



The *Phycological Society of America* (PSA) 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 2008 PSA ANNUAL MEETING:

James L. Wee, *Loyola University, New Orleans*

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*ex-officio member

**ex-officio and non-voting member



OFFICE OF THE PRESIDENT

Dear Members of the Psychological Society of America,

I am sorry I am not able to join you at your 2008 annual meeting but wanted to send a warm welcome to all PSA members. I hope you will enjoy your visit to New Orleans and more particularly to our Loyola University campus. My thanks to Professor Jim Wee for bringing you to our campus.

It looks like your 2008 PSA Annual Meeting will be filled with information, activities and a taste of Louisiana. I note also that you have planned some volunteer activities in the New Orleans area for which I offer my thanks on behalf of the citizens of New Orleans.

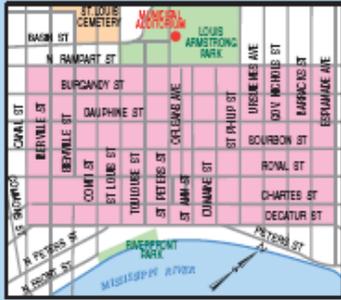
Again, my thanks to all of you for your work, and I hope you enjoy our campus and the metropolitan New Orleans area.

Sincerely,

A handwritten signature in black ink that reads "Kevin Wm. Wildes, S.J., Ph.D." The signature is written in a cursive style with a large, stylized initial 'K'.

Kevin Wm. Wildes, S.J., Ph.D., President

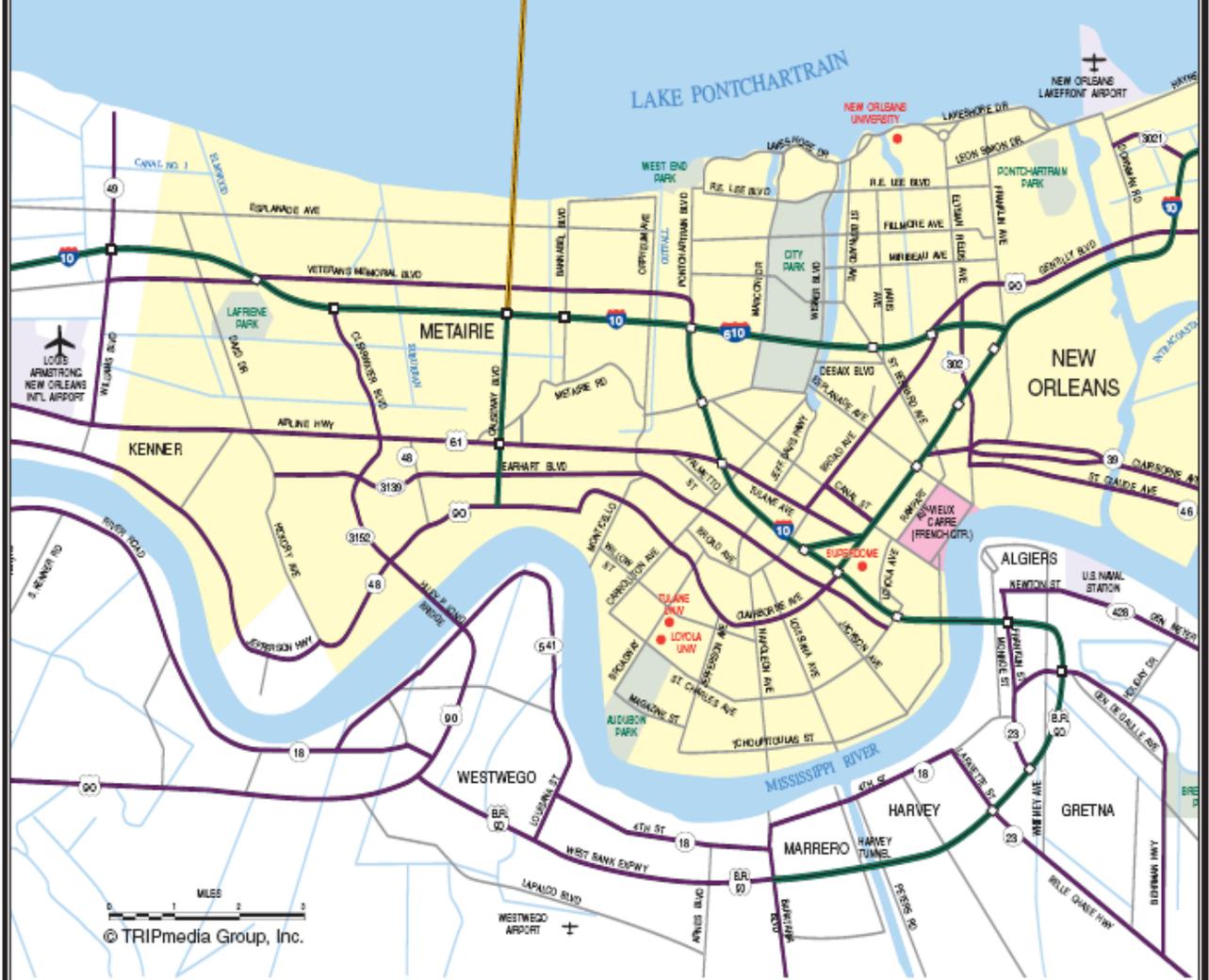
New Orleans



VIEUX CARRE
(The French Quarter)



NEW ORLEANS / LAKE PONTCHARTRAIN

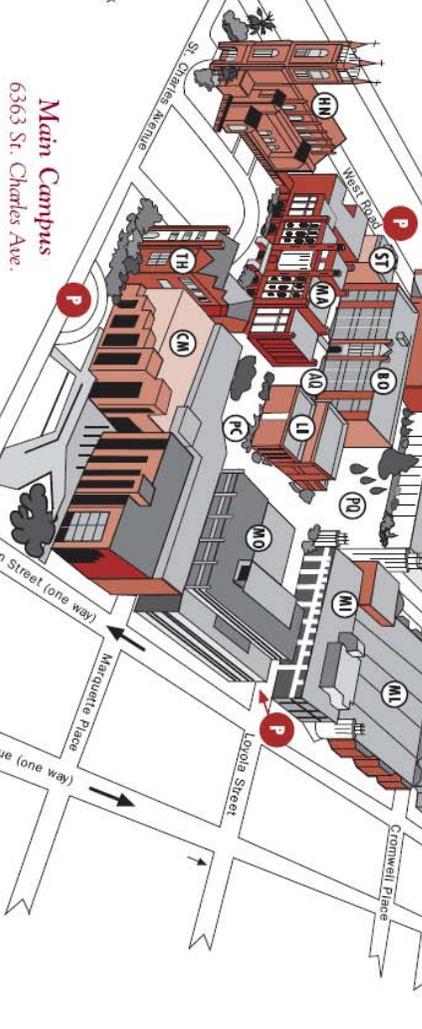
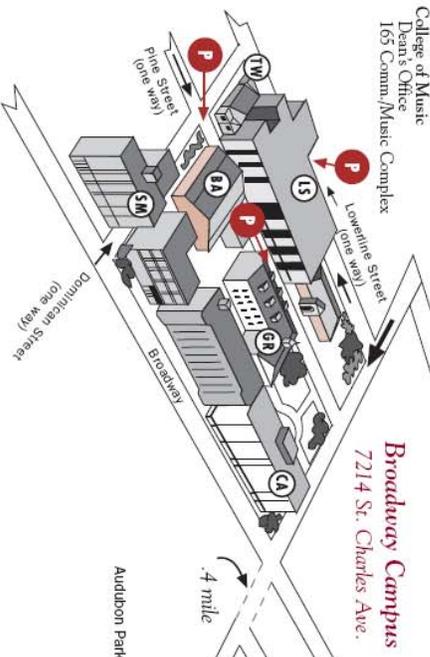


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For more maps, please visit www.TRIPinfo.com

PLACES MOST SOUGHT

- Academic Resource Center
- 405 Monroe Hall
- Admissions
- Undergraduate and Graduate
- 315 Marquette Hall
- Law
- Law School, Broadway Campus
- Alumni Relations
- Greenville Hall
- Audubon Room
- 2nd Floor, Danna Center
- Black Student Union Office
- Lower Level, Danna Center
- Bookstore
- 1st Floor, Danna Center
- Bryant's Office
- 270 Marquette Hall
- Central Receiving
- 125 Monroe Hall
- City College
- Dean's Office, 211 Stallings Hall
- Claborn Rooms
- 1st Floor, Danna Center
- College of Arts and Sciences
- Dean's Office
- 202 Bober Hall
- College of Business Administration
- Dean's Office
- 301 Miller Hall
- College of Music
- Dean's Office
- 165 Comm./Music Complex
- Counseling and Career Services Center
- 213 Danna Center
- Disability Services
- 405 Monroe Hall
- Financial Aid Office
- 110 Marquette Hall
- Human Resources Office
- 102 Merry Hall
- Ignatius Chapel
- 1st Floor, Bober Hall
- International Student Affairs Office
- Merry Hall
- Law
- Law School, Broadway Campus
- Lower Depths Theater
- 1st Floor, Communications/
- Music Complex
- Loyola University Programming Board
- Lower Level, Danna Center
- Marketing, Communications
- Public Affairs/Publications
- 2nd Floor, Greenville Hall
- Maroon Office
- 328 Communications/
- Music Complex
- Marquette Theater
- 2nd Floor, Marquette Hall
- Ninemaker Hall
- 3rd Floor, Monroe Hall
- Ovaria Rooms
- 2nd Floor, Danna Center
- Oleans Room
- 1st Floor, Danna Center
- Purchasing
- 117 Monroe Hall
- Recreational Sports Complex/
- Treret St. Parking Garage
- Main Campus
- Rousel Performance Hall
- 2nd Floor, Communications/
- Music Complex
- Student Finance Office
- 112 Marquette Hall
- St. Charles Room
- 1st Floor, Danna Center



BROADWAY CAMPUS

- BA Broadway Activities Center (& Pine St. entrance)
- CA Cabra Hall (& Pine St./Quad entrance)
- GR Greenville Hall (& rear entrance)
- LS Law School (& Pine St. entrance/entrance left)
- SM St. Mary's Hall Visual Arts (& Dominican St. main entrance)
- TW Tromper Center for Peace Through Justice

MAIN CAMPUS

- AQ Academic Quad
- BE Bever Hall (& main entrance/front)
- BO Bober Hall (& main entrance/back side)
- BU Budding Hall (& main entrance/front)
- CM Communications/Music Complex (& Main entrance/back side)
- DC Danna Center (& main entrance/Peace Quad)
- HN Holy Name of Jesus Church (& West Road entrance)
- LI Old Library, future home of The Center for Visual and Performing Arts
- MA Marquette Hall (& main entrance/back side)
- ME Mercy Hall (& main entrance parking lot)
- MI Miller Hall (& main entrance Loyola S.)
- ML Monroe Library (& main entrance)
- MO Monroe Hall (& main entrance off Palm Court)
- NR New Residence Hall (& from entrance)
- P Parking (& parking)
- PC Palm Court
- PG West Road Parking Garage (& parking)
- PS Public Safety (& main entrance/front)
- PQ Peace Quad
- RC Recreational Sports Complex/Parking Garage (& main entrance/recreational hall side)
- RQ Residential Quad
- ST Stallings Hall (& Holy Name Church side entrance)
- TH Thomas Hall (& horseshoe entrance under arcade)

DRIVING TO CAMPUS

FROM I-10 WEST TRAVELING EAST Follow the signs toward the Central Business District. Take the Carrollton Avenue exit, Exit 232. Follow South Carrollton until it ends in a sharp left-hand curve and becomes St. Charles Avenue. Loyola's main campus is located on the left at 6363 St. Charles Avenue across from Audubon Park. The Broadway campus is located at 7214 St. Charles Avenue at the corner of Broadway.

FROM I-10 EAST TRAVELING WEST As you enter the downtown area, follow the signs to Hwy. 90 Business/West Bank. Exit at St. Charles Avenue/Carondelet Street (do not cross the bridge). At the second traffic light make a right onto St. Charles Avenue. Follow St. Charles Avenue for four miles. Loyola's main campus is on the right at 6363 St. Charles Avenue. The Broadway Campus is located on the left at 7214 St. Charles Avenue.

Interstate 10
From the West
(Carrollton Exit)

Welcome to New Orleans!

Bienvenue a New Orleans!

New Orleans is a city in southern Louisiana, located on the Mississippi River. Most of the city is situated on the east bank, between the Mississippi river to the south/east and Lake Pontchartrain to the north. Because it was built on a great turn of the river, it is known as the Crescent City. New Orleans, with a population of 496,938 (1990 census), is the largest city in Louisiana and one of the principal cities of the South. It was established on the high ground nearest the mouth of the Mississippi, which is 177 km (110 mi) downstream. Elevations range from 3.65 m (12 ft) above sea level to 2 m (6.5 ft) below; as a result, a system of water pumps, drainage canals, and levees has been built to theoretically protect the city from flooding. The city covers a land area of 518 sq km (200 sq mi). New Orleans experiences mild winters and hot, humid summers. Temperatures in January average 13 °C (55 °F), and in July they average 28 °C (82 °F). Annual rainfall is 1.5 m (57 in).

CONTEMPORARY CITY

The population of New Orleans, including Anglos, French, Blacks, Italians, Irish, Spanish, and Cubans, reflects its cosmopolitan past. The Cajuns, or Acadians, are descendants of French émigrés expelled from Nova Scotia (or Acadia) during the 18th century. They speak their own French dialect. The port of New Orleans is one of the world's largest and ranks first in the United States in tonnage handled. Major exports are petroleum products, grain, cotton, paper, machinery, and iron and steel. The city's economy is dominated by the petrochemical, aluminum, and food-processing industries and by tourism.

The most important annual tourist event is Mardi Gras (or 'Fat Tuesday'), which is celebrated for a week before the start of Lent. The Superdome, an enclosed sports stadium, attracts major sporting events and is an element in achieving the city's position as a leading convention center. One of the legacies of the six-month-long 1984 World's Fair, held in New Orleans, is the Ernest N. Morial Convention Center. The New Orleans Jazz & Heritage Festival is celebrated every spring, and draws hundreds of thousands of visitors to an eclectic blend of musical traditions. New Orleans is noted for its fine restaurants, its Dixieland jazz, and its numerous cultural and educational facilities. Tulane (1829), Dillard (1869), and Loyola (1849) universities are major institutions of higher learning. The French Quarter, or 'Vieux Carre' (French for "old square"), is the site of the original city and contains many of the historic and architecturally significant buildings for which New Orleans is famous.

HISTORY

New Orleans was founded as 'Nouvelle-Orléans' in 1718 by Jean Baptiste Le Moyne, sieur de Bienville, and named for the regent of France, Philippe II, duc d'Orleans. The priest-chronicler Pierre François Xavier de Charlevoix described it in 1721 as, "a place of a hundred wretched hovels in a malarious wet thicket of willows and dwarf palmettos, infested by serpents and alligators"; he seems to have been the first, however, to predict for it an imperial future. In 1722 Nouvelle-Orléans was made the capital of French Louisiana, replacing Biloxi in that role. It remained a French colony until 1763, when it was transferred to the Spanish. In 1800, Spain ceded it back to France; in 1803, New Orleans, along with the entire Louisiana Purchase, was sold by Napoleon I to the United States. It was the site of the Battle of New Orleans (1815) in the War of 1812. During the Civil War the city was besieged by Union ships under Adm. David Farragut, and fell on Apr. 25, 1862.

HURRICANE KATRINA

The city suffered from the effects of a major hurricane on and after August 29, 2005, as Hurricane Katrina made landfall in the gulf coast near the city. In the aftermath of the storm, what has been called "the largest civil engineering disaster in the history of the United States" flooded the majority of the city when the levee and floodwall system protecting New Orleans failed. On August 26, tracks which had previously indicated the hurricane was heading towards the Florida Panhandle shifted 150 miles westward, initially centering on Gulfport/Biloxi, Mississippi and later shifted further westward to the Mississippi/Louisiana state line. The city became aware that a possible major hurricane hit was possible and issued voluntary evacuations on Saturday, August 27. Interstate 10 in New Orleans East and Jefferson and St. Charles parishes was converted to all-outbound lanes heading out of the city as well as Interstates 55 and 59 in the surrounding area, a maneuver known as "contraflow."

On the morning of Sunday, August 28, Katrina was upgraded to a top-notched Category 5 hurricane. Around 10 AM, Mayor Nagin issued a mandatory evacuation of the entire city, the first such order ever issued in the city's history. An estimated 1 million people evacuated from Greater New Orleans and nearby areas before the storm. However, some 20% of New Orleans residents were still in the city when the storm hit. This included people who refused to leave home, those who felt their homes were adequate shelter from the storm, and people without cars or without financial means to leave. Some took refuge in the Superdome, which was designated as a "shelter of last resort" for those who could not leave.

The eye of the storm missed the heart of the city by only 20–30 miles, and strong winds ravaged the city, shattering windows, spreading debris in many areas, and bringing heavy rains and flooding to many areas of the city.

The situation worsened when levees on four of the city's canals were breached. Storm surge was funneled in via the Mississippi River Gulf Outlet which breached in multiple places. This surge also filled the Industrial Canal which breached either from the surge or the effects of being hit by a loose barge (the ING 4727). The London Avenue Canal and the 17th Street Canal were breached by the elevated waters of Lake Pontchartrain. Some areas that initially seemed to suffer little from the storm found themselves flooded by rapidly rising water on August 30. As much as 80% of the city — parts of which are below sea level and much of which is only a few feet above — was flooded, with water reaching a depth of 25 feet (7.6 meters) in some areas. Water levels were similar to those of the 1909 Hurricane, but as many areas which were swamp or farmland in 1909 had become heavily settled since, the effects were massively worse. The most recent estimates of the damage from the storm, by several insurance companies, are 10 to 25 billion USD while the total economic loss from the disaster has been estimated at 100 billion USD. Hurricane Katrina surpassed Hurricane Andrew as the costliest hurricane in United States history.

More than 1,100 died in Louisiana alone, though a final count has not yet been possible. Three weeks later, some areas of the city were re-flooded by Hurricane Rita. The city government at first declared the city off-limits to residents and warned that those remaining may be removed by force, supposedly for their health and safety. However, the city was slowly repopulated starting in late September.

While many residents and businesses returned to the task of rebuilding the city, the effects of the Hurricane on the economy and demographics of the city are expected to be dramatic and long term. As of March 2008, around 75% of the population has returned to New Orleans.

	Nunemaker Hall	St. Charles Room	Miller 114	Library Multi-Media 1
MONDAY	PSA Special Session: Harmful Algae (08:00-10:15)			
		Mid-Morning Break (10:15-10:45)		
			Bold Award I (10:45-12:25)	
		Lunch (12:25-13:45)		
			Bold Award II (13:45-15:25)	
		Mid-Afternoon Break (15:25-15:55)		
			Cellular & Molecular Biology (15:55-16:55)	
			<i>PSA Business Meeting</i> (17:00-18:00)	
		<i>PSA Auction and Mixer</i> (18:30-21:30)		

	Nunemaker Hall	St. Charles Room	Miller 114	Library Multi-Media 1
TUESDAY	PSA Special Session: Coastal Ecosystems (08:00-10:10)			
		Mid-Morning Break (10:10-10:40)		
			Phylogenetics & Taxonomy I (10:40-12:20)	Physiology & Biochemistry (10:40-12:20)
		Lunch (12:20-13:40)		
			Phylogenetics & Taxonomy II (13:40-15:40)	Ecology & Population Biology I (13:40-15:40)
		Mid-Afternoon Break (15:40-16:10)		
			Phylogenetics & Taxonomy III (16:10-17:50)	
			<i>Poster Session and Mixer</i> (18:30-20:30)	

WEDNESDAY	Nunemaker Hall	St. Charles Room	Miller 114	Library Multi-Media 1
	PSA Special Session: Algal Biotechnology (08:00-10:10)			
		Mid-Morning Break (10:10-10:40)		
			Ecology & Population Biology II (10:40-12:20)	Algal Biotechnology (10:40-12:20)
		Lunch (12:20-13:40)		
			Phylogenetics & Taxonomy IV (13:40-15:40)	
	<i>PSA Banquet & Awards Ceremony, Louisiana Swamp Exhibit, Audubon Zoo (18:30-22:00)</i> Buses will begin shuttling from hotels/Loyola at ca. 17:45			

Nunemaker Hall is located on the third floor in Monroe Hall (**MO** on the Loyola Campus map).

The **St. Charles Room** is located on the first floor of the Danna Center (**DC** on the Loyola Campus map).

Miller 114 is located on the first floor of Miller Hall (**MI** on the Loyola Campus map).

Library Multi-Media 1 is located on the first floor of the Monroe Library (**ML** on the Loyola Campus map).

The **PSA Headquarters** room will be in **Miller 112** (next to Miller 114).

Computers are available for use in **Monroe Library Computer Laboratory #3**.

SATURDAY, 26 JULY

PSA Board of Trustees Meeting – Library Seminar Room 4, Monroe Library, 13:00 – 18:00

SUNDAY, 27 JULY

PSA Executive Committee Meeting – Library Seminar Room 4, Monroe Library, 13:00 – 18:00

Opening Social and Mixer – St. Charles Room, Danna Center, 18:30-21:30 PM

MONDAY, 28 JULY

Nunemaker Hall; Monroe Hall, Monday Morning:

Plenary Session - Harmful Algal Blooms

Moderator: Robert Andersen, Bigelow Laboratory for Ocean Sciences

08:00 **Opening Remarks**

08:15 **Harmful Algal Blooms in North America: Common Risks**

Karen A. Steidinger

Florida Institute of Oceanography, St. Petersburg, FL, USA

09:15 **Unexpected vectors of brevetoxins to marine mammals**

Leanne J. Flewelling¹, Jerome P. Naar², Jay P. Abbott¹ and Jan H. Landsberg¹

1. Fish and Wildlife Research Institute, Florida Fish and Wildlife Conservation Commission, St. Petersburg, FL, USA; 2. Center for Marine Science, University of North Carolina, Wilmington, NC, USA

09:45 **The evolving story of *Gymnodinium galatheanum* = *Karlodinium micrum* = *Karlodinium veneficum*. A ten year perspective**

Jonathan Deeds

Center for Food Safety and Applied Nutrition, US Food and Drug Administration, College Park, MD, USA

10:15 **COFFEE BREAK** -- St. Charles Room, Danna Center

Miller 114; Miller Hall, Monday Morning:

Bold Award I

Moderator: Kirsten Muller, University of Waterloo

- 10:45 **Reconsideration of the classification of bangiophyte red algae using chloroplast and nuclear gene sequence analysis**
Michael D. Lynch¹, Jamie J. Cannone², Robin R. Gutell² and Kirsten M. Müller¹
1. Department of Biology, The University of Waterloo, Waterloo, ON, Canada; 2. The Institute for Cellular and Molecular Biology, The University of Texas at Austin, Austin, TX, USA
- 11:05 **A Novel Modification of Nitrogen Metabolism Induced by Desiccation in *Porphyra***
Jang K. Kim¹, George P. Kraemer² and Charles Yarish¹
1. Ecology & Evolutionary Biology, University of Connecticut, Stamford, CT, USA; 2. Biology & Environmental Studies, Purchase College, State University of New York, Purchase, NY, USA
- 11:25 **Rethinking native species: evidence for repeated colonizations of *Spyridia filamentosa* (Ceramiales, Rhodophyta) in the Hawaiian archipelago**
Kimberly Y. Conklin and Alison R. Sherwood
Botany, University of Hawaii at Manoa, Honolulu, HI, USA
- 11:45 **Differential gene expression during growth of the harmful marine alga *Alexandrium fundyense***
Lilibeth Miranda and Senjie Lin
Marine Sciences, University of Connecticut, Groton, CT, USA
- 12:05 **A new *Champia* species (Champiaceae, Rhodophyta) from Puerto Rico**
Chad Lozada and David L. Ballantine
Marine Sciences, University of Puerto Rico-Mayaguez Campus, Lajas, PR, USA

12:25 **LUNCH BREAK -- St. Charles Room, Danna Center**

12:25 **EDITORIAL BOARD LUNCHEON -- Library Seminar Room 4, Monroe Library**

Miller 114; Miller Hall, Monday Afternoon:

Bold Award II

Moderator: Kirsten Muller, University of Waterloo

- 13:45 **Using reference site diatom communities for measuring the severity of human impacts on stream ecosystems**
Nathan J. Smucker^{1,2} and Morgan L. Vis^{1,2}
1. Environmental and Plant Biology, Ohio University, Athens, OH, USA; 2. The George V. Voinovich Center for Leadership and Public Affairs, Ohio University, Athens, OH, USA
- 14:05 **Redefining the Genus *Chondria* Agardh: A systematic and morphological approach.**
Constanza Ehrenhaus and Suzanne Fredericq
Biology, UL Lafayette, Lafayette, LA, USA
- 14:25 **Nutrient limitation and productivity of phytoplankton in the lower Laguna Madre, Texas**
Natasha A. Pardo and Hudson DeYoe
Center for Subtropical Studies and Biology Department, University of Texas - Pan American, Edinburg, TX, USA

- 14:45 **Uniflagellar mutants in *Chlamydomonas reinhardtii* provide insights into basal body maturation and flagellar formation**
Brian P. Piasecki and Carolyn D. Silflow
Plant Biology, The University of Minnesota, St. Paul, MN, USA
- 15:05 **Spatial and temporal variability in abundance of the diatom *Pseudo-nitzschia sp.* in coastal Alabama waters**
Justin Liefer¹, William Smith², Carol Dorsey² and Hugh L. MacIntyre¹
1. Marine Science, Dauphin Island Sea Lab/ University of South Alabama, Mobile, AL, USA; 2. Alabama Department of Public Health, Mobile, AL, USA

15:25 **COFFEE BREAK -- St. Charles Room, Danna Center**

Miller 114; Miller Hall, Monday Afternoon:

Cellular & Molecular Biology

Moderator: Senjie Lin, University of Connecticut

- 15:55 **It's not easy being green: the origin of *Euglena longa***
Steven Schwartzbach¹, Maria Takacova², Anna Belicova² and Juraj Krajcovic²
1. Biology Department, University of Memphis, Memphis, TN, USA; 2. Institute of Cell Biology, Comenius University, Bratislava, Slovakia
- 16:15 **The Value of Monitoring the Cell Cycle in Relation to Physiological and Molecular Changes in Phytoplankton**
Mark Hildebrand¹, Luciano G. Frigeri¹, Kimberlee Thamatrakoln² and Aubrey K. Davis¹
1. Marine Biology Research Division, Scripps Inst. of Oceanography, UCSD, La Jolla, CA, USA; 2. Institute of Marine and Coastal Sciences, Rutgers University, New Brunswick, NJ, USA
- 16:35 **Two highly diverging flavodoxin genes and their transcription under iron stress conditions in *Trichodesmium* (Oscillatoriales, Cyanophyceae)**
Senjie Lin¹, Gustaf Sandh², Huan Zhang¹, Jiuju Chen², Keri Perkins¹, Edward J. Carpenter³ and Bergitta Bergman²
1. Marine Sciences, University of Connecticut, Groton, CT, USA; 2. Department of Botany, Stockholm University, Stockholm, Sweden; 3. Romberg Tiburon Center, San Francisco State University, Tiburon, CA, USA
- 16:55 **Assessing Bait Worm Packaging as a Potential Vector of Invasive Species Introductions into Long Island Sound**
Christina Haska¹, Charles Yarish² and Senjie Lin¹
1. Marine Sciences, University of Connecticut, Groton, CT, USA; 2. Ecology and Evolutionary Biology, University of Connecticut, Stamford, CT, USA

Miller 114; Miller Hall, Monday Evening 17:00-18:00:

PSA Business Meeting

Presiding: Robert Andersen, PSA President

St. Charles Room, Danna Center, Monday Evening – 18:30 – 21:30:

Phycological Society of America Annual Auction

Hot and cold hors d'oeuvres and a cash bar – come and bid on an amazing assortment of phycological-related material and support the student funds!

TUESDAY, 29 JULY

Nunemaker Hall; Monroe Hall, Tuesday Morning:

Plenary Session - Coastal Ecosystems

Moderator: Jim Wee, Loyola University

08:00 **Opening Remarks**

08:10 **Climate change, energy scarcity, and sustainable management of the Mississippi delta**

John Day

Dept. of Oceanography and Coastal Sciences, Louisiana State University, Baton Rouge, LA, USA

09:10 **Restoring wetlands to improve hurricane flood protection in the Mississippi river delta.**

Paul Kemp

Gulf Coast Initiative, National Audubon Society, Baton Rouge, LA, USA

09:40 **Harmful Algal Blooms (HABs) and Their Impact on Marine Environments in the Northern Gulf of Mexico**

Sibel Bargu

Oceanography and Coastal Sciences, Louisiana State University, Baton Rouge, LA, USA

10:10 **COFFEE BREAK -- St. Charles Room, Danna Center**

Miller 114; Miller Hall, Tuesday Morning:

Phylogenetics & Taxonomy I

Moderator: Suzanne Fredericq, University of Louisiana - Lafayette

10:40 Oomycetes among algae

J. Craig Bailey

Dept. of Biology and Marine Biology, UNC-Wilmington, Wilmington, NC, USA

11:00 Unravelling the diversity of *Trentepohlia* and *Printzina* (Trentepohliales, Ulvophyceae) by molecular systematic analyses

Fabio Rindi^{1,2}, Daryl W. Lam² and Juan M. Lopez-Bautista²

1. Martin Ryan Institute, National University of Ireland, Galway, Galway, Ireland; 2. Biological Sciences, The University of Alabama, Tuscaloosa, AL, USA

11:20 A multigene approach to inferring the diatom phylogeny: congruence and conflict

Edward C. Theriot^{1,2}, Matthew Ashworth², Robert K. Jansen², Teofil Nakov², Elizabeth Ruck² and Cai Zhengqui²

1. Texas Natural Science Center, University of Texas, Austin, TX, USA; 2. Section of Integrative Biology, University of Texas, Austin, TX, USA

11:40 New observations on the biology of eustigmatophytes, with a description of *Microtalis* gen. nov.

Cory Dashiell and J. Craig Bailey

Department of Biology and Marine Biology, University of North Carolina, Wilmington, NC, USA

12:00 TBA

12:20 LUNCH BREAK -- St. Charles Room, Danna Center

Library Multi-Media 1; Monroe Library, Tuesday Morning:

Physiology & Biochemistry

Moderator: Todd Lane, Sandia National Labs

10:40 Algae in hyperspace: a first foray into mapping the Grinnellian niche of *Chlorella vulgaris* (Chlorophyceae) and *Peridinium cinctum* (Dinophyceae) in relation to ion proportions and amounts

Terence Evens and Randall Niedz

US Horticultural Research Laboratory, USDA-ARS, Ft. Pierce, FL, USA

11:00 Heat Stability and Volatility of a Putative Oogenesis-inducing Male Pheromone in the Brown Alga *Macrocystis integrifolia*

Raymond J. Lewis and Mark R. Johnston

Biology, Wheaton College, Wheaton, IL, USA

- 11:20 **Physiology As A Reflection Of Habitat For Western South African *Porphyra* Species**
Michael S. Stekoll¹, John J. Bolton² and Robert J. Anderson^{3,2}
 1. Department of Natural Sciences, University of Alaska Southeast, Juneau, AK, USA; 2. Department of Botany, University of Cape Town, Cape Town, South Africa; 3. Seaweed Unit, Marine and Coastal Management, Cape Town, South Africa
- 11:40 **A Quantitative Method for Measurement of Neutral Lipids in Chlorophycean Microalgae**
Wei Chen^{1,2}, Chengwu Zhang¹, Lirong Song², Milton Sommerfeld¹ and Qiang Hu¹
 1. Department of Applied Biological Sciences, Arizona State University, Mesa, AZ, USA; 2. State Key Laboratory of Freshwater Ecology and Biotechnology, Institute of Hydrobiology, The Chinese Academy of Sciences, Wuhan, China
- 12:00 **Photosynthetic response of the toxic raphidophyte *Heterosigma akashiwo* during the imposition of, and recovery from, light- and nutrient stress**
Hugh MacIntyre^{1,2}, Marcel Babin¹, Amélie Gelay¹, Emily Goldman², Yannick Huot¹, Antoine Sciandra¹ and Tim Sherman³
 1. Laboratoire d'Océanographie de Villefranche, Villefranche-sur-mer, France; 2. Dauphin Island Sea Lab, Dauphin Island, AL, USA; 3. University of South Alabama, Mobile, AL, USA
- 12:20 **LUNCH BREAK -- St. Charles Room, Danna Center**

Miller 114; Miller Hall, Tuesday Afternoon:

Phylogenetics & Taxonomy - II

Moderator: Juan Lopez-Bautista, University of Alabama

- 13:40 **The correct identity of the species going under the name *Schizymenia dubyi* (Schizymeniaceae, Rhodophyta) in the Azores, based on molecular and morphological evidence**
Daniela Gabriel^{1,2}, Tom Schils³, Ana I. Neto¹ and Suzanne Fredericq²
 1. Department of Biology, University of the Azores, Ponta Delgada, Portugal; 2. Department of Biology, University of Louisiana at Lafayette, Lafayette, LA, USA; 3. Marine Laboratory, University of Guam, Mangilao, GU, USA
- 14:00 **Molecular systematics of *Thorea* (Rhodophyta, thoreales) in Brazil**
Orlando Necchi¹, Patricia Salles¹ and Mariana C. Oliveira²
 1. Zoology and Botany, São Paulo State University, S. Jose Rio Preto, Brazil; 2. Botany, São Paulo University, São Paulo, Brazil
- 14:20 **Phylogeography of *Ishige* with recognition of *I. foliacea* (Ishigeales, Phaeophyceae)**
Kyung Min Lee¹, Ga Hun Boo¹, Jong Arm Shin³, Rafael Riosmena-Rodriguez² and Sung Min Boo¹
 1. Biology, Chungnam National University, Daejeon, South Korea; 2. Marine Biology, UABCS, Las Paz B.C.B., Mexico; 3. Fishery, Cheonnam National University, Yeosu, South Korea
- 14:40 **Subaerial microchlorophytes from West Central Africa: morphological convergence in tropical rain forests**
Haj A. Allali and Juan M. Lopez-Bautista
 Biological Sciences, University of Alabama, Tuscaloosa, AL, USA

- 15:00 **Subaerial Microchlorophyten Diversity of Barro Colorado Island, Panama**
Daryl W. Lam, Fabio Rindi and Juan M. Lopez-Bautista
Biological Sciences, University of Alabama, Tuscaloosa, AL, USA
- 15:20 **Phylogeny of *Thalassionema* Grunow, with discussion of biogeography, stratigraphy, and diagnostic features**
Matthew L. Julius¹ and Yoshihiro Tanimura²
1. Biological Sciences, St. Cloud State University, St. Cloud, MN, USA; 2. Geology and Paleontology, National Museum of Science and Nature, Tokyo, Japan
- 15:40 **COFFEE BREAK -- St. Charles Room, Danna Center**

Library Multi-Media 1; Monroe Library, Tuesday Afternoon:

Ecology & Population Biology - I

Moderator:

- 13:40 **The Seaweeds of Florida**
Clinton Dawes¹ and Arthur Mathieson²
1. Biology, University of South Florida, Tampa, FL, USA; 2. Plant Science, University of New Hampshire, Durham, NH, USA
- 14:00 **Variability in Tissue Nitrogen and Phosphorus of Macroalgae in the Indian River Lagoon, Florida**
M. Dennis Hanisak
Harbor Branch Oceanographic Institute at Florida Atlantic University, Fort Pierce, FL, USA
- 14:20 **Growth and feeding activity of the mixotrophic dinoflagellates *Dinophysis acuminata* and *Dinophysis caudata*: nutrient limitation, food quality, and diel cycle**
Miran Kim¹, Wonho Yih² and Myung Park¹
1. Oceanography, Chonnam National University, Gwangju, South Korea; 2. Oceanography, Kunsan National University, Gunsan, South Korea
- 14:40 **Growth of *Lyngbya wollei*, an invasive mat forming cyanobacterium from Florida springs, under different temperature, light and nutrient regimes.**
Agnieszka Pinowska¹, R. J. Stevenson² and Russell Frydenborg³
1. Valcent Products Inc., Anthony, TX, USA; 2. Zoology, Michigan State University, East Lansing, MI, USA; 3. Environmental Assessment Section, Florida Department of Environmental Protection, Tallahassee, FL, USA
- 15:00 **Are interactions between dominant mesograzers and macroalgae in the Western Antarctic Peninsula, in part, chemically mediated? The anti-grazing capabilities of secondary metabolites produced in Antarctic filamentous macrophytes.**
Craig F. Aumack¹, Charles D. Amsler¹, James B. McClintock¹ and Bill J. Baker²
1. Department of Biology, University of Alabama Birmingham, Birmingham, AL, USA; 2. Department of Chemistry, University of South Florida, Tampa, FL, USA

15:20 **Palatability of *Palmaria decipiens* and its endophyte *Elachista antarctica* to four common Antarctic amphipods**

Philip Bucolo¹, Charles D. Amsler¹, James B. McClintock¹ and Bill J. Baker²

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

15:40 **COFFEE BREAK -- St. Charles Room, Danna Center**

Miller 114; Miller Hall, Tuesday Afternoon:

Phylogenetics & Taxonomy - III

Moderator: Edward Theriot, The University of Texas at Austin

16:10 **Insights into the evolutionary history of the subaerial algal flora**

Juan M. Lopez-Bautista

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

16:30 **Assessing multi-gene candidates for an algal heterokont phylogeny**

Matt Ashworth¹, Elizabeth Ruck¹, Teofil Nakov¹, Cai Zhengqiu¹, Edward Theriot², Robert K. Jansen¹, Robert Andersen³, Matthew Julius⁴, Stefano Draisma⁵ and Hiroshi Kawai⁶

1. *Intergrative Biology, University of Texas at Austin, Austin, TX, USA*; 2. *Texas Memorial Museum, University of Texas at Austin, Austin, TX, USA*; 3. *CCMP, Bigelow Laboratory for Ocean Sciences, West Boothbay Harbor, ME, USA*; 4. *Department of Biological Sciences, St. Cloud State University, St. Cloud, MN, USA*; 5. *Nationaal Herbarium Nederland, Leiden University, Leiden, Netherlands*; 6. *Research Center for Inland Seas, Kobe University, Kobe, Japan*

16:50 **Genetic diversity and reinstatement of *Gracilariopsis chorda* based on *rbcL* and *cox1* sequences**

Suyeon Kim¹, Myung Sook Kim², Eun Chan Yang¹, Paul J. Geraldino¹ and Sung Min Boo¹

1. *Department of biology, Chungnam National University, Daejeon, South Korea*; 2. *Research Institute of Basic Sciences, Pusan National University, Busan, South Korea*

17:10 **Taxonomic studies of the Gonatozygaceae (Desmidiaceae)**

John D. Hall¹ and Charles F. Delwiche²

1. *Science, Cullman Program, New York Botanical Garden, Bronx, NY, USA*; 2. *CBMG, University of Maryland, College Park, MD, USA*

17:30 **Phylogeny of the Characeae (Charophyta) based on chloroplast sequence data**

Kenneth G. Karol¹, Michelle T. Casanova², William Pérez¹, Vernon W. Proctor⁴ and Richard M. McCourt³

1. *Cullman Program, The New York Botanical Garden, Bronx, NY, USA*; 2. *Royal Botanic Gardens, Melbourne, VIC, Australia*; 3. *Department of Botany, Academy of Natural Sciences, Philadelphia, PA, USA*; 4. *Department of Biological Sciences, Texas Tech University, Lubbock, TX, USA*

St. Charles Room; Danna Center, Tuesday Evening 18:30 – 20:30:

Poster Session

Hot and cold hors d'oeuvres and a cash bar

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 18:30 and 19:30.

Presenting authors of EVEN numbered posters are requested to stand with their posters at least between 19:30 and 20:30.

- P1 **Production of Dimethyl sulphide (DMS) and Dimethylsulfoniopropionate (DMSP) by the coccolithophore haptophyte alga *Emiliania huxleyi***
Mostafa M. El-Sheekh¹ and Yoshihiro Shiraiwa²
1. Botany, faculty of Science, Tanta University, Tanta, Egypt; 2. Bioscience, Graduate School of Life and Environmental Sciences, Tsukuba, Japan
- P2 **Filamentous algal endophytes in antarctic macroalgae: incidence and palatability**
Charles D. Amsler¹, Margaret O. Amsler¹, James B. McClintock¹ and Bill J. Baker²
1. Department of Biology, University of Alabama at Birmingham, Birmingham, AL, USA; 2. Department of Chemistry, University of South Florida, Tampa, FL, USA
- P3 **Algal biodiversity and conservation: preparing the next generation of practitioners**
Russell L. Chapman
Center for Marine Biodiversity and Conservation, Scripps Institution of Oceanography, University of California San Diego, La Jolla, CA, USA
- P4 **Untreated Urban Effluent Effects on Phytoplankton Community Structure and Function in Lake Pontchartrain, LA**
James L. Pinckney², James L. Wee¹, Meghan Jelloe², Michael Coggins² and Danielle Johnson²
1. Biological Sciences, Loyola University-New Orleans, New Orleans, LA, USA; 2. Marine Science Program and Biological Sciences Department, University of South Carolina, Columbia, SC, USA
- P5 **Recruitment inhibition, reproductive inundation, and coexistence between dominant subtidal algal crusts and kelps.**
Daniel K. Okamoto, Michael S. Stekoll and Ginny L. Eckert
School of Ocean and Fisheries Sciences, University of Alaska Fairbanks, Juneau, AK, USA
- P6 **Combined Effects of Grazing and Nutrients on Benthic Algae in a Freshwater Marsh, Alaska**
Allison R. Rober¹ and R. J. Stevenson^{1,2}
1. Zoology, Michigan State University, East Lansing, MI, USA; 2. Center for Water Sciences, Michigan State University, East Lansing, MI, USA

- P7 **Effects of experimental nutrient enrichment on benthic algae and algal-derived DOC in a boreal wetland, Alaska**
Kevin H. Wyatt¹ and R. J. Stevenson^{1,2}
1. Zoology, Michigan State University, East Lansing, MI, USA; 2. Center for Water Sciences, Michigan State University, East Lansing, MI, USA
- P8 **Translating Research in Education: A Paleoclimatology Example**
Jeannette Hoffer and Matthew Julius
St. Cloud State University, St. Cloud, MN, USA
- P9 **Influence of habitat's complexity in the toxicity of some marine macroalgae**
Graciela De Lara-Isassi, Sergio Alvarez-Hernandez, Cruz Lozano-Ramirez and Monica Rodriguez-Palacio
Hidrobiologia, Universidad Autonoma Metropolitana-Izatapalapa, Mexico, Mexico
- P10 **Seasonal variation in nutrients and microalgal community composition in Mobile Bay, Alabama, and the northern Gulf of Mexico**
Emily A. Goldman¹, William L. Smith², Kyeong Park¹ and Hugh L. MacIntyre¹
1. Dauphin Island Sea Lab, Dauphin Island, AL, USA; 2. Alabama Department of Public Health, , Mobile, AL, USA
- P11 **Desiccation controls the upper limit of species distribution among blooming ulvoid macroalgae**
Jennifer K. Olson, Lydia D. Imhoff and Timothy A. Nelson
Biology, Seattle Pacific University, Seattle, WA, USA
- P12 **Using underwater video analysis to determine large-scale spatial and temporal changes in macroalgal bloom occurrence**
Lydia D. Imhoff, Jennifer K. Olson and Timothy A. Nelson
Department of Biology, Seattle Pacific University, Seattle, WA, USA
- P13 **Probing The Relationship Between Movement Modalities In *Cylindrotheca closterium* (Bacillariophyceae): Effects Of Osmotic Shock And Cytoskeletal And Metabolic Inhibitors On Movement**
Melba D. Apoya-Horton^{2,1}, Graham J. Underwood³ and Michael R. Gretz²
1. Biological & Environmental Sciences, McNeese State University, Lake Charles, LA, USA; 2. Biological Sciences, Michigan Technological University, Houghton, MI, USA; 3. Biological Sciences, University of Essex, Colchester, United Kingdom
- P14 **Eutrophication Assessment of Lagoonal Detention Ponds in South Carolina, U.S.A.**
Kenneth Hayes¹ and Alan Lewitus²
1. Baruch Institute, University of South Carolina, Summerville, SC, USA; 2. Center for Sponsored Coastal Ocean Research, NOAA, Silver Spring, MD, USA
- P15 **4-Nonylphenol binding to glass as a possible toxicity mechanism in diatoms**
Joshua Stepanek, Robert Janisch and Matthew Julius
St. Cloud State University, St. Cloud, MN, USA
- P16 **Mono- and digalactosylacylglycerol composition of *Lepidodinium chlorophorum*, *Karenia brevis*, and *Kryptoperidinium foliaceum*, three dinoflagellates with aberrant plastids**
Andrew Lasiter and Jeff Leblond
Department of Biology, Middle Tennessee State University, Murfreesboro, TN, USA
- P17 **Euglenophycin-a toxin produced by certain Euglenoids**
Paul Zimba¹, Peter Moeller², Kevin Beauchesne² and Richard Triemer³

1. Catfish Genetics Research Unit, usda/ars, Stoneville, MS, USA; 2. Hollings Marine Lab., NOAA, Charleston, SC, USA; 3. Plant Biology, Michigan St Univ, East Lansing, MI, USA

- P18 **Myosin diversity in the marine pennate diatom *Phaeodactylum tricornutum***
Matthew B. Heintzelman and Matthew E. Enriquez
Biology, Bucknell University, Lewisburg, PA, USA
- P19 **Analyzing The Euglenoid Plastid Genome**
Makbule S. Sahin¹, Richard E. Triemer^{2,1} and Eric W. Linton¹
1. Biology, Central Michigan University, Mount Pleasant, MI, USA; 2. Plant Biology, Michigan State University, East Lansing, MI, USA
- P20 **Development of species-specific, multiplex PCR assays for the detection and quantification of *Prymnesium parvum* Carter (Haptophyta) in natural bloom samples**
Schonna R. Manning and John W. La Claire
Section of Molecular, Cell and Developmental Biology, The University of Texas, Austin, TX, USA
- P21 **Morphology and phenology of *Gelidium elegans* (Rhodophyta)**
Jeongkwang Park
CHUNGNAM NATIONAL UNIVERSITY, Daejeon, South Korea
- P22 **Characterization of Paramylon Morphological Diversity in Photosynthetic Euglenoids**
Emily Bellairs¹, Anna K. Monfils¹ and Richard Triemer²
1. Biology, Central Michigan University, Mt. Pleasant, MI, USA; 2. Plant Biology, Michigan State University, East Lansing, MI, USA
- P23 **The genus *Grateloupia* (Halymeniaceae, Rhodophyta) in Korea**
Ah Young Kim, Paul John L. Geraldino and Sung Min Boo
Biology, Chungnam National University, Daejeon, South Korea
- P24 **Marine Algae and Early Explorations in the Upper North Pacific and Bering Sea.**
Michael J. Wynne
Ecology and Evolutionary Biology and Herbarium, University of Michigan, Ann Arbor, MI, USA
- P25 **Biodiversity survey of Hawaiian red algae, and data display via the Hawaiian Algal Database**
Alison Sherwood¹, Akira Kurihara¹, Kimberly Conklin¹, Norman Wang², Thomas Sauvage¹ and Gernot Presting²
1. Botany, University of Hawaii, Honolulu, HI, USA; 2. Molecular Biosciences and Bioengineering, University of Hawaii, Honolulu, HI, USA
- P26 **A preliminary phylogeny of the Cymbelloid diatoms using molecular data with emphasis on the genera *Didymosphenia* M. Schmidt and *Navicymbula* Krammer**
Teofil Nakov¹, Sarah Spaulding² and Edward Theriot¹
1. Plant Biology, University of Texas at Austin, Austin, TX, USA; 2. US Geological Survey, Boulder, TX, USA
- P27 **Ultrastructure and molecular phylogeny of the genus *Mallomonas* (Synurophyceae) in Korea**
Jo BokYoen and Shin Woongghi
Biology, Chungnam National University, Daejeon, South Korea

- P28 **Zygnemataceae (Zygnematophyceae) from Southern California coastal watersheds**
Rosalina Stancheva¹, Robert G. Sheath¹ and Kirsten M. Müller²
 1. *Biology, California State University San Marcos, San Marcos, CA, USA*; 2. *Biology, University of Waterloo, Waterloo, ON, Canada*
- P29 **Description of a new family, Phacusaceae (Euglenophyta), and multigene analysis of photosynthetic euglenoids**
Jong-Im Kim¹, Richard E. Triemer² and Woongghi Shin¹
 1. *Department of Biology, Chungnam National University, Daejeon, South Korea*; 2. *Department of Plant Biology, Michigan State University, East Lansing, MI, USA*
- P30 **Phylogeny of two unusual chrysophytes, Anthophysa and Phaeodermatium**
 Paul Kugrens², Ian Misner¹, Kristi Sommer¹ and Craig Bailey¹
 1. *Center For Marine Science, University of North Carolina Wilmington, Wilmington, NC, USA*; 2. *Department of Biology, Colorado State University, Fort Collins, CO, USA*
- P31 **Systematics of the Rhapidoophyceae (Heterokontophyta)**
Brooke Stuercke, J. C. Bailey and Carmelo R. Tomas
Center for Marine Science, University of North Carolina Wilmington, Wilmington, NC, USA
- P32 **A molecular comparison of drift and attached green tide species in Narragansett Bay, RI**
Meghan Tracy¹, Brian Wysor¹, Michelle Guidone² and Carol Thornber²
 1. *Department Biology, Marine Biology & Environmental Science, Roger Williams University, Bristol, RI, USA*; 2. *Department of Biological Sciences, University of Rhode Island, Kingston, RI, USA*
- P33 **A preliminary assessment of macroalgal diversity in Bocas del Toro, Caribbean Panama**
Brian Wysor¹, D. Wilson Freshwater², Suzanne Fredericq³ and James Norris⁴
 1. *Department of Biology, Marine Biology & Environmental Science, Roger Williams University, Bristol, RI, USA*; 2. *Center for Marine Sciences, University of North Carolina - Wilmington, Wilmington, NC, USA*; 3. *Department of Biology, University of Louisiana at Lafayette, Lafayette, LA, USA*; 4. *Department of Botany, National Museum of Natural History, Smithsonian Institution, Washington, DC, DC, USA*
- P34 **New Taxonomic Insights in the Red Algal Order Rhodymeniales**
William Schmidt and Suzanne Fredericq
Biology, University of Louisiana at Lafayette, Lafayette, LA, USA
- P35 **Fucus (Heterokontophyta; Phaeophyta) biogeography across North American shores**
Robert G. Young¹, Walter H. Adey² and Kirsten M. Müller¹
 1. *Biology, University of Waterloo, Waterloo, ON, Canada*; 2. *Marine Systems Laboratory, Smithsonian Institution, Washington DC, MD, USA*
- P36 **An experimental elucidation of cell-to-cell communication via pit plugs in the red alga Caloglossa (Harvey) G. Martens (Delesseriaceae, Ceramiales)**
David M. Kravesky and Suzanne Fredericq
Dept. of Biology, University of Louisiana, Lafayette, LA, USA
- P37 **Determining the number of membranes surrounding the chloroplast of three euglenoid species: Lepocinclis acus, Euglena gracilis, and Euglena sanguinea**
Brittany Fritz¹, Richard E. Triemer^{2,1} and Eric W. Linton¹
 1. *Biology, Central Michigan University, Mount Pleasant, MI, USA*; 2. *Plant Biology, Michigan State University, East Lansing, MI, USA*

- P38 **Development of a Modular Integrated Recirculating Aquaculture System Using *Porphyra* for Bioremediation of Marine Finfish Effluent**
Jennifer P. Day¹, Christopher D. Neefus¹ and Charles Yarish²
 1. *Department of Plant Biology, University of New Hampshire, Durham, NH, USA*; 2. *Department of Ecology & Evolutionary Biology, University of Connecticut, Stamford, CT, USA*
- P39 **Is it Safe to Drink the Water?: Filtering Algal Toxins in Rural Settings**
Rachel Lindgren and Matthew Julius
Biology, St. Cloud State University, St. Cloud, MN, USA
- P40 **Isolation, pilot scale mass culture of mono-strain and antioxidant effects of two freshwater microalgae *Pediastrum duplex* and *Dactylococcopsis acicularis* from a rocky pool of natural stream**
Joon-Baek Lee^{1,2}, Abu Affan³, Rohan Karawita¹ and You-Jin Jeon¹
 1. *Faculty of Applied Marine Sciences, College of Ocean Sciences, Cheju National University, Jeju, South Korea*; 2. *Inst. Marine and Coastal Sciences, Rutgers University, New Brunswick, NJ, USA*; 3. *Open & Tropical Ocean Research Division, Korea Ocean Research & Development Institute, Ansan, South Korea*
- P41 **Blooms of *Didymosphenia geminata* in rivers on Vancouver Island 1990 to present: A new invasive species**
Max L. Bothwell¹, D. R. Lynch¹, J. Deniseger² and H. Wright³
 1. *Environment Canada, Nanaimo, BC, Canada*; 2. *British Columbia Ministry of Environment, Nanaimo, BC, Canada*; 3. *British Columbia Conservation Foundation, Nanaimo, BC, Canada*
- P42 **Advances in understanding, predicting and tracking Oregon harmful algal blooms**
 Pete Strutton^{1,6}, Michelle Wood^{2,6}, Jacqui Tweddle^{1,6}, Deb Cannon³, Matt Hunter⁴, Dave Foley^{5,6} and Brittany Scott²
 1. *College of Oceanic and Atmospheric Sciences, Oregon State University, Corvallis, OR, USA*; 2. *Ecology and Evolution, University of Oregon, Eugene, OR, USA*; 3. *Food Safety Division, Oregon Dept. of Agriculture, Salem, OR, USA*; 4. *Marine Resources Program, Oregon Dept. of Fish and Wildlife, Salem, OR, USA*; 5. *West Coast Regional Node, NOAA Coast Watch, Pacific Grove, CA, USA*; 6. *CIOSS: Cooperative Institute for Oceanographic Satellite Studies, Oregon State University, Corvallis, OR, USA*

Wednesday, 30 JULY

Nunemaker Hall; Monroe Hall, Wednesday Morning:

Plenary Session - Algal Biotechnology

Moderator: Donald Cheney, Northeastern University

08:00 Opening Remarks

08:10 **Commercial production of highly unsaturated fatty acids by microalgae: lessons for biofuels production.**

Bill Barclay¹, C. Weaver¹, J. Metz¹, J. Flatt¹ and J. Hansen²

1. Martek Biosciences, Boulder, CO, USA; 2. Martek Biosciences, Winchester, KY, USA

09:10 **Lipid pathways of *Schizochytrium* and their export to heterologous systems.**

Casey Lippmeier

Martek Biosciences, Columbia, MD, USA

09:40 **Manipulation of *Schizochytrium* genes for improved fatty acid production.**

Craig Weaver¹, R. E. Zirkle¹, D. H. Doherty¹, J. Lippmeier² and J. G. Metz¹

1. Martek Biosciences, Boulder, CO, USA; 2. Martek Biosciences, Columbia, MD, USA

10:10 **COFFEE BREAK -- St. Charles Room, Danna Center**

Miller 114; Miller Hall, Wednesday Morning:

Ecology & Population Biology - II

Moderator: Paul Zimba, USDA-ARS

10:40 **Use of heterotrophic “helpers” improves cultivability of phytoplankton**

James J. Morris¹, Robin Kirkegaard¹, Martin J. Szul¹, Zackary I. Johnson², Alison Buchan¹, Martin Keller³ and Erik R. Zinser¹

1. Microbiology, University of Tennessee, Knoxville, TN, USA; 2. Oceanography, University of Hawai'i, Honolulu, HI, USA; 3. Oak Ridge National Laboratory, Oak Ridge, TN, USA

11:00 **The sacoglossan sea slug, *Elysia clarki*, feeds on and sequesters functional chloroplasts from a wide taxonomic range of ulvophyceean algae.**

Nicholas Curtis, Julie A. Schwartz and Sidney K. Pierce

University of South Florida, Tampa, FL, USA

11:20 **Abundance and toxicity of *Karlodinium veneficum* bloom in Weeks Bay National Estuarine Research Reserve, Alabama**

Lucie Novoveska¹, William L. Smith², Allen R. Place³ and Hugh L. MacIntyre¹

1. Dauphin Island Sea Lab and University of South Alabama, Dauphin Island, AL, USA; 2. Alabama Department of Public Health, Mobile, AL, USA; 3. Center of Marine Biotechnology, Baltimore, MD, USA

11:40 **Population genetics and phylogeography of the pantropical alga *Acanthophora spicifera* (Rhodophyta) as revealed by multilocus microsatellite genotyping and DNA sequencing**
Daniel C. O'Doherty and Alison R. Sherwood
Botany, University of Hawaii, Honolulu, HI, USA

12:00 **Monitoring toxic cyanobacteria in western Washington**
Gabriela Hannach¹, D. Bouchard² and J. Frodge²
1. Environmental Lab, King County, Seattle, WA, USA; 2. Water and Land Resources, King County Dept. of Natural Resources and Parks, Seattle, WA, USA

12:20 **LUNCH -- St. Charles Room, Danna Center**

Library Multi-Media 1; Monroe Library, Wednesday Morning:

Algal Biotechnology

Moderator: Ray Lewis, Wheaton College

10:40 **Regulation of Polyunsaturated Fatty Acid Production in the Marine Red Macroalga *Porphyra yezoensis***
Donald Cheney, Angela Silvestro, Yen-Chun Liu and Leslie Graham
Biology, Northeastern University, Boston, MA, USA

11:00 **Microalgae-Based Biofuel: A Perspective on the State of the Science**
Milton R. Sommerfeld and Qiang Hu
Applied Biological Sciences, Arizona State University, Mesa, AZ, USA

11:20 **Characterization of triacylglyceride accumulation in the model diatoms *Thalassiosira pseudonana* and *Phaeodactylum tricorutum*.**
Todd W. Lane¹, Eizadora Yu¹, Frank Zendejas², Pamela Lane¹ and Blake Simmons²
1. Biosystems Research, Sandia National Labs, Livermore, CA, USA; 2. Energy Systems, Sandia National Labs, Livermore, CA, USA

11:40 **Susceptibility and Protective Mechanisms of Motile and Non-Motile Cells of *Haematococcus pluvialis* (Chlorophyceae) to Photooxidative Stress**
Danxiang Han¹, Zhengyu Hu², Milton Sommerfeld¹ and Qiang Hu¹
1. Applied Biological Sciences, Arizona State University, Mesa, AZ, USA; 2. Institute of Hydrobiology, the Chinese Academy of Sciences, Wuhan, China

12:00 **TBA**

12:20 **LUNCH -- St. Charles Room, Danna Center**

Miller 114; Miller Hall, Wednesday Afternoon:

Phylogenetics & Taxonomy - IV

Moderator: J. Craig Bailey, UNC Wilmington

- 13:40 **How ecologically permissive are Pseudanabaenalean (Cyanobacteria) genera? A plethora of new clades when different habitats are contemplated.**
Dale A. Casamatta¹, Jeffrey R. Johansen² and Ralph B. Perkinson¹
1. Biology, University of North Florida, Jacksonville, FL, USA; 2. Biology, John Carroll University, University Heights, OH, USA
- 14:00 **Untangling cyanobacterial systematics: erection of *Emicolynghya* gen. nov. from a polyphyletic clade of *Leptolynghya* (Cyanobacteria).**
Ralph Perkinson¹, Lubomir Kovacik³, Jerry Brand² and Casamatta Dale¹
1. University of North Florida, Jacksonville, FL, USA; 2. School of Biological Sciences, University of Texas, Austin, TX, USA; 3. Department of Botany, Comenius University, Bratislava, Slovakia
- 14:20 **Systematics of the Batrachospermales (Rhodophyta) - A Synthesis**
Timothy J. Entwistle², Morgan L. Vis¹, Wayne B. Chiasson¹, Orlando Necchi³ and Alison R. Sherwood⁴
1. Department of Environmental & Plant Biology, Ohio University, Athens, OH, USA; 2. Botanic Gardens Trust, Mrs Macquaries Road, Sydney, NSW, Australia; 3. Zoology and Botany Department, São Paulo State University, São José do Rio Preto, Brazil; 4. Department of Botany, University of Hawaii, Honolulu, HI, USA
- 14:40 **New insights in the red algae of the Gulf of Mexico**
Suzanne Fredericq, David Kravesky, William Schmidt, Natalia Arakaki, Brigitte Gavio, Showe-Mei Lin, Fred Gurgel, Daniela Gabriel, Boo Yeon Won, Tae Oh Cho and Constanza Ehrenhaus
Biology, University of Louisiana at Lafayette, Lafayette, LA, USA
- 15:00 **Investigation on the Worldwide Distributed Subaerial Green Alga *Cephaleuros virescens***
Sarah M. Noble and Juan M. López-Bautista
Biological Sciences, The University of Alabama, Tuscaloosa, AL, USA
- 15:20 **A molecular phylogenetic study of the red algal parasites *Benzaitenia yenoshimensis*, *Janczewska hawaiiiana*, *J. morimotoi*, and *Ululania stellata* (Rhodomelaceae, Ceramiales) from Hawaii and Japan**
Akira Kurihara¹, Tsuyoshi Abe², Masaya Tani³ and Alison R. Sherwood¹
1. Botany, University of Hawaii, Honolulu, HI, USA; 2. Hokkaido University Museum, Sapporo, Japan; 3. Biological Sciences, Hokkaido University, Sapporo, Japan

Louisiana Swamp Exhibit, Audubon Zoo, Wednesday Evening:

18:30-22:00 – PSA Banquet and Awards Ceremony

ABSTRACTS

ABSTRACTS NUMBERS ARE VERY CLOSE TO ABSTRACT PRESENTATION ORDER .

SEE AUTHOR INDEX ON PAGE 74 TO FIND SPECIFIC ABSTRACTS.

1

Harmful Algal Blooms in North America: Common Risks

Steidinger, Karen A.

Florida Institute of Oceanography, St. Petersburg, FL, USA

All harmful algal blooms (HABs), no matter where they occur, can present common risks to public and natural resources health. For example, HABs can cause obvious effects such as dead floating animals in lakes or seas, toxic shellfish, or they can cause subtle effects such as altering the trophic structure of a community. Why are HABs harmful? First, such blooms often have high biomass that can cause oxygen depletion. Second, many of the microalgal HAB species produce potent toxins, such as brevetoxins, saxitoxins, palytoxins, domoic acid, microcystins, and anatoxins. The major common risk from HABs is the transfer of biotoxins through the food web. Toxins can be vectored through freshwater environments to terrestrial interfaces, for example to birds, or in the marine environment to planktivorous fish to seabirds and marine mammals. The HAB species involved, the vectored toxins, the transfer pathways, and the systems may all differ and the results may vary, but the endpoint will be measured by the risk to public health safety or animal health. Unfortunately, not all chronic risks are studied. The core of the HAB problem in North America, like elsewhere, is the causative species and the respective toxins. Some species are cosmopolitan while others are restricted by geographic area and season. Some toxic species have even been transported to new areas by major currents or in ballast sediment/water. Compounding distribution and occurrence, and therefore the risk of exposure, is an ecophysiological-genetic determinant of whether toxicity is expressed or repressed, or whether there are toxic or nontoxic strains, even in the same locale. By knowing the geographic area, it is possible to speculate which HAB species may be present and consequently determine the public health and environmental risks. Where shellfish poisonings are caused by known phycotoxins, the general risk scenario is known and managed by monitoring and regulating the exposure route to reduce the risk. However, newly discovered toxins or toxic species, as well as newly discovered at-risk populations, together with other unknowns on the horizon, serve to hone response and action plans.

2

Unexpected vectors of brevetoxins to marine mammals

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Brevetoxins produced by the Florida red tide dinoflagellate *Karenia brevis* are known to induce massive fish kills and to cause illness in humans who consume toxic filter-feeding shellfish or inhale aerosolized toxin. Although brevetoxins have been suspected of causing several large-scale mortalities of manatees (*Trichechus manatus latirostris*) and bottlenose dolphins (*Tursiops truncatus*), establishing brevetoxicosis as the cause has often been hindered by limited confirmation of toxin exposure in a fraction of the animals, diagnoses and interpretation of additional complicating

pathologies, and unclear lethal routes of exposure. In each of the last six years, Florida's Gulf coast has witnessed red tide-related marine mammal mortality events; two occurring in the absence of detectable red tides, and shedding light on understudied routes of exposure for brevetoxin to higher vertebrates. In spring of 2002, 34 endangered Florida manatees died in southwest Florida, and in spring of 2004, 107 bottlenose dolphins died in the Florida Panhandle. In both cases, brevetoxin exposure was unambiguously confirmed by elevated concentrations in multiple tissues of all animals tested with extremely elevated concentrations in stomach contents, indicating exposure through ingestion. Field investigations identified high concentrations of brevetoxins in manatee and dolphin food sources, documenting for the first time brevetoxin associations with seagrass and in naturally-exposed fish respectively. Despite almost annual *K. brevis* blooms in the Gulf of Mexico, mass mortalities of marine mammals have been relatively rare. This documentation of brevetoxin accumulation in seagrass and in live fish reveals novel mechanisms for brevetoxin vectoring via the food web, demonstrates that vectored brevetoxins pose a tangible threat to marine mammals, and illustrates the potential for delayed or remote animal exposure to lethal brevetoxins in the absence of a concurrent *K. brevis* bloom.

3

The evolving story of *Gymnodinium galatheanum* = *Karlodium micrum* = *Karlodium veneficum*. A ten year perspective

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Karlodium veneficum (Dinophyceae) was first described as *Gymnodinium galatheanum* from Walvis Bay, Namibia in 1950 during the famed first Danish "Galathea" expedition. The taxonomy of this organism has changed several times in recent years with synonyms now including *G. micrum*, *G. veneficum*, and *K. micrum*. A family of amphipathic ichthyotoxins (karlotoxins - KmTXs) were first described from then *K. micrum* following an investigation of a large mortality event at HyRock fish farm, Maryland, USA in 1996. Interestingly, a toxic compound from a western Atlantic isolate of then *G. veneficum* was described in 1957 but the synonymy of these organisms was only recently determined. The events at HyRock were the first record of *K. veneficum* in the U.S. Prior to this, Maryland authorities had routinely seen this organism but identified it as *Gyrodinium estuariale*. Historical data later revealed that *G. estuariale* in Maryland waters had been associated with several unexplained fish kills. Nearly a decade after their first description, the large (>1300 Da.) linear polyketide structures of two of the karlotoxins, KmTX1 and KmTX2 have now been elucidated. During the past decade, much has been learned on the nature of these compounds. KmTXs function by increasing the ionic permeability of biological membranes resulting in osmotic cell lysis. They kill fish through damage to gill epithelia. The allelopathic, cytotoxic, and anti-fungal properties of KmTXs are due to differential membrane specificity determined by membrane sterol composition, which also appears to be responsible for the apparent immunity of *K. veneficum* to its own toxins. Ecologically, KmTXs appear to serve roles both in allelopathy and mixotrophic feeding. Since 1996, both *K. veneficum* and its toxins have been documented at numerous fish kills both domestically and abroad, most notably in association with seasonal fish mortalities in the Swan River, Western Australia. Researchers worldwide are now investigating various aspects of the ecology and toxicity of *K. veneficum*. It will be interesting to see what discoveries will be revealed in the next ten years for this fascinating organism.

4

Reconsideration of the classification of bangiophyte red algae using chloroplast and nuclear gene sequence analysis

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The red algae are an early-diverged lineage of Eukaryotes occurring globally in a wide range of habitats. These organisms have been traditionally placed into one division (Rhodophyta) and class (Rhodophyceae) and further divided into two subclasses (Bangiophycidae and Florideophycidae). Resolution of phylogenetic signal in ancient events while maintaining relationships among terminal nodes of the tree can be problematic. Consequently, due primarily to the age of the lineage, recent phylogenetic analyses of the Bangiophycidae have either low or inconsistent support for higher-order branching events, making taxonomic conclusions suspect. In these analyses structural information of the nuclear SSU rRNA gene was used to improve alignment of sequences. Additionally, deep phylogenetic relationships were evaluated by focusing analyses on slowly evolving non-stochastic sites including both co-varying sites and sites comprising the eukaryotic core of the ribosomal SSU. Clades of taxa were also screened for orthologous elements of secondary structure, further resolving phylogenies. The incorporation of secondary structure information into phylogenetic analyses significantly increased resolution and phylogenetic support for higher-order branching in the Bangiophycidae *sensu lato* relative to previous studies. This increased resolution provided insights into ancient evolutionary events in the Rhodophyta such as branching order, cladogenesis and the taxonomic relationships among the unicellular Rhodophyta. Additionally, synapomorphic elements of secondary structure of nSSU rRNA were observed for clades within the Bangiophycidae *sensu lato*. As a result, we propose a revised taxonomy of the Bangiophycidae *sensu lato* specifically reflecting higher-order phylogenetic relationships.

5

A Novel Modification of Nitrogen Metabolism Induced by Desiccation in *Porphyra*

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Desiccation determines the upper distribution limits of some algal species and affects the recovery of photosynthesis and nitrogen uptake upon resubmersion. Desiccation-induced changes in nitrogen metabolism are reported for *Porphyra* species. Thalli were cultivated in a greenhouse at natural light intensities, 10 °C, in a medium containing 30 µM nitrate and 3 µM phosphate. During 5-7 days acclimation, simulated semidiurnal tides exposed tissues for 2 or 4 hours during each emersion, and generated tissue water losses of 0% (no emersion), 40±10% (2 h emersion), and 90±5% (4 h emersion). Desiccation was more stressful to the sublittoral species *P. yezoensis* and lower littoral species *P. leucosticta* than to the upper littoral species *P. umbilicalis* in terms of growth. Nitrate uptake and nitrate reductase activity were negatively influenced by desiccation and showed similar diurnal patterns. However, glutamine synthetase activity was not impaired by desiccation and even appeared to be stimulated by desiccation. Interestingly, the desiccated *Porphyra* species contained more tissue N than controls that remained submerged. Also, the tissue N contents dropped during desiccation, and recovered within 0.5 h after re-submergence. Protein concentration also declined during desiccation, and recovered similar to tissue N contents. During desiccation, *Porphyra* may lose stored N, yet after re-submergence, they rapidly replenish their N stores. Since there was no evidence that *Porphyra* grew

during desiccation, *Porphyra* appears to have experienced a net loss of N during desiccation. One possible interpretation of our results is that tissue organic nitrogen was metabolized, releasing ammonia which diffused out of the thallus while *Porphyra* is exposed. Desiccation-induced release may constitute an undescribed biogeochemical pathway linking marine, terrestrial, and atmospheric N reservoirs.

6

Rethinking native species: evidence for repeated colonizations of *Spyridia filamentosa* (Ceramiales, Rhodophyta) in the Hawaiian archipelago

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The red alga, *Spyridia filamentosa*, is widely distributed in tropical and warm temperate locations and can be a dominant component of macroalgal communities in these areas. Recent molecular studies have demonstrated that *S. filamentosa* may consist of multiple, cryptic species. *Spyridia filamentosa* is considered a native alga in the Hawaiian Islands and is currently being evaluated for use in the restoration of habitat for the endemic seagrass, *Halophila hawaiiiana*, in Maunalua Bay, Oahu, by using the highly branched morphology of *S. filamentosa* to capture sediment, priming hard substrate for the later establishment of *H. hawaiiiana*. Morphologies that increase sediment-trapping capabilities may speed up *H. hawaiiiana* replanting efforts on hard substrate. It is necessary to resolve genetic variation within and between *S. filamentosa* populations to determine whether the movement and introduction of specific populations (e.g., highly branched morphs) of the alga can be considered. Two molecular markers were used to assess genetic relatedness of 130 collections of *S. filamentosa* from 52 locations on 13 islands in the Hawaiian archipelago: the mitochondrial *cox2-3* intergenic spacer region and a portion of the nuclear LSU rDNA region. Morphological characters (such as the number of periaxial cells in indeterminate branches) were assessed using herbarium and formalin vouchers. Reconstructed phylogenies based on the two markers placed Hawaiian *S. filamentosa* among worldwide samples in both the Pacific Ocean clade and the Atlantic Ocean/Indian Ocean/Mediterranean Sea clade, showing that considerable variation is present in Hawaiian populations and revealing evidence for repeated colonizations of *S. filamentosa* in Hawaii. Morphological assessments show high levels of plasticity among the clades and suggest Hawaiian *S. filamentosa* may have higher numbers of periaxial cells than previously recorded for this species. The molecular and morphological results of this study provide new insights into the phylogeography of *S. filamentosa* and have implications for its utilization in seagrass habitat restoration.

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Differential gene expression during growth of the harmful marine alga *Alexandrium fundyense*

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Alexandrium fundyense is a toxic dinoflagellate that causes harmful algal blooms (HABs) along the northeast coast of the United States. However, regulation of blooms is still not well understood, largely due to the lack of information on cell division rate (CDR) in situ. CDR is an important component of bloom modeling because, in addition to grazing and other processes, it directly regulates population dynamics. For this study, we are looking for genes that are differentially expressed during the cell cycle as potential molecular markers for estimating in situ CDR. We have constructed full-length cDNA microarrays to investigate global gene expression during the growth of *A. fundyense*. Samples for hybridization were harvested from a semi-continuous culture at different time points during the 24

hr photoperiod. Total RNA extracted was amplified, fluorescently labeled and hybridized to the microarrays. Abundance of the transcripts from different time points are compared and genes showing high levels of up- and down-regulation were validated using quantitative real-time PCR (qRT-PCR). The identification of growth markers will allow a quick snapshot of the cell's growth status, i.e. if the cells are actively dividing, and facilitate further development of qRT-PCR protocol for the estimation of CDR in situ. Results from this study will facilitate measurement of a critical parameter for modeling and predicting *A. fundyense* blooms and could enhance HAB forecasting efforts.

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A new *Champia* species (Champiaceae, Rhodophyta) from Puerto Rico

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Detailed morphological examination and DNA sequence analysis of specimens referable to *Champia parvula* has resulted in the recognition of a new *Champia* species. The new species bears strong resemblance to *C. parvula*, differing in branching pattern (opposite vs typically alternate), number of axes arising from holdfasts (4-7 vs 1-3), and in being monoecious. Molecular differences between *C. parvula* and the new species were confirmed using data from the rubisco large subunit (rbcL) gene and were highly supported for all optimality criteria tested. The new species clades most closely with *Champia parvula*, *C. vieillardii* and *C. compressa*.

9

Using reference site diatom communities for measuring the severity of human impacts on stream ecosystems

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Algae, especially diatoms, are crucial components of stream ecosystems, provide many important functional services, and respond to a variety of chemical and physical variables, making them especially useful in assessing human impacts on streams. For this study, 60 sites were sampled throughout southeastern Ohio for diatoms, chemistry, and land use variables. Of which, 10 were selected as reference sites meeting high quality habitat standards with high forestation in the watershed and no point source pollution. Diatom communities are expected to become less similar structurally to reference site communities as human impacts increase, and this can be used to measure the loss of ecological integrity attributed to stressors. Sites were scored using mean Bray-Curtis similarity to the 10 reference sites. Scores were significantly correlated ($p < 0.05$) with many measures of human disturbance, especially nutrients and cations. A stepwise canonical correspondence analysis selected pH, alkalinity, Ca, Mg, Na, SO₄, PO₄, and drainage area, which explained 31.2% of the variance in the diatom dataset. These variables indicated impairment along an agricultural gradient, and % agriculture was significantly correlated ($p < 0.01$) with the first two CCA axes. Sites were categorized as unimpaired, moderately impaired, and severely impaired based on their scores. ANOVAs detected significantly higher species diversity, less agriculture, and lower nutrients and conductivity in the least impaired sites. An additional 18 sites within the Leading Creek watershed were sampled for characterizing mining affiliated impairments. Scores and diatom communities reflected an acid mine drainage gradient and the effects of a mine waste discharge, as indicated by detrended correspondence analysis and multiple regressions. Diatom communities were very effective in characterizing agricultural and coal mining impairments.

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Redefining the Genus *Chondria* Agardh: A systematic and morphological approach.

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The genus *Chondria* (Rhodomelaceae) is a large genus considered to gather 75 species with a cosmopolitan distribution. Few studies have been performed on the genus as a whole, and the literature has been conflictive about what characters would be appropriate to identify species. Samples going under the name of *Chondria* were studied. For molecular studies the *rbcL* gene was chosen, the samples were also analyzed morphologically including cytoplasmatic and cell wall staining methods. Based on the results obtained we have circumscribed the genus *Chondria* to only species terete or flattened, with acute apices, cell wall thickenings and trichoblasts originating from the central cells. A new genus is proposed based on Falkenberg's subgenus *Coelochondria* represented by terete specimens with blunt apices and trichoblasts originating from the pericentral cells. A third monophyletic clade comprises another genus that gathers specimens terete or flattened with acute or blunt apices, no cell wall thickening and trichoblasts originating from the central cells. According to the data here obtained, the presence of a blunt apex seems to be a basal character, and the secondary flattening of the thallus has evolved multiple times within the group.

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Nutrient limitation and productivity of phytoplankton in the lower Laguna Madre, Texas

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The Lower Laguna Madre (LLM) is a subtropical lagoon in south Texas home to a thriving marine community dominated by seagrass. Significant nutrient inputs coming from municipal sewage treatment plants and agricultural/urban runoff from the Lower Rio Grande Valley (LRGV) including the most eutrophic waterway in Texas, the Arroyo Colorado, likely affect this coastal ecosystem. The fate of these nutrients is uncertain but is likely to stimulate productivity of phytoplankton in affected areas of the lagoon. The growing population in the LRGV will increase nutrient loading to the LLM and could result in nuisance micro- and macroalgal growth. For management purposes, it is critical to know which nutrient limits algal growth in the LLM. The goal of the proposed research is to determine which nutrient, nitrogen (N) or phosphorus (P) (or both, co-limitation), limit phytoplankton growth at three sites differing in nutrient regimes in the LLM: high (GI), medium (BW) and low (ABC). Assays were conducted in June, August, November 2007 and February 2008. For each site, there were four nutrient treatments (control, N, P, and N+ P) applied to triplicate 20-liter carboys of screened lagoon water. After a 1-4 day in situ incubation, photosynthetic rates and biomass accruals were measured. Phytoplankton photosynthetic rates were measured by the light and dark bottle method and monitoring dissolved oxygen change. Biomass accrual was estimated by chlorophyll a quantification. In June, a stimulatory effect of nutrient addition on net primary productivity was seen at BW (P) and GI (N or N+P)($p < .001$, both). In August, a stimulatory effect of nutrient addition on net primary productivity was seen at ABC (N) and GI (N)($p < .05$, both). At ABC N+P addition resulted in higher chlorophyll levels ($p < .05$). At GI, there was a stimulatory effect of N addition on biomass or productivity? in June ($p < .01$) but not August. Besides differences in treatment effects among sites, there were also seasonal differences in treatment response at each site. The results suggest that in order to accurately characterize phytoplankton nutrient limitation in the LLM it is important to consider temporal and spatial heterogeneity.

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Uniflagellar mutants in *Chlamydomonas reinhardtii* provide insights into basal body maturation and flagellar formation

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Chlamydomonas reinhardtii is a unicellular volvocalean green alga used as a model biological system for the study of basal bodies and flagella. *Chlamydomonas* cells are typically biflagellate, but some mutant strains have been identified that contain a high percentage of uniflagellate cells. All uniflagellar mutants preferentially assemble a flagellum from the older basal body positioned *trans* to the eyespot. Previously, we characterized the mutant *uni2* phenotype and the Uni2 protein, a 132 kD phosphoprotein with a large central coiled-coil domain (Piasecki et al., 2008 Mol. Biol. Cell 19, 262). Using an epitope-tagged Uni2 protein, we demonstrated that the Uni2 protein is a component of probasal bodies and basal bodies and provides a useful marker of basal body assembly during the mitotic cycle. This tagged protein can be used to report the position of basal bodies/probasal bodies in a diverse array of strains. To explore the function of the *UNI2* gene, we examined potential interactions with other *UNI* genes. Immunoblot analysis of the Uni2 protein in the *uni1* mutant demonstrated a 10-fold reduction in the phosphorylated Uni2 protein isoform. We generated a *uni1, uni2* double mutant, which contained almost entirely aflagellate cells. Ultrastructural analysis of basal bodies in the double mutant demonstrated it contained enhanced transition zone defects. Serial transverse sections through basal bodies in *uni1* and *uni2* single and double mutant cells revealed a previously undescribed defect in the transition from triplet microtubules of the basal body to doublet microtubules of the axoneme, a defect correlated with failure to assemble flagella. Immunogold electron microscopy revealed that the Uni2 protein localizes at the distal end of basal bodies where the transition of microtubules occurs. These results provide the first mechanistic insights into the pathways mediating the assembly of nine doublet microtubules of the axoneme from the nine triplet microtubule template of the basal body and suggest an overlap in the pathways facilitating microtubule transition and basal body maturation. This work was supported by NSF grant MCB-0344661.

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Spatial and temporal variability in abundance of the diatom *Pseudo-nitzschia* sp. in coastal Alabama waters

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The potentially-toxic diatom *Pseudo-nitzschia* is common in the northern Gulf of Mexico. In coastal Alabama, its abundance is monitored by the departments of Public Health (ADPH) and Environmental Management (ADEM) and the Dauphin Island Sea Lab. Seven sites along the Alabama Gulf Coast are monitored weekly to bi-weekly for potentially-toxic microalgae in the BEACH program. *Pseudo-nitzschia* was detected at densities up to 10⁶ per liter in 380 of 606 routine samples (63%) taken between November, 2003, and May, 2007. A cluster analysis of the frequency distributions of abundance at the sites showed that the site of Little Lagoon Pass had a strong dissimilarity compared to other sites. This was due to a higher frequency of bloom densities and a lower frequency of absences, indicating that it is a regional “hot-spot” for *Pseudo-nitzschia*. Distributions showed no apparent relationship with temperature, over the range 10 -34 C. There was a weak positive relationship between salinity and abundance, over the range 3 - 35 PSU. *Pseudo-nitzschia* was absent more frequently from brackish sites. Peaks in abundance occurred in April-May, with secondary peaks in

fall. Analysis of field surveys within Little Lagoon show a positive relationship between groundwater level and *Pseudo-nitzschia* abundance at this site.

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It's not easy being green: the origin of *Euglena longa*

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Growth of *Euglena gracilis* with various antibacterial agents leads to a permanent loss of green colony forming ability, bleaching. *Euglena longa* resembles a bleached *E. gracilis*. The discovery of a reduced *E. longa* plastome homologous to the *E. gracilis* plastome suggests *E. longa* is not a bleached *E. gracilis*. To evaluate the role of bleaching in *E. longa* evolution, we compared the effects of two bleaching agents, streptomycin, a plastid protein synthesis inhibitor, and ofloxacin, a plastid DNA gyrase inhibitor, on growth and plastid DNA content of *E. gracilis* and *E. longa*. *E. gracilis* growth over six weeks was unaffected by streptomycin and ofloxacin but cells bleached after 24 hours. PCR analysis of 29 chloroplast genes spanning the plastome including genes for tRNAs, rRNAs, ribosomal proteins, photosynthetic proteins, RNA polymerase subunits, tufA, ycf13 and the presumptive replication origin found that levels of a number of chloroplast genes clustered in noncontiguous regions of the genome were unaltered during six weeks of culture while adjacent genes were barely detectable after the first week. Plastome genes are deleted during bleaching at different times in a discontinuous fashion producing a smaller incomplete possibly rearranged genome. Nuclear and mitochondrial gene levels were unaltered. In contrast to *E. gracilis*, streptomycin completely inhibited *E. longa* growth while ofloxacin inhibited growth approximately 50 % indicating growth requires a functional plastid. Neither agent decreased *E. longa* plastid gene levels. These results suggest that the first step in *E. longa* divergence from *E. gracilis* was loss of a nuclear encoded metabolic activity duplicated in the plastid making a functional plastid an absolute requirement for cell growth. Subsequently over time in numerous rounds of a bleaching like process perhaps triggered by bleaching agents, plastid genes were deleted and rearranged. The absolute requirement of a plastid for cell growth coupled with availability of utilizable carbon sources produced a strong selection pressure preventing “housekeeping” gene loss while allowing photosynthetic gene loss eventually producing the reduced rearranged plastome of *E. longa*.

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The Value of Monitoring the Cell Cycle in Relation to Physiological and Molecular Changes in Phytoplankton

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In phytoplankton, cell cycle effects have both general and specific influences over cellular processes, and in turn, different cellular processes can affect progression through the cell cycle. Limitation of growth by different factors (light, specific nutrients) can cause cells to either arrest in, or prolong their time in, particular stages of the cell cycle, which makes it important to distinguish between cell cycle effects and direct effects of limitation. Cell cycle effects can also lead to significant underestimates of kinetic parameters. Synchronized growth that enables progression of cells through the same cell cycle stage at the same time is a powerful tool to determine the specificity of a physiological or molecular response. We developed a silicon starvation-recovery synchrony procedure for the diatom

Thalassiosira pseudonana that enables evaluation of events throughout the cell cycle. This procedure revealed cell-cycle-specific changes in silicon transporter (SIT) mRNA and protein levels, as well as transport activity. The synchrony procedure enabled enrichment of cell wall formation structural intermediates. Cells of *T. pseudonana* starved for silicon became arrested in the early G1 phase of the cell cycle, and after silicate replenishment, girdle band synthesis occurred in a particular period in G1. Cells did not lengthen in accordance with each girdle band added, which has implications for cell growth and separation processes in diatoms. Measurements of silicic acid uptake, intracellular pools, and silica incorporation into the cell wall provided the first direct measurements of silica amounts in individual girdle bands and valves in a diatom. Fluorescence imaging indicated why valves in *T. pseudonana* do not have to reduce in size with each generation. The synchrony procedure also facilitates interpretation of genomic and transcriptomic information.

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Two highly diverging flavodoxin genes and their transcription under iron stress conditions in *Trichodesmium* (Oscillatoriales, Cyanophyceae)

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We analyzed flavodoxin gene sequences and transcription patterns in the marine nitrogen-fixing cyanobacterium *Trichodesmium* Ehrenberg ex Gomont 1892 under contrasting iron and nitrate conditions. While a typical cyanobacterial flavodoxin ortholog (fld1) was identified from cultured and environmental *Trichodesmium* by PCR and Southern blot hybridization, a second flavodoxin (fld2) was identified in the genome sequence. BLAST and phylogenetic analyses indicated that the two fld genes were highly divergent: fld1 clustered with the ortholog common in cyanobacteria, while fld2 homologs were only found in the marine unicellular diazotrophic cyanobacterial genera *Cyanothece* and *Crocospaera*. This cyanobacterial fld2 cluster was nested in non-cyanobacterial diazotrophs such as *Azotobacter* and *Azoarcus*. Real-Time RT-PCR revealed remarkable diel variations in transcription levels of both flds (normalized to 16S rRNA) but failed to show induction under iron stress conditions. Addition of nitrate to cultures depressed nifH and fld2 transcription while elevating the transcription of fld1 in iron-stressed cultures. The data suggest that the two flavodoxins in *Trichodesmium* may be associated with different biochemical pathways.

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Assessing Bait Worm Packaging as a Potential Vector of Invasive Species Introductions into Long Island Sound

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The ecological and economic health of Long Island Sound (LIS) currently is being threatened by introductions of invasive species. To mitigate risk of introducing non-native species, it is important to examine potential vectors and determine whether or not they are contributing to this risk. This project is researching the potential for the seaweed *Ascophyllum nodosum* packaged with bait worms as a vector of invasive or harmful algae to LIS. Oftentimes, this seaweed is discarded into the Sound by either fishermen after using the bait or by retailers discarding spoiled materials, and any spores or cysts

of non-native species included within this seaweed may then be introduced into the water. Bait is purchased from several commercial vendors in Connecticut and New York. Subsamples of the seaweed and associated seagrass are placed in culture medium at three temperatures so that growth of associated macro-algae can be monitored. The remaining seaweed is shaken in seawater and filtered to release any spores or cysts of potentially invasive micro-algae, and this filtrate is also cultured. In addition, microscopic analyses on general algal composition and molecular analyses for specific microalgal species sequences are conducted. Data collected thus far indicate that no harmful or non-native seaweed are likely being introduced through this practice. Two species of toxic microalgae (*Alexandrium* and *Psuedonitzschia*) have been found by molecular methods, supporting the expectation that these methods may be more sensitive in detecting cryptic or unculturable micro-algae. Findings are expected to guide future management control of bait worms and appropriate disposal methods.

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Climate change, energy scarcity, and sustainable management of the Mississippi delta

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The Mississippi delta, one of the largest contiguous coastal ecosystems in the world, was formed by an overlapping series of delta lobes. The delta is important ecologically and economically. It has a vast area of wetlands (5 million ha) that is home to large populations of wildlife and supports one of the largest fisheries in North America. During the 20th century, there was a high rate of coastal wetland loss (up to 100 km²/yr) that was mainly attributable to human impacts such as 1) levee construction along the Mississippi River, resulting in elimination of riverine input to most coastal wetlands, and 2) pervasive hydrologic alterations within the delta due. These hydrologic changes resulted in saltwater intrusion, reduction of sheet flow hydrology, increased flooding of wetlands, and reduction of sediment input to marshes. Historically, the river and delta were managed mainly for navigation and flood control under a complicated array of federal, state, local government regulations. This often resulted in disorganized, contradictory, and ineffective management. Recognition of the severity of the wetland loss problem led to a growing effort to restore the delta. Initially, restoration efforts were focused on small scale, and often unrelated projects. More recently, there has been a realization that restoration must be a comprehensive, integrated effort based on natural functioning of the coast that fundamentally alters the way that people live and work in the coast. Hurricanes Katrina and Rita caused widespread damage to natural ecosystems and human infrastructure and led to the conclusion that effective storm protection is not possible without a restored coast. Before human impacts, river input to the delta was 1-2 orders of magnitude greater than that planned for restoration. Ultimately to restore the delta in a time of climate change and energy scarcity, management will have to approximate the natural functioning of the delta. It is likely that climate and energy will lead to deterioration becoming worse and hypoxia diminishing.

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Restoring wetlands to improve hurricane flood protection in the Mississippi river delta.

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Many of the great port cities of the world are situated in low-lying river deltas that are experiencing to a greater or lesser degree the coupled effects of relative sea level rise and engineered separation of the river from deltaic wetlands. New Orleans and the Mississippi River delta are not unique, and the

flooding that was experienced here in 2005 as a result of a near-miss by Hurricane Katrina, a Category 3 storm, will be repeated elsewhere - and perhaps here again next week or next year -- if important changes are not made to current “brittle” paradigms for overlaying engineered hurricane flood protection on river management, without significant integration. A river delta is an ecological system in which the land is defined by a living skin of vegetation well adapted to maintain its elevation within the intertidal zone. When a storm arrives, this bioactive layer, which can include trees (swamps) as well as grasses (marshes), can provide a powerful buffer for surge and wave reduction, if the hydrologic and sediment transport processes that sustain it are not disrupted. The National Audubon Society has been working with national and local partners including the Lake Pontchartrain Basin Foundation and the Coalition to Restore Coastal Louisiana to encourage the emergence of a “softer,” more reliable and affordable approach to hurricane flood protection that integrates traditional barriers with multiple layers of more natural defenses like restored wetlands and barrier islands.

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Harmful Algal Blooms (HABs) and Their Impact on Marine Environments in the Northern Gulf of Mexico

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Both human populations and marine resources are concentrated in the coastal zones of the United States. Observations of harmful algal blooms (HABs) are increasing around the world’s coastal ocean, with a growing number of reports indicating anthropogenic influences. Excessive phytoplankton growth in response to nutrient increases and/or shifts in nutrient ratios can result in a HAB of a single species that has negative ecosystem impacts. Toxic phytoplankton could potentially poison an ecosystem and have a direct impact on a variety of life forms, including humans, and indirect effects on higher trophic levels through the consumption of toxins accumulated in fish and shellfish. Phytoplankton toxins have been of concern worldwide and have been the subject of regional interest for many decades in the northern Gulf of Mexico. The changes in salinity and nutrient loading may induce shifts in the phytoplankton community assemblage and influence the presence and abundance of harmful algal species in the estuaries and coastal zones. Studies of the northern Gulf of Mexico coastal waters document the occurrence of the toxic diatom *Pseudo-nitzschia*, raphidophytes, several species of toxic dinoflagellates including *Karenia*, *Karlodinium*, *Prorocentrum*, *Heterocapsa*, *Gambierdiscus*, and *Dinophysis*, brown-tide alga *Aureoumbra*, and toxic cyanobacteria populations over the last decades; often in bloom quantities. However, the ecology of these organisms is still under investigation, specifically what controls their toxicity, thus complicating efforts to control outbreaks, or what extend their toxin can be transferred through the food web. Understanding the effects of changing chemical and physical characteristics, and pelagic-benthic coupling in the region may help facilitate their control through management and allow for a more informed understanding of how manipulations such as freshwater diversions of the Mississippi River may impact the occurrence of HABs in the northern Gulf of Mexico.

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Oomycetes among algae

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Genomics data indicate that the nuclear genomes of the oomycetes *Phytophthora sojae* and *P. ramorum* contain genes of probable plastid origin. Work in our laboratory indicates that at least 20 other species of oomycetes belonging to several different genera encode plastid genes that are not localized to the nucleus or mitochondrion. We have obtained partial *psbA* and *rbcL* gene sequences from oomycetes cultured under axenic conditions that are remarkably conserved compared to those from photosynthetic heterokonts. Based upon these data we conclude that oomycetes were once photosynthetic and possess a plastid genome that has yet to be visualized. The idea that oomycetes were once ‘algae’ is not new; Kützing (1841) described them as “achlorophyllous algae”. The life histories of oomycetes and the morphology of their oogonia and antheridia have often been compared to those found in photosynthetic, siphonous *Vaucheria* spp. (Xanthophyceae). Are these striking similarities the result of parallel or convergent evolution or are they evidence of a more recent common ancestry? In this presentation evidence linking oomycetes with certain algae, especially *Vaucheria*, will be reviewed. A brief discussion of plastid evolution will also be presented. The fact that oomycetes were once photosynthetic radically alters our understanding of the evolution of the heterokont algae and their nonphotosynthetic stramenopilous relatives. It also has deeper evolutionary implications and provides among the first tangible evidence supporting the “chromalveolate hypothesis” of plastid evolution.

22

Unravelling the diversity of *Trentepohlia* and *Printzina* (Trentepohliales, Ulvophyceae) by molecular systematic analyses

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Trentepohlia and *Printzina* represent two widespread genera of the Trentepohliales, an order of subaerial microchlorophytes common in regions with humid climates and distributed on a large variety of natural and artificial substrata. These algae appear as small bushes or compact crusts consisting of numerous entangled uniseriate filaments. Their taxonomy has been traditionally plagued by great morphological plasticity related to environmental factors, which has made assessments of the identity and the number of species belonging to these genera so far impossible. Inference on the phylogeny of *Trentepohlia* and *Printzina* was based on sequences of the *rbcL* and 18S rDNA genes. These two datasets provided a generally convergent signal, but the *rbcL* dataset had a much higher nucleotide substitution rate. In both datasets, neither of the two genera were monophyletic, and their separation was therefore not supported. Within the Trentepohliales, species of *Trentepohlia* and *Printzina* were interspersed with other trentepohlialean genera. In this mosaic of taxa, two well-supported clades were inferred. The first clade contained species with a robust habit (such as *Printzina bosseae*, *Trentepohlia flava*, *T. iolithus* and *T. umbrina*). The second clade contained all other strains of Trentepohliales sequenced, including the type species of both *Printzina* (*P. lagenifera*) and *Trentepohlia* (*T. aurea*). All strains of *T. aurea* sequenced had identical *rbcL* and 18S sequences and formed a highly-supported lineage; its position within the second clade, however, differed in *rbcL* and 18S analyses. At present, none of the morphological characters commonly used for identification and classification purposes appears to be phylogenetically relevant. However, our analyses clarified major taxonomic problems (such as the distinctness of *Trentepohlia flava* and *T. abietina*, for which the separation from *T. aurea*

was previously uncertain). These results also suggest that the genetic diversity in these genera is much higher than indicated by the morphology, and that extensive taxon sampling will be necessary to clarify in detail the phylogenetic patterns in these two genera.

23

A multigene approach to inferring the diatom phylogeny: congruence and conflict

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We will report on an analysis of 1336 stramenopile nuclear small subunit ribosomal gene sequences (nSSU: 673 of which are diatoms) downloaded from Genbank as well as a combined analysis of two chloroplast markers (rbcL, psbC) and nSSU genes we have sequenced for more than 70 diatoms. These genes are analysed individually and together, assessing them for combinability and using both model based and parsimony criteria. Previous studies and ours report some incongruity between results from each of these genes. We explore some potential causes for this incongruity, including differences in taxon sampling, and different modes or rates of evolution for the different genes.

24

New observations on the biology of eustigmatophytes, with a description of *Microtalis* gen. nov.

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A new genus, *Microtalis*, including two new species collected from freshwater environments - *M. aquatica* and *M. reticulata* - are established within the heterokont algal class Eustigmatophyceae. Vegetative cells are more-or-less spherical, less than 25 µm in diameter, and possess a prominent red body and vacuole. *Microtalis* is distinguished from previously described eustigmatophytes based upon morphological and reproductive characters as well as nuclear 18S rRNA gene sequence analyses. These data imply that *Microtalis* spp. belongs in the family Goniochloridaceae and are most closely related to species placed in *Goniochloris* and *Pseudostaurastrum*. Cell walls in *Microtalis* spp. are sculptured and comparable to those observed in *Goniochloris sculpta* and their zoospores are putatively astigmatic; these characters both support their classification with the Goniochloridaceae. *Microtalis aquatica* and *M. reticulata* reproduce by means of autospores and zoospores that usually are produced simultaneously within the mother cell wall. Simultaneous production of different reproductive cells has not previously been reported and delimits *Microtalis* from other eustigmatophyte genera. Zoospores in *Microtalis* spp. are highly motile but their flagella (-um) are not visible at the level of the light microscope; in *G. sculpta* and *P. limneticum* zoospores are nonmotile or only weakly motile, respectively. *Microtalis aquatica* and *M. reticulata* are distinguished from one another by the numbers of autospores each produces and by differences in their 18S rRNA gene sequences. In addition, characters traditionally used to delimit eustigmatophytes, new characters of systematic value, and new observations on their life histories and biology will be discussed.

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Algae in hyperspace: a first foray into mapping the Grinnellian niche of *Chlorella vulgaris* (Chlorophyceae) and *Peridinium cinctum* (Dinophyceae) in relation to ion proportions and amounts

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The effects of five ions, NO_3^- , PO_4^{3-} , K^+ , Na^+ and Cl^- on growth rates and cell densities were quantified for *Chlorella vulgaris* (Chlorophyceae) and *Peridinium cinctum* (Dinophyceae) in batch cultures. A five dimensional ion-mixture experimental design was projected across a total ion concentration gradient of 1 to 30 mM to map the ion-based, scenopoetic, or 'Grinnellian' niche space for these two algae in relation to positive growth rates. The two niches overlapped for ca. 95% of the ion mixtures, although the regions of maximal growth rates and cell densities were unique to each alga. Both *C. vulgaris* and *P. cinctum* exhibited very similar positive responses to cations and negative responses to anions in this study. There was no evidence that either K^+ or Na^+ is essential for growth, although both algae exhibited a preference for K^+ . It was determined that total ion concentration for these five ions, from 1 to 30 mM, did not directly affect either growth rate or maximal cell density for either alga, although it did play an interactive role with several ions. This study is the first that we are aware of to attempt the mapping of an ion-based Grinnellian niche. The implications of the experimental design utilized and the potential utility of this type of approach will be discussed.

26

Heat Stability and Volatility of a Putative Oogenesis-inducing Male Pheromone in the Brown Alga *Macrocystis integrifolia*

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Specific female pheromones that are involved in attracting flagellated sperm to eggs are well known in the brown algae. The observation that female gametophytes of species of the order Laminariales will produce more eggs in the presence of males than in their absence indicates the presence of a male pheromone. This effect can be induced by introducing medium from male gametophytes to cultures of females. The objective of this study was to determine the heat stability and volatility of this putative pheromone using *Macrocystis integrifolia*. Male gametophytes were cultured at a constant density in enriched artificial seawater (ESAW) adjusted to 24 psu salinity for 14 days in optimal light and temperature conditions for growth and gametogenesis. Female gametophytes were cultured at a constant density in 24 psu ESAW, and medium from the 14-day old male cultures was exchanged for 80% of the medium in these dishes after 1, 3, 5, and 7 days of culture. The male medium was treated at 30, 45, 60 and 100 °C for 15 minutes in a water bath in an initial experiment, and at 70, 80, 90 and 100 °C in both open and closed screw-cap tubes in a second trial, before cooling the medium and introducing it to the female gametophytes. Oogenesis was determined after 14 days of culture. In the first trial, oogenesis was induced with medium treated at 30-60 °C, but not at 100 °C. In the second trial, oogenesis was induced with medium treated at 70 °C in both open and closed tubes. No significant induction of oogenesis occurred after treatment at 80-100 °C in open tubes. Reduced induction occurred in closed tubes at 80 and 90 °C, and no induction at 100 °C. It appears that the male pheromone may partially break down at approximately 80 °C and completely degrade at 100 °C, and that it evaporates at 70-80 °C.

27

Physiology As A Reflection Of Habitat For Western South African *Porphyra* Species

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Three intertidal, monostromatic *Porphyra* species which are found along the southwestern shores of South Africa were compared with respect to their physiological ecology. *Porphyra capensis* is an abundant, dioecious species found growing epilithically from the mid to high intertidal. It occurs year round. The dark purple *Porphyra saldanhae* is monoecious and co-occurs with *P. capensis*, occupying a similar tidal height and habitat. The monoecious *Porphyra aeodis* grows epiphytically on the red alga *Aeodes orbitosa* as an annual. *Porphyra aeodis* is similar in morphology to the sympatric *P. saldanhae*, but occurs only as an epiphyte and is located in the very low intertidal rarely exposed to desiccation. Physiological ecology experiments were performed with cut out disks from the thalli of these species. Both *P. capensis* and *P. saldanhae* were tolerant to a wider range of salinities than *P. aeodis*. *Porphyra aeodis* growth was photoinhibited at light intensities greater than 100 $\mu\text{mol photons}\cdot\text{m}^{-2}\cdot\text{s}^{-1}$ whereas the other two species showed no photoinhibition. *Porphyra aeodis* growth was maximal at 12°C compared to 15-20°C for *P. capensis* and *P. saldanhae*. Further, whereas *P. capensis* and *P. saldanhae* tolerated and grew at temperatures up to 25°C, *P. aeodis* growth declined rapidly with increasing temperature, not surviving at 25°C. *Porphyra aeodis* responded like a shade-adapted seaweed whereas the other two species were more tolerant to extremes in their environment. *Porphyra aeodis* and *P. saldanhae* overlap morphologically to the extent that identifying specimens on the basis of gametophyte morphology alone is difficult. However, these species are clearly differentiated by their responses to changes in their environment, suggesting that growth is more reflective of habitat as opposed to morphology.

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A Quantitative Method for Measurement of Neutral Lipids in Chlorophycean Microalgae

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The Nile red fluorescence method has been successfully applied to the determination of lipids in a number of microalgae. However, this procedure has been somewhat ineffective in the measurement of the neutral lipid content of some green algae due probably to thick, rigid cell walls that prevent the fluorescence dye from penetrating. In this study, the solvent DMSO was added to green microalgal samples as a stain carrier at an elevated temperature. The cellular neutral lipids were determined and quantified using a 96-well plate and fluorescence spectrophotometry with an excitation wavelength of 530 nm and an emission wavelength of 575 nm. An optimized procedure yielded a high correlation coefficient ($R^2 = 0.998$) with the lipid standard triolein and repeated measurements of replicates. Application of the method to several green algal strains gave very reproducible results, with relative standard errors of 8.5%, 3.9% and 8.6%, 4.5% for repeatability and reproducibility at two concentration levels (2.0 mg/mL and 20 mg/mL), respectively. The detection and quantification limits of the improved Nile red staining method were 0.8 mg/mL and 2.0 mg/mL for the neutral lipid standard, triolein, respectively. The modified method and a conventional gravimetric determination method provided similar results on replicate samples. The modified method enabled the quantitative

assessment of intracellular neutral lipids in representative green microalgae and appears to be a useful high throughput technique for quick screening of a broader spectrum of algae for neutral lipids.

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Photosynthetic response of the toxic raphidophyte *Heterosigma akashiwo* during the imposition of, and recovery from, light- and nutrient stress

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The toxic raphidophyte *Heterosigma akashiwo* was subjected to simultaneous nutrient- and light stress by cutting off the nitrate supply to continuous cultures that were acclimated to growth-saturating irradiance. Cell division ceased on exhaustion of available nitrate and cell volume increased by 60% over 3 days. There was a 2.5x increase in the cellular carbon quota, primarily due to a 6x increase in carbohydrate content. There were no significant changes in cellular nitrogen or chlorophyll quotas. Both the light-limited and light-saturated rates of photosynthesis declined during N-starvation. The reduction in the light-saturated rate was greater than the loss in the light-limited rate (60% vs 30%). This degradation in photosynthetic performance was correlated with losses of ATPase, the PSII reaction center protein D1 and the carboxylating enzyme Rubisco. There was a rise in the de-epoxidation state of the xanthophylls in both saturating light and darkness, in parallel with a loss of D1 relative to Rubisco. This is consistent with the reduced photosynthetic competence arising partially from slippage in the coupling between electron transport and the Calvin Cycle. The cells returned to the acclimated, nutrient-replete state within 36 hours of nitrate being re-supplied. These data suggest that this clone of *H. akashiwo* has a remarkable resistance to and very rapid recovery from photoinhibition arising from light stress during nutrient starvation. This may play a role in its ability to bloom in surface waters with intermittent nutrient supply.

30

The correct identity of the species going under the name *Schizymenia dubyi* (Schizymeniaceae, Rhodophyta) in the Azores, based on molecular and morphological evidence

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Within the Nemastomatales, the genus *Schizymenia* (Schizymeniaceae) has the broadest geographical distribution, with other genera in the order (e.g., *Platoma*, *Predaea*, and *Titanophora*) mainly found in the (sub)tropics. The genus that currently comprises ten species was established by J. Agardh in 1851, with type *Schizymenia dubyi* (Chauvin ex Duby) J. Agardh described from Atlantic France. Seven species names have been recognized as synonyms of *Schizymenia dubyi*, namely *Haematophloea crouaniorum*; *Haematocelis epiphytica*; *Haematocelis rubens*; *Schizymenia minor*; *Schizymenia obovata*; *Schizymenia undulate*; and *Turnerella atlantica*. Comparative *rbcL* sequence analysis indicates that *S. dubyi* specimens from the Azores should be referred to as *S. apoda*, a species described from the Cape Province in South Africa and also known from China and Namibia. *Schizymenia rbcL* sequences from Japan comprise two species; *S. dubyi* and a species here provisionally identified as *S. novae-zelandiae*. *S. pacifica* from Washington, Pacific USA, is the fourth distinct *Schizymenia* species. Morphological observations on *S. apoda* from the Azores are provided,

and the presence of secondary pit connections is newly reported in gametophytes within the Nemastomatales.

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Molecular systematics of *Thorea* (Rhodophyta, thoreales) in Brazil

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This study aimed at evaluate species level taxonomy and phylogenetic relationship among *Thorea* species in Brazil and other regions of the world using two molecular markers - RUBISCO large subunit plastid gene (*rbcL*) and nuclear small-subunit ribosomal DNA (SSU rDNA). Three samples of *Thorea* from Brazil were sequenced, one from São Paulo and two from Mato Grosso do Sul states; a sample from Dominican Republic (DR) was also sequenced for comparison. Tree based on partial *rbcL* sequences (1,282 bp) revealed two major clades, representing genera: *Thorea* and *Nemalionopsis*. *Thorea* clade had two main branches with high bootstrap support ($\geq 90\%$), representing species: *T. violacea* (including *T. gaudichaudii* from Asia and *T. riekei* from U.S.A.) and *T. hispida* (including *T. okadae* from Japan). Sequences of *T. gaudichaudii* formed a distinct clade (100% support) and with a high variation (110-196 bp, 8.6-15.3%) in comparison to the other samples of *T. violacea* (3-151 bp, 0.2-11.6%); they might represent a distinct specific or infra-specific taxon. Tree based on complete SSU rDNA sequences (1,753 bp) was essentially similar to *rbcL* tree with two major clades with high support ($\geq 95\%$), representing the genera *T. hispida* and *Nemalionopsis*. Two clades with high bootstrap support ($\geq 95\%$) were recognized within *Thorea* clade, representing species: *T. violacea* and *T. hispida*. Brazilian specimens were recognized as *T. hispida* on the basis of both SSU and *rbcL* sequences, as well as morphological comparison. However, a relatively high variation in comparison to other samples of this species was observed (112-212 bp = 8,7-16,5% x 1-82 pb = 0,1-6,4% for *rbcL*; 91-158 bp = 4,5-9,5% x 14-68 pb = 0,8-3,9% for SSU). Thus, they might represent a distinct species or a infra-specific taxon of *T. hispida*, but they are provisionally kept as *T. hispida*, since there is no clear basis for distinction. DR sample grouped, as expected, with other North American populations of *T. violacea*. A worldwide revision of *Thorea* is recommended based on molecular and morphological data. Thoreales consistently appeared as monophyletic with high support ($\geq 95\%$) in trees based on both molecular markers.

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Phylogeography of *Ishige* with recognition of *I. foliacea* (Ishigeales, Phaeophyceae)

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Common species occurring between geographically isolated regions are an interesting issue for taxonomy and biogeography. *Ishige Yendo*, previously included two species, inhabits the warm waters of the northwest and the northeast regions of Pacific Ocean. We determined the sequences of mitochondrial *cox3* and plastid *rbcL* from 127 samples of the genus collected over its distribution range. Analyses of the *cox3* and *rbcL* sequences resulted in similar trees that *Ishige* well resolved, but *I. sinicola* (Setchell and Gardner) Chihara consisted of two distinct clades: one for samples from Korea and Japan and the other from Mexico. Based on this result, we reinstated *I. foliacea* Okamura for samples from the northwest Pacific, which was previously synonymized with *I. sinicola* from Mexico. *Ishige foliacea* is circumscribed by large and wide thalli (up to 15 cm), and an epitype for the species is

designated because of the poor visualization of the type. *I. sinicola* is characterized by small, narrow thalli (up to 5 cm). Our results suggest that the genus diverged between the northwest and northeast Pacific.

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Subaerial microchlorophytes from West Central Africa: morphological convergence in tropical rain forests

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While assessing the biodiversity and systematics of subaerial microchlorophytes from African tropical rainforests (Gabon, West Central Africa), several examples of microscopic green algae have been found showing similar thalli morphologies. They represent distantly related lineages from the green algae. Similar examples have been found in other tropical regions. Basically, three main types of thalli characterize the morphology of these subaerial green algae: 1) unicellular, the most widespread in terms of the number of species; 2) sarcinoid (packets formed by a small number of cells), characteristic of one of the most common alga in the world (*Desmococcus*); and 3) uniseriate, found in a relatively limited number of species. These similarities encompass not only thallus morphology, but also growth pattern and pigmentation (there are other biochemical and cytological adaptations). These examples can be interpreted as a case for morphological convergence, defined as the pattern of long-term change in similar directions among remotely related lineages. This is particularly important for the systematics of subaerial algae. In this environment, morphology and reproductive features of microchlorophytes do not reflect phylogenetic patterns. In the absence of abundant morphological characters (as in the case of microchlorophytes) their systematics becomes highly problematic. Furthermore, behind these very limited number of similar morphologies underlies a great deal of genetic diversity. We present cases from the Gabonese tropical rainforests where simplification of the thallus has been favored.

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Subaerial Microchlorophytan Diversity of Barro Colorado Island, Panama

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Barro Colorado Island is a Smithsonian nature preserve located within the Panama Canal waterway. The humid climate of this tropical rainforest promotes the abundant and diverse growth of microscopic subaerial green algae. Microchlorophytes were collected from leaves, tree bark, and man-made structures in the summer of 2007. These algae were identified through microscopic observations. Three morphologies were exhibited in these terrestrial algae: coccoid unicells, sarcinoid packets, and short filaments. Examples of coccoid unicells were found in the genera *Stichococcus* and *Chlorella*. The sarcinoid packet morphology was represented by the genus *Desmococcus*. Filamentous algae of the order Trentepohliales (Ulvophyceae) exhibited the greatest diversity and overall abundance. Our collections revealed the presence of at least 24 species (1 *Cephaleuros*, 6 *Phycopeltis*, 4 *Printzina* and 13 *Trentepohlia*). Two species (*Trentepohlia minima* and *T. treubiana*) were new records for the Americas. Other interesting records included *Printzina bosseae*, *Trentepohlia chapmanii*, *T. depressa*, and *T. dusenii*, species that have been rarely reported in the Americas. Several taxa lacked reproductive structures and therefore could not be unambiguously identified. These samples possibly represent undescribed species. DNA sequence data is currently being gathered to clarify the taxonomic position of these ambiguous algae. In conclusion, this brief collection trip to Barro Colorado Island yielded a relatively high amount of subaerial microchlorophytan diversity and established this area as a

biodiversity hot spot for the order Trentepohliales. Future excursions to Central and South America may well result in the discovery of several new species and green algal lineages.

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Phylogeny of *Thalassionema* Grunow, with discussion of biogeography, stratigraphy, and diagnostic features

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Thalassionema Grunow is widely distributed throughout the world's oceans. Species within this genus are identified from at least the Miocene and are frequently utilized as biostratigraphic and paleoecological reference taxa. Many of the taxa with long histories in the ocean sediments are extant. Species and varieties of these extant forms have been associated with specific oceanic currents. The combination of datasets dealing with modern ecological occurrence and stratigraphic history has led to the development of hypotheses concerning the position and movement of specific oceanic currents. The taxonomy and systematics of this group remain enigmatic despite the utility of these taxa in previous investigations. In these study a phylogenetic hypothesis is developed for species and varieties of *Thalassionema* via cladistic analysis. The best, most parsimonious, cladograms produced in this analysis were compared to known stratigraphic distributions of species and varieties and the biogeographic distribution of taxa among Pacific currents. Stratigraphic occurrence corresponds well with the cladogram topology and reoccurring biogeographic patterns can be observed within clades. Characters used for diagnosis of the species and varieties were also examined. Character distribution on the cladogram revealed that many diagnostic features are likely homologies and that species and varieties in the genus are generally consistent with the phylogenetic species concept. Using the character distributions and the biogeographic and stratigraphic information in conjunction with the phylogenetic hypotheses developed in this study should simplify the use of species and varieties within the genus in paleoenvironmental and other ecological investigations.

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The Seaweeds of Florida

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Historically the study of Florida seaweeds can be divided into three phases: (1) collections that were described in general floras; (2) collections made by visitors and sent to Europe; and (3) collections and publications of American phycologists, mostly during visits from the north. Florida has a 220 million ybp geological record as a carbonate platform, a broad western shelf with low wave energy that permits the formation of mangrove forests in the south and salt marshes in the north. It also has a latitudinal span of 6.5 degrees lying between 24.5 and 31.0 degrees north latitudes that helps permit a diverse set of habitats in which seaweeds occur: salt marshes (45 taxa), mangrove forests (56 taxa), seagrass beds (ca 113 epiphytes, 65 drift species, 20 rhizophytic taxa), as well as hard substrata habitats (e.g. 'live bottoms'), and coral reefs. At least 248 seaweeds occur intertidally on the Florida Keys limestone although they are often stunted and growing within crevices or tide pools. Subtidal communities have been shown to be tropical on both the east and west coasts using SCUBA and Submersible vehicles. Florida is also endowed with a variety of biotic reefs that form substrata for macroalgae including live worm reefs on the southeast coast, mollusc reefs in Florida Bay, *Oculina*

coral banks on the northeast coast, and the hermatypic coral reefs of the Keys. The seaweed flora has at least 694 taxa (224 green, 102 heterokont, 368 red) and a strong subtropical to tropical signature (R+C:P = 4.9). This talk will review some features of the seaweed flora.

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Variability in Tissue Nitrogen and Phosphorus of Macroalgae in the Indian River Lagoon, Florida

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The Indian River Lagoon system (IRL), the longest barrier-island/tidal-inlet system in the continental United States, spans more than one-third of Florida's east coast. The IRL has a richly diverse macroalgal flora, dominated by unattached rhodophytes ("drift algae"). Ongoing research in the central segment of the IRL has identified a nutrient gradient in the water column, with elevated N and P levels, associated with freshwater inputs. Given that existing data indicate that nitrogen is the limiting nutrient for algal growth in this portion of the lagoon, our initial focus was on nitrogen. Tissue nutrient analysis is an excellent integrator of nutrient availability to macroalgae and can be used to determine significant spatial and temporal patterns in the nutrient status of macroalgae relative to sources of anthropogenic inputs. A series of in situ measurements of tissue nitrogen of dominant macroalgal species was initiated. Ultimately the questions to be addressed are: (1) Is the growth of macroalgae in the IRL limited by nitrogen? (2) Does macroalgal growth in the IRL respond to increases in water column nitrogen? An initial assessment was made with monthly monitoring of dominant macroalgae at six stations along the previously identified water quality gradient. The collections were almost exclusively rhodophytes, with the most frequently collected species being *Hypnea spinella*, *Hydropuntia secunda*, and *Gracilaria tikvahiae*. The spatial and temporal patterns of nitrogen content and C:N ratio were similar for the three species, and comparisons to critical internal concentrations for growth identified periods and locations when nitrogen limitation did occur. However, temporal changes in tissue nitrogen were not always directly correlated with changes in nutrient availability in the water column. This disjunction suggests that further research in macroalgal nutrition in the IRL needs to consider other environmental factors that can influence nitrogen uptake by macroalgae and the interactions of these unattached "drift algae" with sediment nutrient pools, as well as with what is available/measured in the water column.

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Growth and feeding activity of the mixotrophic dinoflagellates *Dinophysis acuminata* and *Dinophysis caudata*: nutrient limitation, food quality, and diel cycle

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The photosynthetic species of *Dinophysis* contain plastids of cryptophyte origin and are known as producers of diarrhetic shellfish poisoning toxins. Recent works have shown *Dinophysis* to be obligate mixotroph that requires both light and prey (plastidic ciliate *Myrionecta rubra*) for long-term survival. Whether nutrient limitation and/or food quality enhance feeding (and thus growth) of *Dinophysis*, and its feeding activity depends on time of a day, however, remain still unknown. To study the first issue, we investigated growth of two *Dinophysis* species (*D. acuminata* strain DA-LOHABE01 and *D. caudata* strain DC-LOHABE01) in nutrient-limited (-N, -P, and -N & P treatments) cultures, using the ciliate *M. rubra* (strain MR-MAL01) as prey. For effect of food quality, growth experiments were also

made using prey cells that had been grown under different nutrient conditions (-N, -P, -N & P, and f/2 treatments). To investigate the second issue, diel cycle studies were done over 2 days period during which paired *Dinophysis* cells and feeding activity (as the frequency of *Dinophysis* cells with the attached prey cells) were determined at 3 h intervals. In the meeting, the results will be presented and discussed in context of survival strategy of the mixotrophic dinoflagellates.

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Growth of *Lyngbya wollei*, an invasive mat forming cyanobacterium from Florida springs, under different temperature, light and nutrient regimes.

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Lyngbya wollei is a filamentous cyanobacterium that forms large mats in Florida Springs and in many other lake and river systems in North America. Presence of mats limits the recreational use of affected water body and is a potential health hazard due to algal toxicity. High nitrate levels are blamed for the excess growth of *L. wollei* in many Florida springs. The goal of our study was to determine optimal conditions for the growth of *L. wollei* found in Florida springs. We conducted a series of laboratory experiments using microcentrifuge tubes as microcosms for growing few mm long algal filaments. We found that *L. wollei* had low light requirements and preferred warm waters. We also manipulated conductivity and concentration of macro- (nitrate, ammonia, phosphate) and micro-elements (iron and other metals). *Lyngbya wollei* had high nitrate and phosphate requirements and its growth was negatively affected by high water conductivity and high concentration of ammonia and iron.

40

Are interactions between dominant mesograzers and macroalgae in the Western Antarctic Peninsula, in part, chemically mediated? The anti-grazing capabilities of secondary metabolites produced in Antarctic filamentous macrophytes.

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It is generally believed that evolved chemical defenses are designed to deal with larger, more singularly destructive, predators rather than inconsequential mesograzers. Mesograzers, by themselves, rarely have enough destructive potential to override the physiological costs of secondary defensive metabolites and usually have limited impact on macrophytes because their numbers are controlled by top-down predation. Recent studies though have revealed high abundances and diversities of crustacean mesograzers affiliated with benthic macroalgal communities along the Western Antarctic Peninsula with reported densities of over 300,000 individuals m⁻² algal tissue for the most preferred hosts. Densities along with algal produced amphipod feeding deterrents suggest some ecological or evolutionary relevance exists between the two communities. To test the extent of algal chemical defenses on potential amphipod grazers we conducted feeding assays using two species of amphipods (*Prostebbingia gracilis* and *Gondogeneia antarctica*) commonly found in the benthic community and several finely-branched brown and red algae species from the Antarctic Peninsula. Initial trials encompassed containing amphipods with known quantities of fresh thallus material and calculating grazing rates based on algal tissue loss and time allotted for herbivory. In order to differentiate chemical from physical defenses, subsequent experimentation involved amphipod choice experiments

between palatable alginate pellets or pellets laced with compounds extracted from frozen algae tissue. Initial results indicate that six out of the eight algae species tested exhibit effective defensive properties, in both their hydrophilic and lipophilic extracts, against amphipod grazing. These results indicate the expansive presence of chemical defenses in the local area and influences the mesoherbivore community has had on the adaptive development of western Antarctic Peninsula flora.

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Palatability of *Palmaria decipiens* and its endophyte *Elachista antarctica* to four common Antarctic amphipods

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Although many Antarctic macroalgae are known to produce secondary metabolites that aid in their protection against grazing, it is suspected that the rhodophyte *Palmaria decipiens* is often grazed upon by primary consumers, especially the amphipods and fish. *P. decipiens* is host to a number of epiphytes including the endo/epiphyte, *Elachista antarctica*. *E. antarctica* is a filamentous phaeophyte only found growing within, and emerging out of the thallus of *P. decipiens*. It is surprising that *E. antarctica* is present only on a palatable species of macroalgae considering the standing biomass of other unpalatable species is very high. In order to confirm the palatability of *P. decipiens*, and begin to understand the relationship between *E. antarctica* and *P. decipiens*, feeding assays were conducted with four amphipods commonly associated with *P. decipiens*: *Proteobbingia gracilis*, *Gondogeneia antarctica*, *Oradarea bidentata*, and *Paraphimedia integricauda*. Feeding assays were conducted to determine consumption rates (mg algae mg amphipod⁻¹ h⁻¹) for all four amphipod species in three different trials. In feeding assays, one amphipod was isolated with either *P. decipiens* or *E. antarctica* for set time. Preference experiments where an individual amphipod was given a feeding choice between *P. decipiens* and *E. antarctica* were also conducted using all four amphipod species. Preference experiments were also replicated three times for each species of amphipod. *Gondogeneia antarctica* consumed both species but ate *P. decipiens* at a faster rate than the epiphyte. *Proteobbingia gracilis*, *Paraphimedia integricauda*, and *Oradarea bidentata* fed on *E. antarctica* at much faster rate than *P. decipiens*.

42

Insights into the evolutionary history of the subaerial algal flora

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The community of subaerial algae is one of the most recognizable ecological components in a tropical rain forest. Unfortunately the study of their biodiversity has been hampered by several historical and logistic factors. Our recent studies in these tropical environments have identified some geographic areas as biodiversity hot spots, and we have discovered new taxa and phylogenetic lineages. The use of molecular tools to unravel subaerial algal biodiversity also has been crucial in refinements of their systematics and evolutionary history. The order Trentepohliales is one of these subaerial algal groups under study. This order diverged before the diversification of other orders (mainly marine) such as Dasycladales and Siphonocladales/Cladophorales complex. Published and recently re-discovered fossil evidence of this order date back only 50 mya; however, based on molecular evidence their phylogenetic history may precede the pre-Eocene epoch. A probable explanation of how this subaerial algal group evolved into land habitats is presented. Factors involved during this evolutionary pathway

may include: sea level decline accompanied by pre-adaptive ecological plasticity, an intertidal habit, and other physiological and morphological features.

43

Assessing multi-gene candidates for an algal heterokont phylogeny

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Heterokonts (or stramenopiles) are a group of protists with unequal flagella that include both algal and colorless representatives. The algal heterokonts are currently divided into 16 classes and include over 100,000 described species. Common members include the brown seaweeds, chrysophytes and diatoms. Despite 200 years of light microscopic study, 50 years of electron microscopic study, and 20 years of molecular investigations, phylogenetic relationships among the 16 classes remains unclear. As part of a Tree of Life (ATOL) grant we plan to estimate relationships among these classes by generating a large multi-gene molecular data set. The past year has been devoted to growing cultures and performing a pilot study of 27 taxa. The purpose of the pilot study is to assess candidate molecular markers before a final selection of seven genes (representing the nuclear, mitochondrial and plastid genomes) for the expanded taxon sampling of 270 algal heterokont species and 30 non-photosynthetic relatives. Our preliminary studies include the nuclear genes SSU rRNA, actin, alpha and beta tubulin, the plastid genes *rbcL* and *psbC*, and the mitochondrial genes *cox1* and *cob*. To date, we've assessed and decided to move forward with 1 nuclear (SSU rDNA) and two chloroplast (*rbcL* and *psbC*) genes and are awaiting further data before choosing the remaining 4 molecular markers.

44

Genetic diversity and reinstatement of *Gracilariopsis chorda* based on *rbcL* and *cox1* sequences

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Two different molecular markers, plastid *rbcL* and mitochondrial *cox1* genes, were used to elucidate a taxonomic position of the species currently named under *Gracilaria chorda*, which occurs in the northwest Pacific Ocean region. We analyzed both genes (1222 bp for *rbcL* and 1245 bp for *cox1*) from 18 specimens collected in Korea, Japan and China. Phylogenetic reconstructions of both data revealed that they were not included in *Gracilaria* but in *Gracilariopsis*. These results lead to the conclusion that *Gracilariopsis chorda* (Holmes) Ohmi is the legitimate name for *Gracilaria chorda* Holmes. Within the species, the sequences differed by 8 bp (0.7%) in *rbcL* and 5 bp (0.4%) in *cox1*. Six haplotypes of *cox1* tended to be geographically structured. *Gracilariopsis chorda* is characterized by coarse, elongate terete axes, having short filiform branchlets usually irregular intervals, abrupt transition in cell size from medulla to cortex, cystocarps without tubular nutritive cells connecting the gonimoblast to the upper pericarp and we observed not small but relatively large gonimoblast cells of cystocarp at the specimen collected from Wando, the southern part of Korea.

45

Taxonomic studies of the Gonatozygaceae (Desmidiiales)

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The family Gonatozygaceae (Desmidiiales) includes the genera *Genicularia* and *Gonatozygon* and is characterized by structurally simple cylindrical cells with spines and granules. Compared to other families of desmids, there are very few - fewer than 25 - known species. In order to better understand the relationship between structural characteristics and phylogenetic lineages, several strains of *Gonatozygon* and *Genicularia* were investigated. Their structural characteristics were measured and their phylogenetic relationships were estimated from a three-gene data set of *rbcL*, *psaA* and *coxIII*. We found that *Genicularia spirotaenia* is embedded in *Gonatozygon* and that some species of *Gonatozygon* are not monophyletic. We propose that the species *Gon. brebissonii* as reported in the literature may represent a number of phylogenetically distinct lineages. We conclude that in the family Gonatozygaceae there has been an underestimation of the species diversity. The number of species in other structurally simple groups of desmids and other algae may be similarly underestimated.

46

Phylogeny of the Characeae (Charophyta) based on chloroplast sequence data

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The extant Characeae, commonly called stoneworts or brittleworts, are evolutionarily important with regard to their close relationship to land plants, their extensive fossil record, and their worldwide species diversity. The extant Characeae contain two tribes with six genera: the tribe Chareae, which includes *Chara*, *Lamprothamnium*, *Lychnothamnus*, and *Nitellopsis*; and the tribe Nitelleae, which includes *Tolypella* and *Nitella*. The Characeae exhibit a broad range of gross morphological diversity, including cortication, branching and other features that have been used to delimit subgroups. The monoecious or dioecious condition and the arrangement of gametangia (conjoined or sejoined) have also been utilized in circumscribing species. Given this morphological diversity it is not surprising that numerous taxonomic treatments have been proposed. The most recent and comprehensive treatment (Wood & Imahori 1965) radically altered the taxonomy and classification of the Characeae. More than 400 species were reduced to intra-specific ranks (i.e., variety or forma) or submerged in synonymy yielding approximately 80 broadly defined species. To better understand species diversity and evolution within this cosmopolitan lineage we assembled chloroplast DNA sequence data for *rbcL* and *atpB* from about 500 individuals representing approximately 140 species. Phylogenetic analyses support monophyly of the six genera and the tribe Chareae. The tribe Nitelleae was paraphyletic, however support for this part of the tree was weak. Many sections (*sensu* Wood) were also found to be polyphyletic. These findings along with the discovery of several new species will be presented.

P1

Production of Dimethyl sulphide (DMS) and Dimethylsulfoniopropionate (DMSP) by the coccolithophore haptophyte alga *Emiliana huxleyi*

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The production of DMS and DMSP by the coccolithophore haptophyte alga *Emiliana huxleyi* was studied under different growth conditions. The algal growth was monitored along with chlorophyll content under different growth conditions. The results showed that DMSP and DMS production decreased by increasing the salinity level and the maximum DMS production was obtained at 30‰ as compared with 35‰. Nitrogen and phosphorus limitation affected the growth and chlorophyll content of the alga. DMS was also decreased under nitrogen and phosphorus limitation. Decreased light intensity to half of that of control did not affect the DMS production. The formation of CaCO₃ during the growth course of the alga was also studied.

P2

Filamentous algal endophytes in antarctic macroalgae: incidence and palatability

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Five individuals each from 13 common species of large macroalgae (“macrophytes”) were surveyed for the presence of filamentous algal endophytes both macroscopically and microscopically using dissecting and compound microscopes. No endophytes were observed at all in two macrophyte species. In two other species, most individuals had no visible endophytes but there were very low densities of endophytes in a minority of individuals. The remaining species all supported endophytes in most or usually all individuals with maximum endophyte densities per species ranging from 3% to 75% of the thallus area. Thallus fragments from all individuals with endophytes were placed into culture and 108 individual unialgal strains were isolated. To sort these into species, we sequenced the ITS-1 gene in each strain. Brown algal endophytes grew well in culture and at least 9 species were present. As a previous investigator also found, the green endophytes did not grow well in culture and only two of what is likely four or more green algal species present in the thallus fragments were isolated. No-choice feeding rate bioassays were performed with thallus fragments of all 13 macrophyte species and with cultures of all nine brown endophytes. Feeding rates on the endophytes were 2-3 orders of magnitude higher than rates on 12 of the macrophyte species and 2- to 6-fold higher than on the only truly palatable macrophyte, *Palmaria decipiens*. These data strongly support the hypothesis that antarctic macrophytes are commonly endophytized and that the endophytes benefit from the association by being protected, at least in part, from amphipod herbivory.

P3

Algal biodiversity and conservation: preparing the next generation of practitioners

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In preparing future phycologists who may wish to study, conserve, and/or restore algal biodiversity, programs leading to bachelors, masters, and/or doctoral degrees must seek to provide intensive training

in phycology appropriate to the level of the final degree. Clearly the well-prepared student would also be exposed to several additional relevant areas such as inter alia biogeography, ecology, physiology, botany, and perhaps even some zoology. The exact breadth of coursework would vary, and to some extent student preparation would certainly be interdisciplinary rather than purely phycological. The question arises, how interdisciplinary should the preparation be to ensure that the new phycologists will actually succeed in helping to conserve and/or restore marine algal biodiversity? More specifically, in our world today can they succeed if they are not fully aware of economics, politics, international relations, or communications sensu lato? In the doctoral and masters programs in marine biodiversity and conservation at the Center for Marine Biodiversity and Conservation (CMBC) at Scripps Institution of Oceanography (SIO), students are given a holistic, real world view of the often complex challenges to saving and/or restoring marine biodiversity. An intensive ten-week course (9:00-17:00, five days per week) in marine biodiversity and conservation explicitly covers oceanography, marine biodiversity, paleobiodiversity, informatics, ecological systems, nongovernmental environmental organizations, governance and law, economics, and communications. The interdisciplinary, holistic perspective of the summer course is reinforced through a two-semester course sequence taken by all of the masters and doctoral students enrolled in the intensive summer course, and it is open to all students. Cooperative interdisciplinary group projects and international internships further enhance the development of the interdisciplinary perspective. Very positive student reaction to the program suggests a convincing match between the pedagogical approach and student career plans and interests.

P4

Untreated Urban Effluent Effects on Phytoplankton Community Structure and Function in Lake Pontchartrain, LA

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The recent flooding in the city of New Orleans following Hurricanes Katrina and Rita offered a unique opportunity to observe how ecological processes in Lake Pontchartrain were altered following the addition of untreated urban effluent. Documentation of the impacts of this event on the biota of Lake Pontchartrain provides insight into how coastal ecosystems respond to the synergistic effects of a major climatic perturbation and anthropogenic pollutants. The purpose of this study was to quantify the response and recovery of the phytoplankton community in Lake Pontchartrain to this major environmental disturbance event. Water samples were collected at 27 locations within a 12 km radius from the entrance to the 17th Street Outfall Canal at weekly to biweekly intervals from 15 September to 12 December 2005 (17 - 105 days after the passage of Hurricane Katrina). High performance liquid chromatography (HPLC) was used to determine chemosystematic photosynthetic pigments for phytoplankton algal groups. Photopigment concentrations were analyzed using ChemTax to quantify the relative abundances (in units of $\mu\text{g Chl a l}^{-1}$) for 6 major algal groups. Phytoplankton blooms were limited to a short period following the storm passages and during de-watering operations for New Orleans. Phytoplankton biomass returned to relatively normal levels over much of the study area within forty days after the passage of Katrina. Overall, phytoplankton group diversity declined one month after Katrina and remained relatively constant while group evenness showed little change. Although the relative abundances of algal groups were variable, diatoms constituted over half the phytoplankton biomass ($52\% \pm 18$ of total chl a) when averaged over the study period. Other than a moderate bloom during pumping operations, Hurricanes Katrina and Rita had very little direct impact on phytoplankton biomass, evenness, and diversity in Lake Pontchartrain.

P5

Recruitment inhibition, reproductive inundation, and coexistence between dominant subtidal algal crusts and kelps.

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Subtidal algal crusts of various taxa often dominate the rocky substrate beneath macrophyte canopies. While crusts can tolerate the effects of canopy shading, the reciprocal influence of crust species in regulating the abundance of dominant canopy species, such as kelps, remains unresolved beyond laboratory inference. Because of the widespread abundance of crusts and their ability to transform rock into living substrate, we tested the effect of crust taxa (calcified, non-calcified red, and brown) on recruitment of kelps using both laboratory and field experiments. Laboratory results indicate nearly 100% inhibition of recruitment by microscopic *Saccharina subsimplex* sporophytes by red and brown non-calcified crusts. In contrast, *S. subsimplex* exhibited no significant difference in recruitment on calcified crusts in comparison to bare rock. In the field, we removed algal crusts in experimental plots and compared recruitment therein to unmanipulated plots and control plots (in which we removed everything but crusts). We observed inhibition of recruitment by crusts, with kelps recruiting to small amounts of available bare substrate in nearly all plots, and the highest recruitment in plots with crusts removed. These results indicate that while some crust taxa clearly inhibit localized recruitment of kelps, the high reproductive capacity of kelps facilitates recruitment, even when only miniscule amounts of suitable substrata present themselves in nature. This thereby compensates for the competitive space-occupancy advantage of crusts, explaining why this interaction may not translate to competitive exclusion in nature.

P6

Combined Effects of Grazing and Nutrients on Benthic Algae in a Freshwater Marsh, Alaska

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We studied the independent and interactive effects of snail grazing and nutrient addition on the productivity and composition of the benthic algal community in a boreal marsh, Alaska. Nutrient concentrations were manipulated in-situ with open-ended cylinder enclosures embedded into marsh sediments. Two grazing treatments, caged and un-caged, were nested inside each of three enclosure types; a combination of Nitrogen, Phosphorous, and Silica (NPSi), control, and ambient with four replicates each. We added NPSi to treatment enclosures every four days for 24 days. Caged treatments allowed for benthic algal colonization on natural and artificial substrates in the absence of grazing pressure. Grazing snails (*Lymnaea*) were added to each enclosure to simulate natural abundances. Increased nutrients raised chlorophyll a levels and favored the growth of filamentous green algae (*Mougeotia*), and coccoid blue-green algae (*Chroococcus* and *Gleocapsa*). Natural conditions favored Euglenoid taxa. Intensive grazing reduced total algal abundance, and increased the relative abundance of small blue-green coccoid cells. Our data show that increased nutrients significantly alter benthic algal community composition and grazing significantly decreases algal biomass independent of community composition. These independent and interacting effects are important in understanding the regulatory mechanisms of primary production in boreal wetlands.

P7

Effects of experimental nutrient enrichment on benthic algae and algal-derived DOC in a boreal wetland, Alaska

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Factors that regulate benthic algae have not been extensively studied in boreal wetlands. We investigated the effects of nitrogen (N), phosphorus (P), and silica (Si) enrichment on benthic algal biomass, community composition, and algal-derived dissolved organic carbon (DOC) in a freshwater marsh, Alaska. We constructed 20 mesocosms *in-situ*, and randomly assigned each to one of four nutrient treatments or a control, with four replicates each. We added individual doses of N (1.0 mg L⁻¹ NO₃), P (0.1 mg L⁻¹ PO₄), Si (10 mg L⁻¹ SiO₂), or a combination N, P, and Si (NPSi) to mesocosms every four days for 24 days during the summer growing season. Only the NPSi treatment increased benthic algal biomass to levels significantly higher than the control (ANOVA, $p < 0.05$). DOC concentrations increased with algal cell density across all treatments ($r^2=0.81$), but DOC concentrations in the NPSi treatment were significantly higher than treatments with either nutrient alone (ANOVA, $p < 0.05$). Coccoid cyanobacteria and filamentous green algae such as *Mougeotia* were favored in the NPSi treatment, whereas euglenoid cysts were abundant in individual nutrient treatments and the control. Changes in algal biomass, community composition, and algal-derived DOC with nutrient enrichment could have consequences for wetland biogeochemical processes and food-web dynamics.

P8

Translating Research in Education: A Paleoclimatology Example

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The need for new learning strategies to help students understand Ecology and Evolution is essential in the secondary education curriculum. Certain classes of algae have attributes making them excellent candidates for utilization toward achieving these goals. The intent of this project is to help students understand evolution in the context of long-term historical and environmental records. Diatoms are a particularly useful indicator of modern and past environments. A classroom exercise has been developed to help students understand the way in which these indicator taxa are used in paleo-oceanographic studies. Specific learning components of the exercise include a) developing a classification technique for diatoms that is hands on and visual for students; and b) from this students can then look at decisions made by scientists in identifying environmental parameters. As developed, the exercise also allows opportunity to demonstrate the differences between categorical thinking and tree thinking, along with the opportunity to discuss the strengths and weaknesses of our dataset for inferring environmental change.

P9

Influence of habitat's complexity in the toxicity of some marine macroalgae

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Some macroalgae are able to synthesize toxic molecules; this toxicity may be interpreted as a defense mechanism against predators. Although, it has been established that toxicity is developed by algae in order to defend themselves against herbivores. The process of synthesis induction seems to be more complex, since it can be driven by other physiological, chemical or even spatio-temporal variables. In order to investigate the influence of habitat's complexity in the presence of toxicity, thirty-nine algae samples, corresponding to 31 species were collected in localities with different morphology: a coral reef in Mexican Caribbean, three mixohaline localities in Yucatan Peninsula, and six rocky intertidal localities, four of them in the Mexican Pacific and the other two in the Gulf of Mexico. A potent toxic activity was observed in 19 species, two algae were moderately toxic and ten were non toxic. Algae with potent toxic activity were collected in the reef system, second place of toxic species were the rocky shores algae. The least in number of toxic algae were collected in mixohaline localities. We believe the hypothesis that habitat complexity promotes the presence of toxic species against herbivory is supported. The wide potential of toxic substances for use as molecules with pharmacological and clinical applications or as matrixes for development of other compounds via chemical synthesis is still unknown.

P10

Seasonal variation in nutrients and microalgal community composition in Mobile Bay, Alabama, and the northern Gulf of Mexico

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A transect has been sampled from Mobile Bay, Alabama, to 50 km offshore at monthly to bi-monthly intervals since March 2007. Horizontal salinity gradients have ranged from 8 to 18 PSU in surface waters. Temperature has ranged from 16 to 32 C. Maxima in chlorophyll concentrations and total microalgae numbers were associated with maxima in nutrient concentration. Nutrient concentrations were in turn inversely correlated with salinity, indicating the importance of Mobile Bay as a source. The highest chlorophyll concentrations were found in July-August. The community composition showed a seasonal succession from dinoflagellate- to diatom-dominance in spring, followed by mixed assemblages of chlorophytes, prasinophytes and cryptophytes in summer. There were also horizontal gradients, with dinoflagellate-dominance occurring only in Mobile Bay during a bloom of *Prorocentrum minimum*.

P11

Desiccation controls the upper limit of species distribution among blooming ulvoid macroalgae

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"Green tides" (green macroalgal blooms) can be found globally and are often considered a threat to the environment. A variety of biotic and abiotic factors may limit the abundance and productivity of algal blooms including salinity, irradiance, and temperature. This study compared the desiccation tolerance

of two ulvoids that are often associated with blooms: *Ulvaria obscura* and *Ulva lactuca*. *Ulva* is generally found higher on the beach, while *Ulvaria* is restricted to the subtidal. Recent work suggests that physical factors limit the upper depth limit of distribution for *Ulvaria*, while the lower limit for *Ulva* is set by biotic factors. We suspected that lack of tolerance to desiccation was the key factor in limiting *Ulvaria* to the subtidal. Air and saline drying techniques were used to test this hypothesis. Photosynthetic rates of the two species were calculated before treatment, after treatment, and following a designated recovery period. Both methods of drying illustrated that *Ulvaria* is less tolerant of desiccation than *Ulva* at intermediate stresses. Thus, our results support the idea that *Ulva*'s abundance in the intertidal is primarily due to a higher tolerance of abiotic stressors. Furthermore, our results show that there are substantial physiological and biochemical differences between *Ulva* and *Ulvaria*, which are often assumed to be ecologically redundant species.

P12

Using underwater video analysis to determine large-scale spatial and temporal changes in macroalgal bloom occurrence

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Large blooms of green macroalgae have been associated with anoxia, noxious odors, toxin production, and competition with other marine primary producers. Eelgrass (*Zostera* spp.), in particular, forms an important habitat in the inland waters of Washington State, USA and is particularly impacted by blooms. The growth of green macroalgae is often triggered by nitrogen-rich runoff from human sources, but other factors may also regulate blooms (e.g., light). We used video surveys collected by the Washington State Department of Natural Resources in 2004 and 2005 (most recently available) to compare large scale eelgrass and ulvoid density and depth distribution. We also examined small scale ulvoid bloom and nutrient data collected at 6 beaches around Puget Sound. We found that nutrient concentrations varied widely from site to site and from year to year, and algal bloom cover was often drastically different between neighboring sites. Additionally, ulvoids and seagrasses were found to occupy similar depths, but rarely were found together at high densities. Overall, changes in green algal blooms were unpredictable from one year to the next. Growth of the green algal blooms were not strongly correlated to nitrate concentrations, indicating additional factors are affecting the growth of the algal bloom. The highly varied patterns of growth also suggest that ulvoid growth is strongly affected by small scale, localized influences. In the future, continued use of multiscale sampling will likely be necessary to correctly understand the patterns of these harmful macroalgal blooms

P13

Probing The Relationship Between Movement Modalities In *Cylindrotheca closterium* (Bacillariophyceae): Effects Of Osmotic Shock And Cytoskeletal And Metabolic Inhibitors On Movement

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The wide distribution of *C. closterium* in mudflats has been attributed to its ability to move and physiologically adjust during salinity fluctuations. Video microscopy showed that movement modality changes from the predominant gliding at normal seawater concentration to more non-gliding modalities occurred in response to changes in osmolarity and salinity. Total loss in motility was

observed at extreme osmotic conditions. Sodium and chloride ions are essential for movement; however, salts other than NaCl produced a predominance of non-gliding modalities even at the osmolarity of seawater. This suggests that both osmotic and ionic aspects of salinity changes in the environment influence *C. closterium* movement patterns. Sorbitol and myo-inositol were the preferred neutral osmolytes. Smooth gliding was disrupted by cytoskeletal inhibitors; latrunculin A (actin-assembly inhibitor) and butanedione monoxime (myosin ATPase inhibitor). These also resulted in a reversible total inhibition of all movement modalities. The sodium ionophore, monensin, stopped gliding with concomitant increase in non-gliding movements indicating that such modalities may not be dependent on a sodium motive force. Electron transport uncouplers and inhibitors of polysaccharide and microtubule assembly decreased gliding and promoted non-gliding modalities. Con A-FITC labeling at the poles and central regions support previous hypothesis of the cells' secretion of motility-related EPS at the apical and central raphe endings. Cells subjected to varying salinity increased or decreased in cell volume at hypo- or hyper-osmotic concentrations, respectively. The influence of both osmotic and ionic aspects of salinity stress in *C. closterium* could affect its distribution and consequently influence the species diversity in mudflats through heterotrophic utilization of EPS.

P14

Eutrophication Assessment of Lagoonal Detention Ponds in South Carolina, U.S.A.

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South Carolina's coast is one of the fastest growing regions in the United States, prompting concern for the potential effects of coastal development on estuarine eutrophication. Following the classification scheme of the NOAA National Estuarine Eutrophication Assessment (NEEA) and the USEPA National Coastal Condition Report (NCCR), we applied criteria to storm water detention ponds, lagoonal estuarine systems prevalent along the South Carolina coast. Nitrogen levels were predominantly classified as "high" according to NEEA criteria (based on total dissolved nitrogen, TDN), but were mostly classified as "good" according to NCCR criteria (based on dissolved inorganic nitrogen). Based on the assumption that dissolved organic nitrogen may be an important labile nutrient pool, the inclusion of TDN for eutrophication assessment in these lagoonal systems is considered important. Phosphorous levels were classified as "high" (NEEA) or "poor" (NCCR) in > 75% of samples in all seasons. Chlorophyll a levels were predominantly "high-to-hypereutrophic" (NEEA) or "poor" (NCCR) in the summer and fall/winter periods, while just under 50% of spring samples were included in these categories. Consideration of tidal exchange between lagoonal ponds and estuarine creeks stresses the need to include the former systems when assessing the effects of coastal development on estuarine eutrophication. Evaluating the nutrient and chlorophyll a levels in a representative subset of brackish detention ponds provides an important step toward establishing reference conditions for assessing the eutrophication condition of these lagoonal estuarine systems.

P15

4-Nonylphenol binding to glass as a possible toxicity mechanism in diatoms

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This investigation attempts to confirm the mechanism responsible for 4-nonylphenol's negative impact on diatom health. 4-Nonylphenol is commercially utilized as a surfactant and binds well to glass. The diatom's frustules make the organism particularly susceptible to 4-nonylphenol exposure. The

compound may bind with a diatom's siliceous cell wall and interfere with the organisms ability to interact with its external environment. We tested this hypothesis in two ways. First, siliceous particles of known sizes (including diatom frustules) were exposed to 4-nonylphenol. These exposures a) confirmed that 4-nonylphenol binds to siliceous microparticles and b) demonstrated that the degree of binding corresponds well with siliceous surface area. The second experiment quantified the thickness of extra-cellular products in 4-nonylphenol exposed and control diatoms via atomic force measurements. This confirmed a reduction in extracellular material consistent with 4-nonylphenol's surfactant properties. These results corroborate the hypothesis that 4-nonylphenol's negative impact on diatom health is related to its surfactant properties. These findings are of interest as diatoms are a major component of the aquatic foodweb specifically in terms of their role as a producer and food source for many primary consumers.

P16

Mono- and digalactosylacylglycerol composition of *Lepidodinium chlorophorum*, *Karenia brevis*, and *Kryptoperidinium foliaceum*, three dinoflagellates with aberrant plastids

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The intact molecular forms of monogalactosyl- and digalactosylacylglycerol (MGDG and DGDG, respectively), two important chloroplast membrane lipids, were determined via positive-ion electrospray ionization/mass spectrometry and positive-ion electrospray ionization/mass spectrometry/mass spectrometry for *Lepidodinium chlorophorum*, *Karenia brevis*, and *Kryptoperidinium foliaceum*, three dinoflagellates with non-canonical plastids lacking the typical dinoflagellate carotenoid pigment peridinin, along with *Tetraselmis sp.*, *Emiliania huxleyi*, and *Navicula perminuta*, three potential ancestors, respectively, to these aberrant, tertiary plastids. *Lepidodinium chlorophorum* and *K. brevis* were found to possess 18:5/18:5 MGDG (sn-1/sn-2 regiochemistry), a form observed in several peridinin-containing dinoflagellates, along with forms of MGDG and DGDG not found in peridinin-containing taxa. *Lepidodinium chlorophorum* was found to possess 18:5/16:4 MGDG and 20:5/16:4 DGDG, and *K. brevis* was found to possess 18:5/14:0 MGDG and DGDG as forms of these lipids. *Kryptoperidinium foliaceum* was not observed to produce any C18 fatty acids within its forms of MGDG and DGDG; 20:5/16:3 MGDG and 20:5/16:2 DGDG were the two predominant forms. The MGDG and DGDG composition of the *K. foliaceum*/*N. perminuta* pair was almost an exact match, whereas in the *L. chlorophorum*/*Tetraselmis sp.* and *K. brevis*/*E. huxleyi* pairs, the MGDG and DGDG compositions were similar in some respects, but not others. The significance of these findings, along with the MGDG and DGDG composition of the putative tertiary endosymbionts, is discussed in the context of the evolution of the plastids of these organisms.

P17

Euglenophycin-a toxin produced by certain Euglenoids

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In 2004, Zimba et al. identified two species of euglenoids that caused fish mortality. Evidence included growout of clonal cultures, as well as field exposure studies. Recently the toxin structure was fully elucidated using HPLC, HPLC/MS, MS/MS/TOF, and NMR analyses. The toxin is an alkaloid, having a mass of 304 amu. Toxicity has been observed in five species of fish, as well as mammalian tissue cultured cell lines. The toxin has affinities with fire ant toxin structurally, and may serve as a defense

mechanism.

P18

Myosin diversity in the marine pennate diatom *Phaeodactylum tricornutum*

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Myosins are actin-based molecular motors that participate in a wide range of cellular activities from vesicle transport to signal transduction to cell locomotion. As a prelude to exploring the roles of these mechanoenzymes in the biology of *Phaeodactylum*, we sought to inventory the myosins expressed in this cell. Taking advantage of sequence information available from the *P. tricornutum* genomic database (DOE Joint Genome Institute) and using a battery of degenerate myosin primers, PCR-based strategies have been employed to clone myosins from *Phaeodactylum* cDNA. As is typical of most organisms across the phylogenetic spectrum, *Phaeodactylum* expresses multiple myosins of different types. Comparison of sequences derived from the myosin head (motor) domain was used to assess the similarity of these diatom myosins to each other and to representatives of the established classes of myosins in the myosin superfamily. To date, ten myosins have been identified in *Phaeodactylum* and these segregate into three loose groups, none of which are closely akin to any of the established 24 classes currently defining the myosin superfamily. Even within the three groups of *Phaeodactylum* myosins, significant variations in myosin structure are evident. The diatom myosins range in size from less than 130kDa to greater than 240kDa and exhibit a great range of structural diversity in the three major myosin domains, the head, neck and tail. Analysis of myosin sequences using available algorithms for the prediction of protein domain architecture reveals putative domains common to many myosin classes (N-terminal SH3-like domains, IQ motifs, ankyrin repeats, coiled-coils) as well as some domains that are less common or not yet described in other types of myosins (FYVE zinc-binding domains, CBS domains, PB1 domains). This great diversity of myosins seen in *Phaeodactylum* will likely reflect the wide range of roles that these molecular motors will be discovered to play in the normal structure and function of diatoms.

P19

Analyzing The Euglenoid Plastid Genome

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Euglenoids are unicellular asexual flagellates found in fresh and marine environments having phagotrophic, osmotrophic or phototrophic nutrition. Their chloroplasts contain chlorophylls *a/b* and are surrounded by three membranes suggesting secondary endosymbiosis of a green alga. The existence of non-photosynthetic individuals within several photosynthetic genera indicates multiple losses of photosynthesis. Thus, euglenoids can be a model to study secondary endosymbiosis, chloroplast evolution, gene loss and genome restructuring. This project is to isolate, sequence and annotate the plastid genomes of the photosynthetic *Euglena clara*, *Trachelomonas ellipsoidalis* and *Phacus orbicularis*, and their colorless sister taxa *E. quartana*, *T. reticulata* and *P. ocellatus* respectively, based upon an SSU/LSU phylogeny. This data will be combined with the previously sequenced genomes of *E. longa* (colorless) and *E. gracilis* (photosynthetic) to study the origin and evolution of plastid genomes. We have developed a method of chloroplast isolation using a French press, a discontinuous Percoll gradient, and low speed centrifugations. The chloroplast DNA was isolated using the Qiagen DNeasy Tissue Kit, then amplified using Rolling Circle Amplification

(RCA) or Multiple Displacement Amplification (MDA). All sequencing will be done on a 454 Life Science GS FLX System. The annotation will be performed using the Dual Organellar Genome Annotator (DOGMA) website. Comparisons will be made among all genomes, with the chloroplast genomes being used to infer the green algal ancestor and the non-photosynthetic plastid genomes being used to study gene loss. Comparisons between the two-chloroplast genomes will show if they were gained from the same ancestor or conversely were acquired from different ancestors, or that the genomes have differentially reshuffled. Comparisons between the two non-photosynthetic plastid genomes will show if they have undergone the same gene lost and rearrangements. Here, results of our project are presented.

P20

Development of species-specific, multiplex PCR assays for the detection and quantification of *Prymnesium parvum* Carter (Haptophyta) in natural bloom samples

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The toxic, bloom-forming haptophyte, *Prymnesium parvum* is responsible for massive fish mortalities worldwide, so sensitive, rapid methods of detection are needed to improve management strategies. Multiplex PCR assays were developed for the species-specific detection and quantification of *P. parvum* wherein suites of primers simultaneously amplify four species- and gene-specific products from isolated genomic DNA or whole cells. Primer sets were designed such that the individual amplification products from conventional PCR could be easily resolved by gel electrophoresis as a diagnostic banding pattern. For quantitative PCR (qPCR), gene-specific fluorescent molecular beacons were designed to enable simultaneous detection of the four gene products. Both multiplex PCR assays were capable of detecting as few as 1 or 2 cells in 50 cycles. Isolated genomic DNA and whole-cell concentration gradients were evaluated by qPCR to generate standard curves. The equations derived from linear regression analyses also allowed the estimation of total DNA per cell. Because blooms of *P. parvum* are rarely unialgal, the species- and gene-specificity of the assays were evaluated using various geographic isolates of *P. parvum* combined with related haptophytes and/or outgroup species, using heterogeneous mixtures of cells or isolated DNA. The diagnostic banding pattern in electrophoresis gels and the real-time trace profiles were exclusive to reactions containing *P. parvum* with no interference from the presence of DNA or cells from other algae. As an independent test, the multiplex qPCR assay was used to enumerate *P. parvum* in samples collected from natural blooms. The cell number estimations using qPCR were close to mean values obtained from manual counts using a hemacytometer. These multiplex PCR-based assays present a significant improvement in DNA-based detection technology, enhanced by the rapid and simultaneous confirmation of four species-specific products, and the ability to specifically detect several widely-separated (and previously uninvestigated) geographic isolates of *P. parvum*.

P21

Morphology and phenology of *Gelidium elegans* (Rhodophyta)

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Gelidium is an economically important red algal genus that has a very wide distribution range in temperate to tropical waters. The genus contains about 130 species in the world, but the taxonomy are still difficult due to a lots of morphological variation. To date, approximately 17 species of the genus have been reported in Korea. *Gelidium elegans*, previously named as *G. amansii*, is the most common

gelidioid alga in Korea and is harvested for agar production in the southern province of Korea. We have investigated morphology and phenology of the species since April 2006 in Gampo, located on the southeastern coast of Korea. Thalli grow up to 18 cm in the field and have main branches with slightly sympodial branchlets, which are compressed to cylindrical. Endofibers are produced from the cortical cells and become abundant in the medullar layers. They are filamentous and, under scanning electron microscopy, have holes in the midst. The species has a maximum growth in May to July, and then decreases in October. Thalli in the sublittoral zone tend to be slender with many branchlets than those in the intertidal zone. The morphology of *G. elegans* is very variable, depending on seasons, locations, and depth.

P22

Characterization of Paramylon Morphological Diversity in Photosynthetic Euglenoids

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Paramylon grains are highly crystalline, β -1, 3 glucan storage bodies found in euglenoids. Previous research on *Euglena gracilis*, has indicated an immuno-enhancing biomedical application for paramylon. Within the photosynthetic euglenoids, paramylon grain morphology is highly variable. These varying morphological forms may indicate different underlying chemical structures and forms of β -1,3 glucans, which may affect their overall bioactivity. The preliminary step in determining variable bioactivity of paramylon is to examine the morphological diversity found among euglenoid species prior to chemical analysis and in vitro testing. Scanning electron microscopy was used to examine six species of the order Euglenales (*Euglena gracilis*, *Lepocinclis acus*, *L. ovum*, *Monomorpha pyrum*, *Phacus orbicularis* and *P. pleuronectes*). While a particular grain type may be characteristic of an individual species, all taxa contain the small oval grains (<3 μ m) characteristic of *Euglena gracilis*. In genera such as *Monomorpha*, (represented here by *M. pyrum*), paramylon grains are large shield-shaped lateral plates (approximately 8-10 μ m at their widest point). The major characteristic grain can also vary within a genus. For example, *Lepocinclis acus* has large rod-shaped grains (3-12+ μ m) while *Lepocinclis ovum* has large, curved, ring-shaped grains (greater than 5 μ m in diameter). In *Phacus*, *P. orbicularis* has large plate-shaped grains (documented up to 29 μ m) while *Phacus pleuronectes* has bobbin-shaped paramylon ranging from 7-16 μ m in length. This study demonstrated several distinct paramylon grain morphologies both within a genus and among species. Investigations into grain morphology of divergent photosynthetic euglenoid species are being used to inform research into the chemical structure, bioactivity, and medicinal properties of paramylon.

P23

The genus *Grateloupia* (Halymeniaceae, Rhodophyta) in Korea

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The genus *Grateloupia* C. Agardh, with more than 80 currently recognized species, is by far the largest in the family Halymeniaceae and has a wide distribution in temperate and tropical waters. Vegetative characters of the genus are considered highly homoplasious and difficult to define. However, recent molecular analyses elucidate the taxonomic status up to the species level and also reveal the presence of extensive cryptic diversity. *Grateloupia* is the focus of recent introduction to other areas, and two northeast Asian species, *G. turuturu* and *G. imbricata*, are confirmed to be introduced from the northeast Asian waters to the Atlantic Ocean region. In this study, we analyzed rbcL gene from five

taxa - *G. lanceolata*, *G. elliptica*, *G. imbricata*, *G. turuturu*, and *G. catenata*, of the 23 listed species in Korea. Sequence divergence was calculated for cryptic diversity among samples of *G. elliptica* and *G. lanceolata* from Japan and Korea. Sequences of *G. imbricata* from Korea were compared with those of the species from Canary Island. Further studies will provide a correct taxonomy of the genus from Korea and show genetic diversity within the remaining 18 species of *Grateloupia*.

P24

Marine Algae and Early Explorations in the Upper North Pacific and Bering Sea.

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The inception of the exploration of benthic marine algae in the upper North Pacific and the Bering Sea began with the naturalists approaching from the west, when Steller and Krasheninnikov, as part of the Second Kamchatkan Expedition, spent years living in Kamchatka starting in the winter of 1740. In 1741 Steller joined Vitus Bering on a voyage to discover Alaska. Afterwards, Steller returned to Kamtchatka in 1742 and spent two additional years exploring the Kamtchatka peninsula and making collections. His seaweeds from Kamchatka made their way back to St. Petersburg, and many were described in S.G. Gmelin's (1768) *Historia fucorum*. Another voyage of discovery from Russia was that of the "Northeastern Secret Geographical and Astronomical Expedition" of 1785-94, commissioned by Empress Catherine II of Russia. The commander of the expedition was Capt. J. Billings. Specimens of algae were collected by the naturalist Carl Merck, and unpublished plates and accounts depicting those algae made by Tilesius exist in MEL. This material represents the earliest collections of algae from Alaska. Subsequent voyages, either for commercial purposes or for exploration and discovery, entered the North Pacific. The surgeon-naturalist Archibald Menzies accompanied two voyages, first that with Capt. Colnett's ship 'Prince of Wales' (1786-1789) and later on Capt. Vancouver's 'Discovery' (1791-95). D. Turner in England described a number of Menzies' algal collections. Several other expeditions set out from Russia. The 'Nadeshda' under Capt. Krusenstern (1803-1806), the Romanzof Expedition (1815-1818) with the 'Rurik' under Otto von Kotzebue, and the 'Seniavin' under the command of Lütke (1826-1829). Wilkes commanded the first American voyage of exploration (1838-1842), and some macroalgae and diatoms were described. The Swedish expedition of the 'Vega' (1878-1880) under the command of Nordenskiöld with Kjellman as the botanist entered the Bering Sea from the north, and many algae were collected and described. An American expedition was organized and sponsored by Harriman in the summer of 1899. Marine algae were collected by De A. Saunders from the State of Washington and along the coast of Alaska.

P25

Biodiversity survey of Hawaiian red algae, and data display via the Hawaiian Algal Database

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The red algae of the Hawaiian Islands are extremely diverse, and provide a unique opportunity for detailed study of a tropical insular flora. Hawaiian marine red algae have been the subject of intense morphological examination for a number of decades, and currently approximately 370 species are recognized, with a rate of endemism of approximately 15%. About 10 freshwater red algae are also known from the streams and agricultural fields in the archipelago, and recently several subaerial taxa have also been collected. We are currently in the third year of a biodiversity survey of the red algae of

Hawaii, and have undertaken two seasons of collecting throughout the main Hawaiian Islands. Additional collections are included in the project through deep-water surveys of the main Hawaiian Islands, annual NOAA surveys of the main and Northwestern Hawaiian Islands, archived material at Bishop Museum, and the Census of Marine Life collections from the 2006 CReefs expedition to French Frigate Shoals. All collections are vouchered (as herbarium sheets, formalin vouchers, microscope slides, or dried samples) and DNA extracts are archived for most samples. We are comparing these collections through DNA barcode-like analyses of sequences of three regions: a fragment of the nuclear LSU rRNA gene, a fragment of the plastid 23S rRNA region and part of the mitochondrial COI gene. To date 1,690 red algal samples have been analyzed, representing 19 orders, 139 genera and 317 species. All associated data from the survey (sample photographs and micrographs, collectors, identifiers, georeferenced locality and maps, date of collection, DNA sequences) are housed in the Hawaiian Algal Database (HADB), which will be made publicly available in July 2008. HADB will be demonstrated at the PSA annual meeting as part of this presentation. DNA sequence comparisons indicate that many common taxa in the Hawaiian flora require systematic revision, and we will be working over the next several years to clarify the taxonomy of these algae. Large scale biodiversity surveys, such as this, provide unparalleled opportunities for broad assessment of entire algal floras.

P26

A preliminary phylogeny of the Cymbelloid diatoms using molecular data with emphasis on the genera *Didymosphenia* M. Schmidt and *Navicymbula* Krammer

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Cymbelloid diatoms have been a subject of several recent reviews resulting in either reestablishment of genera (e.g. *Encyonema* Kützing) or introduction of new genera (*Encyonopsis* Krammer, *Cymbopleura* Krammer, *Delicata* Krammer, *Navicymbula* Krammer) based primarily on overall morphological similarity. This preliminary study uses the nuclear encoded SSU rDNA and partial LSU rDNA and the chloroplast encoded *rbcL* and *psbC* to reconstruct a preliminary phylogeny of the Cymbellales with particular interest in the systematic position of *Didymosphenia* M. Schmidt and *Navicymbula*. Phylogenetic analyses place *Didymosphenia* as a sister taxon to a species of *Cymbella* C.A. Agardh confirming the earlier hypothesis based on raphe and apical pore field morphology. Additionally, the genus *Navicymbula* consistently falls within a clade of *Navicula* sensu stricto taxa, which is congruent with frustule and protoplast morphology. Our results indicate that the dorso-ventral asymmetry exhibited by *Navicymbula pusilla* and its varieties may be a homoplastic character secondarily acquired within the naviculoid lineage and may not be homologous with the asymmetry exhibited in the *Cymbellales*. Although data from multiple independent markers support the positions of *Didymosphenia* and *Navicymbula*, we note that the apical pore field bearing genera *Brebissonia* (Grunow) Schütt, *Gomphoneis* Cleve and *Reimeria* Kociolek & Stoermer, and the non-apical porefield genus *Rhoicosphenia* Grunow are absent from this analysis and including them could change the overall topology of the *Cymbellales* tree.

P27

Ultrastructure and molecular phylogeny of the genus *Mallomonas* (Synurophyceae) in Korea

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Taxonomy of the genus *Mallomonas* was investigated by ultrastructure of scale and combined nuclear SSU and LSU rDNA sequence data. For scanning electron microscope (SEM), species were fixed and dehydrated and coated with gold. Specimens were viewed with a LEO-1530 FESEM. The result was added to 6 unrecorded species in Korea; *M. peronoides* var. *bangladeshica*, *M. corymbosa*, *M. cratis*, *M. portaeferreae*, *M. pseudocratis*, *M. heterospina*. Molecular phylogenetic analysis of combined nuclear SSU and LSU rDNA sequence data were performed on 16 *Mallomonas* species and *Ochromonas danica* as outgroup. Bayesian analysis suggested that the genus *Mallomonas* is divided into five clades, representing eight sections: 1) Section *Mallomonas* and *Striatae*, 2) Section *Annulatae* and *Akrokomae*, 3) Section *Torguatae*, 4) Section *Planae*, 5) Section *Punctiferae* and *Insignes*. The section *Mallomonas* and section *Striatae* were grouped together with high supported values in the combined phylogenies. They were also united in the scale characters by the presence of a bristle on every scale and craspedont bristle serration, and presence of v-rib covering the shield. The section *Akrokomae* was sister of the section *Annulatae*, although this topology was not strongly supported. The section *Planae* consisted of four species: *M. caudata*, *M. matvienkoeae*, *M. oviformis*, and *M. peronoides*, which have flat base plate and was highly supported as a monophyletic clade. The section *Punctiferae* and *Insignes* grouped together with high support values. The molecular phylogenetic analysis was not fully resolved but was largely congruent with previous taxonomy.

P28

Zygnemataceae (Zygnematophyceae) from Southern California coastal watersheds

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To date, little is known about Zygnemataceae diversity and distribution in California watersheds, a situation which has limited their application in stream bioassessment. In our extensive sampling of perennial and non-perennial coastal streams from Santa Barbara County to the Mexican border from summer 2007 to spring 2008, we observed that representatives of the Zygnemataceae frequently dominate the periphyton assemblages. *Spirogyra* was the most widespread genus, represented by 16 species, followed by *Zygnema* with five infrageneric taxa and one *Mougeotia* species. Upland, non-perennial streams were characterized by specific a Zygnemataceae flora dominated by *Zygnema sterile*, *Z. stellinum*, *Spirogyra varians*, *S. borgeana*, as well as two newly described species. The new *Zygnema* species, observed only in one of those streams, is similar to *Zygnema oranensis* Gauthier-Lièvre. Both taxa reproduce by aplanospores only, but the new *Zygnema* sp. differs in vegetative cell dimensions and the placement of the aplanospores. The new *Spirogyra* species, distributed in two of the non-perennial streams (including the new *Zygnema* species site) belongs to Section *Conjugata*, Group *Longata*. In its morphology and reproduction, it is closest to *Spirogyra variformis* Transeau, but has much larger zygospores and vegetative cells. From the perennial coastal streams (Malibu Creek, Los Angeles County and San Mateo Creek, Orange County) two new *Spirogyra* species are described. They can be classified in Section *Salmacis* and Section *Conjugata*, Group *Maxima*, respectively. Light microscope and scanning electron microscope images of the four new taxa will be presented and representative samples will be sequenced and compared to related taxa.

P29

Description of a new family, Phacusaceae (Euglenophyta), and multigene analysis of photosynthetic euglenoids

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To evaluate the phylogeny of photosynthetic euglenoids, we conducted Bayesian and ML analyses of the combined multigene data: nuclear SSU rDNA, plastid SSU and LSU rDNA. The combined dataset consisted of 113 strains, of photosynthetic euglenoids (including colorless sister taxa). Three strains of the Eutreptiales were used to outgroup root the tree. Bayesian and Maximum Likelihood (ML) analyses recovered trees of almost identical topology. The results indicated that photosynthetic euglenoids are divided into two groups: Euglenaceae and Phacusaceae. The Euglenaceae was monophyletic with high support and subdivided into four clades: the *Colacium*, the loricate *Trachlomonas* and *Strombomonas*, the *Cryptoglena* and *Monomorphina*, and the *Euglena* and *Euglenaria* clades. The genus *Colacium* was positioned at the basal of the Euglenaceae and was well-supported as a monophyletic lineage. The loricate genera were located at the middle of tree and formed robust monophyletic lineage. The genera *Cryptoglena* and *Monomorphina* also formed a well supported monophyletic clade. The genera *Euglena* and the proposed new genus “*Euglenaria*” emerged as sister groups. The Phacusaceae was also monophyletic with high support values and subdivided into three clades: the *Discoplastis*, the *Phacus* and the *Lepocinclis* clade. The genus *Discoplastis* branched first, and then *Phacus* and *Lepocinclis* emerged as sister groups. These genera shared common characteristics, such as numerous small discoid chloroplasts without pyrenoids and also had the unique molecular synapomorphies in helix D10' to G13 of plastid LSU. These results clearly separated Phacusaceae from the Euglenaceae. Therefore, we propose a new family, Phacusaceae.

P30

Phylogeny of two unusual chrysophytes, *Anthophysa* and *Phaeodermatium*

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The freshwater heterokont algae *Anthophysa vegetans* and *Phaeodermatium rivulare* were reexamined in the light microscope and their phylogenetic positions were investigated using DNA sequence analyses. Parsimony and maximum likelihood analyses of nuclear small subunit ribosomal RNA (18S rRNA) gene sequences confirm placement of both species within the Chrysophyceae. The colorless, phagotrophic colonial flagellate *A. vegetans* is resolved as most closely related to *Poterioochromonas* spp. and *Ochromonas sphaerocystis*. Our results imply that *A. vegetans* lost the capacity for photosynthesis independently from *Oikomonas*, *Paraphysomonas*, and *Spumella*. Evidence is presented for a minimum of four independent losses of photosynthetic capacity within the Chrysophyceae *sensu lato*. *P. rivulare* forms radially organized multistromatic thalli that are macroscopic in size. The species has been placed in the Hydrurales with *Chrysonobula* and *Hydrurus* and/or associated with *Hydrurus* and *Lagynion* on the basis of other features. Our analyses do not support these hypotheses or the hypothesis that *Phaeodermatium* may represent an alternative life history phase for any other known chrysophyte. In our trees *Phaeodermatium* occupies an isolated position among those chrysophytes examined thus far. These results, and others, indicate that the Hydrurales (*sensu* Pascher 1931) is a polyphyletic taxon and should be abandoned.

P31

Systematics of the Raphidophyceae (Heterokontophyta)

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The Raphidophyceae is a comparatively small class of heterokont algae that includes seven genera. Known members of the group take the form of photosynthetic flagellates that lack cell walls. They are often common members of marine and freshwaters, sometimes form blooms, and some species produce toxins. Because they lack cell walls raphidophyte cells may take on a variety of shapes; this has made drawing boundaries between genera and species difficult. To reexamine the systematics of the Raphidophyceae nuclear 18S rRNA and plastid *rbcL* sequences were obtained or newly determined for 10 isolates representing five raphidophyte genera. Cultures of *Haramonas* and *Merotrichia* were unavailable for study. We also encoded and simultaneously analyzed 18 morphological characters for the group. The combined data supported monophyly for *Chattonella*, *Fibrocapsa*, *Gonyostomum*, *Heterosigma*, and *Vacuolaria*. The freshwater genera *Gonyostomum* and *Vacuolaria* formed a strongly supported clade within the class excluding marine species. The absence of fucoxanthin and violaxanthin and the presence of heteroxanthin and vaucherianxanthin derivatives are synapomorphic for these freshwater taxa. *Fibrocapsa* and *Heterosigma*, which both lack diadinoxanthin, are resolved as distantly related in our tree. Most parsimonious optimizations of the presence / absence of various carotenoid pigments on the raphidophyte tree reveals a complex pattern that is difficult to interpret within ecological or evolutionary contexts.

P32

A molecular comparison of drift and attached green tide species in Narragansett Bay, RI

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Green tides are blooms of macroscopic green algae that can affect shallow areas of Narragansett Bay, RI during summer months by contributing to hypoxia or anoxia upon degradation, and negatively impacting fishing and other recreational activities. They are primarily composed of species belonging to the genus *Ulva* (including tubular morphologies formerly classified in the genus *Enteromorpha*), which is well known for exhibiting rampant phenotypic plasticity and morphological convergence. Effective environmental management of green tide biomass relies upon well-resolved species identifications because it may represent important sources of compounds with commercial applications and/or hold clues to important control strategies governed by species-specific interactions. We are attempting to resolve patterns of species richness in Narragansett Bay green tides by sequencing the nuclear rDNA ITS regions and the chloroplast encoded *rbcL* gene. Here we present a preliminary assessment of green tide species richness, and address whether attached and drift populations are identical with regard to these molecular markers.

P33

A preliminary assessment of macroalgal diversity in Bocas del Toro, Caribbean Panama

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The Bocas del Toro province of The Republic of Panama hosts a complex of habitat types ranging from coral and sponge reef, to seagrass meadow and mangrove cay that yields a marine flora and fauna rich in species. Recent investigations have uncovered a biota that is typical of Caribbean Islands, but the short history of biodiversity investigations and high diversity estimates suggest that the region may be more speciose than other, better-studied areas. Our studies on the marine flora of Panama have uncovered one new and numerous putative new species from Bocas del Toro, and reveal that much of marine floristic diversity for Panama is represented by species distributed throughout the Bocas del Toro region. Our current, conservative estimates of species richness for red, green and brown algae are 85, 54 and 24 species. The number of new records for Panama is unsurprisingly high given that limited attention has been paid to algal diversity in the area. A preliminary assessment of macroalgal species richness will be presented for the Bocas del Toro region of Caribbean Panama, in the light of outstanding evolutionary and biogeographic questions and new (molecular-based) approaches to studying seaweed biodiversity.

P34

New Taxonomic Insights in the Red Algal Order Rhodymeniales

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Recent dredging expeditions throughout the Gulf of Mexico (NW: offshore Louisiana and Texas, SW: Gulf of Campeche, Mexico; SE: vicinity of the Dry Tortugas, FL; NE: vicinity of the Florida Middlegrounds, FL) at depths between 45-90 m have revealed an exceptional species-rich diversity of Rhodymeniales. Chloroplast encoded *rbcL* sequences were analyzed from nearly 200 vouchers of Rhodymeniales from the Gulf, and worldwide, belonging to the Rhodymeniaceae, Champiaceae, Faucheaceae, and Lomentariaceae. Emphasis is placed on a critical revision of the generic concepts within each family, the proposal for new species descriptions, and the establishment of new or revised range distributions for pertinent taxa.

P35

***Fucus* (Heterokontophyta; Phaeophyta) biogeography across North American shores**

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The genus *Fucus* (Phaeophyceae) has nine commonly accepted species, five of which inhabit North American shores: *F. gardneri*, *F. serratus*, *F. distichus*, *F. evanescens*, and *F. spiralis*. *Fucus* species inhabit the intertidal zones of the Atlantic, Pacific and Arctic Oceans and due to their highly plastic and morphologically simple phenotypes, are valuable candidates for molecular phylogenetic research. Furthermore, *Fucus* species are useful for biogeographical investigation due to their relatively slow

migration, limited dispersal range, and easily collected distribution. DNA was extracted from 94 samples collected along rocky shores of the Pacific, Arctic, and Atlantic Oceans. For each sample a 700 base pair region of the mitochondrial intergenic spacer between the 23S rRNA gene and the tRNA val gene was amplified and sequenced. Based on neighbor-joining, maximum likelihood and bayesian phylogenetic analyses there were two well-supported and distinct genotypic clades. Taxa from each clade displayed clear geographic groupings across the distribution of North American *Fucus*, from Pacific, Arctic and Atlantic shores. Morphological characters such as winged blades with serrated edges, location and number of air bladders, geographic location, and size of thali were compared among samples and showed little reinforcement of the two distinct genotypes. The presence of different genotypic groups with indistinguishable morphologies, each with their own geographic distribution, suggests the presence of cryptic species within the *Fucus* species of North America.

P36

An experimental elucidation of cell-to-cell communication via pit plugs in the red alga *Caloglossa* (Harvey) G. Martens (Delesseriaceae, Ceramiales)

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Members of the euryhaline genus *Caloglossa* occur throughout tropical, subtropical and temperate regions of the world. The membranous blades consist of a midrib region composed of central and pericentral cells, and of lateral wings that are monostromatic. Abundant secondary pit connections link contiguous kindred and non-kindred cells, but the function of these structures remains unclear. Previous examinations have attempted to elucidate the function of pit plugs/pit connections in other red algal groups. Some studies have stated that translocation occurs between the pit plugs and pit channels while others are of the opinion that such function has yet to be proven. The anatomy of *Caloglossa* demonstrates the potential of this taxon as a model organism for studies on the function of pit plugs versus pit connections. A combination of experiments using microinjection techniques and epifluorescence microscopy confirms that these pit connections are involved in cell-to-cell communication.

P37

Determining the number of membranes surrounding the chloroplast of three euglenoid species: *Lepocinclis acus*, *Euglena gracilis*, and *Euglena sanguinea*

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Previous studies on *Euglena gracilis* revealed chloroplasts bound by three membranes. Secondary symbiosis, a phagotrophic euglenoid ingesting a photosynthetic eukaryote green algae, is thought to be the origin of the three-membrane chloroplast. From this limited data, it was commonly stated that three membranes bind all euglenoid chloroplasts. In light of the vast differences seen in euglenoid chloroplast morphology, it was hypothesized that the number of chloroplast membranes could also differ. Transmission electron microscopy was used to image the number of chloroplast membranes in *Euglena sanguinea* and *Lepocinclis acus*, as well as *E. gracilis*. These new species were chosen to represent the crown and the base of the freshwater euglenoid phylogenetic tree, based on molecular SSU and LSU data. Though images of chloroplasts from *E. sanguinea* were inconclusive, three chloroplast membranes were visible in *E. gracilis* and *L. acus*. This finding supports the position that three membranes bind all euglenoid chloroplasts. Studies including species from the *Discoplastis*,

Phacus, and *Trachelomonas* genera could further corroborate this three-membrane finding.

P38

Development of a Modular Integrated Recirculating Aquaculture System Using *Porphyra* for Bioremediation of Marine Finfish Effluent

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It is crucial to expand the U.S. aquaculture industry in a way that provides a reliable, long term source of food and that minimizes the risk of negative environmental impact. This can be accomplished through integrated multi-tropic aquaculture (IMTA). The simplest form of IMTA combines a “fed” component (e.g. finfish) with an “extractive” component (e.g. seaweed). In an IMTA system metabolic wastes from the fed component become nutrients for the extractive component and are incorporated into valuable biomass. A demonstration-scale modular integrated recirculating aquaculture system (MIRAS) was constructed in a greenhouse adjacent to Great Bay Aquaculture, LLC in Newington, NH. The system integrated the production of Atlantic cod (*Gadus morhua* L.) with the red seaweeds *Porphyra umbilicalis* Kützinger and *P. linearis* Greville and was used to study growth rates of both components and to model nutrient dynamics. Ammonium production and uptake rates of the fish and seaweed, respectively, were used to model the effect of system operating parameters including: water recirculation and replacement rates; fish feed rate or fish biomass; and seaweed biomass on system ammonium dynamics. A second predictive model was developed to optimize seaweed biomass in relation to fish feeding rates to maintain suitable system ammonium concentrations. Optimum operation of the integrated system maintains nutrient levels that are high enough to promote seaweed growth yet safely below stress levels for the fish. Integrated fish/seaweed trials were run in the MIRAS to validate the models using varied feed rates and seaweed biomasses. The models accurately predicted the effect of system parameters on nutrient levels and thus, can be used by an aquaculture operation to balance the needs of both the fish and seaweed components. Overall, the *Porphyra* biofilter removed 88 to 101% of the ammonium from the fish effluent. High quality *Porphyra* (nori) produced in the MIRAS was used in a subsequent study to partially replace fishmeal as a protein source in cod diets.

P39

Is it Safe to Drink the Water?: Filtering Algal Toxins in Rural Settings

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The health and vitality of freshwater lakes and rivers are of the utmost importance to human populations due to the substantial water consumption and recreational needs. As human activity and demand have increased, the need to conserve and manage the welfare of these freshwater systems has been a topic of concern. In recent years the issues of cyanobacterial blooms and the cyanotoxins produced have called into question the safety of freshwater systems. The water systems of Voyageurs National Park, Minnesota allowed me to examine a system where fulltime residents, part-time residents, and summer visitors utilize the water both domestically and recreationally making it imperative that the toxic potential of the water is known. I utilized three types of water monitoring techniques used in determining the human health risk of a freshwater system. These include light microscopy to verify cyanobacteria presence and cell density, polymerase chain reaction (PCR) to establish the presence of the gene *mcyA* in microcystin-LR producing cyanobacteria, and enzyme-linked immunosorbant assays (ELISA) to ascertain the toxin concentration of a water sample.

However, due to weaknesses of each technique and nature of the toxin it is safest to always assume that the water is contaminated as a resident and/or visitor of rural Voyagers National Park. Therefore, water filtration/purification becomes an important and proactive way to reduce toxin risk. These techniques including sand, activated carbon, ultraviolet photolysis, and boiling are typical and/or potential protection methods utilized by residents and visitors of Voyagers National Park. Further examination of commercially available water filter/purification systems allowed me to test the resilience of each system when used repeatedly. Filtering toxic samples through granulated activated carbon yielded the best results reducing the microcystin concentration below the WHO guideline of 1 ug/L (2003). All other methods did not reduce the microcystin-LR concentration and as in the cases of boiling and ultraviolet photolysis, through cell lysis, made the samples more toxic.

P40

Isolation, pilot scale mass culture of mono-strain and antioxidant effects of two freshwater microalgae *Pediastrum duplex* and *Dactylococcopsis acicularis* from a rocky pool of natural stream

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Many efforts have been expended on searching for new compounds, demonstrated in microalgae of all classes. In this study *Pediastrum duplex* and *D. acicularis* were collected from a rocky pool of natural stream in the volcanic Jeju Island, Korea. Isolation was done under the phase contrast inverted microscope using micropipette method. Subculture and mass culture were done with freshwater media enriched with F/2 nutrients, soil extract and trace elements at 25C under fluorescent light on a 14:10 L:D cycle. Mass culture biomass was harvested by filtration after three weeks of culture and finally the collected biomass was freeze dried. Antioxidant properties were determined from the freeze-dried samples. The antioxidant properties of different fractions (n-hexane, chloroform and ethyl acetate) obtained by solvent fractionation of 80% methanolic extracts of two microalgae were investigated for free radical, reactive oxygen species scavenging (superoxide O²⁻, hydrogen peroxide H₂O₂, hydroxyl radical OH, nitric oxide NO, metal chelating (MC) and lipid peroxidation inhibition activities. n-Hexane and ethyl acetate fractions of *P. duplex* and chloroform fraction of *D. acicularis* showed 74.5%, 79.8% and 59.4% effects on DPPH (1,1-diphenyl-2-picrylhydrazyl), respectively, which was remarkable in comparison with commercial antioxidants. H₂O₂ activity was 47.0% and 48.7% from the fractions of chloroform and ethyl acetate of *P. duplex*, and 49.7% from chloroform fraction of *D. acicularis*. Aqueous residue of *P. duplex* and n-hexane fraction of *D. acicularis* exhibited 57.7% and 45.7% activities on NO scavenging, respectively, which were significantly higher than that of commercial antioxidants (α -tocopherol: 25.0 % and BHT: 26.0%). MC effect was 82.4% and 77.6% from the ethyl acetate fraction of *P. duplex* and *D. acicularis*, respectively, which was significantly higher than commercial antioxidants. Fractions of chloroform and ethyl acetate from *P. duplex* showed high lipid peroxidation activities rather than α -tocopherol.

P41

Blooms of *Didymosphenia geminata* in rivers on Vancouver Island 1990 to present: A new invasive species

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Starting in 1989 heavy blooms of *Didymosphenia geminata* began appearing in the Heber River on Vancouver Island. Within 5 years *D. geminata* had spread to 12 catchments on Vancouver Island and was abundant in pristine, nutrient-poor rivers previously known to have very low algal biomass. Investigations to determine the environmental cause of the blooms during the early 1990's proved inconclusive. We have examined a metadata base to explore the possibility that the blooms of *D. geminata* on Vancouver Island in the 1990's might have resulted from an invasion by a new strain of *D. geminata* to Vancouver Island streams associated with intense recreational fishing pressure on the Island in the 1980's.

P42

Advances in understanding, predicting and tracking Oregon harmful algal blooms

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With funding from NOAA's Oceans and Human Health Initiative and MERHAB, we have been combining satellite and in situ data to further our knowledge of the oceanographic conditions that lead to HABs and their interaction with the Oregon coast. The principal phytoplankton genera of interest are *Pseudo-nitzschia* and *Alexandrium* which can cause domoic acid or saxitoxin accumulation (respectively) in coastal shellfish, primarily razor clams, thus presenting a human health hazard. Here we summarize our results thus far. Using historical data on the levels of toxins in shellfish at approximately 20 locations along the Oregon coast, we have identified hot spots of frequent contamination. We have quantified a link between El Nino events and saxitoxin occurrence. Cluster analysis has identified regions of the coast that are subject to shellfish closures at the same time (or not), thus potentially streamlining the process of identifying 'at risk' locations. A new satellite product for bloom identification has been developed and disseminated. Satellite analyses have provided insight into the relationship between bloom development, nearshore winds and landfall of toxic blooms

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Commercial production of highly unsaturated fatty acids by microalgae: lessons for biofuels production.

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Over the past 30 years, a significant amount of research has been conducted focusing on the commercial production of lipid-based compounds using microalgae. Early approaches focused on production of carotenoid-rich microalgae in open ponds, and the mid 1980's and early 1990's saw a flurry of research on closed photobioreactor systems as replacements for these ponds. In the mid 1980's, with developing research pointing to the nutritional importance of DHA (i.e., docosahexaenoic acid (C22:6n-3)) in the human diet, we focused on developing an algae-based technology for producing oils rich in this fatty acid. An alternative source of this fatty acid, fish oil, already existed, but it had numerous organoleptic, stability and contamination issues, most of which still exist today. We decided that the best approach to producing DHA would be to develop a fermentation-based technology. In this talk, we discuss the key milestones in the development of a commercially successful microalgal technology for the production of DHA and describe problems that were overcome during development of this technology. As a result of the high growth rates, cell densities and lipid contents achieved with this approach, the productivity of unsaturated fatty acid-rich lipids in this system represents the highest ever achieved with a microbial technology. With the recent intense interest in the development of biofuel technologies, there has been renewed interest in the use of algae for producing lipids for use in these technologies. Key lessons from development of the DHA technology are directly applicable to problems that will be facing researchers working on algal biofuel technologies. These lessons are described and discussed in light of the potential for developing successful algae-based biofuel technologies.

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Lipid pathways of *Schizochytrium* and their export to heterologous systems.

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Commercially important, biochemical pathways unique to algae have been exported to other more productive or better characterized systems such as bacteria, yeast and higher plants. One such biochemical pathway of great interest has been that of long-chain polyunsaturated fatty acids such as DHA. *Schizochytrium* is a commercially important organism for the production of DHA-containing nutritional oils by fermentation. Two pathways of fatty acid biosynthesis have been discovered in *Schizochytrium*: one mediated by a polyketide synthase-like, polyunsaturated fatty acid synthase, and the other by classical elongases and desaturases. Prior to this study, the latter pathway has only been partially characterized in *Schizochytrium*, however similar desaturase and elongase genes from related algae have been expressed in other model systems such as bacteria, yeast and higher plants. Similarly, the PUFA synthase has also been expressed in these model systems. The characterization and heterologous expression of these and other algal lipid genes will be discussed.

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Manipulation of *Schizochytrium* genes for improved fatty acid production.

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DHA (4,7,10,13,16,19-docosahexaenoic acid; C22:6n3) is an essential nutrient for human development as well as cardiovascular and neurological health. It is presently added to infant formulae and nutritional supplements, and is increasingly used to enhance the nutritional profiles of certain foods. The microorganism *Schizochytrium sp.* ATCC20888 is a commercial source of the omega-3 fatty acid DHA. We have determined that DHA biosynthesis in this organism is carried out by a novel mechanism distinct from those in animals, plants, and most other microorganisms. Development of genetic transformation methods for *Schizochytrium* has allowed the study and manipulation of the biosynthesis of this fatty acid. Gene knock-outs, deletions and replacements with foreign genes are readily achievable. Certain gene modifications result in stable enhancement of DHA productivities and could lead to lower costs and expanded usage. Furthermore, this system represents a model for genetic manipulation of algae and other microorganisms.

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Use of heterotrophic “helpers” improves cultivability of phytoplankton

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Modern molecular methods have revealed a great wealth of diversity in the phytoplankton that is not represented by cultured strains. One of the major challenges facing phycologists in coming years is to develop better strategies for cultivating these organisms. Work in our lab with cultures of the unicellular cyanobacterium *Prochlorococcus* has demonstrated that the removal of the heterotrophic bacteria found in the natural environment has a deleterious impact on these organisms. We hypothesize that this phenomenon is not unique to *Prochlorococcus*, and that standard dilution-to-extinction methods for isolating phytoplankton select against organisms that are dependent on “help” from heterotrophic bacteria. On a recent cruise in Chesapeake Bay we tested this hypothesis by adding cultured bacteria to media used to isolate phytoplankton from a suboxic station. In liquid media, diversity was increased in cultures with added bacteria. On solid media, no phytoplankton grew on plates without added bacteria, while several different species, including some that were rare in the environment, were recovered on the treated plates. Further, similar results were observed on plates treated with catalase instead of bacteria, suggesting that one mechanism for this “helping” phenotype is the reduction of oxidative stress associated with the culture environment.

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The sacoglossan sea slug, *Elysia clarki*, feeds on and sequesters functional chloroplasts from a wide taxonomic range of ulvophycean algae.

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Many Sacoglossan sea slugs have the unusual ability to sequester chloroplasts from their algal food sources and maintain them in specialized cells lining the digestive diverticulum. These sequestered chloroplasts are photosynthetically functional and maintained for just a few days in some species, to up

to 9 months in others, providing significant nutrition to the host animal. In addition, the source of the sequestered chloroplasts determines the color of the host animal. Most Sacoglossans, especially those in which the symbiosis persists for a lengthy period, sequester chloroplasts from a single or only a few species of algae. *Elysia clarki*, a sea slug found in the Florida Keys, can maintain sequestered chloroplasts for up to 4 months, and is unusual in that it sequesters chloroplasts from multiple species of algae from the order Bryopsidales. As part of a comprehensive survey of *E. clarki*'s range in the Florida Keys, we have found several new populations of *E. clarki* and determined the source of their sequestered algal chloroplasts using molecular markers. An analysis of *rbcL* sequences amplified from total DNA extracted from field collected adult sea slugs reveals that *E. clarki* has the ability to sequester chloroplasts from at least 10 species of the Bryopsidales, and at least 2 species of the Dasycladales. Surprisingly, however, *E. clarki* do not feed on some groups of the Bryopsidales that are plentiful in their habitat. *Elysia clarki*'s unusual ability to sequester chloroplasts from such a wide range of algae, and the length of the kleptoplastic association may be due to the presence of horizontally transferred, nuclear encoded, algal chloroplast genes in the animal's genome.

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Abundance and toxicity of *Karlodinium veneficum* bloom in Weeks Bay National Estuarine Research Reserve, Alabama

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Weeks Bay NERR experienced multiple dinoflagellate blooms in 2007. The phytoplankton community was dominated by a bloom of *Prorocentrum minimum* in February followed by *Kryptoperidinium foliaceum* and *Karlodinium veneficum* in July - October. Night time anoxia was recorded in February and in August. Five fish kills occurred within Weeks Bay and its tributaries during the summer. Analyses of the water and the dead fish indicated that karlotoxin contributed to these. We mapped phytoplankton community structure, toxin levels and a range of environmental and optical variables repeatedly during the *Karlodinium* bloom. *Karlodinium* formed spatially localized peaks of cell density and cell toxicity. The highest abundance was 120 million cells/liter (466 µg/l Chla) in the upper reach of the estuary. High cell densities reflected elevated nutrient loading. 67% of the variability in the environmental data (T, S, DIN, DIP and kd) was explained by the first 2 PCs in a principle components analysis. Per-cell toxin concentration was highly correlated with PC2, which was correlated ($p < 0.05$) with DIP ($R = 0.91$) and kd ($R = 0.81$): toxicity was highest at low DIP/high water clarity.

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Population genetics and phylogeography of the pantropical alga *Acanthophora spicifera* (Rhodophyta) as revealed by multilocus microsatellite genotyping and DNA sequencing

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Acanthophora spicifera (Vahl) Borgesen is a common red alga in warm waters throughout the world and has been reported as a nuisance in several widely-spaced Pacific marine ecosystems. We conducted a geographically broad investigation of the population genetics and phylogeography of *A. spicifera* using microsatellite markers and mitochondrial DNA sequences. Analyses revealed an unexpectedly high level of genetic structure and variation. Because *A. spicifera* in Hawaii was recently introduced, is seldom observed in a sexually reproductive state, frequently produces successful clonal

recruits, and has broad dispersal capabilities, genetic analyses were expected to indicate uniformity both within and among Hawaiian populations. In contrast, microsatellite genotyping of Hawaiian samples indicated an unexpected degree of population structure throughout the archipelago and confirmed the widespread occurrence of clonal reproduction. For worldwide phylogeographic analyses, samples from numerous sites in Guam, East and West Australia, New Caledonia, Samoa, Indonesia, Okinawa, Costa Rica, and Puerto Rico were analyzed at the mtDNA COI locus. Sequence polymorphism was found to be conserved on a geographic scale; in the majority of cases a single haplotype was identified from each oceanic island or along vast stretches of coastline. However, the occurrence of ten biogeographically informative haplotypes with pairwise differences ranging from 1-14 base pairs represents unusually high intraspecific polymorphism for COI in rhodophycean lineages. These results indicate the presence of several cryptic intraspecific clades; islands of the Pacific form a closely related haplotype group while samples from Western Australia and the Atlantic differ substantially from each other and the Pacific clade. Additionally, mitochondrial sequence analysis was able to provide insight regarding the original source for Hawaiian populations and revealed the presence of a genetically divergent cryptic haplotype in Guam that may be related to recent reports of invasiveness.

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Monitoring toxic cyanobacteria in western Washington

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There is concern over the increased occurrence of toxic cyanobacteria in Pacific Northwest lakes yet extremely little is still known about the frequency and dynamics of toxic blooms in this region. We present results from two ongoing programs in the State of Washington that are providing much needed data on common cyanobacterial toxins in Washington lakes. In 2002 King County launched the only long term monitoring program for the detection of cyanobacterial toxins in this region. Toxins (hepatotoxic microcystins, and starting 2009, the neurotoxin anatoxin-a) are measured regularly at public beaches and offshore stations in three major urban lakes (Washington, Union and Sammamish) along with environmental parameters in an effort to link toxin production with environmental conditions and species composition. To date, microcystin levels in these lakes have remained below the 1 µg/L World Health Organization threshold for drinking water even though the toxin has been consistently detected in all three lakes. In response to increased public awareness of health risks posed by certain blooms the Washington State Legislature recently established funding for a statewide program to assist local governments in the management of toxic blooms. This program is rapidly providing much needed data on species composition and toxin levels in lakes throughout the region. The data available to date suggests that toxigenic species are common in the region's small lakes and that toxin levels can often exceed thresholds established by the World Health Organization.

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Regulation of Polyunsaturated Fatty Acid Production in the Marine Red Macroalga *Porphyra yezoensis*

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The marine red alga *Porphyra yezoensis* is rich in the polyunsaturated fatty acids (PUFAs) arachidonic acid (AA; C20: 4ω6) and eicosapentaenoic acid (EPA; C20: 5ω3). PUFAs are required for the health

and development of most animals, including aquacultured fish. Past work in our lab has shown that *Porphyra yezoensis* is well accepted in salmonid feed and could be used as a nutritional supplement to increase the sustainability of fish aquaculture. However, the regulation & optimization of PUFA biosynthesis in *P.yezoensis* and other macroalgae is not well understood. In this study, the effects of low temperature with altered nutrient conditions on PUFA production were investigated. It was hypothesized that PUFA content in *P. yezoensis* would increase at low temperature, which is a commonly observed response in microalgae and higher plants. The results of this study indicated that EPA was maximized when nutrients were not limiting, regardless of temperature, while AA was maximized under growth-limiting conditions, such as low temperature and nutrient starvation. In addition, a partial putative fatty acid desaturase gene was identified in *P. yezoensis*. The translated sequence contains an N-terminal cytochrome b5 domain and shows significant similarity to known delta-5 fatty acid desaturases, which are required for the biosynthesis of both AA and EPA. This gene was constitutively expressed and did not appear to be transcriptionally up regulated at low temperature or during nutrient recovery. It showed highest similarity to delta-5 fatty acid desaturases from the oocycetes *Pythium irregulare* and *Phytophthora megasperma*.

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Microalgae-Based Biofuel: A Perspective on the State of the Science

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Microalgae are considered to be a promising alternative source of green feedstock for production of liquid transportation fuels (e.g., biodiesel, green diesel, and jet fuel). Oil yields as high as 200 barrels per hectare of algal mass culture per year have been projected and perceived as an achievable goal. This oil yield, however, has yet to be demonstrated at a production level scale. This presentation will summarize background information and current knowledge on the synthesis and neutral lipid storage in oleaginous microalgae. Since algae oil feedstock production is governed by achievable cell density and cellular oil content, selection for rapidly-growing, high oil-containing and environmentally tolerant strains continues to be a major research focus. Additional areas that require more research and development before biofuels from algae feedstock can approach commercialization include: improved and sustainable production systems, economical and efficient downstream processing procedures (i.e., dewatering and oil extraction), exploitation of co-/by-products, utilization of waste streams (e.g., CO₂, N, and P) for algal biomass production, and overall systems integration.

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Characterization of triacylglyceride accumulation in the model diatoms *Thalassiosira pseudonana* and *Phaeodactylum tricorutum*.

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The recent completion of the sequencing of two marine diatom genomes (*Thalassiosira pseudonana* and *Phaeodactylum tricorutum*) by the Joint Genomes Institute (JGI), the development of rudimentary systems for the genetic manipulation, and the overall advances in molecular biology will allow a more systematic approach to understanding and manipulating the ability of these organisms and other microalgae to form triacylglycerides (TAGs) and potentially serve as feedstocks for the for the production of biodiesel. Our basic research plan is to build upon the preliminary work of the Department of Energy Aquatic Species Program and develop a fuller understanding of the regulation

of the genes encoding the metabolic pathways leading to, and competing with, the formation of TAGs. We have laid the groundwork for this analysis by evaluating TAG formation, in the specific strains sequenced by JGI, induced by nitrate and or silicate starvation by gas chromatography and mass spectrometry. In addition to determining the timing of TAG production, we have quantified the amount of TAGs and identified the major TAG species produced. We are in the process of carrying out a proteomic analysis of the two species under nutrient replete and starvation conditions by two dimensional SDS PAGE followed by a computerized comparison of the expression profile. We have identified several differentially expressed proteins including a number that were induced by starvation. We are extending this analysis by transcription profiling.

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Susceptibility and Protective Mechanisms of Motile and Non-Motile Cells of *Haematococcus pluvialis* (Chlorophyceae) to Photooxidative Stress

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The life cycle of the unicellular green alga *Haematococcus pluvialis* consists of motile and non-motile stages under normal growing conditions, both of which may undergo transformation to form cysts accompanied by accumulation of large amounts of the secondary carotenoid astaxanthin. We have observed that motile cells are more susceptible than non-motile cells to high light, resulting in a decrease in population density and photo-bleaching. In this study, we investigated the cause of cell death and the possible protective mechanisms of the cells that survived the high light, using two *Haematococcus* strains, CCAP 34/12 and SAG34/1b, as model systems. The former is a motile cell dominated strain, whereas the latter is a non-motile cell dominated strain. The death of motile cells under high light was attributed to the generation of excess reactive oxygen species (ROS) which caused severe damage to the photosynthetic components and intracellular membrane system. The motile cells were able to dissipate excess light energy by non-photochemical quenching and also by a partially up-regulated scavenging enzyme system. However, these strategies were not sufficient to protect the motile cells from high light stress. In contrast, non-motile cells were able to cope with and survive under high light by (1) relaxing the potentially over-reduced photosynthetic electron transport chain (PETC) thereby effectively utilizing PETC-generated NADPH to produce storage starch and neutral lipid, and thus preventing formation of excess ROS; (2) down-regulating the level of cytochrome f; (3) partitioning excess energy at PS II via constitutive energy dissipation; and (4) accumulating higher amounts of astaxanthin. The implication of these findings on improving astaxanthin production will be discussed.

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How ecologically permissive are Pseudanabaenalean (Cyanobacteria) genera? A plethora of new clades when different habitats are contemplated.

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Most genera of cyanobacteria have historically been believed to have a global distribution over a wide range of ecologies (e.g., *Aphanizomenon*, *Microcystis*, *Microcoleus* etc.). While a few genera have been reported with very narrow, endemic ranges (e.g., *Rexia*, *Mojavia*, *Halomiconema*), most descriptions have rather broad habitat and ecological ranges for individual species. Members of the

Pseudanabaenales are among the most species-rich, ecologically permissive taxa in the cyanobacteria. Recent examination of phylogenies generated using the 16S rDNA gene sequences from 50 strains have revealed a number of highly supported clades that do not necessarily correspond to traditional morphological characters. Folding patterns of the 16S-23 ITS region have further confirmed these observations. However, many of these clades do correspond to habitat of collection. Strains from desert soils formed several highly supported clades, one of which is sister to the clade containing the type of *Leptolyngbya* (*L. boryana*) that is itself in a highly supported freshwater cluster. Freshwater members fell out in trees to the exclusion of other biotopes, while subaerial taxa clustered with marine, terrestrial and rarely freshwater members. Thus, it appears that many of the genera of Pseudanabaenales do not necessarily contain members in as wide ecological habitats as previously supposed, but seem tied to ecology. Therefore, a reexamination of phylogenetic affiliations with combined ecological and molecular data needs to be undertaken.

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Untangling cyanobacterial systematics: erection of *Emicolynbya* gen. nov. from a polyphyletic clade of *Leptolyngbya* (Cyanobacteria).

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The *Leptolyngbya* contains over 150 taxa making it one of the largest genera within the Oscillatoriales (Cyanobacteria). Previous molecular work using 16S rDNA gene sequence data showed this group was composed of no less than three monophyletic clades, whose members tend to exhibit widely ranging ecologies. In order to characterize monophyletic lineages, the 16S-23S Internal Transcribed Spacer (ITS) region was sequenced from 16 strains currently classified within the genus *Leptolyngbya* based on morphology. In addition, 16S rDNA gene sequences were obtained, and secondary folding structures of the D1-D1' helix, Box-B and V3 helix within the ITS regions were determined to be used as diagnostic characters for further classification. Based on the 16S rDNA sequence data, five strains fell in a well defined clade with several other previously sequenced and described strains. Further, all strains observed in this cluster were subaerial or marine, and produced nodule-like cells unique in the Pseudanabaenaceae. The ITS folding patterns of the D1-D1' helix, Box-B and V3 helix were compared within this clade and against other clades within *Leptolyngbya*. Secondary folding patterns contained unique morphologies that support the 16S rDNA gene sequence data. Thus, in light of the total evidence obtained through this study, we propose the reclassification of these species to a newly erected genus *Emicolynbya*.

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Systematics of the Batrachospermales (Rhodophyta) - A Synthesis

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Recent molecular and morphological data necessitate a major taxonomic revision of the Batrachospermales, an order of red algae found in freshwater habitats throughout the world. This paper is a synthesis of available information with some targeted additional sequence data, resulting in a few

relatively conservative taxonomic changes to begin the process of creating a natural taxonomy for the Batrachospermales. To increase the information content of our taxonomic categories, and in particular to reduce paraphyly, we describe one new genus (*Kumanoa*), and two new sections in *Batrachospermum* (Sections *Australasica* and *Macrospora*); and emend the circumscriptions of the family Batrachospermaceae (to include Lemaneaceae and Psilosiphonaceae), the genus *Batrachospermum* (to exclude the Sections *Contorta* and *Hybrida*, raised to genus level as *Kumanoa*), and the Sections *Aristata*, *Helminthoidea* and *Batrachospermum* of *Batrachospermum*. We also provide a new name, *B. montagnei*, for the illegitimate *B. guyanense*. This taxonomic synthesis increases the level of monophyly within the Batrachospermales, but minimises taxonomic change where data are still needed.

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New insights in the red algae of the Gulf of Mexico

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Recent collections made by SCUBA, ROV and box dredging have revealed a more diversity-rich deepwater (~40-90 meters) marine red algal flora throughout the Gulf of Mexico than was previously reported. Deepwater collections off the northwestern Gulf (Louisiana, Texas), southwestern Gulf (off the Campeche Banks, Mexico), the southeastern Gulf (off the Dry Tortugas) and the northeastern Gulf (off the Florida Middleground) imply complex macroalgal communities. Emphasis will be placed on characterizing the diversity of the dominant red algal families including new algal range extensions, records, and the description of new species.

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Investigation on the Worldwide Distributed Subaerial Green Alga *Cephaleuros virescens*

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Cephaleuros is an understudied genus of subaerial green algae (Chlorophyta) found throughout the Southeastern USA and in many regions of high humidity world-wide. The generitype, *C. virescens*, was originally described as a fungus and reported from almost every tropical and subtropical region, including the Southeastern USA. Habitat requirements and current morphology based classification in *C. virescens* combine to present rather unique research challenges. In order to assess the systematic circumscription and wide spread distribution of *C. virescens*, samples of this taxon have been gathered from the Southeastern USA and overseas. The use of primers specifically designed for the chloroplast-encoded *rbcL* from *Cephaleuros* have been successfully applied in amplifying sequences for phylogenetic analyses. Present results from this study point out that several entities representing different lineages are currently grouped under the name "*Cephaleuros virescens*". These taxa share similar morphology and habitat and possibly represent a case of morphological convergence. Based on topotype material from the Guyanas, *C. virescens*, appears to be restricted to the tropical Central and South America, with several unnamed species of *Cephaleuros* occurring in Southeastern USA and overseas.

A molecular phylogenetic study of the red algal parasites *Benzaitenia yenoshimensis*, *Janczewskia hawaiiiana*, *J. morimotoi*, and *Ululania stellata* (Rhodomelaceae, Ceramiales) from Hawaii and Japan

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Traditionally, red algal parasites have been regarded as adelphoparasites or alloparasites, which are defined by the degree of relatedness to their host species: most fall into the former category and are characterized by the parasites and their hosts being closely related and showing high host specificity. Adelphoparasites are generally classified into the same tribe or at least the same family. On the other hand, alloparasites are not closely related to their hosts and are generally found on hosts from different tribes or families. Molecular phylogenetic studies of red algal parasites over the last 12 years have supported the concept of adelphoparasitism rather than alloparasitism. In the Northwest Pacific and the Hawaiian Islands, *Benzaitenia yenoshimensis*, *Janczewskia hawaiiiana*, *J. morimotoi*, and *Ululania stellata* are known as red algal parasites in the order Ceramiales and are parasitic on some rhodomelacean species belonging to the tribes Chondrieae (*Acanthophora pacifica*, *A. spicifera* and *Chondria crassicaulis*) and Laurencieae (*Laurencia mcdermidiae* and *L. nipponica*). Although *Janczewskia* and *Ululania* have been considered to be in the same tribes as their host species, the taxonomic placement of *Benzaitenia* has been controversial. To infer the phylogenetic positions of these parasites and to clarify the relationships between these parasites and their hosts, we are working on molecular phylogenetic analyses using parts of the nuclear LSU and SSU rRNA genes, plastid LSU rRNA gene and *cox1* gene sequences. Our preliminary nuclear data show that both *Janczewskia* species are positioned within the *Laurencia sensu stricto* clade (where their host plants are also placed), while *B. yenoshimensis* and *U. stellata* are placed in the Chondrieae clade. Our data also show that the two *Janczewskia* species appear not to form a clade, suggesting multiple origins of parasitism within the *Laurencia* complex.

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