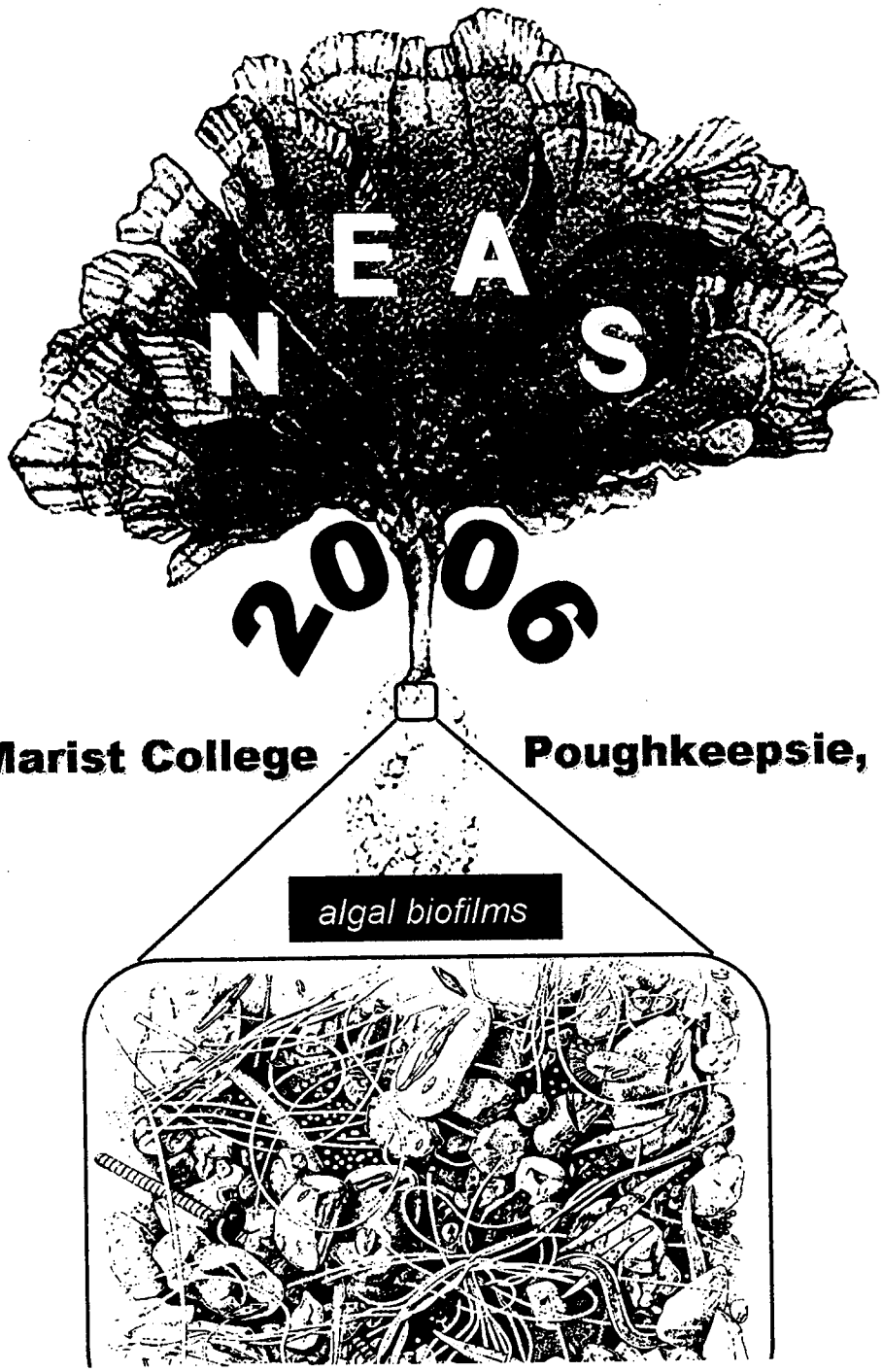
PROGRAM AND ABSTRACTS



Marist College **Poughkeepsie, NY**

21-23 April, 2006

Welcome to the 45th Northeast Algal Symposium, NEAS 2006!

It is our pleasure to welcome you to Marist College in New York's beautiful Hudson River Valley. We will do our best to make this a gratifying meeting and to facilitate the exchange of algological information between meeting attendees. Our goal is to provide you with a solid, cutting-edge scientific program organized to provide a comfortable and supportive atmosphere for students—both graduate and undergraduate—to present the results of their research.

Many of you may not be familiar with Marist College. We hope that you will have an opportunity to learn more about the college during your time here. The hosting of NEAS 2006 is indicative of Marist's commitment to improving the reputation of its programs in the Natural Sciences and we are very happy to be hosting this years meeting.

Perhaps this is your first visit to the Hudson Valley. This area along the middle stretch of the Hudson River boasts world-renowned natural beauty, several sites of historic interest, and a variety of other fun places to visit. We hope you will have an opportunity to take some time, look around, and enjoy some activities in addition to the great symposium we have in store for you.

Best wishes for a scientifically-productive and enjoyable symposium,

Ray Kepner, Marist College
David Domozych, Skidmore College
John Heimke, Russell Sage College
NEAS 2006 Co-Convenors

45th Northeast Algal Symposium

Honorary Chair

H. William "Bill" Johansen

NEAS Chairman 1987-1992

"One fine phycologist, one exceptional human...a true professional, a teacher, colleague and friend to many.

He continues to study and willingly shares his knowledge of the algae and the oceans.

Go well good friend"

Bob T. Wilce

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Activities and Locations

Registration:	Friday at the Courtyard by Marriott. Saturday in the breezeway between Marist College Student Center and Champagnat Hall.
Opening Mixer:	Friday 6-9pm Courtyard by Marriott.
Breakfast:	The Marriott serves a complete breakfast (hot) that is free for registered NEAS attendees staying at the Courtyard.
Program & Oral Presentations:	Student Center (SC) Room 349
Posters:	Posters will be displayed in SC 346 (The Performing Arts Room), SC 348 and their adjoining Hallway.
Saturday Lunch and Banquet:	Student Center Cabaret. Lunch from 12-1:30 Pre-banquet mixer 6:30-7:30, Banquet 7:30-9:30
Executive Comm. Lunch:	Saturday 12-1:30, President's Dining Room A in SC
Vendor Display:	Saturday Rm 348 SC
Break Time:	Hot & cold beverages and light snacks will be available in hallway outside of room 348
Sunday Lunch:	Box lunches will be available following the General Business Meeting outside SC 348.

General Program: 45th Northeast Algal Symposium

Friday, April 21, 2006

6:00 – 9:00pm **Registration and mixer at Courtyard by Marriott**

Saturday, April 22, 2006

Opening remarks (and presentations, Student Center, Marist College)

8:15 – 8:30am **Welcome and Opening Remarks – Raymond Kepner**

SESSION 1 Student Presentations Moderator: Chris Lane

8:30 – 8:45am Wilce Award Candidate
MOLECULAR ANALYSIS OF SPECIES LIMITS OF THE BROWN ALGAL GENUS *FUCUS* IN THE NORTHEAST PACIFIC. **Hana Kucera** and Gary W. Saunders. Centre for Environmental & Molecular Algal Research, Department of Biology, University of New Brunswick, Fredericton, New Brunswick, E3B 6E1, Canada.

8:45 – 9:00am Wilce Award Candidate
EXAMINING ALGAL VIRUS RECEPTORS USING CONFOCAL LASER MICROSCOPY. **Paesani, V.I.**[1],Lawrence, J.E.[1] [1]University of New Brunswick, Fredericton, New Brunswick, E3B 6E4, Canada.

9:00 – 9:15am Wilce Award Candidate
RESURRECTING THE GENUS *GRANIA* FOR *GRANIA EFFLORESCENS* **Susan L. Clayden** and Gary W. Saunders. Centre for Environmental and Molecular Algal Research, Department of Biology, University of New Brunswick, Fredericton, N.B., E3B 6E1, Canada

9:15 – 9:30am Wilce Award Candidate
CHARACTERIZATION OF GROUP IA INTRONS IN THE CHLOROPLAST *RBC*L GENE OF FIVE *PEDIASTRUM* AND TWO *BRACTEACOCCUS* ISOLATES (SPHAEROPLEALES, CHLOROPHYCEAE). **Hilary A. McManus**[1] and Louise A. Lewis[1]. Department of Ecology and Evolutionary Biology, University of Connecticut, Storrs, Connecticut, 06269, USA.

9:30 – 9:45am Wilce Award Candidate
COMPARISON OF DIATOM AND MACROINVERTEBRATE INDICES IN ACID MINE DRAINAGE IMPACTED STREAMS. **Jason T. Zalack** and Morgan L. Vis Department of Environmental and Plant Biology, Ohio University. Athens, OH 45701.

9:45 – 10:00am Wilce Award Candidate
TEMPORAL DYNAMICS OF EPS PRODUCTION, LOSS AND COMPOSITION FOR BIOFILMS WITHIN THE COLNE ESTUARY, U.K. **Brent Bellinger**[1], Graham Underwood[2], and Michael Gretz[1]. [1]Department of Biological Sciences. Michigan Tech University, Houghton, MI 49931 USA
[2]Department of Biological Sciences. University of Essex, Colechester, CO4 3SQ U.K.

10:00 – 10:30am **Break**

SESSION 2 Student Presentations Moderator: Craig Schneider

10:30 – 10:45am Wilce Award Candidate
DESICCATION EFFECTS ON GROWTH RATE AND NITRATE UPTAKE OF *PORPHYRA* SPP. IN RELATION TO TIDAL ELEVATION. **Jang K. Kim**[1,3], George P. Kraemer[2], and Charles Yarish[1] [1]Department of Ecology & Evolutionary Biology, University of Connecticut, Stamford, CT, 06901, USA. [2] Departments of Biology & Environmental Studies, Purchase College, State University of New York, Purchase, NY, 10577, USA. [3]Department of Ecology & Evolutionary Biology, University of Connecticut, Groton, CT, 06340, USA.

10:45 – 11:00am Wilce Award Candidate
MOLECULAR AND ANATOMICAL ANALYSIS OF CRYPTIC SPECIES IDENTIFIED AS *RHODYMENIA* IN AUSTRALIA. **Brian McDonald** & Gary W. Saunders. Department of Biology, University of New Brunswick, Fredericton, N.B., E3B 6E1 Canada.

11:00 – 11:15am Wilce Award Candidate
A MOLECULAR GENETIC INVESTIGATION OF HETEROTROPHIC BACTERIA ASSOCIATED WITH *Aureococcus anophagefferens* (CCMP 1708). **Kristopher M. Baker**[1] and Jackie L. Collier[1]. [1]Marine Science Research Center, Stony Brook University, Stony Brook, NY 11794-5000

11:15 – 11:30am Wilce Award Candidate
PHYLOGENETIC AFFINITIES OF AUSTRALASIAN SPECIMENS OF *BATRACHOSPERMUM* (BATRACHOSPERMALES, RHODOPHYTA) INFERRED FROM MOLECULAR AND MORPHOLOGICAL DATA.
Sarah A. Stewart[1], Morgan L. Vis[1] and Timothy J. Entwisle[2]
[1]Department of Environmental and Plant Biology, Ohio University, Athens, OH 45701, USA. [2]Royal Botanic Gardens and Domain Trust, Mrs. Macquaries Road, Sydney, NSW 2000, Australia.

11:30 – 11:45am President's Award Candidate
AN INVESTIGATION OF THE FACTORS CONTROLLING THE GROWTH OF *GLOEOTRICHIA ECHINULATA* IN AN OLIGOTROPHIC LAKE.
Cayelan C. Carey[1], Kathleen C. Weathers[2], Kathryn L. Cottingham[1], and James F. Haney[3]. [1]Department of Biology, Dartmouth College, Hanover, New Hampshire, 03755, USA. [2]Institute of Ecosystem Studies, Millbrook, New York, 12545, USA. [3]Department of Zoology, University of New Hampshire, Durham, New Hampshire, 03824, USA.

12:00 – 1:30pm **Lunch**
1:30 – 1:45pm **Buffer**

SESSION 3 — Student and Professional Presentations
Moderator: Don Cheney

1:45 – 2:00pm President's Award Candidate
ADHESION STRUCTURES AND MECHANISMS IN THE DESMID, *PLEUROTAENIUM TRABECULA*: BIOFILM DYNAMICS.
Leah E. Elliott and David S. Domozych, Department of Biology, Skidmore College, Saratoga Springs, NY 12866

2:00 – 2:15pm President's Award Candidate
THERMAL STRESS INTENSIFIES PATHOGENIC EFFECTS OF *VIBRIO* BACTERIA ON CLADE SUBSPECIES OF *SYMBIODINIUM* IN REEF BUILDING CORALS.
J.M. Cervino1, **J.M. McClanahan2**, E.A . Lorence3, A. Perovic4, A. Skritnik5, T.J. Goreau6 , R.L. Hayes7

2:15 – 2:30pm Contributed Paper
THE NUCLEOMORPH GENOME OF THE CRYPTOMONAD *HEMISELMIS RUFESCENS* CCMP644 **Christopher E. Lane**[1], Catherine Kozera[2], Sharen Bowman[2], Bruce Curtis[2] and John M. Archibald[1]
[1]Department of Biochemistry and Molecular Biology, Dalhousie University, Halifax, NS, Canada [2] The Atlantic Genome Centre, Institute for Marine Biosciences, Halifax, NS, Canada

2:30 – 2:45pm Contributed Paper
WHOLE-LAKE INORGANIC ^{13}C ADDITIONS AND COMPARATIVE STUDIES REVEAL DIFFICULTIES IN PREDICTING ALGAL ISOTOPE SIGNATURES IN LAKES **Darren L. Bade**[1], Michael L. Pace[1], Jonathan J. Cole[1], and Stephen R. Carpenter[2] [1]Institute of Ecosystem Studies, Millbrook, NY, USA. [2]Center for Limnology, University of Wisconsin-Madison, USA.

2:45 – 3:00pm Contributed Paper
DNA BARCODING: A POWERFUL MOLECULAR TOOL TO UNCOVER DIVERSITY IN THE CANADIAN RED ALGAL FLORA
Line Le Gall and Gary W. Saunders,CEMAR, Dept of Biology, University of New Brunswick, Fredericton, NB, E3B 6E1, CANADA legall@unb.ca

3:00 – 3:15pm Contributed Paper

SESSION 4 **Poster Presentations**

3:15 – 5:00pm

5:00 – 6:00pm

Distinguished Speaker Presentation:
Dr. Graham J. C. Underwood,
Department of Biological Sciences, University of Essex, U.K.
with introduction by David Domozych

Life in Estuarine Biofilms: Small-Scale Complexicity and Large-Scale Importance

6:30 – 7:30pm **Pre-Banquet Mixer**

7:30 – 9:30pm **Banquet, Awards and Auction**

Sunday, April 23, 2006

9:00 – 9:30am **Coffee Break**

SESSION 5 **Mini-symposium: Life on a Surface: Algae and Biofilms**
Moderator: John Heimke

9:30 – 10:15am **D. Domozych,** DESMIDS: THE STORY OF BIOFILM EUKARYOTES OF NORTHERN WETLANDS. Dept of Biology, Skidmore College, Saratoga Springs, NY 12866, USA.

10:15 – 11:00am **R. Jan Stevenson,** BENTHIC ALGAE ARE EVERYWHERE, IMPORTANT. WE NEED TO KNOW MORE! Dept of Zoology, Center for Water Science, Michigan State University, East Lansing, Michigan 48864

11:00 – 11:45am **Z. Lewandowski,** STRUCTURE AND ACTIVITY OF BACTERIAL BIOFILMS, Center for Biofilm Engineering, Montana State University. Bozeman, MT 59717. USA

11:45am – 12:00 **Buffer**

12:00 – 1:00pm **Lunch and General Business Meeting**

1:00 – 1:15pm **Closing Remarks**

Judges:

President's Award (oral and poster presentations)
Chris Lane, Deb Robertson, Brian Wysor

Wilce Award (oral presentations)
Jack Holt, Alison Roberts, Darren Bade

Wilce Award (poster presentations)
Jim Foertch, Eric Roberts, Andy Ryder

POSTER PRESENTATION SUMMARY

Undergraduate (President's Category) Presentations

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IDENTIFICATION OF FLAGELLA CAP PROTEINS FROM *CHLAMYDOMONAS REINHARDTII* MUTANTS USING DIFFERENTIAL FLUORESCENT LABELING. Adel Abdo, Lisa Kortfelt, James Hampton, Mike Adams, Biology Dept, Eastern Connecticut State University, Willimantic, CT 06226

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MORPHOLOGICAL VARIABILITY WITHIN THE GENUS *STENOPTEROBIA* IN NORTH CAROLINA BAYS. Lee Camfield and Peter A. Siver. Department of Botany, Connecticut College, New London, CT, 06320, USA.

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SEARCH FOR CHAPERONE FLAGELLAR PROTEIN COMPLEXES DURING REFLAGELLATION IN *CHLAMYDOMONAS REINHARDTII*. James Hampton, Lisa Kortfelt, Adel Abdo, Mike Adams. , Biology Dept, Eastern Connecticut State University, Willimantic, CT 06226

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STRUCTURE AND DYNAMICS OF WETLAND BIOFILMS: *COSMARIUM* SPECIES AS MAJOR DESMID RESIDENTS. S. Hocine and David S. Domozych, Department of Biology, Skidmore College, Saratoga Springs, NY 12866, USA.

§§

THE EFFECT OF FLAGELLA LENGTH AND NUMBER ON THE KINETICS OF REFLAGELLATION IN *CHLAMYDOMONAS REINHARDTII*. Lisa Kortfelt, James Hampton, Adel Abdo, Mike Adams., Biology Dept, Eastern Connecticut State University, Willimantic, CT 06226

§§

ALTERATION OF CELL DIVISION PROCESSES IN THE DESMID, *PENIUM MARGARITACEUM*: LONG TERM EFFECTS OF BREFELDIN A AND CYTOCHALASINS. Rachel Lay and David S. Domozych, Department of Biology, Skidmore College, Saratoga Springs, NY 12866, USA.

§§

THE EFFECTS OF EXTENDED PERIODS OF ANOXIA ON *VAUCHERIA* PROPAGULES IN CONNECTICUT RIPARAN SEDIMENTS. Alison A. Parpal[1] and Craig W. Schneider[1].
[1]Department of Biology, Trinity College, 300 Summit Street, Hartford, CT 06106-3100, USA.

§§

PROPHAGE: HARMLESS HITCHHIKERS OR CYANOBACTERICIDAL MANIACS?
Alexander Ruck[1] and Raymond Kepner[2]
[1]Department of Microbiology, Marist College, Poughkeepsie, New York 12601, USA
[2]Department of Microbiology, Marist College, Poughkeepsie, New York 12601, USA

§§

ASYMMETRIC CELL WALL DEVELOPMENT IN "SYMMETRIC" DESMIDS.
Ashley A. Serfis and David S. Domozych, Department of Biology, Skidmore College, Saratoga Springs, NY 12866, USA

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IN-STREAM AND RIPARIAN CHARACTERIZATION OF FOUR NEW ZEALAND STREAM SEGMENTS CONTAINING *BATRACHOSPERMUM* SPECIES (RHODOPHYTA).
Katherine F Snyder, Kim J. Brown and Morgan L. Vis. Department of Environmental and Plant Biology, Ohio University, Athens, Ohio, 45701, USA

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THE GOLGI APPARATUS AND EPS SECRETORY MACHINERY OF THE DESMID, *NETRIUM INTERRUPTUM*. Anne L. Thomae and David S. Domozych, Department of Biology, Skidmore College, Saratoga Springs, New York, 12866, USA.

§§

THE EXTRACELLULAR MATRIX OF *COSMARIUM RENIFORME*, A UNIQUE DESMID FOUND IN ADIRONDACK WETLAND BIOFILMS. Richard Wilson, Christine Chang, Catherine E. Domozych and David S. Domozych, Department of Biology, Skidmore College, Saratoga Springs, NY 12866, USA.

Graduate (Wilce Category) Presentations

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WHOLE CELL IMMUNOLOCALIZATION OF THE HEPATOTOXIN MICROCYSTIN IN FRESHWATER CYANOBACTERIA. Heidi Langer Atkinson and Ellen Braun-Howland, University at Albany, School of Public Health, Albany, NY

§§

RESOLVING SPECIES DIVERSITY WITHIN THE ALGAL GENERA *CALLOPHYLLIS, PUGETIA AND EUTHORA* (KALLYMENIACEAE, RHODOPHYTA) USING MOLECULAR TOOLS. 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.

§§

UNRAVELING THE EVOLUTIONARY HISTORY OF GLUTAMINE SYNTHETASE II IN PHOTOSYNTHETIC LINEAGES WITH AN EMPHASIS ON RHODOPHYTES. Sohini Ghoshroy, Aurélien Tartar and Deborah L. Robertson. Department of Biology, Clark University, 950 Main Street, Worcester, MA01610

§§

PROPOSED USE OF THE RED MACROALGA *PORPHYRA* AS A PROTEIN AND FATTY ACID ADDITIVE IN FISH FEEDS. Timothy Hogan, Angela Silvestro, and Donald Cheney. Biology Department, Northeastern University, Huntington Avenue, Boston, MA, 02115, USA.

§§

MICROCYSTIN PRODUCTION IN LAKE ONTARIO. Hotto, A.M., Satchwell, M.F, and Boyer, G.L., SUNY College of Environmental Science and Forestry, 1 Forestry Dr., Syracuse, NY 13210

§§

CHEMICAL CHARACTERIZATION OF DESMID (ZYGNEMATALES) EXTRACELLULAR POLYMERIC SUBSTANCES. IMPLICATIONS FOR EUKARYOTIC EPS FUNCTION IN FRESHWATER BIOFILMS. Sarah N. Kiemle[1], David S. Domozych[2], and Michael R. Gretz[1]
[1]Department of Biological Sciences, Michigan Technological University, Houghton, MI 49931
[2]Department of Biology, Skidmore College, Saratoga Springs, NY 12866

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DESICCATION TOLERANCE IN *PORPHYRA* SPECIES. Yen-Chun Liu[1] and Donald Cheney[2]. [1]Northeastern University, 360 Huntington Avenue, Boston, MA, 02115, USA

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ASSESSING SPECIES RICHNESS AND PHYLOGENETIC RELATIONSHIPS OF THE BROWN ALGAL (PHAEOPHYCEAE) FLORA OF CANADA. Daniel McDevit and Gary Saunders. University of New Brunswick, Fredericton, NB, Canada.

§§

DISTRIBUTION AND RECRUITMENT ECOLOGY OF THE INVASIVE SEAWEED *CODIUM FRAGILE* SSP. *TOMENTOSOIDES* IN MASSACHUSETTS EELGRASS COMMUNITIES. Chris McHan and Donald P. Cheney. Biology Department, Northeastern University, Huntington Avenue, Boston, MA, 02115, USA.

§§

COMPARISON OF TWO ALGAL INDICES FOR USE IN BIOMONITORING OF SOUTHEASTERN OHIO STREAMS. Nathan J. Smucker[1], Emily K. Hollingsworth[1], Robert G. Verb[2] and Morgan L. Vis[1]. [1]Department of Environmental and Plant Biology, Ohio University, Athens, Ohio, 45701, USA.[2]Department of Biological & Allied Health Sciences, Ohio Northern University, Ada, Ohio, 45810, USA.

§§

A BASELINE STUDY USING PERIPHYTON COMMUNITIES IN SHAMOKIN CREEK, AN ACID MINE IMPACTED STREAM IN NORTHUMBERLAND COUNTY, PENNSYLVANIA Laura Wirpsza, Nicole Sweeney, and Jack R. Holt. Department of Biology, Susquehanna University, Selinsgrove, PA 17870, USA.

Professional Poster Presentations

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SEAWEED UPTAKE, CONCENTRATION & DETOXIFICATION OF MARINE POLLUTANTS. Don Cheney[1], Tavi Cruz-Uribe[2], Carrie Fraga[1], and Greg Rorrer[2] [1]Biology Dept., Northeastern University, Boston, MA;[2]Dept. Chem. Engineering, Oregon State University, Corvalis, OR.

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MICROBIOTA OF CRANBERRY BOGS: EASTERN MASSACHUSETTS, USA. Aimlee D. Laderman and Angela Allen, Marine Biological Laboratory, Woods Hole MA 02543.

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AN INVENTORY OF SCALED CHRYSOPHYTES FROM THE MID-ATLANTIC COASTAL PLAIN REGIONS OF MARYLAND AND NEW JERSEY, USA, AND THEIR RELATIONSHIPS TO ENVIRONMENTAL VARIABLES. Anne M. Lott and Peter A. Siver. Department of Botany, Connecticut College, New London, CT, 06320, USA.

§§

UTILIZING ALTERNATE WAVELENGTHS TO INCREASE LEVELS OF THE OMEGA-6 ARACHIDONIC ACID. Audrie-Jo L. M^{c}Conkey and Dr. Catherine T. Enright. Nova Scotia Agricultural College, Department of Plant and Animal Sciences, Truro, NS, B2N 5E3. Canada.

§§

A STUDY OF FRESHWATER SPECIES OF *SYNEDRA* EHRENBERG (BACILLARIOPHYTA) FROM NORTH AMERICAN STREAMS. Eduardo A. Morales, Sarah Hamsher, Erin Hagan & Daniel Mellott. Patrick Center for Environmental Research, The Academy of Natural Sciences, 1900 Benjamin Franklin Parkway, Philadelphia, PA 19130-1195, USA.

§§

A NEW FRESHWATER SPECIES OF *ENCYONOPSIS* KRAMMER (BACILLARIOPHYCEAE) FROM STREAMS IN THE SOUTHERN UNITED STATES. Eduardo A. Morales[1] & Kalina M. Manoylov[2]. [1]Patrick Center for Environmental Research, The Academy of Natural Sciences, 1900 Benjamin Franklin Parkway, Philadelphia, PA 19130-1195, USA. [2]Department of Zoology, Michigan State University, East Lansing, MI 48824, USA.

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ACHNANTHIDIUM SPECIES IN FLOWING WATERS OF THE APPALACHIAN MOUNTAINS. Karin C. Ponader[1] and Marina G. Potapova[2]. [1]Harvard University Herbaria, 22 Divinity Avenue, Cambridge, MA, 02138, USA. [2]Patrick Center for Environmental Research, The Academy of Natural Sciences, Philadelphia, PA, 19103, USA.

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MERHAB – LOWER GREAT LAKES - MONITORING FOR HARMFUL ALGAL BLOOMS IN OUR INLAND SEAS. Mike Satchwell, Amber Hotto, Xingye Yang, Elizabeth Konopko, Steven Ragonese, Karen Howard and Gregory Boyer. State University of New York, College of Environmental Science and Forestry, 1 Forestry Dr, 121 Jahn Lab, Syracuse, New York 13210

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DISCRIMINATING AMONG CRYPTIC SPECIES OF *PLOCAMIUM* IN THE SOUTHERN HEMISPHERE USING DNA BARCODING Gary W. Saunders and Tanya Moore
Centre for Environmental & Molecular Algal Research Department of Biology,
University of New Brunswick Fredericton, NB, Canada E3B 6E1

ABSTRACTS

(Alphabetical by First Author)

45th Northeast Algal Symposium

Marist College, Poughkeepsie, NY
April 21-23, 2006

IDENTIFICATION OF FLAGELLA CAP PROTEINS FROM *CHLAMYDOMONAS REINHARDTII* MUTANTS USING DIFFERENTIAL FLUORESCENT LABELING. Adel Abdo, Lisa Kortfelt, James Hampton, Mike Adams, Biology Dept, Eastern Connecticut State University, Willimantic, CT 06226

There eukaryotic flagellum contains over 300 different proteins, most of which are part of the repeating structure of the axoneme and therefore are present in thousands of copies. However, there is a unique structure at the tip of the flagellum, the cap, where the proteins will be present in single, or few copies. So far there are no reports as to which of the observed proteins might belong to this structure. In order to try and identify the cap proteins two flagella length mutants of *Chlamydomonas reinhardtii* mutants have been used. The long flagella mutant (CC-2287) has flagella three times the length of the short flagella mutant (CC-3663) so the ratio of cap:axonemal proteins should be three times greater in the short. Equal masses of both types are purified and the proteins are labeled with different Alexafluor fluorescent dyes. The short is labeled with a dye fluorescing at 488 nm and the long at 617nm. The two samples are mixed, run on SDS-PAGE, and then examined under UV light. Protein bands showing a pronounced shift to the 488nm end are potential cap proteins and will be examined further.

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WHOLE CELL IMMUNOLOCALIZATION OF THE HEPATOTOXIN MICROCYSTIN IN FRESHWATER CYANOBACTERIA. Heidi Langer Atkinson and Ellen Braun-Howland, University at Albany, School of Public Health, Albany, NY

The cyanobacterial hepatotoxin microcystin has been implicated in numerous poisonings and deaths of humans, livestock and domestic animals worldwide. Microcystin-producing cyanobacteria, such as *Microcystis* and *Anabaena*, are ubiquitous freshwater organisms easily identified by traditional microscopic methods. However, toxicity cannot be established on the basis of morphology. Therefore, additional time-consuming and costly laboratory tests must be performed once a potential toxin-producer is identified in a water supply or recreational water body. In order to enable a one-step approach to the detection of microcystin-producing cyanobacteria, we have initiated the development of a detection method for microcystin based on

the whole-cell immunolabeling of this small, seven-residue, peptide. Whole-cell immunolocalization will permit direct examination of toxin production in field samples and will be a useful tool for studies of toxin segregation within cyanobacterial colonies. To date, whole-cell immunolocalization of microcystin and the constitutively expressed RubisCO enzyme has been evaluated in laboratory cultures of known toxigenicity. Initial results suggest microcystin can be successfully labeled in toxic cyanobacterial species. Microcystin has been labeled in five toxic strains of *Microcystis aeruginosa*, while two non-toxic *M. aeruginosa* strains did not label. RubisCO labeling ensured cells were permeabilized, thus avoiding false negatives. All results were confirmed with the enzyme-linked immunosorbant assay for microcystin (ELISA). Clearly, for environmental samples, this method will combine the specificity of immunological labeling with the certainty of microscopic confirmation. Furthermore, *in situ* detection of toxic cells will supply water management and public health officials with another tool for detection and assessment of ecosystems prone to toxic bloom formation.

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WHOLE-LAKE INORGANIC ^{13}C ADDITIONS AND COMPARATIVE STUDIES REVEAL DIFFICULTIES IN PREDICTING ALGAL ISOTOPE SIGNATURES IN LAKES Darren L. Bade[1], Michael L. Pace[1], Jonathan J. Cole[1], and Stephen R. Carpenter[2]
[1]Institute of Ecosystem Studies, Millbrook, NY, USA. [2]Center for Limnology, University of Wisconsin-Madison, USA.

Determining carbon stable isotope values of algae is a crucial for studies ranging from food web interactions to paleolimnology However, algal carbon isotope signatures are variable within and among lakes because of difference in sources of inorganic carbon and differential isotope fractionation during photosynthesis. Several physiological models have been proposed to explain algal photosynthetic fractionation factors (ε_p). These models generally consider CO_2 concentration, growth rate, or cell morphometry, and have been supported by empirical evidence from laboratory cultures. Using comparative studies and several whole-lake inorganic ^{13}C additions, we explored methods of quantifying algal isotope signatures and tested the applicability of the physiological models to a broad range of lakes with mixed phytoplankton communities. In our largest comparative study, values of $\delta^{13}C$-POC (particulate organic carbon) ranged from -35.1‰ to -21.3‰. Results from the isotope addition demonstrated that algal isotopes signatures can differ substantially form $\delta^{13}C$-POC. Using several methods to estimate algal isotopic signatures, we found high variability in fractionation among lakes. There was no relationship between ε_p and one of the most important predictors in existing models, pCO_2. Measurements and a statistical model from the isotope addition revealed that algal frantionation was often lower (0 - 15‰) than expectations from prior student (ε_p > 20‰). Our work reveals the need for better methods for measuring algal isotope signatures.

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A MOLECULAR GENETIC INVESTIGATION OF HETEROTROPHIC BACTERIA ASSOCIATED WITH *AUREOCOCCUS ANOPHAGEFFERENS* (CCMP 1708). Kristopher M. Baker[1] and Jackie L. Collier[1]. [1]Marine Science Research Center, Stony Brook University, Stony Brook, NY 11794-5000

Aureococcus anophagefferens is a eukaryotic picophytoplankton that forms brown tides in the coastal waters of Long Island, NY, causing the cessation of feeding by bivalves. 17 of the 18 cultures of *Aureococcus* are not axenic, and the one that is axenic is difficult to maintain, suggesting that the prokaryotic contaminants are beneficial to *Aureococcus* growth. We have used universal primers to amplify a ~540 base-pair fragment of the *ureC* gene, encoding the enzyme urease, to examine the bacteria associated with cultures of *Aureococcus anophagefferens*. Total DNA was purified from two nonaxenic CCMP 1708 cultures (one obtained in 2000 from Horn Point Lab, MD, and the other obtained in 2004 from MSRC, NY) and PCR amplified. Thirty-four amplicons were screened and sequenced. Phylogenetic analysis revealed four separate clusters (each with 100% bootstrap support) of virtually identical bacterial sequences were found in both the 2000 and 2004 cultures (a total of 12 sequences). Two other clusters with weaker bootstrap support (56%) also contain an additional 6 sequences found in both cultures. The remaining 16 sequences were unique to one culture or the other. The similarity in bacterial complements is striking considering that these two cultures came from different sources nearly five years apart, and suggests there may be some specific relationship between *Aureococcus* and these bacteria. As expected, only *Aureococcus* sequences were recovered from an axenic *Aureococcus* culture (CCMP1984). Further work will be needed to correctly identify each bacterial species and how it interacts with the eukaryote.

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TEMPORAL DYNAMICS OF EPS PRODUCTION, LOSS AND COMPOSITION FOR BIOFILMS WITHIN THE COLNE ESTUARY, U.K. Brent Bellinger[1], Graham Underwood[2], and Michael Gretz[1].
[1]Department of Biological Sciences. Michigan Tech University, Houghton, MI 49931 USA
[2]Department of Biological Sciences. University of Essex, Colechester, CO4 3SQ U.K.

The development of surface biofilms during low tides is significant in terms of estuarine primary production and also for sediment stabilization. The composition and content of extracellular polymeric substances (EPS) are crucial for the cohesive properties exhibited by these surface biofilms and are primarily the result of diatom production. Hot water soluble (HW) carbohydrates, composed predominately of the intracellular storage polysaccharide chrysolaminarin, showed rapid accumulation during low tide periods (1.92 μg glucose equivalents μg Chl a^{-1} h^{-1}) with the relative abundance of glucose in the extract increasing during photosynthetic periods and declining during tidal cover or during darkness. Tracking carbon flow using ^{13}C-enrichment revealed that recently incorporated carbon was accumulated into the HW fraction rapidly and the label remained for days. Concentrations of labile colloidal carbohydrates, rich in glucose and galactose, were correlated with algal biomass. These carbohydrates were rapidly produced (2.03 μg glucose equivalents μg Chl a^{-1} h^{-1}) by biofilms

during low tide periods, but equally quickly lost (up to 60%) within 2 h of tidal cover. Short and long-term ^{13}C-enrichment of the colloidal fraction indicated this fraction not only served as an immediate carbon overflow, but was later produced from intracellular reserves. The more refractive hot bicarbonate soluble (HB) and hot alkali soluble (HA) polymers showed almost no net accumulation or loss of content over tidal cycles. Cycling of C through the HB and HA fractions was evident from isotopic enrichment, suggesting continuous production and rapid utilization, presumably by heterotrophic bacteria. Compositional analysis and isotopic labeling similarities between the colloidal and HB fraction indicate that degradation of the HB fraction could be contributing to the colloidal carbohydrate pool.

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MORPHOLOGICAL VARIABILITY WITHIN THE GENUS *STENOPTEROBIA* IN NORTH CAROLINA BAYS. Lee Camfield and Peter A. Siver. Department of Botany, Connecticut College, New London, CT, 06320, USA.

Stenopterobia Brébisson is a freshwater diatom genus contained within the Family Surirellaceae in the Phylum Bacillariophyta. Members of this genus have long slender frustules that are either straight or sigmoid-shaped in valve view and possess raphes that encircle the valve and are contained within a keel. During an investigation of Carolina bays situated along the Atlantic Coastal Plain of North Carolina, straight forms of *Stenopterobia* were found to be common, especially in the more acidic localities. The purpose of this study was to examine and characterize populations within this genus using light and scanning electron microscopy (SEM), and to more fully document the valve ultrastructure within this diatom genus. Based on initial results, there appear to be at least four different species, several of which may represent new taxa. The most common species in these habitats are *S. delicatissima* and *S. cuspidata*, however, the true ultrastructure of these species based on the literature and type material is not entirely clear. As a result, we are in the process of attempting to examine either type material or material from the type locality for each of these species with SEM. There apparently is no type material of *S. delicatissima* available for SEM observation. We therefore secured a sediment core from the type locality, Saco Pond in New Hampshire, and plan to examine specimens that date to approximately the point in time that Lewis made the original description of *S. delicatissima* in 1863. We have also secured a small amount of original material for *S. cuspidata* from the Hustedt collection in the hopes of examining the ultrastructure of this organism with SEM.

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AN INVESTIGATION OF THE FACTORS CONTROLLING THE GROWTH OF *GLOEOTRICHIA ECHINULATA* IN AN OLIGOTROPHIC LAKE. Cayelan C. Carey[1], Kathleen C. Weathers[2], Kathryn L. Cottingham[1], and James F. Haney[3].
[1]Department of Biology, Dartmouth College, Hanover, New Hampshire, 03755, USA.
[2]Institute of Ecosystem Studies, Millbrook, New York, 12545, USA.
[3]Department of Zoology, University of New Hampshire, Durham, New Hampshire, 03824, USA.

Gloeotrichia echinulata is an N-fixing cyanobacterium that is well-known for blooming in eutrophic lakes in northern Europe. Intriguingly, *G. echinulata* has recently started colonizing

oligotrophic lakes across the northeastern United States. *G. echinulata* is likely able to colonize an oligotrophic system because it depends on phosphorus in the lake sediment, not in the water column, to bloom. To quantify the temporal and spatial heterogeneity in *G. echinulata* abundance and to explore possible causes of bloom formation, we measured sediment total phosphorus and *G. echinulata* recruitment and surface abundance at 16 sites within an oligotrophic lake in New Hampshire from June-September 2005. *G. echinulata* recruited into the water column throughout the sampling period, with peak recruitment on 12-September. We found that the sediment had high levels of phosphorus in comparison to water column phosphorus concentrations, and that recruitment from shallow (but not deep) sediments substantially contributed to the surface population. *G. echinulata* recruitment did not appear to be related to weather. We also performed ELISA analyses on *G. echinulata* colonies harvested during bloom pulses and confirmed that *G. echinulata* contains the toxin microcystin. *G. echinulata*'s toxicity and ability to colonize low-nutrient systems that historically have had minimal algal populations indicate that this species may have important implications for oligotrophic lake management.

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SEAWEED UPTAKE, CONCENTRATION & DETOXIFICATION OF MARINE POLLUTANTS. Don Cheney[1], Tavi Cruz-Uribe[2], Carrie Fraga[1], and Greg Rorrer[2]
[1]Biology Dept., Northeastern University, Boston, MA;[2]Dept. Chem. Engineering, Oregon State University, Corvalis, OR.

According to a recent report by the EPA on the condition of our nation's coastline, 27% of the Northeast's estuaries have sediments contaminated with PCBs and PAHs at concentrations that can cause harmful ecological effects. Current methods for eliminating PAHs and PCBs from contaminated waters and sediments require sediment dredging and disposal. We are developing a new approach for the removal of such compounds - the use of "phycoremediating" seaweeds. In our initial work, we were able to demonstrate that seaweeds are capable of taking up and metabolizing the explosive compound 2,4,6-triitrotoluene (TNT). We examined two red seaweeds, *Porphyra yezoensis* and *Porteria hornemannii*, and one green *Acrosiphonia coalita*. At a biomass density of 1.2 g/L and an initial TNT conc. of 10 mg/L, both *Porteria hornemannii* and *Porphyra yezoensis* removed 100% of the TNT in just 72 hrs, and reduced TNT to 2-amino-4,6-dinitrotoluene (2-ADNT) and 4-amino-2,6-dinitrotoluene (4-ADNT). In current work, we are investigating the ability of seaweeds to take up and concentrate or metabolize phenanthrene, a three-ringed model compound for PAHs. As a first step, we are testing several seaweeds for their ability to tolerate phenanthrene at concentrations from 0.3 - 1.2 mg/L. So far, the red seaweed *Porteria hormemannii* and the green *Enteromorpha linza* have shown the greatest tolerance; ie. 0.9 mg/L phenathrene for 14 days. Preliminary uptake experiments suggest that *Porteria hormemannii* is able to take up and concentrate 88% of the phenathrene (0.9 mg/L starting conc.) in approximately 100 hrs. The fate of the phenathrene taken up is still being determined.This research was supported by grants from the Office of Naval Research Biotechnology and Environmental Research Program and the USDA Aquaculture Program.

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RESOLVING SPECIES DIVERSITY WITHIN THE ALGAL GENERA *CALLOPHYLLIS, PUGETIA AND EUTHORA* (KALLYMENIACEAE, RHODOPHYTA) USING MOLECULAR TOOLS. 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.

Traditional taxonomy of the red algae (Rhodophyta) has emphasized morphological and anatomical traits. Whereas this approach has generally worked well for resolving species within many genera, taxonomy of the genus *Callophyllis* (Kallymeniaceae) in the Northeast Pacific has proved challenging due to high morphological variability. In addition, members of the genera *Pugetia* (*Pugetia firma* and *P.* chilensis; Norris, 1957) and *Euthora* have been variously included in *Callophyllis* (Hooper and South, 1974). A previous study by Harper and Saunders using nuclear large-subunit ribosomal DNA (LSU) successfully established the generic limits between *Callophyllis*, *Pugetia* and *Euthora*. That study both supported *Euthora* as a viable genus and re-established *P. firma* and *P. chilensis* as members of *Pugetia*, but left unresolved the phylogenetic relationships and diversity of species remaining in *Callophyllis*. The objectives of the current study are to: 1) determine unequivocally the relationships and diversity of species in the genera *Callophyllis*, *Pugetia* and *Euthora* in British Columbia, Canada, using the DNA Barcode marker as an assessment tool; 2) determine which morphological and/or anatomical characteristics are taxonomically viable at the species level in these genera; and 3) resolve the phylogenetic affinities of Kallymeniaceae found in B.C. relative to other genera of this family from other geographical regions using nuclear large-subunit ribosomal DNA (LSU).

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RESURRECTING THE GENUS *GRANIA* FOR *GRANIA EFFLORESCENS* Susan L. Clayden and Gary W. Saunders. Centre for Environmental and Molecular Algal Research, Department of Biology, University of New Brunswick, Fredericton, N.B., E3B 6E1, Canada

Grania efflorescens is a diminutive marine red alga currently classified in the order Acrochaetiales. The phylogenetic relationship of this alga to other acrochaetes remains in question. Its generic assignment has undergone several changes since it was first described by Agardh as *Callithamnion efflorescens* in 1851. In the most recent NEAS key it is listed as *Audouinella efflorescens*, whereas in "AlgaeBase" it is recorded as *Acrochaetium efflorescens*. It is distinguished by its pale red filaments of long narrow cells with spiral shaped plastids, which by current taxonomic thinking excludes it from both the previous genera and is reminiscent of some species in the related red algal order Colaconematales. The triphasic life history of *Grania* is found in some members of both the Acrochaetiales and Colaconematales. To our knowledge there have been no molecular sequences published for this taxon. We present a phylogeny based on large subunit ribosomal DNA (LSU) sequences clearly resolving *G. efflorescens* within the Acrochaetiales. Within the family Acrochaetiaceae it has a unique molecular signature suggesting it differs from and requires separate generic status from other acrochaetes. We propose reinstatement of the available genus *Grania*.

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DESMIDS: THE STORY OF BIOFILM EUKARYOTES OF NORTHERN WETLANDS. David S. Domozych, Department of Biology, Skidmore College, Saratoga Springs, NY 12866, USA.

Desmids (Zygnematophyceae, Streptophyta) are common and often dominant photosynthetic eukaryotes of planktonic and biofilm communities of inland wetlands of the Northern Hemisphere. In biofilms, desmids are often distinguished by their secretion of prodigious amounts of extracellular polymeric substances (EPS). Desmids and their EPS sheaths often create focal collection zones for other microbes in the biofilm community structure. Surprisingly though, very little is known about the structure and maintenance of desmid-associated or –dominant biofilms, the "behavior" of desmids during entry into the biofilm realm, the biochemistry and the role of EPS and the cell biology of biofilm-related events. Over the past 15 years, my laboratory has focused upon desmids and more specifically, the dynamics of desmids in biofilm communities. Desmid EPS consists of complex and poorly understood polysaccharides often rich in fucose, xylose and glucuronic acid and with varying degrees of sulfation. The secretion of the EPS is carefully regulated and is responsible not only for substrate adhesion and cell ensheathment but for gliding motions as well. Desmids have at least two distinct mechanisms for initial adhesion to a substrate: one that entails a secretion-based "glue" and a second that encompasses a series of fibers emanating from the pore organs. In desmids like *Penium margaritaceum* and *Closterium acerosum*, the secretion of adhesion molecules is prevented by pretreatment of cells with calmodulin antagonists, phosphatidyl inositol 3-kinase inhibitors, sodium ionophores, brefeldin A and various membrane ion channel disrupting agents. These agents affect the EPS synthesis machinery of the cell, the delivery mechanism of vesicles to specific loci on the cell surface and the ultimate release of EPS to the extracellular matrix domain including cell wall pore organs or channels. The EPS secretory machinery encompasses the coordinated interaction of an elaborate Golgi Apparatus and associated vesicles, an actin-mediated cytoplasmic streaming network and specific fusion zones at the plasma membrane. Specific environmental triggers initiate a signal cascade that leads to EPS secretion at specific points along the cell wall surface. In many desmids, EPS secretion involved in gliding may also entail polar vacuoles that are filled with barium- or calcium-salts and are juxtaposed to a "spitzenkorper"-like region. The current state of knowledge and future directions for biofilm desmid research will be presented.

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ADHESION STRUCTURES AND MECHANISMS IN THE DESMID, *PLEUROTAENIUM TRABECULA*: BIOFILM DYNAMICS. Leah E. Elliott and David S. Domozych, Department of Biology, Skidmore College, Saratoga Springs, NY 12866

Pleurotaenium trabecula (Zygnematophyceae, Streptophyta) is one of the most common desmids found in biofilms of shallow wetlands of the Adirondack region of New York. After leaving the planktonic phase and adhering to a substrate, the alga often lifts up and remains attached via one end of the cell to its substrate. The adhesion mechanism entails the use of biofilm adhesion centers (BACs) that include the pore complexes that traverse the cell wall. In

this study, we explore the structure and putative mechanisms associated with BACs during *Pleurotaenium*'s entry into the biofilm condition. A BAC consists of a series of stiff 800 nm-long fibrils that emanate from the outer opening of the wall pore. BACs are found only on the secondary wall, label with ConA and form a loose network on the cell surface. The BAC fibrils intermesh with the cell's EPS sheath and remain upon the cell wall after removal of the EPS by physical methods. BACs can be removed from the cell wall by sonication or by treatment with mild bases (e.g. 10 μM NaOH or KOH). Adhesion of the cell to substrates can be prevented by pre-treatment of cells in base but not by chelators or mild acids. There is no preference in which semicell remains attached during post-adhesion events. Based on these studies, it is postulated that BACs are necessary for unspecific but firm adhesion of the cell to the substrate. Possible mechanisms for *Pleurotaenium*'s adhesion dynamics within biofilms will be presented.

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DNA BARCODING: A POWERFUL MOLECULAR TOOL TO UNCOVER DIVERSITY IN THE CANADIAN RED ALGAL FLORA. Line Le Gall and Gary W. Saunders, CEMAR, Dept of Biology, University of New Brunswick, Fredericton, NB, E3B 6E1, CANADA legall@unb.ca

The 'DNA barcode' is a short genetic marker developed with the objective of distinguishing organisms at and above the species level. The 5' end of the mitochondrial gene *cox1* (cytochrome oxidase subunit I) was selected as the preferred marker for researchers working on animals, and this system has also proven useful for reliable and rapid identification of red algae – these at times notoriously difficult to identify based on morphological characters. As partners in the Canadian Barcode of Life Network, we are actively developing a DNA barcode database for the red macroalgae. We provide preliminary results regarding diversity of the Phyllophoraceae (Gigartinales, Rhodophyta) in Canadian waters. We have thus far analyzed ca. 50 individuals from the Atlantic and Pacific coasts resolving ten species based on the Barcode analyses, and subsequent morphological/anatomical observations. We have also included these species in a large-subunit ribosomal DNA phylogeny to resolve their relationships relative to one another and other members of this family.

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UNRAVELING THE EVOLUTIONARY HISTORY OF GLUTAMINE SYNTHETASE II IN PHOTOSYNTHETIC LINEAGES WITH AN EMPHASIS ON RHODOPHYTES. Sohini Ghoshroy, Aurélien Tartar and Deborah L. Robertson. Department of Biology, Clark University, 950 Main Street, Worcester, MA01610.

Glutamine synthetase (GS), an essential enzyme for ammonium assimilation, is found in all organisms. In most photosynthetic eukaryotes, a minimum of two nuclear encoded isoenzymes are present and function in either the cytosol or chloroplast. GSII has been broadly characterized in vascular plants but sequences from other photosynthetic eukaryotes are limited. Rhodophytes occupy a central role in the endosymbiotic evolution of plastids, having acquired a plastid via primary endosymbiosis and being donor of plastids to the chromalveolate super group. We examined the phylogenetic relationship of GSII genes from rhodophytes emphasizing taxon sampling from basal rhodophytes, which have been identified as the putative donor of the

chromalveolate plastid. Five GSII sequences from rhodophytes were generated by PCR amplification. Maximum parsimony and Bayesian analyses consistently yielded trees in which rhodophytes were not monophyletic. Members of the Bangiales (*Porphyra*) and Compsopogonales (*Compsopogon*) formed one clade, while the Cyanidiales (*Cyanidioschyzon* and *Galdieria*), Porphyridiales 1 (*Rhodella* and *Dixoniella*), Porphyridiales 3 (*Flintiella*) and Gelidiales (*Gelidium*) formed a separate clade. The branching pattern within this second clade was similar to phylogenies of other nuclear and plastid encoded genes. Single copies of GSII were obtained from the majority of the rhodophytes. However two GSII sequences (74% identical) were obtained from *Dixoniella grisea* and appear to have arisen from a recent duplication event. The presence of two distinct rhodophyte GSII clades suggests an early duplication event, preceding the divergence of the rhodophytes and the green algal lineages. Analyses of complete ORF's of GSII from *Cyanidioschyzon*, *Galdieria* and *Gelidium* suggest these proteins are localized in cytoplasm. The partial GSII sequences obtained from *Porphyra*, *Compsopogon*, *Dixoniella*, *Flintiella* and *Rhodella* represent approximately 40-80% of the ORF but do not include the N-terminal regions of sequences for determination of cellular localization. Our immediate goal is to obtain complete sequences to identify their cellular functions and increase taxon sampling within the rhodophytes. This will provide a better understanding of gene duplication events of GS in the rhodophytes which eventually may shed light into the secondary endosymbiotic event.

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SEARCH FOR CHAPERONE FLAGELLAR PROTEIN COMPLEXES DURING REFLAGELLATION IN *CHLAMYDOMONAS REINHARDTII*. James Hampton, Lisa Kortfelt, Adel Abdo, Mike Adams. , Biology Dept, Eastern Connecticut State University, Willimantic, CT 06226

All organisms produce a variety of 'chaperone' proteins, whose functions include aiding in the folding and transport of newly-synthesized proteins. If the flagella are removed by pH shock, *Chlamydomonas* can regrow new ones in approximately 90 minutes. We have previously shown that reflagellation also results in an increased synthesis of chaperone proteins, presumably to cope with the added demand of transporting all of the proteins into the new flagella. In order to examine this aspect more closely, we are looking at our ability to identify new protein production in both heatshocked and deflagellated cells. Control and experimental cell samples are lysed by repeated freeze-thaw cycles and the extracted proteins are labeled with different Alexafluor fluorescent dyes. The control proteins are labeled with a dye fluorescing at 488 nm and the experimental at 617nm. The two samples are mixed, run on SDS-PAGE, and then examined under UV light. Protein bands showing a pronounced shift to the 617nm end are potentially proteins synthesized in response to the experimental conditions. We plan to refine the search by immunoprecipitating chaperone:protein complexes in control and regenerating cells to look for the increased presence of flagella-specific proteins in the latter.

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STRUCTURE AND DYNAMICS OF WETLAND BIOFILMS: *COSMARIUM* SPECIES AS MAJOR DESMID RESIDENTS. S. Hocine and David S. Domozych, Department of Biology, Skidmore College, Saratoga Springs, NY 12866, USA.

Over a three year survey of biofilm-based eukaryotes of a southern Adirondack (New York, USA) beaver-engineered wetland system, various *Cosmarium* species were found to be common and in many cases, the dominant algae. One isolate, *Cosmarium* sp. ID# 101 was chosen as a tool organism in our laboratory in the study of biofilm desmids and their "behavior" within the biofilm complex. *C. 101* produced an extensive extracellular polymeric substance (EPS) that included a polysaccharide rich in fucose and acidic sugars. This rapidly-growing desmid produced as much 1 μg of EPS per cell in 4 week old axenic laboratory cultures. EPS secretion from the cell was monitored with the use of fluorescent-lectin and -antibody conjugates. EPS secretion was localized at a series of pores that formed a regular network upon the cell wall. EPS secretion was important in both adhesion to substrates and subsequent gliding movements. Adhesion could be inhibited by pretreatment of cells in weak base or by calmodulin antagonists. Weak base extraction removed a series of stiff fibrils emanating from the wall pore surface. These fibrils represented a "velcro-like" mechanism for attaching to artificial substrates. Light-stimulated gliding movements in *C. 101* were somewhat different that that described for other desmids in that they were periodic and occurred only over short distances. Mechanisms describing EPS secretion in *Cosmarium* species will be presented.

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PROPOSED USE OF THE RED MACROALGA *PORPHYRA* AS A PROTEIN AND FATTY ACID ADDITIVE IN FISH FEEDS. Timothy Hogan, Angela Silvestro, and Donald Cheney. Biology Department, Northeastern University, Huntington Avenue, Boston, MA, 02115, USA.

The need to expand aquaculture production has increased significantly as natural stocks decline due to overfishing, Conservative estimates predict that by 2050 half of the fish consumed will be a product of aquaculture. Since manufactured feeds can account for up to 60% of the operating costs, it is clear that alternatives to the expensive feed ingredients need to be identified. The expensive ingredients, the protein and lipid components, are typically supplied by fish meal and fish oil, considered finite resources. We propose that the red macroalga *Porphyra* represents an excellent and sustainable alternative to typical protein and fatty acid ingredients in fish feeds. In addition to *Porphyra's* high protein content (44-48%), it also has a high content of polyunsaturated fatty acids (PUFAs) and highly unsaturated fatty acids (HUFAs) necessary for normal fish growth. Previous work done at the Seaweed Biotechnology Laboratory at Northeastern University indicates that exposure to low temperature for one week increases total PUFA content. Further preliminary results indicate that this increase in fatty acid content may take place in an even shorter period of time, 24 hours. Ongoing research into the mechanism controlling this change in fatty acid content includes further cold exposure studies as well as expression studies of desaturase genes to better understand this phenomenon at a molecular level. Armed with the knowledge of its high protein content and the ability to rapidly increase existing high levels of nutritionally important fatty acids, the potential of *Porphyra* as a sustainable alternative ingredient in fish feeds seems strong.

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VALORIZATION OF MANURE USING COMBINED ANAEROBIC DIGESTION / ALGAL TAG PRODUCTION. Rhonda Schmidt[1], Alexandra Holland[2], Nam Nguyen[3].
[1]Forest Resources, [2]Chemical Engineering, [3]Material Science and Engineering, University of Washington, Seattle, 98195, USA

Changes in farm animal densities in the state of Washington are producing a concentrated manure surplus, which exceeds the amount usable on local agricultural lands as fertilizer. Simultaneously, persistent increases in the price of petroleum fuels are rendering bioenergy production on the farm an increasingly attractive alternative.
In the context of the NSF MCCE IGERT (Multinational Collaboration on Challenges to the Environment, Integrative Graduate Education and Research Traineeship) at the University of Washington, our interdisciplinary team is looking at the integration of Anaerobic Digestion (AD), biofuel (as Tri-Acyl-Glycerol or TAG) and fertilizer production on the farm. The process concept, based on existing operations (AD) and pilot projects (algae culture in airlift reactors), aims at providing additional revenue to the farm while granting environmental benefits.
Preliminary experiments will assess the robustness of various algal strains documented in the 1998 NREL report: "A Look Back at the U.S. Department of Energy's Aquatic Species Program: Biodiesel from Algae" when given AD effluent as nutrient source. In parallel, as developed in the NREL report, algae populations will be isolated from farm environments, fed on AD effluent, and sorted for fatty acid accumulation by flow cytometry: first, chlorophyll auto-fluorescence will be used to separate heterotrophic bacteria and grazers. Second, Nile Red fluorescence (fatty acid specific dye) to chlorophyll ratio will be used to assess higer lipid contents. The sorted cells will be cultured and tested for lipid production rates.

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MICROCYSTIN PRODUCTION IN LAKE ONTARIO. Hotto, A.M., Satchwell, M.F, and Boyer, G.L., SUNY College of Environmental Science and Forestry, 1 Forestry Dr., Syracuse, NY 13210

Outbreaks of toxic cyanobacteria have been increasing on the Great Lakes. Cyanobacteria in these toxic blooms can produce a family of hepatotoxic peptides, called microcystins. There are two hypotheses surrounding the origin of microcystin production in Lake Ontario: (1) it originates offshore and is circulated throughout the lake via water currents and (2) it is created in eutrophic embayments and is transported to the main lake. To investigate the existence and origin of microcystin production in Lake Ontario, samples were collected in embayments along the southern and eastern shores and from open water. Molecular analysis by PCR revealed the potential for microcystin production, which was then compared to actual microcystin production determined via the biochemical protein phosphatase inhibition assay (PPIA). This information was then used to evaluate the relative contribution of embayments vs. offshore regions to microcystin production in Lake Ontario.

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CHEMICAL CHARACTERIZATION OF DESMID (ZYGNEMATALES) EXTRACELLULAR POLYMERIC SUBSTANCES. IMPLICATIONS FOR EUKARYOTIC EPS FUNCTION IN FRESHWATER BIOFILMS. Sarah N. Kiemle[1], David S. Domozych[2], and Michael R. Gretz[1]
[1]Department of Biological Sciences, Michigan Technological University, Houghton, MI 49931
[2]Department of Biology, Skidmore College, Saratoga Springs, NY 12866

Desmids represent a group of advanced green algae that are often residents of freshwater biofilms. Most biofilm-associated desmids secrete large amounts of extracellular polymeric substances (EPS) that function in adhesion, post-adhesion movements and ensheathment within the biofilm complex. The EPS of desmids is poorly characterized and it was the goal of this project to initiate a comprehensive biochemical analysis of EPS macromolecules of the following desmids isolated from biofilms: *Penium margaritaceum*, *Pleurotaenium trabecula*, *Cosmarium* sp., *Tetmemorus brebissonii* and *Netrium oblongum*. EPS was characterized by monosaccharide and methylation analysis, and components localized with lectin-fluorescein isothiocyanate. Polysaccharides were the major components (30-42%) of the desmid EPS examined with xylosyl and fucosyl residues predominate for all desmid species with the exception of T. *brebissonii* and *N. oblongum*. *P. margaritaceum* was found to contain glycosyl linkages/substitutions corresponding to t-Xyl_p and 3,4-GlcA residues. In *Cosmarium sp.*, 2-Fuc, 4-Fuc, t-Fuc, $4_p/5_f$-Xyl were identified and lectin labeling revealed α-2-L-Fuc (UEA I) and C-acetyl-α-D-galactosaminyl (HPA). *Pl. trabecula* EPS polysaccharide residues include 3,4-Fuc, 3-Fuc, t-Fuc, 2-Xyl_f, t-Xyl_p, 4-GalA and the polymer was sulfated (10% w/w). Fuc and Gal were the major sugars in *T. brebissonii* EPS with glycosyl linkages of 3,4-Fuc t-Fuc, and t-Xyl_P and significant ester sulfate (15% w/w). The major sugars present in *N.oblongum* EPS were Gal and Xyl, major glycosyl linkages were 3-Fuc, 6-Gal, and 4-Glc, with labeling of C-acetyl-α-D-galactosaminyl (HPA), α-Man (ConA), α-Glc (ConA), and WGA (N-acetyl-β-D-Glc and D-acetyl-β-D-glucsamine oligomers) evidenced with FITC conjugates. The importance of desmid EPS in freshwater biofilms has been underestimated and preliminary chemical analysis has shown potential roles of EPS in water retention (related to the hydrophilic nature of the polymers), and metal-binding (anionic side groups). We are just beginning to understand the structure and function of desmid EPS, its secretory and regulatory pathways, its role in desmid behavior in biofilms, and its significance in biofilm heterotrophy.

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DESICCATION EFFECTS ON GROWTH RATE AND NITRATE UPTAKE OF *PORPHYRA* SPP. IN RELATION TO TIDAL ELEVATION. Jang K. Kim[1,3], George P. Kraemer[2], and Charles Yarish[1] [1]Department of Ecology & Evolutionary Biology, University of Connecticut, Stamford, CT, 06901, USA.[2] Departments of Biology & Environmental Studies, Purchase College, State University of New York, Purchase, NY, 10577, USA.[3]Department of Ecology & Evolutionary Biology, University of Connecticut, Groton, CT, 06340, USA.

Intertidal zonation is the distinctive pattern of an organism's vertical distribution. Organisms in the intertidal habitat are exposed daily by low tides. During exposure, sessile organisms, such as seaweeds, experience stresses including nutrient limitation, extremes of light intensity, ultraviolet light, temperature and desiccation. The ability to acquire essential resources following emersion may be a critical factor controlling vertical distribution pattern of seaweeds. The objective of this study was to determine whether *Porphyra* species at different vertical elevations on the shore respond differently to the desiccation stress, in terms of growth rate and nitrate uptake. *Porphyra umbilicalis* occurs throughout the eulittoral zone, whereas *Porphyra amplissima* occurs in the low eulittoral and sublittoral zones and is seldom exposed to air. Both *Porphyra* species were cultivated at 100–150 $\mu molm^{-2}s^{-1}$ light intensities, 500 μM nitrate concentration and 10 °C (*P. umbilicalis*) and 15 °C (*P. amplissima*) for three weeks (*P. umbilicalis*) and three days (*P. amplissima*). Photoperiod was 12:12h L:D. Samples were exposed daily to air for 0, 30 min, 30-50% water loss, and 2 hrs, 90% water loss, 4 hrs after light exposure. Desiccation was more stressful to the sublittoral species, *P. amplissima,* than to the eulittoral species, *P. umbilicalis*. When the tissues were exposed for 2 hrs daily, *P. amplissima* lost weight and pigments, while the growth rate of *P. umbilicalis* was approximately 70% of that of continually submerged blades. For 30 min exposure, the growth rates were about 77% (*P. umbilicalis*) and 50% (*P. amplissima*) of that of continually submerged blades. Nitrate uptake rate of sublittoral *P. amplissima* was only 73% (30-50% water loss) and 62% (90% water loss) of that of continually submerged tissues. Nitrate uptake rates of *P. umbilicalis* were greater than 90% of uptake by continually submerged tissues in both desiccation treatments. These results suggest that species in the eulittoral zone, which have longer exposure times, may have higher time-use efficiency than the sublittoral species in terms of nitrate uptake. There may be a correlation between nitrate uptake and observed vertical distribution patterns.

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THE EFFECT OF FLAGELLA LENGTH AND NUMBER ON THE KINETICS OF REFLAGELLATION IN *CHLAMYDOMONAS REINHARDTII.* Lisa Kortfelt, James Hampton, Adel Abdo, Mike Adams., Biology Dept, Eastern Connecticut State University, Willimantic, CT 06226

The eukaryotic flagellum is a complex structure, containing over 300 different proteins. Although flagella normally stay at fixed length, they are in dynamic equilibrium, with new proteins being added at the tip and old ones being removed at the base. If the flagella are removed, *Chlamydomonas* can regenerate them within 90-120 minutes, with the rate of regrowth showing an asymptotic curve. The kinetics of this process are likely to be controlled by three factors, the concentration of flagellar proteins in the cytoplasm, the rate at which they can be transported to the tip and the rate at which proteins are being removed from the base. It is possible to alter the ratio of pool size:flagella by looking at the *uni* mutant since, although this has a single flagellum, we have shown it contains a normal pool of proteins. Likewise, we can observe the effect of changing the time needed to transport proteins to the tip by using mutants that contain abnormally long or short flagella.

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MOLECULAR ANALYSIS OF SPECIES LIMITS OF THE BROWN ALGAL GENUS *FUCUS* IN THE NORTHEAST PACIFIC. Hana Kucera and Gary W. Saunders. Centre for Environmental & Molecular Algal Research, Department of Biology, University of New Brunswick, Fredericton, New Brunswick, E3B 6E1, Canada.

Two species of the genus *Fucus* are recognized in the Northeast Pacific: *F. gardneri* and *F. spiralis*. In addition, there are reports of a *F. cottonii*-like morph. *Fucus gardneri* and *F. spiralis* are found growing in a continuous band in the rocky intertidal, the former reported to inhabit the mid, and the latter the upper intertidal. The zone between the two extremes is inhabited by plants that variously display morphological characteristics of both species. This intermediate zone may be the result of phenotypic plasticity of one or both species, hybridization between the two species, or some combination of these events. Alternatively, the individuals may be morphological expressions of a single species at varying heights in the intertidal.

In order to test these hypotheses, we sequenced the DNA barcode marker (ca.600 bp of the mitochondrial cytochrome oxidase I gene) and the nuclear internal transcribed spacer (ITS) to evaluate species limits for the genus *Fucus* in Canada. We then looked in detail at *Fucus* in the Northeast Pacific. We used a small, variable fragment of the ITS to evaluate whether hybridization was occurring between *F. gardneri* and *F. spiralis* and to genetically identify plants of intermediate morphology. Both DNA barcode and ITS results showed *F. spiralis* and *F. gardneri* to be distinct species. Intermediate morphologies were primarily *F. gardneri* and there was no evidence of hybridization. We also found that individuals of *F. cottonii* morphology were assignable to *F. gardneri*.

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MICROBIOTA OF CRANBERRY BOGS: EASTERN MASSACHUSETTS, USA. Aimlee D. Laderman and Angela Allen, Marine Biological Laboratory, Woods Hole MA 02543.

Water, submerged vegetation and moist emergent surfaces of natural, renaturalized, and cultivated cranberry bogs were sampled in summer and fall 2005. Burrage Pond WMA (6 sites in Halifax/Hanson), east ditch of Lower Coonamessett Bog (Falmouth), and Windswept Bog and Tawpawshaw Bog (Nantucket Island) were studied. A portion of each sample was preserved in each of 3 ways: in 70% ethanol, in Lugol's Iodine, and dried in standard herbarium fashion. Living collections were stored under natural daylight at 62-75 F, examined microscopically (phase contrast inverted scope) to 400x, photographed digitally, images transferred and recorded digitally and prepared for inclusion in the digital herbarium of MBL/WHOI, Woods Hole, MA . The survey is organized in a Filemaker Pro database and interactive website, linked to the global protistan database and website "micro*scope" at the MBL/WHOI Library. Multicellular zooplankton (e.g., rotifers, annelids, copepods), protozoa with and without visible pigment, and unicellular and filamentous chlorophytes were abundant. Green filamentous Zygnemataceae (e.g., *Mougeotia, Spirogyra*) dominated many sites; diverse populations of filamentous and unicellular Desmidiaceae were found. A dark red dense bloom of *Euglena sanguinea* covered one site.

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THE NUCLEOMORPH GENOME OF THE CRYPTOMONAD *HEMISELMIS RUFESCENS* CCMP644. Christopher E. Lane[1], Catherine Kozera[2], Sharen Bowman[2], Bruce Curtis[2] and John M. Archibald[1] [1]Department of Biochemistry and Molecular Biology, Dalhousie University, Halifax, NS, Canada [2] The Atlantic Genome Centre, Institute for Marine Biosciences, Halifax, NS, Canada

The cryptomonads are an enigmatic group of microalgae that have acquired photosynthesis via secondary endosymbiosis, an ancient event that has likely occurred three times during evolutionary history. Secondary endosymbiosis occurs when a phagotrophic eukaryote engulfs a photosynthetic eukaryote, but retains the organism, and eventually enslaves it as a plastid (chloroplast), rather than digest it. This process has given rise to an enormous diversity of algal lineages, but cryptomonads are unusual in that they retain the nucleus of their eukaryotic endosymbiont in a highly reduced form, called a nucleomorph. The 551 Kb nucleomorph genome of the cryptomonad *Guillardia theta* has already been sequenced and is incredibly gene dense (~1 gene/Kb). Little is known about the nucleomorph in other cryptomonads but in those investigated thus far, the nucleomorph genome is spread across three chromosomes of varying size, each with sub-telomeric ribosomal DNA (rDNA) cistrons. We have recently found exceptions to this genomic arrangement in the genus *Hemiselmis*, where the middle-sized nucleomorph chromosome has no rDNA locus. To elucidate the structure and content of the *Hemiselmis rufescens* nucleomorph we have sequenced its 580 Kb genome. Using the *G. theta* nucleomorph genome as a comparison we find that the general properties expected in nucleomorphs (high A/T content and gene density) hold true, but there are some surprising differences. The genes of the two nucleomorphs exist in short blocks of synteny (~2-4Kb), but recombination has scrambled the gene order of each *H. rufescens* chromosome, relative to *G. theta*. Additionally, intergenic spacers in *H. rufescens* are approximately double those of *G. theta*, providing a possible explanation for the observed size differences among nucleomorph genomes. The implications of these new data regarding nucleomorph evolution and the process of secondary endosymbiosis will be discussed.

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ALTERATION OF CELL DIVISION PROCESSES IN THE DESMID, *PENIUM MARGARITACEUM*: LONG TERM EFFECTS OF BREFELDIN A AND CYTOCHALASINS. Rachel Lay and David S. Domozych, Department of Biology, Skidmore College, Saratoga Springs, NY 12866, USA.

Desmids (Zygnematophyceae, Streptophyta) possess a unique morphology that entails two "identical" semicells positioned around a central isthmus zone. Competent cell division leading to the expression of this unique morphology entails a precisely-coordinated series of complex events that include components of the endomembrane system, cytoskeletal/cytomotile network and extracellular matrix. In this study, we demonstrate that alteration of the actin network of the cell by long term treatment with cytochalasins, or the Golgi Apparatus (GA) and secretory mechanism with brefeldin A, alter the normal cell division process. Resultant division products consist of regular chains of cells attached end-to-end. This "filamentous" morphotype is

reversible upon removal of inhibitors. High resolution imaging of the cell wall surface by variable pressure scanning electron microscopy reveals significant changes to wall architecture in treated cells. This is supplemented by an analysis of labeling of specific cell wall macromolecules with the monoclonal antibodies, JIM5, JIM7 and LM7 along with the lectin, ConA. Ultrastructural analysis reveals significant structural alteration to the GA and vesicle production in brefeldin A-treated cells and distinct destabilization of the peripheral actin network in cells treated with cytochalasins. We propose that the alteration of post-cytokinetic secretory competency results in the formation of "filamentous" morphotypes.

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STRUCTURE AND ACTIVITY OF BACTERIAL BIOFILMS Zbigniew Lewandowski, Center for Biofilm Engineering, Montana State University. Bozeman, MT 59717. USA

Biofilms are studied in such disparate areas as bioremediation of toxic compounds, oral hygiene, souring of oil formations, microbially influenced corrosion, wastewater treatment, and infection of implantable prosthetic devices. Two types of biofilm-related research activities emerge from this complex picture: research devoted to understanding fundamental biofilm processes and research devoted to biofilm technology. The leading discipline in the biofilm research devoted to understanding fundamentals of biofilm processes is microbial ecology where biofilms are seen as highly organized structures of microorganisms having qualities comparable to tissues. Microorganisms in biofilms are not randomly distributed. Instead, they form communities in which various microbial species have various functions, and they communicate with each other using chemical signals. This internal organization of bacterial biofilms, documented by confocal images and molecular probes, stimulated imagination and spawned new ideas sometimes bordering science fiction. The most exciting hypotheses presently tested include the active role of biofilms in controlling their own structure; greater structural heterogeneity encourages delivery of substrates to deeper layers of the biofilm. New Scientist, a British science magazine, published an article in August 1996 emphatically comparing biofilms to cities built by microorganisms. This analogy reflects the popular image of biofilms as self-assembled microbial structures, able to optimize their functions. The effects of biofilms on various technological processes constitute the domain of biofilm engineering, which is mostly devoted to controlling biofilm processes. Among various types of biofilm oriented research projects, biomedical research attracts much attention; graphic images of biofilms on implantable prosthetic devices make convincing examples of the importance of biofilms and biofilm processes. Much has been done to understand and to mitigate the effects of biofilms in other than biomedical technologies, exemplified by the biodeterioration of stone, microbially influenced corrosion and biofouling of filtration membranes. Biofilms are also used to enhance the desirable technological processes, such as bioremediation of contaminated ground waters or wastewater treatment.

This presentation is designed as an introduction to biofilms and biofilm processes. It focuses on the development of the conceptual models of biofilm structure, and on the functions of various components of biofilm systems - the surface, the biofilm matrix, the liquid phase, and the gas phase. Quantifying biofilm structure and activity is illustrated using results of several studies.

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DESICCATION TOLERANCE IN *PORPHYRA* SPECIES. Yen-Chun Liu[1] and Donald Cheney[2]. [1]Northeastern University, 360 Huntington Avenue, Boston, MA, 02115, USA

Intertidal seaweeds provide unique model systems for dessication study because they face rapid changes of water content twice a day, and therefore, intertidal seaweeds must have to possess unique mechanisms to survive. In general, there are two types of desiccation resistance mechanisms: avoidance and tolerance. Also, there are two ways to achieve stress resistance: adaptation and acclimation. We chose to study the desiccation tolerance mechanisms in *Porphyra* species because of two reasons. First, they can be easily grown in the lab and this allows us to study solely desiccation tolerance, not other environmental stresses, such as high light and extreme temperatures, in combined. Secondly, because of their simple morphology, the results won't be confounded by structural protection. In addition, their morphology allows us to study a response to severe desiccation rapidly. We have established *P. umbilicalis* and *P. yezoensis* culture in lab. Preliminary results show that *P. umbilicalis* is more resistant to desiccation than *P. yezoensis*. Both species lose more than 95% of their water in two total hours and the final relative water content is virtually the same. Thus, the resistance in *P. umbilicalis* is not due to acclimation or avoidance of water loss. Massive membrane leakage was observed in the susceptible species *P. yezoensis* but not in *P. umbilicalis*. However, neither species shows an increase in membrane peroxidation after desiccation, and, *P. umbilicalis* appears to accumulate more reactive oxygen species (ROS). We plan to investigate whether sugars and late embryogenesis abundant (LEA) proteins play a role in desiccation tolerance in *P. umbilicalis*.

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AN INVENTORY OF SCALED CHRYSOPHYTES FROM THE MID-ATLANTIC COASTAL PLAIN REGIONS OF MARYLAND AND NEW JERSEY, USA, AND THEIR RELATIONSHIPS TO ENVIRONMENTAL VARIABLES. Anne M. Lott and Peter A. Siver. Department of Botany, Connecticut College, New London, CT, 06320, USA.

The purpose of this study was to catalog the diversity of silica-scaled Chrysophyceae and Synurophyceae from a suite of lakes located within two primary regions along the Mid-Atlantic Coastal Plain regions of Maryland and New Jersey, and to relate the distributions to environmental variables. Phytoplankton, periphyton, and surface sediments from each of the 18 sites were collected in June of 2004 and later analyzed extensively with both scanning electron microscopy (SEM) and light microscopy (LM) for scaled chrysophytes and diatoms. In addition, water samples were used to measure a suite of chemical characteristics, including specific conductivity, pH, alkalinity, total phosphorus, total nitrogen, chloride, sulfate and base cation concentrations. New Jersey waterbodies were located within the Pinelands National Preserve, which represents a 1.1 million acre mosaic of forests, wetlands, ponds, streams and farms situated on the outer Atlantic Coastal Plain in southern New Jersey. Maryland sites were located within the Delmarva Peninsula, an area bordered by the Chesapeake Bay on the west, and the Delaware River, Delaware Bay, and Atlantic Ocean on the east. Overall, waterbodies in each locality were found to be rich and abundant in scaled chrysophytes. To date, we have identified over 62 taxa of silica-scaled Chrysophyceae and Synurophyceae, representing six genera. The

number of taxa found per lake ranged from 0 to 30 and observations include new records of several rarely reported species such as *Mallomonas americana* and *M. guttata* f. *simplex*. Dominating the flora were *Synura sphagnicola, S. echinulata, S. petersenii, S. spinosa, Mallomonas punctifera, and Chrysodidymus synuroideus*. The use of this flora in reconstructing paleolimnological environments will be discussed.

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THERMAL STRESS INTENSIFIES PATHOGENIC EFFECTS OF *VIBRIO* BACTERIA ON CLADE SUBSPECIES OF *SYMBIODINIUM* IN REEF BUILDING CORALS. J.M. Cervino1, J.M. McClanahan2, E.A . Lorence3, A. Perovic4, A. Skritnik5, T.J. Goreau6 , R.L. Hayes7

Corresponding Address: Pace University, Department of Biological Sciences
1 Pace Plaza, New York, NY 10038

Recent in vitro studies show that four yellow-band (YBD) inducing *Vibrio* pathogens primarily target the symbiotic zooxanthella (*Symbiodinium* sp.) harbored in the tissues of reef building Caribbean corals, causing in-situ apoptosis of endosymbiotic zooxanthellae. Current comparative analysis of the 16s rDNA genome sequences reveal identical species matches between Pacific and Caribbean YB-causing *Vibrio* sp. Recent *in vivo* analysis has shown that related clades of *Symbiodinium* from the Pacific and Caribbean are the targets of *Vibrio* infection, rather than the coral host tissue itself. Studies show that *Vibrio* infection intensifies when surrounding seawater temperatures are abnormally high. It has been speculated that this is due to increased pathogen virulence, increased susceptibility of the algae cells, or a combination of both. Cultured zooxanthellae clade subtypes C1 and D subjected to heat shock (33C) followed by inoculation with *Vibrio* species show lower % mitotic index of the symbiotic zooxanthellae and algal cell densities compared to non-heat shocked, *Vibrio*-incoulated controls (25C). Cytological analysis of zooxanthellae treated with *Vibrio* show a decline in chlorophyll pigments and cell size, increases in cell lysis and degenerative cells, characteristics that were higher in heat treated infected zooxanthellae and not evident in controls. These data suggest that thermally-stressed symbiotic algae are more susceptible to *Vibrio* infection.

Key Words: Zooxanthellae clades, *Vibrio* spp., 16S rDNA, yellow-band disease, thermal stress

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UTILIZING ALTERNATE WAVELENGTHS TO INCREASE LEVELS OF THE OMEGA-6 ARACHIDONIC ACID. Audrie-Jo L. M^{c}Conkey and Dr. Catherine T. Enright. Nova Scotia Agricultural College, Department of Plant and Animal Sciences, Truro, NS, B2N 5E3. Canada.

Selected species from the classes Prasinophyceae, Coscinodiscophyceae and Prymnesiophyceae were grown in triplicate under different light wavelength environments of red (680 nm), blue (425 nm), green (550 nm) and a standard florescent light to determine if growth and the lipid content of arachidonic acid (ArA) (20:4n-6) would be altered. The role of ArA is linked to several health benefits with a particular association to the human nervous system. Supplementary diets have been produced including ArA for products such as baby formula and aquaculture

feeds. Growth for all tested classes was found to be greatest under the influence of red wavelengths ($p=0.001$), proceeded by blue, then green and the standard respectively. After a growth curve was established, the cultures were inoculated so that samples could be drawn and analyzed during exponential phase under each wavelength. The levels of ArA were determined through gas chromatography. Levels of ArA as % by weight units for the class Prymnesiophyceae 0.16 ± 0.02 (red), 0.20 ± 0.015 (blue), $0.09 \pm (0.01)$ (green), and 0.12 ± 0.005 (standard); Prasinophyceae 2.63 ± 0.08 (red), 2.34 ± 0.21 (blue), 0.91 ± 0.11 (green), 0.73 ± 0.03 (standard); Coscinodiscophyceae 6.08 ± 0.02 (red), 6.11 ± 0.01 (blue), 4.78 ± 0.26 (green), 3.91 ± 0.83 (standard). Overall, levels of ArA are greater in red and blue ($p<0.05$) over green and standard wavelengths.

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ASSESSING SPECIES RICHNESS AND PHYLOGENETIC RELATIONSHIPS OF THE BROWN ALGAL (PHAEOPHYCEAE) FLORA OF CANADA. Daniel McDevit and Gary Saunders. University of New Brunswick, Fredericton, NB, Canada.

The brown algae (Phaeophyceae) are a diverse and economically important group of organisms. Unfortunately, morphological identification within the Phaeophyceae is often difficult and thus there are numerous taxonomic uncertainties in the literature. Molecular barcoding is emerging as a solution for species identification problems. We are testing the utility of the DNA barcode (~700bp region of the mitochondrial Cytochrome c oxidase 1 gene) for differentiating between species of Phaeophyceae. To accomplish this, we are comparing sequence variation in the barcode to a nuclear marker - the ribosomal internal transcribed spacer region – shown in numerous studies to differentiate effectively between species. In the process of testing the barcode, this study will aid in answering a number of questions related to distribution and amphi-oceanic species, life history stages and morphological plasticity as well as possibly uncover a number of cryptic or overlooked species. In addition, there has yet to be a comprehensive study of the Canadian brown algal flora. LSU sequence data will provide the first comprehensive phylogenetic picture of the Canadian Phaeophyceae. Here we present preliminary data indicating that the barcode shows significant variation to differentiate between species, there are several cryptic species in the Canadian brown algal flora and there is need for taxonomic revision within the Phaeophyceae.

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MOLECULAR AND ANATOMICAL ANALYSIS OF CRYPTIC SPECIES IDENTIFIED AS *RHODYMENIA* IN AUSTRALIA. Brian McDonald & Gary W. Saunders. Department of Biology, University of New Brunswick, Fredericton, N.B., E3B 6E1 Canada.

The family Rhodymeniaceae is described based on reproductive morphology, including organisms with four-celled carpogonial branches, cruciate and intercalary tetrasporangia, and an absence of a *tela arachnoidea.* The Australian members of the type genus *Rhodymenia* currently include eight different recognized species. Most of these possess anatomical features that are characteristic of the type. However, the species *Rhodymenia verucossa*, *R. cunneata*, and some collections of *R. sonderi* possess anatomical characteristics that are anomalous to those of the

type species. Molecular analysis of large subunit ribosomal DNA from collections of these species has supported the distinction from this genus. Plants collected as *Rhodymenia verucossa* in particular form a separate cluster that is sister to the genus *Halichrysis*. These molecular and anatomical data support the repositioning of *R. verucossa* as a member of the Faucheaceae family.

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DISTRIBUTION AND RECRUITMENT ECOLOGY OF THE INVASIVE SEAWEED *CODIUM FRAGILE* SSP. *TOMENTOSOIDES* IN MASSACHUSETTS EELGRASS COMMUNITIES. Chris McHan and Donald P. Cheney. Biology Department, Northeastern University, Huntington Avenue, Boston, MA, 02115, USA.

The invasive green macroalga *Codium fragile* ssp. *tomentosoides* can be found on both shores of the North Atlantic as well as Australia, New Zealand, and South Africa. Due to its invasive nature and rapid spread from a single introduction (Long Island, NY-1957), *Codium* has been the subject of many previous investigations concerning its distribution, reproduction, physiological tolerances, and ecology. One area of *Codium* research that is not well understood is its interaction with *Zostera marina* L., or eelgrass. Understanding these interactions is essential to the conservation and management of eelgrass communities and the resources they support. This study will examine the distribution and abundance of *Codium* within eelgrass beds along Massachusetts' southern shore and islands, as well as the associated seasonal patterns of variation. In addition, the study will investigate the underlying factors which control the recruitment and persistence of *Codium* in eelgrass beds. For example, the role of living substrates (in particular *Crepidula fornicata*) on the recruitment of *Codium* "spores" into seagrasses. Previous sampling of drift specimens collected on beaches adjacent to vast seagrass meadows have shown up to 98% of plants attached to *Crepidula forniacata* alone. A unique aspect of this study is the incorporation of a GIS (Geographic Information System) to manage, analyze, and express the data collected. By incorporating the GIS, both field collected data and results from experiments can be visually expressed and reproduced in an easily interpreted format, which can be incorporated into management systems throughout the region.

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CHARACTERIZATION OF GROUP IA INTRONS IN THE CHLOROPLAST *RBC*L GENE OF FIVE *PEDIASTRUM* AND TWO *BRACTEACOCCUS* ISOLATES (SPHAEROPLEALES, CHLOROPHYCEAE). Hilary A. McManus[1] and Louise A. Lewis[1]. Department of Ecology and Evolutionary Biology, University of Connecticut, Storrs, Connecticut, 06269, USA.

Group IA introns located in the chloroplast-encoded *rbc*L (large subunit ribulose-1,5-bisphosphate carboxylase/oxygenase) gene have been reported in several genera of the colonial Volvocales (Chlorophyceae). The introns found within the Volvocales are inserted at position 462 of the rbcL exon (*rbc*L-462), and they range from 549 bases to 1,447 bases in length. Some of the introns contain an open reading frame (ORF) that encodes a putative homing endonuclease. A survey of additional chlorophyceaen taxa within the Sphaeropleales has revealed that five isolates of *Pediastrum* (Hydrodictyaceae) and two of *Bracteacoccus* also

contain an intron within the *rbc*L gene. The *Pediastrum* intron occurs at position 462, like those found in the Volvocales, while the *Bracteacoccus* intron occurs at position 700. The newly determined introns are over 1,000 bases in length, exhibit a secondary structure typical of group IA introns and like the Volvocales, contain ORFs. Phylogenetic analyses of the conserved intron regions and comparisons to the host phylogeny will assist in the determination of the intron relationships and whether these introns are vertically inherited from a common ancestor or if they have been more recently acquired.

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A NEW FRESHWATER SPECIES OF *ENCYONOPSIS* KRAMMER (BACILLARIOPHYCEAE) FROM STREAMS IN THE SOUTHERN UNITED STATES. Eduardo A. Morales[1] & Kalina M. Manoylov[2]. [1]Patrick Center for Environmental Research, The Academy of Natural Sciences, 1900 Benjamin Franklin Parkway, Philadelphia, PA 19130-1195, USA. [2]Department of Zoology, Michigan State University, East Lansing, MI 48824, USA.

A new diatom species was observed during analysis of periphyton samples collected from Alabama by the U.S. Geological Survey's National Water Quality Assessment Program (NAWQA). Subsequently, other populations of the same entity were found in material collected for an Environmental Protection Agency (EPA) project also from Alabama streams. The species was originally identified as *Navicula* aff. *subminuscula* Manguin, although there is a significant size difference, the new taxon being much smaller. EPA material yielded larger populations allowing for the observation of additional features that suggested that the taxon is better placed within *Encyonopsis*. Due to the small size of the valves (3.8-14 μm), the usual dorsi-ventrality observed in other species of this genus is difficult to detect in the new taxon. Other features of the new entity include elliptical valves with rounded ends, 3.8-14 μm long and 1.5-3.7 μm wide. The striae vary from parallel in the middle portion of the valve to radiate toward the apices and sometimes one shortened stria can be seen in the ventral side of the valve. Striae density is 18-28 in 10 μm. Ecologically, the new taxon is found in warm waters with high conductivity. So far, only freshwater stream populations have been found with no records from lakes.

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A STUDY OF FRESHWATER SPECIES OF *SYNEDRA* EHRENBERG (BACILLARIOPHYTA) FROM NORTH AMERICAN STREAMS. Eduardo A. Morales, Sarah Hamsher, Erin Hagan & Daniel Mellott. Patrick Center for Environmental Research, The Academy of Natural Sciences, 1900 Benjamin Franklin Parkway, Philadelphia, PA 19130-1195, USA.

The genus *Synedra* Ehrenberg includes species with primarily freshwater distribution, many of which are considered cosmopolitan and highly variable in their morphologic features. The nomenclatural history of the genus is abstruse and clarification is difficult due to loss of the type and incorrect lectotypification. One of the most common species is *Synedra ulna* (Nitzsch) Ehrenberg, depicted in the literature as a taxon with a wide tolerance to environmental factors and high phenotypic variability, but adequate argumentation for such broad characterization is

often lacking. We have studied several populations of *Synedra ulna* and other species within the genus reported from the United States during analyses of material collected by NAWQA (National Water Quality Assessment Program dependent from the U.S. Geological Survey) and Montana's Department of Environmental Quality. The goal of this project is to review the variability of *Synedra*, particularly *S. ulna*, and determine if there are measurable morphologic differences and variations in the geographic distribution of morphs observed in various streams.

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EXAMINING ALGAL VIRUS RECEPTORS USING CONFOCAL LASER MICROSCOPY. Paesani, V.I.[1],Lawrence, J.E.[1] [1]University of New Brunswick, Fredericton, New Brunswick, E3B 6E4, Canada.

Viral infection begins with the interaction of a virus particle with receptors on the surface of a host cell. These 'receptors' are naturally expressed cell-surface molecules exploited by viruses. We are developing methods for examining this first step of algal virus infection using the *Heterosigma akashiwo* - HaNIV system. Since viruses and receptors cannot be detected using traditional light microscopy, we are labelling viruses with SYTOX Orange and using confocal laser microscopy to examine their binding pattern. SYTOX Orange fluoresces outside the range of natural chlorophyll fluorescence allowing detection of bound viruses on the surface of photosynthetic cells. In addition to mapping receptor sites, we are incubating *H. akashiwo* with proteases, glycoprotein-digesting enzymes, cellulase and a lectin; the interruption of infection by any of these will provide information on the biochemical nature of the receptor. The two approaches, visualization and biochemical tests, will be used to determine the abundance, distribution and biochemical nature of viral receptors. This will provide critical information on the initial interactions between virus and host, which is fundamental for understanding the propagation of infection.

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THE EFFECTS OF EXTENDED PERIODS OF ANOXIA ON *VAUCHERIA* PROPAGULES IN CONNECTICUT RIPARAN SEDIMENTS. Alison A. Parpal[1] and Craig W. Schneider[1]. [1]Department of Biology, Trinity College, 300 Summit Street, Hartford, CT 06106-3100, USA.

Species of the yellow green alga *Vaucheria* (Vaucheriaceae, Heterokontophyta) are found throughout the world in salt, brackish, and freshwater sediments. We have previously demonstrated that this resilient genus has demonstrated the ability to survive extreme environmental stresses by depositing hardy, dormant "seed banks" of propagules into the sediments in which it grows. The present study investigates the effect of extended periods of anoxia on the survival of *Vaucheria* propagules. Sediment samples from a moist streambed in Ashford, Connecticut, a habitat where seven species of *Vaucheria* have been known to grow, were used in this study. The raw mud samples were homogenized and divided into small circular cakes, which were then placed in individual BioBags™ relieved of oxygen, and then stored in N_2-filled desiccation chambers in a dark cold-room. Every thirty days, a single, moist 7.5 cm cake was removed from anoxic conditions and transferred to a growth chamber with a 16L/8D

diurnal cycle at 15°C. Cultures were observed twice weekly for germination and ultimately reproduction. Our results demonstrate that at least three species, *Vaucheria aversa, V. uncinata* and *V. undulata,* are able to survive at least 150 d. of anoxic dormancy, with two surviving 360 d. of treatment.

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ACHNANTHIDIUM SPECIES IN FLOWING WATERS OF THE APPALACHIAN MOUNTAINS. Karin C. Ponader[1] and Marina G. Potapova[2]. [1]Harvard University Herbaria, 22 Divinity Avenue, Cambridge, MA, 02138, USA. [2]Patrick Center for Environmental Research, The Academy of Natural Sciences, Philadelphia, PA, 19103, USA.

Representatives of the genus *Achnanthidium* are often the most abundant benthic diatoms in rivers and streams of the Appalachian Mountains. The identification of *Achnanthidium* taxa is difficult, due to their small cell size and insufficient information in the literature. We studied the taxonomy and ecology of *Achnanthidium* from Appalachian rivers by analyzing samples and environmental information collected during various water quality surveys. The following species were identified using scanning electron and light microscopy: *A. alpestre* (Lowe & Kociolek) Lowe & Kociolek, *A. atomus* (Hustedt) Monnier, Lange-Bertalot & Ector, *A. deflexum* (Reimer) Kingston, *A.* cf. *kranzii* (Lange-Bertalot) Round & Bukhtiyarova, *A. latecephalum* Kobayasi, *A. minutissimum* (Kützing) Czarnecki (sensu lato), *A. reimeri* (Camburn) comb. nov., *A. rivulare* Potapova & Ponader, and *A. thienemannii* (Hustedt) Lange-Bertalot. Distribution of *Achnanthidium* species in relation to water chemistry was studied by fitting species abundances to non-parametric regression models, such as LOESS, Generalized Additive Models (GAMs), and Non-Parametric Multiplicative Regression Models (NPMR). Although most *Achnanthidium* species were found to be indicative of low-nutrient concentrations and generally clean waters, they varied considerably in ecological preferences. *A. deflexum*, and *A. thienemannii* could withstand some mining pollution without acid drainage because of their preference to higher ionic content. *A. minutissimum* was the only species that was able to tolerate acid mine drainage because of its tolerance to lower pH. *A. reimeri* had highest abundance in rivers with high silt content, often polluted by nutrients. *A. rivulare* and *A. minutissmum* were also shown to tolerate some nutrient pollution. *A. atomus* was abundant in rivers with a narrow range of pH about 8-8.3, while *A. alpestre* was found only in streams with very low ionic content in the Great Smoky Mountains region.

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PROPHAGE: HARMLESS HITCHHIKERS OR CYANOBACTERICIDAL MANIACS? Alexander Ruck[1] and Raymond Kepner[2]
[1]Department of Microbiology, Marist College, Poughkeepsie, New York 12601, USA
[2]Department of Microbiology, Marist College, Poughkeepsie, New York 12601, USA

Previous work has shown that both mitomycin-C (mito-C) and Cu have been successful in stimulating prophage excision in some cyanobacteria, while the impact of Cd on phage activity has never been investigated. Our work focused on investigating the ability of mito-C and Cd to release lytic cyanophage from 5 strains of arctic cyanobacteria. Strains were grown in 96-well microplates following isolation via sterile pipetting techniques combined with antibiotic

treatments to reduce heterotrophic bacterial contaminants. Cultures of each of the 5 cyanobacterial strains were treated with 1.0 mg L^{-1} of mito-C and 2 of the 5 strains were treated with 0.5 mg L^{-1} of Cd^{2+}. Three days later cultures were ultrasonicated to release any free cyanophage and filtered extracts were added to actively growing cultures in microwell plates. Neither of the 2 tested strains showed any response to the Cd-treated culture extract addition. In two of the strains (E-066b and WHE1b) we observed a decrease in growth associated with the mito-C-treated culture extract addition. Further work will have to be performed in order to determine whether growth inhibition in E-066b and WHE1b was due to lytic cyanophage release or another factor.

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MERHAB – LOWER GREAT LAKES - MONITORING FOR HARMFUL ALGAL BLOOMS IN OUR INLAND SEAS. Mike Satchwell, Amber Hotto, Xingye Yang, Elizabeth Konopko, Steven Ragonese, Karen Howard and Gregory Boyer. State University of New York, College of Environmental Science and Forestry, 1 Forestry Dr, 121 Jahn Lab, Syracuse, New York 13210

The North American Great Lakes located between the United States and Canada collectively contain approximately 10% of the World's fresh water and provide drinking water for more than 22 million people. In recent years, these inland seas have suffered harmful algal blooms in the form of toxic cyanobacteria. Toxic blooms of *Microcystis* are well documented in the relatively shallow western basin of Lake Erie where concentrations of the hepatotoxic microcystin LR (MC-LR) have exceeded 20 μg L^{-1}. Similarly, both microcystins and the neurotoxin anatoxin-a have led to animal fatalities in the Lake Champlain basin. Lake Ontario, with its numerous nutrient-impacted embayments along the New York Coastline and deep offshore waters, also has a documented history of cyanobacterial blooms. MERHAB-LGL is specifically focused on developing monitoring strategies for these important waters using a combination of molecular, chemical and classical techniques combined with remote sensing, and hydrodynamic modeling to safe guard our drinking water supplies. The results of our field sampling in Lakes Erie, Champlain and Ontario will be presented.

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DISCRIMINATING AMONG CRYPTIC SPECIES OF *PLOCAMIUM* IN THE SOUTHERN HEMISPHERE USING DNA BARCODING Gary W. Saunders and Tanya Moore
Centre for Environmental & Molecular Algal Research Department of Biology, University of New Brunswick Fredericton, NB, Canada E3B 6E1

The genus *Plocamium* includes over 40 recognized species that are widely distributed throughout the world. Whereas most species are clearly defined on the basis of anatomical features and biogeography, the type, *P. cartilagineum,* has a reportedly cosmopolitan distribution and a wide range of morphological and anatomical attributes. Using molecular tools, Saunders and Lehmkuhl (2005) greatly restricted the taxonomic and biogeographic scope of *P. cartilagineum* and, in doing so, established that this species complex includes at least six distinct species in the Northern Hemisphere, four in northern European waters. In that study cryptic entities from this species complex were also identified in the southern Hemisphere.
In light of the earlier findings, we are using the DNA barcode (mitochondrial 5' *coxI*) as a

molecular tool to assess the diversity of *Plocamium* spp. in the Southern Hemisphere with an emphasis on Australia and New Zealand. Preliminary results will be provided which indicate that as few as 50% of the species of *Plocamium* in these waters have been identified to date with most clustered into complexes of *P. cartilagineum, P. angustum* and *P. cirrhosum* – like algae.

§§

ASYMMETRIC CELL WALL DEVELOPMENT IN "SYMMETRIC" DESMIDS.
Ashley A. Serfis and David S. Domozych, Department of Biology, Skidmore College, Saratoga Springs, NY 12866, USA.

Placoderm desmids (Zygnematophyceae, Streptophyta) are characterized by two "identical" semi-cells symmetrically connected at a central isthmus. The reproduction of this symmetry during every cell cycle requires the coordinated interaction of multiple subcellular mechanisms including the synthesis of a new cell wall around the new and expanding daughter semi-cell. In a comprehensive analysis of cell wall microarchitecture and morphogenesis in the simple model desmid, *Penium margaritaceum*, the production of new cell walls in daughter semi-cells during several division cycles does not always yield the expected symmetry. Immunolabeling and subsequent culturing of live cells with the anti-homogalacturonan (HGA) antibodies, JIM5, JIM7, LM7, 2F4 and PAM1 or the general marker of neutral wall sugars, the lectin, ConA, reveal that wall polymer distribution is not symmetrically manifested in the cytokinetic and post-cytokinetic phases of daughter semicells. In the first round of cell division, the production of "esterified" HGAs, as monitored by JIM7 labeling, is localized in a narrow band in the isthmus zone of dividing cells or at the polar termini of expanding daughter semi-cells. De-esterification of the HGA occurs adjacent to these zones and allows for Ca^{2+}-crosslinking and the subsequent strengthening of the wall. This can be monitored by labeling with the other HGA-specific antibodies and ConA. However, after the first division round, the anticipated cell wall labeling patterns upon the new daughter semi-cell are mostly not found. These results suggest that new cell wall components may be inserted between segments of old wall components during cell wall morphogenesis. The significance of this mechanism in *P. margaritaceum*, a desmid that produces only a primary cell wall, will be presented.

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COMPARISON OF TWO ALGAL INDICES FOR USE IN BIOMONITORING OF SOUTHEASTERN OHIO STREAMS.
Nathan J. Smucker[1], Emily K. Hollingsworth[1], Robert G. Verb[2] and Morgan L. Vis[1]. [1]Department of Environmental and Plant Biology, Ohio University, Athens, Ohio, 45701, USA.[2]Department of Biological & Allied Health Sciences, Ohio Northern University, Ada, Ohio, 45810, USA.

Periphyton and water chemistry data from 43 stream segments in the unglaciated Western Allegheny Plateau of Ohio were sampled as part of a larger EPA STAR grant to determine the interrelationship of physical, chemical and biological data for monitoring impairments. These streams were expected to have high water quality based on historical chemistry, fish and invertebrate data. The periphyton index of biotic integrity (PIBI) and the diatom index of biotic integrity (DIBI) were calculated with minor modifications. For the purpose of calculating these

indices, five reference streams were determined using a qualitative habitat evaluation index and land use data. The PIBI for these sites ranged from 43-81 on a 100 point scale with higher scores indicative of better water quality, and likewise the DIBI scores ranged considerably from 36-91. Pearson product-moment correlation was used to determine relationships among metrics and indices. Some of the metrics used in these indices were correlated, which may over emphasize the effect of particular stressors on overall scores within each index. The two indices were expected to score sites similarly. The data showed a weak yet significant correlation ($r = 0.35$, $p<0.05$) for all sites and a very strong correlation for reference sites only ($r = 0.96$, $p<0.01$). Since there was no significant relationship ($r=0.22$, $p=0.17$) among non-reference sites, we suspect the weak correlation of all sites was driven by the strong correlation of reference sites. Also, the DIBI relies heavily on the full environmental gradient being represented; therefore, the weak correlation may be compounded by sampling only high water quality streams. Further sampling of degraded streams next year may strengthen the correlation between the indices.

§§

IN-STREAM AND RIPARIAN CHARACTERIZATION OF FOUR NEW ZEALAND STREAM SEGMENTS CONTAINING *BATRACHOSPERMUM* SPECIES (RHODOPHYTA).
Katherine F Snyder, Kim J. Brown and Morgan L. Vis. Department of Environmental and Plant Biology, Ohio University, Athens, Ohio, 45701, USA.

Four forested stream segments from the South Island and Stewart Island of New Zealand were sampled to determine physical and chemical parameters which might characterize the habitat for *Batrachospermum* species. At each site, water color, pH, specific conductance and water temperature were recorded. Water depth, current velocity, light above the water, light at algae level, substratum types and percent algal cover were measured in numerous quadrats within a defined stream segment. The riparian vegetation was characterized by noting the species composition, forest canopy gap frequency and light reduction due to canopy structure. *Batrachospermum* species investigated were *B. atrum, B. anatinum* forma *confusum* and *B. pseudogelatinosum* in two streams. The four stream segments varied in pH, specific conductance and temperature, but were all clear and tea-colored. Overall, algal cover showed a significant positive correlation to current velocity, water depth, percent boulder and percent sand. In individual streams, the physical parameters were variously correlated to algal cover. It would appear that *Batrachospermum* prefers larger substrata in deeper portions of the stream with moderate current velocities. Light was not correlated with percent cover in most instances, but may have been due to the measurements being instantaneous rather than integrated throughout the day. Characteristics of the forest riparian community which define the in-stream habitat of *Batrachospermum* will be discussed.

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BENTHIC ALGAE ARE EVERYWHERE, IMPORTANT: WE NEED TO KNOW MORE!
R. Jan Stevenson, Department of Zoology, Center for Water Science, Michigan State University, East Lansing, Michigan 48864

Benthic algae occur in many habitats in significant quantities, from streams, wetlands, and coastal zones to deserts. As important sources of primary production, nutrient sinks, and habitat, they also are highly affected by human activities. Results of large scale surveys and experiments have been integrated to teach us much about function of these assemblages and how they are strongly and complexly regulated by abiotic and biotic factors. These factors have shaped evolution of an extraordinary diversity of organisms. Is this diversity important in ecosystem function? Do humans affect benthic algal diversity? How would we manage human activities to sustain diversity sufficiently that ecosystem services can be maintained?
Responses of ecological systems, such as benthic algae, to contaminants and habitat alterations by humans may be affecting species richness as well as other measures of biodiversity. However, this evidence is far from certain and the scale at which this is important is largely unknown. Relative abundances of sensitive native taxa do decrease with human disturbance, but do they go extinct, either locally, regionally, or globally? Is local extinction important or will functionally redundant taxa sustain ecological function? Can regional and even global dispersal repopulate habitats where populations were extirpated? New evidence indicates limitations in algal biogeography, thus local and regional extirpation may be important. Preliminary process-based models indicate a few cells of an introduced species can rapidly support ecological function, but these models are highly sensitive to poorly understood rates of dispersal and colonization success.
The scientific and legal foundation for managing human activities exists in many countries to protect algal biodiversity at sufficient levels for sustainable support of ecosystem services; but like so many environmental issues, great gaps exist in what we know and how certainly we know it. We need to know it with sufficient detail and certainty to convince large portions of the population that problems exist and specific management strategies have a high likelihood of successful protection or restoration of the valued ecological attributes – in this case – benthic algae. The public does care and they want guidance. We need to know more to help.

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PHYLOGENETIC AFFINITIES OF AUSTRALASIAN SPECIMENS OF *BATRACHOSPERMUM* (BATRACHOSPERMALES, RHODOPHYTA) INFERRED FROM MOLECULAR AND MORPHOLOGICAL DATA. Sarah A. Stewart[1], Morgan L. Vis[1] and Timothy J. Entwisle[2] [1]Department of Environmental and Plant Biology, Ohio University, Athens, OH 45701, USA. [2]Royal Botanic Gardens and Domain Trust, Mrs. Macquaries Road, Sydney, NSW 2000, Australia.

Specimens of *Batrachospermum pseudogelatinosum, B. camplyclonum, B. bourrelleyii, B. theaquum, B. atrum, B. australicum* and *B. virgato-decaisneanum* were collected from locations in Australia, New Caledonia and New Zealand. DNA sequence data from a 1282-base pair portion of the plastid *rbc*L gene is used to infer interspecies relationships for all taxa. The two specimens of *B. bourrelleyii* were sister to the *B. pseudogelatinosum/B. camplyclonum* clade. There was much sequence variation among the four *B. theaquum* specimens, but they formed a well-supported clade. Likewise, there was intraspecific variation among specimens of *B. atrum*, *B. australicum* and *B. virgato-decaisneanum*, yet these species were monophyletic. Ten new specimens that could be attributed to *B. pseudogelatinosum* or *B. camplyclonum* were added to the seven previously sequenced specimens. Most of these specimens formed a clade. However,

two specimens were more closely related to *Nothocladus* species. The utilization of morphological and supplementary molecular data for *B. pseudogelatinosum* and *B. camplyclonum* to determine potential patterns of cryptic speciation will be discussed.

§§

THE GOLGI APPARATUS AND EPS SECRETORY MACHINERY OF THE DESMID, *NETRIUM INTERRUPTUM*. Anne L. Thomae and David S. Domozych, Department of Biology, Skidmore College, Saratoga Springs, New York, 12866, USA.

Netrium is a commonly-encountered saccoderm desmid of low nutrient wetlands of the Adirondack Region of New York. Many species are found attached to substrates and are residents of biofilm communities. *Netrium* is also noted for its production of large amounts of extracellular polymeric substances (EPS) that are often in the form of thick, clear mucilages. In this study, we undertook an examination of the cell biology of EPS production in *N. interruptum*. Its EPS consists of a complex polysaccharide rich in fucose, xylose and acidic sugars. Sulfation levels within the EPS are relatively low in comparison with the EPSs of other desmids. The EPS is processed and packaged within an elaborate endomembrane system consisting of 150-200 Golgi bodies per cell and an associated network of large EPS-containing vesicles. Upon exit from the Golgi Apparatus, the EPS vesicles enter an active cytoplasmic streaming network located just under the plasma membrane. This represents a large supply of EPS readily available for rapid secretion at the specific sites on cell surface. Once secreted, the EPS passes through a pore-less cell wall. Polyclonal antibodies were raised against EPS fractions and used in an immunocytochemical mapping of EPS transit through the cell. A model mechanism describing EPS secretory mechanics is presented.

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LIFE IN ESTUARINE BIOFILMS: SMALL-SCALE COMPLEXICITY AND LARGE-SCALE IMPORTANCE. Graham J. C. Underwood[1] [1] Department of Biological Sciences, University of Essex, U.K.

Golden brown and bright green patches of colour on the surface of intertidal mudflats and sand flats are the signs of abundant populations of microphytobenthic algae. Species-rich and physiologically versatile, these intertidal assemblages nicely illustrate some of the key features of biofilms. This paper will describe the distribution of biofilms in shallow-water marine environments and the patterns and causes of changes in species composition and richness. Biofilms are three dimensional structures, with cells held within a matrix of sediment particles and extracellular polymeric substances (EPS). Irradiance levels at the biofilm's surface can be extremely high, and species of microphytobenthos show distinct migratory behaviour, in response to light gradients, and use vertical migration within the biofilm as a mechanism of photoacclimation, combined with physiological responses to deal with light stress. Changing light and nutrient conditions also mediate patterns of production of different EPS fractions within biofilms, with EPS production coupled to degradation by specific bacterial groups. High rates of production, nutrient uptake and oxygen production, lead to estuarine biofilms playing an important role in the biogeochemistry of shallow estuarine and coastal waters, and by

implication, in other clear water environments, such as coral reefs, where much biofilm research is still required to be done.

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THE EXTRACELLULAR MATRIX OF *COSMARIUM RENIFORME*, A UNIQUE DESMID FOUND IN ADIRONDACK WETLAND BIOFILMS. Richard Wilson, Christine Chang, Catherine E. Domozych and David S. Domozych, Department of Biology, Skidmore College, Saratoga Springs, NY 12866, USA.

Cosmarium reniforme is a desmid often found in Adirondack wetland biofilms and one that is commonly encountered as a pioneer species colonizing new substrates. This alga has become an important tool organism in our laboratory in the investigation of desmid pore apparatus structure, the extracellular polymeric substance (EPS) secretory mechanism and biofilm "behavioral" mechanics of desmids. The extracellular matrix (ECM) of *C. reniforme* includes the cell wall (CW), the CW pore apparatus and a thin but exceptionally adhesive EPS. The primary CW is thin and quickly sloughed off by a striking, regularly-lobed secondary CW. This wall is 1.2 μm thick and possesses a network of pores, spaced roughly 2.3 μm apart. Variable pressure scanning electron microscopy highlights a regular distribution of the pores in a hexagonal pattern around each CW lobe. The CW readily labels with BSI and *Helix pomatia* lectins as well as the cell wall-specific monoclonal antibodies JIM5, LM5, LM6, LM7 and CCRCM2. The distinct lobes of the CW are hollow and are filled with extensions of a multi-branched chloroplast. The CW pore consists of a narrow channel that extends from the outer surface of the CW to a bulb-like protrusion of the inner CW surface. The bulb appears to be a focal point for the collection and putative fusion of large, Golgi-derived vesicles. These vesicles emerge from the peripheral cisternae of medial to trans face Golgi cisternae and most likely contain EPS. EPS extrusion from the CW allows for an unusual creeping or gliding by the cell upon surfaces.

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A BASELINE STUDY USING PERIPHYTON COMMUNITIES IN SHAMOKIN CREEK, AN ACID MINE IMPACTED STREAM IN NORTHUMBERLAND COUNTY, PENNSYLVANIA Laura Wirpsza, Nicole Sweeney, and Jack R. Holt. Department of Biology, Susquehanna University, Selinsgrove, PA 17870, USA.

We present the results of a three month study as part of on-going monitoring program using periphyton communities found in Shamokin Creek, a tributary of the Susquehanna River affected by acid mine drainage (AMD) in Northumberland County, Pennsylvania. We sampled five sites, three located on the main stem (Hospital, 61 Bridge, Waste Water Treatment) and two located on the upper tributaries (North, and South) for a period of three months at three week intervals. AMD originated in the upper portion of Shamokin Creek while agricultural influences also occurred in the lower reaches of the stream. Diatometers and chlorophyll samples were collected for analysis in the laboratory. Water chemistry collected included standard physical chemistry (pH, oxygen, total dissolved solids (TDS), oxidation-reduction potential (ORP), turbidity, and temperature) and chemical (ammonium, phosphate, nitrate, and hardness). Diatometers were

preserved in the field and prepared for microscopic examination by the ethanol dehydration method, thus allowing dominant and common taxa in the biofilm to be classified and counted. Chlorophyll was analyzed using spectrophotometric analysis and confirmed our results of the biofilm examination. We cleaned scrapings of the biofilms from rocks, sticks, and leaves with concentrated nitric-sulfuric acids to generate slides of cleaned diatom frustules for species determination and enumeration with scanning electron and differential interference contrast microscopy. Our results show the common species of diatoms present to be *Eunotia exigua, Navicula pupula, Cocconeis placentula, Cymbella tumida,* and *Cyclotella meneghiana.* In the coal mining region, *Frustrulia rhomboides* and *Eunotia exigua* were dominant, which is in agreement with earlier studies as key species indicating the presence of AMD. All sites had low pH (4-6) and high oxygen levels, but the turbidity, ORP, and TDS varied site to site. These results demonstrate that AMD has a significant general impact on Shamokin Creek.

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COMPARISON OF DIATOM AND MACROINVERTEBRATE INDICES IN ACID MINE DRAINAGE IMPACTED STREAMS. Jason T. Zalack and Morgan L. Vis
Department of Environmental and Plant Biology, Ohio University. Athens, OH 45701

In Ohio, macroinvertebrates are the organisms of choice for assessment of biological condition in wadable streams. Macroinvertebrates are used to calculate the invertebrate community index (ICI) which assigns a site a score of 0-60, and classification of Excellent, Good, Fair, or Poor. This study aims to show the utility of the diatom community in classifying streams as well as the ICI. To accomplish this task, macroinvertebrates, diatoms and water samples were collected from 40 stream segments in southeast Ohio. Macroinvertebrates were collected from multi-plate artificial substrate samplers that were colonized in-stream for six weeks. Diatoms were sampled by scraping a total of 70^2 cm of cobble from riffles. Water samples were analyzed for nutrients (P, N, S) and metals (Fe, Al, Mn). Sites ranged from minimally disturbed reference conditions to sites heavily impacted by acid mine drainage (AMD), as this is the major source of stream impairment in Southeast Ohio. Macroinvertebrate ICI scores were compared to Diatom Index of Biotic Integrity (DIBI) scores using linear regression. ICI and DIBI scores were plotted against stream pH and iron concentration; variables indicative of AMD impairment. CART analysis was used to identify diatom species and community metrics that characterize the 4 water quality classes based on the ICI scores.

NEAS 2006
Distinguished Lecturer
Professor Graham Underwood

***CURRICULUM VITAE:* Professor Graham James Charles Underwood.**

Department. of Biological Sciences, University of Essex, Colchester, Essex. CO4 3SQ.
Tel: (01206) 873337, FAX (01206) 873416, email *gjcu@essex.ac.uk*

Education

1983 - 1986 University of Reading, Whiteknights, Reading.
1986 B.Sc. (Hons.) First Class, Zoology with Microbiology as a subsidiary subject.
1986 University Prize, University of Reading.
1986 Alison Grisley Prize, University of Reading.
1986-1989 University of Sussex, Falmer, Brighton.
1989 Degree of Doctor of Philosophy, Univ. of Sussex.
NERC CASE award with Freshwater Biological Association. *Interactions between freshwater pulmonate snails, macrophytes and epiphytes.*

Employment

1989-1991. Post-doctoral Research Assistant, Department of Zoology, University of Bristol. Dept. of Energy funded research into algal stabilisation of estuarine sediments.
1991-1992. Post-doctoral Research Assistant. Departments of Botany and Geology, University of Bristol. NERC funded research into microbial production and utilisation of extracellular material in estuarine sediments.
1992 - 1998. Lecturer in Department of Biology, University of Essex.
1998 – 2002. Senior Lecturer, Department of Biological Sciences, University of Essex.
2002 – 2004. Reader, Department of Biological Sciences, University of Essex
2004-present. Professor, Department of Biological Sciences, University of Essex

Research interests, activity and funding

- The role of microphytobenthos (benthic microalgae) in marine coastal ecosystems.
- Photosynthesis and production of exopolymers (EPS) by benthic diatoms.
- Effect of environmental conditions on benthic biofilm physiology
- Carbon and nitrogen cycling in marine sediments
- Interactions between benthic primary producers in coastal biogeochemical cycles
- Nutrient cycling across sediment - water interfaces

- Response of algal assemblages to nutrient enrichment
- Benthic diatom diversity, taxonomy and response to environmental gradients
- Saltmarsh erosion, sediment biostabilisation and the impact of toxic substances

Successful Research funding since 1992
Major research grants and programmes

1. **Nov. 1992**, £167,678, NERC, Investigation of primary productivity by microphytobenthos in intertidal mudflats. (£156,126 awarded. (joint with St. Andrews) Essex component, £52,239).
2. **Nov. 1993**, £45, 000, Anglian Water Services Ltd, Phosphorous cycling and algal dynamics in Alton reservoir (fully funded Ph.D., joint supervision with P Daldorph, Anglian Water).
3. **Jun. 1994,** £142,000, DoE, Influence of benthic algal biofilms on nutrient fluxes across the sediment-water interface (with DB Nedwell).
4. **June 1995**, ECU 278,000. EU. MAST III proposal. Nitrogen cycling in estuaries. 1.4 mECU awarded, Essex component ≈ £187,000 Jan. 1996 (with DB Nedwell).
5. **Oct. 1995**, £64,356, NRA, Investigation of sediment, phytobenthic and water quality interactions in the River Deben estuary, Suffolk. (with DB Nedwell).
6. **Aug. 1996**, £400,000 NERC ED. Sublethal effects of herbicides on saltmarshes £80,000 awarded in first phase, (with C.F. Mason et al.).
7. **Jun. 1997** £164,646 Department of the Environment, Environmental limitation of phytoplankton in estuaries (with DB Nedwell).
8. **Mar 1998** £142,879 NERC Determination of individual cell contributions to *in situ* microphytobenthic photosynthesis. (PI, with NR Baker, DM Paterson).
9. **June 2001** £25,500 Environment Agency. Ph.D. studentship, developing and estuarine trophic diatom index.
10. **June 2001** $370,000, Exopolymer production by diatoms US National Science Foundation. £51,034, Essex component of award to Gretz (Michigan Tech.) and Underwood (Essex).
11. **Dec 2001.** £199,404 NERC. Carbohydrate degradation and bacterial-algal coupling in intertidal sediments (PI, with Osborn and Ball).
12. **Sept 2003,** £29,824 NERC. Continuous culture systems for studying microbial community dynamics in marine environments. (co PI with Geider RJ et al.).
13. **Dec 2003,** £193,608 NERC. Strategies for tolerance to high light stress in diatoms (PI, with NR Baker).

14. **July 2004** £193,583 NERC. Development of an instrument for sequential imaging of chlorophyll a fluorescence and Light-Induced Breakdown Spectroscopy (LIBS) at the single cell level. (Co-I, with K. Oxborough, R. Geider)

15. **July 2005** £187,240 NERC. roles of DMSP and GBT in protection from photoinhibition/photooxidative stress and consequences for DMS and NH3 production. (SOLAS thematic programme, Co-I with R. Geider, N.R. Baker)

16. **Dec 2005** £267,152 NERC. Degradation of dissolved complex polysaccharides in estuarine littoral zones. (PI, with CoI T. McGenity).

17. **Feb 2006** £64,458 NERC. Is increased chemical complexity of extracellular polymeric substances (EPS) related to increasing salinity in polar sea ice? (PI, with CoI ~D. Thomas, Bangor).

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2. **Underwood, G.J.C.** and Baker, J.H. (1991). The effect of various aquatic bacteria on the growth and senescence of duckweed (*Lemna minor*). *Journal of Applied Bacteriology*. **70**, 192-196.

3. **Underwood, G.J.C.** (1991). Note: Colonization and invasion of leaves of the aquatic macrophyte *Ceratophyllum demersum* L. by epiphytic bacteria. *Microbial Ecology*. **21**, 267-275.

4. **Underwood, G.J.C.** (1991). Growth enhancement of the macrophyte *Ceratophyllum demersum* in the presence of the snail *Planorbis planorbis*: The effect of grazing and chemical conditioning. *Freshwater Biology*. **26**, 325-334.

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51. Abdullahi, A.S., **Underwood, G.J.C.**, Gretz, M.R. (in press) Extracellular matrix assembly in diatoms (Bacillariophyceae). V. Environmental effects of polysaccharide synthesis in the model diatom *Phaeodactylum tricornutum. J. Phycol.*

52. Apoya, M. D. Yin, L. **Underwood G.J.C**. and Gretz, M.R. Movement modalities and responses to environmental changes of the mudflat diatom *Cylindrotheca closterium* (Bacillariophyceae) (in press) *J. Phycol.*

Invited reviews

53. **Underwood, G.J.C**. & Kromkamp, J. (1999). Primary production by phytoplankton and microphytobenthos in estuaries. *Advances in Ecological Research,* **29**, 93-153.

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National and international research profile

Sept. 2001, Keynote Speaker, joint Society of General Microbiology / British Phycological Society Symposium "*Microbial Interactions in Aquatic Environments*", University of East Anglia, U.K.

Oct 2002, Invited Speaker, Diatom ecology and taxonomy: a marriage of necessity. University of Szczecin, Californian Academy of Sciences, Szcecin, Poland.

Jan 2003, Keynote speaker, 19th Congress of the Phycological Society of Southern Africa.

Aug 2003, Invited speaker, Microphytobenthos functioning colloquium, Royal Netherlands Academy of Arts and Sciences, Amsterdam.

April 2005 *European Geophysical Union Congress, Vienna, 25-29th April 2005*. Invited keynote speaker in a special Biofilms session, co-organised by the biogeochemistry section of the EGU and the International Society for Microbial Ecology. *Cell-specific activity, photosynthesis and exopolymer dynamics in transient marine diatom biofilms.*

June 2005 *American Society for Limnology and Oceanography* meeting, Santiago, Spain, June 19-24. Invited keynote speaker, special session Biogeochemistry of tidal flats.June 2005,

April 2006 *North East Algal Symposium*, New York, USA Plenary speaker,. Biofilms.

Media articles and appearances

BBC1 Look East, May 2003 "Mud mud, glorious mud"

BBC1 "*The Politics Show*", 21st Sept. 2003, Discussion on ecological impacts of offshore wind farms.

BBC East, January 2004, contribution on offshore sediment extraction and ecological effects.

BBC1, Sept 2004. *The British Isles, a natural history.* Programme 3. *After the ice.*

BBC Radio 4 "*Home Planet*" Environment discussion programme dealing with topical issues, regular panel member dealing with marine biology, 2003 – 200

BBC Radio 4. *The Natural World*, BBC Radio 4, *Changing Places*

1995-2000 Member of Editorial Board of *Microbiology*, published by the Society for General Microbiology.

1998-2003 Environmental Microbiology Committee Member, Society for General Microbiology.

2000-2006 Adjunct Professor, Biological Sciences, Michigan Technical University, Michigan. USA.

1999-2004 Scientific Review Committee member, Natural Environment Research Council. Centre for Coastal and Marine Sciences.

2002-2005, 2006-2009 Council Member, British Phycological Society.

2002–2005 Marine Sciences Peer Review College Committee member, Natural Environment Research Council. UK.

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Marist College

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NEAS 2006 Registered Participants

Adel Abdo
Eastern Connecticut State University
Willimantic, CT 06226
860-465-5305

Mike Adams
Eastern Connecticut State University
Willimantic, CT 06226
860-465-5305
adams@easternct.edu

Darren Bade
Institute of Ecosystem Studies
Millbrook, NY 12545
845-677-5343
baded@ecostudies.org

Kristopher Baker
Stony Brook University
Stony Brook, NY 11794
631-495-1757
krbaker@ic.sunysb.edu

Kathryn Beldowski
Marist College
Poughkeepsie, NY 12601
845-575-2285
katieb5984@hotmail.com

Brent Bellinger
Michigan Technological University
Houghton, MI 49931
414-719-1588
bjbellin@mtu.edu

Edmund Bonneau
North Grosvenordale, CT 06255
860-923-9351
bonneau@charter.net

Peter Bradley
Worcester State College
Worcester, MA 01602-2597
508-929-8571
pbradley@worcester.edu

Lee Camfield
Connecticut College
New London, CT 06320
860-439-2520
lmcam@conncoll.edu

Cayelan Carey
Dartmouth College
Hanover, NH 03755
518-577-0332
cayelan.carey@dartmouth.edu

Christine Chang
Skidmore College
Saratoga Springs, NY 12866
518-580-5075
c_chang@skidmore.edu

Donald Cheney
Northeastern University
Boston, MA 02115
617-373-2489
d.cheney@neu.edu

Bridgette Clarkston
University of New Brunswick
Fredericton, NB E3B 6E1
506-452-6086
bridgette.clarkston@unb.ca

Susan Clayden
University of New Brunswick
Fredericton, NB E3B 6E1
506-452-6086
z9dc@unb.ca

Philip Cook
University of Vermont
Underhill, VT 05489
802-899-9928
philip.cook@uvm.edu

Catherine Domozych
Skidmore College
Saratoga Springs, NY 12866
518-580-5075
cdomozyc@skidmore.edu

David Domozych
Skidmore College
Saratoga Springs, NY 12866
518-580-5075
ddomoz@skidmore.edu

Leah Elliott
Skidmore College
Saratoga Springs, NY 12866
518-580-7244
llelliot@skidmore.edu

Jim Foertch
Millstone Environmental Lab
Waterford, CT 06385
860-444-4237
james_f_foertch@dom.com

Sohini Ghoshroy
Clark University
Worcester, MA 01610
508-415-1913
sghoshroy@clarku.edu

Rebecca Gladych
University of Connecticut
Stonington, CT 06378
860-287-9767
rebecca.gladych@uconn.edu

Michael Gretz
Michigan Technological University
Houghton, MI 49931
906-487-2025
mrgretz@mtu.edu

Erin Hagan
Philadelphia Acad. of Natural Sciences
Philadelphia, PA 19103
215-405-5084
hagan@acnatsci.org

James Hampton
Eastern Connecticut State University
Willimantic, CT 06226
860-465-5305

Sarah Hamsher
Philadelphia Acad. of Natural Sciences
Philadelphia, PA 19103
215-405-5084
hamsher@acnatsci.org

John Heimke
Russell Sage College
Troy, NY 12180
518-279-9073
heimkj@sage.edu

Sami Hocine
Skidmore College
Saratoga Springs, NY 12866
603-209-6608
s_hocine@skidmore.edu

Tim Hogan
Northeastern University
Boston, MA 02115
617-373-7738
hogan.ti@neu.edu

Emily Hollingsworth
Ohio University
Athens, OH 45701-2979
740-593-1134
eh175005@ohio.edu

Jack Holt
Susquehanna University
Selinsgrove, PA 17870
570-372-4205
holt@susqu.edu

Amber Hotto
SUNY-ESF
Syracuse, NY 13210
315-470-6844
ahotto@syr.edu

H. William "Bill" Johansen
Clark University
Worcester, MA 01610
508-829-9512
hjohansen@verizon.net

Venkatesh Kandadai
Marist College
Poughkeepsie, NY 12601
845-575-2285
venkatesh.kandadai@marist.edu

Raymond Kepner
Marist College
Poughkeepsie, NY 12601
845-575-2285
ray.kepner@marist.edu

Sarah Kiemle
Michigan Technological University
Houghton, MI 49931
906-487-2025
snkiemle@mtu.edu

Jang Kim
University of Connecticut
Groton, CT 06340
860-405-9089
jang.kim@uconn.edu

Lisa Kortfelt
Eastern Connecticut State University
Willimantic, CT 06226
860-465-5305

Hana Kucera
University of New Brunswick
Fredericton, NB E3B 6E1
506-452-6086
hana.kucera@unb.ca

Aimlee Laderman
Marine Biological Laboratory
Woods Hole, MA 02543
508-548-5618
aladerman@mbl.edu

Christopher Lane
Dalhousie University
Halifax, NS B3H 1X5
902-494-2536
c.lane@dal.ca

Ellen Lavoie
University of New Hampshire
Wakefield, NH 03872
603-799-9638
elavoie@unh.edu

Janice Lawrence
University of New Brunswick
Fredericton, NB E3B 6E1
506-458-7842
jlawrenc@unb.ca

Rachel Lay
Skidmore College
Saratoga Springs, NY 12866
518-580-5075
r_lay@skidmore.edu

Line LeGall
University of New Brunswick
Fredericton, NB E3B 6E1
506-453-3537
legall@unb.ca

Molly Letsch
University of Connecticut
Storrs, CT 06269
860-468-2298
molly.letsch@uconn.edu

Mike Levandowsky
Pace University
New York, NY 10038
212-346-1861
mlevandowsky@pace.edu

Zbigniew Lewandowski
Montana State University
Bozeman, MT 59717
406-994-4770
zl@erc.montana.edu

Larry Liddle
Southampton College-Long Island Univ.
Southampton, NY 11968
631-283-7376
lliddle@southampton.liu.edu

Yen-Chun Liu
Northeastern University
Boston, MA 02115
617-373-7738
liu.ye@neu.edu

Anne-Marie Lott
Connecticut College
New London, CT 06320
860-439-2520
aliz@conncoll.edu

Audrie-Jo McConkey
Nova Scotia Agricultural College
Truro, NS B2N 5E3
902-893-6533
amcconkey@nsac.ca

Daniel McDevit
University of New Brunswick
Fredericton, NB E3B 1E7
506-452-6086
dan.mcdevit@unb.ca

Brian McDonald
University of New Brunswick
Fredericton, NB E3B 6E1
506-452-6086
n7wmb@unb.ca

Chris McHan
Northeastern University
Boston, MA 02115
617-373-2489
mchan.c@neu.edu

Hilary McManus
University of Connecticut
Storrs, CT 06269
860-486-2289
hilary.mcmanus@uconn.edu

Tanya Moore
University of New Brunswick
Fredericton, NB E3B 6E1
506-453-3537
moore@unb.ca

Eduardo Morales
Philadelphia Acad. of Natural Sciences
Philadelphia, PA 19103
215-299-1102
morales@acnatsci.org

Vanessa Paesani
University of New Brunswick
Fredericton, NB E3B 6E1
506-455-9947
v.paesani@unb.ca

Karin Ponader
Harvard University Herbarium
Cambridge, MA 02138
617-495-2365
kponader@hotmail.com

Emily Porter-Goff
RPI
Troy, NY 12180
portee@rpe.edu

Kirwin Providence
Ithaca College
Ithaca, NY 14850
607-274-3979
kprovidence@ithaca.edu

Curt Pueschel
Binghamton University
Binghamton, NY 13902
607-777-2602
curtp@binghamton.edu

Haseeb Randhawa
University of New Brunswick
Fredericton, NB E3B 6E1
506-458-7592
haseeb.randhawa@unb.ca

Alison Roberts
University of Rhode Island
Kingston, RI 02881
401-874-4098
aroberts@uri.edu

Eric Roberts
Rhode Island College
Providence, RI 02908
401-456-9632
eroberts@ric.edu
Deborah Robertson
Clark University
Worcester, MA 01610
508-793-7515
debrobertson@clarku.edu

Alexander Ruck
Marist College
Poughkeepsie, NY 12603
845-304-1384
krnocopia@aol.com

Andrew Ryder
Marist College
Poughkeepsie, NY 12601
845-575-3000
andrew.ryder@marist.edu

Priya Sampath-Wiley
University of New Hampshire
Durham, NH 03824
603-862-3857
psampath@cisunix.unh.edu

Mike Satchwell
SUNY-ESF
Syracuse, NY 13210
315-470-6844
mfsatchw@syr.edu

Gary Saunders
University of New Brunswick
Fredericton, NB E3B 6E1
506-452-6216
gws@unb.ca

Craig Schneider
Trinity College
Hartford, CT 06106
860-297-2233
cschneid@trincoll.edu

Ashley Serfis
Skidmore College
Saratoga Springs, NY 12866
518-580-5075
a_serfis@skidmore.edu
Angela Silvestro
Northeastern University
Boston, MA 02115
617-373-2489
silvestro.a@neu.edu

Peter Siver
Connecticut College
New London, CT 06320
860-439-2160
pasiv@conncoll.edu

Nathan Smucker
Ohio University
Athens, OH 45701-2979
440-821-2970
ns218005@ohio.edu

Katie Snyder
Ohio University
Athens, OH 45701-2979
740-593-1134
ks818604@ohio.edu

R. Jan Stevenson
Michigan State University
East Lansing, MI 48824
517-432-8038
rjstev@msu.edu

Sarah Stewart
Ohio University
Athens, OH 45701-2979
740-593-1134
sarahastewart@gmail.com

Nicole Sweeney
Susquehanna University
Selinsgrove, PA 17870
570-372-3192
sweeney@susqu.edu

Anne Thomae
Skidmore College
Saratoga Springs, NY 12866
617-797-5905
a_thomae@skidmore.edu

Glen Thursby
U. S. Environmental Protection Agency
Narragansett, RI 02882
401-782-3178
thursby.glen@epa.gov

Francis Trainor
University of Connecticut
Storrs, CT 06268
860-486-4151
f.r.trainor@uconn.edu

Graham Underwood
University of Essex
Colchester, UK CO4 3SQ
44-0-1206-873337
gjcu@essex.ac.uk

Morgan Vis
Ohio University
Athens, OH 45701-2979
740-593-1134
vis-chia@ohio.edu

John Wehr
Fordham University
Armonk, NY 10504
914-273-3078
wehr@fordham.edu

Robert Wilce
University of Massachusetts
Amherst, MA 01003
413-545-1342
rwilce@bio.umass.edu

Richard Wilson
Skidmore College
Saratoga Springs, NY 12866
518-580-5075
r_wilson@skidmore.edu

Laura Wirpsza
Susquehanna University
Selinsgrove, PA 17870
609-432-7773
wirpsza@susqu.edu

Brian Wysor
Roger Williams University
Bristol, RI 02809
401-254-3014
bwysor@rwu.edu

Jason Zalack
Ohio University
Athens, OH 45701-2979
740-593-1134
jz165804@ohio.edu