red algae. We applied these methods to the marine flora of Bermuda, an isolated archipelago located at the interface of tropical and warm temperate zones. Based on work done over the last decade, it is clear that a number of Bermuda's algal species have been misidentified, and the level of endemism in these islands is likely underestimated. Molecular data show that several Bermudian species possessing morphologies convergent with their Caribbean and western Atlantic counterparts are in fact novel species. Among the groups studied thus far, we have uncovered 44 species currently classified as 18 biological entities, 24 of which we believe are potentially novel taxa. These include members of the *Centroceras clavulatum* complex, for which one taxon is currently recognized. Our MAAT analyses revealed the existence of five separate taxa, with two potentially novel species. The *Laurencia obtusa* complex is another group under investigation because it forms two distinct clades in phylogenetic analysis, neither of which includes the type locality. Additionally, the genus *Peyssonnelia* is resolved into a minimum of seven distinct species in our analyses, four of which are likely novel.

WHAT IS THE ROLE OF ALGAE IN THE RECENT COLLAPSE OF THE GREAT LAKES FOOD WEB? Euan D. Reavie, Natural Resources Research Institute, University of Minnesota Duluth, 1900 East Camp Street, Ely, MN 55731, USA.

The EPA's Great Lakes National Program Office (GLNPO) is now in its 27th year of comprehensive monitoring of the Great Lakes. Pelagic monitoring includes physical and chemical parameters, phytoplankton, zooplankton and benthic invertebrates. Monitoring data have revealed significant changes in whole-lake conditions, particularly within the last decade, thus justifying GLNPO's mandate to track changes under the Great Lakes Water Quality Act of 1978. Major drivers in these changes appear to be establishment of non-native filter feeders, shifts in chemical parameters such as nutrients and chloride and climate-related changes such as increased water temperature, less ice and longer periods of stratification. Unfortunately, causal mechanisms for the dramatic declines in phytoplankton and invertebrates remain uncertain. Trends in Great Lakes phytoplankton are provided alongside trends in other organisms and chemical parameters in order to identify relationships among trophic levels. New findings on possible causal factors, and remaining unknowns, are summarized. These trends convey the dramatic changes that are taking place in the Great Lakes, and so indicate the importance of long-term monitoring for phytoplankton.

New and innovative applications for these phytoplankton collections are also presented. The algae, particularly diatoms, are known powerful indicators of environmental change. Pelagic and coastal Great Lakes algae have been calibrated to water quality conditions and are shown to reflect water quality and human stressors. At a time when long-term data are needed to distinguish natural from human trends, and to reveal the causes and magnitudes of environmental insults, contemporary monitoring alone is not sufficient to answer important management questions regarding climate change, pollution and invasive species. Algal indicators and paleoecological applications will serve to address the myriad environmental issues that require long-term data in order to make critical remedial decisions in the Great Lakes.

DEVELOPMENT OF SEAWEED CULTURE SYSTEM TECHNOLOGIES TO SUPPORT INTEGRATED MULTI-TROPHIC AQUACULTURE AND SEA VEGETABLE AQUACULTURE IN NEW ENGLAND COASTAL WATERS. Sarah Redmond & Charles Yarish. Departments of Ecology & Evolutionary Biology & Marine Sciences, University of Connecticut, CT, 06901, U.S.A.

The marine aquaculture industry in the United States has been mainly restricted to finfish and shellfish, and growth has been limited due to environmental concerns and social sustainability. Seaweed aquaculture represents a bioextractive solution (=bioremediation) to excess inorganic nutrients generated in coastal waters, while also providing biomass for biofuels, food, phycocolloids, and other valuable phycoproducts. By adapting techniques developed in Asia for our native varieties of the kelp and *Gracilaria* spp., we aim to develop scalable modular nursery culture systems for commercial scale mass production of young seaweeds, and then transfer this technology to the commercial sector. The development of a seaweed aquaculture industry in the United States could be important for the growth of other cultured species through integrated multi-trophic aquaculture, sea vegetable production, or bioremediation of coastal waters. We have developed a scalable culture system for *Saccharina latissima* (Linnaeus) C.E.Lane, C.Mayes, Druehl & G.W.Saunders, and are currently culturing young plants both in the Gulf of Maine and in Long Island Sound. The next phase of the project will be focusing on *Gracilaria* spp., including *Gracilaria tikvahiae* McLachlan, a potential commercially important species of red algae in southern New England.

OVERWINTERING STRATEGIES OF *ULVA* SPP. IN NARRAGANSETT BAY, RI
Shelby Rinehart, Michele Guidone, and Carol Thornber. Department of Biological Sciences, University of Rhode Island, Kingston, RI, 02881, U.S.A.

Ulva spp. blooms negatively impact marine coastal organisms, commerce, and recreation. In order to fully understand how *Ulva* spp. blooms begin to proliferate in the spring, we need to understand their overwintering strategies. Two previous studies showed that *Ulva* spp. can overwinter as fragments and/or germlings. In our study, we examined the winter abundance of *Ulva* blade fragments at three bloom-impacted sites in Narragansett Bay, RI. At two of these sites, we conducted monthly intertidal surveys (November 2010-March 2011), to determine *Ulva* percent cover. The *Ulva* blades were collected in the field and then identified to species and weighed in the lab. In addition, to look for submerged and/or buried fragments, we took two sediment cores and a subtidal net sweep at each sampling point. At our third site, we collected sediment cores only. In the laboratory, all sediment samples were sieved, and *Ulva* spp. fragments removed, counted, and weighed. We tested the viability of our *Ulva* spp. by culturing selected fragments from the January and February sediment cores.

We found that *Ulva* blade fragments were present in the water column and the sediment throughout the winter. For the intertidal surveys, *Ulva* spp. biomass differed significantly amongst months and sites, with the greatest biomass present during December. By contrast, the abundance of fragments in the sediment cores did not differ significantly amongst months or sites. Culturing demonstrated that *Ulva* spp. fragments were viable; most fragments increased in mass in our cultures. Our results indicate that bloom-forming *Ulva* spp. in Narragansett Bay can successfully overwinter as fragments, which may allow these species to proliferate in the spring as soon as favorable temperatures and nutrient levels occur.

POST-TRANSCRIPTIONAL REGULATION OF NITROGEN ASSIMILATION IN MARINE DIATOMS. Deborah L. Robertson, Grant Goodrich, Minoli Perera, and Priyanka Kapur. Clark University, 950 Main Street, Worcester, MA 01610.

In all living cells, the regulation of gene expression is a multifaceted and dynamic process. While there has been much focus on patterns of coordinated gene transcription, there are now examples from both prokaryotes and eukaryotes of coordinated post-transcriptional regulation of mRNAs. Previous work established that transcripts encoding nitrate reductase (NR) accumulate in diatom cells that are nitrogen(N)-starved, suggesting that the mRNA is sequestered within the cell. NR transcripts are rapidly translated when nitrate is resupplied and the addition of ammonium results in the rapid degradation of these transcripts. We have shown that ammonium addition stimulates the degradation of transcripts encoding other enzymes and transporters involved in nitrate assimilation. These results suggest that post-translational processes are important in the coordination and regulation of N-assimilation in marine diatoms. The overarching goal of our current research is to test the hypothesis that post-transcriptional regulation of genes involved in N-transport and -assimilation in marine diatoms allows for rapid metabolic response to perturbations in nutrient source or supply and is mediated by changes in mRNA stability.

RNA-binding proteins (RBPs) play an important role in the post-transcription regulation of gene expression. Members of several RBP families are represented in diatom genomes, including PUF/pumilo, KH-I, and Bruno-like homologs. The structure and evolutionary history of these RBPs will be presented. Many RBP regulatory motifs have been identified in the 3'-untranslated regions (UTRS) of mRNAs. Therefore, we amplified and cloned the 3'-UTR sequences of NR and glutamine synthetase (GSII) from two marine diatoms, *Thalassiosira pseudonana* and *Skeletonema costatum*. EMSA analyses indicated that proteins bind to the *S. costatum* GSII 3'UTR. We are currently examining protein binding profiles under differing growth conditions with the goal of identifying changes in protein binding in response to environmental perturbations.

A PRELIMINARY INVESTIGATION OF THE *BATRACHOSPERMUM BORYANUM* SPECIES COMPLEX (BATRACHOSPERMALES, RHODOPHYTA) IN NORTH AMERICA AND EUROPE. Eric D. Salomaki & Morgan L. Vis. Environmental and Plant Biology, Ohio University, Athens, OH, 45701, U.S.A.

For the past two decades, molecular systematics has revolutionized our methods for delineating species and has revealed cryptic taxa, unknown from morphological studies. Previous research, using the *rbcL* gene and to a lesser extent SSU sequence data, has placed the freshwater red alga, *Batrachospermum boryanum*, in a well-supported clade with *B. confusum*, *B. confusum* forma *anatinum*, *B. heterocorticum*, and *B. involutum*. Furthermore, all of the aforementioned taxa share the morphological synapomorphy of heterocortication. In this study, specimens that fit within the current circumscription of *B. boryanum* have been collected from 25 locations in 16 states throughout the USA as well as Great Britain, Poland, Lithuania, Latvia, Estonia and Finland. Using *rbcL* gene sequence data, the relationship among these specimens was analyzed. Results of maximum parsimony and Bayesian analyses showed *B. boryanum* to be paraphyletic within the clade of heterocorticated taxa. From these preliminary data, there appear to be 7 genetically distinct heterocorticated taxa, but more may be delineated with the addition of new specimens and data from other DNA regions. The clades from the molecular data are not geographically structured and many of these taxa appear to overlap in their ranges. Future research will focus on type specimens of these species and linking them to this genetic data. This research will lead to the description of new species, reevaluation of morphological characters, and, upon completion, the nomenclature will be emended.

IDENTIFICATION AND DELIMITATION OF SPECIES WITHIN *POLYSIPHONIA* (RHODOPHYTA) IN THE NORTHWEST ATLANTIC USING MOLECULAR TOOLS. Amanda Savoie and Gary. W. Saunders. Center for Environmental & Molecular Algal Research, Department of Biology, University of New Brunswick, Fredericton, N.B., E3B 5A3, Canada.

The identification and classification of red algae (Rhodophyta) can be a very difficult task due to their phenotypic plasticity, convergent evolution and simple morphology. A relatively new solution to problems associated with traditional taxonomy is to use molecular tools such as DNA barcoding (COI-5P). When used together with morphological based classification, DNA barcoding can give a more complete and accurate assessment of species diversity within a taxonomic group. DNA barcoding has been shown to work well in red algae and can quickly and easily assign specimens to known species. This tool is thus a highly efficient way to resolve the difficulties in identifying and studying red algae. *Polysiphonia* (Rhodomelaceae, Rhodophyta) is the largest genus of red algae with 195 species currently recognized worldwide. This genus has been historically a source of taxonomic difficulty. Twelve species of *Polysiphonia sensu lato* (including the closely related genera *Vertebrata* and *Neosiphonia*) are found along the northeastern coast of North America. Despite considerable taxonomic study, there remain a number of uncertainties with regards to species diversity and respective biogeography in the North American flora. This study investigates the species diversity of the genus *Polysiphonia sensu lato* along the northeastern coast of North America using an integrative taxonomic approach. We have identified 14 unique genetic species groups for *Polysiphonia* from the northwest Atlantic through COI-5P and *rbcL* sequence data. Many of our genetic groups key out to the same morphological species concept, and, despite extensive sampling, we have not collected four of the 12 currently recognized species. These results indicate that there is hidden species diversity within the genus *Polysiphonia* in the northwest Atlantic.

BIOCHEMICAL ECOLOGY OF *MICROCYSTIS*. Justine R. Schmidt, Katherine A. Perri, Jeremy M. Sullivan, & G.L. Boyer. Department of Chemistry, State University of New York, College of Environmental Science and Forestry, Syracuse, NY, 13210, USA.

Cyanobacterial blooms are commonly found in many freshwater lakes during the summer. Monitoring for these blooms depends on understanding what factors affect cyanobacterial growth. *Microcystis aeruginosa* is a common unicellular species with an interesting biochemical ecology. It is known to produce hepatotoxins and this toxin production has been linked to iron availability. To investigate the biochemical ecology of this species, cells were grown in BG11 and used for pigment, toxin, and siderophore analysis. HPLC and a liquid waveguide capillary cell were used to identify the pigments in this algal genus and separate it from the green alga *Chlorella* and some strains of *Anabaena* using a similarity index. Toxin production in *Microcystis* was measured using liquid chromatography-mass spectroscopy (LC-MS). The major toxin produced by this species is the hepatotoxic peptide microcystin-LR. *Microcystis* also contains a number of other bioactive peptides. To look for potential siderophores or other iron-binding compounds, cell extracts were tested using a combination of HPLC and LC-MS techniques. Results from these studies will be presented along with their importance in the biochemical ecology of this species and its application to monitoring and management.

THE NORTHEAST ALGAL SOCIETY: A BRIEF HISTORY OF THE FIRST HALF CENTURY. Craig W. Schneider, Department of Biology, Trinity College, Hartford, CT, 06106, USA.

Beginning as an informal gathering of a handful of NYC phycologists known as the Metropolitan Area Algal Discussion Group in 1966, the Northeast Algal Society has developed and grown to become a vibrant affiliate of the Phycological Society of America over the past 50 years with annual meetings, publications and sponsored travel for student members. The small gatherings in New York were soon supplanted with ever larger groups of participants from a broader northeastern US geographical region by the later years of the 1960s beginning with the Universities of Connecticut and Massachusetts. These two meetings in 1969 were convened by Frank Trainor, Joanna Page, Robert Wilce and James Sears. The Society formalized its practices and hierarchy in the early 1980s, and has grown financially to support increasingly larger numbers of students attending annual meetings. Historical data will be presented for Society “founding members,” officers, annual meetings, finances, prizes and recipients, conveners, keynote speakers and honorary chairs illustrated with archival photographs.

THE GIRAFFE PIPE: USING ALGAL MICROFOSSILS TO RECONSTRUCT THE PAST AND INFORM THE FUTURE. Peter A. Siver¹, Alex P. Wolfe² and Anne Marie Lizarralde¹.

¹Botany Department, Connecticut College, New London, CT, U.S.A.; ²Department of Earth & Atmospheric Sciences, University of Alberta, Edmonton, Alberta, Canada.

Siliceous microfossils abound in lake sediments deposited in the Giraffe kimberlite diatreme, a Middle Eocene maar situated in the Northwest Territories of Canada during the Cenozoic hot house. The lake persisted between the time of kimberlite emplacement at 48 Ma and final paludification at 40 Ma, as constrained by ⁸⁷Rb/⁸⁷Sr and fission-track ages. An exploration drill core taken from the crater in 1999 contains 113.1 m of organic sediment, including 44.8 m of peaty material underlain by 68.3 m of stratified lacustrine sediment, in many places finely laminated, and rich in siliceous microfossils. Overall, an astonishing diversity of siliceous microfossils representing the Chrysophyceae, Synurophyceae and Bacillariophyceae dominate the lacustrine facies. Although a suite of taxa are believed extinct, numerous organisms display remarkable morphological similarities with their modern counterparts implying extended periods of evolutionary stasis. In addition to siliceous features, we have documented similarities in organelle ultrastructure in the diatom *Aulacoseira* and cell architecture in the synurophyte *Mallomonas*. Findings from the Giraffe core represent new mileposts for scaled chrysophytes, extend the antiquity of the Thalassiosirales lineage, and establish that nonmarine biraphid diatoms as a whole are more ancient than previously believed, dating to at least 45 Ma. Results are being used to inform molecular-based investigations on phylogeny, evaluate modern biogeography and examine Arctic systems during hot house climates.

CHARACTERIZATION OF LONG ISLAND COASTAL CYANOPHAGE COMMUNITIES. Sme, N. A., and Marston, M. F. Department of Biology and Marine Biology, College of Arts and Sciences, Roger Williams University, Bristol, RI.

Viruses infecting cyanobacteria, including *Synechococcus* spp., are abundant and genetically diverse in coastal environments. These viruses likely influence the abundance and composition of marine cyanobacterial communities. Most cyanophages belong to one of three major viral families: Myoviridae, Podoviridae, or Siphoviridae. Although most studies have focused only on myoviruses, in this study we characterize the myoviral and podoviral cyanophage communities at two sites on Long Island: Long Beach and Oyster Bay. Seawater samples were collected at seven different time points over the course of a year and viral abundances were determined using the most probable number assay with *Synechococcus* strain WH7803. Individual viral genotypes were isolated using extinction dilution enrichment. Viral isolates were initially screened using PCR primers for the myoviral DNA polymerase gene. Viral isolates that did not belong to the Myoviridae family were screened using Podovirus DNA polymerase gene primers. Myoviruses were detected in every water sample and twenty-six distinct myoviral strains have been observed. Eight of these strains have never been detected in 10 years of sampling Rhode Island coastal waters and may be unique to Southern Long Island coastal waters. Podoviruses were detected in less than half of the samples; however, in some months the majority of the isolates characterized were podoviruses. Notably, all of the podoviruses isolated thus far belong to the same strain. This podoviral strain is commonly found in Rhode Island during the late summer months, but was isolated from Long Island samples in both the spring and fall months. We are continuing to analyze additional Long Island samples to further assess temporal changes in cyanophage community composition at these locations.

MULTIVARIATE ANALYSES OF MACROALGAL BLOOMS. Carol S. Thornber¹, Michele Guidone¹, Christopher Deacutis². ¹Department of Biological Sciences, University of Rhode Island, Kingston, RI 02881, U.S.A. ²Narragansett Bay Estuary Program, University of Rhode Island Coastal Institute, URI Bay Campus, Box 27, Narragansett, RI 02882.

Macroalgal blooms are frequent occurrences in estuarine systems worldwide. These blooms typically consist of a suite of rapidly growing species drifting in the water column, including genera such as *Ulva*, *Cladophora*, and many others. In Narragansett Bay, RI, USA, blooms have been recorded since the early 1900s, but have rapidly increased in duration and frequency over the past few decades. Through a combination of repeated intertidal and subtidal quantitative surveys over 5 years, as well as larger-scale aerial photography, we assessed the distribution, density, and composition of blooms in this bay through univariate and multivariate statistical techniques. The most common bloom species included flat bistrromatic blades of *Ulva*, numerous tubular, branched *Ulva* species, the red algae *Gracilaria tikvahiae* and *G. vermiculophylla*, and *Agardhiella subulata*. However, more than 30 other species also occurred in bloom formations. The highest biomass density recorded was 149g/0.25m² (wet weight) for intertidal habitats, and 47g/m³ (for subtidal habitats). We found significant spatial and temporal (both seasonal and yearly) variation in bloom composition and abundance, with strong local variation (<2km) in bloom density. Our data indicate the likelihood of rapid shifts in bloom location and composition in estuarine systems.

EVALUATION OF CHLOROPLAST GENES FOR RESOLVING ORDINAL PHYLOGENETIC RELATIONSHIPS IN CHLOROPHYCEAE. Nicholas P. Tippery, Louise A. Lewis & Paul O. Lewis. Department of Ecology and Evolutionary Biology, University of Connecticut, Storrs, CT 06269-3043, U.S.A.

Relationships among chlorophycean algae are being resolved with ever increasing frequency due to an abundance of molecular data and phylogenetic methods. Despite the current bulk of data, however, many crucial phylogenetic relationships remain insufficiently resolved. In addition, analyses using different sources of molecular data often obtain incongruent results. Following an initial reliance on relatively few genes (e.g., 18S, *rbcL*), current studies employ data from several loci simultaneously. With whole chloroplast genome sequences available for a sparse sample of all major Chlorophyceae lineages, we are poised to evaluate the relative utility of various chloroplast genes for resolving phylogenetic relationships, and thus to make informed decisions about the most useful genes to pursue in future phylogenetic studies. To this end, we investigated (1) the ability of nine chloroplast genes (*atpA*, *atpB*, *psaA*, *psaB*, *psbA*, *psbB*, *psbC*, *psbD*, *rbcL*) to resolve ordinal relationships in Chlorophyceae, (2) the effect of increased taxon sampling on the topology and support values for four of these gene regions (*psaA*, *psaB*, *psbC*, *rbcL*), and (3) the topology achieved by analyzing multiple gene regions simultaneously. Several relationships were recovered in a majority of single-gene analyses (e.g., the monophyly of Chaetopeltidales + Chaetophorales + Oedogoniales and Sphaeropleales + Volvocales), occasionally with high statistical support. Inclusion of additional taxa in single-gene analyses did not appreciably alter branch support for ordinal relationships. Analyses of combined data from multiple genes, however, achieved the highest overall branch support and congruence with expected relationships. Preliminary results support *psaA*, *psaB*, and *psbC* as candidate regions for resolving ordinal relationships in Chlorophyceae, whereas *rbcL* data produced trees that were less well resolved at deeper nodes and less consistent with the current understanding of chlorophycean phylogenetic relationships.

IRON LIMITATION EFFECTS ON THE ASCORBATE-GLUTATHIONE CYCLE OF THE CHLOROPHYTE ALGAL DUNALIELLA TERTIOLECTA. Hannah Traggis and Leland Jahnke. Biological Sciences, University of New Hampshire, Durham NH, 03824, USA.

Ubiquitous in the neritic ocean, it is now believed that iron-limitation is the most important factor controlling primary production in oceanic phytoplankton. To investigate the effects of iron deficiency, *Dunaliella tertiolecta* was cultured under limiting (100 nM Fe) and replete (1 μ M Fe) iron concentrations. The physiological status and the Water-Water antioxidant defense system were evaluated. Iron limitation effected a 21% drop in PSII efficiency (replete= 0.634 ± 0.012 ; limiting= 0.507 ± 0.012) concurrent with a 17.5% reduction in photosynthetic rates (replete= $265.8 \text{ umol } O_2/\text{mg chl/hr} \pm 5.7$; limiting= $219.3 \text{ umol } O_2/\text{mg chl/hr} \pm 5.7$). Growth rates in replete and limited cultures show no significant differences at 0.84 ± 0.37 and 0.62 ± 0.37 , respectively. Both heme and non-heme based antioxidant enzyme activities were assessed. Heme-based Ascorbate peroxidase (APX), exhibits an 84% iron limited rate reduction (replete and limited = 36.23 and $5.72 \text{ umol ascorbate mg prot}^{-1} \text{ hr}^{-1} \pm 2.96$, respectively). Conversely, the flavin-based Monodehydroascorbate reductase (MDHAR), exhibits a significant rate increase, 2.16 ± 0.19 (replete) to $3.86 \pm 0.19 \text{ umol NADH mg prot}^{-1} \text{ hr}^{-1}$ under iron-limitation. These investigations suggest that *D. tertiolecta* is able to maintain a stable growth rate under iron limitation by re-allocating its subcellular usage of available iron. Further investigations will determine the presence of additional iron/flavin based molecules involved in the photosynthetic apparatus and anti-oxidant scavenging mechanisms.

ALGAL PHYLOGENETICS AND BIOGEOGRAPHY IN THE HIGH-THROUGHPUT AGE. Heroen Verbruggen. Phycology Research Group, Ghent University. Krijgslaan 281 (S8), 9000 Ghent, Belgium.

High-throughput sequencing technologies permit generating massive datasets of algal DNA sequences at moderate cost. I will give an overview of how high-throughput technologies, including DNA barcoding, have and will continue to influence the fields of algal phylogenetics and biogeography. A great advantage of the large datasets produced with high-throughput technologies is that their size allows inferring older relationships and testing more complex hypotheses. Due to the fact that we have to process much larger datasets and test more complex hypotheses using model-based inference, biology will become a more computational discipline. I will discuss recent computational methods that permit making better use of the data and the resulting trees for evolutionary and biogeographic inferences and use algal examples to illustrate these new developments.

ENCRUSTING EPILITHIC ALGAE: AN UNDERSTUDIED FRESHWATER ASSOCIATION? John Wehr, Kam Truhn, & Alissa Perrone. Louis Calder Center – Biological Field Station, Fordham University, Armonk, NY 10504 USA.

Early in the 20th century, many eminent phycologists including F.E. Fritsch, L. Geitler, R.W. Butcher, J.W.G. Lund, G. Israelsson, and E. Kann, described a diverse assemblage of encrusting algae, species that colonize rocks and boulders in streams and lakes. Nearly all these studies were conducted in Europe, with a corresponding paucity of records from North America and Asia. As ecological and floristic studies of freshwater algae developed in the United States and Canada, emphasis was placed on planktonic species in lakes, and primarily diatoms, or simply “periphyton” in rivers. As a result, reports of encrusting algal species other than diatoms are uncommon, and when discovered, are typically cited as “rare” or in some cases “new” species. Our studies of epilithic, encrusting algal associations in North American rivers reveal many of the same taxa that have been described from Europe. We report on the algal flora of more than 100 streams and rivers from eastern and western North America, with special note on records of species once thought to be absent or rare from this continent, including *Coleodesmium wrangelii*, *Chamaesiphon amethystinus*, *Caposira brebissonii*, *Stauromatonema viride* (Cyanobacteria), *Gongrosira fluminensis*, *G. incrustans*, *Protoderma frequens* (Chlorophyta), *Chrysocapsa cf. maxima* (Chrysophyta), *Heribaudiella fluviatilis*, and *Pleurocladia lacustris* (Phaeophyta). Many of these, while rarely reported, may form conspicuous, macroscopic colonies or tufts visible with the naked eye. We also document the apparent loss of certain uncommon or rare algal species from habitats altered by urbanization and agriculture. We offer recommendations to improve methods for freshwater algal biodiversity surveys and suggest the need for a North American “red list” for algae, as has been adopted in many European countries.

MORPHOLOGICAL AND MOLECULAR STUDIES ON *SPHAEROSPERMOPSIS TORQUES-REGINAE* (CYANOBACTERIA, NOSTOCALES) FROM SOUTH AMERICAN WATER BLOOMS. Vera R. Werner¹, H. Dail Laughinghouse IV^{2,3}, Marli F. Fiore⁴, Célia L. Sant'Anna⁵, Caroline Hoff⁴, Kleber R. Santos⁵, Emanuel B. Neuhaus¹, Renato J. Molica⁶, Ricardo Y. Honda⁴ and Ricardo O. Echenique⁷. ¹MCN-FZB/RS, Porto Alegre, RS, Brazil; ²Botany, NMNH-SI, Washington, DC, USA; ³CMNS, UMD, College Park, MD, USA; ⁴CENA-USP, Piracicaba, SP, Brazil; ⁵Phycology, IBt-São Paulo, SP, Brazil; ⁶UFRPE, Garanhuns, PE, Brazil; ⁷Phycology, FCNyM-UNLP, La Plata, Argentina.

Sphaerospermopsis torques-reginae (Komárek) comb. nov. was originally described as *Anabaena torques-reginae* Komárek from planktonic populations of Cuban eutrophic environments, characterized by presenting twisted trichomes with spherical akinetes adjacent to heterocytes. Recently, all planktonic *Anabaena* Bory de Saint-Vincent ex Bornet et Flahault morphospecies were transferred into the genus *Dolichospermum* (Ralfs ex Bornet et Flahault) Wacklin et al., including *D. torques-reginae* (Komárek) Wacklin et al. However, by polyphasic characterization of strains of *Anabaena reniformis* Lemmermann and *Aphanizomenon aphanizomenoides* (Forti) Horecká et Komárek (= *Anabaena aphanizomenoides* Forti), these planktonic species were reclassified into *Sphaerospermum* Zapomělová et al. This was an illegitimate name, so the genus was renamed *Sphaerospermopsis*. This study's main objective was to morphologically and molecularly characterize cyanobacterial populations identified as *D. torques-reginae* from different aquatic ecosystems in South America. The 16S rRNA gene of two *D. torques-reginae* strains (ITEP024 and ITEP026) was sequenced and phylogenetically analysed for the first time. The morphological and phylogenetic analyses demonstrated the affiliation of our populations with the genus *Sphaerospermum* and were denominated *Sphaerospermopsis torques-reginae*. Furthermore, geographic distribution, ecology, and toxicity of the species are discussed. *Sphaerospermopsis torques-reginae* was observed in different aquatic environments, natural and artificial, tropical and subtropical in Brazil, temperate in Argentina, and tropical in Colombia, suggesting a wide distribution in South America. It normally occurred in dense freshwater blooms, although also found in water with low salinity. *Sphaerospermopsis torques-reginae* toxic blooms, identified as *Anabaena spiroides* Klebahn, with production of anatoxin-a(s) have been reported in tropical water bodies in northeastern Brazil.

DIATOM COLONIZATION PATTERNS IN A SUBURBAN STREAM AFFECTED BY GRAZING PRESSURE. Sarah B. Whorley & John D. Wehr. Louis Calder Center – Biological Field Station, Fordham University. Armonk, NY, 10504, USA.

Diatom assemblages are important ecosystem producers and food sources in stream food webs. Increasingly, stream ecosystems are profoundly affected by urbanization, yet most properties, including periphyton colonization and grazing activity, are known mainly from pristine systems. As regulatory agencies aim to improve water quality in streams along urban-to-rural gradients, we predict that periphyton communities will differ in species composition and nutritional quality, as food sources for higher trophic levels. This study explores how newly developing periphyton communities vary species composition, biomass, and nutritional quality (C, N, P content and fatty acid content) under contrasting grazing pressure. Cleaned rocks were placed in a fourth-order suburban stream (Bronx River, NY), with half the substrata rimmed with petroleum gel to exclude macroinvertebrate grazers. Periphyton communities were randomly sampled daily. While not significantly different, biomass and nutritional measurements (periphyton N, P, and fatty acids) tended to be greater among grazed samples than ungrazed samples, regardless of sample date. These results suggest that further exploration is needed to determine whether grazing pressure influences either periphyton nutritional quality or diatom species composition in suburban streams at early stages of colonization and succession.

THE BENTHIC MARINE ALGAE OF THE TROPICAL AND SUBTROPICAL WESTERN ATLANTIC: CHANGES IN OUR UNDERSTANDING IN THE LAST HALF CENTURY. Michael J. Wynne. Ecology and Evolutionary Biology and Herbarium, University of Michigan, Ann Arbor, MI 48108, U.S.A.

The volume “Marine algae of the eastern tropical and subtropical coasts of the Americas” produced by W. R. Taylor in 1960 was a comprehensive treatment of the benthic seaweeds of this region and remains a useful compendium for the breadth of its coverage, its detailed descriptions, and excellent artwork. But in the 50 years since that floristic treatment, numerous regional treatments have appeared, many new taxa described, and many new records have been published. Wynne has produced several checklists over the years (1968, 1998, 2005) in efforts to gather the pertinent literature from this broad region from Cape Hatteras, North Carolina, in the north to southern Brazil in the south. The just published third revision (Wynne, 2011, *Nova Hedwigia* Beiheft vol. 140, 166 pages) gives us the opportunity to see the dramatic changes in the schemes of classification and in the treatment of genera of green, brown, and red algae from the new information provided by the flood of phylogenetic data. These changes will be discussed with some general and specific examples.

454 PYROSEQUENCING FOR EUKARYOTIC MICROBES: DINOFLAGELLATES AS A FOCUS. Yunyun Zhuang, Huan Zhang and Senjie Lin. Department of Marine Sciences, University of Connecticut, 1080 Shennecossett Road, Groton, CT06340, USA.

454 pyrosequencing has proven to be powerful in unraveling prokaryotic microbial biodiversity but the power, which is even greater now due to the increased read length, has not been much exploited for eukaryotic microbes. Dinoflagellates are the second most important eukaryotic primary producers in the ocean, and are most important contributors of harmful algal blooms and biotoxins in the coastal ocean. It is very important to understand their community structure and its spatiotemporal changes relative to those of other eukaryotic microbes. In this study, we designed eukaryote-universal (18Scom) and dinoflagellate-specific (Dino18S) 18S rDNA primers to fit the read length of 454 GSFLX Titanium sequencing. 18Scom embraces variable regions V7-V9, while Dino18S embraces V1-V3 and part of V4. We tested the feasibility of this protocol by analyzing a coastal plankton sample collected in May 2010 from Long Island Sound, USA. 18Scom retrieved organisms from nearly all eukaryotic kingdoms, including Metazoa, Fungi, Amoebozoa, Plantae, Chromalveolata, and Rhizaria. Among the most abundant phyla, diatoms, chlorophytes, dinoflagellates, arthropod (mainly copepods), and ciliates accounted for approximately 23, 15, 9, 9 and 8% of the community, respectively. The dataset also revealed a “rare biosphere” comprising 17 low-abundance phyla such as Glaucophyta, Haplosporidia, and Hyphochytriomycota. For dinoflagellates, 18Scom and Dino18S retrieved 37 and 22 classified genera, respectively (totally 42 genera), with *Gyrodinium*, *Heterocapsa* and *Gymnodinium* being the most abundant, whereas about 40% of the reads represent uncultured environmental dinoflagellates. Our results show that the new primers and our sequencing protocol will be useful for uncovering the biodiversity of eukaryotic microbes and the combination of the two primer sets maximizes dinoflagellate diversity recovery.

MICHAEL HALL GRAHAM

Moss Landing Marine Laboratories
8272 Moss Landing Road
Moss Landing, Ca. 95039
WWW: <http://phycology.mlml.calstate.edu>

office: (831) 771-4481
lab: (831) 771-4421
fax: (831) 632-4403
email: mgraham@mlml.calstate.edu

EDUCATION

- 2000 **Doctor of Philosophy in Oceanography**, Scripps Institution of Oceanography, UC San Diego, Supervisor: Dr. Paul K. Dayton
Dissertation: *Planktonic patterns and processes in the giant kelp *Macrocystis pyrifera**
- 1995 **Master of Science in Marine Science**, Moss Landing Marine Laboratories, San Jose State University, Supervisor: Dr. Michael S. Foster
Thesis: *Regulation of the shallow limit of giant kelp, *Macrocystis pyrifera*, at three sites along the Monterey Peninsula*
- 1992 **Bachelor of Arts in Aquatic Biology/Geography**, UC Santa Barbara

EXPERIENCE

- 2008-pres. **Fellow**, California Academy of Sciences
- 2008-pres. **Scientific Consultant**, PBS *Octonauts*
- 2007-pres. **Associate Professor of Marine Ecology**, Moss Landing Marine Laboratories, San Jose State University
- 2003-2007. **Assistant Professor of Marine Ecology**, Moss Landing Marine Laboratories, San Jose State University
- 2003-pres. **Collaborating investigator**, Center for Advanced Studies in Arid Zones (CEAZA, Chile)
- 2001-2002 **University of California Faculty Fellow**, UC Davis. Supervisor: Dr. Richard K. Grosberg
- 2001-2002 **National Center for Ecological Analysis & Synthesis**, Working Group: Long-Term Ecological Records of Marine Environments, Populations and Communities (Leader: Dr. Jeremy B. C. Jackson)
- 2001-2002 **Lecturer**, U.C. Davis (*Marine Ecology*)
- 2000 **Lecturer**, Scripps Institution of Oceanography (*Statistical Techniques*)
- 2000 **Scientific Consultant**, Pixar Animation Studios *Finding Nemo*
- 1999-2000 **Statistical Consultant**, Cabrillo National Monument
- 1997-2000 **Guest Lecturer**, UC San Diego/Scripps Institution of Oceanography (*Benthic Ecology, Marine Ecology*), Univ. of San Diego (*Oceanography*), Hawaii Pacific University (*Ecology*)

GRANTS

- 2008-2012 **NSF #0752523**. Effects of ocean climate change on recruitment of kelp populations. **\$571,027 (PI, w/ C. Harley)**
- 2008-2011 **NOAA/ California Sea Grant**. Seaweed strain selection and preservation to optimize harvest yields for abalone culture. **\$301,479 (PI)**
- 2006-2008 **NOAA/ California Sea Grant**. Integrated culture of seaweeds and red abalone in Monterey Harbor. **\$239,387 (PI)**
- 2005 **NOAA/ California Sea Grant**. Development of rope-culture methods for red seaweed aquaculture in California. **\$9,993 (PI)**
- 2004-2008 **NSF #0351778**. Collaborative Research: Biodiversity and ecosystem function in seaweed communities. **\$266,489 (PI, collaborative grant w/ J. Stachowicz)**

- 2004-2006 **EPA**. Development of a regional monitoring program for central California wetlands. **\$180,500 (PI)**
- 2003-2006 **NSF #0320972**. MRI/RUI: Acquisition of a high-speed digital motion analysis system for studying multi-scale interactions in a fluid environment. **\$196,195 (PI, w/ L. Ferry-Graham, J. Geller)**
- 2003-2004 **NSF #0407937**. US-Chile: Planning visit to incorporate Chilean kelp forests into study of kelp life history evolution. **\$5,241 (PI)**
- 2001-2002 **NOAA/ California Sea Grant**. Reproductive biology of *Undaria pinnatifida*, a seaweed recently introduced to southern California: assessing the potential for establishment and spread. **\$9,916 (PI w/ J. Stachowicz, C. Thornber)**
- 2001-2002 **NSF #0120789**. Integrative approaches to natural history. **\$10,950 (PI w/ S. Gilman)**
- 2000-2001 **NSF #0087359**. Natural history in the 21st century: A student symposium. **\$9,250 (co-PI w/ P. Dayton)**
- 1998-2000 **NOAA/California Sea Grant #R/CZ-141**. Effect of spore abundance on recruitment and maintenance of subtidal kelps. **\$100,654 (co-PI w/ P. Dayton)**

PUBLICATIONS

Peer-reviewed Publications

- Demes, KW and **MH Graham**. Abiotic regulation of investment in sexual vs. vegetative reproduction in the clonal kelp, *Laminaria sinclairii* (Laminariales, Phaeophyceae) *Journal of Phycology* (In press).
- Henriquez, LA, AH Buschmann, MA Maldonado, **MH Graham**, MC Hernandez-Gonzalez, SV Pereda, and MI Bobadilla. Grazing on giant kelp microscopic phases and the recruitment success of annual populations of *Macrocystis pyrifera* (Laminariales, Phaeophyta) in southern Chile *Journal of Phycology* (In press).
- Graham, MH**, J Parker, and PK Dayton (eds). *The Essential Naturalist: Timeless Readings in Natural History*. University of Chicago Press (In press).
- Graham, MH**, BP Kinlan, and RK Grosberg. 2010. Post-glacial redistribution and shifts in productivity of giant kelp forests. *Proceedings of the Royal Society of London: Biological Sciences* 277:399-406.
- Demes, KW, **MH Graham**, and TS Suskiewicz. 2009. Phenotypic plasticity reconciles incongruous molecular and morphological taxonomies: giant kelp, *Macrocystis* (Laminariales, Phaeophyceae), is a monospecific genus. *Journal of Phycology* 45:1266-1269.
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- Stachowicz, JJ, **MH Graham**, MES Bracken, and AI Szoboszlai. 2008. Diversity enhances cover and stability of seaweed assemblages: the importance of environmental heterogeneity and experimental duration. *Ecology* 89:3008-3019.
- Stachowicz, JJ, RJ Best, MES Bracken, and **MH Graham**. 2008. Complementarity in marine biodiversity manipulations: reconciling divergent evidence from field and mesocosm experiments. *Proceedings of the National Academy of Sciences USA* 105:18842-18847.
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- Erlandson, JM, **MH Graham**, RS Steneck, JA Estes, BJ Bourque, and D Corbett. 2007. Peopling the Americas via a kelp highway. *Journal of Island and Coastal Archeology* 1:161-174.

- Graham, MH.** 2007. Sea-level change, effects on coastlines. Deny, MW and SD Gaines (eds), *Encyclopedia of Tidepools*, University of California Press, pp. 497-498.
- Graham, MH,** BP Kinlan, LD Druehl, LE Garske and S Banks. 2007. Deep-water kelp refugia as potential hotspots of tropical marine diversity and productivity. *Proceedings of the National Academy of Sciences USA* 104:16576-16580.
- Graham, MH,** JA Vasquez and AH Buschmann. 2007. Global ecology of the giant kelp *Macrocystis*: from ecotypes to ecosystems. *Oceanography and Marine Biology: an Annual Review* 45:39-88.
- Hernandez-Carmona, G, B Hughes, and **MH Graham.** 2006. Reproductive longevity of drifting kelp *Macrocystis pyrifera* (Phaeophyceae) in Monterey Bay, USA. *Journal of Phycology* 42:1199-1207
- Kinlan BP, **MH Graham,** JM Erlandson. 2005. Late Quaternary changes in the size and shape of the California Channel Islands: implications for marine subsidies to terrestrial communities. *Proceedings of the California Islands Symposium* 6:119-130
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- Graham, MH.** 2004. Effects of local deforestation of the diversity and structure of southern California giant kelp forest food webs. *Ecosystems* 7:341-357
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- Graham, MH.** 2003. Confronting multicollinearity in ecological multiple regression. *Ecology* 84:2809-2815
- Graham, MH.** 2003. Coupling propagule output to supply at the edge and interior of a giant kelp forest. *Ecology* 85:1250-1264
- Kinlan, BP, **MH Graham,** E Sala, and PK Dayton. 2003. Arrested development of giant kelp (*Macrocystis pyrifera*, Phaeophyceae) embryonic sporophytes: a mechanism for delayed recruitment in perennial kelps? *Journal of Phycology* 39:1-12
- Graham, MH,** PK Dayton, and JM Erlandson. 2003. Ice ages and ecological transitions on temperate coasts. *Trends in Ecology and Evolution* 18:33-40
- Steneck, RS, **MH Graham,** BJ Bourque, D Corbett, JM Erlandson, JA Estes, and MJ Tegner. 2002. Kelp forest ecosystems: biodiversity, stability, resilience and their future. *Environmental Conservation* 29:436-459
- Graham, MH,** PK Dayton, and MA Hixon (editors). 2002. Paradigms in Ecology: Past, Present, and Future. *Special Feature in Ecology* 83:1479-1480
- Graham, MH** and PK Dayton. 2002. On the evolution of ecological ideas: paradigms and scientific progress. *Ecology* 83:1481-1489
- Graham, MH.** 2002. Prolonged reproductive consequences of short-term biomass loss in seaweeds. *Marine Biology* 140:901-911
- Sala, E and **MH Graham.** 2002. Community-wide distribution of predator-prey interaction strength in kelp forests. *Proceedings of the National Academy of Sciences USA* 99:3678-3683
- Graham, MH** and MS Edwards. 2001. Statistical significance vs. fit: estimating relative importance of individual factors in ecological analysis of variance. *Oikos* 93:505-513
- Graham, MH.** 1999. Identification of kelp zoospores from in situ plankton samples. *Marine Biology* 135:709-720
- Graham, MH** and BG Mitchell. 1999. Obtaining absorption spectra from individual macroalgal spores using microphotometry. *Hydrobiologia* 398/399:231-239
- Graham, MH.** 1999. Where will all the PhDs go? *Trends in Ecology and Evolution* 5:208

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- Graham, MH,** Harrold, C, Lisin, S, Light, K, Watanabe, J, and MS Foster. 1997. Population dynamics of *Macrocystis pyrifera* along a wave exposure gradient. *Marine Ecology Progress Series* 148:269-279
- Graham, MH.** 1996. Effect of high irradiance on recruitment of the giant kelp, *Macrocystis* (Phaeophyta), to shallow water. *Journal of Phycology* 32:903-906

In preparation:

- Graham, MH.** Geographic variability in life history traits leads to variable population persistence in the annual kelp *Postelsia palmaeformis*. To be submitted to *Ecology*.
- Graham, MH** and E Sala. A general unified approach to estimate the strength of species interactions. To be submitted to *Ecology Letters*.

AWARDS

- 2005 **Young Investigator of the Year**, SJSU Foundation
- 2001 **Best Published Paper** (2nd out of 80), MarinAlg Best Paper Competition
- 2000 **Best Student Paper**, Western Society of Naturalists Annual Meeting
- 1999 **E. W. Fager Award** for contributions in quantitative ecology, SIO

UNIVERSITY SERVICE

- 2003-pres. Governing Board member, Moss Landing Marine Laboratories
- 2003-pres. MLML Committee service: Diving Control Board (chair), Aquarium Committee, Tech Committee, Museum Committee, Development Committee, Curriculum Committee, Moss Landing Marine Laboratories
- 2002 Search Committee, Physical Oceanographer, Moss Landing Marine Labs
- 1998-2000 Diving Control Board, SIO
- 1998-1999 Editorial and Publications Committee, SIO

PROFESSIONAL SERVICE

- 2011-pres Applied Phycology Committee, *Phycological Society of America*
- 2007-2011 Associate Editor, *Ecology/Ecological Monographs*
- 2007-2011 Associate Editor, *Journal of Phycology*
- 2007-pres Nominations Committee, *Phycological Society of America*
- 2008-2009 Member-at-large, *Western Society of Naturalists*
- 2006-2011 Editorial Board, *Botanica Marina*.
- 2006-2009 Editorial Board, *Journal of Phycology*.
- 2005-2008 Associate Editor, *Encyclopedia of Ecology* (Elsevier)
- 2005 Working Group Member, *California Invasive Seaweeds*
- 2004 Conservation Working Group, *Monterey Bay National Marine Sanctuary*
- 2004-2005 Member-at-large, *Western Society of Naturalists*
- 2002-pres. Editorial Advisory Staff, *Marine Ecology Progress Series*

Advising:

- Undergraduates:** Christian Hansen (1996, UCSD), Everett Yee (1997, UCI), Brian Kinlan (1998, Yale University), Greg Schroeder (2006, SJSU), Gabe Rodriguez (2007-2008, CSUMB), Jasmine Ruvalcaba (2007-2008, CSUMB), Sam Rivera (2008-2009, SJSU), Sarah Jeffries (current, CSUMB),
- Masters:** Tim Schaadt (2005, MLML), Brent Hughes (2007, MLML), Amber Szoboszlai (2007, MLML), Diana Kohtio (2007, MLML), Jenn Jorve (2008, MLML), Aurora Alifano (2008, MLML), Kyle Demes (2009, MLML), Max Overstrom Coleman (2009, MLML),

Selena McMillan (Current, MLML), Thew Suskiewicz (Current, MLML), Rosemary Romero (Current, MLML), Catalina Reyes (MLML), Arley Muth (Current, MLML), Megan Wehrenberg (Current, MLML), Brynn Hooton (Current, MLML), Sonya Sankaran (Current, MLML), Sara Hutto (Current, MLML), Michael Fox (Current, MLML), Jasmine Ruvalcaba (Current, MLML), Sara Worden (Current, MLML), Alexis Howard (Current, MLML)

PhD committees: Wendy Cover (Current, UCSC), Brenna Mahoney (Current, UCSC)

Post-doctoral fellows: Dr. Bernat Hereu (2005-2007, Fulbright Fellow University of Barcelona), Dr. Gage Dayton (2005-2007, Texas A&M University).

COMMUNITY SERVICE

2007-Pres. Director, *Marina High School Monterey Bay Stewards Program*

2007-Pres. President, *Marina Youth Soccer Association*

2007-2009. President, *Marina Pony Baseball Softball*

PROFESSIONAL MEMBERSHIPS

American Society of Limnologists and Oceanographers, Ecological Society of America, International Seaweed Association, Phycological Society of America, Sigma Xi, Western Society of Naturalists

INVITED SYMPOSIA, SEMINARS AND WORKSHOPS

Causes and consequences of global kelp deforestation. International Isoyake Symposium, August 2, 2008. Tokyo, Japan.

Function of global kelp systems. Departmental Seminar at iMar, Puerto Montt Chile, July 14, 2008.

Temperate kelps in deep tropical waters. Departmental Seminar, Bamfield Marine Science Centre, June 21, 2007.

Functional role of seaweeds in marine systems. Departmental Seminar, Hawaii Institute of Marine Biology, May 29, 2007.

Temperate kelp populations in deep tropical waters. Evolutionary History of Kelps Symposium at 27th International Seaweed Symposium, April 21-25, 2007. Kobe, Japan.

Causes and Consequences of kelp deforestation in California. Isoyake Symposium at 27th International Seaweed Symposium, April 21-25, 2007. Kobe, Japan.

Temperate kelps in deep tropical waters *Moss Landing Marine Labs Seminar*, January 2007.

Algal diversity manipulations: How do seaweeds structure rocky shores? Presented in: Macroalgae as ecological probes at *Phycological Society of America Annual Meeting*. Juneau, Alaska, July 2006.

Life history evolution and the dynamics of kelp recruitment. *Bodega Marine Labs Seminar*, July 2005, *Pontificia Universidad Católica de Chile Ecology Seminar*, July 2005, and *San Jose State University*, October 2005.

Predicting past and future effects of climate change on kelp distribution and productivity. *International Symposium on Construction of Seaweed Forests*, September 14-18, 2004. Gangneung, South Korea.

Predicting past and future effects of climate change on kelp distribution and productivity. Kelps and Climate Change Symposium at *International Seaweed Symposium*, June 21-25, 2004. Bergen, Norway.

Life history evolution and the persistence of kelp populations. *University of California Santa Barbara Departmental Seminar*, March 9, 2004.

Life history evolution and the persistence of kelp populations. *University of Chicago Departmental Seminar*, March 2, 2004.

Ice age kelp forests: climate-driven changes in kelp forest distribution since the last glacial maximum. Seaweeds and Climate Change Symposium at *Phycological Society of America Annual Meeting*, June 12-18, 2003, Salishan, Oregon.

Foundation species and the dynamics of natural communities: a kelp forest case study. *UC Santa Cruz Ecology Seminar*, May 2002 and *Bodega Marine Labs Seminar*, May 2002.

Kelps as foundation species: from population to community dynamics. *Moss Landing Marine Labs Ecology Seminar*, April 2002.

Contemporary and historical processes in kelp population and community dynamics. *University of Washington*, Zoology Department Seminar, April 2001 and *UC Davis*, Center for Population Biology Seminar, April 2001.

Contemporary and historical processes in kelp population dynamics. *San Diego State University*, Ecology Seminar, February 2001 and *Moss Landing Marine Labs Ecology Seminar*, March 2001.

The secret life of kelps: planktonic processes and population dynamics. Ecology of big brown algae symposium at *Phycological Society of America Annual Meeting*. San Diego, July 2000.

PUBLIC OUTREACH

Ocean Day Presentation, Miss Barbara's Child Development Center (pre-Kindergarden), Spring 2008.

Kelp Week Presentation, Olson Elementary School (K-5), September 2007.

Invited speaker. *Understanding the functional role of seaweed's in nearshore marine systems*. Public seminar, Friends of MLML, October 2007.

Ocean Day Presentation, Miss Barbara's Child Development Center (pre-Kindergarden), Spring 2007.

Invited speaker. *The of Monterey's seaweed systems*. Public seminar, American Cetacean Society, April 2007.

Kelp Week Presentation, Olson Elementary School (K-5), September 2006.

Ocean Day Presentation, Miss Barbara's Child Development Center (pre-Kindergarden), Spring 2006.

Invited speaker. *Understanding the functional role of seaweed's in nearshore marine systems*. Annual Board Meeting, San Jose State University Foundation, September 22, 2005

Public seminar. *Diversity benefits from the bottom up: how seaweeds structure rocky shores*. Friends of Moss Landing Marine Laboratories, September 16, 2005

Public seminar. *Wakame: a kelp invasion of Monterey Harbor*. Open House, Moss Landing Marine Laboratories, April 27, 2003

Invited speaker. *Current health of California's kelp forests*. Annual retreat of US Congressman Sam Farr and Associates, January 29, 2004

Ocean Day Presentation, Miss Barbara's Child Development Center (pre-Kindergarten), Spring 2004