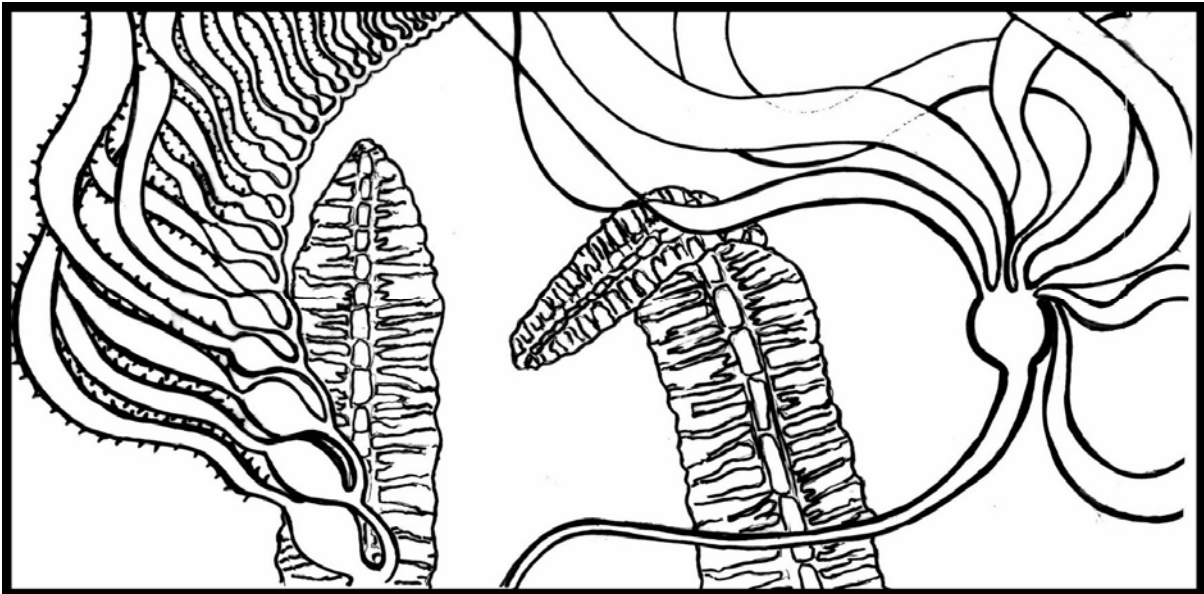


The Phycological Society of America

60th Annual Meeting

With the Northwest Algal Symposium



University of Alaska Southeast

Juneau, Alaska USA

6 - 12 July 2006

Meeting Program





THE PHYCOLOGICAL SOCIETY OF AMERICA



The *Phycological Society of America* was founded in 1946 to promote research and teaching in all fields of Phycology. The society publishes the *Journal of Phycology* and the *Phycological Newsletter*. Annual meetings are held, often jointly with other national or international societies of mutual member interest. *Phycological Society of America* awards include the **Bold Award** for best student paper at the annual meeting, the new **Student Poster Award** for the best student poster at the annual meeting, the **Provasoli Award** for outstanding papers published in the *Journal of Phycology*, and the **Prescott Award** for the best Phycology book published within the previous two years. The society provides financial aid to graduate student members through **Croasdale Fellowships** for enrollment in phycology courses at biological stations, **Hoshaw Travel Awards** for travel to the annual society meeting, and **Grants-In-Aid** for supporting research. To join the *Phycological Society of America*, contact the membership director. Society Webpage: <http://www.psaalgae.org/>

LOCAL ORGANIZER FOR 2006 PSA ANNUAL MEETING: Michael S. Stekoll, *University of Alaska*

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PSA Scientific and Social Events Room Schedule

DAY & DATE	MILLER ROOM	HAMMOND ROOM	HICKEL ROOM	SHEFFIELD BALLROOM 1	EGAN ROOM	SHEFFIELD BALLROOM 2	SHEFFIELD BALLROOM 3	OFF-SITE
THURSDAY 6 July								BOT Meeting 1:00 - 6:00 PM
FRIDAY 7 July		Meeting Registration 2:00 - 6:30 PM						EC Meeting 8:30 AM - 6:00 PM ----- Chancellor's Reception 7:00 - 10:00 PM (1st bus at 6:30)
SATURDAY 8 July	Speaker Preparation Room 8:00 AM - 5:00 PM	PSA Headquarters 8:00 AM to 5:00 PM	Relaxation and Discussion 8:00 AM to 5:00 PM	Plenary/Mini-Syposium & Featured Contributed Papers Macroalgal Ecology 8:00 AM - 12:00 PM ----- Bold Award 1 1:30-3:30 PM ----- Education Workshop 4:00 - 6:00 PM		Posters Available for Viewing		Auction/Mixer 7:30 - 9:30 PM
SUNDAY 9 July	Speaker Preparation Room 8:00 AM - 5:00 PM	PSA Headquarters 8:00 AM to 5:00 PM	Relaxation and Discussion 8:00 AM to 5:00 PM	Plenary/Mini-Syposium & Featured Contributed Papers Algal Genomics 8:00 - 11:30 AM ----- Bold Award 2 1:00-3:15 PM ----- Ecology & Pop. Biology 1 3:45-5:00 PM ----- PSA Business Meeting 5:00 - 6:30 PM		Applied Phycology 3:45-5:00 PM	Posters Available for Viewing	<i>Journal of Phycology</i> Editorial Board Luncheon
MONDAY 10 July	Speaker Preparation Room 2:00-7:00 PM					Poster Session and Mixer 7:00 - 9:30 PM	Poster Session and Mixer 7:00 - 9:30 PM	Optional Field Trips during morning and afternoon
TUESDAY 11 July	Speaker Preparation Room 8:00 AM - 5:00 PM	PSA Headquarters 8:00 AM to 5:00 PM	Relaxation and Discussion 8:00 AM to 5:00 PM	Plenary/Mini-Syposium & Featured Contributed Papers Phytoplankton Evolution 8:00 - 11:30 AM ----- Phylogenetics & Taxonomy 1 1:00-3:00 PM ----- Phylogenetics & Taxonomy 2 3:30-5:30 PM		Physiology/Biochemistry & Cellular/Molecular Biology 1:00-3:00 PM ----- Ecology & Pop. Biology 2 3:30-5:00 PM ----- NWAAS Business Meeting 5:30-6:00 M	Posters Available for Viewing	PSA Banquet/Awards Cer. Buses leaving 7:00-7:30 PM
WEDNESDAY 12 July	Speaker Preparation Room 8:00 - 10:00 AM		Relaxation and Discussion 8:00 - 11:30 AM	Plenary/Mini-Syposium & Featured Contributed Papers Diatom Ecology & Evolution Heterokont Ecol. & Evolution 8:30 AM - 12:00 PM				

PSA 2006 MEETING SPONSOR:



The University of Alaska Southeast Juneau campus is the scholastic home to about 700 full-time and 2,000 part-time students. It offers a variety of degree and certificate programs including master's and bachelor's degrees. The Juneau campus' natural setting along the shores of the Inside Passage lends itself to the study of marine biology and environmental science. All degree programs, and especially programs in public administration and business administration, take advantage of our location in the state capital. Small classes, personal attention and interaction with faculty, a dynamic location and real educational value are all key components of a UAS education.

UAS is surrounded by the last great expanse of temperate rainforest left in North America and our programs are designed with that in mind. The Tongass National Forest is our living classroom. It is a place in which our students find solace, inspiration, and opportunities to be challenged both academically and physically. Students can find the Mendenhall Glacier, the shores of the Inside Passage and stands of old growth forest all within three miles of campus.



HOST CITY: JUNEAU

Called America's most scenic state capital, Juneau is surrounded by intercoastal waterways, lush rainforests, rugged mountainsides, and awe-inspiring, accessible glaciers. The Mendenhall Glacier, an arm of the 1,500 square mile Juneau Icefield, is one of the few glaciers in Alaska you can reach by car. The Tongass Rainforest climate provides Juneau with lush terrain and vibrant wildflowers.

Originally fishing grounds for local Tlingit Indians, the Gastineau Channel area became a focus of attention in the late 1800 's when a Tlingit named Kowee of the Auk Tlingit Tribe provided gold ore samples in response to a reward offered by George Pilz, a Sitka engineer. Pilz grubstaked prospectors Richard Harris and Joseph Juneau in August 1880. They found plenty of color in Gold Creek, but did not follow the gold to its source. At Kowee 's urging, Pilz sent the pair back again. Harris and Juneau climbed Snow Slide Gulch at the head of Gold Creek and looked down into the mother lode of Quartz Gulch and Silver Bow Basin.

On October 18, they staked a 160 acre town site on the beach where, the following month, they were joined by the first boatloads of prospectors bound for the new strike on Gastineau Channel. The stampede was on. The discovery was the first that resulted in the founding of an Alaskan town.

Juneau grew from a boomtown to a center for large-scale hard-rock mining when the loose gold in the stream beds ran out. On the mainland side of the Channel, two great mills were created: the Alaska-Juneau at the south end of Juneau and the Alaska-Gastineau at Thane, farther south. On Douglas Island, the ground reverberated with 960 stamps of the world-renowned Treadwell Gold Mining Company.

Treadwell production peaked in 1915. Two years later, a cave-in flooded three of the four mines, effectively ending the Treadwell era. In Juneau, the Alaska-Gastineau folded from high costs in 1921. A-J was halted by the war in 1944.

Juneau was established as Alaska's capital in 1906 when the government was transferred from Sitka. Today, federal, state and local government employs one out of every two Juneau workers. Tourism is the largest private employer and continues to grow. Commercial fishing and mining continue to play a role in Juneau's economy.

Juneau is a marvel - an unexpected blend of fishermen and teachers, legislators and artists, homemakers and lawyers, union workers and frontier entrepreneurs, students and Native elders, all sharing an active port city within an inspiring wilderness setting. Juneau offers unparalleled glacier viewing from Tracy Arm Fjord, Mendenhall Glacier, the Juneau Icefield, and Glacier Bay National Park. Outdoor enthusiasts will love Juneau's extraordinary kayaking, dogsledding, rafting, biking, hiking, and glacier hiking. Abundant salmon and halibut fishing is also available minutes from downtown. Wilderness cabins and fishing lodges cater to anglers seeking the remote Alaska fishing experience. Juneau flightseeing excursions feature spectacular scenery. Incredible wildlife inhabits areas in and around Juneau. The downtown area is served by tramway up Mt. Roberts, where wilderness is instantly accessible. Nearby Admiralty Island National Monument, features one of the largest concentrations of brown bear in the world. Icy Strait offers unprecedented whale watching.

The outstanding hiking, kayaking, sportfishing, flyfishing, whale watching, and wildlife viewing add to the city's distinctive character. With Glacier Bay National Park, Tracy Arm, and Admiralty Island National Monument nearby, Juneau offers all the experiences for which Alaska is legendary.

CENTENNIAL HALL ROOM INFORMATION

THE PSA HEADQUARTERS ROOM will be located in the **Hammond Room**. Meeting t-shirts and a variety of other psychological items will be on sale there. In addition, many of the items up for sale at the PSA Auction will be on display there on prior to the auction.

The **SPEAKER PREPARATION ROOM** will be the **Miller Room**.

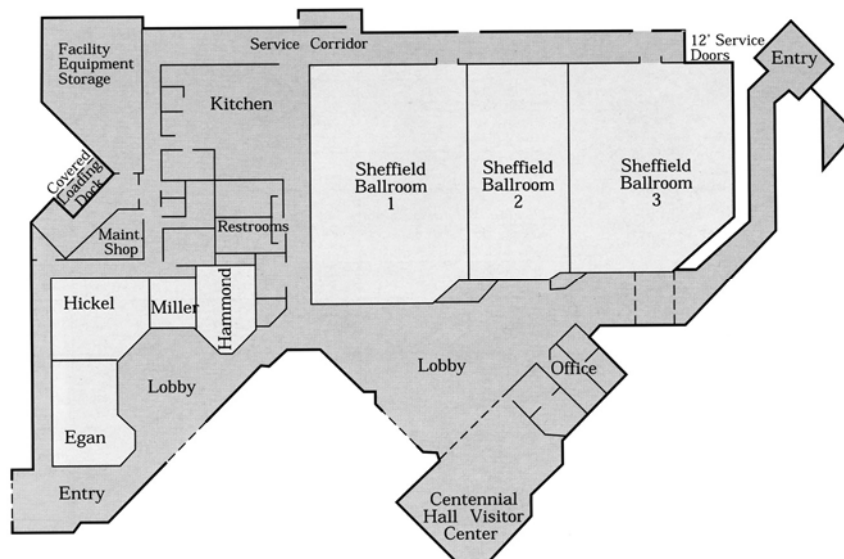
The **Hickel Room** will be available for **RELAXATION AND DISCUSSIONS**.

ORAL PRESENTATIONS will be in **Sheffield Ballroom 1** and the **Egan Room**.

POSTERS will be in **Sheffield Ballroom 2**.

The **AUCTION AND MIXER** and the **POSTER SESSION MIXER** will be in **Sheffield Ballroom 3** (which will be open to Sheffield Ballroom 2 during the Poster Session Mixer).

*Note that **Wireless Internet** is available throughout Centennial Hall Convention center at no charge.*

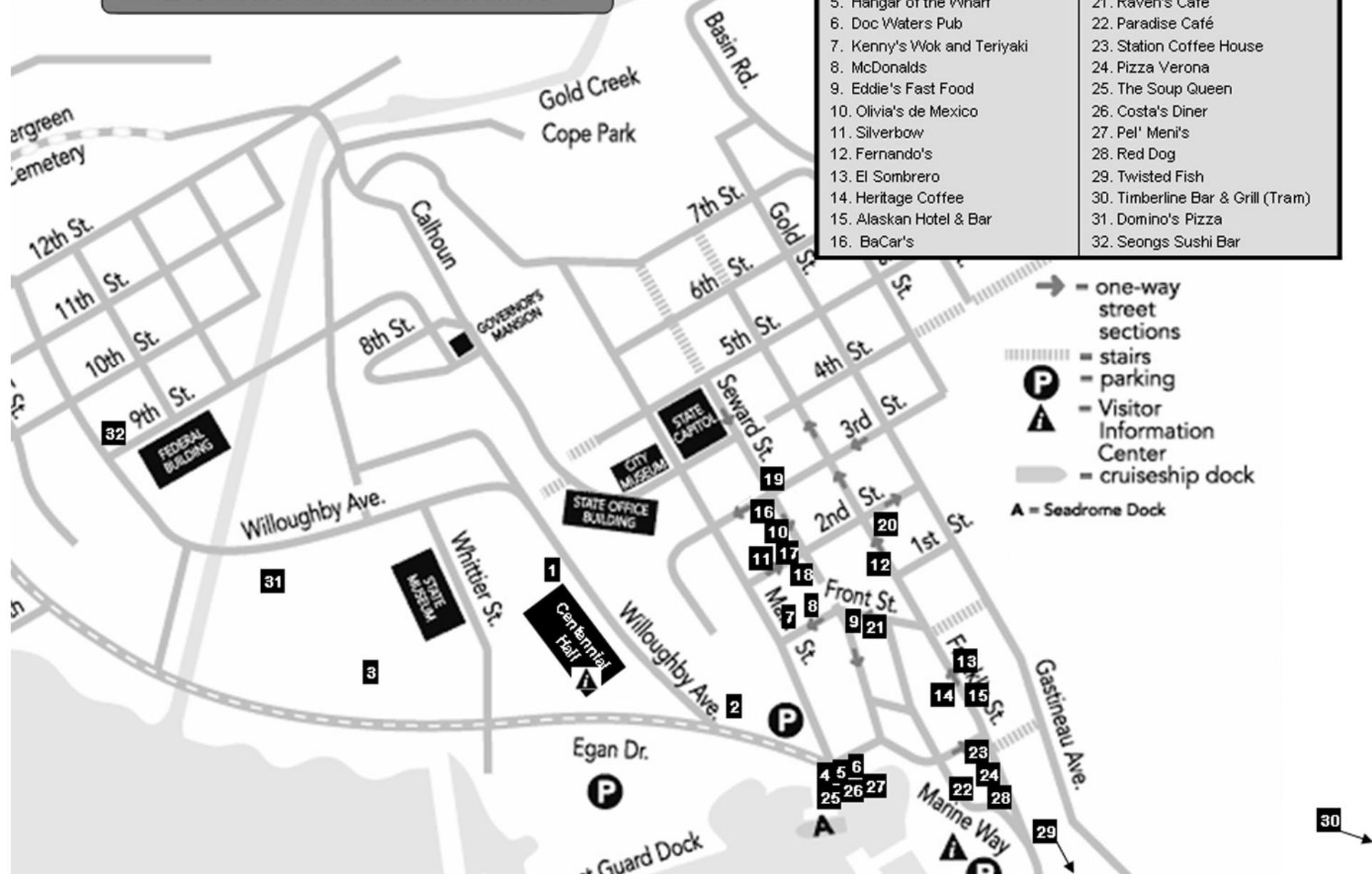


JUNEAU

Downtown Restaurants

Restaurant locations are marked with boxes: **13**

- | | |
|-----------------------------|-----------------------------------|
| 1. Bullwinkle's Pizza | 17. Oriental Express |
| 2. Goldbelt | 18. Wild Spice |
| 3. Prospector | 19. Subway |
| 4. Pizzeria Roma | 20. Capital Café |
| 5. Hangar of the Wharf | 21. Raven's Café |
| 6. Doc Waters Pub | 22. Paradise Café |
| 7. Kenny's Wok and Teriyaki | 23. Station Coffee House |
| 8. McDonalds | 24. Pizza Verona |
| 9. Eddie's Fast Food | 25. The Soup Queen |
| 10. Olivia's de Mexico | 26. Costa's Diner |
| 11. Silverbow | 27. Pel' Meni's |
| 12. Fernando's | 28. Red Dog |
| 13. El Sombrero | 29. Twisted Fish |
| 14. Heritage Coffee | 30. Timberline Bar & Grill (Tram) |
| 15. Alaskan Hotel & Bar | 31. Domino's Pizza |
| 16. BaCar's | 32. Seongs Sushi Bar |



PROGRAM OF SESSIONS AND EVENTS

THURSDAY AFTERNOON, 6 JULY – University of Alaska Southeast Campus

PSA Board Of Trustees Meeting, 1:00 to 6:00 PM

FRIDAY, 7 JULY – University of Alaska Southeast Campus

PSA Executive Committee Meeting, 8:30 AM to 6:00 PM

Registration Table Open In Centennial Hall Convention Center, 2:00 to 6:30 PM

Pre-Meeting Field Trips

Vouchers for the pre-meeting tours can be picked up at your hotel unless you have made prior arrangements with the Local Organizer, Mike Stekoll (ffmss@uaf.edu, cell phone 907-723-1514). Information will be included with the vouchers concerning where and when to meet for each tour.

Chancellor's Reception (Opening Social and Mixer), 7:00 to 10:00 PM

Buses will leave from Centennial Hall at 6:30 and 7:00

Buses back to Centennial Hall from campus will leave at 9:30 and 9:50

SATURDAY MORNING, 8 JULY – Sheffield Ballroom 1

8:00 PSA and NWSA welcoming remarks

Special Session: The Experimental Ecology - Macroalgae Connection

Introducing and Presiding: Chuck Amsler, University of Alabama at Birmingham

8:15 **PLENARY LECTURE: Reflections Of A Phycological Zoologist: Macroalgae As Powerful Experimental Probes Of How Natural Communities Are Organized**

Paine, Robert

Department of Biology, University of Washington, Seattle, WA, USA

9:00 **Algal Diversity Manipulations: How Do Seaweeds Structure Rocky Shores?**

Graham, Michael H.¹, Szoboszlai, Amber¹, Bracken, Matthew E.² & Stachowicz, John J.^{2,3}

¹Moss Landing Marine Labs, Moss Landing, CA, USA; ²Bodega Marine Lab, Bodega Bay, CA, USA;

³Section of Evolution and Ecology, University of California, Davis, CA, USA

9:30 **Macroalgae Reveal The Underappreciated Role Of Resources In Structuring Benthic Marine Communities**

Nielsen, Karina J.

Department of Biology, Sonoma State University, Rohnert Park, CA, USA

10:00 **BREAK**

Presiding: Robert Paine, University of Washington

10:30 Synergistic Serial Depletion Of Marine Invertebrates Leads To The Decline Of A Keystone Grazer And The Alteration Of A Coastal Ecosystem

Salomon, Anne K.

Department of Biology, University of Washington, Seattle, WA, USA

Featured Contributed Papers: The Experimental Ecology - Macroalgae Connection

11:00 Disturbance Maintains High Local Diversity In *Ecklonia radiata* Kelp Forests

Kendrick, Gary A., Toohey, Ben D. & Harvey, Euan S.

Department of Plant Biology, University of Western Australia, Crawley, WA, Australia

11:15 Demographic Consequences Of Inbreeding And Population Structure In Kelp

Pfister, Catherine & Wootton, J T.

Department of Ecology & Evolution, University of Chicago, Chicago, IL, USA

11:30 Determining Recovery In Rocky Intertidal Systems: Relative Performance Of Recovery Endpoints

Klinger, Terrie

Marine Affairs, University of Washington, Seattle, WA, USA

11:45 Rates Of Selfing And Outcrossing In Two Species Of Intertidal Kelp (*Postelsia palmaeformis* And *Alaria nana*) From Geographically Separated Parents

Collens, Julie

Department of Ecology and Evolution, University of Chicago, Chicago, IL, USA

Lunch on your own 12:00 to 1:30

SATURDAY AFTERNOON, 8 JULY – Sheffield Ballroom 1

Bold Award 1

Presiding: Kirsten Müller, University of Waterloo

1:30 Phylogeny And Evolutionary Ecology Of Thalassiosiroid Diatoms

Alverson, Andrew^{1,2} & Theriot, Edward¹

¹*Plant Biology Graduate Program, The University of Texas at Austin, Austin, TX, USA;* ²*Texas Memorial Museum, The University of Texas at Austin, Austin, TX, USA*

1:45 Linking Light Attenuation And Suspended Sediment Loading To Benthic Productivity Within An Arctic Kelp Bed Community

Aumack, Craig F.^{1,2}, Dunton, Kenneth H.², Burd, Adrian B.³ & Funk, Dale W.⁴

¹*Department of Biology, University of Alabama at Birmingham, Birmingham, AL, USA;* ²*Department of Marine Science, The University of Texas Marine Science Institute, Port Aransas, TX, USA;* ³*Department of Marine Science, University of Georgia, Athens, GA, USA;* ⁴*LGL Alaska Research Associates, Inc., Anchorage, AK, USA*

- 2:00 **Effects Of Nutrient Enrichment On Biomass And Primary Production Of Sediment Microalgae In *Halodule wrightii* Ascherson (Shoalgrass) Seagrass Beds**
Bucolo, Anthony P.¹, Sullivan, Michael J.² & Zimba, Paul V.³
¹*Department of Biology, University of Alabama at Birmingham, Birmingham, AL, USA;* ², *Florida State University Marine Lab, St. Teresa, FL, USA;* ³*USDA, , Stoneville , MS, USA*
- 2:15 **Photosynthetic Activities Of *Sargassum* spp. And *Lobophora variegata* In Tung Ping Chau Marine Park, Hong Kong Sar,China**
Fai Fai, Yeung¹ & Put, Ang O.²
¹*Department of Environmental Science, The Chinese University of Hong Kong, Hong Kong, Hong Kong;* ²*Department of Biology, The Chinese University of Hong Kong, Hong Kong, Hong Kong*
- 2:30 **Distribution Of Symbiotic Algae Within The Intertidal Sea Anemone *Anthopleura xanthogrammica* In Alaska And Oregon**
Kitaeff, Pema & Muller-Parker, Gisele
Department of Biology, Western Washington University, Bellingham, WA, USA
- 2:45 **Characterization Of A Nitrogen-Regulated Cell-Surface Protein In The Marine Coccolithophore, *Emiliana huxleyi***
Landry, Dori M.¹, Read, Betsy² & Palenik, Brian¹
¹*Marine Biology, Scripps Institution of Oceanography, San Deigo, CA, USA;* ²*Biological Sciences, California State University, San Marcos, San Marcos, CA, USA*
- 3:00 **ISSR-Estimated Intraspecific Genetic Variation And Phylogenetic Position Of A Population Of The Red Alga *Bangia maxima***
Lynch, Michael D.¹, Müller, Kirsten M.¹ & Sheath, Robert G.²
¹*Department of Biology, University of Waterloo, Waterloo, ON, Canada;* ²*Provost's Office, Division of Academic and Student Affairs, California State University San Marcos, San Marcos, CA, USA*
- 3:15 **Molecular Phylogeography And Species Discrimination Of Freshwater *Cladophora* (Cladophorales, Chlorophyta) In North America**
Ross, Sara J.¹, Sheath, Robert G.² & Müller, Kirsten M.¹
¹*Department of Biology, University of Waterloo, Waterloo, ON, Canada;* ²*Department of Biology, California State University at San Marcos, San Marcos, CA, USA*
- 3:30 **BREAK**
- 4:00 to 6:00 ***Education Workshop: Algae and the Broader Impacts of Science***
Organized by Richard Triemer (Michigan State University) and Gisèle Muller-Parker (National Science Foundation and Western Washington University) for the PSA Education Committee

Dinner on your own 6:00 to 7:30

7:30 to 9:30 **PSA AUCTION AND MIXER – Sheffield Ballroom 3**

SUNDAY MORNING, 9 JULY – Sheffield Ballroom 1

Special Session: Molecular, Biochemical, And Genomics Approaches For Phytoplankton Research

Introducing and Presiding: John La Claire, University of Texas at Austin

8:00 PLENARY LECTURE: Application Of Molecular And Genomics Tools To Diatoms

Hildebrand, Mark

Scripps Institution of Oceanography, UCSD, La Jolla, CA, USA

9:00 Molecular Genetic Approaches To Studying Silica Biomineralization In Diatoms

Poulsen, Nicole & Kröger, Nils

Department of Chemistry & Biochemistry, Georgia Institute of Technology, Atlanta, GA, USA

9:30 BREAK

Presiding: Mark Hildebrand, Scripps Institution of Oceanography

10:00 Molecular Approaches To Understanding Biomineralization In *Emiliana huxleyi*

Read, Betsy A.

Department of Biological Sciences, Cal State University, San Marcos, CA, USA

Featured Contributed Papers: Algal Genomics

10:30 Molecular Archeology: Sequencing Stramenopile Chloroplast DNA

Cattolico, Rose Ann^{1,2}, Jacobs, Michael³, Rocap, Gabrielle² & Zhou, Yang³

¹Biology, University of Washington, Seattle, WA, USA; ²Oceanography, University of Washington, Seattle, WA, USA; ³Genome Center, University of Washington, Seattle, WA, USA

10:45 Putative Rubisco Activase CfxQ In The Toxic Alga *Heterosigma akashiwo*

Lee, Kun-Lin¹, Hoyt, Amanda¹ & Cattolico, Rose Ann^{2,3}

¹Biochemistry, University of Washington, Seattle, WA, USA; ²Biology, University of Washington, Seattle, WA, USA; ³Ocean Sciences, University of Washington, Seattle, WA, USA

11:00 Functional Genomics Of The Harmful Alga, *Prymnesium parvum* (Haptophyta)

La Claire, John W.

MCD Biology, U. Texas at Austin, Austin, TX, USA

11:15 Genes And Genomes In The Charophyte Green Algae

Delwiche, Charles F.

Cell Biology and Molecular Genetics, University of Maryland - College Park, College Park, MD, USA

Lunch on your own 11:30 to 1:00

***Journal of Phycology* Editorial Board Luncheon, 11:30 to 1:00**

SUNDAY EARLY AFTERNOON, 9 JULY – Sheffield Ballroom 1

Bold Award 2

Presiding: Kirsten Müller, University of Waterloo

- 1:00 **Identification Of Geosmin Producing Cyanobacteria In Lake Ontario Using DGGE**
Gill, Andrea¹, Muller, Kirsten M.¹ & Watson, Susan B.²
¹*Department of Biology, University of Waterloo, Waterloo, ON, Canada;* ²*National Water Research Institute (NWRI), Environment Canada, Burlington, ON, Canada*
- 1:15 **An Early Light-Inducible Protein (ELIP) Is Produced During Cold Acclimation Of *Spirogyra varians* (Zygnematales)**
Han, Jong Won¹, Yoon, MinChul², Lee, Key Pyoung¹ & Kim, Gwang Hoon²
¹*Department of Chemistry, Kongju National University, Kongju, South Korea;* ²*Department of Biology, Kongju National University, Kongju, South Korea*
- 1:30 **The Mitochondrial Genome Of A Tertiary Endosymbiont Retains Genes For Electron Transport Proteins**
Imanian, Behzad¹, Carpenter, Kevin J.^{3,2} & Keeling, Patrick J.^{3,2}
¹*Genetics Graduate Program, University of British Columbia, Vancouver, BC, Canada;* ²*Department of Botany, University of British Columbia, Vancouver, BC, Canada;* ³*Canadian Institute for Advanced Research, Vancouver, BC, Canada*
- 1:45 **The Effect Of Water Flow Induced Carbon Limitation On The Physiology Of *Laminaria saccharina***
Jordan, Terry L.¹, Koch, Evamaria W.¹ & Davison, Ian R.²
¹*Horn Point Laboratory, University of Maryland Center for Environmental Sciences, Cambridge, MD, USA;* ²*Academy of Natural Sciences, Philadelphia, PA, USA*
- 2:00 **Phylogenetic Affinities Of Australasian *Batrachospermum* Specimens (Batrachospermales, Rhodophyta) Inferred From Molecular And Morphological Data**
Stewart, Sarah A.¹, Vis, Morgan L.¹ & Entwisle, Timothy J.²
¹*Environmental and Plant Biology, Ohio University, Athens, OH, USA;* ²*Royal Botanic Gardens and Domain Trust, Sydney, NSW, Australia*
- 2:15 **Facilitative Effect Of Intertidal Macroalgal Canopies On *Pelvetiopsis* Recruitment**
Szoboszlai, Amber
Moss Landing Marine Labs, San Jose State University, Moss Landing, CA, USA
- 2:30 **Comparative Sequence Analysis Of Diatom Silicon Transporters: Towards A Molecular Model Of Silicon Transport**
Thamatrakoln, Kimberlee¹, Alverson, Andrew J.² & Hildebrand, Mark¹
¹*Scripps Institution of Oceanography, La Jolla, CA, USA;* ²*Section of Integrative Biology and Texas Memorial Museum, The University of Texas at Austin, Austin, TX, USA*
- 2:45 **Experimental Evaluation Of Reduced Resource Allocation On The Growth And Reproduction Of *Sargassum siliquastrum* (Turn.) Ag. In Hong Kong Sar, China**
Wong, Suet Ying¹ & Ang, Put O. Jr.²
¹*Environmental Science Programme, The Chinese University of Hong Kong, Hong Kong, China;* ²*Biology Department, The Chinese University of Hong Kong, Hong Kong, China*

3:00 **Development And Evaluation Of A Diatom Based Index Of Biotic Integrity For Acid And Metal Impacted Streams**

Zalack, Jason T. & Vis, Morgan L.

Environmental and Plant Biology, Ohio University, Athens, OH, USA

3:15 **BREAK**

SUNDAY LATE AFTERNOON, 9 JULY – Sheffield Ballroom 1

Ecology & Population Biology 1

Presiding: Michael Graham, Moss Landing Marine Lab

3:45 **Towards A Global Phylogeography Of *Gracilaria salicornia* (Gracilariaceae, Rhodophyta), An Invasive Species In Hawaii, Based On Chloroplast And Mitochondrial Markers**

Gurgel, Carlos F.¹, Terada, Ryuta², Abbott, Isabella A.³, Fredericq, Suzanne⁴ & Norris, James N.⁵

¹*Smithsonian Marine Station, Smithsonian Institution, Fort Pierce, FL, USA;* ²*Faculty of Fisheries, Kagoshima University, Shimoarata, Japan;* ³*Dept. of Botany, University of Hawai`i at Manoa, Honolulu, HI, USA;* ⁴*Dept. of Biology, University of Louisiana, Lafayette, LA, USA;* ⁵*Dept. of Botany, Smithsonian Institution, Washington, DC, USA*

4:00 **Dopamine In A Green Alga: Localization, Release, And Community Effects**

Nelson, Tim¹, Van Alstyne, Kathryn L.² & Jackson, Dana³

¹*Blakely Island Field Station, Seattle Pacific University, Seattle, WA, USA;* ²*Shannon Point Marine Center, Western Washington University, Anacortes, WA, USA;* ³*Biology, Paine College, Augusta, GA, USA*

4:15 **Assessment Of Coral Reefs Using Herbivory/Nutrient Assays And Indicator Groups Of Benthic Primary Producers: A Critical Synthesis, Proposed Protocols, And Critique Of Management Strategies**

Littler, Mark M.¹ & Littler, Diane S.²

¹*Department of Botany, Smithsonian Institution, Washington, DC, USA;* ²*Marine Science, Harbor Branch Oceanographic, Fort Pierce, FL, USA*

4:30 **Macroalgal Communities In Indian River Lagoon, Florida: Spatial And Temporal Variability**

Hanisak, M. Dennis

Harbor Branch Oceanographic Institution, Fort Pierce, FL, USA

4:45 **Changing Seaweed Communities On Southern California Shores**

Murray, Steven N.^{1,2}, Smith, Jayson¹, Bullard, Aimee¹, Gerrard, Amanda¹ & Kido, Janine¹

¹*College of Natural Sciences and Mathematics, California State University, Fullerton, Fullerton, CA, USA;* ²*Department of Biological Science, California State University, Fullerton, Fullerton, CA, USA*

5:00 to 6:30 ***PSA Business Meeting***

8:00 to ??? ***PSA/NWAS Student Organized Evening Out (for students only). Location TBA***

SUNDAY LATE AFTERNOON, 9 JULY – Egan Room

Applied Phycology

Presiding: Thierry Chopin, University of New Brunswick

- 3:45 **Integrated Multi-Trophic Aquaculture: Seaweeds And Beyond... The Need Of An Interdisciplinary Approach To Develop Sustainable Aquaculture**
Chopin, Thierry¹, Robinson, Shawn², MacDonald, Bruce¹, Haya, Kats², Page, Fred², Ridler, Neil¹, Szemerda, Michael³, Sewuster, John⁴ & Boyne-Travis, Sharon⁵
¹University of New Brunswick, Saint John, NB, Canada; ²Fisheries & Oceans, St. Andrews, NB, Canada; ³Cooke Aquaculture Inc., St. George, NB, Canada; ⁴Acadian Seaplants Limited, Dartmouth, NS, Canada; ⁵CFIA, Blacks Harbour, NB, Canada
- 4:00 **Photoautotrophic Growth Of Microalgae In Tubular Photobioreactors**
Ugwu, Charles U., Aoyagi, Hideki, Uchiyama, Hiroo & Tanaka, Hideo
Institute of Life Sciences and Bioengineering, University of Tsukuba, Japan, Tsukuba city, Japan
- 4:15 **Developing A Land-Based, Low-Cost Polyculture System Accessible To Coastal Maori**
Miller, Sheryl¹, Heath, Philip² & Williams, Tiratu³
¹Te Kuwaha, National Institute of Water & Atmospheric Research Ltd, Wellington, New Zealand; ²Aquaculture and Fisheries Enhancement, National Institute of Water and Atmospheric Research Ltd, Wellington, New Zealand; ³Hongoeka Community Development Trust, Wellington, New Zealand
- 4:30 **Nutraceuticals From Red Microalgae As Hypocholesterolemic Agent**
Dvir, Irit¹, Chayoth, Reuven², Madar, Zecharia³ & Arad (Malis), Shoshana¹
¹The Institute for applied biotechnology, Ben-Gurion University of the Negev, Beer Sheva 84105, Israel; ²Life science, Ben-Gurion University of the Negev, Beer Sheva 84105, Israel; ³Faculty of Agriculture, The Hebrew University of Jerusalem, Rehovot 76100, Israel
- 4:45 **Biodiesel From Algae: Lessons Learned Over The Past 60 Years And Future Perspectives**
Hu, Qiang, Zhang, Chengwu & Sommerfeld, Milton
Department of Applied Biological Sciences, Arizona State University, Mesa, AZ, USA
- 5:00 to 6:30 ***PSA Business Meeting (in Sheffield Ballroom 1)***
- 8:00 to ??? ***PSA/NWAS Student Organized Evening Out (for students only). Location TBA***
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MONDAY, 10 JULY

Field trips during morning and afternoon

Vouchers for the mid-meeting tours should be included with your registration packet. Information about where and when to meet for the tours will be included with the vouchers. For help with the tours contact the Local Organizer, Mike Stekoll (ffmss@uaf.edu, cell phone 907-723-1514).

The Intertidal Collecting and Freshwater Collecting field trips will leave from Centennial Hall. The Intertidal field trip will leave at 6 AM. The Freshwater trip will leave at 12:00 noon.

MONDAY EVENING, 10 JULY – Sheffield Ballrooms 2 and 3

Poster Session and Mixer: 7:00 to 9:30 PM

Presenting authors are encouraged to stand with their posters throughout the evening.

Presenting authors of ODD numbered posters are requested to stand with their posters at least between 7:00 and 7:45.

Presenting authors of EVEN numbered posters are requested to stand with their posters at least between 7:45 and 8:30.

Posters can be put up in Sheffield Ballroom 2 on Saturday and can be left up until Wednesday morning. Authors are encouraged to have their posters on display for as long as possible.

- 1 **Demographic Similarities And Differences Between *Zostera japonica* In Its Native (Korea) And Introduced (Willapa Bay) Habitats**
DeAmicis, Stacey¹, Hong, Jae-Sang² & Ruesink, Jennifer¹
¹*Biology, University of Washington, Seattle, WA, USA;* ²*Oceanography, Inha University, Incheon, South Korea*
- 2 **The Relationships Between Delayed And Prompt Fluorescence In Monitoring Photosynthetic Traits Of Phytoplankton**
Kurzbaum, Eyal¹, Eckert, Werner² & Beer, Sven¹
¹*Plant science, Tel Aviv university, Tel Aviv, Israel;* ²*The Yigal Allon Kinneret Limnological Laboratory, Israel Oceanographic and Limnological Research, Migdal, Israel*
- 3 **Domoic Acid Production By *Pseudo-nitzschia* spp. In Response To Estuarine Nutrient Dynamics**
Ohana-Richardson, Andrew & Shapiro, Lynda
Oregon Inst. of Marine Biology, University of Oregon, Charleston, OR, USA
- 4 **The Influence Of Temperature, Salinity, And Nutrients On Cyanobacterial Density In Costal Waters Of Bandar Abbas, Persian Gulf**
Nejatkah Manavi, Parisa¹ & Korei, H.²
¹*Marine Biology, Islamic Azad University, North Tehran Branch, Tehran, Iran;* ²*Marine Biology, Islamic Azad University, North Tehran Branch, Tehran, Iran*
- 5 **Delayed Development In Kelp Forest Systems**
Carney, Laura & Edwards, Matthew S.
Biology, San Diego State University, San Diego, CA, USA
- 6 **Six Easy Steps To (Hopefully) Plating Your Favorite Phytoplankton Species**
Lakeman, Michael B.¹ & Cattolico, Rose Ann^{1,2}
¹*Biology, University of Washington, Seattle, WA, USA;* ²*Ocean Sciences, University of Washington, Seattle, WA, USA*
- 7 **A Re-Evaluation Of The Trophic State Of Mountain Lake, Virginia**
Parker, Bruce C.¹ & Deshler, David²
¹*Department of Biological Sciences, Virginia Tech, Blacksburg, VA, USA;* ²*The Wilderness Conservancy at Mountain Lake, Pembroke, VA, USA*

- 8 **Decline Of The Native Kelp *Kjellmaniella crassifolia* Miyabe On The Eastern Coast Of Korea**
Kim, Hyung Geun¹, Park, Joong Goo¹, Lee, Sung Bok¹, Son, Yong Soo² & Sohn, Chul Hyun³
¹*Faculty of Marine Bioscience and Technology, Kangnung National University, Gangneung, South Korea;*
²*East Sea Fisheries Research Institute, NFRDI, Gangneung, South Korea;* ³*Department of Aquaculture, Pukyong National University, Busan, South Korea*
- 9 **Characterization Of The Macroalgal Community Associated With The High Energy Zone Of Punta Yu Yum, Quintana Roo, Mexico**
Fikes, Ryan L.¹, Smith, Leslie C.² & Lehman, Roy L.¹
¹*Physical & Life Sciences, Texas A&M University-Corpus Christi, Corpus Christi, TX, USA;* ²*Center for Coastal Studies, Texas A&M University-Corpus Christi, Corpus Christi, TX, USA*
- 10 **Potential Chemical Defenses Against Endophytes And Epiphytes In Antarctic Macroalgae**
Aumack, Craig F.¹, Backstrom, Ian C.¹, Amsler, Charles D.¹, McClintock, James B.¹ & Baker, Bill J.²
¹*Department of Biology, University of Alabama at Birmingham, Birmingham, AL, USA;* ²*Department of Chemistry, University of South Florida, Tampa, FL, USA*
- 11 **Population Structure Of *Padina australis* Hauck (Dictyotales, Phaeophyta) In Two Locations In Phuket Province, Thailand**
 Wichachucherd, Bongkot¹, Prathep, Anchana¹ & Liddle, Larry B.²
¹*Department of Biology, Prince of Songkla University, Hat Yai, Thailand;* ²*Department of Marine Science, Southampton College of Long Island University, Southampton, NY, USA*
- 12 **Effects Of Herbivory And Season Of Clearing On Species Composition And Algal Succession In A Tropical Intertidal Shore, Phuket, Thailand**
 Mayakun, Jaruwat¹, Prathep, Anchana¹, Kim, Jeong Ha² & Liddle, Larry B.³
¹*Department of Biology, Prince of Songkla University, Hat Yai, Thailand;* ²*Department of Biological Science, Sungkyunkwan University, Suwon, South Korea;* ³*Marine Science, Southampton College of Long Island University, Southampton, NY, USA*
- 13 **Differences In *Skeletonema* Distribution Among Three Distant Temperate Coastal Sites**
Saggiomo, Maria¹, Kooistra, Wiebe H.¹, Sarno, Diana¹, Montresor, Marina¹, Burns Lopez, Cary², Cloern, James E.², Hargraves, Paul H.^{3,4} & Zingone, Adriana¹
¹*Stazione Zoologica A. Dohrn, Naples, Italy;* ²*U.S. Geological Survey MS496, Menlo Park, CA, USA;*
³*University of Rhode Island, Narragansett, RI, USA;* ⁴*Harbor Branch Ocean. Inst., Ft. Pierce, FL, USA*
- 14 **Sympagic Diatoms In The Annual Pack Ice Of Terra Nova Bay, Ross Sea, Antarctica**
Saggiomo, Maria¹, De Stefano, Mario², Mangoni, Olga³, Saggiomo, Vincenzo¹, Sarno, Diana¹ & Zingone, Adriana¹
¹*Stazione Zoologica Anton Dohrn, Naples, Italy;* ²*Seconda Università di Napoli, Caserta, Italy;* ³*Università di Napoli "Federico II", Naples, Italy*
- 15 **Phototactic Responses Of *Elachista antarctica* Skottsberg Spores**
Bucolo, Anthony P.¹, Amsler, Charles D.¹, McClintock, James B.¹ & Baker, Bill J.²
¹*Department of Biology, University of Alabama at Birmingham, Birmingham, AL, USA;* ²*Department of Chemistry, University of South Florida, Tampa, FL, USA*

- 16 **Dramatic Blooms Of A Bioluminescent Dinoflagellate And A Potentially Toxic Prymnesiophyte In The Salton Sea, California**
 Wolny, Jennifer^{2,3}, Steidinger, Karen^{2,3}, Tiffany, Mary A.¹ & Garrett, Matthew³
¹Biology, San Diego State University, San Diego, CA, USA; ²Florida Fish and Wildlife Conservation Commission, Fish and Wildlife Research Institute, St. Petersburg, FL, USA; ³Florida Institute of Oceanography, St. Petersburg, FL, USA
- 17 **Initial Observations And Monitoring Of *Grateloupia turuturu* Yamada Along The Connecticut Coast In Long Island Sound**
Gladych, Rebecca A.¹, Keser, Milan² & Yarish, Charles³
¹Department of Marine Sciences, University of Connecticut, Groton, CT, USA; ²Millstone Environmental Laboratory, Dominion Nuclear Connecticut, Waterford, CT, USA; ³Ecology and Evolutionary Biology, University of Connecticut, Stamford, CT, USA
- 18 **Diatom Polymers Of Colne Estuary (U.K.) Biofilms: Functional Roles Of EPS Based On Structural Characteristics**
Bellinger, Brent J.¹, Underwood, Graham J.² & Gretz, Michael¹
¹Department of Biological Sciences, Michigan Technological University, Houghton, MI, USA; ²Department of Biological Sciences, University of Essex, Colechester, United Kingdom
- 19 **Notes From Underground: Bryopsidalean Green Algal Holdfasts In Psammophytic Habitats**
Bedinger, Laura A. & Bell, Susan S.
 Department of Biology, University of South Florida, Tampa, FL, USA
- 20 **Ecological Evaluation Of Algal Communities From Western Streams In Us**
Manoylov, Kalina M.¹, Stevenson, R. J.¹ & Pan, Yangdong²
¹Zoology, Michigan State University, East Lansing, MI, USA; ²Environmental Sciences and Resources, Portland State University, Portland, OR, USA
- 21 **Rapid Assessment Of A Benthic Community Using Molecular Tools**
Manoylov, Kalina M.¹, Marsh, Terrance² & Stevenson, R. J.¹
¹Zoology, Michigan State University, East Lansing, MI, USA; ²Microbiology & Molecular Genetics, Michigan State University, East Lansing, MI, USA
- 22 **Movement Modalities As Adaptive Response To Salinity Changes Of The Mudflat Diatom *Cylindrotheca closterium* (Bacillariophyceae)**
Apoya-Horton, Melba D.¹, Underwood, Graham J.² & Gretz, Michael R.¹
¹Biological Sciences, Michigan Technological University, Houghton, MI, USA; ²Department of Biological Sciences, University of Essex, Essex, United Kingdom
- 23 **Comparison Of Two Algal Indices For Use In Biomonitoring Of Southeastern Ohio Streams**
Smucker, Nathan J.¹, Hollingsworth, Emily K.¹, Verb, Robert G.² & Vis, Morgan L.¹
¹Environmental and Plant Biology, Ohio University, Athens, OH, USA; ²Biological & Allied Health Sciences, Ohio Northern University, Ada, OH, USA
- 24 **Morphology And Distribution Of *Thalassiosira lacustris* (Grunow) Hasle: An Exotic Diatom In Southeastern Ohio Streams**
Smucker, Nathan J.¹, Edlund, Mark B.² & Vis, Morgan L.¹
¹Environmental and Plant Biology, Ohio University, Athens, OH, USA; ²St. Croix Watershed Research Station, Science Museum of Minnesota, Marine on St. Croix, MN, USA

- 25 **A Phycomate Prasinophyte From Puget Sound, Washington, USA**
Kodner, Robin B.¹ & Helm, Rebecca²
¹*Organismic and Evolutionary Biology, Harvard University, Cambridge, MA, USA;* ²*Eckerd College, St. Petersburg, FL, USA*
- 26 **Algae From Cryptogamic Crusts, Santa Fe, New Mexico**
Wallace, Stacey L., Santiago, Jonathan & Mosto, Patricia
Biology, Rowan University, Glassboro, NJ, USA
- 27 **Using Machine Learning Environments To Extract Taxonomic Information From Text: An Example From Print And Digital Texts On Algae**
McCourt, Richard¹, Cui, Hong², Monique, Feist³ & Michael, Guiry⁴
¹*Botany, Academy of Natural Sciences, Philadelphia, PA, USA;* ²*University of Western Ontario, London, ON, Canada;* ³*University of Montpellier, Montpellier, France;* ⁴*National University of Galway, Galway, Ireland*
- 28 **Morphological And Ecological Variation Within *Achnanthydium minutissimum* (Bacillariophyta) Species Complex**
Potapova, Marina¹ & Hamilton, Paul²
¹*Academy of Natural Sciences, Philadelphia, PA, USA;* ²*Canadian Museum of Nature, Ottawa, ON, Canada*
- 29 **A Study Of Freshwater Species Of *Synedra Ehrenberg* (Bacillariophyta) From North American Streams**
Morales, Eduardo, Hamsher, Sarah, Hagan, Erin & Mellott, Daniel
Patrick Center for Environmental Research, Academy of Natural Sciences, Philadelphia, PA, USA
- 30 **Oomycota: The Systematics Of Nonphotosynthetic, Coenocytic Stramenopiles**
Bailey, Craig, Padgett, David E., Peterson, Russ, Webster, LaShawnda C. & Henry, Anna C.
Department of Biology and Marine Biology and Center for Marine Science, UNC-Wilmington, Wilmington, NC, USA
- 31 **Divergence Order Of Chlorophyte Green Algal Lineages As Inferred From The Chloroplast And Mitochondrial Genomes**
Pombert, Jean-François, Bélanger, Anne-Sophie, De Cambiaire, Jean-Charles, Gagnon, Jonathan, Otis, Christian, Lemieux, Claude & Turmel, Monique
Biochimie et Microbiologie, Université Laval, Quebec, QC, Canada
- 32 **An Evolutionary Novelty From The Subaerial Algal Flora Of The Hawaiian Islands: *Spongiocrhysis hawaiiensis* (Cladophorales, Ulvophyceae)**
Rindi, Fabio¹, Lopez-Bautista, Juan M.¹, Sherwood, Alison R.² & Guiry, Michael D.³
¹*Biological Sciences, The University of Alabama, Tuscaloosa, AL, USA;* ²*Botany, University of Hawaii, Honolulu, HI, USA;* ³*Martin Ryan Institute, National University of Ireland, Galway, Ireland*
- 33 **Phylogeny Of The Euglenales Inferred From Chloroplast 23S rDNA**
Shin, Woongghi, Son, Mi-Sun & Jo, Bok-Yeon
Department of Biology, Chungnam National University, Daejeon, South Korea
- 34 **Color Atlas Of Photosynthetic Euglenoids**
Ciugulea, Ionel & Triemer, Richard E.
Plant Biology, Michigan State University, East Lansing, MI, USA

- 35 **Zoochlorellae Symbionts Of *Anthopleura* Form A Distinct Monophyletic Taxon Regardless Of Host Species Or Geographic Location**
Letsch, Molly R.¹, Lewis, Louise A.¹ & Muller-Parker, Gisèle T.²
¹*Ecology and Evolutionary Biology, University of Connecticut, Storrs, CT, USA;* ²*The Department of Biology, Western Washington University, Bellingham, WA, USA*
- 36 **An Unusual Fat *Alaria* Found Near Juneau, Alaska**
Stekoll, Michael S.¹ & Hansen, Gayle I.²
¹*Department of Natural Sciences, University of Alaska, Juneau, AK, USA;* ²*Department of Botany and Plant Pathology, Oregon State University, Newport, OR, USA*
- 37 **Species And Genera Of The Order Laminariales From Russian Pacific Coasts That Are Unfamiliar To Western Phycologists**
 Selivanova, Olga¹, Zhigadlova, Galina¹ & Hansen, Gayle I.²
¹*Kamchatka Branch, Pacific Institute of Geography, Petropavlovsk-Kamchatskii, Russian Federation;* ²*Botany and Plant Pathology, Oregon State University, Newport, OR, USA*
- 38 **Molecular Characterization Of The "*Cottonii*" Form Of *Fucus* In The Northeastern Pacific Versus The Atlantic**
 Serrão, Ester¹, Vliet, Mirjam¹, Hansen, Gayle I.², Maggs, Christine³ & Pearson, Gareth¹
¹*Center of Marine Sciences, Universidade do Algarve, Gambelas, Portugal;* ²*Department of Botany and Plant Pathology, Oregon State University, Newport, OR, USA;* ³*School of Biological Sciences, Queen's University Belfast, Belfast, United Kingdom*
- 39 **Phylogenetic Studies On The Genus *Nostoc* (Cyanobacteria)**
Han, Danxiang & Hu, Zhengyu
Institute of hydrobiology, the Chinese Academy of Sciences, Wuhan, China
- 40 **Phylogenetic Relationships Of The Fucales (Phaeophyceae) Based On The Photosystem I Coding pssA Sequences**
Cho, Ga Youn¹, Rousseau, Florence², de Reviers, Bruno² & Boo, Sung Min¹
¹*Department of Biology, Chungnam National University, Daejeon, South Korea;* ²*Département Systématique et Evolution, Muséum National d'Histoire Naturelle, Paris, France*
- 41 **The Life History And Molecular Phylogeny Of *Kuetzingiella battersii* (Ectocarpales, Phaeophyceae)**
 Ling, Huai Yian¹, Cho, Ga Youn¹, Müller, Dieter G.² & Boo, Sung Min¹
¹*Biology, Chungnam National University, Daejeon, South Korea;* ²*Biology, Konstanz University, Konstanz, Germany*
- 42 **Identification Of Conserved Plastid Regions Through Comparative Genomics**
 Presting, Gernot
Molecular Biosciences and Bioengineering, University of Hawaii, Honolulu, HI, USA
- 43 **The Identity Of Two New *Ceramium* Species (Ceramiaceae, Ceramiales) From West And East Florida As Inferred From Molecular And Morphological Data**
Cho, Tae O.¹, Won, Boo Y.¹, Yates, Kim K.² & Fredericq, Suzanne¹
¹*Biology, University of Louisiana at Lafayette, Lafayette, LA, USA;* ²*U.S. Geological Survey, 600 4th, street South, St. Petersburg, FL, USA*

- 44 **Biogeography Of Alaskan Seaweeds**
Lindstrom, Sandra
Department of Botany, University of British Columbia, Vancouver, BC, Canada
- 45 ***www.seaweedsfalaska.com*—A Photo-Rich Portal To The Taxonomy Of Alaskan Seaweeds And Their Habitats**
Lindeberg, Mandy², Lindstrom, Sandra¹ & Saupe, Susan³
¹*Department of Botany, University of British Columbia, Vancouver, BC, Canada;* ²*Auke Bay Laboratories, Alaska Fisheries Science Center NOAA/NMFS, Juneau, AK, USA;* ³*Cook Inlet Regional Citizens Advisory Council, Kenai, AK, USA*
- 46 **The Broader Impacts Of Algae: Algae As Teaching Tools In The National Science Foundation Graduate Teaching Fellows Program**
Gower, Jessie¹, Jackson, Brenda², Masters, Alyce³, Muhlin, Jessica F.⁴ & Brawley, Susan H.⁴
¹*Newburgh Elementary School, Newburgh, ME, USA;* ²*Viola Rand School, Bradley, ME, USA;* ³*Dr. Lewis S. Libby School, Milford, ME, USA;* ⁴*School of Marine Sciences, University of Maine, Orono, ME, USA*
- 47 **Purification, Characterization, And cDNA Cloning Of A Novel N-acetyl-D-glucosamine/ N-acetyl-D-galactosamine-Binding Lectin From The Green Alga *Bryopsis plumosa***
Yoon, Kang-Sup¹, Lee, Key Pyoung² & Kim, Gwang Hoon¹
¹*Department of Biology, Kongju National University, Kongju, South Korea;* ²*Department of Chemistry, Kongju National University, Kongju, South Korea*
- 48 **Iron And The Complex Story Of Reactive Oxygen Species Production By *Heterosigma akashiwo***
Overman, Richard L., Lakeman, Michael B. & Cattolico, Rose Ann
Biology, University of Washington, Seattle, WA, USA
- 49 **Inorganic Carbon Acquisition In The Chrysophyte Algae**
Bhatti, Shabana & Colman, Brian
Biology, York University, Toronto, ON, Canada
- 50 **The *Chlamydomonas reinhardtii* Fea1 Protein Has Iron-Assimilating Functions**
Sayre, Richard¹, Ihemere, Uzoma¹, Chiu, Wai Ting¹, Oda, Saharu¹ & Siritunga, Dimuth²
¹*Plant Cellular and Molecular Biology, Ohio State University, Columbus, OH, USA;* ²*Biology, University of Puerto Rico, Mayaguez, Puerto Rico*
- 51 **A Novel Pigment Biomarker For Identification Of Some Euglenophyceae**
Triemer, Richard¹, Bennett, Matthew¹, Zimba, Paul², Moeller, Peter³ & Beauchesne, Kevin³
¹*Department of Plant Biology, Michigan State University, East Lansing, MI, USA;* ²*United States Department of Agriculture, Agricultural Research Service, Stoneville, MS, USA;* ³*National Ocean Service, Hollings Marine Laboratory, Charleston, SC, USA*
- 52 **Characterization Of Carbonic Anhydrases From The Marine Diatom *Phaeodactylum tricornutum***
Colman, Brian & Szabo, Eva
Biology, York University, Toronto, ON, Canada

- 53 **The Exopolymers Of Desmids (Conjugatophyceae, Streptophyta): Chemistry, Structural Analyses And Implications In Wetland Biofilms**
 Kiemle, Sarah¹, Domozych, David S.² & Michael, Gretz R.¹
¹Department of Biological Sciences, Michigan Technological University, Houghton, NY, USA; ²Biology, Skidmore College, Saratoga Springs, NY, USA
- 54 **Seasonal Variation Of Major Nitrogen Pools In Two High Latitude Red Algal Species**
Buckley, Cadie L.¹ & Stekoll, Michael S.²
¹School of Fisheries and Ocean Sciences, University of Alaska Fairbanks, Juneau, AK, USA; ²Department of Natural Sciences, University of Alaska Southeast, Juneau, AK, USA
- 55 **Differential Expression Gene (DEG) Method Used For The Identification And Isolation Of Genes Expressed In Response To Cold Stress In A Green Alga, *Spirogyra varians* (Zygnematales)**
Han, Jong Won¹, Yoon, MinChul², Lee, Key Pyoung¹ & Kim, Gwang Hoon²
¹Department of Chemistry, Kongju National University, Kongju, South Korea; ²Department of Biology, Kongju National University, Kongju, South Korea
- 56 **Temporal Changes In The Chemical Composition Of Six Seaweeds Of A Tropical Environment**
 Costa, Tatiana M., Barbarino, Elisabete & Lourenço, Sergio O.
 Marine Biology, Universidade Federal Fluminense, Niteroi, Brazil
- 57 **A Fresh Look At An Invasive Species, *Didymosphenia geminata*: Chemical And Structural Analysis Of The Extracellular Polymers**
Gretz, Michael R.¹, Riccio, Michelle L.¹, Hungwe, Tendeukai R.¹, Burger, Holly M.¹, Kiemle, Sarah N.¹, Apoya-Horton, Melba D.¹, Domozych, David S.² & Spaulding, Sarah A.³
¹Biotechnology Research Center, Michigan Technological University, Houghton, MI, USA; ²Department of Biology, Skidmore College, Saratoga Springs, NY, USA; ³EPA Region VII, U.S. Geological Survey / EPA, Denver, CO, USA
- 58 **Effects Of Photon Flux Density On Carotenogenesis In *Haematococcus pluvialis* (Chlorophyceae): Comparison Between Wild Type And Astaxanthin-Overproduction Mutant**
Li, Yantao^{1,2}, Wang, Jiangxin¹, Sommerfeld, Milton¹, Chen, Feng² & Hu, Qiang¹
¹Department of Applied Biological Sciences, Arizona State University, Mesa, AZ, USA; ²Department of Botany, The University of Hong Kong, Hong Kong, China
- 59 **Does An Extracellular Bromoperoxidase Of Marine Diatoms Halogenate DOC?**
Hill, Valerie L. & Manley, Steven L.
 Biological Sciences, California State University, Long Beach, CA, USA
- 60 **Detection Of The Microcystin Synthetase Genes (*mcy*) In Phytoplankton In Lake Victoria, Africa**
Chhun, Aline¹, Gikuma-Njuru, Peter^{1,2}, Müller, Kirsten¹ & Guildford, Stephanie¹
¹Department of Biology, University of Waterloo, Waterloo, ON, Canada; ²Lake Victoria Environmental Mangement Programme (LVEMP), Water Quality Management Component, Kisumu, Kenya
- 61 **Phylogenetic Analysis And Differential Expression Of Glycosyl Transferase Gene Homologues From The Model Diatom *Thalassosira pseudonana***
Abdullahi, Abass S., Wusirika, Ramakrishna & Gretz, Michael R.
 Department of Biological Sci., Michigan Tech. University, Houghton, MI, USA

- 62 **Carotenoids And Carotenoid Pathway Enzymes Of The Primitive Red Alga *Cyanidioschyzon merolae***
Cunningham, Jr, Francis X., Lee, Hansel & Gantt, Elisabeth
Department of Cell Biology and Molecular Genetics, University of Maryland, College Park, MD, USA
- 63 **How Symmetrical Are Desmids? Cell Wall Chemistry And Development In *Penium margaritaceum***
Domozych, David S.¹, Kiemle, Sarah², Domozych, Catherine E.¹ & Gretz, Michael R.²
¹*Biology, Skidmore College, Saratoga Springs, NY, USA;* ²*Biological Sciences, Michigan Technological University, Houghton, MI, USA*
- 64 **Temporal Relationship Between Chloroplast DNA Replication And The Cell Cycle**
Burger, Megan L.¹, Hoyt, Amanda¹, O'Brien-Labayen, Shalana B.² & Cattolico, Rose Ann^{1,3}
¹*Biochemistry, University of Washington, Seattle, WA, USA;* ²*Biology, University of Washington, Seattle, WA, USA;* ³*Ocean Sciences, University of Washington, Seattle, WA, USA*
- 65 **Cloning, Identification And Characterization Of Several Superoxide Dismutases (SOD) Genes In *Haematococcus pluvialis***
Wang, Jiangxin¹, Li, Yantao^{1,2}, Sommerfeld, Milton¹ & Hu, Qiang¹
¹*Department of Applied Biological Sciences, Arizona State University, Mesa, AZ, USA;* ²*Department of Botany, Hong Kong University, Hong Kong, China*
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TUESDAY MORNING, 11 JULY – Sheffield Ballroom 1

Special Session: The Evolution Of Modern Marine Eukaryotic Phytoplankton

Introducing and Presiding: Morgan Vis, Ohio University

- 8:00 **PLENARY LECTURE: How, When, And Why Secondary Red Symbiotic Algae Rose To Ecological Prominence On The Contemporary Ocean**
Falkowski, Paul G.
Institute of Marine and Coastal Sciences and Dept. of Geological Science, Rutgers University, New Brunswick, NJ, USA
- 9:00 **Origin And Diversification Of Light Harvesting Complexes During Plastid Evolution**
Durnford, Dion
Biology, University of New Brunswick, Fredericton, NB, Canada
- 9:30 **BREAK**

Presiding: Paul Falkowski, Rutgers Univeristy
- 10:00 **Whole Genome Analyses Of Diatoms: Insights Into Ecology And Evolution**
Armbrust, Virginia
School of Oceanography, University of Washington, Seattle, WA, USA

Featured Contributed Papers: Phytoplankton Evolution

- 10:30 **Plastid Genes In The Nonphotosynthetic Dinoflagellate *Cryptocodinium cohnii***
Sanchez-Puerta, Maria V.¹, Lippmeier, J C.², Apt, Kirk E.² & Delwiche, Charles F.¹
¹*Cell Biology and Molecular Genetics, University of Maryland, College Park, MD, USA;* ²*Martek Biosciences Corp., Columbia, MD, USA*
- 10:45 **Were The Oceans Ever Green? Evaluating The Evidence For Green Algae In The Geologic Record**
Kodner, Robin B.¹, Summons, Roger E.² & Knoll, Andrew H.¹
¹*Department of Organismic and Evolutionary Biology, Harvard University, Cambridge, MA, USA;* ²*Earth, Atmospheric, and Planetary Sciences, Massachusetts Institute of Technology, Cambridge, MA, USA*
- 11:00 **Cryptic Evolution In Laboratory Cultures**
Lakeman, Michael B.¹ & Cattolico, Rose Ann^{1,2}
¹*Biology, University of Washington, Seattle, WA, USA;* ²*Ocean Sciences, University of Washington, Seattle, WA, USA*
- 11:15 **Phylogenetic Relationships And Taxonomy Of Several Unicellular Algae Of The CW Group (Chlorophyceae)**
Watanabe, Shin
Department of Biology, Faculty of Science, University of Toyama, Toyama, Japan

Lunch on your own 11:30 to 1:00

TUESDAY EARLY AFTERNOON, 11 JULY – Sheffield Ballroom 1

Phylogenetics & Taxonomy 1

Presiding: Rick Zechman, California State University, Fresno

- 1:00 **Molecular Phylogeny Of *Discosporangium mesarthrocarpum* (Phaeophyceae) With A Reassessment Of The Order Discosporangiales**
Kawai, Hiroshi¹, Hanyuda, Takeaki¹, Draisma, Stafano G.² & Dieter, Mueller G.³
¹*Research Center for Inland Seas, Kobe University, Kobe, Japan;* ²*University of Leiden branch, National Herbarium Nederland, Leiden, Netherlands;* ³*Faculty of Biology, University of Konstanz, Konstanz, Germany*
- 1:15 **Phylogeography Of *Costaria costata* (Laminariales, Phaeophyceae) Based On Mitochondrial *cox3* Genes And Nuclear ITS Region**
Cho, Ga Youn¹, Cho, Yun Jin¹, Druehl, Louis², Miller, Kathy A.³ & Boo, Sung Min¹
¹*Department of Biology, Chungnam National University, Daejeon, South Korea;* ²*Bamfield Marine Station, Bamfield, BC, Canada;* ³*University Museum, University of California, Berkely, Berkely, CA, USA*

- 1:30 **Perspectives On The Trans-Arctic Distribution Of Families And Genera Of Red Algae**
Hommersand, Max H.
Department of Biology, University of North Carolina, Chapel Hill, NC, USA
- 1:45 **Molecular Evidence Reveals Diversity In Alaskan Isolates Of *Ceramium pacificum***
Carlile, Amy¹, Waaland, J. R.¹ & Hall, Benjamin D.^{1,2}
¹*Biology, University of Washington, Seattle, WA, USA;* ²*Genome Sciences, University of Washington, Seattle, WA, USA*
- 2:00 **Revising The Genus *Halymenia* (Cryptonemiales, Rhodophyta) In The Northeast Pacific Using Sequence Data**
Gabrielson, Paul
Herbarium, University of North Carolina, Chapel Hill, Chapel Hill, NC, USA
- 2:15 **Phylogeny And Distribution Of The Red Algal Genus *Campylaeophora* (Ceramiaceae, Ceramiales), Including The Transfer Of *Microcladia californica* To The Genus**
Cho, Tae O.¹, Hommersand, Max² & Fredericq, Suzanne¹
¹*Biology, University of Louisiana at Lafayette, Lafayette, LA, USA;* ²*Biology, University of North Carolina, Chapel Hill, NC, USA*
- 2:30 **Origin Time Of The Florideophyceae And Ceramiales (Rhodophyta)**
Yang, Eun Chan¹, Boo, Sung Min¹, Yoon, Hwan Su² & Bhattacharya, Debashish²
¹*Department of Biology, Chungnam National University, Daejeon, South Korea;* ²*Department of Biological Sciences and Roy J. Carver Center for Comparative Genomics, University of Iowa, Iowa City, IA, USA*
- 2:45 **Phylogenetic Relationships Of Members Of The Freshwater Red Algal Family Lemnaneaceae From North America, Europe And Africa**
Sheath, Robert¹, Müller, Kirsten², Sherwood, Alison³ & Shea, Troina⁴
¹*Department of Biology, California State University San Marcos, San Marcos, CA, USA;* ²*Department of Biology, University of Waterloo, Waterloo, ON, Canada;* ³*Department of Botany, University of Hawaii, Honolulu, HI, USA;* ⁴*Department of Biological Sciences, University of Calgary, Calgary, AB, Canada*
- 3:00 **BREAK**

TUESDAY EARLY AFTERNOON, 11 JULY – Egan Room

Physiology & Biochemistry and Cellular & Molecular Biology

Presiding: Elma Gonzalez, University of California at Los Angeles

- 1:00 **Nitrogen Uptake By Gametophytes Of *Porphyra dioica* (Bangiales, Rhodophyta) Under Controlled Culture Conditions**
Pereira, Rui^{1,2}, Yarish, Charles², Kraemer, George³ & Sousa-Pinto, Isabel^{1,4}
¹*Coastal Biodiversity Laboratory, CIIMAR, Porto, Portugal;* ²*Ecology and Evolutionary Biology, University of Connecticut, Stamford, CT, USA;* ³*Department of Environmental Sciences, State University of New York, Purchase, NY, USA;* ⁴*Department of Botany, University of Porto, Porto, Portugal*

- 1:15 **Effects Of Desiccation On Nitrate Uptake And Growth Rate In Two Native *Porphyra* Species Occurring In Different Tide Levels Along The New England Coast**
Kim, Jang K.^{1,3}, Kraemer, George P.² & Yarish, Charles³
¹*Department of Ecology & Evolutionary Biology, University of Connecticut, Groton, CT, USA;*
²*Departments of Biology & Environmental Studies, Purchase College, State University of New York, Purchase, NY, USA;* ³*Department of Ecology & Evolutionary Biology, University of Connecticut, Stamford, CT, USA*
- 1:30 **A Unique Tropical Marine Cyanobacterium That Facilitates Dinitrogen Fixation**
Li, Zhongkui & Brand, Jerry J.
Culture Collection of Algae and MCD-Biology, Univ. of Texas at Austin, Austin 78712, TX, USA
- 1:45 **Characterization And Molecular Cloning Of A Bryohealin Lectin From The Green Alga *Bryopsis plumosa***
Yoon, Kang-Sup¹, Lee, Key Pyoung² & Kim, Gwang Hoon¹
¹*Department of Biology, Kongju National University, Kongju, South Korea;* ²*Department of Chemistry, Kongju National University, Kongju, South Korea*
- 2:00 **Regeneration Of A Cell From Extruded Protoplasm Of The Marine Coenocytic Green Alga *Bryopsis plumosa***
Gwang Hoon, Kim & Tatyana A., Klochkova
Department of Biology, Kongju National University, Kongju, South Korea
- 2:15 **Novel Genes Induced By Short Term Cu Exposure In The Diatom *Thalassiosira pseudonana***
Davis, Aubrey, Hildebrand, Mark & Palenik, Brian
Scripps Institution of Oceanography, UCSD, La Jolla, CA, USA
- 2:30 **Bacterial Quorum-Sensing Interference By *Chlamydomonas reinhardtii***
Sayre, Richard^{1,2}, Rajamani, Sathish², Teplitski, Max³ & Bauer, W. Dietz⁴
¹*Plant Cellular and Molecular Biology, Ohio State University, Columbus, OH, USA;* ²*Biophysics, Ohio State University, Columbus, OH, USA;* ³*Dept of Soil and Water Science, University of Florida, Gainesville, FL, USA;* ⁴*Plant Science, University of California, Davis, Davis, CA, USA*
- 2:45 **Genes Encoding Plastid Terminal Oxidase In *Haematococcus pluvialis*: cDNA Cloning, Characterization, And Expression Under Oxidative Stress**
Wang, Jiangxin, Sommerfeld, Milton & Hu, Qiang
Department of Applied Biological Sciences, Arizona State University, 7001 E. Williams Field Road, Mesa, AZ, USA
- 3:00 **BREAK**

TUESDAY LATE AFTERNOON, 11 JULY – Sheffield Ballroom 1

Phylogenetics & Taxonomy 2

Presiding: Paul Gabrielson, University of North Carolina, Chapel Hill

3:30 A Combined SSU And LSU rDNA Phylogeny Of The Euglenales With A Description Of The New Genus *Discoplastis*

Linton, Eric W.¹ & Triemer, Richard E.²

¹*Biology, Central Michigan University, Mt. Pleasant, MI, USA;* ²*Department of Plant Biology, Michigan State University, East Lansing, MI, USA*

3:45 Distribution Of Freshwater Dinoflagellates In North America

Carty, Susan

Biology, Heidelberg College, Tiffin, OH, USA

4:00 Mapping Ultrastructural Characteristics On Gene Phylogenies Of The Conjugating Green Algae
Hall, John D. & Delwiche, Charles F.

Cell Biology and Molecular Genetics, University of Maryland, College Park, MD, USA

4:15 A Reassessment Of *Geminella* (Chlorophyta) Based Upon Photosynthetic Pigments, DNA Sequence Analyses And Electron Microscopy

Durako, Maris R. & Bailey, Craig

Biology and Marine Biology and Center for Marine Science, UNC-Wilmington, Wilmington, NC, USA

4:30 What Two Genes And Many Isolates Reveal About Species Relationships And Geographic Distribution Of The Freshwater Family Hydrodictyaceae (Sphaeropleales)

McManus, Hilary A. & Lewis, Louise A.

Ecology and Evolutionary Biology, University of Connecticut, Storrs, CT, USA

4:45 First Insights Into The Systematics Of The Family Trentepohliaceae (Chlorophyta, Ulvophyceae)

Lopez-Bautista, Juan M. & Rindi, Fabio

Department of Biological Sciences, The University of Alabama, Tuscaloosa, AL, USA

5:00 Are *Acrosiphonia arcta* (Dillwyn) Gain And *A. spinescens* (Kützinger) Kjellman (Acrosiphoniales, Chlorophyta) Conspecific? Evidence From Morphology, Ecology And Molecules

Zechman, Frederick¹, Mathieson, Arthur C.², Ashworth, Matt¹ & Ebner, Ethan²

¹*Department of Biology, California State University, Fresno, Fresno, CA, USA;* ²*Department of Plant Biology and Jackson Estuarine Laboratory, University of New Hampshire, Durham, NH, USA*

5:15 Universal Primers Amplify A Plastid Marker For Biodiversity Assessment Of Eukaryotic Algae And Cyanobacteria

Sherwood, Alison R.¹ & Presting, Gernot G.²

¹*Department of Botany, University of Hawaii, Honolulu, HI, USA;* ²*Molecular Biosciences and Bioengineering, University of Hawaii, Honolulu, HI, USA*

5:30 to 6:00 ***NWAS Business Meeting (in Egan Room)***

7:00 to 10:00 ***PSA Banquet and Awards Ceremony – Gold Creek Salmon Bake***

Buses leaving Centennial Hall at 7:00, 7:15, and 7:30

TUESDAY LATE AFTERNOON, 11 JULY – Egan Room

Ecology & Population Biology 2 and Other

Presiding: Steve Murray, California State University, Fullerton

- 3:30 **Effect Of Time And Irradiance On Intertidal Multi-Species *Euglena* Patches In Oregon**
Kingston, Michael B.¹ & Gough, Jennifer²
¹*Biology Department, Elon University, Elon, NC, USA;* ²*Environmental Studies Program, Elon University, Elon, NC, USA*
- 3:45 **Cellular Basis For Mechanical Strength In *Calliarthron Genicula***
Martone, Patrick T.
Hopkins Marine Station, Stanford University, Pacific Grove, CA, USA
- 4:00 **Cyanobacterial Diversity And Halotolerance In A Variable Hypersaline Environment**
Kirkwood, Andrea^{1,3}, Buchheim, Julie², Buchheim, Mark² & Henley, William¹
¹*Department of Botany, Oklahoma State University, Stillwater, OK, USA;* ²*Department of Biological Science, The University of Tulsa, Tulsa, OK, USA;* ³*Department of Biological Sciences, University of Calgary, Calgary, AB, Canada*
- 4:15 **Population Genetic Structure Of *Fucus vesiculosus* L. In The Northwestern Atlantic**
Muhlin, Jessica F. & Brawley, Susan H.
School of Marine Sciences, University of Maine, Orono, ME, USA
- 4:30 **A Slow Death? Failure By Fatigue In Seaweeds**
Mach, Katharine J.
Hopkins Marine Station, Stanford University, Pacific Grove, CA, USA
- 4:45 **Integrating Research And Education Through The University Of Maine's NSF GK-12 Graduate Teaching Fellows Program**
Jackson, Brenda¹, Masters, Alyce², Gower, Jessie³, Muhlin, Jessica F.⁴ & Brawley, Susan H.⁴
- 5:30 to 6:00 ***NWAS Business Meeting (in Egan Room)***
- 7:00 to 10:00 ***PSA Banquet and Awards Ceremony – Gold Creek Salmon Bake***
Buses leaving Centennial Hall at 7:00, 7:15, and 7:30
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WEDNESDAY MORNING, 12 JULY – Sheffield Ballroom 1

***Special Session: The Scale Of Taxonomic, Biogeographic, And Paleontologic Resolution
And How It Affects Our Understanding Of Diatom Ecology And Evolution***

Introducing and Presiding: Craig Bailey, University of North Carolina at Wilmington

8:30 PLENARY LECTURE: Scale And Resolution In Protistan Evolution: Is The Fossil Record Sufficient To Capture Characteristic Patterns Of Morphological Evolution In Protists?

Theriot, Edward C.

Texas Memorial Museum, The University of Texas at Austin, Austin, TX, USA

9:30 The Intersection Of History And Environment In Diatom Biogeography

Spaulding, Sarah

Fort Collins Science Center, US Geological Survey, Denver, CO, USA

10:00 BREAK

Presiding: Edward Theriot, The University of Texas at Austin

10:30 Fossil Freshwater Diatoms: Providing Key Insights Into Systematics, Evolution And Ecology

Kociolek, John P.

California Academy of Sciences, San Francisco, CA, USA

Featured Contributed Papers: Heterokont Ecology, Evolution, and Systematics

11:00 Biogeography And Species Diversity Within The Phytoplanktonic Diatom Genus *Skeletonema*

Kooistra, Wiebe H., Zingone, Adriana, Saggiomo, Maria & Sarno, Diana

Marine Botany, Stazione Zoologica, Naples, Italy

11:15 Baseline Analysis Of Periphyton Community Structure In Agriculturally Impacted Lotic Systems In West-Central Ohio

Verb, Robert G. & Katrina, Glascock I.

Department of Biological & Allied Health Sciences, Ohio Northern University, Ada, OH, USA

11:30 Phylogenetic Analyses Of GSIII And GSII: Evidence For A Shared Evolutionary History Among Heterokonts And Haptophytes?

Tartar, Aurélien, Ghoshroy, Sohini & Robertson, Deborah

Clark University, Worcester, MA, USA

11:45 Species Diversity Among Coccoid Eustigmatophyceae (Heterokontophyta)

Bailey, Craig¹, Fawley, Marvin² & Fawley, Karen²

¹*Biology and Marine Biology and Center for Marine Science, UNC-Wilmington, Wilmington, NC, USA;*

²*Biological Sciences, North Dakota St. University, Fargo, ND, USA*

Post-Meeting Field Trip to Sitka (Participants will be contacted individually)

Safe Travels Home. See you at PSA 2007 in Providence, Rhode Island!

Abstracts

ABSTRACTS NUMBERS ARE VERY CLOSE TO ABSTRACT PRESENTATION ORDER WITH POSTERS AT THE END.
SEE AUTHOR INDEX ON PAGE 86 TO FIND SPECIFIC ABSTRACTS.

1

REFLECTIONS OF A PHYCOLOGICAL ZOOLOGIST: MACROALGAE AS POWERFUL EXPERIMENTAL PROBES OF HOW NATURAL COMMUNITIES ARE ORGANIZED

Paine, Robert

Biology, University of Washington, Seattle, WA, USA

Three fundamental ecological processes are increasingly acknowledged to dominate how benthic assemblages are organized and function: dispersal, competition and predation. All three will be explored with macroalgal scenarios. 1]. Herbivory can alter the species composition of local plots with *Alaria marginata* replacing *Hedophyllum* or coralline algae, depending on the identity of the excluded grazer. Depending on treatment, net primary production will vary by orders of magnitude. 2]. Coralline algae compete vigorously for space. Experiments on multi-species systems (7-11 species) show that the identity of winners and their relative abundances change with the herbivore "load", and that the guild becomes competitively hierarchical when grazing is reduced. 3]. *Postelsia* populations at given sites vary numerically or in percent cover between years by orders of magnitude. Localized, adjacent disturbance seems to be required for persistence; short-distance dispersal should increase the probability of persistence. Estimates of annual dispersal kernels and experimental disturbance to mussel beds confirm this expectation.

2

ALGAL DIVERSITY MANIPULATIONS: HOW DO SEAWEEDS STRUCTURE ROCKY SHORES?

Graham, Michael H.¹, Szoboszlai, Amber¹, Bracken, Matthew E.² & Stachowicz, John J.^{2,3}

¹*Moss Landing Marine Labs, Moss Landing, CA, USA*; ²*Bodega Marine Lab, Bodega Bay, CA, USA*; ³*Section of Evolution and Ecology, University of California, Davis, CA, USA*

Regulation of the structure and diversity of algal assemblages has been broadly addressed in the ecological literature, yet we know relatively little about the functional consequences of that diversity to associated communities. Previous marine studies have been limited primarily to short-term mesocosm studies and many have focused on animal rather than algal diversity, limiting our ability to generalize across systems due these methodological differences. Here, we report the first results from an ongoing multi-year manipulation of perennial algal diversity on intertidal benches in central California, USA. Specifically, we are assessing the role of intertidal macroalgal diversity on primary production, standing algal biomass and cover, and the diversity and abundance consumer species in 1.5 m diameter plots in the mid-high intertidal. This zone is dominated by a spatial mosaic of 4 macroalgae: *Cladophora columbiana*, *Endocladia muricata*, *Mastocarpus papillatus*, and *Pelvetiopsis limitata*. Our manipulations consisted of weeding plots to contain a monoculture of each of these 4 dominant species or a polyculture of the 4 species; unmanipulated plots served to control for weeding artifacts. After 2 years, we find the total richness of associated animal species (amphipods, gastropods, polychaetes, etc.) is greater in the polycultures, although total invertebrate abundance does not differ among treatments. Furthermore, the cover of our target algal species in the monoculture plots has stabilized, with total algal cover in the polyculture plots exceeding that in any of the component monocultures. Importantly, the cover of our target algal species in the monoculture plots does not exceed the cover of these individual species in the polyculture plots. This was unpredicted given the previous assertion that the spatial mosaic of these 4 algae in central California is regulated by algal-algal competition. Thus, the positive effects of algal diversity on animal assemblages in this zone may be driven by both preferential animal-algal associations, as well as higher total algal coverage in polycultures due to non-overlapping environmental tolerances and resource requirements of the algae.

3

MACROALGAE REVEAL THE UNDERAPPRECIATED ROLE OF RESOURCES IN STRUCTURING BENTHIC MARINE COMMUNITIES

Nielsen, Karina J.

Biology, Sonoma State University, Rohnert Park, CA, USA

Our perception of how the natural systems function is often biased by which aspects are easiest to observe or experimentally manipulate. Paradigmatic views of the important factors controlling algal abundances vary sharply

depending on the size of the alga. For example, phytoplankton abundance is strongly controlled by water column structure and additional factors that influence the supply of light and nutrients. Phytoplankton abundance in turn can strongly influence the productivity of entire marine food chains, a phenomenon easily observed during extreme ENSO events. Thus pelagic marine communities are thought to be controlled in large part via the supply of resources (or bottom-up factors). In contrast, benthic marine communities provide us with classic examples of how communities are structured by the actions of consumers (or top-down factors). Sea otters and seastars have enormous direct and indirect effects on their respective communities that cascade down to impact benthic macroalgae. In general, our understanding of how benthic marine communities function has been dominated by a paradigm of predation. Consumers are challenging to manipulate in pelagic systems and resource supply is challenging to manipulate in benthic systems. Thus strong evidence of the influence of these factors has been limited and contributes to the dominance of bottom-up and top-down paradigms in our perception of how pelagic and benthic communities are structured, respectively. Despite these deeply entrenched world views, it is becoming clear that both bottom-up and top-down factors play important roles in determining the structure of marine communities. Evidence for the influence of resource supply on the structure of intertidal communities is accumulating. The abundance and diversity of macroalgal assemblages growing on wave-swept rocky shores is strongly influenced by the supply of nutrients and light, not just by food-chain length. In the face of increasing anthropogenic impacts on oceanic climate and the abundance of consumers, it is becoming increasingly important that we understand the interplay between both bottom-up and top-down factors in structuring marine communities.

4

SYNERGISTIC SERIAL DEPLETION OF MARINE INVERTEBRATES LEADS TO THE DECINE OF A KEYSTONE GRAZER AND THE ALTERATION OF A COASTAL ECOSYSTEM

Salomon, Anne K.

Biology, University of Washington, Seattle, WA, USA

I investigated the relative roles of natural factors and shoreline harvest leading to localized declines of the black leather chiton, *Katharina tunicata*, on the Kenai Peninsula, Alaska. Field surveys of the significant predictors of *K. tunicata* across 11 sites suggest that its current spatial variation is significantly related to human exploitation and sea otter predation. Traditional ecological knowledge further revealed that several benthic marine invertebrates (sea urchin, crab and clams) have declined sequentially, with reduced densities of *K. tunicata* being the most recent. I propose that a restriction in alternative prey species availability has led to recent intensified per capita predator impacts on *K. tunicata*. Experimental *K. tunicata* removals in the low intertidal revealed that at high densities, *K. tunicata* reduced the production of *Alaria marginata* by 94% and species richness by 38%, and altered algal and invertebrate community structure. Across-site comparisons showed that *A. marginata* biomass was 7 times greater at exploited versus unexploited sites. Furthermore, community structure differed significantly as a function of predation pressure. These results provide evidence of a trophic cascade and reveal the extent to which fishing and natural predation, via the reduction of a shared keystone resource, indirectly alter a temperate coastal ecosystem.

5

DISTURBANCE MAINTAINS HIGH LOCAL DIVERSITY IN *ECKLONIA RADIATA* KELP FORESTS

Kendrick, Gary A., Toohey, Ben D. & Harvey, Euan S.

Plant Biology, University of Western Australia, Crawley, WA, Australia

Gaps in marine kelp forests, similar to gaps in the canopy of terrestrial forests, are sites of high local diversity. Physical disturbance removes kelps creating gaps that are re-established with kelp over years to decades. This study describes a kelp canopy clearing experiment, designed to simulate early winter swell-driven disturbance of beds of the temperate kelp *Ecklonia radiata*. The recovery and re-establishment of the macroalgal assemblage is then described and compared to theories of treefall gap recovery in terrestrial forests. Six replicate reefs within each of three locations were cleared of their *Ecklonia radiata* canopy in 314 m² circular areas. The patterns of macroalgal recolonisation in these replicate clearances were assessed at 7, 10, 22, 34 and 46 months after clearance, and compared to control sites where canopy was not cleared. Similar to treefall gaps in terrestrial forests, species diversity increased in recolonised gaps as a response to release from intense interspecific competition for light. Also, biomass increased for common understory species when exposed to higher light climates of gaps. Canopy disturbance in kelp forests, like terrestrial forests, created a mosaic of different patch types that formed islands of high diversity against a background of low diversity under kelp canopies. The pattern of recolonisation began with the establishment of a species-rich assemblage of foliose and filamentous algae which persisted for up to 7 months. By 10 months after removal of kelps, a multiple species canopy of *Sargassum* developed and this

canopy persisted until *Ecklonia radiata* started to replace it 22 months after clearance. The biomass of *E. radiata* in cleared sites was approximately 70% of biomass in control sites after 46 months suggesting kelp canopy had not completely recovered by this stage. Also, a few cleared sites formed an alternate state of turf algae and remained unchanged over the duration of the experiment. These patterns of recolonisation of gaps in the canopy of the kelp *Ecklonia radiata* are similar to those observed in temperate and tropical forests, where light is also a major limiting factor for growth of understory.

6 DEMOGRAPHIC CONSEQUENCES OF INBREEDING AND POPULATION STRUCTURE IN KELP

Pfister, Catherine & Wootton, J T.

Ecology & Evolution, University of Chicago, Chicago, IL, USA

Kelp species are characterized by a variety of life histories that cooccur in the same environment. Key to understanding the persistence of these algae is connecting events at the level of the individual to population level fluctuations. Demographic data from several species of kelp (*Alaria nana*, *Pleurophycus gardneri*, *Postelsia palmaeformis*) show that annual kelp species should be especially vulnerable to environmental variation relative to perennial species. Here we examine the role of inbreeding and population density on the persistence of the annual kelp, *Postelsia palmaeformis*. The negative demographic effects of inbreeding are countered by positive effects of high density and suggest that short-term inbreeding has a relatively small negative effect on *Postelsia* populations.

7 DETERMINING RECOVERY IN ROCKY INTERTIDAL SYSTEMS: RELATIVE PERFORMANCE OF RECOVERY ENDPOINTS

Klinger, Terrie

Marine Affairs, University of Washington, Seattle, WA, USA

Determination of recovery following pulse disturbance to rocky intertidal communities is difficult because recovery endpoints are difficult to define, especially in highly dynamic systems such as the temperate rocky intertidal zone. To address this problem through direct experimental manipulation, we established a long-term manipulative field experiment at a rocky intertidal site in Kasitsna Bay, Alaska. We cleared experimental plots in the summers of 1999 and 2000 and followed their recovery through July 2005. We tested whether 1) disturbed plots would resemble their starting conditions after a recovery period; 2) disturbed plots would resemble undisturbed (control) plots after a recovery period; and 3) the abundance of focal taxa in disturbed plots would fluctuate in parallel with those in undisturbed plots after a recovery period. We found that after a 5-6 year recovery period, disturbed plots did not differ significantly from undisturbed control plots on the same beach, but did differ from their original starting condition and from the condition of plots on adjacent beaches. The abundance of focal taxa in disturbed plots fluctuated in parallel with undisturbed plots after a recovery period of about 2 years. Our results suggest that 1) recovery to pre-disturbance conditions is not a reasonable endpoint because the systems themselves are dynamic; 2) recovery can lead to convergence between disturbed and undisturbed plots where the scale of disturbance is small and the physical distance between disturbed and undisturbed plots is very short; but 3) convergence may not occur over larger scales of comparison, for example, between beaches.

8 RATES OF SELFING AND OUTCROSSING IN TWO SPECIES OF INTERTIDAL KELP (*POSTELSIA PALMAEFORMIS* AND *ALARIA NANA*) FROM GEOGRAPHICALLY SEPARATED PARENTS

Collens, Julie

Ecology and Evolution, University of Chicago, Chicago, IL, USA

It is expected that organisms with the capacity for both selfing and outcrossing have theoretically optimized levels of selfing and outcrossing to minimize deleterious alleles in a population, while maintaining flexibility for the founding of new populations from one or few individuals. In kelp, there is evidence of inbreeding depression, leading to an expectation of selection against selfing when outcrossing opportunities exist. Conversely, if dispersal is limiting sexual reproduction between individuals from different geographic locations, then there should be greater than random outcrossing between all individuals when the opportunity for long-distance mating is present. I experimentally examined mate preference and mating success in kelp by determining parentage for individuals from crosses where either selfing or outcrossing was possible among 2 genetically distinct parents. Reproductive individuals of *Alaria nana* and *Postelsia*

palmaeformis were collected from geographically disparate areas from Barkley Sound on Vancouver Island to the southern extent of the range to California for *P. palmaeformis*, and to Oregon for *A. nana*. Parents used in each cross came from distances of less than one meter to hundreds of kilometers. 10 000 spores of each of two individuals were settled and cultured until offspring reached approximately 1-2mm. DNA extracted from offspring were analyzed for the homozygous or heterozygous condition using non-coding genomic sequence data (SNP). Preliminary results reveal more selfing than expected under random mating, suggesting a role for reproductive compatibility in maintaining the spatially explicit patterns of genetic divergence observed in natural kelp populations.

9 PHYLOGENY AND EVOLUTIONARY ECOLOGY OF THALASSIOSIROID DIATOMS

Alverson, Andrew^{1,2} & Theriot, Edward¹

¹*Plant Biology Graduate Program, The University of Texas at Austin, Austin, TX, USA;* ²*Texas Memorial Museum, The University of Texas at Austin, Austin, TX, USA*

Salinity is a significant barrier to diatom distribution, and though it is generally understood that diatoms are ancestrally marine, the number of times diatoms independently colonized freshwater and the physiological adaptations that facilitated these colonizations remain outstanding questions in diatom evolution. Resolving the exact number of freshwater colonizations will require a large-scale reconstruction of the diatom phylogeny with dense sampling of marine and freshwater taxa. We pursued a more tractable approach by focusing on a single lineage, Thalassiosirales, which has high diversity in marine and fresh waters. Thalassiosirales species are divided into marine Thalassiosiraceae and freshwater Stephanodiscaceae, reflecting the more generally held hypothesis that diatoms are naturally split along marine-freshwater lines. The fossil record suggests that Stephanodiscaceae traces to a single colonization of freshwater in the mid-Miocene. Stephanodiscaceae species share a suite of complex cell wall characters, corroborating the hypothesis that they share a recent common ancestor. Phylogenetic analyses provide evidence for multiple colonizations of freshwater and soundly reject previous colonization hypotheses. Results further show that part of Stephanodiscaceae is an early diverging lineage within Thalassiosirales, providing evidence that these two distantly related and separately derived Stephanodiscaceae lineages independently evolved a similar set of complex morphological characters upon the colonization of freshwater. Several fossils were used as calibration points to estimate absolute divergence times in the phylogeny, and results showed that Stephanodiscaceae colonized and diversified in freshwater much earlier than the independent, Miocene colonization by the rest of the family. Results from these and other studies show that Thalassiosirales provides an excellent model system for studying many important questions in diatom biology.

10 LINKING LIGHT ATTENUATION AND SUSPENDED SEDIMENT LOADING TO BENTHIC PRODUCTIVITY WITHIN AN ARCTIC KELP BED COMMUNITY

Aumack, Craig F.^{1,2}, Dunton, Kenneth H.², Burd, Adrian B.³ & Funk, Dale W.⁴

¹*Department of Biology, University of Alabama at Birmingham, Birmingham, AL, USA;* ²*Department of Marine Science, The University of Texas Marine Science Institute, Port Aransas, TX, USA;* ³*Department of Marine Science, University of Georgia, Athens, GA, USA;* ⁴*LGL Alaska Research Associates, Inc., Anchorage, AK, USA*

Annual growth and productivity of kelp in the Stefansson Sound Boulder Patch, located along the arctic coast of Alaska, is regulated almost entirely by photosynthetically active radiation (PAR) received during the summer open water period. Increased water turbidity during summer, often in response to storm activity, has been linked to low levels of ambient PAR and measurable decreases in kelp elongation. However, the relationship between PAR and water transparency has not been quantified, which compromises efforts to assess the effects of changing climate and weather conditions on kelp production. During the 2001-2002 summer periods, the inherent optical properties (IOPs) of Stefansson Sound waters were measured in conjunction with total suspended sediment (TSS) concentrations, which differed significantly between the two years, for input into a radiative transfer equation (RTE). In both years, highest TSS levels (24.2 - 18.5 mg L⁻¹ in 2001 and 2002 respectively) occurred in nearshore areas and were coincident with increased light attenuations (13.8 m⁻¹ and 8.3 m⁻¹). Lower TSS concentrations and attenuations were measured offshore. Data input to the RTE provided a TSS concentration specific attenuation coefficient that was used in a productivity model to estimate annual kelp productivities throughout the Boulder Patch based on modeled irradiance and averaged site specific TSS concentrations. Production estimates varied across the Boulder Patch, but were lower in 2001 (0.12 - 0.34 g C gdw⁻¹ yr⁻¹) compared to 2002 (0.24 - 0.80 g C gdw⁻¹ yr⁻¹). Production in both years was greater in offshore locations with lower TSS loads. Results suggest PAR availability during the summer is heavily influenced by TSS concentrations and that changes in storm intensity and

frequency, associated with current warming trends, may have significant effects on the primary production of these unique benthic algal communities.

11 EFFECTS OF NUTRIENT ENRICHMENT ON BIOMASS AND PRIMARY PRODUCTION OF SEDIMENT MICROALGAE IN *HALODULE WRIGHTII* ASCHERSON (SHOALGRASS) SEAGRASS BEDS

Bucolo, Anthony P.¹, Sullivan, Michael J.² & Zimba, Paul V.³

¹Department of Biology, University of Alabama at Birmingham, Birmingham, AL, USA; ², Florida State University Marine Lab, St. Teresa, FL, USA; ³USDA, Stoneville, MS, USA

Eutrophication of coastal waters often leads to excessive growth of microalgal epiphytes attached to seagrass leaves. If the growth of the epiphytes is excessive, seagrass communities may disappear and be replaced by sediment microalgal assemblages. The effect of increased nutrient levels on sediment microalgae has not been studied within seagrass communities. *In situ* applications of a slow release Osmocote fertilizer were implemented to enrich the sediment microalgae beneath beds of shoal grass, *Halodule wrightii* in Big Lagoon, Perdido Key, FL. Enrichment treatments were positioned at the center and edge of the beds, as well as outside the beds in unvegetated sediments 2 m and 6 m from the edge. Sediment microalgal GPP, and biomass measured using HPLC, beneath fertilized and control *H. wrightii* beds were measured following two consecutive enrichment periods of four weeks during June and July 2004. There was no effect of position on sediment microalgal GPP or biomass. However, nutrient enrichment significantly increased GPP in both June and July, whereas sedimentary chlorophyll *a* and fucoxanthin (proxies of total microalgal and diatom biomass respectively) were significantly increased during the June incubation period. These results suggest that sediment microalgae could fill some of the void in primary production where seagrass beds disappear.

12 PHOTOSYNTHETIC ACTIVITIES OF *SARGASSUM* SPP. AND *LOBOPHORA VARIEGATA* IN TUNG PING CHAU MARINE PARK, HONG KONG SAR, CHINA

Fai Fai, Yeung¹ & Put, Ang O.²

¹Environmental Science, The Chinese University of Hong Kong, Hong Kong, Hong Kong; ²Biology, The Chinese University of Hong Kong, Hong Kong, Hong Kong

Monthly photosynthetic activities of *Sargassum* spp., and *Lobophora variegata* (both Phaeophyceae) in Tung Ping Chau Marine Park, Hong Kong, were monitored *in situ* from April 04 to July 05 and diurnal activities were investigated for *Sargassum* spp. on 2 August 04 and *Lobophora variegata* on 4 August 04. The effective quantum yield of photosynthesis of the seaweeds and photosynthetically-active radiation (PAR) were measured using the diving PAM (Pulsed Amplitude Modulation) fluorometer. Both *Sargassum* spp. and *Lobophora variegata* showed similar temporal variation of effective quantum yield with higher yield recorded in winter (*Sargassum* spp. 0.776, *Lobophora variegata* 0.695) than in summer (*Sargassum* spp. 0.703, *Lobophora variegata* 0.583). *Sargassum* spp., showing higher effective quantum yield of photosynthesis, are generally more efficient in utilizing the solar energy for photosynthesis than *Lobophora variegata* at all depths and times. Photo-inhibition at noon time was observed for *Lobophora variegata* but not for *Sargassum glaucescens* in diurnal experiment. The effective quantum yield of both *Sargassum* spp. and *Lobophora variegata* showed significant but weak linear relationship with depth and with PAR (Regression Analysis, $p < 0.01$) in monthly monitoring studies with less than 40% of the variation (all R^2 values < 0.4) accounted for by this linear relation.

13 DISTRIBUTION OF SYMBIOTIC ALGAE WITHIN THE INTERTIDAL SEA ANEMONE *ANTHOPLEURA XANTHOGRAMMICA* IN ALASKA AND OREGON

Kitaeff, Pema & Muller-Parker, Gisele

Biology, Western Washington University, Bellingham, WA, USA

Along the northeast Pacific coast temperate sea anemones in the genus *Anthopleura* may host up to 3 different types of photosynthetic symbionts: a chlorophyte (zoochlorellae), and 2 dinophyte species in the genus *Symbiodinium* (zooxanthellae). In this study, patterns of algal distribution in *A. xanthogrammica* were examined at two widely separated locations to test the hypothesis that environmental factors (such as temperature, light, and microhabitat) associated with latitude affect the distribution of symbionts. In Sitka in Southeast Alaska (135.40°W, 57.11°N), *A. xanthogrammica* host only zoochlorellae; zooxanthellae were not found in any of the 127 Alaskan anemones sampled. In Coos Bay in Southern

Oregon (124.40°W, 43.30°N), *A. xanthogrammica* exhibited patterns previously established for symbiotic algae. In Alaska, *A. xanthogrammica* contained on average 40% higher density of zoochlorellae than their southern counterparts in Oregon (among low intertidal anemones). Both low and high intertidal anemones at 3 study sites in Sitka contained as much as 1.4×10^6 zoochlorellae/mg anemone protein in their tentacles, compared with 1.0×10^6 zoochlorellae/mg protein in low intertidal anemones in Coos Bay. The distribution of symbionts within body regions of *A. xanthogrammica* was also examined. Thirty-one whole anemones (average size = $70.52 \text{ cm}^3 \pm 64.54 \text{ s.d.}$) were divided into crown (tentacles), middle, and base (pedal disc) sections which were analyzed separately. A clear pattern was found with densities of zoochlorellae up to seven times higher in the crown regions than in the bases of zoochlorellate anemones in both Alaska and Oregon. For zooxanthellate anemones in Oregon mean densities of zooxanthellae were up to three times higher in the crowns than in the bases. These conclusions suggest the existence of a northern “transition zone” along the coastal northeastern Pacific beyond which zooxanthellae are not found due to environmental factors. In addition, this study is the first characterization of algal symbiont distribution within *A. xanthogrammica* bodies and provides evidence for microhabitat-based density patterns within host anemones.

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CHARACTERIZATION OF A NITROGEN-REGULATED CELL-SURFACE PROTEIN IN THE MARINE COCCOLITHOPHORE, *EMILIANA HUXLEYI*

Landry, Dori M.¹, Read, Betsy² & Palenik, Brian¹

¹Marine Biology, Scripps Institution of Oceanography, San Deigo, CA, USA; ²Biological Sciences, California State University, San Marcos, San Marcos, CA, USA

Emiliana huxleyi (Lohmann) Hay et Mohler is a unicellular eukaryote classified as a coccolithophore because it is able to cover its external surface with calcium carbonate scales, termed coccoliths. *E. huxleyi*, comprising up to 80% of the global coccolithophore population, is widespread in its distribution and can form blooms. Nitrogen-regulated protein 1, nrp1, is a cell-surface protein in *E. huxleyi* that is present under nitrogen stressed conditions and absent during phosphate stressed or nutrient replete conditions. Although nrp1 is known to be present under nitrogen stressed conditions, little is known about its function in nitrogen metabolism. Polyclonal antibodies were generated to nrp1 purified from nitrogen stressed cultures. Anti-nrp1 preferentially labeled nitrogen stressed cells of multiple strains of *E. huxleyi*. In addition, anti-nrp1 was used to detect the presence of nrp1 in environmental samples. Protein sequence fragments were obtained from nrp1 and were used to mine the genomic trace archives at NCBI using BLAST to determine the sequence of the gene that encodes nrp1. The genomic and full length cDNA sequences of this gene give little clue as to its function, but preliminary data suggests it may have some activity with nitrogenous compounds.

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ISSR-ESTIMATED INTRASPECIFIC GENETIC VARIATION AND PHYLOGENETIC POSITION OF A POPULATION OF THE RED ALGA *BANGIA MAXIMA*

Lynch, Michael D.¹, Müller, Kirsten M.¹ & Sheath, Robert G.²

¹Department of Biology, University of Waterloo, Waterloo, ON, Canada; ²Provost's Office, Division of Academic and Student Affairs, California State University San Marcos, San Marcos, CA, USA

An inter simple sequence repeat (ISSR) PCR-based DNA fingerprint analysis was used to study the genetic variation within a population of the red alga *Bangia maxima* Gardner located on seven separated littoral boulders in Bolinas Bay, CA collected in April 2004. Although *B. maxima* is not widely distributed, due to its large size (up to 35 cm long x 6 mm in diameter) it is the only readily distinguishable *Bangia* morphotype and is potentially an important species for resolving taxonomic problems in *Bangia*. Banding patterns from up to 20 male filaments from seven boulders for five ISSR primers were used to develop both band presence/absence and distance matrix (using Jaccard's coefficient) datasets. Banding patterns of *B. maxima* isolates were highly polymorphic among boulders and consistent among individuals from the same boulder. UPGMA and Neighbour-Joining analyses were performed and reliably separated individuals from each boulder indicating genetic homogeneity within localized groups and limited genetic transfer between boulders. Additionally, in phylogenetic analysis of nuclear small subunit ribosomal DNA *B. maxima* was observed to group with local populations of previously and concurrently collected *Bangia fuscopurpurea*. These results help in clarifying both the population genetics of *B. maxima* and further understanding of genetic diversity within species of the Bangiophycidae. Further study of *B. maxima* and its implications for *Bangia* evolution is warranted.

MOLECULAR PHYLOGEOGRAPHY AND SPECIES DISCRIMINATION OF FRESHWATER *CLADOPHORA* (CLADOPHORALES, CHLOROPHYTA) IN NORTH AMERICARoss, Sara J.¹, Sheath, Robert G.² & Müller, Kirsten M.¹¹Department of Biology, University of Waterloo, Waterloo, ON, Canada; ²Department of Biology, California State University at San Marcos, San Marcos, CA, USA

Cladophora is a widespread freshwater filamentous chlorophyte genus and is frequently observed in eutrophic waters where it can produce large nuisance blooms. These blooms can have direct impacts on water intake for power generation, irrigation canals and can be aesthetically unpleasant. Much of the ecological and physiological studies on *Cladophora* have assumed that the populations of this genus in North America belong to the species *Cladophora glomerata*. However, this has never been tested despite that it is well-documented that identifying freshwater *Cladophora* to the species level is difficult due morphological variability under different ecological conditions. In addition, the species epithets for freshwater *Cladophora* are based on European collections and it is not clear if these should be applied to North America. This study examines approximately 40 collections of *Cladophora* from the Laurentian Great Lakes and 43 from various locations in North America ranging from the Northwest Territories to Puerto Rico. Initially we determined the nucleotide sequences of the internal transcribed spacer (ITS) region of the nuclear ribosomal cistron and observed sequence divergence to be low (0-3%), demonstrating an inability for this marker to resolve species delineation as divergence of this region was low. Amplification of the inter-simple sequence repeat (ISSR) regions were used to analyze microsatellite motif frequency throughout the genome to evaluate the biogeography relationships, including diversity, of freshwater *Cladophora* sp. five different primers were used on 70 individuals. UPGMA analyses of the presence/absence of bands demonstrate that each of the Great Lake populations separate into groups according to the Lake they were initially sampled from. However, collections from North America are highly variable and do not form well supported biogeographic clades. In addition, these collections appear to be distinct from type cultures of freshwater *Cladophora* from Europe.

APPLICATION OF MOLECULAR AND GENOMICS TOOLS TO DIATOMS

Hildebrand, Mark

Scripps Institution of Oceanography, UCSD, La Jolla, CA, USA

Molecular approaches are essential to elucidate unexplored aspects of phytoplankton biology. The success of a species under different environmental conditions depends upon molecular components involved in environmental interaction and metabolic processing. In diatoms, we have focused on the molecular characterization of silicon metabolism and the cellular response to different nitrogen sources. Due to lack of characterized genes, our initial application of molecular tools was a subtraction technique to isolate any gene induced by silicon. This led to the discovery of the silicon transporters (SITs) and nitrate transporters (NATs) in diatoms. For both of these transporter types, RACE techniques to obtain full-length sequence, hybridizations to estimate genome copy numbers, sequencing of genomic DNA to determine gene structure, and analysis of changes in mRNA levels under different conditions were applied to characterize the genes and their responses to different stimuli. Monitoring gene expression changes at the mRNA level can provide a powerful tool for investigating cellular responses. Such analysis showed that one level of regulation in the cell's preference for ammonium over nitrate was transcription of the NATs, which was not the case for ammonium transporter genes which were cloned later. The recent availability of phytoplankton genome sequences provides a tremendous information resource to facilitate gene identification and enable genome-wide surveys. We used genomic information in the first proteomics investigation into diatom silicification (which would not otherwise been feasible), and applied a whole genome microarray approach to identify novel genes involved in this process. Information gained by proteomic and genomic approaches is augmented by in-depth molecular analysis, including transgenic approaches. Molecular tools available to diatom researchers (including classical biochemical approaches) are reaching a high level of sophistication, which when coupled with genetic manipulation approaches, will greatly facilitate our understanding of diverse aspects of phytoplankton biology.

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MOLECULAR GENETIC APPROACHES TO STUDYING SILICA BIOMINERALIZATION IN DIATOMS

Poulsen, Nicole & Kröger, Nils

Chemistry & Biochemistry, Georgia Institute of Technology, Atlanta, GA, USA

Diatoms are a large group of unicellular microalgae encased by elaborate silica cell walls that exhibit species-specific micro- and nanopatterns. Recently, a unique family of silica associated phosphoproteins (termed silaffins) implicated in silica formation have been isolated from the diatoms *Cylindrotheca fusiformis* and *Thalassiosira pseudonana*. Structural characterization of the five major silaffins from *T. pseudonana* revealed that they share no sequence homology to silaffins from *C. fusiformis* but exhibit similar amino acid composition and posttranslational modifications. Interestingly, alternative processing of two silaffin precursor polypeptides gives rise to mature silaffins with rather different chemical properties. *In vitro* silica formation experiments suggest that the alternative processing of silaffins is an important step for cell wall morphogenesis. Numerous unsuccessful attempts to functionally analyze *C. fusiformis* silaffins *in vivo* led us to develop a molecular genetic transformation system for *T. pseudonana*, enabling the regulated expression of introduced genes. Using these tools we have investigated the cellular localization of GFP-tagged silaffins.

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MOLECULAR APPROACHES TO UNDERSTANDING BIOMINERALIZATION IN *EMILIANA HUXLEYI*

Read, Betsy A.

Biological, Cal State University, San Marcos, CA, USA

With the impending release of the draft sequence of the *Emiliana huxleyi* genome we are well poised to make significant advances in our understanding of the genes and proteins it encodes, and how they relate to biomineralization and coccolithogenesis in this most prominent coccolithophore. We have developed molecular and information tools and resources that will contribute to the annotation of the *E. huxleyi* genome sequence and will facilitate experimental and functional genomics research aimed at identifying genes and proteins involved in calcification processes. These resources include cDNA libraries representing transcripts from calcifying and non-calcifying cultures from which over 80,000 expressed sequence tags have been generated. A genomic BAC (bacterial artificial chromosome) library providing 5X coverage of the *E. huxleyi* genome has been developed, clones of which will be used: 1) to construct a physical map for annotation, and 2) to screen other coccolithophore libraries for comparative genomics studies. *E. huxleyi* specific microarrays have been produced from cDNA and long oligonucleotides and candidate biomineralization targets have been identified. We have also developed database systems to manage and disseminate genomics data for *E. huxleyi*. Our multifaceted approach to develop molecular tools and information to understand calcification will be described in this presentation.

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MOLECULAR ARCHEOLOGY: SEQUENCING STRAMENOPILE CHLOROPLAST DNA

Cattolico, Rose Ann^{1,2}, Jacobs, Michael³, Rocap, Gabrielle² & Zhou, Yang³

¹Biology, University of Washington, Seattle, WA, USA; ²Oceanography, University of Washington, Seattle, WA, USA;

³Genome Center, University of Washington, Seattle, WA, USA

Most chloroplast genomes have been sequenced by cloning chloroplast (cpDNA) into plasmid vectors, selecting cpDNA-containing clones, and then sequencing the clones using both plasmid and chloroplast-specific primers. This process is very labor intensive and involves isolation of highly purified cpDNA, which is often difficult or impossible to obtain from many algal taxa. Instead, we have developed a fosmid cloning approach for chloroplast genome sequencing. This technique is faster and more cost effective because it obviates the need to isolate cpDNA and avoids significant difficulties often encountered with assembly of the large inverted repeat - a feature that is found in most chloroplast genomes. The entire plastid genome has now been sequenced for two *Heterosigma akashiwo* strains (CCMP 452: East Pacific and NIES 293: West Atlantic). This unicellular raphidophyte forms destructive blooms worldwide in coastal regions. Analysis of the sequenced *Heterosigma* chloroplast genome has revealed findings that would not have been predicted based on our current knowledge of chloroplast chromosome architecture (derived almost entirely from terrestrial plants). The *Heterosigma* chloroplast genome is 160 kb in size and exist as two isomers. These variants result from recombination within the 22kb inverted repeat at putative “*dif* sites” which are docking domains for the chloroplast-encoded Xer C-like recombinase protein. Chloroplast gene order in *Heterosigma* is distinct from that of chlorophytes, rhodophytes or the two other stramenopiles sequenced to date (*Odontella* and *Thalassiosira*). Analyses of *Heterosigma*

cpDNA reveals genes not previously reported in any plastid genome. Several genes appear to have a regulatory role and thus could influence the functional program of the plastid. Analysis of the *Heterosigma* chloroplast genome documents the presence of numerous inverted and tandem repeats that represent approximately 2% of the total genome. Repeats have a median size of about 40 bp. All repeats are present between genes, many at the termini of specific genes. A discussion of the evolutionary significance of repeat structures in strameopile, haptophyte and rhodophyte chloroplast genomes will be presented.

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PUTATIVE RUBISCO ACTIVASE CFXQ IN THE TOXIC ALGA *HETEROSIGMA AKASHIWO*

Lee, Kun-Lin¹, Hoyt, Amanda¹ & Cattolico, Rose Ann^{2,3}

¹Biochemistry, University of Washington, Seattle, WA, USA; ²Biology, University of Washington, Seattle, WA, USA;

³Ocean Sciences, University of Washington, Seattle, WA, USA

CO₂ entry into the Calvin Cycle of many autotrophic organisms is driven by the enzyme Ribulose 1,5-Bisphosphate Carboxylase/Oxygenase (RuBisCO). In the *Viridiplantae*, activity of RuBisCO is catalyzed by an ATP-dependent enzyme, RuBisCO Activase. The chloroplast-encoded *cfxQ* gene in the raphidophyte *Heterosigma akashiwo* shows sequence homology to *cbbX*, a protein which enhances the performance of RuBisCO in bacterial systems. *cfxQ* is present and highly conserved in all published chloroplast genomes of rhodophytes, stramenopiles and haptophytes. We hypothesize that *Heterosigma CfxQ* is a RuBisCO Activase. The *Heterosigma cfxQ* gene is being studied at three different levels: genomic, transcriptional, and proteomic. At the genomic level, the presence of single nucleotide polymorphisms (SNPs) has been documented among geographically distinct algal populations. Five variants of the *cfxQ* gene have been identified among twenty one *Heterosigma* strains that have been sequenced. The nucleotide changes that have been observed cause both synonymous and non-synonymous amino acid alterations in the resulting proteins. CfxQ has been putatively modeled using sequence homology to the mouse ATPase P97. Nonrandom clustering of SNP-related amino acids localize on one face of the modeled protein, indicating mutations may be functionally selected. At the transcriptional level, expression patterns of *cfxQ* and the RuBisCO operon were analyzed over the synchronized 12-hour-light-12-hour-dark *Heterosigma* growth cycle (12L:12D). Cell samples were taken every three hours during a thirty-hour time period, subjected to RNA extraction, and analyzed by reverse-transcriptase-quantitative PCR. It was found that levels of *rbcL* and *cfxQ* expression oscillate in a similar fashion. Transcriptional abundance peaks at 12D/0L, gradually decreases though the light and reaches a minimum at 6D. At the proteomic level, we have over-expressed the *cfxQ* gene with a Topo T7 bacterial vector in *E. coli*. ATPase assays on extracted recombinant protein have shown that CfxQ has ATPase activity. Simultaneous approaches at the genomic, transcriptional and proteomic levels of this gene will elucidate the function of the CfxQ protein.

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FUNCTIONAL GENOMICS OF THE HARMFUL ALGA, *PRYMNESIUM PARVUM* (HAPTOPHYTA)

La Claire, John W.

MCD Biology, U. Texas at Austin, Austin, TX, USA

Prymnesium parvum N. Carter forms ichthyotoxic blooms that are increasing in frequency in several parts of the U.S., including Texas. In order to begin investigating the genetic basis of bloom formation and toxin production in this alga, a non-normalized cDNA library was constructed using poly(A⁺) RNA isolated from late log-phase cultures. Eight thousand clones were isolated and single-pass 5' nucleotide sequences of ~6,300 clones met length and quality criteria necessary to be incorporated into an expressed sequence tag (EST) database. Collectively, 3,415 tentative unique genes (TUGs) were distinguished from singlets or were assembled from clusters of 2 to 44 ESTs. Only 34% of the TUGs (~1,100) were identifiable from gene database searches [expect (*E*) values $\leq 10^{-10}$]. These represented most functional classes (KOG) of proteins as well as many metabolic pathways (KEGG). The vast majority of TUGs, including 12 of the 50 most commonly-encountered transcripts, encode potentially novel proteins that require further characterization. With respect to toxicity, the actual biosynthetic pathway of the unique prymnesin toxins is unknown. However, the toxins themselves have been structurally characterized as being polyketide glycolipids. TUGs that putatively encode polyketide synthase, oligoketide cyclase, methylmalonyl-CoA mutase, and β -ketoacyl-ACP synthase were identified, all being potential players in the toxin synthesis pathway(s). The large number of TUGs identified as functioning in vesicle transport and secretion may also be significant in this context, because the toxins are known to be secreted. Regarding bloom growth, one of the most abundant ESTs among the 50+ TUGs involved in ion/molecule transport, putatively encodes an ABC-type phosphate transport system component. This suggests that active and efficient phosphate transport may correlate with

bloom formation, which might help to explain why *P. parvum* out-competes other algae when it forms toxic blooms under low levels of phosphate. Microarray-based expression studies of all the TUGs should provide important insights into the biochemical and physiological nature of *P. parvum* cells when forming toxic blooms.

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GENES AND GENOMES IN THE CHAROPHYTE GREEN ALGAE

Delwiche, Charles F.

Cell Biology and Molecular Genetics, University of Maryland - College Park, College Park, MD, USA

Phylogenetic studies indicate that the closest algal relatives of land plants are found among the charophytes sensu Mattox and Stewart (1984), also known as the basal streptophytes. With growing recognition of the importance of comparative methods in genome analysis, the value of obtaining genomic data from charophyte algae is clear. Unfortunately relatively little is known about genome size or organization in these organisms. Expressed Sequence Tag (EST) analysis of cDNA data has been an effective method for acquiring preliminary genome-scale data from organisms with poorly characterized genomes, and this approach has recently been applied to *Mesostigma*, a unicellular flagellate closely related to the charophytes. I will describe our ongoing efforts to acquire genomic information from other charophytes, and will discuss the interaction between genomic and phylogenetic data.

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IDENTIFICATION OF GEOSMIN PRODUCING CYANOBACTERIA IN LAKE ONTARIO USING DGGE

Gill, Andrea¹, Muller, Kirsten M.¹ & Watson, Susan B.²

¹*Biology, University of Waterloo, Waterloo, ON, Canada;* ²*National Water Research Institute (NWRI), Environment Canada, Burlington, ON, Canada*

During late August and early September geosmin outbreaks due to planktonic Cyanobacteria frequently occur in Lake Ontario source water causing taste and odour episodes. These outbreaks often elicit consumer concern and are wrongly associated with poor drinking water quality. This study evaluates denaturing gradient gel electrophoresis (DGGE) as a molecular tool for monitoring potential taste and odour-causing Cyanobacteria in environmental samples. A DGGE standard using a variable region of the 16S rRNA gene was developed for single isolates of various planktonic geosmin-producing and non-producing cyanobacterial species. This standard was then applied to various environmental collections from Lake Ontario (August 2005). Included in the standard was the suspected primary contributor to Lake Ontario taste and odour, *Anabaena lemmermannii*. Profiles of sites that had a matching *An. lemmermannii* band were excised and sequenced for verification. GC-MS data of geosmin concentrations as well as identification of *An. lemmermannii* in fixed samples at each site was determined and compared to the molecular data from DGGE. There is a good correlation of detectable geosmin levels at the sites with the presence of microscopically identified *An. lemmermannii* and this correlates with the presence of these species noted in DGGE. Using DGGE to examine cyanobacterial communities can show shifts in the population of geosmin producing Cyanobacteria and with further development may be useful in predicting geosmin episodes in source waters.

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AN EARLY LIGHT-INDUCIBLE PROTEIN (ELIP) IS PRODUCED DURING COLD ACCLIMATION OF *SPIROGYRA VARIANS* (ZYGNEMATALES)

Han, Jong Won¹, Yoon, MinChul², Lee, Key Pyoung¹ & Kim, Gwang Hoon²

¹*Department of Chemistry, Kongju National University, Kongju, South Korea;* ²*Department of Biology, Kongju National University, Kongju, South Korea*

Simultaneous comparison of differentially expressed protein profiles of a freshwater alga, *Spirogyra varians*, grown under two different temperature conditions (4 and 20 degree) indicated the presence of cold stress-responsive proteins. Results from two dimensional electrophoresis (2-DE) showed that 21 proteins were up-regulated or newly appeared and 9 proteins were down-regulated under 4 degree condition. We isolated a 20 KDa protein (pI 4.5) which was most strongly up-regulated in 4 degree (about 500-fold higher than in 20 degree). Partial amino acid sequence of this protein was obtained using Ettan-MALDI TOF mass spectrometry. As the protein was never been reported before we named it as SVCR1 (*Spirogyra varians* cold regulated) protein. The cDNA encoding SVCR1 was cloned using a degenerated primers designed from the internal amino acid sequence of the protein and a cDNA library of *Spirogyra varians*. This cDNA consisted of 745bp containing open reading frame(ORF) of 549bp and 47bp/ 149bp of 5'/3'-untranslated region, respectively.

Interestingly, the deduced amino acid had a high sequence similarity with early light-inducible proteins (ELIPs) which are known as nuclear-encoded chloroplast proteins induced by light stress. The northern blot results showed that the accumulation of SVCR1 mRNA could be induced by cold treatment (4 degree) even under the dark condition whereas the high light stress conditions does not produce it.

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THE MITOCHONDRIAL GENOME OF A TERTIARY ENDOSYMBIONT RETAINS GENES FOR ELECTRON TRANSPORT PROTEINS

Imanian, Behzad¹, Carpenter, Kevin J.^{3,2} & Keeling, Patrick J.^{3,2}

¹Genetics Graduate Program, University of British Columbia, Vancouver, BC, Canada; ²Department of Botany, University of British Columbia, Vancouver, BC, Canada; ³Canadian Institute for Advanced Research, Vancouver, BC, Canada

Mitochondria and plastids originated through endosymbiosis, and subsequently reduced and integrated with the host in similar ways. However, plastids also spread between lineages through further endosymbioses of eukaryotic algae, resulting in secondary or even tertiary endosymbiotic algae. In contrast, mitochondria appear to have originated once and not spread between lineages. Mitochondria are also generally lost in secondary and tertiary endosymbionts, where only the host mitochondria remain. The exception to this is the diatom tertiary endosymbiont of dinoflagellates like *Kryptoperidinium foliaceum* where both host and endosymbiont are reported to contain mitochondria. Here, we describe the first mitochondrial genes from this system: cytochrome c oxidase 1 (*cox1*), cytochrome oxidase 3 (*cox3*), and cytochrome b (*cob*). Phylogenetic analyses demonstrated that all characterized genes were derived from the pennate diatom endosymbiont, and not the host. We also demonstrated that all three genes are expressed; *cox1* contains spliced introns; and *cob* and *cox3* form an operon, all like their diatom relatives. The endosymbiont mitochondria not only retain a genome, but also express their genes, and are actively involved in electron transport. Ultrastructural examination confirmed the endosymbiont mitochondria retain normal tubular cristae. Interestingly, we found the endosymbiont mitochondria abundant while host mitochondria were not observed, suggesting they are rare or perhaps have been lost. Overall, these data suggest the endosymbiont mitochondria have not reduced at the genomic or functional level, so essential functions may be divided between the two, or the endosymbiont mitochondrion may even be replacing the host organelle.

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THE EFFECT OF WATER FLOW INDUCED CARBON LIMITATION ON THE PHYSIOLOGY OF LAMINARIA SACCHARINA

Jordan, Terry L.¹, Koch, Evamaria W.¹ & Davison, Ian R.²

¹Horn Point Laboratory, University of Maryland Center for Environmental Sciences, Cambridge, MD, USA; ²Academy of Natural Sciences, Philadelphia, PA, USA

We examined acclimation of the photosynthetic metabolism to water flow in the brown alga *Laminaria saccharina*. Our hypotheses were that 1) increased boundary layer thickness at low flows would increase carbon limitation, and 2) the alga would respond by increasing the efficiency of carbon uptake by up-regulating mechanisms such as external carbonic anhydrase. We compared physiological characteristics of algae from high and low flow sites and in algae grown in a laboratory flume under three flow regimes (0, 1, and 13 cm s⁻¹). DIC uptake kinetics indicated that *L. saccharina* experiences carbon limitation in situ. Growth and carbon tissue levels were significantly lower under zero flow than 1 or 13 cm s⁻¹ suggesting that the flow-induced carbon limitation threshold is between 0 and 1 cm s⁻¹. Dark respiration and pigment levels were not significantly affected by water flow in the laboratory or the field. External carbonic anhydrase (CA_{ext}) activities were highest at the low flow site in the field and stagnant conditions in the flume experiment, indicating that CA_{ext} responds to boundary layer limitation, independent of water column concentrations. P_{max} was highest under stagnant conditions reflecting the increase in CA_{ext}, but these results were not statistically significant. Non-photochemical quenching (qN) increased in all groups of algae when they were transferred from high flow to stagnant conditions, but low-flow acclimated algae exhibited an increased capacity to dissipate light energy via qN both in response to increased carbon limitation at low flows or when exposed to high light. These data suggest that the capacity of *L. saccharina* to utilize light decreases under boundary layer limiting conditions and the resulting high light stress is dissipated via non-chemical quenching. Overall our data support the hypothesis that *L. saccharina* acclimates to low current velocities by increasing its ability to generate free CO₂ in the boundary layer via increased CA_{ext} concentrations. In addition, an increased ability to dissipate excess light energy is a key component of the acclimation response to low water flow

induced carbon limitation.

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PHYLOGENETIC AFFINITIES OF AUSTRALASIAN *BATRACHOSPERMUM* SPECIMENS (BATRACHOSPERMALES, RHODOPHYTA) INFERRED FROM MOLECULAR AND MORPHOLOGICAL DATA

Stewart, Sarah A.¹, Vis, Morgan L.¹ & Entwisle, Timothy J.²

¹*Environmental and Plant Biology, Ohio University, Athens, OH, USA;* ²*Royal Botanic Gardens and Domain Trust, Sydney, NSW, Australia*

Batrachospermum pseudogelatinosum, *B. campyloclonum*, *B. kraftii*, *B. bourrellyi* and *B. theaquum* were collected from Australia, New Caledonia and New Zealand. Sequence data from the *rbcL* gene was used to infer relationships among taxa. *B. pseudogelatinosum* and *B. campyloclonum* may represent a species complex, or harbor cryptic species, overlapping in morphological characters, and being difficult to distinguish. Ten new specimens attributable to *B. pseudogelatinosum* or *B. campyloclonum* were added to seven previously sequenced specimens. Fifteen specimens formed a clade; however, two specimens were not within this clade and sister to *Nothocladus*. Genetic variability among the fifteen specimens ranged from 0-5%, with some specimens identified as *B. campyloclonum* being identical to individuals of *B. pseudogelatinosum*. The two *B. bourrellyi* samples were variable in their position, either sister to this clade or part of it. Support for alternative hypotheses was equivocal. The *B. theaquum* specimens formed a well-supported clade. The position of *B. kraftii* specimens in the analyses will be discussed. The relationship among *B. pseudogelatinosum*, *B. campyloclonum* and *B. bourrellyi* was further investigated using the *cox2-3* gene spacer. The topology within the *B. pseudogelatinosum/B. campyloclonum* clade was similar to the *rbcL* analyses and showed *B. bourrellyi* sister to this clade. The phylogenetic utility of some commonly-used morphometric characters was evaluated using CART software. The clades obtained in the molecular analyses were used as a predictive framework to assess the morphometric data, but these clades could not be characterized by the morphometric data, demonstrating much morphological variability within and among the genetic clades. There is evidence for *B. bourrellyi* sister to *B. pseudogelatinosum*, but those data are equivocal. Further collections are needed to assess the position of *B. kraftii* within the Batrachospermales.

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FACILITATIVE EFFECT OF INTERTIDAL MACROALGAL CANOPIES ON *PELVETIOPSIS* RECRUITMENT

Szoboszlai, Amber

Moss Landing Marine Labs, San Jose State University, Moss Landing, CA, USA

During this study, I examined the facilitative effect of intertidal macroalgal canopies on the recruitment success of *Pelvetiopsis limitata*. Intertidal algal canopies can modify the micro-habitat and impact the survival & recruitment of algal propagules. *Endocladia muricata* and *Pelvetiopsis limitata* coexist in a patchy distribution, and they form canopies in the upper intertidal across much of central California. Initial observations of *Pelvetiopsis* recruits growing within the turf-like thallus of *Endocladia* suggested the presence of a facilitative relationship between *Endocladia* and *Pelvetiopsis*. I designed an experiment to manipulate algal canopy cover of different intertidal algal species in the field and established permanent plots with *Endocladia* only, *Pelvetiopsis* only, and complete removal of algal cover. I then counted visible *Pelvetiopsis* recruits <1cm high in the different treatments monthly for one year. Results indicated that *Pelvetiopsis* recruitment was enhanced by the presence of algal canopies, but that algal canopy species composition had no effect. This observation was further supported by the springtime appearance of *Porphyra* sp. in the plots and subsequent high numbers of *Pelvetiopsis* recruits. Proximity and position of reproductive adult *Pelvetiopsis* also appeared to positively influence recruitment success. The relationship between algal canopy cover and recruitment success of *Pelvetiopsis* has important implications for understanding patterns of species distribution and diversity.

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COMPARATIVE SEQUENCE ANALYSIS OF DIATOM SILICON TRANSPORTERS: TOWARDS A MOLECULAR MODEL OF SILICON TRANSPORT

Thamatrakoln, Kimberlee¹, Alverson, Andrew J.² & Hildebrand, Mark¹

¹*Scripps Institution of Oceanography, La Jolla, CA, USA;* ²*Section of Integrative Biology and Texas Memorial Museum, The University of Texas at Austin, Austin, TX, USA*

Silicon, an important element in biology from unicellular algae to humans, can act as a structural material for both plants and animals, as well as a metabolite or regulator of gene expression. Molecular details of biological interaction with silicon are poorly understood. Diatoms, the largest group of silicifying organisms in the ocean, are a good model system for studying this interaction. The first proteins shown to directly interact with silicon were diatom silicon transporters (SITs), and although other silicon-interacting proteins have since been identified, SITs are the only proteins known to interact with soluble silicon without polymerizing it into silica. Five SIT genes were first identified in the pennate diatom, *Cylindrotheca fusiformis*, and genome sequencing of the centric diatom, *Thalassiosira pseudonana* led to the identification of three SIT genes. SITs are a novel family of transporters with no known homologs. Relatively little is known about how SITs bind and transport silicon. Because the fundamental basis for substrate recognition lies within the amino acid sequence of a protein, residues important for function are likely retained during evolution. Identification of conserved amino acids would provide insight into the mechanism of SIT function, however, lack of SIT sequences from diverse diatoms, and high sequence conservation in known SITs has precluded identification of such residues. In this study, PCR was used to amplify partial SIT sequences from diverse diatom species. Multiple gene copies were found and phylogenetic analysis showed SITs tended to group according to species. Comparative amino acid analysis identified conserved regions that may be important for silicon transport, including repeats of the motif GXQ. A model for silicon uptake is presented that is consistent with known aspects of transport.

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EXPERIMENTAL EVALUATION OF REDUCED RESOURCE ALLOCATION ON THE GROWTH AND REPRODUCTION OF *SARGASSUM SILIQUASTRUM* (TURN.) AG. IN HONG KONG SAR, CHINA

Wong, Suet Ying¹ & Ang, Put O. Jr.²

¹Environmental Science Programme, The Chinese University of Hong Kong, Hong Kong, China; ²Biology Department, The Chinese University of Hong Kong, Hong Kong, China

Individuals of *Sargassum siliquastrum* were tagged and trimmed to 15 cm of shoot length or to holdfast at different times within two successive years to test for the effects of reduced resources at different growth stages on their growth and reproduction. Manipulations were conducted in Aug 2004 and 2005, before the active growing period of the seaweeds, and in Nov 2004 and 2005, before their reproductive period. The length, reproductive state and number of new shoots emerging from the holdfast of the tagged plants were then monitored monthly. Individuals trimmed to 15cm in Aug showed reduced growth [max mean (SD) length = 72.8 ± 44.1 cm for 2004 treatment and 51.7 ± 20.5 cm for 2005 treatment] and delayed reproduction when compared with tagged controls [max mean length = 178.0 ± 48.2 cm for 2004 treatment and 95.6 ± 21.2 cm for 2005 treatment]. Only 70% of the plants trimmed in Aug 2004 and 60% of those trimmed in Aug 2005 became reproductive in Feb 2005 and 2006 respectively, compared with 100% of the tagged controls that became reproductive in Dec 2004 and Jan 2006. Plants trimmed to 15 cm in Nov 2004 and 2005 remained at ≈ 25 cm in length throughout the reproductive period. However, around 45% (2004 treatment) and 50% (2005 treatment) of them still became reproductive in Feb 2004 and 2005 respectively although their sizes were smaller than the min size of 40 cm of the reproductive control plants. Treatment plants also produced fewer receptacles when compared with the control plants. More new shoots emerged from those trimmed to holdfast in Nov 2004 and 2005 than in those trimmed in Aug, suggesting that more reserved resources were available in the holdfast in Nov, after the plants had gone through rapid growth in autumn. None of these plants however, ever became reproductive. All these results suggested differential allocation of resources by *S. siliquastrum*, with the ultimate effect of propagating itself through sexual reproduction or vegetative growth.

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DEVELOPMENT AND EVALUATION OF A DIATOM BASED INDEX OF BIOTIC INTEGRITY FOR ACID AND METAL IMPACTED STREAMS

Zalack, Jason T. & Vis, Morgan L.

Environmental and Plant Biology, Ohio University, Athens, OH, USA

Acid mine drainage (AMD) is caused when pyrite minerals naturally occurring in coal are exposed to oxygen and water producing sulfuric acid; the low pH facilitates metal dissolution. This acidic and metal rich effluent then flows into streams. In Ohio, macroinvertebrates and fish are used for assessing the biological condition in wadable streams. Macroinvertebrates are used to calculate the invertebrate community index (ICI), assigning sites a score of 0-60, and a classification of Excellent, Good, Fair, or Poor. Recently a diatom index of biotic integrity (DIBI) using seven metrics was developed in Kentucky to monitor agriculturally impacted streams. Our study sought to evaluate the sensitivity of

these DIBI metrics to AMD pollution by relating them to water chemistry and the ICI. Also to assemble promising metrics into an index that would characterize health of streams along an AMD gradient. To accomplish this task, diatoms, macroinvertebrates and water samples were collected using standard methods from 41 stream segments in southeast Ohio. Water chemistry was analyzed for a variety of chemicals including nutrients and metals. Macroinvertebrate metrics showed significant ($p < 0.05$) correlations with many stream chemistry variables. Three diatom metrics used in the DIBI showed significant correlations with two or more chemical variables. The DIBI and ICI were significantly ($r = 0.31$, $p < 0.05$) correlated to each other. Classification and regression tree (CART) analysis produced a tree using five of the seven diatom metrics to characterize streams based on the macroinvertebrate narrative groupings (excellent, good, fair, poor). A modified diatom index was created using three of the original metrics plus six additional metrics that were shown to be particularly sensitive to AMD stress. The modified index proved to have a much improved relationship with the ICI ($r = 0.72$, $p < 0.0001$). This modified DIBI may be a useful tool for assessing biotic integrity when obtaining an ICI score is not feasible.

33 **INTEGRATED MULTI-TROPHIC AQUACULTURE: SEaweEDS AND BEYOND... THE NEED OF AN INTERDISCIPLINARY APPROACH TO DEVELOP SUSTAINABLE AQUACULTURE**

Chopin, Thierry¹, Robinson, Shawn², MacDonald, Bruce¹, Haya, Kats², Page, Fred², Ridler, Neil¹, Szemerda, Michael³, Sewuster, John⁴ & Boyne-Travis, Sharon⁵

¹University of New Brunswick, Saint John, NB, Canada; ²Fisheries & Oceans, St. Andrews, NB, Canada; ³Cooke Aquaculture Inc., St. George, NB, Canada; ⁴Acadian Seaplants Limited, Dartmouth, NS, Canada; ⁵CFIA, Blacks Harbour, NB, Canada

Integrated multi-trophic aquaculture (IMTA) is based on an age-old, common sense, farming practice in which the by-products (wastes) from one species become inputs for another: fed aquaculture (fish or shrimp) is combined with extractive inorganic (seaweed) and extractive organic (shellfish) aquaculture. We are developing such a system at an industrial pilot scale by co-cultivating salmon (*Salmo salar*), kelp (*Laminaria saccharina* and *Alaria esculenta*) and blue mussel (*Mytilus edulis*) at three sites in the Bay of Fundy, Canada. The project has 5 modules: seaweeds, mussels, food safety, environment and socio-economics. Data acquired through this interdisciplinary approach support the establishment of IMTA systems for environmental sustainability (bioremediation), economic diversification (from fish filets to bioactive compounds) and social acceptability (better management practices). Kelp culture techniques have been improved. Increased growth rates of kelps (46%) and mussels (50%) cultured in proximity to fish farms, compared to reference sites, reflect the increase in food availability and energy. Nutrient, biomass and oxygen levels are being monitored to model the bioremediation potential of an IMTA site. Over 5 years, none of the therapeutants used in salmon aquaculture have been detected in kelps and mussels collected from the IMTA sites; levels of heavy metals, arsenic, PCBs and pesticides are always below regulatory limits. Most participants of a focus group study felt that IMTA has the potential to reduce the environmental impacts of salmon farming, benefit community economies and employment opportunities, and improve the industry competitiveness and sustainability. All felt that seafood produced in IMTA systems would be safe to eat and 50% were willing to pay 10% more for these products if labelled as such. Preliminary data of a bio-economic model show that the addition of seaweed and mussel to salmon farming is profitable and helps reduce risks. We are now scaling-up the systems and working on an appropriate food safety regulatory and policy framework that will allow the development of commercial IMTA operations.

34 **PHOTOAUTOTROPHIC GROWTH OF MICROALGAE IN TUBULAR PHOTOBIOREACTORS**

Ugwu, Charles U., Aoyagi, Hideki, Uchiyama, Hiroo & Tanaka, Hideo
Life Sciences and Bioengineering, University of Tsukuba, Japan, Tsukuba city, Japan

The use of fossil fuels as the main industrial and transportation energy sources has increased drastically leading to global warming. Unfortunately, these fossil fuels are not renewable and their excessive use have led to various environmental problems. In order to keep the environment clean and free of pollutants, there is an urgent need to develop alternative energy source. Solar light energy is very promising because it is clean, cheap and abundant in nature. Development of efficient methods for utilization of solar light energy will help to solve the present world energy and environmental problems. Photosynthetic microorganisms are capable of utilizing solar light energy and can also be used for bio-fixation of carbon dioxide from the atmosphere. Furthermore, photosynthetic microorganisms have various advantages in terms of carbon recycling systems such as high growth rates, possibility of cultivating them both in seas and deserts, as well as

their usefulness in production of foods and bioactive substances. We have been trying to develop efficient outdoor photobioreactor systems for cultivation of photosynthetic microorganisms. Among the cultivation systems which we have investigated, tubular photobioreactors seem to have high potentials for mass cultivation of microalgae. Thus, we developed efficient tubular photobioreactor with high mass transfer capacity. Outdoor mass cultivation of *Chlorella sorokiniana* and *Synechocystis aquatilis* in these photobioreactors were also studied. In order to improve the efficiency of our tubular photobioreactors, we installed mixing devices (static mixers) in them, and this resulted to high biomass yields, as well as high CO₂ fixation rates (Ugwu *et al* 2002. *Appl Microbiol Biotechnol.* 58, 600 - 607). Volumetric and areal productivities obtained in our tubular photobioreactors were 1.5 g L⁻¹ d⁻¹ and 34 g m⁻² d⁻¹, respectively. Growth of these microalgae depended on the prevailing light intensity, temperature, standing biomass concentration, and other culture parameters. This work was partly funded through the 'Grant-in-Aid for Scientific Research' program of the Japan Society for Promotion of Science.

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DEVELOPING A LAND-BASED, LOW-COST POLYCULTURE SYSTEM ACCESSIBLE TO COASTAL MAORI

Miller, Sheryl¹, Heath, Philip² & Williams, Tiratu³

¹*Te Kuwaha, National Institute of Water & Atmospheric Research Ltd, Wellington, New Zealand;* ²*Aquaculture and Fisheries Enhancement, National Institute of Water and Atmospheric Research Ltd, Wellington, New Zealand;* ³*Hongoeka Community Development Trust, Wellington, New Zealand*

In New Zealand, indigenous involvement within land-based aquaculture activities is considerably less than their participation in commercial wild fisheries due primarily to high capital costs, unsuitable seawater supply and lack of capacity. NIWA has entered into a research partnership with an indigenous Maori group to develop a low-cost, land-based polyculture system and appropriate husbandry techniques as a means of providing sustainable employment and as a source of customary foods. The proposed system will be modular, and scaleable to meet the requirements of individual applications whilst establishing techniques for existing and new high-value species that can be cultured economically in small volumes. A pilot system, 1/8 the size of the proposed system, has been built for experimental purposes. NIWA is an established leader in paua (abalone) farming hence paua was chosen as the primary crop. Other species being investigated for use within this system include oysters, mussels, seaweed and sea cucumbers. This presentation will give an overview of the project and detail some of the preliminary results to date.

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NUTRACEUTICALS FROM RED MICROALGAE AS HYPOCHOLESTEROLEMIC AGENT

Dvir, Irit¹, Chayoth, Reuven², Madar, Zecharia³ & Arad (Malis), Shoshana¹

¹*The Institute for applied biotechnology, Ben-Gurion University of the Negev, Beer Sheva 84105, Israel;* ²*Life science, Ben-Gurion University of the Negev, Beer Sheva 84105, Israel;* ³*Faculty of Agriculture, The Hebrew University of Jerusalem, Rehovot 76100, Israel*

The cells of the red microalga *Porphyridium* sp. are encapsulated in a cell wall composed of sulfated polysaccharides (about 50-70% of the biomass); the external part of which dissolves into the medium. The cell-wall polysaccharides are composed of 10 different sugars and it is negatively charge due to the presence of sulfate groups and glucuronic acid. The algal cells contain essential PUFA such as eicosapentaenoic acid [EPA - 20:5 (n-3)]. The purpose of this study was to investigate the dietary effects of the red microalga *Porphyridium* sp. on lipid metabolism in rats fed a cholesterol rich diet. Pellets from the biomass (red microalgal cells) or the algal sulfated polysaccharide were use as the dietary fibers diet, for a period of 15 days. The algal polysaccharide and biomass significantly lowered total serum cholesterol levels, increased the HDL/LDL ratio, lowered triglycerides and reduced liver weight and hepatic cholesterol levels, as compared with the respective control (pectin or cellulose). Consumption of the biomass increased fecal bile acid excretion by two fold and significantly enhanced neutral steroid excretion in the polysaccharide fed rats. Both algal polysaccharide and biomass were found to be potent hypocholesterolemic agents active at low concentrations. The results presented in this study support the use of products from red microalgae as a novel nutraceutical in the health food market.

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BIODIESEL FROM ALGAE: LESSONS LEARNED OVER THE PAST 60 YEARS AND FUTURE PERSPECTIVES

Hu, Qiang, Zhang, Chengwu & Sommerfeld, Milton

The concept of using microalgae for biodiesel was first explored during and shortly after the World War II when there were shortages of petroleum fuel supplies, particularly for transportation. Major efforts were initiated during the 1970s when the oil crisis occurred worldwide and alternative fuel sources were sought. The nearly twenty-year long "Aquatic Species Program, or ASP" funded by the U.S. Department of Energy from the late 1970's through the early 1990's represented the single largest effort to determine the technical and economic feasibility of microalgae-based biodiesel. Over the past 60 years, more than 120 species/strains of high oil-containing microalgae have been characterized. The unicellular green algae and diatoms were among the most frequently tested organisms and were generally found to contain higher lipid or oil content. Cyanobacterial species/strains were found to contain the least amounts of lipids/oil (<10% of dry weight). The most effective culture conditions that influenced the cellular oil content were the depletion of the major nutrients nitrogen and silicon. As algal cultures transition from nutrient-rich to nutrient-depleted conditions, the cellular oil content increases, on average, from 20.2% to 43.8% of dry weight in green algae, and from 22.7% to 37.8% of dry weight in diatoms. Open ponds have been the primary culture systems evaluated for mass culture of microalgae for biodiesel feedstock. However, establishing algal cultures of high biomass yield with high lipid content in open pond systems is very difficult. Recent soaring oil prices, reduction in world oil reserves, international instability, and the environmental deterioration associated with fossil fuel consumption have generated renewed interest in algae-based biodiesel. Four research areas deserve attention in order for the algae-for-biodiesel concept to become viable in the marketplace: 1) development of cost-effective, large-scale photobioreactors; 2) integration of algal biodiesel feedstock production with waste-stream treatment; 3) genetic improvement of algal strains for higher oil content and/or enhanced culture performance; and 4) co-production of value-added products.

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TOWARDS A GLOBAL PHYLOGEOGRAPHY OF *GRACILARIA SALICORNIA* (GRACILARIACEAE, RHODOPHYTA), AN INVASIVE SPECIES IN HAWAII, BASED ON CHLOROPLAST AND MITOCHONDRIAL MARKERS

Gurgel, Carlos F.¹, Terada, Ryuta², Abbott, Isabella A.³, Fredericq, Suzanne⁴ & Norris, James N.⁵

¹Smithsonian Marine Station, Smithsonian Institution, Fort Pierce, FL, USA; ²Faculty of Fisheries, Kagoshima University, Shimoarata, Japan; ³Dept. of Botany, University of Hawai'i at Manoa, Honolulu, HI, USA; ⁴Dept. of Biology, University of Louisiana, Lafayette, LA, USA; ⁵Dept. of Botany, Smithsonian Institution, Washington, DC, USA

Gracilaria salicornia, a benthic red alga invasive in the main Hawaiian Islands, has produced a massive, uncontrolled growth near the Waikiki Aquarium, Honolulu, Oahu Island, creating an almost monotypic, thick-stand, and therefore a conspicuous loss of local biodiversity. The uncontrolled growth of this species may pose a threat to other Hawaiian marine ecosystems. Introduced to Oahu in the 1970's, its original source is unknown but ought to be from somewhere in the tropical and subtropical Indian Ocean or Indo-Pacific where it is native. In this study we present preliminary phylogeographic analyses based on *rbcL-rbcS* (chloroplast) and *cox2-cox3* (mitochondrial) spacers from populations sampled from a wide geographic range across the Western Pacific Ocean and Hawaii. Results revealed that the Waikiki invasive populations have multiple sources of independent introduction with haplotypes also present in all surveyed countries: Malaysia, Micronesia, Indonesia, Thailand, Japan, Guam, and Philippines. However results from both markers show strong presence (high frequency) of haplotypes from Guam, Philippines and Japan in the Waikiki population, suggesting the formation of the genetic "super invasive" concept, where invasive populations present higher genetic diversity than in their native populations, caused by multiple events of introduction from isolated sources. Genetic survey of *G. salicornia* populations in Oahu also discovered the presence of at least one cryptic (unknown) species, so far endemic to Hawaii. This is possibly due to the wide range of distinct morphological phenotypes (habits) seen in presumed *G. salicornia* that accounts for the several synonyms currently merged into this species. A more extensive sampling across the Pacific and within the main Hawaiian Islands may reveal new patterns of dispersal and cryptic species for this economically and ecology important benthic red macroalgae.

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DOPAMINE IN A GREEN ALGA: LOCALIZATION, RELEASE, AND COMMUNITY EFFECTS

Nelson, Tim¹, Van Alstyne, Kathryn L.² & Jackson, Dana³

¹Blakely Island Field Station, Seattle Pacific University, Seattle, WA, USA; ²Shannon Point Marine Center, Western Washington University, Anacortes, WA, USA; ³Biology, Paine College, Augusta, GA, USA

Ulvaria obscura var. *blyttii* is a major contributor to "green tides" in the Northwestern United States and Western Canada. This alga releases dopamine at its death, causing the thallus to turn brown or black. If placed in a liquid medium at death, the alga will cause the liquid to turn pink, then reddish-brown, and finally a black precipitate will form as the medium clears. These effects are caused by the release of dopamine, its conversion to quinones by polyphenol oxidase, and subsequent polymerization of the quinones and organic molecules. *Ulvaria* is less favored by grazers than other Ulvacean algae and its extracts are toxic to a variety of algae and invertebrates. Dopamine has been identified as a grazer deterrent, and shown to inhibit *Fucus* germination and *Ulva* growth. Dopamine was localized within cells using the glyoxylic acid technique. It occurs in vesicles near the outer cell surfaces of *Ulvaria*. These vesicles appear to release their contents to the apoplast of the alga when the cells are damaged or dying.

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ASSESSMENT OF CORAL REEFS USING HERBIVORY/NUTRIENT ASSAYS AND INDICATOR GROUPS OF BENTHIC PRIMARY PRODUCERS: A CRITICAL SYNTHESIS, PROPOSED PROTOCOLS, AND CRITIQUE OF MANAGEMENT STRATEGIES

Littler, Mark M.¹ & Littler, Diane S.²

¹Department of Botany, Smithsonian Institution, Washington, DC, USA; ²Marine Science, Harbor Branch Oceanographic, Fort Pierce, FL, USA

1. Rapid assessment protocols for determining and monitoring the status of any given coral reef are provided and include measuring: (a) standing stocks of functional indicator groups, (b) herbivore populations, (c) water-column nutrient levels, (d) tissue C:N:P ratios, (e) algal physiological-response assays, and (f) herbivory assays. These measurements can reveal quantitative tipping-point levels beyond which resilience to undesirable phase shifts begins to become critically reduced. Universal tipping-point approximations are reviewed for inorganic nutrients, and posited for the first time for herbivory. 2. The relative roles of top-down and bottom-up controls in determining benthic community structure and the health of coral reefs are especially important management concerns. This paper specifically addresses the top-down effects of herbivory and bottom-up effects of nutrient enrichment on critical indicator groups; i.e. reef-building corals, crustose coralline algae, dense turf algae, and frondose macroalgae. 3. A predominance of (a) massive corals and calcareous coralline algae relative to frondose macroalgae and algal turfs indicates a healthy spatially heterogeneous condition reflecting low nutrients and high herbivory. An abundance of (b) frondose macroalgae illustrates the least desirable condition of elevated nutrient levels and reduced herbivory, possibly reflecting pollution in concert with destructive herbivore fishing practices. High coverage of (c) coralline algae suggests healthy high herbivory levels, but problems with elevated nutrients that are inhibitory to some corals. Domination by (d) dense turf algae indicates desirably low nutrient levels, but an inadequate herbivory component. The experimental results demonstrate flaws in some of the previously published manipulative methods and provide insights for the improvement of in-situ nutrient studies on coral reefs. 4. The fast growth and turnover rates of fleshy algae compared to other reef organisms highlight their value as early-warning indicators of reef degradation.

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MACROALGAL COMMUNITIES IN INDIAN RIVER LAGOON, FLORIDA: SPATIAL AND TEMPORAL VARIABILITY

Hanisak, M. Dennis

Harbor Branch Oceanographic Institution, Fort Pierce, FL, USA

From November 1993 to November 1995, a study was conducted in Indian River Lagoon (IRL) to determine relationships of light attenuation, water quality, and submerged aquatic vegetation (SAV) at six stations representing a range of water quality conditions. As part of the quarterly SAV effort, macroalgal species composition, cover, and biomass were determined. The grand mean macroalgal cover for all stations was 15%, but varied considerably (from 1 to 41%); the grand mean macroalgal biomass was 17 g dry weight/m² (ranging among stations from 1 to 42 g dry weight/m²). The macroalgal community at these stations was almost exclusively unattached "drift" algae; 65% of the total biomass belonged to the red algal genus *Gracilaria*. Macroalgal cover, total macroalgal biomass, and *Gracilaria* biomass increased along the north-south gradient of stations. Despite strong seasonal patterns at individual stations, there was no consistent temporal pattern in macroalgal cover and biomass among stations. A significant interannual difference occurred at only one station. This study provides baseline data to determine long-term changes in community structure of IRL macroalgae. While much attention has appropriately been paid to the importance of seagrass in estuarine waters, such as IRL, more work is needed to describe the spatial and temporal variability of macroalgae, to understand the causes of these variation,

and to determine the consequences of such variability to other tropic levels and to biogeochemical cycles in these systems.

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CHANGING SEAWEED COMMUNITIES ON SOUTHERN CALIFORNIA SHORES

Murray, Steven N.^{1,2}, Smith, Jayson¹, Bullard, Aimee¹, Gerrard, Amanda¹ & Kido, Janine¹

¹*College of Natural Sciences and Mathematics, California State University, Fullerton, Fullerton, CA, USA;* ²*Department of Biological Science, California State University, Fullerton, Fullerton, CA, USA*

Environmental conditions have changed along the southern California coast during the past five decades. Coastal habitats have been increasingly influenced by the activities of a rapidly expanding human population. In addition, coastal waters have undergone shifts in ocean climate, including a regime shift affecting coastal plankton, fish, and sea bird populations that began in the mid-1970s and persisted through the late 1990s. Changes in the abundances of intertidal seaweeds over this 50-year period are less well known. E. Y. Dawson developed seaweed species lists and made subjective estimates of abundance at 44 sites along the southern California coast in the late 1950s. During the mid-1970s, Mark Littler and colleagues performed intensive ecological studies at an additional 22 southern California sites. We re-located and re-sampled 14 of Dawson's and Littler's study sites between 1998 and 2002 using quantitative line transect or plot-based methods and compared seaweed community compositions and abundances with prior data. We found that macrophyte communities have changed at these sites since the original benchmark sampling. Seaweed communities are now increasingly dominated by low-producing, crustose, articulated coralline, and turf-forming algae while abundances of many larger, more productive, frondose algae have declined. These shifts have changed the principal contributors to community primary productivity on southern California shores and reduced the influences of mid-intertidal algal canopies. The ability to correlate changes in southern California intertidal seaweed communities with environmental variables is limited by the robustness of available data and complexities associated with the many environmental factors potentially affecting these coastal habitats.

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HOW, WHEN, AND WHY SECONDARY RED SYMBIOTIC ALGAE ROSE TO ECOLOGICAL PROMINENCE ON THE CONTEMPORARY OCEAN

Falkowski, Paul G.

Institute of Marine and Coastal Sciences and Dept. of Geological Science, Rutgers University, New Brunswick, NJ, USA

The community structure and ecological function of contemporary marine ecosystems are critically dependent on eukaryotic phytoplankton. Although numerically inferior to cyanobacteria, these organisms are responsible for the majority of the flux of organic matter to higher trophic levels and the ocean interior. Photosynthetic eukaryotes evolved over 2 billion years ago in the Proterozoic oceans, however it was not until the Mesozoic Era (251-65 million years ago), that the three principal phytoplankton clades which came to dominate the modern seas rose to ecological prominence. In contrast to their pioneering predecessors, the dinoflagellates, coccolithophores and diatoms all contain plastids derived from an ancestral red alga via secondary symbiosis. In this talk, I will we examine the geological, geochemical and biological processes that contributed to the rise of these three, distantly related, phytoplankton groups, and how their rise to ecological prominence altered the Earth's carbon and oxygen cycles.

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ORIGIN AND DIVERSIFICATION OF LIGHT HARVESTING COMPLEXES DURING PLASTID EVOLUTION

Durnford, Dion

Biology, University of New Brunswick, Fredericton, NB, Canada

The Light-harvesting complexes (LHCs) are a large superfamily of chlorophyll and carotenoid-binding proteins present in nearly all photosynthetic eukaryotes. Though the most obvious role of these proteins is the collection and transfer of light energy into the reaction centres, the LHCs are also essential for photoprotection. The fine-tuning of these roles over time has led to tremendous functional divergence of the LHCs, the scope of which has only been extensively examined in plants. Though novel pigment-protein complexes have evolved independently in several groups, the LHCs are the dominant antennae system in the majority of photosynthetic eukaryotes. The similarity of LHCs in diverse groups and the absence of homologs in cyanobacteria suggests they are a eukaryotic invention that occurred following the endosymbiotic origin of the plastid. This talk will trace the evolutionary history of the LHCs from cyanobacterial precursors through to

the diverse photosynthetic groups possessing primary or secondary plastids and discuss events leading to the diverse antenna systems observed today. In particular, I will concentrate on the chlorophyll a/b-binding family of antenna proteins and discuss our recent progress in understanding the diversification of the antennae systems of green algae and organisms possessing green algal-derived plastids. This work stems from several expressed sequence tag (EST) projects initiated by the Protist EST Project that included a taxonomically broad range of chlorophyll a/b-containing protists. With the prevalence of genomics, the complexity of the LHC antennae systems in different groups is becoming apparent, though the reason for such complexity and the function of individual members is largely unknown. However, the extensive knowledge of the structure and function of the plant antenna system provides a convenient framework upon which the antenna systems of other chlorophyll a/b-containing organisms can be compared and the functional capabilities inferred. It is through such approaches that we hope to gain an understanding of the evolution of the antenna systems and the origin of light harvesting and photoprotective strategies.

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WHOLE GENOME ANALYSES OF DIATOMS: INSIGHTS INTO ECOLOGY AND EVOLUTION

Armbrust, Virginia

School of Oceanography, University of Washington, Seattle, WA, USA

Whole genome sequences for two diatoms, *Thalassiosira pseudonana* (centric diatom) and *Phaeodactylum tricornutum* (pennate diatom) have been completed and are (or soon will be) publicly available. Whole genome sequencing of the toxigenic diatom *Pseudo-nitzschia multiseries* is now underway and is scheduled to be completed in 2007. This growing data base of sequence information provides new insights into the ecology and evolution of this important group of phytoplankton. Diatoms are derived from a secondary endosymbiotic event in which a eukaryotic heterotroph engulfed a eukaryotic autotroph, most likely a red alga. Not surprisingly, we find genomic evidence that diatoms possess a diverse array of capabilities that distinguish them from the higher plant/green/red alga lineage. I will discuss how we are using a wide diversity of approaches to gain insights into aspects of diatom physiology that may have helped to make them such successful components of the marine phytoplankton.

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PLASTID GENES IN THE NONPHOTOSYNTHETIC DINOFLAGELLATE *CRYPTHOCODINIUM COHNII*

Sanchez-Puerta, Maria V.¹, Lippmeier, J.C.², Apt, Kirk E.² & Delwiche, Charles F.¹

¹*Cell Biology and Molecular Genetics, University of Maryland, College Park, MD, USA;* ²*Martek Biosciences Corp., Columbia, MD, USA*

Dinoflagellates are a diverse group of flagellate protists closely related to apicomplexan parasites, comprising photosynthetic and heterotrophic species, as well as parasitic ones. About half of all dinoflagellates are photosynthetic, and it is uncertain whether the non-photosynthetic members of the group are primitively so, or have lost photosynthesis. *Cryptocodinium cohnii* is an early divergent non-photosynthetic marine dinoflagellate. We have completed an EST analysis of *C. cohnii* and examined the data for presence of genes that appear to be of plastid origin. This represents the first extensive genomic analysis of a heterotrophic dinoflagellate. Out of 5,505 unique sequences in the dataset, 415 were most similar to genes from cyanobacteria or plants using BLAST tool from NCBI. To more precisely determine their evolutionary history, these genes were subjected to detailed phylogenetic analysis. Among the candidate genes, at least 18 are very likely to have been derived from a plastid, and at least 10 appear to be plastid-targeted. These data imply that *C. cohnii* is not only derived from a photosynthetic ancestor, but very likely retains a non-photosynthetic plastid. Analyses of putative gene function suggest that heme biosynthesis, non-mevalonate isoprenoid biosynthesis, amino-acid metabolism, and Fe-S cluster assembly may occur in the plastid. These observations are also consistent with the "Chromalveolate hypothesis," which proposes that several major groups of eukaryotes, including ciliates, apicomplexa, oomycetes, and others, may form a monophyletic group, and be derived from photosynthetic ancestors.

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WERE THE OCEANS EVER GREEN? EVALUATING THE EVIDENCE FOR GREEN ALGAE IN THE GEOLOGIC RECORD

Kodner, Robin B.¹, Summons, Roger E.² & Knoll, Andrew H.¹

¹*Organismic and Evolutionary Biology, Harvard University, Cambridge, MA, USA;* ²*Earth, Atmospheric, and Planetary Sciences, Massachusetts Institute of Technology, Cambridge, MA, USA*

In the modern oceans, red-lineage phytoplankton are responsible for the majority of eukaryotic photosynthesis. It is commonly believed that these groups, that arose in the early Mesozoic, replace green-algal-dominated marine ecosystems. We have reevaluated the evidence for green algae in the pre-Mesozoic rock record. The molecular fossil and microfossil records are interpreted in light of comparative biology and biochemistry of extant green algae. Two classes of molecular fossils, steroidal lipids and the algaenan biopolymer, are currently associated with green algae. We have conducted survey studies on cultured organisms for these compounds and evaluated them in the context of the phylogenetic relationships of these algae. It appears that algaenan, a highly aliphatic biopolymer, is likely a complicated class of compounds that is difficult to distinguish with current extraction and analysis methods. Furthermore, there is no specific phylogenetic relationship among algaenan producing organisms. C_{29} sterols and their fossil sterane derivatives, are commonly attributed to the green algal lineage. Analysis of sterols from all major groups of green algae show that they do produce C_{29} sterols, but many taxa contribute C_{28} sterols in equal abundance. A prominent feature of the earliest fossil biomarker record shows a strong dominance of C_{29} steranes. We have also examined the chemical nature and ultrastructure of putative green algal microfossils and their modern analogues. We have done the first chemical and ultrastructure analysis of modern prasinophyte green algal phycoma *Halosphaera* sp?. Though it is still difficult to make a positive identification of leiospherids microfossils as *Halosphaera*, our work adds to a body of knowledge indicating cryptic diversity within leiospherids and to new ideas about microfossil preservation. Though there is support for the presence of green algae in ancient oceans, more work on chemical and ultrastructural analysis of modern phycoma and leiospherid fossil, as well as taphonomic investigations of alga biomass is required to make generalized statements about their presence in pre-Mesozoic ecosystems.

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CRYPTIC EVOLUTION IN LABORATORY CULTURES

Lakeman, Michael B.¹ & Cattolico, Rose Ann^{1,2}

¹Biology, University of Washington, Seattle, WA, USA; ²Ocean Sciences, University of Washington, Seattle, WA, USA

Over recent decades surprising diversity has been revealed within phytoplankton populations. Over time, appreciation of this variation has moved to smaller and smaller scales. Initially inter-specific diversity was thoroughly documented, then variation within species was noted through the use of different strains or isolates of the same species. More recently, field studies have even demonstrated significant inter-individual diversity within a single bloom population. However, this level of resolution has not frequently been applied to analysis of laboratory cultures. The potential for intra-clonal diversity has largely been ignored and we will discuss one possible reason for this omission; the perception that strains or isolates of phytoplankton are snap-shots in time and space. We will also present theoretical considerations and empirical data that suggest that, if phytoplankton strains were examined with sufficient resolution, laboratory cultures would be revealed to be surprisingly dynamic populations, almost certainly harboring cryptic diversity. For example, data collected from sister cultures curated in parallel show that considerable divergence in stress responses has occurred during routine maintenance, possibly due to mutation accumulation. We also demonstrate selection for mutants arising spontaneously during a single batch culture generation. Such intra-clonal population dynamics have implications for the use of laboratory strains in comparative ecological studies. However these dynamics also demonstrate an opportunity to begin to actually perform manipulative experiments in which the micro-evolutionary response of phytoplankton to well controlled changes in environmental conditions can be investigated.

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PHYLOGENETIC RELATIONSHIPS AND TAXONOMY OF SEVERAL UNICELLULAR ALGAE OF THE CW GROUP (CHLOROPHYCEAE)

Watanabe, Shin

Department of Biology, Faculty of Science, University of Toyama, Toyama, Japan

Using 18S rDNA sequence data and morphological features, phylogenetic relationships of 13 species (8 genera) of the CW group were inferred. *Deasonia proliferum* and *Urnella terrestris*, both of which have multinucleate vegetative cells with sponge-like chloroplasts, and produce zoospores covered by single layered cell walls, formed a monophyletic branch separate from a clade of *Protosiphon* whose chloroplast is sponge-like but zoospores are naked. Two species of *Neosporiocolocum* that is distinguished from *Deasonia* in possessing uninucleate vegetative cells were resolved in separate branches from the latter. Three species of *Nautococcus* formed a single branch in the sister position to *Ettlia minuta*. The former organisms are distinguished from the latter in having partial thick cell walls around vegetative cells, but resemble it in having single-layered striated cell walls that have been already indicated by Kouwets (1994). *Ettlia*

carotinos was resolved away from *E. minuta*, but formed a monophyletic branch with *Haematococcus pluvialis*. *E. carotinos* and *H. pluvialis* are common to one another in producing red pigment of astaxanthin. *Chlorogonium fusiforme* was separate from other species of the genus, but sister to the *Dunaliella* clade of marine species. *Axilosphaera vegetata* forming tetrads of daughter cells and *Radiosphaera negevensis* forming single vegetative cells commonly possessed axile chloroplasts and constructed a monophyletic clade. *Actinochloris sphaerica* with the radiate chloroplast in multinucleate vegetative cells and *Borodinellopsis texensis* forming tetrads of daughter cells with asteroid chloroplasts were separately resolved from each other and from *Axilosphaera* or *Radiosphaera*. Based on the phylogenetic analysis, some taxonomic discussion is made on the organisms.

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MOLECULAR PHYLOGENY OF *DISCOSPORANGIUM MESARTHROCARPUM* (PHAEOPHYCEAE) WITH A REASSESSMENT OF THE ORDER DISCOSPORANGIALES

Kawai, Hiroshi¹, Hanyuda, Takeaki¹, Draisma, Stafano G.² & Dieter, Mueller G.³

¹Research Center for Inland Seas, Kobe University, Kobe, Japan; ²University of Leiden branch, National Herbarium Nederland, Leiden, Netherlands; ³Faculty of Biology, University of Konstanz, Konstanz, Germany

A molecular phylogenetic analysis of the little studied filamentous brown alga *Discosporangium mesarthrocarpum* using *rbcL* and partial 18S rDNA sequences revealed that the species forms a monophyletic clade with *Choristocarpus tenellus* that is sister to all other brown algae. Although *D. mesarthrocarpum* has unique disc-shaped plurilocular reproductive organs, *D. mesarthrocarpum* and *C. tenellus* share the following basic morphological features which are considered to be plesiomorphic characters in the brown algae: 1) Apical (and diffuse) growth; 2) Uniseriate, subdichotomously branched filaments; 3) Multiple chloroplasts per cell without pyrenoids; 4) Lack of heterotrichy and phaeophycean hairs. The *rbcL* DNA sequence of an Australian *D. mesarthrocarpum* specimen showed considerable deviation from Mediterranean and Macaronesian specimens. Therefore, the presence of a second species in the genus is suggested, however, the taxonomic treatment of this putative species is suspended in the present report. Regarding the higher rank systematic position of *D. mesarthrocarpum*, reappraisal of Discosporangiaceae and Discosporangiales is proposed. In culture conditions of 15-25 °C LD and SD, Mediterranean *D. mesarthrocarpum* showed a direct type of life history, with successions of uniseriate filamentous thalli bearing characteristic disc-shaped plurilocular zoidangia, but did not survive at 10 °C and below.

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PHYLOGEOGRAPHY OF *COSTARIA COSTATA* (LAMINARIALES, PHAEOPHYCEAE) BASED ON MITOCHONDRIAL COB AND COX3 GENES AND NUCLEAR ITS REGION

Cho, Ga Youn¹, Cho, Yun Jin¹, Druehl, Louis², Miller, Kathy A.³ & Boo, Sung Min¹

¹Department of Biology, Chungnam National University, Daejeon, South Korea; ²Bamfield Marine Station, Bamfield, BC, Canada; ³University Museum, University of California, Berkeley, Berkeley, CA, USA

Costaria costata is an edible kelp species that occurs intertidally to subtidally in the north Pacific Ocean, having an umbrella-shaped distribution with southern limits in Korea and USA, respectively. Since the nearshore coastal ecosystems are under pressure from ocean warming, there is an urgent need to conserve the cold kelp species in its southern limits such as Korea and USA. In order to know genetic variation of the species and to explain its current distribution pattern, we collected 76 samples from Korea, Japan, Russia, Canada, and USA, and analyzed nuclear noncoding ITS region and two mitochondrial coding genes, *cob* (apocytochrome b) and *cox3* from the samples. *Costaria costata* was very variable, having up to 20 haplotypes in ITS (719 bp), 13 in *cob* (826 bp), and 11 in *cox3* (562 bp). Statistical parsimony networks of individual and combined data are congruent, showing that *C. costata* comprised two divergent clades, the west and east groups. Despite more samples collected in the east side (44 specimens) than the west (32 specimens), each of nuclear and mitochondrial haplotypes was higher in the northwest than the northeast. The results reveal that geographical fragmentation has played an important role in genetic structuring between samples of *C. costata* from the northwest and east Pacific coasts. Evolutionary processes resulting in the current distribution of the two genetic lineages are briefly discussed. This is the first report to use the mitochondrially encoded *cob* gene for phylogeography of marine algae.

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PERSPECTIVES ON THE TRANS-ARCTIC DISTRIBUTION OF FAMILIES AND GENERA OF RED ALGAE

Hommersand, Max H.

Department of Biology, University of North Carolina, Chapel Hill, NC, USA

Phylogenetic and morphological evidence support the following postulates: (1) Except for the Rhodophysemataceae and Palmariaceae, and perhaps the Bangiaceae, most Northern Hemisphere families and tribes are connected to antecedents that originated in the Southern Hemisphere in the vicinity of Australia and New Zealand. (2) Some of these migrated along the edge of the Western Pacific to Japan and East Asia. (3) Others migrated westward to South America and north to Pacific North America reaching Alaska and East Asia. (4) Still others migrated through West Antarctica to southern Africa with some species undergoing amphitropical distribution to Western Europe. (5) Species that reached the North Pacific underwent further radiation in the vicinity of the Bering Sea and the Sea of Okhotsk. (6) Some of these underwent trans-Arctic distribution from the North Pacific to the North Atlantic Ocean prior to the opening of the Bering Strait. (7) Some North Pacific species migrated eastward and some North Atlantic species migrated westward through the Arctic Ocean to reach the North Atlantic or the North Pacific after the opening of the Bering Strait. (8) None of the taxa that reached Europe or Atlantic North America from southern Africa or that originated within the Tethyan Ocean underwent trans-Arctic distribution at a later date. Evidence supporting these postulates come from phylogenetic studies of members of the families: Dumontiaceae, Gloiosiphoniaceae, Kallymeniaceae, Schizymeniaceae, Tichocarpaceae, Furcellariaceae, Cystocloniaceae, Phyllophoraceae, Gigartinaceae, Ceramiaceae, Delesseriaceae and Rhodomelaceae.

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MOLECULAR EVIDENCE REVEALS DIVERSITY IN ALASKAN ISOLATES OF *CERAMIUM PACIFICUM*

Carlile, Amy¹, Waaland, J. R.¹ & Hall, Benjamin D.^{1,2}

¹Biology, University of Washington, Seattle, WA, USA; ²Genome Sciences, University of Washington, Seattle, WA, USA

Ceramium pacificum (Collins) Kylin is a conspicuous red algal species found in the species rich family Ceramiaceae. This species is widely distributed on the western coastlines of North and South America and is recognized by its prolific spine-like side branches throughout the thallus. Phylogenetic analysis of nuclear (*RPB1*) and plastid (*rbcL*) encoded genes revealed a specimen from Alaska identified as *Ceramium pacificum* that was not monophyletic with collections of the same species from Washington, British Columbia and another location in Alaska. These preliminary data along with data showing the phylogenetic placement of this species with respect to other Pacific Northwest *Ceramium* species will be presented.

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REVISING THE GENUS *HALYMENIA* (CRYPTONEMIALES, RHODOPHYTA) IN THE NORTHEAST PACIFIC USING SEQUENCE DATA

Gabrielson, Paul

Herbarium, University of North Carolina, Chapel Hill, Chapel Hill, NC, USA

Sequencing of type material has shown that *Halymenia gardneri* (Kylin) P. G. Parkinson, type locality Whidbey I., WA, *Halymenia schizymenioides* Hollenberg *et* I. A. Abbott, type locality Mission Point, near Carmel, CA and *Grateloupia maxima* (N. L. Gardner) Kylin, type locality Fort Point, San Francisco, CA, represent a single species. *rbcL* sequence data indicates that this species belongs in *Grateloupia*. *Halymenia hollenbergii* I. A. Abbott, type locality Imperial Beach, San Diego Co., CA, is a distinct species that also belongs in *Grateloupia* and is sister to *Grateloupia maxima*. *Halymenia californica* G. M. Smith *et* Hollenberg, type locality Pacific Grove, CA, is a distinct species that does not group with other species of *Halymenia* or *Grateloupia* and appears to represent a new genus. The habitats and distributions of these entities in the NE Pacific will be discussed.

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PHYLOGENY AND DISTRIBUTION OF THE RED ALGAL GENUS *CAMPYLAEPHORA* (CERAMIACEAE, CERAMIALES), INCLUDING THE TRANSFER OF *MICROCLADIA CALIFORNICA* TO THE GENUS

Cho, Tae O.¹, Hommersand, Max² & Fredericq, Suzanne¹

¹Biology, University of Louisiana at Lafayette, Lafayette, LA, USA; ²Biology, University of North Carolina, Chapel Hill, NC, USA

The four described species in the genus *Campylaephora* J. Agardh (1852), tribe Ceramiaceae, namely, *Campylaephora hypnaeoides* J. Agardh, *C. borealis* Seo, Cho *et* Boo, *C. crassa* (Okamura) Nakamura, and *C. japonica* Noda are only known from the western North Pacific (Korea, Japan, China, Russia). *Campylaephora* is characterized by the presence of rhizoidal filaments in the cortex and by a discoid holdfast. A new combination within this genus is proposed for plants referred to as *Microcladia californica* Farlow (1875), described from Santa Cruz, CA. The species has rhizoidal inner

cortical cells, a multilayered cortex, 6 periaxial cells per axial cell, alternate branching, spermatangia developing on cortical cells, tetrasporangia covered by cortical cells and developing from inner cortical and periaxial cells, and carposporangia associated with or without involucrel branchlets. In our molecular study inferred from plastid-encoded *rbcL* sequence analysis, the sequence of *C. californica* from San Mateo, CA was nested with strong support inside the *Campylaephora* clade, separate from the *Microcladia* clade. Our molecular phylogenetic analyses also revealed sufficient % sequence divergence among the species of *Campylaephora* to recognize *C. californica* comb. nov. as a natural entity: 3.7% between *C. californica* and *C. borealis*, 2.9-3.0% between *C. californica* and *C. hypnaeoides*, and 3.0-3.7% between *C. californica* and *C. crassa*. The phylogenetic position of *Campylaephora* within the tribe Ceramieae will be discussed.

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ORIGIN TIME OF THE FLORIDEOPHYCEAE AND CERAMIALES (RHODOPHYTA)

Yang, Eun Chan¹, Boo, Sung Min¹, Yoon, Hwan Su² & Bhattacharya, Debashish²

¹Department of Biology, Chungnam National University, Daejeon, South Korea; ²Department of Biological Sciences and Roy J. Carver Center for Comparative Genomics, University of Iowa, Iowa City, IA, USA

Despite ecological, evolutionary and economic importance of florideophycean red algae, a lack of fossil records make origin time of the algae unconvincing. Recent morphological and molecular data recognize the monophyletic Florideophyceae as the sister group of the Bangiophyceae in red algae. However, a comprehensive study of divergence time estimation using large concatenated data of protein coding genes is lacking. We have analyzed plastid protein-coding proteins to address specific questions concerning phylogeny and origin time of the Florideophyceae and the large order Ceramiales. To construct molecular clock for the Florideophyceae, we included Bacillariophyceae, Cyanidiophyceae, Phaeophyceae, Raphidophyceae, Xanthophyceae and land plant as well as six recently established classes of Rhodophyta. To address the possible misleading effects of mutational saturation of DNA sequence, we used protein data (1260 aa) from 80 species of the algae and land plants. Trees were reconstructed with parsimony and Bayesian methods, and evolutionary timescale was estimated using the Bayesian local clock methods. We found that major lineages of the Florideophyceae had arisen before periods of global glaciation in the Precambrian and then several lineages originated prior to the Cambrian Explosion. According to our molecular clock, the time of the first divergence of the Ceramiales was estimated 375-482 MYA.

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PHYLOGENETIC RELATIONSHIPS OF MEMBERS OF THE FRESHWATER RED ALGAL FAMILY LEMANEACEAE FROM NORTH AMERICA, EUROPE AND AFRICA

Sheath, Robert¹, Müller, Kirsten², Sherwood, Alison³ & Shea, Troina⁴

¹Biology, California State University San Marcos, San Marcos, CA, USA; ²Biology, University of Waterloo, Waterloo, ON, Canada; ³Botany, University of Hawaii, Honolulu, HI, USA; ⁴Biological Sciences, University of Calgary, Calgary, AB, Canada

Specimens of *Lemanea* and *Paralemanea* (Lemaneaceae, Batrachospermales) from three continents were sequenced for the *rbcL* gene and the ITS1-5.8S-ITS2 region to determine if the two genera and currently recognized species continue to be distinct in a broad geographic sampling. In the two gene sequence analyses from the whole data set, the two genera are well separated with strong nodal support. In terms of *Lemanea*, European and North American samples were positioned in separate and strongly supported clades. While the members of these clades are not readily distinguishable morphologically, they do appear to represent separate species. An additional trend was evident in the *Lemanea* data set; that is, North American specimens can be separated into eastern and western clades in both sequence analyses. The number of *Paralemanea* samples is relatively low, thereby limiting taxonomic conclusions, but it is evident that the collection from Kenya is well separated from those of North America and Europe.

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NITROGEN UPTAKE BY GAMETOPHYTES OF *PORPHYRA DIOICA* (BANGIALES, RHODOPHYTA) UNDER CONTROLLED CULTURE CONDITIONS

Pereira, Rui^{1,2}, Yarish, Charles², Kraemer, George³ & Sousa-Pinto, Isabel^{1,4}

¹Coastal Biodiversity Laboratory, CIIMAR, Porto, Portugal; ²Ecology and Evolutionary Biology, University of Connecticut, Stamford, CT, USA; ³Department of Environmental Sciences, State University of New York, Purchase, NY, USA; ⁴Department of Botany, University of Porto, Porto, Portugal

Aspects of the nutrient uptake physiology of *Porphyra dioica* collected in Porto, Portugal, were investigated under laboratory conditions. The nitrogen (N) uptake and accumulation capacity of *P. dioica* were determined for two different N forms, ammonium (NH₄⁺) and nitrate (NO₃⁻). The influence of the light-dark cycle and of the simultaneous presence of NH₄⁺ and NO₃⁻, as well as the effects of phosphorus (P) enrichment on the growth, nutrient uptake and accumulation were also evaluated. *Porphyra dioica* was able to uptake and accumulate equally well both forms of nitrogen. The form of N used also did not influence the growth rate. The photosynthetic pigments increased significantly with the increase of the available N in the medium, for both N forms. The form of N available did not influence the phycobiliprotein content, whereas the chlorophyll a content was higher in thalli that used nitrate as source of N. In the presence of both N forms, *P. dioica* removed preferentially NH₄⁺, with a clear day and night influence. The algae removed 70% of the NH₄⁺ available during the day and only 35% during the dark period. The P enrichment did not influence the growth rate or the amount of P removed from the medium, suggesting lack of ability to store P. These results confirm that *P. dioica* is a good candidate for application in integrated aquaculture.

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EFFECTS OF DESICCATION ON NITRATE UPTAKE AND GROWTH RATE IN TWO NATIVE PORPHYRA SPECIES OCCURRING IN DIFFERENT TIDE LEVELS ALONG THE NEW ENGLAND COAST

Kim, Jang K.^{1,3}, Kraemer, George P.² & Yarish, Charles³

¹Department of Ecology & Evolutionary Biology, University of Connecticut, Groton, CT, USA; ²Departments of Biology & Environmental Studies, Purchase College, State University of New York, Purchase, NY, USA; ³Department of Ecology & Evolutionary Biology, University of Connecticut, Stamford, CT, USA

Organisms in the intertidal habitat are exposed daily to the rise and fall of tides. During exposure, 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 species were cultivated at 100-150 μmolm⁻²s⁻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 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 tissues were exposed for 2 hrs daily, *P. amplissima* lost weight and pigments, while the growth rate of *P. umbilicalis* was approximately 70% of the continually submerged blades. For 30 min exposure, growth rates were about 77% (*P. umbilicalis*) and 50% (*P. amplissima*) of the continually submerged blades. Nitrate uptake rate of *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 not significantly different from 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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A UNIQUE TROPICAL MARINE CYANOBACTERIUM THAT FACILITATES DINITROGEN FIXATION

Li, Zhongkui & Brand, Jerry J.

Culture Collection of Algae and MCD-Biology, Univ. of Texas at Austin, Austin 78712, TX, USA

An unusual strain of non-heterocystous, non-branching filamentous cyanobacterium was isolated from the South China Sea. Portions of the filaments coiled and twisted into knot-like structures (nodules) when cultures were grown under low light intensity (<13 μmol photons m⁻² s⁻¹). Nodules occurred as discrete aggregates which varied in size and shape. Electron microscopy showed that nodules are well-defined units. Each individual portion of the filament within a nodule retains its own distinct sheath, while the entire nodule is surrounded by an additional thick sheath. Proximal portions of filaments that are not contained in nodules are surrounded by thick sheaths resembling the sheaths that surround nodules, while more distal portions of the same filaments contain only a thin mucilaginous sheath. When observed by various microscopic techniques, the overall morphology and internal structure of individual cells appear identical in nodules and in non-aggregated portions of filaments. DNA sequence data, morphological observations and physiological tests indicate that this cyanobacterium is related to *Lyngbya*, but with unusually broad environmental tolerances. It is capable of

growing at a wide range of salinities, from fresh water media to double-strength sea water. The optimal pH, temperature and light intensity were 8.0, 25°C and 60 $\mu\text{mol photons m}^{-2} \text{ s}^{-1}$, respectively. Axenic cultures of this cyanobacterium do not grow in media devoid of combined nitrogen. However, non-axenic cultures are capable of growing indefinitely (for at least two years) in the absence of combined nitrogen. Primers developed from a consensus sequence obtained from diverse *nifH* genes were used to amplify a homologous sequence in the new cyanobacterium. A putative *nifH* gene was found in non-axenic cultures but not in axenic cultures. Preliminary acetylene reduction experiments indicate that this cyanobacterium may harbor non-photosynthetic bacteria in a niche that facilitates dinitrogen fixation.

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CHARACTERIZATION AND MOLECULAR CLONING OF A BRYOHEALIN LECTIN FROM THE GREEN ALGA *BRYOPSIS PLUMOSA*

Yoon, Kang-Sup¹, Lee, Key Pyoung² & Kim, Gwang Hoon¹

¹Department of Biology, Kongju National University, Kongju, South Korea; ²Department of Chemistry, Kongju National University, Kongju, South Korea

Bryohealin is an algal lectin isolated from a marine green algae *Bryopsis plumosa*. This lectin has been reported as a strong candidate protein taking part in the wound healing process of *Bryopsis plumosa* cells. The lectin molecule is composed of two identical 27kDa subunits cross-linked by disulfide bond and shows binding specificity to N-acetyl D-glucosamine and N-acetyl D-galactosamine. Based on the amino acid sequence of the N-terminal and internal regions, a degenerate primers was synthesized and polymerase chain reaction (PCR) was performed to clone bryohealin-cDNA. The full-length cDNA of bryohealin consisted of 1,101 bp with 24 bp of 5' untranslated region (UTR) and 201 bp of 3' UTR. It had an open reading frame (ORF) of 768 bp encoding a 256 amino acid residues. The N-terminal sequence of the mature bryohealin polypeptide started at amino acid 21 of the deduced sequence from the cDNA, indicating 20 amino acids lost due to post-translational modification. The multi-alignment analysis based on the amino acid sequence of cDNA clone indicated that the bryohealin has unique structures among the other lectins, exhibiting a high degree of sequence similarities to eel-Fucolectin Tachylex-4 Pentraxin-1 (FTP) domain. These related proteins containing this domain in their sequence belong to either the Pentraxin family or to the Fucolectin family, all members of the lectin superfamily. Interestingly, these lectin families have a useful immune system for host defense. Hence, this protein may be involved in host defense against microbial invasion

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REGENERATION OF A CELL FROM EXTRUDED PROTOPLASM OF THE MARINE COENOCYtic GREEN ALGA *BRYOPSIS PLUMOSA*

Gwang Hoon, Kim & Tatyana A., Klochkova

Department of Biology, Kongju National University, Kongju, South Korea

When cell membrane of *Bryopsis plumosa* is destructed, the protoplasm expelled in seawater generates numerous new cells in vitro. Five essential steps of protoplast formation were identified: (1) agglutination of extruded cell organelles into protoplasmic masses in seawater; (2) changes in protoplasmic masses from an irregular to a spherical shape; (3) formation of a primary envelope around protoplasmic masses; (4) replacement of the envelope by a cell membrane; and (5) development of a cell wall. Then, the newly formed cells develop into fully differentiated *Bryopsis* plants. Whereas we described some events of the protoplast formation process previously, the new aspects were revealed by the use of time-lapse video microscopy. Agglutination of the extruded cell organelles into protoplasmic masses during protoplast formation occurs by a lectin-carbohydrate complementary system, and a novel lectin, bryohealin, involved in this process was purified and partially characterized. There are mechanisms preventing incorporation of foreign organisms or materials into the protoplast during its formation. Cytoskeletal changes were observed during protoplast formation using specific fluorescent chemicals, different inhibitors, and time-lapse video microscopy. Protoplasts were naked without the cell membrane from the beginning of formation, and this developed within several hours after wounding, presumably by recycling of the disintegrated original cell membrane. The protoplast primary envelope was composed of polysaccharides, but it acted in a similar way to the cell membrane. The proteome of the protoplast changes dramatically at each step of its formation, and there are special groups of genes expressed at each step. The wound-induced protoplast formation in vitro might be a natural dispersal mechanism from fatal injuries that serves multiple functions, such as regeneration of organisms from cell fragments and contribution to the natural dispersal.

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NOVEL GENES INDUCED BY SHORT TERM CU EXPOSURE IN THE DIATOM *THALASSIOSIRA PSEUDONANA*

Davis, Aubrey, Hildebrand, Mark & Palenik, Brian
Scripps Institution of Oceanography, UCSD, La Jolla, CA, USA

Copper pollution is increasing in the coastal marine environment and may be adversely affecting organisms such as diatoms, which are important coastal primary producers. Although an essential element for aerobic organisms, copper becomes toxic at high concentration. In order to prevent cellular damage, organisms have developed multiple methods of tightly regulating intracellular copper concentration and activity as well as mechanisms for dealing with copper stress. Using a subtractive cDNA approach, we identified genes in the diatom *Thalassiosira pseudonana* up-regulated by short term exposure to elevated concentrations of copper. Real-time PCR (RT-PCR) using gene specific primers confirmed changes in mRNA concentrations upon copper exposure. Sequence similarity searches against the complete genome of *T. pseudonana* revealed that several of these genes are located within inverted repeats and hence are duplicated. A subset of genes were determined to be strongly induced at the mRNA level by copper concentrations that do not affect cell growth and were not equivalently induced by exposure to either H₂O₂ or Cd, suggesting some specificity in the response. One subset of genes displayed a dose-dependent response to Cu and constitute a multi-gene family encoding relatively small proteins enriched in amino acids that could potentially bind metals. Another subset of genes were highly induced upon exposure to a threshold level of copper, however, this level did not affect cell growth. Most of the identified copper induced genes cannot be assigned function based on sequence similarity and may represent a novel response to copper stress.

64 BACTERIAL QUORUM-SENSING INTERFERENCE BY *CHLAMYDOMONAS REINHARDTII*

Sayre, Richard^{1,2}, Rajamani, Sathish², Teplitski, Max³ & Bauer, W. Dietz⁴
¹*Plant Cellular and Molecular Biology, Ohio State University, Columbus, OH, USA;* ²*Biophysics, Ohio State University, Columbus, OH, USA;* ³*Dept of Soil and Water Science, University of Florida, Gainesville, FL, USA;* ⁴*Plant Science, University of California, Davis, Davis, CA, USA*

Quorum sensing (QS) is a cell-population density dependent process that regulates several physiological functions in bacteria. Gram-negative bacteria use signaling molecules known as acylated homoserine lactones (AHLs), as well as other signaling molecules to activate a number of bacterial genes including those related to virulence, symbiosis, antibiotic production, and biofilm formation. Plants and other eukaryotes have been shown to produce mimic compounds that interfere with bacterial AHL signals. At this time, no plant mimic compound structures have been solved. Using culture filtrates from the unicellular green alga, *Chlamydomonas reinhardtii*, we have demonstrated the production of quorum sensing mimic compounds. Solvent partitioning of the cell filtrate and RP-HPLC coupled bacterial reporter bioassays indicated the presence of AHL mimic compounds. Bacterial reporter strains encoding LasR and CepR receptor that specifically detects their cognate signals 3-oxo-C12-HSL and C8-HSL respectively also detected several stimulatory activities from the algae HPLC fractions. Further biochemical studies with CepR stimulatory activities have demonstrated that these compounds contain conserved lactone ring structures. Structure determinations of these compounds are underway using Mass spectrometry and NMR techniques. We also describe the development of transgenic algae expressing AHL lactonase enzyme, which inactivates AHL signals for use as model for eukaryote-bacteria interaction studies.

65 GENES ENCODING PLASTID TERMINAL OXIDASE IN *HAEMATOCOCCUS PLUVIALIS*: CDNA CLONING, CHARACTERIZATION, AND EXPRESSION UNDER OXIDATIVE STRESS

Wang, Jiangxin, Sommerfeld, Milton & Hu, Qiang
Department of Applied Biological Sciences, Arizona State University, 7001 E. Williams Field Road, Mesa, AZ, USA

Plastid terminal oxidase (PTOX) is a plastoquinol oxidase involved in carotenoid biosynthesis in plants and algae. It may also represent the elusive oxidase in chlororespiration. *Haematococcus pluvialis* is a green alga that has the ability to synthesize and accumulate under oxidative stress large amounts of the red carotenoid astaxanthin (ca. 4% of dry weight). However, the biological role of PTOX in astaxanthin synthesis is unknown. In this study, two *Haematococcus* cDNAs for PTOX (PTOX1 & 2) were cloned and sequenced. The deduced *Haematococcus* PTOX amino acid sequences show high identity and similarity to that of other algae and higher plants. The expression of *ptox1* and *ptox2* at a transcriptional level

was studied by real-time RT-PCR under low (ca. 20 $\mu\text{mol m}^{-2} \text{s}^{-1}$) and high light (ca. 250 $\mu\text{mol m}^{-2} \text{s}^{-1}$) conditions. The mRNA expression of *ptox1* and *ptox2* underwent transient up-regulation under high light. A rapid increase in mRNA transcripts occurred in *ptox2* in response to high light stress, reaching a maximum level (ca. 2.8-fold) after 12 hours. The mRNA transcripts reduced to a basal level (at onset of high light) after 96 hours. A delayed expression pattern occurred in *ptox1* which exhibited a maximum transcript level (ca. 10-fold) after 48 hours of high light, followed by gradual decline. Phytoene desaturase (PDS), a key enzyme in the carotenogenesis, showed an identical mRNA expression pattern to that of *ptox2* under high light. Inhibition of PTOXs and PDS with 2 μM Octyl gallate and 10 μM Norflurazon, respectively, resulted in transient over-expression of their mRNA transcripts. However, astaxanthin synthesis and photosynthetic oxygen evolution were reduced, whereas the lipid peroxidation was enhanced. This may suggest that overproduction of reactive oxygen species (ROS) using photosynthesis-generated molecular oxygen is the cause and also the consequence of high light-induced oxidative stress. The role of PTOX1 & 2 is to prevent the formation of ROS by reducing molecular oxygen to water using electrons derived from PDS-mediated phytoene desaturation, thereby protecting the cells against oxidative stress.

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A COMBINED SSU AND LSU rDNA PHYLOGENY OF THE EUGLENALES WITH A DESCRIPTION OF THE NEW GENUS *DISCOPLASTIS*

Linton, Eric W.¹ & Triemer, Richard E.²

¹Biology, Central Michigan University, Mt. Pleasant, MI, USA; ²Department of Plant Biology, Michigan State University, East Lansing, MI, USA

A combined SSU and LSU rDNA gene sequences from 84 strains of plastid-containing euglenophytes representing eleven genera—were analyzed by the Bayesian likelihood criterion. The analysis resulted in a tree with three major clades: a *Phacus* and *Lepocinclis* clade, a *Euglena*, *Colacium*, *Trachelomonas*, *Strombomonas*, *Monomorphina* and *Cryptoglena* clade and a *Discoplastis* clade. The genus *Euglena* formed a well-supported clade, except for two species, which formed a separate clade near the base of the tree. A new genus, *Discoplastis*, was erected to accommodate these taxa making the genus *Euglena* monophyletic. The monophyly of *Colacium*, *Trachelomonas*, *Strombomonas*, *Monomorphina* and *Cryptoglena*, was supported as two sister subclades to the *Euglena* clade. *Colacium*, *Trachelomonas* and *Strombomonas*, all of which produce copious amounts of mucilage to form loricas or mucilaginous stalks, formed a well-supported lineage. The retention of *Strombomonas* and *Trachelomonas* as separate genera was strongly supported. *Monomorphina* and *Cryptoglena* formed two well-supported clades that were sister to the *Colacium*, *Trachelomonas* and *Strombomonas* clade. *Phacus* and *Lepocinclis*, both of which have numerous small discoid chloroplasts without pyrenoids and lack peristaltic euglenoid movement (metaboly), formed a well-supported monophyletic lineage sister to the larger *Euglena* through *Cryptoglena* clade. The increased taxon sampling and combined multi-gene datasets provided strong support for internal tree nodes and resulted in well-resolved relationships among the major genera in the photosynthetic euglenoid lineage.

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DISTRIBUTION OF FRESHWATER DINOFLAGELLATES IN NORTH AMERICA

Carty, Susan

Biology, Heidelberg College, Tiffin, OH, USA

A compilation of dinoflagellate records from North America has been assembled for the first time since 1934 when the last publication (“Freshwater dinoflagellates of North America”) by G.H. Wailes was released. Dinoflagellate species are difficult to identify and thus are under-reported in the literature. I am working to compile the distribution of 130 species in North America (Canada, Greenland, United States, Mexico, Central America and the Caribbean). Thirty species have single reports, and of these, twelve are the original new species report. All reports have to be critically evaluated. The most reliable records are those including accurate original line drawings, followed by reports from experienced investigators, lastly are reports (usually part of a species list) without any taxonomic references in the literature cited. Some species such as *Ceratium hirundinella* and *Peridinium cinctum* are widely reported. Although all reports lacking illustration are suspect, I accept published reports even though many records of *P. cinctum* are probably really *P. gatunense* and the forms of *C. hirundinella* are rarely used by United States researchers. In the course of this work, many taxonomic problems have been encountered such as the stage in the life cycle to which the genus is attached, as well as invalidly described species. These and other problems encountered in this investigation are discussed and the distribution of some exemplar taxa is reported.

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MAPPING ULTRASTRUCTURAL CHARACTERISTICS ON GENE PHYLOGENIES OF THE CONJUGATING GREEN ALGAE

Hall, John D. & Delwiche, Charles F.

Cell Biology and Molecular Genetics, University of Maryland, College Park, MD, USA

The conjugating green algae are the most structurally diverse group of charophyte green algae. Besides diversity of general form, the conjugating green algae also exhibit a wide range of ultrastructural characteristics including cell division, chloroplast shape and cell wall ornamentation. This study used a molecular phylogeny of structurally diverse conjugating green algae and mapped ultrastructural characteristics to that phylogeny. The relationships among these characteristics are discussed as well as their use as phylogenetic and taxonomic characters.

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A REASSESSMENT OF *GEMINELLA* (CHLOROPHYTA) BASED UPON PHOTOSYNTHETIC PIGMENTS, DNA SEQUENCE ANALYSES AND ELECTRON MICROSCOPY

Durako, Maris R. & Bailey, Craig

Biology and Marine Biology and Center for Marine Science, UNC-Wilmington, Wilmington, NC, USA

A cultured microalgal strain (UTEX 2540) originally identified as *Heterotrichella gracilis* Reising (Xanthophyceae) was examined using various techniques. HPLC analyses of photosynthetic pigments indicated the presence of chlorophylls a and b, β -carotene, and violaxanthin whereas TEM revealed the presence of starch stored inside the plastid. These data, as well as 18S rRNA gene sequence analyses, indicate that the alga belongs in the Chlorophyta not the Xanthophyceae. DNA sequence analyses imply that among green algae UTEX 2540 is most closely related to *Geminella terricola* and certain *Microspora* spp. that possess peculiar H-shaped cell walls, both of which are currently classified in the Ulotrichales. However, unlike other *Geminella* species UTEX 2540 exists as single cells or forms poorly organized short (2-8 celled) ephemeral pseudofilaments. In nature a conspicuous extracellular sheath characterizes *Geminella* species but this feature is lacking in UTEX 2540. Furthermore, our analyses - as well as previously published TEM observations of flagellar architecture - convincingly demonstrate that *Geminella* and some isolates of *Microspora* do not belong in the Ulotrichales. Our results imply that (1) the concept for *Geminella* should be relaxed to include species that are fundamentally unicellular and lack an apparent mucilaginous envelope, (2) *Geminella* and some *Microspora* spp. form a well supported clade, and (3) the closest relatives of our *Geminella* and *Microspora* isolates may be found among the Trebouxiophyceae. On the other hand, the latter relationship is weakly supported and it is possible that *Geminella* and allies may represent an as yet unaccounted for (i.e., independent) evolutionary lineage within the green algae.

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WHAT TWO GENES AND MANY ISOLATES REVEAL ABOUT SPECIES RELATIONSHIPS AND GEOGRAPHIC DISTRIBUTION OF THE FRESHWATER FAMILY HYDRODICTYACEAE (SPHAEROPLEALES)

McManus, Hilary A. & Lewis, Louise A.

Ecology and Evolutionary Biology, University of Connecticut, Storrs, CT, USA

A data set of over 100 ingroup taxa, representing four continents, was used to address species relationships and geographic distribution patterns of the family Hydrodictyaceae (Chlorophyceae). Maximum likelihood and Bayesian phylogenetic methods were applied to molecular sequence data collected from the nuclear large subunit (26S rDNA) and the chloroplast large subunit of ribulose-1,5-bisphosphate carboxylase/oxygenase (rbcL), totalling over 3,000 aligned characters. These analyses offer increased support for some relationships and aid in better defining previously ambiguous placements recovered in earlier phylogenetic estimations of fewer isolates. *Hydrodictyon*, *Pediastrum duplex* and *P. angulosum* form a clade, with *P. duplex* forming two separate groups, one of which contains *P. angulosum*. The *P. duplex* isolates separate according to geographic locations, with one group consisting mainly of isolates from Europe, North and South America, and the other group including isolates from Australia as well as *P. angulosum*. Four isolates with *P. duplex* var. *gracillimum* morphology make up another clade separate from these two *P. duplex* groups and outside the *Hydrodictyon* + *P. duplex* + *P. angulosum* complex, indicating this particular variety may represent a separate taxonomic entity from *P. duplex*. In addition, the analyses of the expanded taxon sampling offer support, as well as raise doubts, regarding some of the recent taxonomic revisions made within the family.

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FIRST INSIGHTS INTO THE SYSTEMATICS OF THE FAMILY TRENTEPOHLLIACEAE (CHLOROPHYTA, ULVOPHYCEAE)

Lopez-Bautista, Juan M. & Rindi, Fabio

Biological Sciences, The University of Alabama, Tuscaloosa, AL, USA

The family Trentepohlliaceae contains subaerial green algae abundant in tropical and subtropical regions. This family includes six genera: *Cephaleuros*, *Phycopeltis*, *Physolinum*, *Printzina*, *Stomatochroon* and *Trentepohllia*, which have been traditionally separated based only on morphological features and for which phylogenetic relationships are still inadequately studied. Molecular data from the nuclear-encoded 18S rDNA and the chloroplast-encoded *rbcL* have been obtained from our laboratory and represent most of the genera in this family. Our current results are compared with the traditional system of classification based on morphological features. These analyses indicate that the morphological criteria used for the circumscription of genera and species of Trentepohlliaceae do not correspond with their phylogenetic patterns. Although the genus *Cephaleuros* forms a well-supported monophyletic clade in all analyses, *Trentepohllia* (*sensu lato*) is non-monophyletic, and representatives of *Phycopeltis*, *Printzina* and *Physolinum* are mixed together in several lineages. Characters such as subcuticular habit, heteromorphic life history and clustered zoosporangia appear to be phylogenetically significant. On the other hand, characters commonly used to separate species and genera, such as shape and size of cells, prostrate/erect habit, and substratum colonized have no phylogenetic relevance at this level. Current efforts have been initiated to develop a framework of molecular and morphological data to circumscribe genera and species from tropical and subtropical regions and construct a modern revisionary taxonomic treatment for this group. This research is being funded by an NSF grant (DEB 0542924) to JLB.

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ARE ACROSIPHONIA ARCTA (DILLWYN) GAIN AND A. SPINESCENS (KÜTZING) KJELLMAN (ACROSIPHONIALES, CHLOROPHYTA) CONSPECIFIC? EVIDENCE FROM MORPHOLOGY, ECOLOGY AND MOLECULES

Zechman, Frederick¹, Mathieson, Arthur C.², Ashworth, Matt¹ & Ebner, Ethan²

¹*Department of Biology, California State University, Fresno, Fresno, CA, USA;* ²*Department of Plant Biology and Jackson Estuarine Laboratory, University of New Hampshire, Durham, NH, USA*

A review of the *Spongomorpha-Acrosiphonia* complex (Acrosiphonales, Chlorophyta) is provided, as well as varying interpretations of the distinctiveness of two of its species, *Acrosiphonia arcta* (Dillwyn) Gain and *A. spinescens* (Kützing) Kjellman. Morphological, cellular, and ecological differences were documented from sympatric *A. arcta* and *A. spinescens* plants on Appledore Island, Maine USA. Mean frond length, weight, and cell dimensions of *A. arcta*-type plants exceeded those of the *A. spinescens*-types. Both plants have abundant rhizoids, while hooks are only present in densely entangled *A. spinescens* populations from wave-exposed habitats. Contrasting ecologies, including varying zonations, tolerances to wave action and estuarine conditions, and different seasonal patterns (i.e. phenologies) suggest that the two plants are distinct. A genetic distinction is confirmed by analyses of rDNA ITS sequences for Appledore populations and globally distributed isolates of *Acrosiphonia*. However, absence of morphological data for isolates of published GenBank *A. arcta* sequences and the resulting phylogeny leaves uncertain the issue of whether these should be considered distinct species. Supported in part by a grant from the National Science Foundation DEB-0128977.

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UNIVERSAL PRIMERS AMPLIFY A PLASTID MARKER FOR BIODIVERSITY ASSESSMENT OF EUKARYOTIC ALGAE AND CYANOBACTERIA

Sherwood, Alison R.¹ & Presting, Gernot G.²

¹*Botany, University of Hawaii, Honolulu, HI, USA;* ²*Molecular Biosciences and Bioengineering, University of Hawaii, Honolulu, HI, USA*

Designing universal algal primers is uniquely challenging due to the vast array of evolutionary lineages contained within this informally-named group of organisms. A comparative genomics approach was used previously to identify conserved primers flanking a region of the 23S ribosomal RNA plastid genome. Our present research illustrates the feasibility of amplifying and sequencing this marker across multiple lineages, including cyanobacteria and a number of eukaryotic algal groups. Here we present DNA sequence frameworks based on several hundred samples, primarily representing the red,

green and brown algae, and the cyanobacteria, with smaller representation for diatoms and euglenoids. Such universal primers have great potential in the developing field of environmental sampling with the ability to detect the presence of any plastid-containing organism above a threshold level. Applications are likely to include detection assays for alien or invasive algae in ballast waters or on biofouled ship hulls.

74 EFFECT OF TIME AND IRRADIANCE ON INTERTIDAL MULTI-SPECIES *EUGLENA* PATCHES IN OREGON

Kingston, Michael B.¹ & Gough, Jennifer²

¹Biology Department, Elon University, Elon, NC, USA; ²Environmental Studies Program, Elon University, Elon, NC, USA

In mid-June 2003, large green patches composed of a multi-species *Euglena* complex (*E. agilis*, *E. geniculata*, *E. deses*, and a 4th unidentified species) were observed in the high intertidal areas of Nye Beach in Oregon. This study examined the effect of time of day and shading on the density of the *Euglena* population on the sediment surface. Surface sediment samples were collected throughout the day to examine the general pattern of vertical migration. Diel sampling revealed a diurnal effect with higher cell densities recorded within two hours of solar noon but no appreciable tidal effect. Neutral density light filters and opaque canisters were used to shade 6 small replicate areas to 56% incident light (I_0), 22% I_0 , 2% I_0 , and 0% I_0 . After one hour, a small sample of sand was collected from each area as well as 6 replicate unshaded areas. One-way ANOVA revealed that darkness and high irradiance had a significant negative effect on the number of cells on the surface. The number of cells at 22% I_0 was significantly greater than that at 100% I_0 and 0% I_0 suggesting that these *Euglena* species respond to darkness and full sunlight by migrating downward.

75 CELLULAR BASIS FOR MECHANICAL STRENGTH IN *CALLIARTHRON* GENICULA

Martone, Patrick T.

Hopkins Marine Station, Stanford University, Pacific Grove, CA, USA

Articulated coralline algae thrive in wave-swept environments around the world thanks to joints, called genicula, which lend flexibility to their otherwise rigid calcified thalli. While providing this freedom of movement, genicula are also at the greatest risk of mechanical failure and articulated thalli usually break at these joints. A recent study demonstrated that genicula are composed of a material that is many times stronger than other seaweed materials and suggested that, as fronds grow, genicula strengthen their constitutive materials to avoid breaking. Corallinoid genicula are composed of thousands of long fiber-like cells, which each help to tie together adjacent calcified segments. Until now, the characteristics of these genicular cells have not been well-described. Here I present results from a histological study quantifying the number, dimensions, and cell wall thickness of the fiber-like cells in *Calliarthron* genicula. All genicula are composed of similarly-sized cells, but larger genicula have significantly more cells. Genicula from older fronds are composed of cells with thicker cell walls, which likely explains the increased material strength observed in older genicula. Moreover, cells at the periphery of genicula have significantly thicker cell walls than more central cells, which may fortify genicula against bending stresses. At the tissue level, vast numbers of thick-walled cells clearly underlie the great strength of genicula: older genicula may be as much as 50% cell wall. However, at the cellular level, whether constitutive cell walls are made of a uniquely strong material remains an open question. I adjust previous breaking stress measurements by percent cell wall and estimate the mechanical strength of the geniculum cell wall alone. Surprisingly, data suggest that genicula cell walls are not much stronger than other algal cell walls. Instead, genicula gain their strength from the sheer quantity of cell wall material they pack into their cross-section.

76 CYANOBACTERIAL DIVERSITY AND HALOTOLERANCE IN A VARIABLE HYPERSALINE ENVIRONMENT

Kirkwood, Andrea^{1,3}, Buchheim, Julie², Buchheim, Mark² & Henley, William¹

¹Botany, Oklahoma State University, Stillwater, OK, USA; ²Biological Science, The University of Tulsa, Tulsa, OK, USA;

³Biological Sciences, University of Calgary, Calgary, AB, Canada

The Great Salt Plains (GSP) in north-central Oklahoma, USA is an expansive salt flat (~65 km²) that is part of the federally protected Salt Plains National Wildlife Refuge. Also designated as the "Salt Plains Microbial Observatory" by the National Science Foundation, the GSP serves as an ideal environment to study the microbial diversity of a terrestrial,

hypersaline system that experiences wide fluctuations in freshwater influx and diel temperature. Our study focused on cyanobacterial diversity at the GSP by assessing the taxonomic and physiological diversity of GSP isolates, and the 16S rRNA phylogenetic diversity of isolates and environmental clones from three sites (north, central and south). Taxonomic diversity of isolates was limited to a few genera (mostly *Phormidium* and *Geitlerinema*), but physiological diversity based on halotolerance ranges was strikingly more diverse, even between strains of the same phylotype. The phylogenetic tree revealed diversity that spanned a number of cyanobacterial lineages, though diversity at each site was dominated by only a few phylotypes. Unlike other hypersaline systems, a number of environmental clones from the GSP were members of the heterocystous lineage. Though a number of cyanobacterial isolates were close matches with prevalent environmental clones, it is not certain if these clones reflect the same halotolerance ranges of their matching isolates. This caveat is based on the notable disparities we found between strains of the same phylotype and their inherent halotolerance. Our findings support the hypothesis that variable or poikilotrophic environments promote diversification, and in particular, select for variation in ecotype more so than phylotype.

77 POPULATION GENETIC STRUCTURE OF *FUCUS VESICULOSUS* L. IN THE NORTHWESTERN ATLANTIC

Muhlin, Jessica F. & Brawley, Susan H.
School of Marine Sciences, University of Maine, Orono, ME, USA

Intertidal organisms on the northeastern coast of North America were strongly affected by the last glacial maximum (ca. 18,000 years ago). The current southern limits of populations of species such as the marine alga *Fucus vesiculosus* L. (Phaeophyceae) may be part of a refugial population and have higher levels of genetic diversity than recently recolonized (i.e. northern) areas. Regardless, there may be significant genetic differentiation across the current range limits related to glaciation and subsequent recolonization. We are testing the scale of genetic differentiation of *F. vesiculosus* in the northwestern Atlantic, including whether populations exhibit a pattern of isolation by distance. Six microsatellite loci were used to characterize genetic structure at Beaufort, NC; Lewes, DE; Avery Point, CT; Schoodic and Pemaquid Pts., ME; and Mabou and Yarmouth, NS. Preliminary results demonstrate significant isolation by distance (Mantel test, $p < 0.0236$). Pairwise F_{ST} comparisons indicate significant genetic differentiation among all sites surveyed (F_{ST} values range from 0.023 - 0.5589, $p < 0.00007$). The different populations of *F. vesiculosus* share alleles at each locus; however, allele frequencies differ among sites. *Fucus vesiculosus* populations form two distinct regional groups; a southern region comprised of NC and DE and northern region with ME and NS. Northern sites that were recolonized following the Pleistocene ice age exhibit more genetic diversity than the southern sites that did not experience glaciation. Interestingly, the NC site appears to be monomorphic at each locus, suggesting a severe bottleneck event (Supported by NSF OCE-99043).

78 A SLOW DEATH? FAILURE BY FATIGUE IN SEaweEDS

Mach, Katharine J.
Hopkins Marine Station, Stanford University, Pacific Grove, CA, USA

In the wave-swept intertidal zone, many seaweeds experience dislodgment and breakage seasonally as well as throughout the year. Yet evaluation of algal material properties often predicts no, or very little, breakage in algal populations. Algal material properties, such as breaking strength, are typically measured with pull-to-break tests involving application of a single, increasing load until breakage occurs. Then, comparison of measured strength and maximum wave drag forces yields predictions of breakage rates. Discrepancies between observed and predicted rates of failure have been explained by external mechanisms not included in breakage models. For example, herbivory or abrasion may concentrate stress at flaws, entanglement of stipes may increase imposed loads, and occasional extreme waves may impose large forces, all increasing likelihood of thallus breakage. Alternatively, the mode of loading in the field—constant fluctuating wave forces—may cause failure by fatigue. That is, loads well below measured material strength, repeated over time, may cause gradual formation and extension of cracks that weaken seaweed materials and ultimately lead to failure. Here, I describe a standard method of fatigue analysis that can be used to predict the fatigue life—loading cycles required for failure to occur through fatigue cracking—for macroalgae in field loading conditions. These techniques also allow assessment of the effects of seasonal wave-force variation on fatigue processes. Examination of fatigue in seaweeds may help clarify the discrepancy between known and predicted breakage rates and the extent to which other external mechanisms cause observed breakage.

INTEGRATING RESEARCH AND EDUCATION THROUGH THE UNIVERSITY OF MAINE'S NSF GK-12 GRADUATE TEACHING FELLOWS PROGRAM

Jackson, Brenda¹, Masters, Alyce², Gower, Jessie³, Muhlin, Jessica F.⁴ & Brawley, Susan H.⁴

¹*Viola Rand School, Bradley, ME, USA;* ²*Dr. Lewis S. Libby School, Milford, ME, USA;* ³*Newburgh Elementary School, Newburgh, ME, USA;* ⁴*School of Marine Sciences, University of Maine, Orono, ME, USA*

The University of Maine's NSF's GK-12 program integrates research and science education from kindergarten to graduate school (www.umaine.edu/NSFGK-12). This goal is achieved by providing fellowships to outstanding science, technology, mathematics, and engineering (STEM) students. Through an outreach component, Fellows developed lesson plans and demonstrated science in K-12 classrooms ca. 8 hours/week. The program provides professional development opportunities to K-12 teachers and has created cooperation between University faculty and K-12 schools. Activities supported by the program include microscopic studies of phytoplankton, field trips to the intertidal zone and marine laboratories, and participation of students in novel and long-term research projects. This program was successful for all participants: Fellows state that the fellowship led to increased self-confidence and improved time management, communication, and organizational skills. Teachers report that their involvement has broadened their ability to teach in a variety of science areas with greater expertise. This program also provided teachers an opportunity to attend national and international scientific meetings and to earn graduate level credit for continuing education. Most importantly, K-12 students were exposed to a positive role model, improved their understanding of the scientific method, and felt more comfortable doing experiments. By integrating research and education, we are promoting a younger generation of students who are curious, creative, and passionate about science. Such students are future members of PSA (Supported by NSF DGE-0231642).

SCALE AND RESOLUTION IN PROTISTAN EVOLUTION: IS THE FOSSIL RECORD SUFFICIENT TO CAPTURE CHARACTERISTIC PATTERNS OF MORPHOLOGICAL EVOLUTION IN PROTISTS?

Theriot, Edward C.

Texas Memorial Museum, The University of Texas at Austin, Austin, TX, USA

Protists are presumed to evolve gradually after speciation events because of large population size, high dispersal capacity, and low reproductive barriers. There are no particular biological reasons to believe that protists should evolve slowly. For example, while large population size inhibits PROBABILITY of change in cases of drift between adaptive peaks, large population size can, in fact, allow for very high rates of morphological evolution under other scenarios, including under directional selection which is frequently proposed as a causal factor. Moreover, published examples suggests that it is highly premature to generalize about rates of evolution in protists. The resolving capacity of most sedimentary depositional environments is not sufficient to capture morphological change at rates which have been proposed as possible for diatoms from heritability studies or that have been shown to occur in lacustrine sediments. It has been claimed that phylogenetic (e.g., cladistic) analysis is irrelevant to the study of morphological evolution in mineralized protists, but this paper will show that phylogenetic analysis is essential to understanding the fossil record of protists.

THE INTERSECTION OF HISTORY AND ENVIRONMENT IN DIATOM BIOGEOGRAPHY

Spaulding, Sarah

Fort Collins Science Center, US Geological Survey, Denver, CO, USA

The geographic distribution of freshwater diatoms is the result of both history and environmental factors. The question concerning a given taxon is, "Where do history and environment intersect in controlling the distribution of that taxon?" How are we to discern the processes that led to modern patterns, and how does the role of history and environment change for different taxa? In this presentation, I will examine modern distributions of diatom species and lineages. Not surprisingly, sampling methods have a strong impact on perceptions of biodiversity and lead to disparate conclusions about biogeography. Diatoms in permanently ice-covered Antarctic lakes, ancient tectonic basins, fens of Iowa, and streams of western North America all illustrate varying roles of history and environmental processes. On the Antarctic continent, geographic isolation leads to speciation and a high proportion of endemic taxa. On the other hand, non-isolated sub-Antarctic regions also have high numbers of endemic taxa. Can the processes be resolved? In another example, the ancient tectonic basin of Lake Ohrid in Macedonia contains a number of closely related species. Such endemic species

flocks are well known features of ancient lakes, yet ancient river drainages contain also endemic lineages. Geologically old erosional surfaces have received less attention than geologically old lakes, but contain similar species flocks. Finally, we have not recognized the degree to which freshwater diatom species are spread by human activities. Geographic distributions of freshwater diatoms are rapidly changing due to alteration of aquatic environments as well as by direct human transport of organisms.

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FOSSIL FRESHWATER DIATOMS: PROVIDING KEY INSIGHTS INTO SYSTEMATICS, EVOLUTION AND ECOLOGY

Kociolek, John P.

California Academy of Sciences, San Francisco, CA, USA

Despite keen interest in past climate change events in the earth's history, there are fewer freshwater micropaleontologists today than a generation ago. This presentation reviews the temporal, spatial, and taxonomic diversity of fossil freshwater diatoms, and reviews topics in systematic biology, evolutionary biology, and ecology where the group has been, or could be, provided examples or key insights into topics such as extinction, tempo and mode of evolution, and adaptive radiation. Key challenges and opportunities to further applying these organisms to critical questions are explored.

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BIOGEOGRAPHY AND SPECIES DIVERSITY WITHIN THE PHYTOPLANKTONIC DIATOM GENUS SKELETONEMA

Kooistra, Wiebe H., Zingone, Adriana, Saggiomo, Maria & Sarno, Diana

Marine Botany, Stazione Zoologica, Naples, Italy

Recent explorations into the diversity of the cosmopolitan phytoplanktonic diatom *Skeletonema costatum* demonstrated the existence of several morphological and genetically distinct species. Here we assess how drastically increased sample size and global coverage affect our delineation of species and our ideas on their distribution. Thereto, we analyzed ca. 200 *Skeletonema* strains from coastal regions all over the world. The strains were identified through light- and electron microscopic observations of their silica frustules and through sequence comparison of their nuclear LSU rDNA hyper-variable regions. Results show that all species described in previous studies except *S. marinoi* and *S. dohrnii* retain their genetic and morphological distinctness, though several cryptic relatives were detected within many of the morphologically defined species. Based on our still limited sample coverage all species seem widespread but none appears truly cosmopolitan; some abound in the northern and southern temperate latitudes whereas others appear to have subtropical to tropical distribution patterns, though gaps seem to occur in these patterns. This study also contains a taxonomic update of all *Skeletonema* strains currently available in AC, CCAP, CCMP, CSIRO, MBA and NIES to aid interpretation of results obtained in previous research projects using these strains.

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BASELINE ANALYSIS OF PERIPHYTON COMMUNITY STRUCTURE IN AGRICULTURALLY IMPACTED LOTIC SYSTEMS IN WEST-CENTRAL OHIO

Verb, Robert G. & Katrina, Glascock I.

Department of Biological & Allied Health Sciences, Ohio Northern University, Ada, OH, USA

The Scioto Marsh region in west-central Ohio is the former location of an 18,000-acre Wisconsin age lake, which eventually progressed into a fen habitat. The region was effectively drained by the early 1900's to expose the rich peat laden soils (Carlisle Muck) of the fen for agriculture. Since that time the region has been intensively farmed with vegetable crops such as onions (historically) and carrots. In addition, it was announced in 2005 that this basin would be site of a 4,500-head dairy Concentrated Animal Feeding Operation (CAFO). The objective of this study was to quantify the periphyton community dynamics and water quality in small tributaries of the Upper Scioto River Watershed prior to the installation of the CAFO. Periphyton samples were collected seasonally along with selected water quality parameters. Initial sampling revealed that systems in the region are presently impacted by high levels of sedimentation reflected by high numbers of motile diatoms such as *Navicula* and *Surirella*. Sampling efforts will continue in the future to determine if the CAFO (during construction and during production) and the spread of its liquid manure waste onto the neighboring 4,500 acres will have an impact on the surrounding aquatic systems.

PHYLOGENETIC ANALYSES OF GSIII AND GSII: EVIDENCE FOR A SHARED EVOLUTIONARY HISTORY AMONG HETEROKONTS AND HAPTOPHYTES?

Tartar, Aurélien, Ghoshroy, Sohini & Robertson, Deborah
Clark University, Worcester, MA, USA

Glutamine synthetase (GS) is an essential enzyme for ammonium assimilation and glutamine biosynthesis. Three distinct gene families (GSI, GSII, and GSIII) have been identified and are distributed among the major lineages of prokaryotes and eukaryotes. Although most photosynthetic eukaryotes express isoenzymes that function in either the cytosol or chloroplast, the evolutionary events that gave rise to the isoenzymes vary among lineages. For example, the GS isoenzymes in vascular plants arose by relatively recent GSII gene duplications while in contrast, members of the GSII and GSIII gene families encode the diatom chloroplast- and cytosolic-localized isoenzymes, respectively. Here we report a similar pattern of GS isoenzyme expression in the haptophyte *Emiliania huxleyi* Hay et Mohler. GSIII sequences of three diatoms, *E. huxleyi*, and four sequences from the Sargasso Sea environmental samples were found in a well-supported clade in phylogenetic analyses of prokaryotic and eukaryotic GSIII proteins. The cyanobacterial GSIII sequences formed a well-supported group with no association with heterokont+haptophyte GSIII sequences. GSIII sequences were also retrieved from the *Dictyostelium discoideum* and *Entamoeba histolytica* genome projects. Although there was only weak phylogenetic support for the monophyly of eukaryotic GSIII sequences, the presence of GSIII in several eukaryotic lineages suggests members of this gene family were present in the nuclear genomes of early eukaryotes. Phylogenetic analyses of GSII sequences revealed strong support among members of photosynthetic lineages (Plants+Chlorophytes+Rhodophytes+Heterokonts+Haptophytes). GSII from diatoms (*Thalassiosira pseudonana* [Hustedt] Hasle et Heimdal and *Skeletonema costatum* [Greville] Cleve) and *E. huxleyi* formed a well-supported clade; however, GSII sequences from heterokonts (diatoms and oomycetes) were not monophyletic. We propose that the evolution of GS isoenzymes in diatoms and haptophytes reflects the endosymbiotic history of these lineages and that phylogenies of GSIII and GSII indicate a clear link between the host and symbiont genomes of heterokonts and haptophytes.

SPECIES DIVERSITY AMONG COCCOID EUSTIGMATOPHYCEAE (HETEROKONTOPHYTA)

Bailey, Craig¹, Fawley, Marvin² & Fawley, Karen²

¹Biology and Marine Biology and Center for Marine Science, UNC-Wilmington, Wilmington, NC, USA; ²Biological Sciences, North Dakota St. University, Fargo, ND, USA

We have brought into clonal culture ca. 100 coccoid eustigmatophytes from freshwater habitats using single cell isolation techniques. Cells are characterized by the presence of a distinctive ‘red body’ and cell wall visible at the light microscopic level. Photosynthetic pigment profiles obtained for selected isolates using HPLC analyses match those previously published for other eustigmatophytes. Cell size variation within- and among-cultures is not significantly different and cursory TEM examinations revealed no differences among cells of those cultures examined. In short, these isolates are morphologically indistinguishable from one another. Nevertheless, different isolates reared in liquid or on agar mediums exhibit widely varying growth rates and temperature preferences indicative of physiological differentiation. Nuclear 18S rRNA and plastid rbcL gene sequences for those isolates investigated thus far are all unique. In fact, phylogenetic analyses clearly indicate that our freshwater coccoid eustigmatophytes are only distantly related to other eustigmatophytes for which published data are available. Furthermore, none of the isolates can be placed in any of the four currently recognized families within the Eustigmatales. To accommodate this diversity we propose the erection of two (possibly three) new eustigmatophyte families and three genera including at least seven species that are new to science. Also, we transfer *Goniochloris* to the Eustigmatophyceae on the basis of DNA sequence data obtained from the type species, *G. sculpta* (SAG 29.96). This study doubles the number of known eustigmatophyte species.

DEMOGRAPHIC SIMILARITIES AND DIFFERENCES BETWEEN *ZOSTERA JAPONICA* IN ITS NATIVE (KOREA) AND INTRODUCED (WILLAPA BAY) HABITATS

DeAmicis, Stacey¹, Hong, Jae-Sang² & Ruesink, Jennifer¹

¹Biology, University of Washington, Seattle, WA, USA; ²Oceanography, Inha University, Incheon, South Korea

Biological invasions are understudied in marine systems, despite the fact that coastal ecosystems are heavily invaded. The

small eelgrass species *Zostera japonica* arrived in western North America around 1957, probably with oyster imports. To understand *Z. japonica*'s invasion process, we studied its demography and morphology in Willapa Bay, WA. Sampling occurred at near monthly intervals at two tidal elevations at each of three sites in 2004-2005. We found that i) *Z. japonica* is perennial but its shoot density declines by 50-80% over winter; ii) sexual reproduction is substantial (at least 30% of shoots flower) and successful (new recruits contribute 10-65% of all shoots in the spring); and iii) growth is rapid (1 cm/d), with total annual production estimated at 4.79×10^6 kg DW/yr, or 14% of native eelgrass production. A recent publication from Korea allowed us to compare *Z. japonica* in its native and introduced ranges. Some seasonal patterns were similar, in particular, peak germination in April, peak growth rate in mid-late summer, and reproduction from June to September. In contrast, the Korean population showed little seasonal variation in shoot density, and plants there tended to be larger, with lower proportions of flowering shoots. We suspect that *Z. japonica*'s successful invasion stems in part from high reproductive ability that enables it to overcome stressful overwinter conditions.

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THE RELATIONSHIPS BETWEEN DELAYED AND PROMPT FLUORESCENCE IN MONITORING PHOTOSYNTHETIC TRAITS OF PHYTOPLANKTON

Kurzbaum, Eyal¹, Eckert, Werner² & Beer, Sven¹

¹Plant science, Tel Aviv university, Tel Aviv, Israel; ²The Yigal Allon Kinneret Limnological Laboratory, Israel Oceanographic and Limnological Research, Migdal, Israel

When plants are exposed to light, part of the energy captured by chlorophyll is emitted directly as fluorescence ("prompt fluorescence"). This type of fluorescence can be utilised for measuring quantum yields and photosynthetic electron transport rates (ETR) in so-called pulse amplitude modulated (PAM) fluorimeters. Another type of fluorescence is obtained after turning off the light ("delayed fluoresce", DF), which is due to a back-flow of electrons in the photosynthetic electron transport chain (until charges across the thylakoid membrane have been neutralised). Such fluorescence can be utilised in a DF spectrometer for determining the concentration of "active" chlorophyll, as well as for distinguishing between different major groups of phytoplankton based on differential excitation of their pigments. DF spectrometry is sensitive, and can be used for continuous monitoring natural phytoplankton populations in aquatic environments. However, there is no reliable information regarding the relationship between DF fluorescence and quantum yield or photosynthetic rates. In this work, DF spectrometry was compared with PAM fluorometry in order to establish whether the former method could yield any measure of the photosynthetic activity of phytoplankton. This was done by monitoring direct and delayed fluorescence, together with pH, temperature, irradiance (PAR), chlorophyll and dissolved oxygen (DO) concentrations, continuously during several diel cycles, in a *Chlorella* culture kept in an open transparent plastic tank submerged at the surface of Lake Kinneret, Israel. It was found that the DF signal correlated with effective quantum yield measured by PAM fluorometry on a daily cycle, with high values during nights and lowered values during days. DO measurements, on the other hand, correlated with PAM-fluorometry derived ETRs. Thus, it seems that the DF signal is a good proxy for quantum yields and for ETR calculations. In addition to the continuous monitoring of biomass of different taxonomical groups, our findings suggest that DF spectrometry also carries the potential to measure photosynthetic rates in natural phytoplankton assemblages.

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DOMOIC ACID PRODUCTION BY *PSEUDO-NITZSCHIA* SPP. IN RESPONSE TO ESTUARINE NUTRIENT DYNAMICS

Ohana-Richardson, Andrew & Shapiro, Lynda

Oregon Inst. of Marine Biology, University of Oregon, Charleston, OR, USA

The South Slough National Estuarine Research Reserve, the southern arm of the larger Coos Estuary, is a model protected ecosystem that can be utilized to study the processes affecting Oregon's coastal zone. Throughout spring and summer, the Slough becomes mostly marine due to a minimal input of freshwater. During this time, coastal marine phytoplankton populations are able to move into the Slough on flood tides. *Pseudo-nitzschia*, a toxic genus of diatoms, is generally found to be abundant coastally during this time and has been found within the South Slough. *Pseudo-nitzschia* is a producer of the potent neurotoxin domoic acid that has plagued Oregon's shellfish industry in the past few years. Better understanding of the diatom's ability to produce the toxin within the estuarine ecosystem would aid in the future monitoring for shellfish toxicity in bays and estuaries. This study is currently undertaking a monitoring regime for cell abundance, species identification, and nutrient concentrations within Slough waters during flood tide. Preliminary results indicate cell movement to the furthest reaches of tidally driven water in the upper estuary. Work is being performed to identify toxic

species and level of toxicity during population blooms. It is our hope that this data may be used together with a model of nutrient dynamics currently in development to strengthen predictive capabilities related to limits of toxic population movement in coastal inlets such as the South Slough.

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THE INFLUENCE OF TEMPERATURE, SALINITY, AND NUTRIENTS ON CYANOBACTERIAL DENSITY IN COSTAL WATERS OF BANDAR ABBAS, PERSIAN GULF

Nejatkhah Manavi, Parisa¹ & Korei, H.²

¹*Marine Biology, Islamic Azad University, North Tehran Branch, Tehran, Iran;* ²*Marine Biology, Islamic Azad University, North Tehran Branch, Tehran, Iran*

Cyanobacteria respond to changes in growth condition by a variety of adaptive means which allow them to dominate over other phytoplankton groups and lead to their mass occurrence. In one year (2003-2004) data set was used to investigate changes in temperature, salinity, phosphorus, nitrate and cell density of cyanobacteria in fishery and oil wharfs which is located on the Persian Gulf in Bandar Abbas in the present study. Concentration of total P increased from 0.02 to 0.9 ug/l in fishery and oil wharf transects. And also concentration of total N increased from 0.01 to 21 ug/l, too. Water temperature in highest was 35 c in June and August, while the lowest (21 c) measured in December. Cyanobacteria lost their dominant position while nutrients decreased. And the cell density increased following a rise in the water temperature, with the highest cell density occurrence in late spring and middle summer. Results were consistent with the prediction; cyanobacterial cell density was favoured by nutrients and warm water, and water temperature has been found to be the main factor controlling the initiation of cyanobacterial cell density increase.

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DELAYED DEVELOPMENT IN KELP FOREST SYSTEMS

Carney, Laura & Edwards, Matthew S.

Biology, San Diego State University, San Diego, CA, USA

Identifying the factors that drive kelp forest persistence is fundamental to understanding how temperate coastal marine ecosystems are regulated in time and space. Recent declines in north Pacific kelp forests linked to large-scale oceanographic disturbances have altered the abundance and distribution of species that rely on kelp forests for habitat and food. Recovery from large-scale disturbances such as El Nino has been delayed in some regions (e.g. near the southern range limit) for years to decades. For some species in these regions at least, recovery may depend on the presence of a bank of microscopic propagules that survive these disturbances and produce new adults when conditions improve. Macroalgal propagule banks are formed by the microscopic early life stages which delay their development on the surface of rocky substratum below the adults. Little is known, however, about which kelp species rely on this mechanism or the processes that regulate delayed development in these life stages. Further, given the recent advances in our understanding of the deleterious consequences of self-fertilization within kelps, it may be important to know if delayed development in these stages decreases the rate of self-fertilization by increasing the probability of encountering unrelated individuals that accrue over time. Just as it is widely recognized that understanding the factors required to break seed dormancy are critical to agriculture and land management, understanding microscopic development of seaweeds is critical for the successful management of existing kelp forests, as well as currently mandated restoration efforts of those that have declined. Investigations are underway to determine which of the most conspicuous kelp species in the northeastern Pacific form seed banks via delayed development, which microscopic life stage delays, and which environmental conditions control the delay and resumed development of these stages. Preliminary results from laboratory experiments suggest that 1) the gametophytes of several kelp species can delay their development and that 2) increasing both nitrate concentration and irradiance can induce resumed development and subsequent adult recruitment from these gametophytes.

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SIX EASY STEPS TO (HOPEFULLY) PLATING YOUR FAVORITE PHYTOPLANKTON SPECIES

Lakeman, Michael B.¹ & Cattolico, Rose Ann^{1,2}

¹*Biology, University of Washington, Seattle, WA, USA;* ²*Ocean Sciences, University of Washington, Seattle, WA, USA*

Phycologists most often use liquid cultures to study phytoplankton. If the cells in a culture are all identical, then we can accept that the properties measured from that culture are the properties of each individual cell. However, the cells within a batch culture are almost certainly functionally or genetically diverse, and the properties of these diverse individuals can

only be addressed by isolating single cells. Plating represents one of the most simple, quick, inexpensive and high-throughput techniques for generating single-cell isolates. However, plating of phytoplankton has been restricted to taxa which are suitable for this approach. Wall-less algae are especially problematic, because growth on a surface (i.e. at the solid-gaseous interface) exposes such cells to physical demands which are beyond the capabilities of the organism to withstand. We will present results of experiments aimed at developing and optimizing an embedded plating technique for the wall-less raphidophyte alga *Heterosigma akashiwo*. Important variables ensuring success in plating this organism are the source and concentration of agarose used to solidify the growth medium and the light level under which incubation occurs. Plating efficiency is independent of the growth rate of the parent culture and plating density. Recovery of colonies into liquid medium is shown to be straightforward. Data will be presented illustrating some potential uses of this plating technique, focusing specifically on applications which investigate population diversity present within a batch culture. We demonstrate direct PCR from colonies, facilitating quantitative assay of genetic variation within a liquid culture. We also show that this plating technique allows quantitation of the frequency of phenotypes such as tolerance of nutritional stress. Finally, preliminary data will be presented illustrating that this simple technique can be adapted for use with other photoautotrophic unicells including species belonging to the *Synuraphyceae*, *Haptophyceae* and *Dinophyceae*.

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A RE-EVALUATION OF THE TROPHIC STATE OF MOUNTAIN LAKE, VIRGINIA

Parker, Bruce C.¹ & Deshler, David²

¹Department of Biological Sciences, Virginia Tech, Blacksburg, VA, USA; ²The Wilderness Conservancy at Mountain Lake, Pembroke, VA, USA

Mountain Lake, the only natural lake of any significant size in the unglaciated southern Appalachians, is unique: Its 1.0 km-long basin overlies three geological formations, it originated through partial damming of a stream by gradual downslope movement of sandstone blocks, and it has subterranean losses of >50% of all entering water through the partial dam. Mountain Lake is oligotrophic primarily from low phosphate inducing low phytoplankton densities and low productivity, albeit high algal diversity totaling 448 taxa in 17 investigations. Periodic re-evaluations of Mountain Lake's trophic state has been urged by Virginia's Department of Environmental Quality. Thus, we collected surface and 8 meter depth water samples every two weeks May-September, 2005-the period of thermal stratification when nutrients, biomass, and productivity are highest. Samples were processed for orthophosphate, total phosphate, nitrate, nitrite, ammonium, total nitrogen, chlorophyll a, and dissolved organic carbon using mostly methods of earlier studies. Comparisons of results with those of earlier studies show that orthophosphate has increased, inorganic nitrogen has decreased, yet the N:P ratio remains higher than 17:1 (i.e., 19:1 -99:1) indicating that P remains the limiting nutrient sustaining oligotrophy of Mountain Lake. Chlorophyll a was 64% of average values measured 1985-90, and dissolved organic carbon was slightly higher than 1988-90 values. Total P and N, not previously measured in this lake, was slightly higher than orthophosphate and inorganic nitrogen, confirming with chlorophyll a the relatively low organic production. The few samples examined for algae disclosed essentially the same communities of the past three decades. Thus, the trophic state of Mountain Lake appears unchanged-oligotrophy and a pristine natural lake persists.

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DECLINE OF THE NATIVE KELP *KJELLMANIELLA CRASSIFOLIA* MIYABE ON THE EASTERN COAST OF KOREA

Kim, Hyung Geun¹, Park, Joong Goo¹, Lee, Sung Bok¹, Son, Yong Soo² & Sohn, Chul Hyun³

¹Faculty of Marine Bioscience and Technology, Kangnung National University, Gangneung, South Korea; ²East Sea Fisheries Research Institute, NFRDI, Gangneung, South Korea; ³Department of Aquaculture, Pukyong National University, Busan, South Korea

Native kelp *Kjellmaniella crassifolia* populations were distributed in deeper water (15~30m depth) while the *Laminaria* populations were in upper shallower water (0~15m depth) in Gangneung, the eastern coast of Korea. We surveyed the culture condition, biomass and density of *K. crassifolia* in field from 1994 to 2003. Juvenile sporophytes of *K. crassifolia* grew to optimal blade length only under specific culture conditions (10°C, 40 µmol m⁻²s⁻¹) while *Laminaria* was good in various water temperatures (10~20°C) and light levels (40~120 µmol m⁻²s⁻¹). Algal standing crops of *K. crassifolia* were 3~4 kg/m² in 1994. Biomass declined to 2~3 kg/m² in May and August 1997; by November 1997 these populations had disappeared. This kelp bed recovered the next year and remained healthy. In September 2002, this kelp bed was destroyed

again. Density followed similar pattern; in January, May and August 1997, over 20 *Kjellmaniella* /m² were collected in the kelp bed. However in November 1997, water temperature increased because of a warm current and this kelp bed was destroyed. In 1998 this kelp bed recovered reaching a density of 25 individuals/m², and remained healthy until August 2002 when again the population disappeared. Two possible explanations for this biomass decline are changes in seawater temperature and increase in turbidity. Particularly, the water temperature increased suddenly in 1996~1997 and a heavy storm which produced much freshwater run off occurred in September 2002.

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CHARACTERIZATION OF THE MACROALGAL COMMUNITY ASSOCIATED WITH THE HIGH ENERGY ZONE OF PUNTA YU YUM, QUINTANA ROO, MEXICO

Fikes, Ryan L.¹, Smith, Leslie C.² & Lehman, Roy L.¹

¹Physical & Life Sciences, Texas A&M University-Corpus Christi, Corpus Christi, TX, USA; ²Center for Coastal Studies, Texas A&M University-Corpus Christi, Corpus Christi, TX, USA

Macroalgal community structure was characterized for a high energy portion of the lower midlittoral, upper infralittoral zone of a rocky point on the eastern coast of Mexico's Yucatan peninsula. This intertidal zone of Punta Yu Yum has historically been inaccessible due to high energy wave action. However, meteorological conditions during a 2005 summer research expedition made it possible to conduct intensive sampling. A species checklist was developed for the macroalgal community, and three sets of voucher specimens were collected of each species encountered. A random design of 132 quadrats (20cm X 30cm), imaged with a Sony 4.1 mega pixel Cyber-shot digital camera, were used to collect data. Images were evaluated with Coral Point Count (CPC), which assigned 25 random points per image. Each organism per point was identified to lowest possible taxon. Datasets were analyzed for species diversity, richness, evenness, and relative cover using both CPC and Quantitative Analysis in Ecology programs. Maximum Shannon diversity was found to be 1.51, following normal trends of low diversity in high energy habitats, and evenness was 0.591. Species richness was found to be 31, with class Florideophyceae constituting 10 species, Phaeophyceae 9 species, and Chlorophyceae 10 species. In total, 10 orders of marine macroalgae were represented. *Chondrophyucus papillosa* [Laurencia papillosa] had the greatest relative cover at 37.08 percent, followed by *Turbinaria tricostrata* with 17.64 percent cover.

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POTENTIAL CHEMICAL DEFENSES AGAINST ENDOPHYTES AND EPIPHYTES IN ANTARCTIC MACROALGAE

Aumack, Craig F.¹, Backstrom, Ian C.¹, Amsler, Charles D.¹, McClintock, James B.¹ & Baker, Bill J.²

¹Department of Biology, University of Alabama at Birmingham, Birmingham, AL, USA; ²Department of Chemistry, University of South Florida, Tampa, FL, USA

Several studies have shown that high densities of epiphytes can be detrimental to their macrophytic hosts. Their presence reduces light availability, interferes with gas exchange, and increases the competition for limiting nutrients. In the western Antarctic, particular species of macroalgae are rarely fouled despite the presence of corroding diatoms and epiphytic macroalgae in early life stages. Previous studies have shown that many Antarctic macroalgae produce chemical defenses to deter grazing but little work has been done to explore their use as anti-fouling agents. In the present study, we tested the effects of organic and aqueous extracts from *Desmarestia anceps* and *Plocamium cartilagineum* on two species of macroalgae (*Geminocarpus geminatus* and *Desmarestia antarctica*) known to have early epiphytic life-stages. Small filaments (0.25 - 0.35 mm) of *G. geminatus* and *D. antarctica* were placed in individual holding trays containing media treated with either 0x, 0.3x, 1x, and 3x the standard concentration of organic or aqueous solutions from *D. anceps* or *P. cartilagineum*. The cultures were maintained in optimal growth conditions for 15 days. Treated and untreated media was replaced every five days to ensure constant extract concentration within the trays. Digital pictures were taken prior to initial incubation and after the designated culture period to photo-document growth and were used in conjunction with image analysis software (Image-Pro Plus) to determine the surface area of algal filaments. Ultimately, we hope to demonstrate that extracts from Antarctic macroalgae provide a chemical defense against potentially invasive and harmful macroalgal epiphytes.

POPULATION STRUCTURE OF *PADINA AUSTRALIS* HAUCK (DICTYOTALES, PHAEOPHYTA) IN TWO LOCATIONS IN PHUKET PROVINCE, THAILAND

Wichachucherd, Bongkot¹, Prathep, Anchana¹ & Liddle, Larry B.²

¹Department of Biology, Prince of Songkla University, Hat Yai, Thailand; ²Department of Marine Science, Southampton College of Long Island University, Southampton, NY, USA

The genus *Padina*, a brown alga (Phaeophyta), has a worldwide distribution in tropical and subtropical climate zones. All species of *Padina* have a fan-shaped blade, an infurled apical meristem and a felty holdfast. *Padina* attaches to any solid substrate and may be partially or wholly buried in sand periodically. Reproductive sori are formed in concentric bands gradating in maturity from the apex to the base of the blade. They alternate in We posed the question: How does *Padina* increase the number of individuals and what factors support its reproduction? The purpose of this project is to study the population structure of *Padina australis* Hauck in two locations on Koh Phuket. The hypothesis includes the idea that characteristic patterns of growth, reproductive cell formation and recruitment in the natural habitats will determine the distribution of particular phases of the life history, the numbers of each phase and the annual cycle of growth, maturation, death and then recruitment of new individuals. The two populations at the contrasting habitats of Koh Pling and Tang Khen, undoubtedly show similarities and differences over the year of study. Thirty samples have been collected at 20 meter intervals from the shoreline in the intertidal zones. The length, radius, maturity phase, quantity of reproductive cells and quantity of released reproductive cells were recorded for each individual. Specimens were put into size classes defined by length and radius. The frequency of these classes was calculated. The maturity phase is categorized according to a maturity index. The recruitment study was carried out on hard substrata in situ. Three permanent plots 0.25 m² were studied every 20 meters. Intraspecific competition was calculated from percentage of recruitment at the two sites. The research started in September 2005 and it will be finished in September 2006. The preliminary results presented here on reproductive potential and recruitment are for eight months. They help describe the distribution of the life history stages and the different strategies in the two locations. Growth rates at the two sites are also compared.

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EFFECTS OF HERBIVORY AND SEASON OF CLEARING ON SPECIES COMPOSITION AND ALGAL SUCCESSION IN A TROPICAL INTERTIDAL SHORE, PHUKET, THAILAND

Mayakun, Jaruwan¹, Prathep, Anchana¹, Kim, Jeong Ha² & Liddle, Larry B.³

¹Department of Biology, Prince of Songkla University, Hat Yai, Thailand; ²Department of Biological Science, Sungkyunkwan University, Suwon, South Korea; ³Marine Science, Southampton College of Long Island University, Southampton, NY, USA

The effects of herbivory and season of clearing on species composition and algal succession were experimentally tested in a tropical intertidal shore, Phuket Island, Thailand. To determine the effect of season of clearing on algal succession, dead coral patches were cleared, and cages were set up to exclude fish herbivory. The experimental design comprised 1 gap size of clearing (20 cm × 20 cm), 2 seasons of clearing (January 2004 and July 2004) and 2 categories of herbivory: five fully caged (25 cm × 25 cm × 20 cm, mesh size was 2 cm × 2 cm) and five uncaged plots both experimental and control plots. The results indicated that the pattern of algal community development during succession was in the middle stage and algal succession followed 'an inhibition model'. In this succession process, an ephemeral alga, *Ulva paradoxa* was the early colonist which inhibited the settlement of the later species, *Polysiphonia sphaerocarpa* and *Dictyosphaeridia* stage of *Padina*. Seasons of clearing influenced the abundances in the algal succession. *U. paradoxa* was able to reproduce and recruit throughout the year. Algal abundance was not influenced by grazing. It might be a result of resident herbivorous damselfishes excluded other herbivores from their territories and maintained algae as algal farms. Unexpectedly, the *U. paradoxa* cover in the caged plots (without fish), had a lower algal coverage. These excluded fish plots could allow smaller grazers to feed on the new colonized algae, thus reducing the algal cover within the cages. Further experiments on these roles of herbivory are still needed for a better understanding of their roles. Other aspects of disturbances on algal succession should be investigated in this tropical intertidal shore.

DIFFERENCES IN *SKELETONEMA* DISTRIBUTION AMONG THREE DISTANT TEMPERATE COASTAL SITES

Saggiomo, Maria¹, Kooistra, Wiebe H.¹, Sarno, Diana¹, Montresor, Marina¹, Burns Lopez, Cary², Cloern, James E.², Hargraves, Paul H.^{3,4} & Zingone, Adriana¹

¹Stazione Zoologica A. Dohrn, Naples, Italy; ²U.S. Geological Survey MS496, Menlo Park, CA, USA; ³University of Rhode Island, Narragansett, RI, USA; ⁴Harbor Branch Ocean. Inst., Ft. Pierce, FL, USA

Most species of the genus *Skeletonema* were until recently identified as *S. costatum*, which was considered ubiquitous and opportunistic. However morphological and molecular studies have revealed that the latter taxon actually includes several distinct species, now described under new names. To understand whether all these species retain an opportunistic and ubiquitous nature, cultures and natural samples of *Skeletonema* were investigated from three different areas, the Gulf of Naples (GON, Mediterranean Sea), San Francisco Bay (SFB, Pacific Ocean) and Narragansett Bay (NB, Atlantic Ocean), using morphological and molecular techniques (LSU rDNA). The three sites differed markedly in both species composition and seasonal cycles of *Skeletonema* species. In the GON, *S. dohrnii*, *S. pseudocostatum*, *S. tropicum* and *S. menzelii* succeeded one another over the annual cycle, from late winter to autumn. In SFB, *S. dohrnii* was found in all seasons and over a wide salinity range (16-36 PSU), whereas *S. costatum* and *S. menzelii* were recorded occasionally. In NB, *S. japonicum* was responsible for the autumn-winter bloom in two different years whereas a different, still unidentified species was found in summer samples. The strains of *S. japonicum* from NB were genetically identical to those from other areas of the world, whereas *S. dohrnii* showed molecular differences between SFB and GON material. Strains of *S. dohrnii* from the two areas were morphologically similar, all showing variability in the band ultrastructure, which is the only character that distinguishes this species from the closely related *S. marinoi*. Strains of *S. dohrnii* from both SFB and GON had very low growth rates ($<0.5 \text{ div. day}^{-1}$) at 5-10°C, whereas they showed constantly high growth rates (1.5-2.5 div. day^{-1}) between 15 and 24°C; therefore differences in their seasonality cannot be explained by differences in temperature tolerance. Differences recorded over the seasonal cycle and among the areas investigated suggest that *Skeletonema* species are not ecologically equivalent, but the physiological and/or environmental factors that account for their distinct spatial and temporal distributions need further investigation.

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SYMPAGIC DIATOMS IN THE ANNUAL PACK ICE OF TERRA NOVA BAY, ROSS SEA, ANTARCTICA

Saggiomo, Maria¹, De Stefano, Mario², Mangoni, Olga³, Saggiomo, Vincenzo¹, Sarno, Diana¹ & Zingone, Adriana¹

¹Stazione Zoologica Anton Dohrn, Naples, Italy; ²Seconda Università di Napoli, Caserta, Italy; ³Università di Napoli "Federico II", Naples, Italy

The pack ice is a semisolid matrix permeated by a network of channels and micrometric pores filled with salt brine; it is inhabited by micro-algae, mainly diatoms as well as by a variable heterotrophic community. While the major contribution of diatoms to the Antarctic primary production is well known, floristic investigations on pack ice communities are very scarce. We analysed the vertical distribution of total algal biomass and diatom species in the annual pack ice in Terra Nova Bay during the austral spring of 1999. A 240 cm ice core was divided into four 55 cm and one 20 cm parts, the latter including the bottom-ice at the water interface. In addition, material from the underneath platelet ice was examined. The total biomass (Chla) was analysed with a spectrofluorometer, whereas quantitative analysis and taxonomic identification of diatoms were performed using light and electron microscopy. Biomass concentrations increased slightly from the surface to the bottom layer (from < 1 to $1.30 \mu\text{g l}^{-1}$ Chla); markedly higher concentrations ($90 \mu\text{g l}^{-1}$ Chla) were recorded in the platelet ice. Diatom abundances ranged from 0.3×10^6 to 3.4×10^6 cells l^{-1} in the pack ice and attained 22.7×10^6 cells l^{-1} in the platelet ice. Planktonic species constituted about 98% of the diatom assemblages from the surface layer of the ice core down to 220 cm. Some species, such as *Fragilariopsis curta*, *F. rhombica*, *F. sublinearis*, *F. obliquecostata*, *F. cylindrus*, *Thalassiosira gracilis* and *T. lentiginosa*, were present along the entire ice core. *Asteromphalus parvulus*, *T. graviga* and *T. maculata*, occurred only in the upper layers of the ice core while benthic species were about 30% of the diatoms in the bottom and platelet ice (e.g. *Berkeleya* sp., *Entomoneis* spp., *Navicula directa*, *Navicula* spp., *Nitzschia stellata*). The distribution of diatoms along the ice core reflects the seasonal occurrence of the different species in the sea. Planktonic species are trapped in the ice as the water freezes in autumn and most likely play a role in seeding the water column at ice melting. By contrast, the presence of benthic diatoms in the bottom and platelet ice is probably due to colonization and/or *in situ* growth.

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PHOTOTACTIC RESPONSES OF *ELACHISTA ANTARCTICA* SKOTTSBERG SPORES

Bucolo, Anthony P.¹, Amsler, Charles D.¹, McClintock, James B.¹ & Baker, Bill J.²

¹Department of Biology, University of Alabama at Birmingham, Birmingham, AL, USA; ²Department of Chemistry, University of South Florida, Tampa, FL, USA

The endophyte *Elachista antarctica*, a filamentous brown alga found throughout the waters surrounding the Antarctic Peninsula, South Shetland, and Macquarie Islands appears to be restricted to one host macrophyte, *Palmeria decipiens*. *E. antarctica* spores released from unilocular sporangia develop into filamentous microthalli forming plurilocular reproductive structures. Physical factors such as temperature, topography, current movements, and light can significantly affect swimming behavior of released spores. In this study we measured phototactic capabilities of *E. antarctica* spores after release. *E. antarctica* isolates collected near Anvers Island were cultured in the laboratory using Provasoli's Enriched Natural Seawater (PES) in a 12:12 photoperiod at 1.5°C. After swimming spores were concentrated they were pipetted onto glass slides and imaged on a thermal stage using red light. A fiberoptic light source supplied white light from one side of the microscope stage at a range of irradiance levels using different slides for each light treatment. Phototactic capabilities of spores released from this brown endophyte were determined using computer-assisted motion analysis software. Responses to light may influence dispersal and aid in detection of suitable settlement locations in marine microenvironments. Phototactic behavior of spores may influence duration of spore motility directing the spores to areas of settlement on *P. decipiens*.

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DRAMATIC BLOOMS OF A BIOLUMINESCENT DINOFLAGELLATE AND A POTENTIALLY TOXIC PRYMNESIOPHYTE IN THE SALTON SEA, CALIFORNIA

Wolny, Jennifer^{2,3}, Steidinger, Karen^{2,3}, Tiffany, Mary A.¹ & Garrett, Matthew³

¹Biology, San Diego State University, San Diego, CA, USA; ²Florida Fish and Wildlife Conservation Commission, Fish and Wildlife Research Institute, St. Petersburg, FL, USA; ³Florida Institute of Oceanography, St. Petersburg, FL, USA

In early 2006, unusual algal blooms of two species occurred in the Salton Sea, a large salt lake in southern California. In mid-January local residents reported bioluminescence in the Sea. Starting in February, large rafts of long-lasting foam were observed as well. In fact, the foam was also bioluminescent. Microscopical investigations were initiated and *Alexandrium margalefii*, previously unreported from the Sea, was found to be highly abundant. Other dinoflagellate species, usually present in earlier studies, were extremely rare or not detected. A sample from January had no detectable levels of *Prymnesium parvum* but had 240 cells ml⁻¹ of the dinoflagellate. On March 19 a sample collected from Red Hill Marina, where white caps glowed at night and shoreline foam about 0.5 m thick glowed brightly, contained 950 cells ml⁻¹ of *A. margalefii* and 82,000 cells ml⁻¹ of *P. parvum*. A shore sample from an intensely bioluminescent location, collected on March 31, had 50,100 cells ml⁻¹ of *A. margalefii* and 5,240 cells ml⁻¹ of *P. parvum*. Mid-lake phytoplankton samples collected on the same date had modest levels of both species, along with high abundance of two species of chain-forming *Cyclotella*. It appears that the foam was caused by the *P. parvum* bloom and its glow was due to the bloom of entrained *A. margalefii*. We will describe on-going laboratory studies on these species.

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INITIAL OBSERVATIONS AND MONITORING OF *GRATELOUPIA TURUTURU* YAMADA ALONG THE CONNECTICUT COAST IN LONG ISLAND SOUND

Gladych, Rebecca A.¹, Keser, Milan² & Yarish, Charles³

¹Marine Sciences, University of Connecticut, Groton, CT, USA; ²Millstone Environmental Laboratory, Dominion Nuclear Connecticut, Waterford, CT, USA; ³Ecology and Evolutionary Biology, University of Connecticut, Stamford, CT, USA

The presence of non-indigenous species in new environments has had tremendous ecological impacts on the local environment. With increased ship travel between the oceans of the world, the rate of species introduction is constantly increasing. The red alga *Grateloupia turuturu* Yamada, native to Japan, has been reported as particularly invasive, and may compete and displace the native *Chondrus crispus* populations. *Grateloupia turuturu* has been reported as being tolerant of nutrient enriched waters, and has been found in salinities from 15‰ to 37‰, and from 4°C to 28°C. *Grateloupia turuturu* was first found in Europe in 1969 and was later recorded in Narragansett Bay, Rhode Island, in 1994. It has recently (September, 2004) been found at Millstone Point, Waterford, Connecticut. This population of *G. turuturu* has been monitored monthly since its discovery. This species has been found primarily in subtidal and low

intertidal areas, growing on cobbles and most recently on a rocky platform. Epiphytes primarily consist of *Polysiphonia* spp. and *Porphyra* spp. It has been found growing among beds of *C. crispus* and has diverse morphologies. The fronds that were found exposed during extreme low tides were bleached during the winter, suggesting that they may not be tolerant of freezing temperatures. Future determination of specific physiological traits and continued monitoring of this new invasive species in Long Island Sound will give a better understanding of the ecology of the species, and its rate of spread into Long Island Sound.

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DIATOM POLYMERS OF COLNE ESTUARY (U.K.) BIOFILMS: FUNCTIONAL ROLES OF EPS BASED ON STRUCTURAL CHARACTERISTICS

Bellinger, Brent J.¹, Underwood, Graham J.² & Gretz, Michael¹

¹Biological Sciences, Michigan Technological University, Houghton, MI, USA; ²Biological Sciences, University of Essex, Colchester, United Kingdom

Pennate diatoms are significant components of intertidal biofilms found within the Colne Estuary, U.K. These diatoms are capable of producing copious amounts of extracellular polymeric substances (EPS), an important component of the biofilm matrix of estuarine sediments. Hot water soluble (HW) carbohydrates, composed predominately of the intracellular storage polysaccharide chrysolaminarin, showed rapid accumulation during low tide periods, with the relative abundance of Glc in the extract increasing during photosynthetic periods and declining during tidal cover or during darkness. Labile colloidal carbohydrates, rich in Glc and Gal, were significantly correlated with algal biomass. These carbohydrates were rapidly produced by biofilms during low tide periods, but quickly lost (up to 60%) within 2 h of tidal cover. Refractive polymers isolated using hot bicarbonate (HB) showed almost no net accumulation or loss over tidal cycles. Pulse-chase labeling of biofilms using ¹³C-bicarbonate showed rapid uptake and incorporation of carbon in the HW fraction and into EPS. Subsequent ¹³C-enrichment of extracellular polymers suggests continuous production, with losses due to tidal wash-away or rapid utilization, presumably by heterotrophic bacteria. Comparing monosaccharide and linkage data from field sites with data generated from two cultured diatoms native to the system, we found significant correlations. *Navicula phyllepta* and *Nitzschia epithemioides* produce extracellular polymers rich in Gal, Man, Xyl and to a lesser extent Fuc and Rha, but differ in how their polymers are substituted and linked. *N. epithemioides* produces a GalUA rich HB polymer, while *Navicula phyllepta* produces a highly O-methylated Fuc- and Gal- rich HB polymer. Our results indicate a structurally complex polymer matrix in diatom dominated biofilms. The chemical nuances of EPS produced by individual species are significant to the functional roles of the polymers, both in terms of biotic and abiotic interactions. Overall, diatom polymers represent a significant source of carbon and are central to the highly successful communities found within estuarine biofilms.

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NOTES FROM UNDERGROUND: BRYOPSIDALEAN GREEN ALGAL HOLDFASTS IN PSAMMOPHYTIC HABITATS

Bedinger, Laura A. & Bell, Susan S.

Biology, University of South Florida, Tampa, FL, USA

Rhizophytic algae of the order Bryopsidales (*Caulerpa*, *Halimeda*, *Udotea*, *Penicillus*, *Rhipocephalus*, and *Avrainvillea*) are large and abundant primary producers in tropical and subtropical psammophytic communities and their ability to grow attached in unconsolidated sediments is unique among the algae. Despite this, their rhizoids and holdfasts have not been well studied. On the west coast of Florida north of Tampa Bay we have observed large sediment clumps (holdfasts) associated with the rhizoids of these rhizophytic algae. Though highly variable, these belowground structures extend from the sediment surface to mean depth of 5.3 ± 1.6 cm (S.D.) and can occupy a volume as large as $27,815$ ml/m³ in a dense mixed rhizophytic algal community. Analysis of holdfast volume and dry weight on a per species basis yielded the following respective results (mean \pm S.E.): *Halimeda incrassata* 12.15 ± 1.5 ml and 10.9 ± 1.7 g (n=30), *Penicillus capitatus* 14.1 ± 1.6 ml and 13 ± 1.6 g (n=26), *Udotea conglutinata* 15.3 ± 1.4 ml and 15.2 ± 1.3 g (n=19). Mean organic content of holdfasts was $5 \pm 1\%$, which is 2.5 ± 1.3 (S.D.) % more than that of surrounding sediments, which are also permeated by a fine net of algal rhizoids. Surprisingly, the amount of above ground vegetation was a poor indicator of the below ground holdfast size for all species ($R^2 = 0.13$). Given that the holdfasts of rhizophytic algae occupy large amounts of belowground space in sediments we investigated the impact of the rhizoids on water percolation in shallow sediments using experimental set-ups with natural levels of *P. capitatus* and *H. incrassata* holdfasts, assuming that percolation rate is a proxy for water permeability. In over 70% of our manipulations, rhizophytic algal holdfasts reduced water percolation

11-36% as compared with controls made up of similar sediment without holdfasts. These results reveal that structures produced by rhizophytic algae may be important in subtidal sediments because they alter physical properties of sediments by mechanisms not previously examined. Moreover, these changes may have geochemical implications that could affect benthic organisms that live in close proximity to the rhizoids.

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ECOLOGICAL EVALUATION OF ALGAL COMMUNITIES FROM WESTERN STREAMS IN US

Manoylov, Kalina M.¹, Stevenson, R. J.¹ & Pan, Yangdong²

¹Zoology, Michigan State University, East Lansing, MI, USA; ²Environmental Sciences and Resources, Portland State University, Portland, OR, USA

The ecology and distribution of soft bodied algae are rarely reported for large national surveys. We assessed algae in 879 samples from streams from 5 western ecoregions during 2002-2004. Diatoms were identified as live and dead, while soft bodied algae were identified to the lowest taxonomic unit. 89.5 % of the streams were dominated by diatoms. Algal species abundance was related to environmental variables and weighted average environmental optima were calculated for most species. All major algal groups were observed; filamentous Cyanophyta had the widest distribution in all 5 ecoregions, due mainly to abundance and distribution of *Homoeothrix janthina* (Bornet et Flahault) Starmach. In a few sites, the largest proportion of algal biomass was attributed to species like *Nostoc linckia* (Roth) Bornet & Thuret, *Aphanizomenon flos-aquae* (Linnaeus) Ralfs, and *Cladophora glomerata*, (Linnaeus) Kützing. Ecological evaluations based on species weighted average optima were presented for 40 % of the identified soft algae. This information can be used in addition to diatom community evaluations and as a valuable source of information when diatoms do not dominate communities. Dead diatoms varied from 5 to 53 % of all observed diatoms; and we were unable to relate the appearance of large numbers of dead diatoms with changes in another algal group.

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RAPID ASSESSMENT OF A BENTHIC COMMUNITY USING MOLECULAR TOOLS

Manoylov, Kalina M.¹, Marsh, Terrance² & Stevenson, R. J.¹

¹Zoology, Michigan State University, East Lansing, MI, USA; ²Microbiology & Molecular Genetics, Michigan State University, East Lansing, MI, USA

In ecology linking natural communities with information derived with molecular technology will permit realistic estimate of species biodiversity and ultimately will allow timely and accurate environmental assessment. As part of a larger project to develop a rapid, culture-independent technique for analyses of phototrophic communities (freshwater), we characterized a natural benthic community morphologically and then the same community was assessed with culture independent molecular analysis. We utilized the evolutionary-based taxonomic information encoded in organismal rRNA to phylogenetically profile the community. Both bacterial and eukaryotic populations were targeted with domain-specific primers for 16S and 18S rRNA genes. Bacterial sequences were analyzed through the Ribosomal Database Project using Classifier and 18S rRNA sequences through GenBank with Blast. 16S rRNA sequences yield 97 % similarity with *Nitzschia frustulum* (observed in the sample) and similarity to marine diatoms. In the prokaryotic assessment 23 % of the isolates were photosynthetic, while morphologically most of those cyanobacteria were not observed in the natural community. In the eukaryotic community 13 % of the sequences corresponded with the phototrophic algae observed morphologically in the sample. With the available primers the three domains, Bacteria, Archaea, and Eukaryotes were adequately quantified. Algal morphology and sequence information was successfully matched, based on the 16S rRNA genes. Pure algal cultures (as positive controls) are expected to increase our success rate of assessment of natural communities using 18S rRNA.

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MOVEMENT MODALITIES AS ADAPTIVE RESPONSE TO SALINITY CHANGES OF THE MUDFLAT DIATOM *CYLINDROTHECA CLOSTERIUM* (BACILLARIOPHYCEAE)

Apoya-Horton, Melba D.¹, Underwood, Graham J.² & Gretz, Michael R.¹

¹Biological Sciences, Michigan Technological University, Houghton, MI, USA; ²Department of Biological Sciences, University of Essex, Essex, United Kingdom

Cylindrotheca closterium (Ehrenberg) Reiman et Lewin is a raphid diatom widely distributed in mudflat assemblages. Video microscopy showed various movement modalities defined as, smooth and corkscrew gliding, pirouette, pivot, rock

and roll, rollover, and simultaneous pirouette and gliding. Z-axis projection analysis of images revealed a unique gliding motif with corkscrew motions which may have important ecological implications for *C. closterium* movement in muds. The general response to salinity alteration was a decrease in gliding movements with concomitant increase in other modalities listed above. Short-term responses to salinity change include dramatic alteration in modalities in hyposaline conditions and cessation of motility in extreme hypersaline environments. Modality changes were rapid and occurred within five seconds in response to hypersaline conditions. Hypo- or hyper-saline conditions resulted in decreased gliding speed in standard media. Five- and fifteen-day acclimation to salinity change resulted in progressive reduction in gliding movement and increased non-gliding modalities. The movement responses of *C. closterium* in response to salinity changes may form part of an adaptive strategy to survive in mudflats and could be useful as bioindicators of environmental changes.

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COMPARISON OF TWO ALGAL INDICES FOR USE IN BIOMONITORING OF SOUTHEASTERN OHIO STREAMS

Smucker, Nathan J.¹, Hollingsworth, Emily K.¹, Verb, Robert G.² & Vis, Morgan L.¹

¹Environmental and Plant Biology, Ohio University, Athens, OH, USA; ²Biological & Allied Health Sciences, Ohio Northern University, Ada, OH, 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 the 43 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 ($r=0.96$, $p<0.01$). We suspect the weak correlation of all sites was driven by the strong correlation of reference sites because there was no significant relationship ($r=0.22$, $p=0.17$) among non-reference sites. 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.

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MORPHOLOGY AND DISTRIBUTION OF *THALASSIOSIRA LACUSTRIS* (GRUNOW) HASLE: AN EXOTIC DIATOM IN SOUTHEASTERN OHIO STREAMS

Smucker, Nathan J.¹, Edlund, Mark B.² & Vis, Morgan L.¹

¹Environmental and Plant Biology, Ohio University, Athens, OH, USA; ²St. Croix Watershed Research Station, Science Museum of Minnesota, Marine on St. Croix, MN, USA

Thalassiosira lacustris (Grunow) Hasle has been reported primarily in the phytoplankton from marine coastal regions and large rivers around the world. Observations of *T. lacustris* from inland waters of North America have been rarely made, but published accounts report its distribution being confined to Lake Erie where introduction from Europe or Asia in the 1970s by ship ballast water is suspected. During the summer of 2005, periphyton samples were collected from 43 wadeable streams throughout the Unglaciated Western Allegheny Plateau of southeastern Ohio for the purpose of assessing water quality. *Thalassiosira lacustris* was found in five samples collected strictly from epilithic habitats in riffles; one with relatively high abundance (6% per 500 valves) and four with $\leq 1\%$ per 500 valves. All five sites were within 20 miles of the Ohio River, but were from four watersheds, in three different USEPA Level IV ecoregions. Drainage areas of four sites ranged from 11-68.4 mi² and 200 mi² for the fifth. Scanning electron and light microscopy were used to observe morphological features. Observations were fairly similar to published accounts of *T. lacustris*; however, inconsistencies in the morphology of girdle band structure, occluded processes, marginal fultoportulae, and rimoportulae were noted. These variations may lead to the determination of a new variety of *T. lacustris* because two morphotypes, distinguished in the SEM, appear to be present within the same sample. Valve diameter varied from 11-34 μm , which extends previously reported size ranges (17-55 μm ; 20-75 μm). As valve diameter decreased, the number of

central fultoportulae decreased. Continued sampling in 2006 will provide more data on the distribution, environmental response, and seasonal occurrence of *T. lacustris* in southeastern Ohio.

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A PHYCOMATE PRASINOPHYTE FROM PUGET SOUND, WASHINGTON, USA

Kodner, Robin B.¹ & Helm, Rebecca²

¹*Organismic and Evolutionary Biology, Harvard University, Cambridge, MA, USA;* ²*Eckerd College, St. Petersburg, FL, USA*

Prasinophytes are a group of related early divergent lineages green algae. This group is typically the only green algae abundant in the phytoplankton of most marine ecosystems today. Three genera, belonging to the most basal lineage within the prasinophytes, produce a large resistant cyst called a phycoma as part of their life cycle. Little is known about the formation of these cysts and reports of their appearance are limited in the literature. It appears they are a seasonal phenomenon, and are often abundant when found. These cysts are of interest because of their striking morphological and ultrastructural resemblance to many microfossils in the paleozoic and some as old as 1.6 Ga. Here we report on a monotypic population of phycomate prasinophytes collected in the waters of Puget Sound, Washington. This species, belonging to the genus *Halosphaera*, was collected from January to April, 2005. Though recognized in this area by others back into the 1970s, there are no published reports of this population in the literature. We have characterized this group with LM, SEM, TEM, and time lapse video of development of the phycoma. In addition, we have used the 18s ribosomal gene to place the phycoma within a phylogeny of flagellates from known phycomate producing groups.

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ALGAE FROM CRYPTOGAMIC CRUSTS, SANTA FE, NEW MEXICO

Wallace, Stacey L., Santiago, Jonathan & Mosto, Patricia

Biology, Rowan University, Glassboro, NJ, USA

Cryptogamic crusts are common in desert and arid regions of the western United States. These dark, lumpy communities consist of cyanobacteria, eukaryotic algae, lichens, mosses, and fungi. Algae from 10 crusts collected from Santa Fe National Forest in New Mexico were isolated. Algae were grown in liquid media, and transferred to agar plates for isolation and identification. Monocultures were transferred back to liquid for DNA analysis. Genomic DNA protocols were developed by modifying Qiagen Dneasy Plant DNA Isolation Mini Kit protocols. Preparation of optimal DNA samples for sequencing and species comparison is underway. Morphological identifications will be corroborated with the DNA findings. To date, 106 isolates were found, 33 identified to genus and 7 to species. Further isolation and identification will be carried out for the next two years. Furthermore, cryptogamic crusts collected from the Southern New Jersey Pine Barrens will be isolated, identified, and compared with the Santa Fe crusts' algae.

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USING MACHINE LEARNING ENVIRONMENTS TO EXTRACT TAXONOMIC INFORMATION FROM TEXT: AN EXAMPLE FROM PRINT AND DIGITAL TEXTS ON ALGAE

McCourt, Richard¹, Cui, Hong², Monique, Feist³ & Guiry, Michael⁴

¹*Botany, Academy of Natural Sciences, Philadelphia, PA, USA;* ²*University of Western Ontario, London, ON, Canada;*

³*University of Montpellier, Montpellier, France;* ⁴*National University of Galway, Galway, Ireland*

Taxonomic descriptions are a vital part of the systematic literature. Each one is the distilled set of descriptive terms about a taxon's distinguishing characters. These descriptions hold their value because new systematic works must refer to the original descriptions and subsequent revisions. Accessing the information in taxonomic works poses interesting logistical as well as intellectual challenges. Many print descriptions were published in rare or difficult to find publications, and even for electronically accessible information, the volume of data is enormous. We report here on a method involving machine learning in which a computer is used to automatically structure data from text descriptions and compile them into an online database (using open source GreenStone Digital Library software) that is fully searchable using text strings (e.g., taxon names, morphology, etc.). We used MARTT (MARK-upper for Taxonomic Treatments), a machine learning environment for marking up formal morphological descriptions with XML (extensible Markup Language). In one mode, MARTT enables a human user to annotate morphological descriptions with XML tags (e.g., morphology, name, etc.) to be used as training examples for computer learning algorithms. MARTT then uses an XML schema and the training examples to automatically mark up descriptions. In a different mode, MARTT tries to derive names of organs and other

concepts from morphological descriptions automatically therefore eliminates the need of hand prepared training examples. We used MARTT to process descriptions of several dozen genera of fossil and extant charophytes from a published treatise (University of Kansas) and 4,000 genus descriptions from AlgaeBase. MARTT produced a structured, searchable database viewable with a web browser. These databases can be used to assist in taxonomic identification, monographic research, and capture of information from older, rare or out-of-print works.

116 MORPHOLOGICAL AND ECOLOGICAL VARIATION WITHIN *ACHNANTHIDIUM MINUTISSIMUM* (BACILLARIOPHYTA) SPECIES COMPLEX

Potapova, Marina¹ & Hamilton, Paul²

¹Academy of Natural Sciences, Philadelphia, PA, USA; ²Canadian Museum of Nature, Ottawa, ON, Canada

Variation of frustular morphology within the *Achnantheidium minutissimum* (Bacillariophyta) species complex was studied in type populations of 12 described taxa and in 30 recent North American samples. The SEM observations in this study and other publications showed that ultrastructural characters do not discriminate between taxa within the *A. minutissimum* complex. Therefore, an attempt was made to use other characters, such as valve shape and striation pattern to investigate morphology within this species complex. The sliding landmarks method was used to obtain valve shape descriptors. These shape variables were combined with conventional morphological characters in multivariate analyses. From this analytical approach it was shown that some types (*A. macrocephalum*, *A. straubianum*, *A. affine*, *A. saprophilum*) are morphologically distinct, while others, such as *A. minutissimum*, *A. microcephalum*, *A. lineare*, *A. jackii*, and “*Achnanthes minutissima* var. *cryptocephala*” are more difficult to differentiate. Similarity between type populations of 12 historic taxa did not correspond to their taxonomic hierarchy in contemporary diatom floras. Morphometric analyses of a dataset of 728 specimens from North American rivers revealed six morphological clusters, although it was impossible to draw clear boundaries between them. These six morphological groups identified within the North American dataset differed significantly in their ecological characteristics, and can be recommended as indicators of water quality. Application of the discriminant functions based on shape variables and striation pattern showed that North American specimens could be more consistently classified into six groups identified in our analysis than into historical taxa. Therefore, our bioassessments are expected to be more informative if the identifications of diatoms from notoriously difficult species complexes were based on careful studies of local diatom floras rather than on the common practice of “fitting” specimens into historical morphospecies.

117 A STUDY OF FRESHWATER SPECIES OF *SYNEDRA* EHRENBERG (BACILLARIOPHYTA) FROM NORTH AMERICAN STREAMS

Morales, Eduardo, Hamsher, Sarah, Hagan, Erin & Mellott, Daniel

Patrick Center for Environmental Research, Academy of Natural Sciences, Philadelphia, PA, USA

The genus *Synedra* Ehrenberg includes species with primarily freshwater distribution, many of them considered cosmopolitan and highly variable in their morphologic features. The nomenclatural history of the genus is very confusing 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 a broad characterization is often lacking. We 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). Twenty six different morphotypes were isolated using both light microscopy (LM) and scanning electron microscopy (SEM). Many of the morphotypes appear to have restricted distributions as shown by preliminary ecological/geographical analyses. Unfortunately, none of the studied populations can be associated with “*ulna*” since the identity of this taxon remains unresolved until type material is found or a lectotype/neotype is erected. Meanwhile, it is recommended that the morphotypes presented here, as well as any other morphological variation, are kept separate during ecological studies since these variants might be indicators of different ecological conditions.

118 OOMYCOTA: THE SYSTEMATICS OF NONPHOTOSYNTHETIC, COENOCYTTIC STRAMENOPILES

Bailey, Craig, Padgett, David E., Peterson, Russ, Webster, LaShawnda C. & Henry, Anna C.

Biology and Marine Biology and Center for Marine Science, UNC-Wilmington, Wilmington, NC, USA

The Phylum Oomycota includes non-photosynthetic stramenopiles vegetatively composed of coenocytic siphons. Taxa are saprobic detritivores or facultative plant or animal pathogens, some of which are of great economic importance. Genera have traditionally been defined on the basis of sporangial discharge (zoospore release and behavior) and sporangial renewal patterns. The morphology, development, and position of sexual structures (antheridia and oogonia) have also been emphasized in taxonomic treatments. Out-crossing is, however, rarely observed and is replaced by self-fertilization or asexual reproduction only. We have re-investigated the phylogeny of the Oomycota using morphological data and DNA sequence data from multiple nuclear or mitochondrial loci. Results indicate that there is very little congruence between DNA-based phylogenies and any taxonomic scheme based on morphology. Curiously, we find that features associated with asexual reproduction are more reliable phylogenetic markers than are those derived from examination of sexual structures. Significantly, we have found that some genera are not monophyletic and this group includes a number of the most damaging crop pathogens. Some isolates form clades that, when compared to better known and equally well-characterized taxa, obviously should be recognized at the rank of genus. Other single isolates and clades containing but a few isolates occupy unsupported positions in our tree(s) and probably warrant recognition as well, although at what rank is unclear. Although asexual morphological features provide a useful, but not perfect, guide for recognizing some genera we conclude that the recognition of any species on the basis of morphology alone is - literally and practically - impossible. Truly useful species concepts for oomycetes will, in the future, have to be based on a combination of morphological and 'molecular' characters. Our results imply that the number of recognized species in some genera should be reduced, whereas in other genera the number of species recognized will likely increase.

119 DIVERGENCE ORDER OF CHLOROPHYTE GREEN ALGAL LINEAGES AS INFERRED FROM THE CHLOROPLAST AND MITOCHONDRIAL GENOMES

Pombert, Jean-François, Bélanger, Anne-Sophie, De Cambiaire, Jean-Charles, Gagnon, Jonathan, Otis, Christian, Lemieux, Claude & Turmel, Monique

Biochimie et Microbiologie, Université Laval, Québec, QC, Canada

The green algae are currently divided into five classes: the Charophyceae, Prasinophyceae, Ulvophyceae, Trebouxiophyceae and Chlorophyceae. Members of the Charophyceae are the closest relatives of land plants and belong to the Streptophyta lineage, whereas those of the four remaining classes belong to the sister lineage Chlorophyta. In the latter phylum, the prasinophytes form a non-monophyletic assemblage that predates the divergence of the Ulvophyceae, Trebouxiophyceae and Chlorophyceae (UTC); however, the branching order of the UTC lineages remains uncertain. To unravel the relationships among these three chlorophyte lineages, our group has adopted a comparative genomics approach based on organelle genomes. We have previously reported that comparative analyses of structural features from the chloroplast and mitochondrial genomes as well as phylogenetic analyses of protein sequences encoded by the mitochondrial genome are consistent with the idea that the Trebouxiophyceae represents the most basal lineage of the UTC clade. In contrast, we found that phylogenetic analyses of protein sequences encoded by the chloroplast genome support the notion that the Chlorophyceae is the most basal divergence of the UTC clade. To resolve this conflict, we have undertaken phylogenetic analyses of protein and gene sequences encoded by the mitochondrial and chloroplast genomes from a broader selection of taxa (including three trebouxiophytes, two ulvophytes and three chlorophycean green algae) using recently developed methods to detect phylogenetic inconsistencies in large datasets. Overall, the results of our study provide robust support for the basal placement of the Trebouxiophyceae within the UTC clade.

120 AN EVOLUTIONARY NOVELTY FROM THE SUBAERIAL ALGAL FLORA OF THE HAWAIIAN ISLANDS: SPONGIOCHRYSIS HAWAIIENSIS (CLADOPHORALES, ULVOPHYCEAE)

Rindi, Fabio¹, Lopez-Bautista, Juan M.¹, Sherwood, Alison R.² & Guiry, Michael D.³

¹Biological Sciences, The University of Alabama, Tuscaloosa, AL, USA; ²Botany, University of Hawaii, Honolulu, HI, USA; ³Martin Ryan Institute, National University of Ireland, Galway, Ireland

Despite records dating back to 1876, current knowledge of the subaerial algal flora of the Hawaiian Islands is still very rudimentary. In the course of a recent survey, an undescribed alga was discovered forming bright golden coatings on the bark of many trees on several beaches along the windward coast of O'ahu. Because of its habit, it was initially confused with members of the common subaerial genus *Trentepohlia*. However, a combination of morphological features and molecular data supports the establishment of a new genus and species, *Spongiochrysis hawaiiensis*. Cells are rounded or

oval, 10-20 µm in diameter, with a single axial, stellate chloroplast. The only known reproduction is a specialized form of autosporulation, previously known only in the trebouxiophycean genera *Marvania* and *Stichococcus*, in which a budding-like division of the mother cell produces daughter cells of different sizes. Phylogenetic analyses, including the complete 18S rRNA sequence of two separate populations show that this entity allies with the Cladophorales/Siphonocladales lineage of the class Ulvophyceae and is positioned with good support in the so-called “*Aegagropila* group”. This research is partially funded by an NSF grant (DEB 0542924) to JLB.

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PHYLOGENY OF THE EUGLENALES INFERRED FROM CHLOROPLAST 23S rDNA

Shin, Woongghi, Son, Mi-Sun & Jo, Bok-Yeon

Department of Biology, Chungnam National University, Daejeon, South Korea

The phylogeny of the Euglenales was estimated by maximum likelihood, maximum parsimony, Distance, and Bayesian methods using plastid 23 rDNA data. Bayesian analysis suggested that the Euglenales is divided into nine clades: 1) a *Phacus* clade, 2) a *Lepocinclis* clade, 3) a *Trachelomonas* clade, 4) a *Colacium* clade, 5) a *Strombomonas* clade, 6) a *Cryptoglena* clade, 7) a *Monomorphina* clade, and 8) two *Euglena* clades. However, our plastid 23S rDNA data and previous data (nuclear 18S rDNA and 26S rDNA data) disagreed regarding genus- and species-level relationships within the Euglenales. The placement of the genera, *Monomorphina*, *Cryptoglena*, *Strombomonas*, *Colacium*, *Trachelomonas*, was incongruent, but other genera, *Euglena*, *Phacus*, and *Lepocinclis* were congruent with previous studies. The *Phacus* and *Lepocinclis* were a basal monophyletic assemblage while the genus *Euglena* was polyphyletic and diverged into two independent clades (*Euglena* clade and *Anabeana* clade). The analysis also supported that *Trachelomonas*, *Colacium*, *Strombomonas*, *Cryptoglena*, and *Monomorphina* are monophyletic. The loricate genera *Trachelomonas* and *Strombomonas* formed two well-supported clades, but not a monophyletic assemblage. At species-level relationships within the genus *Euglena*, *E. deses* and *E. mutabilis* formed a well supported subclade and placed at most basal of the *Euglena* clade. This result suggested that both species be retained in the subgenus *Calliglena*.

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COLOR ATLAS OF PHOTOSYNTHETIC EUGLENOIDS

Ciugulea, Ionel & Triemer, Richard E.

Plant Biology, Michigan State University, East Lansing, MI, USA

Euglenoids are commonly found in eutrophic ponds throughout the world. Most of the photosynthetic forms can easily be keyed to genus. However, species level descriptions are often based on original line drawings which frequently lack detail and vary from author to author. Therefore, there is a need for an easy way to clearly visualize the diversity within euglenoids and accurately identify taxa to the species level. With the advent of modern digital microscopy, it is no longer difficult to obtain high resolution color images of taxa. We are assembling images of the common representative taxa from each photosynthetic genus into a Color Atlas of Photosynthetic Euglenoids. The Atlas will have full color plates of approximately 150 taxa. Information about taxon names will be up to date and supported by the most recent molecular and morphological studies. The Atlas will contain an introductory section describing the phylogeny of euglenoids, the cellular organization, the specific morphological features used in identification and information on the habitats of euglenoids and instructions on how to collect them. Additionally, a Glossary of common terms and a Bibliography of the literature will be included. The Atlas is designed to be useful not only for phycologists, but for biology students, ecologists, naturalists and to those who monitor water quality.

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ZOOCHLORELLAE SYMBIONTS OF ANTHOPLEURA FORM A DISTINCT MONOPHYLETIC TAXON REGARDLESS OF HOST SPECIES OR GEOGRAPHIC LOCATION

Letsch, Molly R.¹, Lewis, Louise A.¹ & Muller-Parker, Gisèle T.²

¹*Ecology and Evolutionary Biology, University of Connecticut, Storrs, CT, USA;* ²*The Department of Biology, Western Washington University, Bellingham, WA, USA*

In the North Pacific intertidal the sea anemones *Anthopleura xanthogrammica* and *A. elegantissima* can each form an intracellular symbiosis with a unicellular green alga (Chlorophyta). Previous studies of this symbiont system have focused on ecological questions dealing with the influence of light and temperature on carbon allocation and symbiont distribution. A recent phylogenetic analysis of single sequences from the nuclear 18S rDNA and the plastid encoded *rbcl*

gene region placed this symbiont in the Trebouxiophyceae. Though called “zoochlorellae,” this symbiont is not a true *Chlorella* (sensu Huss et al. 1999) but is more closely related to *Trebouxia* and *Coccomyxa* (Lewis and Muller-Parker 2004). In order to determine if this symbiont is a new taxon, we have gathered morphological and molecular data from samples of *A. xanthogrammica* and *A. elegantissima* tissue containing green symbionts from their known range along the North Pacific coast, including Alaska, Oregon and Washington. Anemones of different sizes located in distinct microhabitats (sun, shade) were sampled from sheltered bays and exposed coastlines. The symbiont cells we observed using TEM were small, under 10 microns in diameter, non-motile, and reproduce by binary fission. As expected, the morphology visible in these TEMs was not sufficient to classify zoochlorellae as a distinct taxonomic group. Our molecular analysis of 18S rDNA shows monophyly of all zoochlorellae isolated directly from anemone samples, regardless of host species or geographic location. A close relationship to *Hemichloris* and *Elliptochloris* (and several lichen photobionts such as *Coccomyxa*) is also indicated. The 18S sequences of the zoochlorellae, however, all share a short (4 bp) insertion at position 1659 that is absent from all other aligned sequences. Phylogenetic analysis of the rbcL data support the results obtained using 18S rDNA. Therefore, we propose that the zoochlorellae of *A. xanthogrammica* and *A. elegantissima* are a distinct taxon.

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AN UNUSUAL FAT ALARIA FOUND NEAR JUNEAU, ALASKA

Stekoll, Michael S.¹ & Hansen, Gayle I.²

¹Department of Natural Sciences, University of Alaska, Juneau, AK, USA; ²Department of Botany and Plant Pathology, Oregon State University, Newport, OR, USA

Species of the genus *Alaria* (Laminariales) dominate the lower intertidal and upper subtidal zones of many parts of Alaska. More than 12 species of *Alaria* have been reported from Alaska, but many of these still need molecular clarification. Our study involves an unusual *Alaria* species that occurs only in the semi-sheltered areas of southeast Alaska. Its known range is very narrow, restricted to just a few kilometers of the coastline near Juneau. The species is an annual. When it first develops in the spring, it appears to be a typical young *Alaria* with a mid-ribbed vegetative blade and a terete trunk (stipe + rachis) that is up to 8 cm tall. However, as the alga matures and the sporophylls begin to develop, an unusual phenomenon occurs. The trunk expands laterally to form a flattened disk up to 3 cm wide that is narrowed at the holdfast. The sporophylls begin their development near the disk apex as small 1-2 ranked ligulate projections. The projections then rapidly expand, forming large thin blades that vary in shape from broadly spatulate (up to 7 x 25 cm) to broadly obovate (up to 12 x 8 cm), all with narrowly attenuated bases. The mature sporophylls are spaced out along the upper third of the disk margin with the youngest occurring apically, indicating the continued growth of the apical disk margin. Sori develop basally and cover the lower one-third to one-half of each sporophyll. Zoospores are released from late spring into the summer and the plants disintegrate by fall. We have just begun to speculate on the relationship of this plant to other *Alaria* species in Alaska, and we are currently searching for a molecular biologist to join us on the project.

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SPECIES AND GENERA OF THE ORDER LAMINARIALES FROM RUSSIAN PACIFIC COASTS THAT ARE UNFAMILIAR TO WESTERN PHYCOLOGISTS

Selivanova, Olga¹, Zhigadlova, Galina¹ & Hansen, Gayle I.²

¹Kamchatka Branch, Pacific Institute of Geography, Petropavlovsk-Kamchatskii, Russian Federation; ²Botany and Plant Pathology, Oregon State University, Newport, OR, USA

Members of the Laminariales are widespread in cold temperate areas of the North Pacific on both Asian and American coasts. Some species of *Laminaria* are recorded only from Russia: *L. gurjanovae* A. Zinova (Zinova, 1964; 1969), *L. appressirhiza* Ju. Petr. et V. Vozzh. and *L. inclinorhiza* Ju. Petr. et V. Vozzh. (Petrov and Vozzhinskaja, 1970), *L. multiplicata* Ju. Petr. et M. Suchov. (Petrov and Suchovejeva, 1976). There are also some species of *Laminaria* with forms described by Russian phycologists: e.g. *L. angustata* Kjellman f. *sibirica* Ju. Petr. et M. Suchov. (Petrov and Suchovejeva, 1972), *L. cichorioides* Miyabe f. *sinuicola* Ju. Petr. (Petrov, 1972), *L. gurjanovae* A. Zinova f. *lanciformis* Ju. Petr. (Petrov, 1972). These species and forms can be considered endemic to Russian Pacific coasts. In fact, they seem to be unknown to the overwhelming majority of phycologists outside Russia. The same may be said about some species of other genera in the Laminariales described by Russian scientists: *Phylariella ochotensis* Ju. Petr. et V. Vozzh. (Petrov and Vozzhinskaja, 1966), *Costularia kurilensis* Ju. Petr. et I. Guss. (Gussarova and Petrov, 1970), *Feditia simuschirensis* Ju. Petr. et I. Guss. (Gussarova and Petrov, 1972), and *Tauya basicrassa* Kloczc. et Krupn. (Klochkova and Krupnova, 2004). However, the generic status of *Tauya* is questionable. It resembles *Laminaria* in habit, and the peculiar morphology of the

lamina may represent an anomalous growth form of this genus. *L. philippinensis* Ju. Petr. et M. Suchov. (Petrov *et al.*, 1973) was described far from Russia in the Philippine Sea, but it has also been overlooked by western scientists. The status of these taxa and their phylogenetic relations with other members of the Laminariales all need clarification.

126 MOLECULAR CHARACTERIZATION OF THE "COTTONII" FORM OF *FUCUS* IN THE NORTHEASTERN PACIFIC VERSUS THE ATLANTIC

Serrão, Ester¹, Vliet, Mirjam¹, Hansen, Gayle I.², Maggs, Christine³ & Pearson, Gareth¹

¹Center of Marine Sciences, Universidade do Algarve, Gambelas, Portugal; ²Department of Botany and Plant Pathology, Oregon State University, Newport, OR, USA; ³School of Biological Sciences, Queen's University Belfast, Belfast, United Kingdom

Along the west coast of North America, three species of *Fucus* are reported to occur: *F. gardneri* Silva, *F. spiralis* Linnaeus, and the controversial *F. cottonii* Wynne & Magne. Our study investigates the identity of *F. cottonii* in this area and compares it with isolates from the Northeastern Atlantic. The thalli from both areas vegetatively resemble one another, lacking midribs, and they occur in similar salt marsh habitats. The dwarf *Fucus* grows in mats so high in the intertidal zone that it is often intermixed with vascular plants and mosses. The Pacific entity is unattached and/or embedded in mud and reproduces mainly by fragmentation. However, it also reproduces sexually in some populations. These thalli become fertile in the winter. Ellipsoidal and/or pointed receptacles develop at the tips of the axes and form bisexual conceptacles with 8 eggs/oogonium as is typical of the genus. After reproduction, the receptacles drop off the plants and are generally undetectable by late spring. To date, *F. cottonii* has been found in the northeastern Pacific from southcentral Alaska to southern Oregon. Our molecular study targets sites in Oregon and in Ireland. In Oregon, 25 samples of each form of *Fucus* occurring in two estuaries, South Slough and Yaquina Bay, were examined for 5 microsatellite loci. The data revealed that *F. cottonii* in this region is a differentiated form derived from *F. gardneri* with common alleles at all loci but one that appears to be diagnostic for the form. *F. spiralis* was genetically distinct, but it was often morphologically very similar to *F. gardneri*. The Oregon forms are being compared with *F. cottonii*, *F. spiralis* and *F. vesiculosus* in Ireland, the type locality of *F. cottonii*. Samples of "cottonii" forms of fucoids from a site in northwestern Ireland revealed a mixture of both *Pelvetia canaliculata* and a differentiated form of *Fucus* with unique alleles not found in nearby populations of *F. vesiculosus* or *F. spiralis*.

127 PHYLOGENETIC STUDIES ON THE GENUS *NOSTOC* (CYANOBACTERIA)

Han, Danxiang & Hu, Zhengyu

Institute of hydrobiology, the Chinese Academy of Sciences, Wuhan, China

Nostoc is a genus of non-branching filamentous heterocytous cyanobacteria that is widely distributed in both terrestrial and aquatic ecosystems. Much of the success of *Nostoc* in terrestrial habitats is related to its ability to remain desiccated for months or years and to recover metabolic activity rapidly after rehydration. We reconstructed the phylogeny of *Nostoc*, on the basis of 16S rRNA sequences. The results indicate that the phylogenetic analysis on *Nostoc* is sensitive to search algorithm and taxa sample bias. The statistic tests support the maximum-likelihood tree (ML) reflect the phylogenetic relation for the data set better than alternative topologies obtained by other search algorithms. The ML trees show that the genus *Nostoc* is not monophyletic. One monophyletic *Nostoc* spp. clade is defined as the genus *Nostoc* according to the phylogeny and identity of 16S rRNA sequences. However, the morphological criteria, hormogonia formation and sheath, cannot be used as taxonomic criteria to distinguish it from other groups. The stabilities of 16S rRNAs secondary structures, indicated by free energy change of folding, were compared among *Nostoc* and other related species. The results suggest that 16S rRNA secondary structures of the desiccation-tolerant *Nostoc* strains are more stable than that of planktonic species belonging to Nostocaceae. The stabilizing mutations were divided into two categories, those causing GC to replace other types of base pairs in stems and those causing extension of stems. By mapping stabilizing mutations onto the *Nostoc* phylogenetic tree based on 16S rRNA gene, it was shown that most of stabilizing mutations had evolved during adaptive radiation among *Nostoc* spp.. The evolution of 16S rRNA along the *Nostoc* lineage is suggested to be selectively advantageous under the desiccation stress. In addition, we performed a case study in *Nostoc* to evaluate *rpoC1*, *hetR*, *rbcLX* and 16S rRNA- tRNAIle - tRNAAla-23S rRNA ITS as phylogenetic markers. The results indicated that the gene trees of these loci are not congruent with the species phylogeny based on 16S rRNA gene. The mechanisms contributing to the incongruence include randomized variation, recombination and positive selection.

PHYLOGENETIC RELATIONSHIPS OF THE FUCALES (PHAEOPHYCEAE) BASED ON THE PHOTOSYSTEM I CODING PSA A SEQUENCES

Cho, Ga Youn¹, Rousseau, Florence², de Reviers, Bruno² & Boo, Sung Min¹

¹Department of Biology, Chungnam National University, Daejeon, South Korea; ²Département Systématique et Evolution, Muséum National d'Histoire Naturelle, Paris, France

Fucalean brown algae are ecologically important for maintaining intertidal to subtidal ecosystems and are currently a subject for DNA phylogenies. We analyzed the photosystem I coding psaA gene (1488 base pairs) from 26 taxa in all families of the Fucales including *Nemoderma tingitanum* and *Microzonia velutina* as outgroup species. A total of 41 taxa including published sequences from three fucalean and 13 brown algae were used for phylogenetic analyses. The psaA phylogenies confirmed previous ideas, based on previous studies using morphology and nuclear ribosomal genes, suggesting that the fucalean algae are monophyletic, including the Durvillaeaceae and Notheiaceae. However, in all analyses of the psaA data, the Notheiaceae, endemic to Australasia, occupied a basal position within the order. All families except the Cystoseiraceae are monophyletic. The psaA data together with previous nuclear rDNA data and autapomorphic morphological characters strongly support that the genera *Bifurcariopsis* and *Xiphophora* should be separated from the Cystoseiraceae and the Fucaceae, respectively. Two new families, Bifurcariopsidaceae and Xiphophoraceae, are proposed to accommodate each of the genera. The psaA data concur with the morphological and biogeographical hypotheses that fucalean algae might have originated from Australasian waters and moved to northern hemisphere. The present results indicate that the psaA region is a new tool for a better understanding of phylogenetic relationships within fucalean algae.

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THE LIFE HISTORY AND MOLECULAR PHYLOGENY OF *KUETZINGIELLA BATTERSII* (ECTOCARPALES, PHAEOPHYCEAE)

Ling, Huai Yian¹, Cho, Ga Youn¹, Müller, Dieter G.² & Boo, Sung Min¹

¹Biology, Chungnam National University, Daejeon, South Korea; ²Biology, Konstanz University, Konstanz, Germany

Kuetzingiella battersii is a very tiny filamentous brown alga that is distributed in the Atlantic, Mediterranean, East Africa and Indian Ocean. It has been classified in the family Chordariaceae on the basis of morphology. In order to recheck the classification, we studied life history and molecular phylogeny of the species. The life history in culture shows that both sporophytes and gametophytes are macroscopic. Each cell includes several discoid plastids with one pyrenoid per plastid. However, in the Chordariaceae, sporophytes are macroscopic, and gametophytes are microscopic, and each plastid includes several pyrenoids. We analyzed rbcL and psaA in plastids, cox3 in mitochondria, and ITS2 in nucleus. Topology of all four gene trees were identical in the position of *Kuetzingiella* in the Acinetosporaceae and its sister relations with the clade of *Geminocarpus* and *Pylaiella*. The molecular results support that life history and pyrenoids are important characters for phylogeny of the species. As *Kuetzingiella* is very similar to the Acinetosporaceae in life history and the number of pyrenoids, we are carefully proposing to move *Kuetzingiella* from the Chordariaceae to the Acinetosporaceae.

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IDENTIFICATION OF CONSERVED PLASTID REGIONS THROUGH COMPARATIVE GENOMICS

Presting, Gernot

Molecular Biosciences and Bioengineering, University of Hawaii, Honolulu, HI, USA

Detailed computer-assisted comparison of 37 complete plastid genomes has led to the identification of all highly conserved regions of this organellar genome. These regions are of interest because they are indicative of strong selection pressure. The majority of conserved sites are located in the inverted repeat (IR) region, but several sites in the single copy region (predominantly in tRNA and psb genes) are conserved among all higher plants. Two oligonucleotides, separated by 362 nucleotides, are found in all cyanobacterial, red, brown and green algal, as well as diatom, euglenid, apicomplexan and land plant GenBank accessions that have been examined to date. Analysis of 160 GenBank accessions illustrates that the resulting amplicon discriminates many algae at the species level. This marker should find application in the biodiversity assessment of algal lineages and lichens, as well as environmental sampling. More rapidly evolving regions of the plastid genome, also identified here, serve as a starting point to design and test useful markers for more narrowly defined lineages, including the more recently diverged angiosperms.

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THE IDENTITY OF TWO NEW CERAMIUM SPECIES (CERAMIACEAE, CERAMIALES) FROM WEST AND EAST FLORIDA AS INFERRED FROM MOLECULAR AND MORPHOLOGICAL DATA

Cho, Tae O.¹, Won, Boo Y.¹, Yates, Kim K.² & Fredericq, Suzanne¹

¹Biology, University of Louisiana at Lafayette, Lafayette, LA, USA; ²U.S. Geological Survey, 600 4th, street South, St. Petersburg, FL, USA

On the basis of comparative rbcL sequence data, and vegetative and tetrasporophytic morphology, two distinct *Ceramium* species are newly described from Florida, USA. *Ceramium* sp. nov. 1 grows epiphytically on *Thalassia testudinum*, is 2-3 cm long, and is characterized by branch apices of unequal length, incomplete cortication, 7 periaxial cells per axial cell, 5-6 acro- and basipetal cortical cell initials per periaxial cell, and tetrasporangia that are covered by cortical cells and restricted to adventitious branchlets; the species was collected in Brevard Co. (Atlantic FL) and in Santa Rosa Co. (Gulf of Mexico). *Ceramium* sp. nov. 2 is an epiphyte on *Digenea simplex*, is 0.5-0.8 cm long, has incurved branch apices, incomplete cortication, 4-5 periaxial cells per axial cell, 2 acropetal cortical cell initials per periaxial cell, 1-2 tetrasporangia cut off from single periaxial cells on the abaxial side; the species was collected from Miami (Atlantic FL) and Tampa Bay (Gulf of Mexico). These two new taxa will be compared morphologically to the other ten *Ceramium* species we recently collected from Florida.

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BIOGEOGRAPHY OF ALASKAN SEaweEDS

Lindstrom, Sandra

Department of Botany, University of British Columbia, Vancouver, BC, Canada

A recent survey of seaweed specimens collected in Alaska over the past two centuries, together with the application of molecular techniques to recent collections, has revealed a surprisingly diverse flora given the history of glaciation, large areas of unsuitable habitat, and otherwise harsh environmental conditions. The number of recognized species has increased from 376 in 1977 to about 550 today. Species show a variety of biogeographic patterns: species that occur primarily to the south and have their northern limit in Alaska, species that occur primarily to the west and have their eastern limit in Alaska, species that are primarily Atlantic but extend through the Arctic to Alaska, and a number of endemics and more localized patterns often involving disjunctions. These disjunctions, the occurrence of endemic species, patterns of genotype distributions, and the overall richness of the seaweed flora support the idea that marine refugia must have existed in Alaska during Pleistocene glaciations. Knowledge of seaweeds and their distributions is critical to identifying and understanding ecological and evolutionary processes in the region. Many contemporary as well as historical efforts are contributing to this understanding.

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WWW.SEaweEDSOFALASKA.COM—A PHOTO-RICH PORTAL TO THE TAXONOMY OF ALASKAN SEaweEDS AND THEIR HABITATS

Lindeberg, Mandy², Lindstrom, Sandra¹ & Saupe, Susan³

¹Department of Botany, University of British Columbia, Vancouver, BC, Canada; ²Auke Bay Laboratories, Alaska Fisheries Science Center NOAA/NMFS, Juneau, AK, USA; ³Cook Inlet Regional Citizens Advisory Council, Kenai, AK, USA

SeaweedsOfAlaska.com has been developed to complement and aid ongoing habitat mapping and research in the coastal areas of Alaska. The website provides a searchable taxonomic database linked to dynamic web pages. Imagery includes Alaskan seaweeds in their natural habitats, herbarium specimens, and photomicrographs. Baseline information covers taxonomic classification and geographic distribution. At present, 125 species commonly encountered in coastal Alaska are represented. More species will be added as the site is developed, and detailed descriptions for these species are being solicited. Additional site information includes maps, descriptions of the regions, and examples of coastal habitat classifications. Through multiple partnerships and sponsorship by the Cook Inlet Regional Citizens Advisory Council, this website will serve as a valuable resource for researchers studying the nearshore of Alaska and complement other online databases.

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THE BROADER IMPACTS OF ALGAE: ALGAE AS TEACHING TOOLS IN THE NATIONAL SCIENCE FOUNDATION GRADUATE TEACHING FELLOWS PROGRAM

Gower, Jessie¹, Jackson, Brenda², Masters, Alyce³, Muhlin, Jessica F.⁴ & Brawley, Susan H.⁴

¹Newburgh Elementary School, Newburgh, ME, USA; ²Viola Rand School, Bradley, ME, USA; ³Dr. Lewis S. Libby School, Milford, ME, USA; ⁴School of Marine Sciences, University of Maine, Orono, ME, USA

The algae are used extensively in science lessons through the University of Maine's National Science Foundation (USA) Graduate Teaching Fellows program. This program began in the US and at UMaine in 1999. NSF's primary goals are to support graduate research by outstanding science, math, and engineering students while, through an outreach component, improving K-12 science education. Algae provide versatile teaching tools because they are applicable to many subject areas and all grade levels. Elementary students learned to use microscopes while studying cell structure and diversity with a variety of freshwater and marine algae. Older students visited the rocky intertidal zone where they identified and quantified different marine algae and used such data to learn to graph. Students at all grade levels studied the application and uses of algal products in daily life. Students tasted a variety of sea vegetable products, prepared authentic Irish Moss pudding with *Chondrus crispus*, and participated in a sensory analysis of ice cream with and without carrageenan. In 2005, fifth graders participated in a doctoral research project that investigated population genetic structure of *Fucus vesiculosus* L. and nearshore circulation patterns around coastal promontories. Participation in an authentic study gave the students a keen appreciation of the research and its implications. These lessons and activities are examples of how to foster positive attitudes of K-12 students to science and the importance of algae (Supported by NSF DGE-0231642 and OCE-99043).

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PURIFICATION, CHARACTERIZATION, AND CDNA CLONING OF A NOVEL N-ACETYL-D-GLUCOSAMINE/ N-ACETYL-D-GALACTOSAMINE-BINDING LECTIN FROM THE GREEN ALGA *BRYOPSIS PLUMOSA*

Yoon, Kang-Sup¹, Lee, Key Pyoung² & Kim, Gwang Hoon¹

¹Department of Biology, Kongju National University, Kongju, South Korea; ²Department of Chemistry, Kongju National University, Kongju, South Korea

A novel lectin was isolated and purified from *Bryopsis plumosa* and named as BPL. This lectin showed specificity to N-acetyl-D-galactosamine as well as N-acetyl-D-glucosamine and agglutinated erythrocytes of all human blood type showing slight preference to the O blood group. SDS-PAGE and MALDI-TOF mass spectrometry data showed that BPL was a monomeric protein with molecular weight of ~12 kDa. BPL was a non-glycoprotein with pI values of ~ 7.0. It is stable in high temperature up to 85 degree and exhibited optimum activity in pH 4 -11. A sugar N-acetyl-D-galactosamine was the most potent inhibitor of BPL hemagglutinating activity (minimal inhibitory concentration = 62.5 mM) followed by N-acetyl-D-glucosamine, 125 mM. The N-terminal and internal amino acid sequences of the lectin were determined by Edman degradation and enzymatic digestion, which showed no sequence homology with any other reported proteins. The full sequence of the cDNA encoding the lectin was obtained from PCR using the cDNA library and first-stranded cDNA and the degenerated primer designed from the internal peptide amino acid sequences of purified BPL lectin. The N-terminal and internal amino acid sequence was verified by the full sequence of cDNA cloned. The size of the cDNA was 622 bp and containing single ORFs encoding the lectin precursor. The homology analysis of the full gene sequence of BPL indicated that this protein belong to a new class of lectin. This lectin showed same sugar specificity to bryohealin, a previously reported lectin in this plant. Therefore, BPL may be involved in the aggregation of cell organelles during protoplast reformation from extruded cytoplasm of *B. plumosa*.

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IRON AND THE COMPLEX STORY OF REACTIVE OXYGEN SPECIES PRODUCTION BY *HETEROSIGMA AKASHIWO*

Overman, Richard L., Lakeman, Michael B. & Cattolico, Rose Ann

Biology, University of Washington, Seattle, WA, USA

The marine alga *Heterosigma akashiwo* forms harmful blooms that kill fish in coastal waters globally. Iron often limits the growth of this alga. A proposed mechanism for the toxic effect of *Heterosigma* is the production of reactive oxygen species (ROS) that attack fish gill tissue. The production of ROS may be an adaptive solution for increasing the

availability of organically trapped iron in the environment. ROS is hypothesized to free iron from chelates, increasing its solubility, potentially making it available for uptake by *Heterosigma* cells. Previous research in our laboratory has produced low-iron tolerant mutants that were selected through prolonged iron limitation. These mutants provide a good system for investigating the relationship between ROS production and iron availability. Low-iron selected mutants grown in low-iron media, and controls grown in replete media were compared in our study. Concentrations of hydrogen peroxide and superoxide, two types of ROS, were monitored during culture growth, using high-throughput, plate based, fluorescent Amplex Red and luminescent MCLA assays respectively. Data show that, relative to replete controls, low-iron selected cultures had consistently reduced hydrogen peroxide concentrations, but higher superoxide concentrations. Net positive levels of hydrogen peroxide (relative to media blanks) were observed in both treatments only at high cell densities. Net positive superoxide concentrations were only seen in the low-iron treatment at low cell densities. All other data reveal ROS levels in cultures to be lower than sterile media blanks, suggesting degradation of ROS in the presence of *Heterosigma*. By spiking cell cultures with ROS, we have confirmed that *Heterosigma* is capable of degradation of ROS in its environment. We hypothesize that this degradation is enzymatic, and will present data testing that hypothesis. It also appears that abiotic factors such as light exposure and the presence of metals (e.g. iron) also affect ROS concentration and under certain conditions have a greater impact than biotic factors.

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INORGANIC CARBON ACQUISITION IN THE CHRYSOPHYTE ALGAE

Bhatti, Shabana & Colman, Brian

Biology, York University, Toronto, ON, Canada

Many algae have the capacity to take up CO₂ and HCO₃⁻ by active transport and accumulate dissolved inorganic carbon intracellularly. This process is called a 'CO₂ concentrating mechanism' (CCM) in which CO₂ is concentrated in the site of the primary carboxylating enzyme Rubisco thereby increasing photosynthesis and reducing the rate of photorespiration. Some algae appear to lack CCMs and rely on diffusive uptake of CO₂. Chrysophytes, the golden brown algae, have a relatively wide ecological distribution but a rather poorly understood physiology and therefore little is known about the mechanism of inorganic carbon acquisition. Photosynthetic characteristics of the chrysophyte *Mallomonas papillosa* were investigated to determine whether this species has some form of CCM. The effect of external pH on the photosynthetic rate of air-grown cells demonstrated an optimum in the range pH 5.0 to 7.0. This species lacked external carbonic anhydrase, the cells has no capacity for direct bicarbonate uptake and had a low affinity for dissolved inorganic carbon. Measurement of the fluxes of CO₂ and O₂ in photosynthesizing cells at pH 7.0 by mass spectrometry, displayed no rapid uptake but only a slow depletion of CO₂ from the medium upon illumination. Furthermore, CO₂ uptake and O₂ evolution by *Mallomonas* was greatly reduced by iodoacetamide, an inhibitor of CO₂ fixation. The overall internal pH of *Mallomonas* as determined by distribution between the cells and medium, of ¹⁴C-benzoic acid over the pH range 5.5 to 6.0, and [2-¹⁴C]-5,5-dimethylloxazolidine-2,4-dione over the pH range 6.5 to 7.0. As the external pH was lowered from 7.0 to 5.5, there was a decrease in the internal pH of the *Mallomonas* cells, from 8.31 to 7.75. The ΔpH was great enough to allow the accumulation of inorganic carbon by the diffusive uptake of CO₂. To establish whether *Mallomonas* can accumulate Ci, a time-course of Ci accumulation was obtained using the silicone-oil centrifugation technique. As the external pH increases from 6.5 to 8.0 the Ci accumulation ratio decreases and the internal concentration never rises to that of the external medium, that is there is no accumulation. Similar work was done with the chrysophyte alga, *Synura petersenii*.

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THE CHLAMYDOMONAS REINHARDTII FEA1 PROTEIN HAS IRON-ASSIMILATING FUNCTIONS

Sayre, Richard¹, Ihemere, Uzoma¹, Chiu, Wai Ting¹, Oda, Saharu¹ & Siritunga, Dimuth²

¹Plant Cellular and Molecular Biology, Ohio State University, Columbus, OH, USA; ²Biology, University of Puerto Rico, Mayaguez, Puerto Rico

The FEA1 gene of *Chlamydomonas reinhardtii* encodes an iron transport protein whose expression is inducible under high CO₂, iron depletion and cadmium stress. Iron deficiency is a common problem in many environments particularly in developing countries. Iron deficiency in humans manifests mainly as anemia, which is a consequence of a reduction in hemoglobin and myoglobin in the blood. Anemia could result in compromised immunity, tiredness, reduced mental development in children and could lead to increased mortality during pregnancy. To investigate the role of the Fea1 protein in iron transport, we transformed *Arabidopsis thaliana* (ecotype Columbia) with the *Chlamydomonas* FEA1 gene using two different plasmids, where its expression is under the regulation of the constitutive 2X 35S CAMV or the root-

specific patatin promoter. The transformants were confirmed by PCR and the expression of the FEA1 gene by RT-PCR. Our results show that the transgenic plants where the FEA1 gene is expressed under the control of the root-specific patatin promoter grow better under iron-limiting conditions than wild-type plants. To further investigate the role of Fea1 protein in iron assimilation, we transformed the *Arabidopsis thaliana* IRT1 mutant, impaired in iron transport, with *Chlamydomonas* FEA1 gene. The results show that the FEA1 gene complemented the IRT1 mutant imparting the transgenic plants with the capability to survive in the soil without the exogenous iron supplementation. Further studies are ongoing to fully characterize the mechanism of action of the Fea1 protein.

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A NOVEL PIGMENT BIOMARKER FOR IDENTIFICATION OF SOME EUGLENOPHYCEAE

Triemer, Richard¹, Bennett, Matthew¹, Zimba, Paul², Moeller, Peter³ & Beauchesne, Kevin³

¹Department of Plant Biology, Michigan State University, East Lansing, MI, USA; ²United States Department of Agriculture, Agricultural Research Service, Stoneville, MS, USA; ³National Ocean Service, Hollings Marine Laboratory, Charleston, SC, USA

Pigment biomarkers are extremely useful for characterizing algal populations. For maximal utility, these biomarkers should be unique compounds found within specific divisions or lower taxonomic rankings. A unique pigmented compound was isolated from select species from eight genera of euglenoids representing all of the major photosynthetic lineages. The compound does not match the published absorbance or atomic mass for pigments found in this division. This novel compound, currently thought to be a carotenoid and tentatively named euglenoxanthin, has a maximal absorbance at 464nm in acetone, and a mass weight of 520-564 AMU and appears to have utility in separating euglenophytes from the chlorophytes.

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CHARACTERIZATION OF CARBONIC ANHYDRASES FROM THE MARINE DIATOM *PHAEODACTYLUM TRICORNUTUM*

Colman, Brian & Szabo, Eva

Biology, York University, Toronto, ON, Canada

One form of carbonic anhydrase (CA) has previously been isolated from a strain of the marine diatom *Phaeodactylum tricornutum* (UTEX 642) and found to be a β -CA localized to the chloroplast. In our study we isolated and identified CA isozymes from three other strains of *P. tricornutum* (UTEX 640, NEPC B31 & CCAP 1052/1A). External and internal CA activities were detected by potentiometric assay of intact cells and cell homogenates of air and high CO₂-grown cells. External CA was detected only in UTEX 640 grown under CO₂-limited conditions and present in trace amounts in cells grown on high CO₂. CA isozymes in cell extracts were separated by cellulose acetate electrophoresis and by SDS-PAGE. All three strains had two CA bands in common, while UTEX 640 had a third, faster-running band which was absent from extracts of high CO₂-grown cells and thus was the external isozyme. The internal CA isoforms of the UTEX 640 strain were shown to have molecular masses of 28 and 25 kDa, and the external 24 kDa. A fourth external CA isozyme with a molecular weight of 23.5 kDa was later detected using a polyclonal CA antibody. The CA isozymes were low-CO₂-inducible proteins, since Western blot analysis and immunogold electron microscopy (EM) studies indicated that CA expression was repressed in high CO₂-grown cells. CA localization in air-grown cells, using both immunofluorescence and immunogold techniques, indicated that the external CA was located in the periplasmic space and on the cell membrane, whereas in high CO₂-grown cells only internal CA was detected. This is the first study to show the presence of two internal CA isoforms in the marine diatom *P. tricornutum* and to demonstrate the localization of its extracellular CA in the periplasmic space. Future studies will include sequencing of the isozymes and comparison with already existing *P. tricornutum* sequence data base.

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THE EXOPOLYMERS OF DESMIDS (CONJUGATOPHYCEAE, STREPTOPHYTA): CHEMISTRY, STRUCTURAL ANALYSES AND IMPLICATIONS IN WETLAND BIOFILMS

Kiemle, Sarah¹, Domozych, David S.² & Michael, Gretz R.¹

¹Department of Biological Sciences, Michigan Technological University, Houghton, NY, USA; ²Biology, Skidmore College, Saratoga Springs, NY, USA

Desmids represent a group of advanced green algae that are commonly found in biofilm communities of freshwater

wetlands. Most of these desmids secrete significant amounts of poorly-characterized extracellular polymeric substances (EPSs) that function in adhesion, gliding-based movements and ultimate ensheathment within the biofilm complex. It was the goal of this project to initiate comprehensive biochemical and structural analyses of the EPS macromolecules of five desmids isolated from biofilms from the southeastern Adirondack region of New York including *Penium margaritaceum*, *Pleurotaenium trabecula*, *Cosmarium sp.*, *Tetmemorus brebissonii* and *Netrium oblongum*. All of the EPSs form extensive mucilaginous sheaths external to the cell wall (CW). These exopolymers are processed in the Golgi apparatus, transported to the cell surface by large secretory vesicles and secreted through specialized CW pores, simple CW channels or through the CW proper. The EPS was composed primarily of proteins (2-10%), and sulfated polysaccharides (52-76%) with significant uronic acid content. *N. oblongum* polysaccharide was uronic acid rich (29.3% w/w) and *Pl. trabecula* and *T. brebissonii* had the highest amounts of ester sulfate (10.2% and 14.7%, respectively). Xyl and Fuc were the predominant neutral monosaccharides with the major glycosyl linkages t-Xylp, 3,4-Fuc, t-Fuc, and 3,4-GlcA. 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). The establishment of this baseline biochemistry provides the foundation for the future dissection of core EPS molecules and associated functional groups and studies of specific stages in biofilm development (e.g. adhesion).

142 SEASONAL VARIATION OF MAJOR NITROGEN POOLS IN TWO HIGH LATITUDE RED ALGAL SPECIES

Buckley, Cadie L.¹ & Stekoll, Michael S.²

¹*School of Fisheries and Ocean Sciences, University of Alaska Fairbanks, Juneau, AK, USA;* ²*Department of Natural Sciences, University of Alaska Southeast, Juneau, AK, USA*

Seaweeds may play an important role in nutrient recycling in the near shore marine environment by their ability to efficiently uptake and store nitrogen. Patterns of uptake and storage of nitrogen may vary as a function of the life cycle of the seaweeds and/or the exposure of the coastline. The seasonal variation of major nitrogen pools in two red algal species, *Palmaria mollis* (an annual) and *Constantinea* spp. (a perennial), were investigated at two locations, Sunshine Cove (exposed) and Auke Bay (sheltered), near Juneau, Alaska. Samples were collected from January 2005 to January 2006 and analyzed for total nitrogen, total protein, phycoerythrin, phycocyanin, free amino acids and total amino acid content. Seawater samples were collected from each site at the time of sampling, as well as, water temperature and salinity. The highest levels of protein and total nitrogen in *Palmaria* occurred in early spring. Protein and total nitrogen in *Palmaria* from both locations had peak values of approximately 20% and 5% (based on dry weight), respectively. *Palmaria* from Auke Bay showed a pulse of high nitrogen and protein levels in early April, whereas, *Palmaria* from Sunshine Cove had continuous high levels from early February to late April. There was a sharp decline in nitrogen and protein in May with low values of 5% and 1.5%, respectively. There was significant decrease in protein and total nitrogen in late spring. Phycobilin concentrations showed bi-modal profile with combined peak phycobilin concentrations of 6.1 mg/g in early February and 6.4 mg/g in early April. Phycoerythrin had values that tracked with phycocyanin. Nitrogen values in *Constantinea* also peaked in the early spring, but did not decline as precipitously as in the *Palmaria*.

143 DIFFERENTIAL EXPRESSION GENE (DEG) METHOD USED FOR THE IDENTIFICATION AND ISOLATION OF GENES EXPRESSED IN RESPONSE TO COLD STRESS IN A GREEN ALGA, *SPIROGYRA VARIANS* (ZYGNEMATALES)

Han, Jong Won¹, Yoon, MinChul², Lee, Key Pyoung¹ & Kim, Gwang Hoon²

¹*Department of Chemistry, Kongju National University, Kongju, South Korea;* ²*Department of Biology, Kongju National University, Kongju, South Korea*

When the plant cells are exposed to cold stress, various genes encoding specific stress proteins with possible protective functions are produced. The identification of cDNAs, representing up-regulated genes induced by cold stress, was achieved by differential expressed gene (DEG) technique of mRNAs isolated from freshwater alga, *Spirogyra varians* under differential temperature conditions (4 and 20 degree). Five distinct genes which were most strongly up-regulated in 4 degree were isolated and identified. These genes were designated as SVCR (*Spirogyra varians* cold regulated) gene group. Four mRNA species were amplified by the polymerase chain reaction (PCR) using cDNA library and sequenced. These genes showed sequence similarity with cold-shock induced genes (SVCR2), DNA-directed RNA polymerase sigma subunit (SVCR3), shikimate dehydrogenase (SVCR4) and transmembrane protein (SVCR5), respectively. Northern blot

analysis demonstrated that transcript level of SVCR increased minimum 10 fold at low temperature (4 degree) condition than at warm (20 degree) conditions.

144 TEMPORAL CHANGES IN THE CHEMICAL COMPOSITION OF SIX SEAWEEDS OF A TROPICAL ENVIRONMENT

Costa, Tatiana M., Barbarino, Elisabete & Lourenço, Sergio O.
Marine Biology, Universidade Federal Fluminense, Niteroi, Brazil

The chemical composition of *Colpomenia sinuosa*, *Cryptopleura ramosa*, *Hypnea musciformis*, *Pterocliadiella capillacea*, *Sargassum vulgare*, and *Ulva rigida* was studied throughout a 24-month survey in a coastal environment of Rio de Janeiro State, Brazil. The site is thought to have lower concentrations of dissolved nutrients and no relevant anthropic impacts. The species showed significant differences of concentrations of many substances, especially protein. Higher concentrations of protein were found in red algae, especially in *C. ramosa* (ca. 20% d.w.) and maximum concentrations of total carbohydrate (up to 55% d.w.) occurred in the agarophyte *P. capillacea*. Higher concentrations of chlorophyll were found in the green alga *U. rigida*. All species studied showed changes in the concentrations of the substances in the thalli throughout time, however they did not show any regular cyclic seasonal pattern. There is not evidence of nitrogen- or phosphorus-limitation in any season, neither sampling site. The concentrations of dissolved nutrients at the site were typically low, but sufficient to generate high concentrations of protein and chlorophyll in the thalli of the tested species. The set of results points to the physiological basis that determine the remarkable capability of tropical seaweeds grow well under reduced to moderate levels of dissolved nutrients.

145 A FRESH LOOK AT AN INVASIVE SPECIES, *DIDYMOSPHENIA GEMINATA*: CHEMICAL AND STRUCTURAL ANALYSIS OF THE EXTRACELLULAR POLYMERS

Gretz, Michael R.¹, Riccio, Michelle L.¹, Hungwe, Tendeukai R.¹, Burger, Holly M.¹, Kiemle, Sarah N.¹, Apoya-Horton, Melba D.¹, Domozych, David S.² & Spaulding, Sarah A.³

¹Biotechnology Research Center, Michigan Technological University, Houghton, MI, USA; ²Department of Biology, Skidmore College, Saratoga Springs, NY, USA; ³EPA Region VII, U.S. Geological Survey / EPA, Denver, CO, USA

Impact of the invasive diatom *Didymosphenia geminata* is primarily due to the production of prodigious amounts of extracellular polymers organized into stalks. The capability to secrete large quantities of highly organized extracellular polymer arrays differentiates *D. geminata* from other related benthic diatoms. Mats of stalk material, which usually include trapped *D. geminata* cells, other organisms and sediments, accumulate and cause unsightly masses resembling raw sewage, clog water intakes and generally create negative impact. The stalk is composed primarily of proteins and sulfated polysaccharides with significant uronic acid content. Galactose, xylose, and mannose were the major neutral monosaccharides with the predominate glycosyl linkages 3,4-Gal, 4,6-Man, and 4/5-Xyl. Striated parallel bands were highlighted after staining for anionic polysaccharides and sulfated polymers. Based on preliminary results, *D. geminata* stalks have chemical similarities to the stalks and pads of benthic diatoms *Cymbella mexicana*, *Cymbella cistula*, and *Gomphonema olivaceum*.

146 EFFECTS OF PHOTON FLUX DENSITY ON CAROTENOGENESIS IN *HAEMATOCOCCUS PLUVIALIS* (CHLOROPHYCEAE): COMPARISON BETWEEN WILD TYPE AND ASTAXANTHIN-OVERPRODUCTION MUTANT

Li, Yantao^{1,2}, Wang, Jiangxin¹, Sommerfeld, Milton¹, Chen, Feng² & Hu, Qiang¹

¹Department of Applied Biological Sciences, Arizona State University, Mesa, AZ, USA; ²Department of Botany, The University of Hong Kong, Hong Kong, China

The green alga *Haematococcus pluvialis* can produce large amounts (ca. 4% of dry weight) of the red carotenoid astaxanthin under high photon flux density (PFD) or other oxidative stress conditions. However, the regulation and physiological role of carotenogenesis in response to stress is not well understood. In this study, the concentrations of the major carotenoids (e.g., lutein, beta-carotene, and astaxanthin) were measured in cells of the wild type (WT) and an astaxanthin-overproduction mutant (M2877) exposed to different PFDs (20, 50, 125, 300, and 600 $\mu\text{mol m}^{-2} \text{s}^{-1}$). No net increase in cellular lutein and beta-carotene content occurred under various PFDs, suggesting their limited role in

protection in this organism. A PFD-dependent increase in astaxanthin was observed. The mRNA expression of five genes (i.e., isopentenyl-diphosphate δ -isomerase gene, *ipi*; phytoene synthase gene, *psy*; phytoene desaturase gene, *pds*; β -carotenoid oxygenase gene, *crtO*; and β -carotenoid hydroxylase gene, *crtR-b*) involved in astaxanthin synthesis was monitored by real-time RT PCR under different PFDs. As PFD increased from 20 to 300 $\mu\text{mol m}^{-2} \text{s}^{-1}$, transient increases in mRNA level of these genes occurred in both the WT and M2877 with similar expression patterns: the higher the PFD, the higher the maximum mRNA transcript level and the earlier the maximum transcript level occurred. As a result, more astaxanthin was produced, indicating PFD-dependent transcriptional regulation of astaxanthin synthesis. Significantly higher mRNA transcript levels of *ipi*, *pds* and *crtR-b* in the M2877 were responsible for overproduction of astaxanthin (by ca. 100%). When PFD was increased to 600 $\mu\text{mol m}^{-2} \text{s}^{-1}$, little increase in maximum mRNA transcripts of these genes and astaxanthin was observed in the WT and M2877. The cell mortality was associated with PFD: the higher the PFD, the high the cell mortality. The M2877 exhibited improved survival rate at higher PFDs due to its enhanced photoprotection through overproduction of astaxanthin.

147 DOES AN EXTRACELLULAR BROMOPEROXIDASE OF MARINE DIATOMS HALOGENATE DOC?

Hill, Valerie L. & Manley, Steven L.

Biological Sciences, California State University, Long Beach, CA, USA

Short-term dark incubations of marine diatoms in a buffered NaCl based medium have been shown to brominate and iodinate externally supplied organic substrates in the presence of added hydrogen peroxide. Several diatom species show this ability, especially those known to produce polyhalogenated methanes, such as *Porosira glaciales* (CCMP #651) and *Nitzschia* sp. (CCMP #580). Lower level activity has also been detected from the stalk former *Achnanthes longipes* (CCMP#101) and other species. The bromoperoxidase is located extracellularly in the apoplast, based on the type of substrates halogenated during the experiments and based on cell fractionation studies. Under optimum conditions, the amount of oxidized halogens (e.g. HOBr or equivalents) produced are 12 femto moles bromine/hour/cell and 740 femto moles iodine/hour/cell for *P. glaciales*. The effects of pH, hydrogen peroxide concentration, halide concentration and cell age on this activity are presented. The result of adding these organic substrates to diatom cultures significantly reduces the production of polyhaomethanes (e.g. bromoform). This suggests that reactive bromine and iodine formed via this extracellular bromoperoxidase reacts with a component of DOC to form polyhalomethanes.

148 DETECTION OF THE MICROCYSTIN SYNTHETASE GENES (MCY) IN PHYTOPLANKTON IN LAKE VICTORIA, AFRICA

Chhun, Aline¹, Gikuma-Njuru, Peter^{1,2}, Müller, Kirsten¹ & Guildford, Stephanie¹

¹Department of Biology, University of Waterloo, Waterloo, ON, Canada; ²Lake Victoria Environmental Mangement Programme (LVEMP), Water Quality Management Component, Kisumu, Kenya

Lake Victoria, the world's second largest lake, is highly eutrophic due to anthropogenic influences. The lake is susceptible to cyanobacterial blooms and cyanotoxins have been reported in Mwanza Gulf, Tanzania, Murchison Bay, Uganda and at a nearshore station in Nyanza (Winam) Gulf, Kenya. Our study, conducted in November 2005 detected the presence of the genes for biosynthesis of microcystin using PCR, in phytoplankton at all locations along a transect from within Nyanza Gulf extending to the open, international waters of Lake Victoria. The sites were different with respect to depth, thermal stratification and had different amounts of phytoplankton and quite different phytoplankton assemblages as detected using a FluoroProbe underwater spectral fluorometer. The shallow Gulf station had over 30 $\mu\text{g L}^{-1}$ total chlorophyll with 18 $\mu\text{g L}^{-1}$ Cyanobacteria while the deeper, open lake station had much lower biomass and was dominated by Cryptophytes with only 1.5 $\mu\text{g L}^{-1}$ Cyanobacteria. Our study is the first to report the potential for microcystin production in the off shore open lake and demonstrates the need for concern for toxins in the whole lake not just the near shore areas.

149 PHYLOGENETIC ANALYSIS AND DIFFERENTIAL EXPRESSION OF GLYCOSYL TRANSFERASE GENE HOMOLOGUES FROM THE MODEL DIATOM THALASSOSIRA PSEUDONANA

Abdullahi, Abass S., Wusirika, Ramakrishna & Gretz, Michael R.

Biological sci., Michigan Tech. University, Houghton, MI, USA

Centric diatoms such as *Thalassiosira* species are mainly planktonic organisms that produce highly crystalline beta chitin

fibers which are postulated to enable positioning within the water column, where they float or sink depending on a variety of physical and chemical parameters. Phylogenetic analysis and transcriptional regulation of four chitin synthases (CHSs) as well as one glucan synthase (GS), three mannosyl transferases (MTs), and two sulfotransferases (STs) were investigated in the model diatom, *Thalassiosira pseudonana*, during different growth phases and in response to salinity variation. Diatom chitin synthases weakly clustered with class V CHSs from filamentous fungi and GS was closer to fungal and plant beta 1,3-glucan synthases. The three diatom mannosyl transferases clustered with beta 1,4, alpha 1,2, and alpha 1,6 MTs, whereas the two sulfotransferases grouped with membrane STs. Increased expression of these genes was observed in response to growth phase status and hypo- or hyper-saline growth conditions. Our results suggest that certain components of extracellular matrix (ECM) polymers and transcript abundance of candidate genes encoding for enzymes involved in ECM biosynthesis may be up- or down- regulated in response to changing environmental conditions, indicating a high level of genetic control to enable flexibility in response to environmental cues. This suggests that these enzymes play important roles in the growth as well as environmental adaptation of diatoms to different habitats.

150 CAROTENOIDS AND CAROTENOID PATHWAY ENZYMES OF THE PRIMITIVE RED ALGA CYANIDIOSCHYZON MEROLAE

Cunningham, Jr, Francis X., Lee, Hansel & Gantt, Elisabeth

Department of Cell Biology and Molecular Genetics, University of Maryland, College Park, MD, USA

The unicellular red alga *Cyanidioschyzon merolae* is possibly a very primitive photosynthetic eukaryote. The photosynthetic apparatus in this alga may provide the closest approximation to that of the cyanobacterial ancestor of the modern day chloroplast. Of special interest is the evolution of the pathway that provides for the synthesis of the carotenoids, pigments that are integral and essential constituents of the photosynthetic apparatus. Accordingly, genes of *C. merolae* that encode polypeptides similar in sequence to known carotenoid pathway enzymes were identified, the major carotenoid pigments accumulated by *C. merolae* were ascertained, and the activities of two gene products of particular interest, the putative lycopene cyclase (LCY) and β -carotene hydroxylase (CrtR) enzymes, were examined. The pigment composition of *C. merolae* was found to be relatively simple, with Chl a, zeaxanthin, and β -carotene as the major pigments, and β -cryptoxanthin as a minor constituent. Carotenoids with ϵ -rings (i.e. lutein and α -carotene), found in many of the more advanced red algae, were not detected in pigment extracts of *C. merolae*. The lycopene cyclase (LCY) of *C. merolae*, when expressed in lycopene-accumulating *E. coli*, was found to form only carotenoids with β -rings, in contrast to LCY of certain cyanobacteria that produce carotenoids with both β - and ϵ -rings. The enzyme responsible for the synthesis of zeaxanthin from β -carotene in *C. merolae* is unrelated to the β -carotene hydroxylase enzymes (CHY) present in flowering plants. What at first appeared to be a likely candidate for a β -carotene hydroxylase-encoding gene in *C. merolae*, a chloroplast gene similar in sequence to cyanobacterial-type β -carotene hydroxylase genes (crtR), did not produce an active enzyme when expressed in *E. coli*. The polypeptide encoded by this *C. merolae* plastid gene is truncated by 20 or more a. a. at the N terminus when compared to cyanobacterial crtR gene products. A comparable truncation was found to inactivate the CrtR of *Synechocystis* PCC6803. Could this be a nonfunctional relic of the ancestral chloroplast progenitor, or a cryptic gene?

151 HOW SYMMETRICAL ARE DESMIDS? CELL WALL CHEMISTRY AND DEVELOPMENT IN *PENIUM* *MARGARITACEUM*

Domozych, David S.¹, Kiemle, Sarah², Domozych, Catherine E.¹ & Gretz, Michael R.²

¹*Biology, Skidmore College, Saratoga Springs, NY, USA;* ²*Biological Sciences, Michigan Technological University, Houghton, MI, USA*

Placoderm desmids represent a group of conjugating green algae that are noted for their symmetry. This symmetry is based on two “identical” semicells that are attached at a common point, the central isthmus zone. During each cell division, a new daughter semicell must develop whose morphology ultimately matches the shape of a parent semicell. This includes production of a new cell wall (CW). *Penium margaritaceum* represents a simple model desmid system for understanding CW development and semicell morphogenesis. This is due to its simple morphology and production of only a primary CW. The CW of *Penium* consists of cellulose and pectins, the latter includes various esterified and de-esterified homogalacturonans (HGAs). The synthesis and incorporation of the HGAs into the CW during semicell development can be carefully monitored by live-labeling the cells with the monoclonal antibodies, JIM5 (de-esterified HGAs) and JIM7 (esterified HGAs). De-esterified HGAs are secreted in the septum zone of the dividing cell and at the polar tips of the

newly forming semicells. The HGAs are de-esterified and complex Ca^{2+} to ultimately form a rigid CW. When allowed to proceed through multiple cell divisions, the pattern of CW development is not symmetric. Rather, our immunofluorescence data typically shows two asymmetric JIM5-labeled bands of CW in the daughter cell division products. When labeled cells are centrifuged at 10,000 rpm for 4 minutes and placed back in culture, only single JIM5-labeled bands are found. JIM7-labeled bands are always associated with the nucleus. We propose multiple possible hypotheses for what is occurring in this desmid during semicell development as well as the existence of CW secretory sites that are located near pre-determined cytokinetic planes.

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TEMPORAL RELATIONSHIP BETWEEN CHLOROPLAST DNA REPLICATION AND THE CELL CYCLE

Burger, Megan L.¹, Hoyt, Amanda¹, O'Brien-Labayen, Shalana B.² & Cattolico, Rose Ann^{1,3}

¹Biochemistry, University of Washington, Seattle, WA, USA; ²Biology, University of Washington, Seattle, WA, USA;

³Ocean Sciences, University of Washington, Seattle, WA, USA

The survival of a photoautotrophic organism requires that the multiple copies of its plastid genome are reproduced with high fidelity and that these replicated chromosomes are efficiently distributed to the next chloroplast generation. Though the presence of DNA in chloroplasts was reported over 40 years ago, we still know very little concerning the mechanisms that drive the replication and distribution of this genetic material to daughter plastids. *Heterosigma akashiwo*, a multiplastidic stramenopile, and a recognized model system for chloroplast biogenesis studies, was used in these analyses. The objective of our study was to determine the time at which *Heterosigma* chloroplast DNA replicates when this alga is synchronously maintained on a 12-hour light/12-hour dark photoperiod. Quantitative real-time PCR (qPCR) was used to detect a doubling of the chloroplast DNA. The presence of 1000 to 2000 copies of each chloroplast gene in a *Heterosigma* cell augments the feasibility of this approach. Primers of the ideal length and specificity for qPCR were designed for several chloroplast genes, including *rbcL*, *psbA*, and *xerC*. qPCR was optimized using total DNA extracted from *Heterosigma* cells. Control qPCR experiments demonstrated that very small amounts of template were needed to reveal a two-fold increase in DNA concentration. The qPCR technique was further optimized using freshly frozen *Heterosigma* cells in place of extracted DNA in the reactions. The substitution was possible because this alga is naturally wall-less and releases its cellular contents easily upon freeze/thawing. *Heterosigma* cells were harvested at hourly intervals over a 26-hour period during the logarithmic growth phase. qPCR was performed in triplicate for each time point. Chloroplast DNA replication was found to occur between the fourth and tenth hours of darkness. Chloroplast DNA replication occurs after chloroplast division in these synchronized cultures.

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CLONING, IDENTIFICATION AND CHARACTERIZATION OF SEVERAL SUPEROXIDE DISMUTASES (SOD) GENES IN HAEMATOCOCCUS PLUVIALIS

Wang, Jiangxin¹, Li, Yantao^{1,2}, Sommerfeld, Milton¹ & Hu, Qiang¹

¹Department of Applied Biological Sciences, Arizona State University, Mesa, AZ, USA; ²Department of Botany, Hong Kong University, Hong Kong, China

Superoxide dismutase (SOD) is an enzymatic antioxidant that regulates superoxide concentration in the cell by dismutation of superoxide to hydrogen peroxide, which is then converted to water by peroxidases or dismutated to water and oxygen by catalase. The green alga *Haematococcus pluvialis* (Chlorophyceae) cells can cope with oxidative stress via rapid transformation from the green vegetative form to red cysts. However, little is known about the expression and regulation of SOD in response to oxidative stress in this organism. In this study, native gel electrophoresis of free-cell extracts of *Haematococcus* exposed to high light revealed two major and four minor superoxide dismutase (SOD) bands. One major band and the four minor bands were deduced to be Mn-type SOD, whereas another major band was a Fe-type SOD, based upon their susceptibility to KCN and H_2O_2 . Of four Mn SOD isoforms detected, two were constitutive and two others were induced by various stressors (e.g., high light, salinity, and heavy metals). Using degenerated primers derived from known Mn-containing SOD genes, two cDNAs encoding Mn SOD 1 and Mn SOD 2 were cloned and their full length sequences were obtained with RACE technique. The two SODs share over 50% of identity at the cDNA sequence level, and contributed to about 50% of total SOD activity measurable in the cell. Real-time RT-PCR analysis revealed that the expression of *sod1* and *sod2* were stress-regulated: the higher the light intensity (from 20 to 300 $\mu\text{mol m}^{-2} \text{s}^{-1}$), the higher the maximum mRNA transcripts. Also, the higher the light intensity, the earlier the maximum mRNA transcript levels were reached, and the faster the cell transformation.

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