

The Psychological Society of America
58th Annual Meeting



Williamsburg, Virginia USA
6 - 12 August 2004

Meeting Program





THE PHYCOLOGICAL SOCIETY OF AMERICA



The *Phycological Society of America* was founded in 1946 to promote research and teaching in all fields of Phycology. The society publishes the *Journal of Phycology* and the *Phycological Newsletter*. Annual meetings are held, often jointly with other national or international societies of mutual member interest. *Phycological Society of America* awards include the **Bold Award** for best student paper, 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 2004 PSA ANNUAL MEETING: Sharon T. Broadwater, *College of William and Mary*

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PSA Scientific and Social Events Room Schedule

DAY & DATE	WARWICK ROOM	JAMESTOWN PARLOR	HUNTINGTON ROOM	EMPIRE ROOM A	EMIPRE ROOM C	WILLIAMSBURG PARLOR	OTHER HOTEL & OFF-SITE
FRIDAY 6 Aug.	Board of Trustees Meeting 12:00 - 7:00 PM						
SATURDAY 7 Aug.	Executive Committee Meeting 8:00 AM - 7:00 PM	PSA Headquarters 3:00 - 7:00 PM	Speaker Preparation Room 3:00 - 5:00 PM				Opening Mixer/Reception Hospitality House Cortyard 7:00 - 10:00 PM
SUNDAY 8 Aug.	Speaker Preparation Room 8:00 AM - 5:00 PM	PSA Headquarters 9:00 AM - 5:00 PM	Relaxation and Discussion 8:00 AM - 5:00 PM	Presidential Welcome: 9:00 AM ----- Contributed Oral Paper Session: Bold Award 9:10 - 12:00 AM ----- Symposium: PSA History 1:30 - 5:00 PM		Posters Set-up	<i>Journal of Phycology</i> Editorial Board Luncheon Berret's Restaurant 12:00 - 1:30 PM ----- PSA Auction and Social Westminster Ball Room 7:00 - 10:00 PM
MONDAY 9 Aug.	Speaker Preparation Room 8:00 AM - 5:00 PM	PSA Headquarters 8:00 AM - 5:00 PM	Relaxation and Discussion 8:00 AM - 5:00 PM	Symposium: Educational Workshop 8:10 - 12:00 AM ----- Contributed Oral Paper Session: Phylogeny and Taxonomy 1:30 - 5:00 PM ----- PSA Business Meeting 7:15 - 8:30 PM	Contributed Oral Paper Session: Ecology and Population Biology 1:50 - 5:00 PM	Posters Available for View	
TUESDAY 10 Aug.	Speaker Preparation Room 8:00 AM - 5:00 PM					Poster Session and Mixer 7:00 - 10:00 PM	Optional Field Trips during morning and afternoon
WEDNESDAY 11 Aug.	Speaker Preparation Room 8:00 AM - 5:00 PM	PSA Headquarters 8:00 AM - 5:00 PM	Relaxation and Discussion 8:00 AM - 5:00 PM	Symposium: Progress in Green Algal Systematics 8:05 AM - 2:30 PM ----- Contributed Oral Paper Session: Ecology and Population Biology 3:00 - 5:00 PM	Contributed Oral Paper Session: Applied Phycology 3:00 - 4:40 PM	Posters Available for View	PSA Banquet & Awards Mariner's Museum 7:00 - 1:30 PM Busses leave Hospitality House at 6:15
THURSDAY 12 Aug.	Speaker Preparation Room 8:00 - 10:00 AM	PSA Headquarters 9:00 - 11:00 AM	Relaxation and Discussion 8:00- 11:30 AM	Contributed Oral Paper Session: Phylogeny and Taxonomy 9:10 - 11:30 AM	Contributed Oral Paper Session: Physiology, Biochemistry, Cell Biology and Molecular Biology 9:10 - 11:10 AM		

THE HISTORIC TRIANGLE

“THE LARGEST LIVING MUSEUM IN THE WORLD”

The Colonial Parkway, a twenty two mile stretch of scenic highway, connects three of the most historically significant towns in America – Jamestown, Williamsburg, and Yorktown. Jamestown, settled in 1607 was the first permanent English settlement in the United States (13 years before the Pilgrims landed!). Jamestown served as the capitol of Virginia until 1699 when the capitol was moved to Williamsburg. Today, the Jamestown historic area consists of a museum and state park at Jamestown and a national park on Jamestown Island. The latter includes the original site of the 1607 fort which is currently being excavated. The excavation has provided a wealth of historical data including the structure of the fort and vignettes of life in the early colony based on more than 500,000 artifacts. Jamestown is the birthplace of America as eloquently said on their website: *“For it is from Jamestown that we as Americans can trace who and what we are as a people and as a nation. It is from here that the first permanent English settlement laid its roots in 1607. It is from here that the first representative legislative assembly in North America met in 1619. It is from here that three continents came together as Europeans encountered American Indians, and later brought enslaved Africans to this land. As the seat of Virginia government Jamestown became the focal point of Bacon’s rebellion in 1676.”*

Williamsburg, perhaps the best known of the three sites, is somewhat unusual in that there is no “town.” Williamsburg consists primarily of Colonial Williamsburg (CW), the College of William & Mary (WM) and many tourist attractions. “For 81 years (1699-1780), Williamsburg was the political, cultural, and educational center of what was then the largest, most populous, and most influential of the American colonies. It was here that the fundamental concepts of our republic – responsible leadership, a sense of public service, self-government, and individual liberty – were nurtured under the leadership of patriots such as George Washington, Thomas Jefferson, George Mason, and Peyton Randolph.” (quoted from website) After the capitol was moved to Richmond in 1780, Williamsburg gradually faded from the limelight until 1926 when John D. Rockefeller agreed to reclaim a piece of history. Today 4 million people a year visit CW. It is an ongoing archaeological project with continuing efforts to present an accurate view of the early life of the town. There are museums, taverns where arguments were waged between Loyalists and Revolutionaries, restored buildings, and recreations of colonial life and work, At the courthouse you might be asked to serve on a jury, and if you wish, you can join a ghost tour or try out the “stocks” for size.

Yorktown is located on the York River just across from the Virginia Institute of Science at Gloucester Point. Yorktown gains fame as the site of the last major battle of the Revolutionary War. “Between September 28 and October 19, 1781, General George Washington and his allied American and French army of 17,600 troops surrounded and besieged General Charles Lord Cornwallis’ 8,300 British, German and American loyalist forces, which were fortified within the port of Yorktown. Over the course of 9 days, over 15,000 rounds of siege artillery were fired upon the British. On October 17, Lord Cornwallis requested a cease-fire; two days later, he surrendered in an open field, now known as “Surrender Field.” Upon hearing the news of the defeat, the British Prime Minister is said to have clutched his chest and exclaimed, “Oh God, it’s all over.” And indeed it was. After two years of diplomatic negotiations, Great Britain signed the Treaty of Paris, formally recognizing independence for the United States of America.” (quoted from website). While there, you can visit the Yorktown Victory Museum, the Waterman’s museum, the Yorktown battlefield, a small beach, and art galleries.

THE COLLEGE OF WILLIAM AND MARY

The College of William and Mary was chartered on February 8, 1693, by King William III and Queen Mary II as the second college in the American colonies. It severed formal ties with Britain in 1776, became state-supported in 1906, and became coeducational in 1918. William and Mary achieved modern university status in 1967. Phi Beta Kappa and the honor code system of conduct were founded at William and Mary. The Sir Christopher Wren Building is the oldest academic building in continuous use in the United States. It was constructed between 1695 and 1699, before Williamsburg was founded, when the capital of the colony of

Virginia was still located at Jamestown. Classes are still held in the Wren Building, which also is home to several faculty offices.

The William and Mary campus covers approximately 1,200 acres including picturesque Lake Matoaka and the College Woods. Adjacent to Colonial Williamsburg, the Ancient Campus section is restored to 18th-century appearance. Enrollment is 7,650 of whom approximately 5,700 are undergraduates. Students come from all 50 states plus the District of Columbia and Guam as well as 43 foreign countries. The faculty currently numbers 567 in the Schools of Arts and Sciences, Marine Science, Business Administration, Education, and Law.

IMPORTANT FIELD TRIP INFORMATION

As noted on the web site and printed registration materials, most of the optional Field Trips required a 15 person minimum to allow for group rates. At the time of printing this program book, only the VIMS trip had enough registrants. Some others were very close to meeting this minimum and might by the time the meeting starts. **Updated information on the status of each field trip will be posted at registration.** Most of the field trips sites would have used public transportation anyway and so would still be available, simply not at discounted group rates. People who have registered and paid for field trips that do not meet the minimum will, of course, be reimbursed by PSA.

ROOM INFORMATION

MEETING REGISTRATION will be held next to **Empire Room A** on the second floor.

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

EXHIBITORS will be set up in the **Berkeley Room**, directly across the hall from the PSA Headquarters Room in the lower lobby.

The **SPEAKER PREPARATION ROOM** will be the Huntington Room on the second floor on Saturday and the **Warwick Room** on the second floor thereafter.

The **Huntington Room** on the second floor will be available from Sunday on for **RELAXATION AND DISCUSSIONS**.

PROGRAM OF SESSIONS AND EVENTS

FRIDAY AFTERNOON, 6 AUGUST

12:00-7:00 PM - Warwick Room

MEETING: PSA-Board of Trustees

SATURDAY MORNING and AFTERNOON, 7 AUGUST

8:00 AM – 7:00 PM - Warwick Room

MEETING: PSA-Executive Committee Meeting

SATURDAY EVENING, 7 AUGUST

7:00-10:00 PM - Hospitality House Courtyard

SOCIAL: Opening Social and Mixer

SUNDAY MORNING, 8 AUGUST

9:00-9:10 AM - Empire A

PRESIDENTIAL WELCOME

Presiding: THIERRY CHOPIN, *University of New Brunswick*

SUNDAY MORNING, 8 AUGUST

9:10-10:10 AM - Empire A

CONTRIBUTED PAPERS: Bold Award 1

Presiding: JEFFREY LEBLOND, *Middle Tennessee State University*

- 9:10 **Phylogenetic analyses of the Caulerpales (Ulvophyceae, Chlorophyta) based on *rbcL* gene sequences.** Lam, Daryl; Zechman, Frederick. *Department of Biology, California State University, Fresno, Fresno, CA, USA*
- 9:30 **A Multi-gene approach to the phylogeny of the Dasycladales (Ulvophyceae, Chlorophyta).** Ashworth, Matt; Zechman, Rick. *Department of Biology, California State University, Fresno, Fresno, CA, USA*
- 9:50 **A potential biological control agent, bacterium SG-3: Mode of action and effect on two economically important cyanobacteria.** Wilkinson, Kathryn Joan¹; Walker, H. Lynn²; Lembi, Carole A.¹. (1) *Botany and Plant Pathology, Purdue University, West Lafayette, IN, USA.* (2) *School of Biological Sciences, Louisiana Tech University, Ruston, LA, USA.*

SUNDAY MORNING, 8 AUGUST

10:10-10:40 AM

BREAK

SUNDAY MORNING, 8 AUGUST

10:40-12:00 AM - Empire A

CONTRIBUTED PAPERS: Bold Award 2

Presiding: JEFFREY LEBLOND, *Middle Tennessee State University*

10:40 **A carbon ($\delta^{13}\text{C}$) and nitrogen ($\delta^{15}\text{N}$) stable isotope analysis of macrophyte contributions to mussel (*Mytilus californianus*) diets on southern California shores.** Gilbane, Lisa; Murray, Steve. *Department of Biological Science, California State University, Fullerton, CA, USA.*

11:00 **Isolation and coexistence: Macroalgal species richness along the south coast of Australia.** Goldberg, Nisse Aloma; Kendrick, Gary A. *School of Plant Biology, University of Western Australia, Crawley, WA, Australia.*

11:20 **Shifting Macrophyte abundances and the primary productivity of southern California shores.** Bullard, Aimee M.; Murray, Steven N. *Department of Biological Science, California State University, Fullerton, CA, USA.*

11:40 **Culturing coccolithophorid algae for carbon dioxide bioremediation.** Moheimani, Navid Reza; Borowitzka, Michael A. *Department of Biological Sciences and Biotechnology, Murdoch University, Murdoch, WA, Australia.*

SUNDAY AFTERNOON, 8 AUGUST

12:00-1:30 PM

LUNCH BREAK (on own)

SUNDAY AFTERNOON, 8 AUGUST

12:00-1:30 PM - Berret's Seafood Restaurant

***JOURNAL OF PHYCOLOGY* - Editorial Board Luncheon**

SUNDAY AFTERNOON, 8 AUGUST

1:30-2:50 PM - Empire A

SYMPOSIUM: *The Phycological Society of America: Reflections on its History in a Historic Venue*

Presiding: DENNIS HANISAK, *Harbor Branch Oceanographic Institute*

1:30 **Welcome and Introduction.** Hanisak, M. Dennis. *Harbor Branch Oceanographic Institute*

1:40 **The Phycological Society of America: its roots and early years.** Parker, Bruce C. *Department of Biology, Virginia Tech, Blacksburg, VA, USA.*

2:20 **The Journal of Phycology: from Luigi Provasoli to electronic publishing.** Lembe, Carole A. *Purdue University.*

SUNDAY AFTERNOON, 8 AUGUST

3:00-3:30 PM

BREAK

SUNDAY AFTERNOON, 8 AUGUST

3:30-5:00 PM - Empire A

SYMPOSIUM: *The Psychological Society of America: Reflections on its History in a Historic Venue*

Presiding: DENNIS HANISAK, *Harbor Branch Oceanographic Institute*

3:30 **PSA's Endowment: from dream to reality.** Hanisak, M. Dennis. *Harbor Branch Oceanographic Institute*

4:10 **Round Table Discussion**

SUNDAY EVENING, 8 AUGUST

5:00 PM – 7:00 PM

DINNER BREAK (on own)

SUNDAY EVENING, 8 AUGUST

7:00-10:00 PM - Westminster Ball Room

SOCIAL: PSA Auction

MONDAY MORNING, 9 AUGUST

8:10-9:55 AM - Empire A

SYMPOSIUM: *Educational Workshop and Symposium*

Presiding: ROY LEHMAN, *Texas A&M University-Corpus Christi*

8:10 **Life in glass houses.** Pickett-Heaps, Jeremy David. *Department of Botany, Univ. of Melbourne, Melbourne, VIC, Australia.*

9:10 **Ecological field methods for marine benthic macroalgal assessment: a comparison of traditional and modern methods.** Lehman, Roy L. *Department of Physical & Life Sciences, Texas A&M University-Corpus Christi, Corpus Christi, TX, USA.*

MONDAY MORNING, 8 AUGUST

9:55-10:25 AM

BREAK

MONDAY MORNING, 9 AUGUST

10:25-12:00 AM - Empire A

SYMPOSIUM: *Educational Workshop and Symposium*

Presiding: ROY LEHMAN, *Texas A&M University-Corpus Christi*

- 10:25 **The joys and pitfalls of accessing non-model systems in the genomic age: what happens when evolution, development, physiology, systematics and genomics fuse in the kitchen sink of science.** Mandoli, Dina F. *Department of Biology & Center for Developmental Biology, University of Washington, Seattle, WA, USA.*
- 11:25 **Remarkable plants: The Oedogoniales (green algae).** Pickett-Heaps, Jeremy David. *Department of Botany, Univ. of Melbourne, Melbourne, VIC, Australia.*
- 11:55 **Closing Remarks**

MONDAY AFTERNOON, 9 AUGUST

12:00-1:30 PM LUNCH BREAK (on own)

MONDAY AFTERNOON, 9 AUGUST

1:30-3:10 PM - Empire A

CONTRIBUTED PAPERS: Phylogenetics and Taxonomy 1

Presiding: RICK MCCOURT, *Academy of Natural Sciences of Philadelphia*

- 1:30 **Systematics and Evolution of the euglenophyta: a phylogenetic approach based on combined analysis of SSU and LSU rDNA.** Triemer, Richard¹; Shin, Woongghi³; Linton, Eric W.¹; Nudelman, Maria A.¹; Brosnan, Stacy²; Monfils, Anna K.¹; Bennett, Matthew S.¹ (1) *Michigan State University, East Lansing, MI, USA.* (2) *Rutgers University, New Brunswick, NY, USA.* (3) *Chungnam National University, Daejeon, South Korea.*
- 1:50 **Structure and phylogenetic usefulness of the euglenoid beta-tubulin gene.** Linton, Eric W.; Triemer, Richard E. *Department of Plant Biology, Michigan State University, East Lansing, MI, USA.*
- 2:10 **Are cyanobacteria endemic? A case study employing newly described *Leptolyngbya* sp. (Cyanobacteria) isolated from desert soils based on morphology and 16S rDNA sequence data.** Casamatta, Dale Anthony; Johansen, Jeffrey R. *Dept. of Biology, John Carroll University, University Heights, OH, USA.*
- 2:30 **Two new cyanobacterial taxa from the Great Smoky Mountains National Park (USA).** Johansen, Jeffrey R.; Casamatta, Dale A.; Gomez, Shannon R. *Department of Biology, John Carroll University, University Heights, OH, USA.*
- 2:50 **Water bloom forming *Raphidiopsis* (Cyanobacteria): Its taxonomy, phylogeny and toxins.** Li, Renhui¹; Carmichael, Wayne M.²; Watanabe, Makoto M.³; Wilhelm, Steven W.¹. (1) *Department of Microbiology, University of Tennessee, Knoxville, TN, USA.* (2) *Department of Biological Sciences,*

MONDAY AFTERNOON, 9 AUGUST

1:50-3:10 PM - Empire C

CONTRIBUTED PAPERS: Ecology and Population Biology 1

Presiding: CHARLIE YARISH, *University of Connecticut*

- 1:50 **Macroalgal recruitment on coral reefs: Dynamics and roles of ecological processes.** Diaz-Pulido, Guillermo¹; McCook, Laurence J². (1) *Programa de Biología & Instituto de Investigaciones Tropicales INTROPIC, Universidad del Magdalena, Santa Marta, Magdalena, Colombia.* (2) *Great Barrier Reef Marine Park Authority, Townsville, QLD, Australia.*
- 2:10 ***Nereocystis luetkeana* as recruitment habitat for fish and invertebrates in southeast Alaska.** Stekoll, Michael S^{1,2}; Calvert, Elizabeth L²; Meyer, Erin¹; Rasher, Doug¹. (1) *Department of Natural Sciences, University of Alaska Southeast, Juneau, AK, USA.* (2) *Juneau Center School of Fisheries and Ocean Sciences, University of Alaska Fairbanks, Juneau, AK, USA.*
- 2:30 **Lack of phlorotannin induction by UV radiation in two species of dominant Antarctic macroalgae.** Fairhead, VA¹; Amsler, CD¹; McClintock, JB¹; Baker, BJ². (1) *Department of Biology, University of Alabama at Birmingham, Birmingham, AL, USA.* (2) *Department of Chemistry, University of South Florida, Tampa, FL, USA.*
- 2:50 **Stream macroalgae of the Hawaiian islands: a floristic analysis.** Sherwood, Alison R. *Department of Botany, University of Hawaii, Honolulu, HI, USA.*

MONDAY AFTERNOON, 9 AUGUST

3:10-3:40 PM

BREAK

MONDAY AFTERNOON, 9 AUGUST

3:40-5:00 PM - Empire A

CONTRIBUTED PAPERS: Phylogenetics and Taxonomy 2

Presiding: MIKE WYNNE, *University of Michigan*

- 3:40 **Diversity in *Grateloupia filicina* (Halymeniales, Rhodophyta) with special emphasis on cyptic diversity in the Atlantic Ocean.** De Clerck, Olivier¹; Fredericq, Suzanne²; Gavio, Brigitte²; Coppejans, Eric¹. (1) *Department of Biology, Ghent University, Ghent, Belgium.* (2) *Department of Biology, University of Louisiana at Lafayette, Lafayette, LA, USA.*
- 4:00 ***Centroceras clavulatum* (Ceramiaceae, Rhodophyta): a cosmopolitan red algal species?** Won, Boo Y.; Cho, Tae Oh; Fredericq, Suzanne. *Department of Biology, University of Louisiana, Lafayette, LA, USA.*

- 4:20 ***Antithamnion nipponicum* Yamada & Inagaki (Ceramiaceae, Rhodophyta) is a recent introduction along the coast of North Carolina and the correct name of the species known as *A. hubbsii* in Pacific North America and *A. pectinatum* in Western Europe.** Cho, Tae Oh; Won, Boo Y.; Fredericq, Suzanne. *Department of Biology, University of Louisiana, Lafayette, LA, USA.*
- 4:40 "A seaweed goes to war" --- Taxonomic status of the agarophyte *Gracilaria "confervoides"* harvested in North Carolina during WWII. Hommersand, Max H.¹; Freshwater, D. Wilson². (1) *Department of Biology, University of North Carolina, Chapel Hill, NC, USA.* (2) *Center for Marine Science, Univ. of North Carolina at Wilmington, Wilmington, NC, USA.*

MONDAY AFTERNOON, 9 AUGUST

3:40 – 5:00 PM - Empire C

CONTRIBUTED PAPERS: Ecology and Population Biology 2

Presiding: GUILLERMO DIAZ-PULIDO, *Universidad del Magdalena*

- 3:40 **Metaphytic algal succession of a newly constructed wetland in northwestern Ohio.** Hamsher, Sarah E.¹; Casamatta, Dale A.²; Luckeydoo, Lee M.³; Fausey, Norman R.³. (1) *Division of Water, City of Lancaster, Lancaster, OH, USA.* (2) *Department of Biology, John Carroll University, University Heights, OH, USA.* (3) *Agricultural Research Service, United States Dept of Agriculture, Columbus, OH, USA.*
- 4:00 **The role of environmental factors on the dynamic of the phytoplankton in streams of South Mississippi.** Anzola, Nestor Raul¹; Pessoney, George F¹; Hernandez, Carmen Liliana. *Department of Biological Sciences, University of Southern Mississippi, Hattiesburg, MS, USA.*
- 4:20 **Diversity and ecology of freshwater *Nannochloropsis* (Eustigmatophyceae).** Fawley, Karen Phillips; Fawley, Marvin. *North Dakota State University, Fargo, ND, USA.*
- 4:40 **Power law relationships among hierarchical taxonomic categories in algae reveal a new paradox of the plankton.** Passy, Sophia I.¹; Legendre, Pierre². (1) *Department of Biology, University of Texas at Arlington, Arlington, TX, USA.* (2) *Department of Biological Sciences, University of Montreal, Montreal, QC, Canada.*

MONDAY EVENING, 9 AUGUST

5:00 PM – 7:15 PM **DINNER BREAK (on own)**

MONDAY EVENING, 9 AUGUST

7:15-8:30 PM - Empire A

MEETING: PSA-Business Meeting (all PSA members)

TUESDAY MORNING AND AFTERNOON, 10 AUGUST

Various Times - all field trips leave from the Hospitality House

OPTIONAL FIELD TRIPS – SEE IMPORTANT NOTICE ON PAGE 3

TUESDAY EVENING, 10 AUGUST

7:00 – 10:00 PM - Williamsburg Parlor

POSTER SESSION AND MIXER

Presenting authors are encouraged to stand with their posters at any or all times throughout the evening.

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

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

1. **Species diversity in *Fragilaria sensu lato* from selected sites in the Great Lakes.** Ferguson, Michael Joseph¹; Scotese, Kyle¹; Morales, Eduardo²; Johansen, Jeffrey R¹. (1) *Biology Department, John Carroll University, University Heights, OH, USA.* (2) *Academy of Natural Sciences, Philadelphia, PA, USA.*
2. **Erradication program of *Undaria pinnatifida* (Harvey) Suringar (Laminariales, Phaeophyta) in Mexico.** Aguilar-Rosas, Luis Ernesto; Zertuche-Gonzalez, J. A.; Aguilar-Rosas, R.; Avila-Serrano, G. *Biología, Universidad Autónoma de Baja California, Ensenada, Baja California, Mexico.*
3. ***Undaria pinnatifida* (Harvey) Suringar (Laminariales, Phaeophyta) in Mexico.** Aguilar-Rosas, Raul¹; Aguilar-Rosas, Luis Ernesto²; Avila-Serrano, Guillermo¹. (1) *Facultad de Ciencias Marinas, Universidad Autónoma de Baja California, Ensenada, Baja California, Mexico.* (2) *Instituto de Investigaciones Oceanológicas, Universidad Autónoma de Baja California, Ensenada, Baja California, Mexico.*
4. ***Porphyra pendula* Dawson (Bangiaceae, Rhodophyta) in the Pacific coast of Mexico: Endemic species from the Gulf of California.** Aguilar-Rosas, Luis Ernesto¹; Aguilar-Rosas, Raul²; Sanchez Rodriguez, Ignacio³; Broom, Judy⁴; Nelson, Wendy⁵. (1) *Instituto de Investigaciones Oceanológicas, Universidad Autónoma de Baja California, Ensenada, Baja California, Mexico.* (2) *Facultad de Ciencias Marinas, Universidad Autónoma de Baja California, Ensenada, Baja California, Mexico.* (3) *Centro Interdisciplinario de Ciencias Marinas, Instituto Politecnico Nacional, La Paz, Baja California Sur, Mexico.* (4) *Department of Biochemistry, University of Otago, Dunedin, New Zealand.* (5) *Museum of New Zealand Te Papa Tongarewa, Wellington, New Zealand.*
5. **The Dinoflagellates of Twin Cays, Belize: Biodiversity.** Faust, Maria A. *Department of Botany, Smithsonian Institution, Washington D.C., DC, USA.*
6. **Feeding behavior and conditioning in three *Pfiesteria*-like dinoflagellates.** Egerton, Todd; Marshall, Harold G. *Department of Biological Sciences, Old Dominion University, Norfolk, VA, USA.*
7. **Comparison of algal growth on trees at various ozone levels (elevations) in Great Smoky Mountains National Park (USA).** Olsen, Catherine E.; Johansen, Jeffrey R. *Biology Department, John Carroll University, University Heights, OH, USA.*
8. **Morphology and physiology of a novel *Pfiesteria*-like-dinoflagellate from a Chesapeake Bay estuary.** Cerbin, Slawomir; Stem, Todd; Egerton, Todd; Marshall, Harold G. *Department of Biological Sciences, Old Dominion University, Norfolk, VA, USA.*
9. **The effects of forest harvesting practices on phytoplankton community structure in boreal lakes: establishing a reference condition.** Rattan, Kim; Gordon, Andrew M.; Sibley, Paul K. *Department of Environmental Biology, University of Guelph, Guelph, ON, Canada.*

10. ***Caulerpa sertularioides*, a green alga spreading aggressively over coral reef communities in Culebra Bay, North Pacific of Costa Rica.** Fernandez, Cindy. *CIMAR, University of Costa Rica, San Pedro, San José, Costa Rica.*
11. **Taxonomy, distribution and temporal changes in the abundance of phytoplankton in Taal Lake, Batangas, Philippines.** Perez, Teresita Ramos. *Dept. of Environmental Science, Ateneo de Manila University, Quezon City, Philippines.*
12. **A preliminary diatom community analysis of the Upper Roanoke River, southwest Virginia.** Buccellato, Michele T.; Cawley, Jon C. *Department of Biology, Roanoke College, Salem, VA, USA.*
13. **Morphological characteristics and occurrence of the diatom *Aulacoseira herzogii* from a dystrophic lake in southeastern Virginia, U.S.A.** Marshall, Harold G¹; Burchardt, Lubomira²; Cerbin, Slawomir¹. (1) *Department of Biological Sciences, Old Dominion University, Norfolk, VA, USA.* (2) *Department of Hydrobiology, Adam Mickiewicz University, Poznan, Poland.*
14. **Effects of temperature on rates of photosynthesis and respiration in *Caulacanthus ustulatus* (Rhodophyta), a new addition to the California seaweed flora.** Galvan, Victor C.; Murray, Steven N. *Department of Biological Science, California State University, Fullerton, Fullerton, CA, USA.*
15. **Latitudinal variation in *Egrecia menziesii*: Investigations of morphology, physiological response and gene flow.** Henkel, Sarah K. *Department of Ecology, Evolution, and Marine Biology, University of California, Santa Barbara, Santa Barbara, CA, USA.*
16. **Spatial and temporal patterns of abundance in southern California populations of *Caulacanthus ustulatus* (Rhodophyta).** Whiteside, Kim E.; Murray, Steven N. *Department of Biological Science, California State University, Fullerton, Fullerton, CA, USA.*
17. **A comprehensive evaluation of the palatability and chemical defenses of subtidal macroalgae from the Antarctic Peninsula.** Amsler, Charles D.¹; Iken, Katrin^{1,4}; McClintock, James B.¹; Amsler, Margaret O.¹; Peters, Kevin J.¹; Hubbard, Joanna M.²; Baker, Bill J.³. (1) *Department of Biology, University of Alabama at Birmingham, Birmingham, AL, USA.* (2) *Anchorage School District, Anchorage, AK, USA.* (3) *Department of Chemistry, University of South Florida, Tampa, FL, USA.* (4) *Institute of Marine Science, University of Alaska, Fairbanks, Fairbanks, AK, USA.*
18. **A comparative analysis of the biochemical and elemental composition of macroalgae from the western Antarctic Peninsula.** Peters, Kevin J.¹; Amsler, Charles D.¹; Amsler, Margaret O.¹; McClintock, James B.¹; Dunbar, Robert B.²; Baker, Bill J.³. (1) *Department of Biology, University of Alabama at Birmingham, Birmingham, AL, USA.* (2) *Department of Geological and Environmental Sciences, Stanford University, Stanford, CA, USA.* (3) *Department of Chemistry, University of South Florida, Tampa, FL, USA.*
19. **Back to phytoplankton 101: An evaluation of *Karenia brevis* strain differences.** Schaeffer, Blake; Kamykowski, Dan; Milligan, Edward; McKay, Laurie; Sinclair, Geoff. *Department of Marine, Earth, & Atmospheric Sciences, North Carolina State University, Raleigh, NC, USA.*
20. **Motility and aggregation of the mudflat diatom *Cylindrotheca closterium* (Bacillariophyceae) under varying environmental conditions.** Apoya, Melba Duhilag¹; Gretz, Michael R.¹; Underwood, Graham J.C.². (1) *Department of Biological Sciences, Michigan Technological University, Houghton, MI, USA.* (2) *Department of Biological Sciences, University of Essex, Colchester, Colchester, United Kingdom.*

21. **Lipid composition of Chlorarachniophytes (Chlorarachniophyceae): Unusual polar lipids and the role of the nucleomorph in sterol biosynthesis.** Dahmen, Jeremy L.¹; Leblond, Jeffrey¹; Seipelt, Rebecca L.¹; Elrod-Erickson, Matthew J.¹; Cahoon, Bruce¹; Kincaid, Rodney¹; Evens, Terence J.²; Chapman, Peter J.³. (1) *Department of Biology, Middle Tennessee State University, Murfreesboro, TN, USA.* (2) *United States Horticultural Research Laboratory, Ft. Pierce, FL, USA.* (3) *United States Environmental Protection Agency, Gulf Ecology Division, Gulf Breeze, FL, USA.*
22. **ARS-MEDIA: A new software program for the analysis, design and optimization of algal culture media.** Evens, T.J.; Niedz, Randall P. *USDA-ARS, Ft. Pierce, FL, USA.*
23. **The effect of temperature on diatom cell size, growth rates and biogenic silica content.** Johnson, Amber; Wilkerson, Frances; Dugdale, Richard. *Romberg Tiburon Center, San Francisco State University, Tiburon, CA, USA.*
24. **Astaxanthin's role in protecting *Haematococcus pluvialis* against oxidative stress: new evidence from an astaxanthin-overproduction mutant.** Hu, Z. Y.^{1,2}; Sommerfeld, Milton R.¹; Hu, Q.². (1) *School of Life Sciences, Arizona State University, Tempe, AZ, USA.* (2) *Department of Phycology, Institute of Hydrobiology, Wuhan, Hubei, China.*
25. **Seasonal changes in the effects of ultraviolet radiation on carbon partitioning in phytoplankton.** Franklin, Linda A.; Neale, Patrick J. *Smithsonian Environmental Research Center, Edgewater, MD, USA.*
26. **Cellular responses of *Chlorella zofingiensis* to selenium application.** Pelah, Dan; Cohen, Ephraim. *Ben-Gurion University, Beer-Sheva, Israel.*
27. **The chloroplast genome sequence of the haptophyte *Emiliana huxleyi*.** Sanchez Puerta, Maria Virginia; Bachvaroff, Tsvetan R.; Delwiche, Charles F. *Department of Cell Biology and Molecular Genetics, University of Maryland, College Park, MD, USA.*
28. **Heat-Shock Proteins expression in the coccolithophore *Emiliana huxleyi* under nutrient-replete and phosphorus limited conditions.** Kaufman, Jessica Annissa; Gonzalez, Elma. *Department of Organismic Biology, Ecology, and Evolution, UCLA, Los Angeles, CA, USA.*
29. **Unique architecture of the chloroplast genome in the green alga *Pseudendoclonium akinetum*.** Pombert, Jean-Francois; Otis, Christian; Lemieux, Claude; Turmel, Monique. *Biochimie et Microbiologie, Universite Laval, Quebec, QC, Canada.*
30. **The chloroplast genome sequence of the chlorophycean alga *Scenedesmus obliquus*: a comparative analysis with its *Chlamydomonas* homolog.** de Cambiaire, Jean-Charles; Otis, Christian; Lemieux, Claude; Turmel, Monique. *Biochimie et Microbiologie, Universite Laval, Quebec, QC, Canada.*
31. **Studying Species abundance and gene expression in marine diatoms using real-time PCR.** Takabayashi, Misaki; Wilkerson, Frances. *Romberg Tiburon Center, San Francisco State University, Tiburon, CA, USA.*
32. **Observations on binucleate dinoflagellates using long term fluorescent nuclear staining.** Rizzo, Peter Jacob Morris, Rodney; Tyler, Kristy; Shields, Robyn. *Department of Biology, Texas A&M University, College Station, TX, USA.*
33. **Fatty acid analyses of 8 *Craticula cuspidata* clones.** Zimba, Paul V.¹; Weaver, Mark²; Sullivan, Michael J.³; Czarnecki, Dave⁴. (1) *Catfish Genetics Research unit, USDA/ARS/MSA, Stoneville, MS, USA.* (2)

Southern Weed Research Unit, USDA/ARS, Stoneville, MS, USA. (3) Department of Biology, Mississippi St. University, Starkville, MS, USA. (4) Biology, Ioras College, Dubuque, IA, USA.

34. **Growth and agar quality of *Gracilaria heteroclada* Zhang et Xia grown in a filter tank of a finfish broodstock tank.** Luhan, Maria Rovilla J.; Rodriguez, Jesus. *Aquaculture Department, Southeast Asian Fisheries Development Center, Tigbauan, Iloilo, Philippines.*
35. **Morphometric and toxicity data for *Pyrodinium bahamense* from Florida.** Wolny, Jennifer L.¹; Steidinger, Karen A¹; Flewelling, Leanne J²; Abbott, Jay²; Richardson, R William²; Landsberg, Jan H². (1) *Florida Marine Research Institute, Florida Institute of Oceanography, St. Petersburg, FL, USA.* (2) *Florida Marine Research Institute, Fish and Wildlife Conservation Commission, St. Petersburg, FL, USA.*
36. **An historical account of the depiction of marine algae: a preview.** Wynne, Michael J. *Department of Ecology & Evolutionary Biology, University of Michigan, Ann Arbor, MI, USA.*
37. **Observations on *Purpureofilum apyrenoidigerum* gen. et sp. nov. from Australia and *Bangiopsis subsimplex* from India (Stylonematales, Bangiophyceae, Rhodophyta).** West, John A.¹; Zuccarello, Giuseppe C.²; Scott, Joe³; Pickett-Heaps, Jeremy¹. (1) *School of Botany, University of Melbourne, Parkville, VIC, Australia.* (2) *National Herbarium Netherlands, University of Leiden, Leiden, Netherlands.* (3) *Biology, College of William and Mary, Williamsburg, VA, USA.*
38. **Diversity and distribution of *Trentepohlia* and *Printzina* (Trentepohliales, Chlorophyta) in the Hawaiian islands.** Rindi, Fabio²; Sherwood, Alison R.¹; Guiry, Michael D². (1) *Department of Botany, University of Hawaii, Honolulu, HI, USA.* (2) *Department of Botany, Martin Ryan Institute, National University of Ireland, Galway, Ireland.*
39. **Towards the production of a photographic guide of macroalgal seagrass epiphytes in Tampa Bay, Florida.** Cho, Tae Oh¹; Fredericq, Suzanne¹; Yates, Kim². (1) *Department of Biology, University of Louisiana, Lafayette, LA, USA.* (2) *U.S Geological Survey, Petersburg, FL, USA.*
40. **Comparative DNA sequence analyses and morphological evidence reveal a diverse marine red algal flora in Tampa Bay, Florida.** Cho, Tae Oh¹; Won, Boo Y.¹; Gurgel, Fred¹; Fredericq, Suzanne¹; Yates, Kim². (1) *Biology, University of Louisiana, Lafayette, LA, USA.* (2) *U.S. Geological Survey, St. Petersburg, FL, USA.*
41. **Evidence for polyphyly of *Ulothrix* and *Monostroma*, and other novel relationships in the Ulotrichales (Ulvophyceae).** Wysor, Brian; O'Kelly, Charles J.; Bellows, Wendy K.; Brown, Jeffrey F. *Bigelow Laboratory for Ocean Sciences, West Boothbay Harbor, ME, USA.*
42. **A preliminary account of the seaweeds of Alabama, north central Gulf of Mexico.** Lopez-Bautista, Juan M¹; Tragemann, Todd W.¹; Noble, Sarah M.¹; Sturm, Diana². (1) *Department of Biological Sciences, The University of Alabama, Tuscaloosa, AL, USA.* (2) *Mobile Bay National Estuary Program, Mobile, AL, USA.*
43. **Classification of the Gonatozygaceae and its relation to *Roya* spp.** Hall, John D.¹; McCourt, Richard²; Delwiche, Charles¹. (1) *Cell Biology and Molecular Genetics, University of Maryland, College Park, MD, USA.* (2) *Botany Department, The Academy of Natural Sciences, Philadelphia, PA, USA.*
44. **Species groups in *Peridinium* I. The Umbonatum Group.** Carty, Susan. *Department of Biology, Heidelberg College, Tiffin, OH, USA.*

45. **Broad Diversity of *Dunaliella* at the Salt Plains National Wildlife Refuge (OK, USA): Inferences from nuclear-encoded rDNA data.** Buchheim, Julie Ann¹; Kirkwood, Andrea²; Henley, William²; Buchheim, Mark Alan¹. (1) *Department of Biological Science, The University of Tulsa, Tulsa, OK, USA.* (2) *Department of Botany, Oklahoma State University, Stillwater, OK, USA.*
46. **Diversity of Chlamydomonadalean algae at Itasca State Park.** Veit, Mariah¹; Buchheim, Julie Ann¹; Portman, Richard¹; Fawley, Karen²; Fawley, Marvin²; Buchheim, Mark Alan¹. (1) *Department of Biological Science, The University of Tulsa, Tulsa, OK, USA.* (2) *Biological Sciences, North Dakota State University, Fargo, ND, USA.*
47. **Diversity of Microalgae and Cyanobacteria at the Salt Plains National Wildlife Refuge (OK, USA).** Buchheim, Julie¹; Kirkwood, Andrea²; Henley, William²; Buchheim, Mark¹. (1) *Department of Biological Science, The University of Tulsa, Tulsa, OK, USA.* (2) *Department of Botany, Oklahoma State University, Stillwater, OK, USA.*
48. **Phylogenetic affinities of *Batrachospermum* specimens from French Guiana.** Vis, Morgan L.¹; Chiasson, Wayne B¹; Sheath, Robert G². (1) *Department of Env. & Plant Biology, Ohio University, Athens, OH, USA.* (2) *Office of the Provost, California State University San Marcos, San Marcos, CA, USA.*
49. **Phylogeny and taxonomic revision of the loricates *Trachelomonas* and *Strombomonas* (Euglenophyta) based on SSU rDNA and ultrastructure.** Nudelman, Maria A.; Triemer, Richard E. *Department of Plant Biology, Michigan State University, East Lansing, MI, USA.*
50. **Online algae discussion and identification.** McCourt, Richard M.¹; Sprouffske, Kathleen²; Mellott, Daniel²; Ratnayaka, Chamira². (1) *Department of Botany, Academy of Natural Sciences of Philadelphia, Philadelphia, PA, USA.* (2) *Patrick Center for Environmental Research, Academy of Natural Sciences of Philadelphia, Philadelphia, PA, USA.*
51. **Phylogenetic relationship of *Coolia tropicalis* and *Prorocentrum* species isolated from Belizean barrier reef and oceanic mangrove systems relative to other dinoflagellates.** Vandersea, Mark W.¹; West, Mellisa A.¹; Kibler, Steven R.¹; Faust, Maria A.²; Litaker, R. Wayne¹; Tester, Patricia A.¹. (1) *Center for Coastal Fisheries Habitat Research, NOS / NOAA, Beaufort, NC, USA.* (2) *Department of Botany, National Museum of Natural History, Smithsonian Institution, Suitland, MD, USA.*
52. **A comparison of ITS sequences and cell wall structure of *Scenedesmus* and *Desmodesmus*.** Johnson, Joni L.; Fawley, Karen Phillips; Fawley, Marvin W. *North Dakota State University, Fargo, ND, USA.*
53. **A new and distinctive *Leptolyngbya* species from aerial habitats in the Czech Republic.** Kovacik, Lubomir¹; Casamatta, Dale A.²; Johansen, Jeffrey R.². (1) *Department of Botany, Comenius University, Bratislava, Slovakia.* (2) *Department of Biology, John Carroll University, University Heights, OH, USA.*
54. **Phenotypic plasticity, molecules and species boundaries in *Pediastrum Meyen 1829*.** McManus, Hilary A.; Lewis, Louise A. *Department of Ecology and Evolutionary Biology, University of Connecticut, Storrs, CT, USA.*
55. **Marine microfilamentous green algae: new lineages in the Ulotrichales/Ulvales complex (Ulvophyceae).** O'Kelly, Charles J.; Wysor, Brian; Bellows, Wendy K.; Brown, Jeffrey F. *Bigelow Laboratory for Ocean Sciences, West Boothbay Harbor, ME, USA.*
56. **Phylogeography of *Batrachospermum macrosporum* (Batrachospermales, Rhodophyta) in North and South America.** Hodge, J. Cameron¹; Necchi, Orlando²; Vis, Morgan L¹. (1) *Department of Env. & Plant*

Biology, Ohio University, Athens, OH, USA. (2) Depto. Zoologia e Botanica, UNESP Campos de Sao Jose do Rio Preto, Sao Jose do Rio Preto, Brazil.

WEDNESDAY MORNING, 11 AUGUST

8:05-9:45 AM - Empire A

SYMPOSIUM: *Twenty Years of Research: Progress in Green Algal (Chlorophyta) Systematics Since Mattox and Stewart (1984)*

Presiding: RICK ZECHMAN, *California State University, Fresno*

- 8:05 **Introduction to the Symposium.** Buchheim, Mark A. *Department of Biological Science, The University of Tulsa, Tulsa, OK, USA.*
- 8:15 **The challenge of green algal diversity.** Fawley, Marvin W.; Fawley, Karen P. *Department of Biological Sciences, North Dakota State University, Fargo, ND, USA.*
- 8:45 **An evaluation of the phylogenetic signal present in morphological data across chlorophycean green algae.** Lewis, Louise A.¹; Watanabe, Shin². (1) *Ecology and Evolutionary Biology, University of Connecticut, Storrs, CT, USA.* (2) *Laboratory of Biology, Department of Education, Toyama University, Toyama, Japan.*
- 9:15 **Chlamydomonadalean Diversity and Phylogeny.** Buchheim, Mark Alan; Buchheim, Julie Ann. *Department of Biological Science, The University of Tulsa, Tulsa, OK, USA.*

WEDNESDAY MORNING, 11 AUGUST

9:45-10:15 AM

BREAK

WEDNESDAY MORNING, 11 AUGUST

10:15 -11:45 AM - Empire A

SYMPOSIUM: *Twenty Years of Research: Progress in Green Algal (Chlorophyta) Systematics Since Mattox and Stewart (1984)*

Presiding: MARK BUCHHEIM, *University of Tulsa*

- 10:15 **What are Trebouxiophyceae?** Friedl, Thomas; Hepperle, Dominik. *Department of Experimental Phycology and SAG, University of Goettingen, Goettingen, Germany.*
- 10:45 **Phylogeny of the Ulvophyceae green algae: Morphological and molecular evolution of siphonous and hemisiphonous lineages.** Zechman, Frederick. *Department of Biology, California State University, Fresno, Fresno, CA, USA.*
- 11:15 **The Ulvophyceae: history, novel diversity and phylogenetic issues, with special reference to the orders Ulotrichales and Ulvales.** O'Kelly, Charles J. *Bigelow Laboratory for Ocean Sciences, West Boothbay Harbor, ME, USA.*

WEDNESDAY AFTERNOON, 11 AUGUST

11:45 AM - 1:15 PM

LUNCH BREAK (on own)

WEDNESDAY AFTERNOON, 11 AUGUST

1:15 – 2:30 PM - Empire A

SYMPOSIUM: *Twenty Years of Research: Progress in Green Algal (Chlorophyta) Systematics Since Mattox and Stewart (1984)*

Presiding: MARVIN FAWLEY, *North Dakota State University*

- 1:15 **Phylogeny of the Trentepohliaceae (Chlorophyta; Ulvophyceae).** Lopez-Bautista, Juan Manuel¹; Chapman, Russell L.^{2,3}; Rindi, Fabio⁴; Guiry, Michael D.⁴. (1) *Department of Biological Sciences, The University of Alabama, Tuscaloosa, AL, USA.* (2) *Department of Biological Sciences, Louisiana State University, Baton Rouge, LA, USA.* (3) *Department of Oceanography and Coastal Sciences, Louisiana State University, Baton Rouge, LA, USA.* (4) *Department of Botany, Martin Ryan Institute, Galway, Ireland.*
- 1:45 **A chloroplast genome sequencing program to unravel phylogenetic relationships among chlorophytes.** Turmel, Monique; Charlebois, Patrick; de Cambiaire, Jean-Charles; Gagnon, Jules; Otis, Christian¹; Pombert, Jean-Francois¹; Lemieux, Claude. *Department of Biochimie et Microbiologie, Universite Laval, Quebec, QC, Canada.*
- 2:15 **Panel Question and Answer**

WEDNESDAY AFTERNOON, 11 AUGUST

2:30-3:00 PM

BREAK

WEDNESDAY AFTERNOON, 11 AUGUST

3:00 – 5:00 PM - Empire A

CONTRIBUTED PAPERS: Ecology and Population Biology 3

Presiding: PAT WHEELER, *Oregon State University*

- 3:00 **High phytoplankton productivity in a mangrove embayment, Belize, Central America.** Tester, Patricia A.¹; Kibler, Steven R.¹; Vandersea, Mark W.¹; Litaker, R. Wayne¹; Faust, Maria A.². (1) *Plankton Ecology and Physiology, National Ocean Service, NOAA, Beaufort, NC, USA.* (2) *Department of Botany, Smithsonian Institution, National Museum of Natural History, Suitland, MD, USA.*
- 3:20 **Dinoflagellates in a naturally eutrophied mangrove embayment in Belize.** Kibler, Steven R.¹; Chrost, Ryszard J.²; Faust, Maria A.³; Vandersea, Mark W.¹; Litaker, R. Wayne¹; Tester, Patricia A.¹. (1) *National Ocean Service/NOAA, Beaufort, NC, USA.* (2) *Department of Microbial Ecology, Warsaw University, Institute of Microbiology, Warsaw, Poland.* (3) *Department of Botany, National Museum of Natural History, Smithsonian Institution, Suitland, MD, USA.*
- 3:40 ***Heterocapsa triquetra* bloom dynamics in Newport River, NC, during a cold subtropical winter.** Ornolfsdottir, Erla Bjork; Tester, Patricia A.; Litaker, R. Wayne. *Center for Coastal Fisheries and*

Habitat Research, NOAA, Beaufort, NC, USA.

- 4:00 **Pico-eukaryotic dominance of the Arctic Ocean phytoplankton.** Bonilla, Sylvia^{1,4}; Lovejoy, Connie²; Roy, Suzanne³; Vincent, Warwick F¹. (1) *Centre d' Etudes Nordiques, Universite Laval, Quebec, QC, Canada.* (2) *Institut Ciencas de Mar, Barcelona, Spain.* (3) *Institut des Sciences de la Mer, Universite du Quebec a Rimouski, Quebec, QC, Canada.* (4) *Facultad de Ciencias, Universidad de la Republica, Montevideo, Uruguay.*
- 4:20 **Modeling of ecological indicators: characterizing estuarine phytoplankton and trophic state using artificial neural networks.** Millie, David F.^{1,6}; Weckman, Gary R.²; Pinckney, James L.³; Paerl, Hans W.⁴; Bendis, Brian J.⁵; Pigg, Ryan J.⁶. (1) *Florida Institute of Oceanography, University of South Florida, St. Petersburg, FL, USA.* (2) *Department of Industrial & Manufacturing Systems Engineering, Ohio University, Athens, OH, USA.* (3) *Department of Oceanography, Texas A & M University, College Station, TX, USA.* (4) *Institute of Marine Sciences, University of North Carolina-Chapel Hill, Morehead City, NC, USA.* (5) *AMJ Equipment Corporation, Lakeland, FL, USA.* (6) *Florida Marine Research Institute, Fish & Wildlife Conservation Commission, St. Petersburg, FL, USA.*
- 4:40 **Phytoplankton blooms and ecosystem management: one approach to bringing them together.** Thompson, Peter Allan¹; Armstrong, Paul^{2,1}; Parslow, John¹; Herzfeld, Michael¹; Wild-Allen, Karen¹. (1) *Marine, CSIRO, Hobart, TAS, Australia.* (2) *School of Aquaculture, University of Tasmania, Launceston, TAS, Australia.*

WEDNESDAY AFTERNOON, 11 AUGUST

3:00 – 4:40 PM - Empire C

CONTRIBUTED PAPERS: Applied Phycology

Presiding: MIKE STEKOLL, *University of Alaska*

- 3:00 **Cultivation of *Laminaria saccharina* as the extractive inorganic component of an integrated multi-trophic aquaculture system (salmon-kelp-mussel).** Chopin, Thierry B.¹; Bastarache, Susan¹; Sawhney, Manav¹; Belyea, Ellen¹; MacDougall, Julie²; Stewart, Ian³; Fitzgerald, Patrick⁴. (1) *Centre for Coastal Studies and Aquaculture, University of New Brunswick, Saint John, NB, Canada.* (2) *Canadian Food Inspection Agency, Blacks Harbour, NB, Canada.* (3) *Atlantic Silver Inc., St. George, NB, Canada.* (4) *Heritage Salmon Company Inc., Blacks Harbour, NB, Canada.*
- 3:20 **Development of a TNT-detoxifying strain of the seaweed *Porphyra yezoensis* through genetic engineering.** Bernasconi, Paula¹; Cruz-Uribe, Tavi²; Rorrer, Gregory²; Bruce, Neil³; Cheney, Donald¹. (1) *Northeastern University, Boston, MA, USA.* (2) *Oregon State University, Corvallis, OR, USA.* (3) *University of York, York, United Kingdom.*
- 3:40 **The bioremediation opportunities of *Porphyra* spp. in an integrated land-based aquaculture system with finfish in coastal New England.** C. Yarish¹, G. Kraemer², C.D. Neefus³, R. Carmona^{1,4}, D. Snellgrove¹, P. He^{1,5}, Tang^{1,6}, R. Pereira^{1,7} and G.C. Nardi⁸. (1) *Department of Ecology & Evolutionary Biology, University of Connecticut, Stamford, CT, USA.* (2) *Division of Natural Sciences, Purchase College, State University of New York, Purchase, NY, USA.* (3) *Department of Plant Biology, Office of Biometrics, University of New Hampshire, Durham, NH, USA.* (4) *Departamento de Ecologia, Facultad de Ciencias, University of Malaga, Malaga, Spain.* (5) *Shanghai Fisheries University, Shanghai, China.* (6) *Laboratory of Marine Genetics and Breedings, Division of Life Science and Technology, Ocean University of China, Qingdao, China.* (7) *Dept. Botanica FCUP, Centre for Marine*

and Environmental Research, University of Porto, Porto, Portugal. (8) GreatBay Aquaculture LLC, Portsmouth, NH, USA.

- 4:00 **Spectral fingerprinting as a novel approach to biofilm analysis and biomonitoring.** Larson, Chad Allen; Passy, Sophia I. *Department of Biology, The University of Texas at Arlington, Arlington, TX, USA.*
- 4:20 **Studies on algae-metal interaction based on cytological, biochemical and radio- tracer techniques.** Banerjee, S. ¹; Chakravorty, N. ¹; Mukherjee, A. ¹; Pal, Ruma ¹; Nayak, D. ²; Lahiri, S. ². (1) *Botany, University of Calcutta, Kolkata, West Bengal, India.* (2) *Chemical Science Division, Saha Inst. Of Nuclear Physics, Kolkata, India.*

WEDNESDAY EVENING, 11 AUGUST

7:00-13:00 PM - Mariner's Museum

Busses leave from Hospitality House at 6:15 PM

Return busses leaving Mariners Museum 10:30-11:00 PM

SOCIAL: PSA Banquet and Awards Ceremony

THURSDAY MORNING, 12 AUGUST

8:40-9:10 AM PRE-TALKS "BREAK" WITH COFFEE AND BREAK FOODS

THURSDAY MORNING, 12 AUGUST

9:10-11:30 AM - Empire A

CONTRIBUTED PAPERS: Phylogenetics and Taxonomy 3

Presiding: JUAN LOPEZ-BAUTISTA, *University of Alabama, Tuscaloosa*

- 9:10 **Phylogeny of dinoflagellates based on mitochondrial cytochrome b and nuclear small subunit rDNA sequence comparisons.** Zhang, Huan ¹; Bhattacharya, Debashish ²; Lin, Senjie ¹. (1) *Department of Marine Sciences, University of Connecticut, Groton, CT, USA.* (2) *Department of Biological Sciences and Center for Comparative Genomics, University of Iowa, Iowa City, IA, USA.*
- 9:30 **Using ITS rRNA Sequences to define dinoflagellate species.** Litaker, Wayne; Vandersea, Mark; West, Melissa; Kibler, Steven; Tester, Patrica. *Center for Coastal Fisheries and Habitat Research, National Ocean Service, NOAA, Beaufort, NC, USA.*
- 9:50 **Insights into brown algal phylogenetics using chloroplast and nuclear genes.** Phillips, Naomi ¹; Burrowes, Renaud ³; Rousseau, Florence ³; de Reviers, Bruno ³; Saunders, Gary W. ². (1) *Department of Biology, University of New Brunswick, Fredericton, NB, Canada.* (2) *Zoology, University Of Florida, Gainesville, FL, USA.* (3) *Department de Systematique , UPMC, MNHN, IRD, CNRS FRE 2634, Paris, France.*
- 10:10 **Preliminary investigations on the subaerial Trentepohliales (Ulvophyceae, Chlorophyta) in the Southeastern USA.** Noble, Sarah Marie; Lopez-Bautista, Juan M. *Department of Biological Sciences, The University of Alabama, Tuscaloosa, AL, USA.*

- 10:30 **Evolution of the Chlorophyceae and Trebouxiophyceae: Inferences from chloroplast genes.** Buchheim, Mark Alan; Vergheese, Bindhu. Department of Biological Science, The University of Tulsa, Tulsa, OK, USA.
- 10:50 **Morphological Species in *Coleochaete*.** Delwiche, Charles Francis. *Department of Cell Biology and Molecular Genetics, University of Maryland - College Park, College Park, MD, USA.*
- 11:10 **Phylogeny of *Spirogyra* and *Sirogonium* based on *rbcL* sequence data.** Drummond, Christopher⁴; Hall, John²; Karol, Kenneth G.³; Delwiche, Charles F.²; McCourt, Richard M.¹. (1) *Department of Botany, Academy of Natural Sciences of Philadelphia, Philadelphia, PA, USA.* (2) *Cell Biology and Molecular Genetics, University of Maryland, College Park, MD, USA.* (3) *Department of Biology, University of Washington, Seattle, WA, USA.* (4) *Department of Biology, Georgetown University, Washington, DC, USA.*

THURSDAY MORNING, 12 AUGUST

9:10-11:10 AM - Empire C

CONTRIBUTED PAPERS: Physiology, Biochemistry, Cell Biology, and Molecular Biology

Presiding: LINDA FRANKLIN, *Smithsonian Environmental Research Center*

- 9:10 **New approaches to the design of algal media formulations for nutrition studies: the anionic/cationic balance problem.** Evens, T.J.; Niedz, Randall P. *USHRL, USDA-ARS, Ft. Pierce, FL, USA.*
- 9:30 ***Haematococcus* lipid bodies: isolation, composition and biogenesis.** Liu, G. X.^{2,1}; Hu, Z. Y.²; Sommerfeld, M.¹; Hu, Q.¹. (1) *School of Life Sciences, Arizona State University, Tempe, AZ, USA.* (2) *Department of Hydrobiology, Institute of Hydrobiology, Wuhan, Hubei, China.*
- 9:50 **Time-lapse videography on the photomovement in the filamentous green alga *Spirogyra* (Chlorophyta, Zygnemataceae).** Kim, Gwang Hoon¹; Klotchkova, Tatiana A.¹; Yoon, Min-Chul¹; Spurk, Tim²; West, John A.². (1) *Department of Biology, Kongju National University, Kongju, Chungnam, South Korea.* (2) *Department of Botany, Melbourne university, Melbourne, VIC, Australia.*
- 10:10 **Novel dinoflagellate clock-related genes identified through microarray analysis.** Okamoto, Oswaldo Keith¹; Hastings, John Woodland². (1) *Experimental Research Center, Albert Einstein Research & Education Institute, Sao Paulo, SP, Brazil.* (2) *Molecular & Cellular Biology, Harvard University, Cambridge, MA, USA.*
- 10:30 **Effects of ambient calcium concentration on calcium oxalate crystals in marine red algae.** Pueschel, Curt¹; West, John². (1) *Department of Biology, SUNY Binghamton, Binghamton, NY, USA.* (2) *School of Botany, University of Melbourne, Parkville, VIC, Australia.*
- 10:50 **Mitochondrial cytochrome b mRNA editing in wide range of dinoflagellates and possible evolutionary association.** Lin, Senjie; Zhang, Huan. *Department of Marine Sciences, University of Connecticut, Groton, CT, USA.*

Abstracts

ABSTRACTS NUMBERS ARE VERY CLOSE TO ABSTRACT PRESENTATION ORDER.

SEE AUTHOR INDEX AT END TO FIND SPECIFIC ABSTRACTS.

1. Daryl Lam* ; Frederick Zechman

Biology, California State University, Fresno, Fresno, CA

Phylogenetic Analyses of the Caulerpales (Ulvophyceae, Chlorophyta) Based On *rbcL* Gene Sequences.

In a review of caulerpalean green algal taxonomy, Hillis-Colinvaux (1984) recognized two suborders (Bryopsidineae and Halimedineae) on the basis of anatomical, physiological, and habitat characteristics. The freshwater caulerpalean algal taxon, *Dichtomosiphon tuberosus*, however, had uncertain affinity to the two suborders. Previous phylogenetic analyses based on 18S rRNA sequence data (Zechman *et al.* 1990) supported the hypothesis of two monophyletic suborders within the Caulerpales, however, analyses of morphological characters (Vroom *et al.* 1998) inferred monophyly in only the Halimedineae. Low numbers of ingroup taxa and limited character sampling in these previous studies prompted a reanalysis of this diverse group of green algae based on chloroplast-encoded *rbcL* gene sequences. Thirty-two caulerpalean ingroup taxa and four dasycladalean outgroup taxa were analyzed with Bayesian inference, maximum likelihood, and maximum parsimony methods. Results of all analyses suggested that the Halimedineae and Bryopsidineae form separate monophyletic assemblages. Within the suborder Bryopsidineae, the families Bryopsidaceae, Derbesiaceae, and Codiaceae each formed monophyletic lineages in all analyses, however, the relationships among these families differed among optimality criteria. For example, parsimony suggested that the Codiaceae is the most basal family of the Bryopsidineae, while model-based methods suggested that the Derbesiaceae is most primitive. Within the Halimedineae, the Caulerpaleae was monophyletic in all analyses, however, only parsimony supported monophyly of the Udoteaceae. The freshwater alga, *D. tuberosus*, was found to be the basal-most lineage of the Halimedineae clade with strong support in all analyses. These results will be discussed in the context of molecular and morphological character evolution. Supported in part by NSF grant DEB-0128977 to FWZ.

2. Matt Ashworth* ; Rick Zechman

Department of Biology, California State University, Fresno, Fresno, CA

A Multi-gene Approach to the Phylogeny of the Dasycladales (Ulvophyceae, Chlorophyta).

The Dasycladales is an ancient order of tropical benthic marine green algae, unique in their radially arranged unicellular thalli and a well-preserved fossil record. The inference of an accurate phylogeny for the Dasycladales is important in order to better understand their stratigraphy, character evolution, and classification. Previous phylogenetic analyses based on *rbcL* and 18S rDNA suggested that the family Acetabulariaceae is monophyletic, but that the family Dasycladaceae is a basal paraphyletic assemblage. However, the two data sets disagreed regarding genus- and species-level relationships within the Dasycladales. For example, the placement of the genera, *Halicoryne*, *Bornetella* and *Cymopolia* were incongruent. Given the conflicting results of these previous analyses, the current project examined two additional genes: nuclear-encoded 26S rDNA and chloroplast-encoded *atpB*. Phylogenetic analyses of aligned sequences was performed with parsimony and model-based methods. Family-level relationships based on new sequences were largely congruent with previous studies: the Acetabulariaceae is monophyletic while the Dasycladaceae is paraphyletic. In addition, acetabulariacean genera are not monophyletic, suggesting that the presence of a corona inferior and calcification of gametes may not be appropriate to define genera. Within the Dasycladaceae, the current tribal groupings based on gametangial position are not monophyletic. Also, the basal positions of *Cymopolia* and *Neomeris* were supported by 26S rDNA, a result congruent with *rbcL* and stratigraphy but not with 18S rDNA data. These results will be discussed in the context of morphological character evolution, fossil stratigraphy and family, tribal and generic relationships among these living algal fossils. Supported in part by NSF grant DEB-0128977 to FWZ.

3. Kathryn J. Wilkinson*¹; H. L. Walker²; Carole A. Lembi¹

1. Botany and Plant Pathology, Purdue University, West Lafayette, IN; 2. School of Biological Sciences, Louisiana Tech University, Ruston, LA

A Potential Biological Control Agent, Bacterium SG-3: Mode of Action and Effect on Two Economically Important Cyanobacteria.

Bacterium SG-3 is capable of killing many species of cyanobacteria; however, its mode of action remains unknown. Assays were conducted to determine the method by which SG-3 lyses susceptible species of cyanobacteria. Is contact or penetration necessary or does a secreted compound cause cell death? Although the mechanism is unknown, we hypothesize that a large molecule is responsible for the lytic activity of SG-3. Activity was retained after filtration of a bacterial culture through a 0.45 μm filter, but lost after filtration through a 0.2 μm filter. When filtered through a 0.45 μm

filter and centrifuged at 40,000 g for 2 hours, activity was retained in both the supernatant and the pellet. Transmission electron microscopic observation of the pellet reveals membrane bound structures with electron dense centers that vary in diameter from 30-100 nm. These vesicle-like structures contain no DNA or RNA and are believed to be the cause of cell lysis. We tested the sensitivity of two cyanobacteria; *Pseudanabaena limnetica* and *Cylindrospermopsis raciborskii*, to SG-3. These two genera of cyanobacteria are of great concern to lake and reservoir managers because *P. limnetica* produces off-flavor compounds, and *C. raciborskii* produces numerous toxins including potent neurotoxins and hepatotoxins. One isolate of *P. limnetica* from Eagle Creek Reservoir in Indiana and two isolates of *C. raciborskii* from Lake Griffin and Lake Yale in Florida were tested. Cyanobacteria were treated at a final concentration of 5.3×10^6 plaque forming units/mL. Treatment of *P. limnetica* with SG-3 resulted in a 62% reduction in chlorophyll *a* and a 99.7% reduction in filament number as compared to the initials. Both isolates of *C. raciborskii* were also highly sensitive to SG-3. Chlorophyll *a* for the Lake Griffin strain was reduced by 92.8% and filament number by 99.8%. Chlorophyll *a* and filament number were each reduced by > 99% for the Lake Yale strain of *C. raciborskii*. *Pseudanabaena limnetica* and *C. raciborski* are very important organisms from a water quality standpoint and their sensitivity to SG-3 increases its potential as a biological control agent.

4. Lisa Gilbane* ; Steve Murray

Biological Science, California State University, Fullerton, CA

A Carbon ($\delta^{13}\text{C}$) and Nitrogen ($\delta^{15}\text{N}$) Stable Isotope Analysis of Macrophyte Contributions to Mussel (*Mytilus californianus*) Diets on Southern California Shores.

Benthic intertidal consumers obtain food derived directly and indirectly from both phytoplankton and macrophyte (algae and seagrass) production sources. Carbon ($\delta^{13}\text{C}$) and nitrogen ($\delta^{15}\text{N}$) stable isotopes have been used successfully to show that macrophyte production, particularly through detrital pathways, is an important contributor to benthic consumer diets in colder seas characterized by large, local algal beds. The purpose of this study was to examine macrophyte contributions to food webs on urban, southern California shores by focusing on *Mytilus californianus*, an abundant suspension-feeding mussel found in the region. Dietary inputs to mussels were determined by comparing $\delta^{13}\text{C}$ and $\delta^{15}\text{N}$ stable isotope signatures from multiple macrophyte and phytoplankton (POM) production sources with signatures obtained from mussel tissues. Mussels were collected from a single island and multiple mainland intertidal habitats, characterized by variable local macrophyte standing stocks. $\delta^{13}\text{C}$ for all sites averaged -14.8 ‰ for macrophyte signatures and -21.0 ‰ for POM. Using these carbon isotope signatures in a two-source mixing model, we calculated that macrophytes contributed over 50 % of the carbon to mussel diets at all of the mainland sites, even sites lacking large, local algal beds. Mussel $\delta^{15}\text{N}$ signatures were similar among sites with a mean of 11.0 ‰ and were enriched by 1.5 ‰ over the nitrogen isotope signatures obtained for macrophyte and POM sources. Mussels from the offshore island, an oligotrophic site, had distinct and more depleted $\delta^{13}\text{C}$ signatures (-18.7 ‰) compared with mussels from the mainland sites, indicating a greater dietary contribution from phytoplankton sources and less utilization of carbon derived from macrophyte sources. We conclude that mussels assimilate macrophyte-derived carbon at all of our sites in southern California, with a greater dietary contribution found on the mainland compared with our island site.

5. Nisse A. Goldberg* ; Gary A. Kendrick

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

Isolation and coexistence: Macroalgal species richness along the south coast of Australia.

We characterized the subtidal flora of the Recherche Archipelago, located along the south coast of Western Australia; related patterns of diversity to abiotic factors; and evaluated higher-taxonomic richness to that of the temperate Australian flora. Macroalgal assemblages were compared between island locations, wave exposures, and depth. Macroalgae were harvested (6-0.25 m² quadrats per site) from sites at two exposures (sheltered and exposed to wave energy), three depths (<10, 10-20, and 21-28 m), and two island groups (inside and outside Esperance Bay; n = 3 islands per group). Multivariate tests were used to evaluate differences in assemblages with depth and island group. Assemblages were clearly different with exposure and were used as a standard to compare assemblages grouped into higher taxonomic levels with species-level data. 216 species were recorded with species richness per 0.25 m² ranging between 13 and 29 species. Assemblages consisted of a multi-specific overstory of fuclean species with one kelp (*Ecklonia radiata*), and a species-rich understory. 60% of all species contributed <5 g wet-weight per 0.25 m². Density of overstory species decreased with depth. Differences with depth and exposure, and to a lesser extent island group, were driven by abundant overstory and understory species. Within-habitat variability and overall species richness were due to turnover of uncommon species. Although widely-distributed, these species did not contribute to observed patterns with exposure, depth, and island group. Macroalgal species belonged to 114 genera, 51 families, and 18 orders. Speciose orders (i.e. Ceramiales, Gigartinales, Fucales) and families (i.e. Cystoseiraceae, Sargassaceae, Rhodomelaceae) in the Recherche Archipelago were also

speciose along southern Australian coasts, indicating commonalities in habitat and evolutionary history over 1000 kilometers of coastline. Genus groupings detected similar differences with exposure, suggesting that species within a genus have similar ecological requirements. Species pool and coexistence hypotheses are presented as possible explanations for high species richness observed in the archipelago.

6. Aimee M. Bullard* ; Steven N. Murray

Biological Science, California State University, Fullerton, Fullerton, CA

Shifting Macrophyte Abundances and the Primary Productivity of Southern California Shores.

During the last five decades, southern California intertidal communities have shifted towards greater cover of crustose and turf-forming macrophytes and reduced abundances of larger, fleshy seaweeds. Because crustose and turf-forming algae are known to be low producers, we hypothesized that these shifts in macrophyte abundances would result in lower community primary productivity. To test this hypothesis, we determined cover and light-saturated, net photosynthetic rates for macrophyte populations at two sites believed to support contrasting macrophyte communities. Intertidal macrophyte cover (70.4 % in winter; 66.0 % in summer) was lower at Corona del Mar (CDM), a site dominated by coralline and crustose algae, and varied little between sampling periods. Higher macrophyte cover occurred at Dana Point (DPT), a site supporting greater abundances of fleshy seaweeds, and varied seasonally, ranging from 73.4 % in winter to 98.8 % in summer. Maximum net photosynthetic rates of individual macrophytes varied little between sites and seasons and were comparable to previously reported values for the same southern California species. Community productivity at CDM ranged from 188.4. in winter to 146.2 mg C m⁻² h⁻¹ in summer, and was 8 to 35 % lower than productivity estimates for DPT (winter: 206.0 mg C m⁻² h⁻¹; summer: 225.7 mg C m⁻² h⁻¹). Turf-forming articulated corallines and crustose algae contributed the majority (54 to 79 %) of the macrophyte productivity at CDM, whereas fleshy algae accounted for 55 to 84 % of the primary production at DPT. Our results support the hypothesis that reductions in the abundances of larger, fleshy seaweeds can significantly affect the primary productivity of southern California intertidal communities and indicate that production is dominated by different types of seaweeds and that these communities are less productive today compared with times past.

7. Navid R. Moheimani* ; Michael A. Borowitzka

Biological Sciences and Biotechnology, Murdoch University, Murdoch, WA, Australia

Culturing coccolithophorid algae for carbon dioxide bioremediation.

Culturing coccolithophorids is an attractive alternative for application in the sequestration or recycling of carbon dioxide. Coccolithophorids can fix carbon both by photosynthesis and also by producing calcium carbonate plates known as coccoliths. They also produce high amounts of lipids which can possibly be used as a renewable fuel. We studied the mass cultivation of *Pleurochrysis carterae* CCMP647 in number of photobioreactors including airlift, carboys, plate reactors, tubular (Biocoil) reactors and outdoor raceway ponds. This species grew well in all types of photobioreactors examined except for the Biocoil. Culture in outdoor raceway ponds (paddle wheel mixed) was the most successful. We have maintained semicontinuous cultures for a period of 12.5 months. The highest biomass achieved has been 3.9 g total dry weight. L⁻¹ with the coccolith weight of 0.319 g.L⁻¹ during the spring and summer period. The most sustainable mean generation time of 2 ± 0.9 days was achieved during the same period of time. Productivity of 0.1 g.L⁻¹.d⁻¹ was also achieved in raceway photobioreactors. Total lipid content of the cells ranged between 30-50% of total dry weight. Bacterial, algal and protozoan contaminations did not present significant difficulties during cultivation.

8. Bruce C. Parker *

Department of Biology, Virginia Tech, Blacksburg, VA

The Phycological Society of America: Its Roots and Early Years.

The Phycological Society of America [PSA] came into being on December 30, 1946 during the American Association for the Advancement of Science [AAAS] meeting at the Copley-Plaza Hotel, Boston, Massachusetts. The founders consisted of a mere 8(-11) botanists dabbling or specializing in freshwater or marine algae. G.W. Prescott (Michigan State College, East Lansing) convened the small gathering in his hotel room, convincing all present of the benefits that could derive through establishing the first society in the world devoted exclusively to the subject of algae. One of the more eminent phycologists in America then also was attending the AAAS meeting, namely Gilbert Morgan Smith (Stanford University). On being approached, he agreed to serve as President for the fledgling society during its first year, with Prescott serving as Treasurer (and much more). From the 1947 Charter Member list totaling 157 amateur and more professional algal enthusiasts to the present membership exceeding 1600, PSA has faced nearly six decades of struggles and accomplishments. The early struggles and accomplishments especially did much to pave the way for PSAs future strides and continuing successes as a leading phycological society with an international reputation.

9. M. D. Hanisak^{*1}; J. R. Waaland²

1. Harbor Branch Oceanographic Institution, Fort Pierce, FL; 2. Department of Biology, University of Washington, Seattle, WA

PSA's Endowment: From Dream to Reality.

The Phycological Society of America's Endowment Fund resulted from the vision of members of our society in the 1970's. The Endowment was established through donations and fund raising activities "to support awards, special projects and programs to promote various aspects of phycology" and is supervised by the PSA Board of Trustees. In 1979, the initial Endowment consisted of five accounts: the General Fund (supports Endowment management and fund raising), the Education and Research Fund (supports educational activities and student research through Grants-in-Aid of Research), the Publication Fund (supports non-Journal phycological publications), the Lecture Fund (supports symposia at annual meetings), and the Bold Award Fund (for the best student paper at the annual meeting). Additional accounts were established as the Endowment grew and additional needs were identified by the Society: the Prescott Award Fund (1982, for the best algae monograph or book published in the preceding one or two years), the Provasoli Award Fund (1984, for the best paper appearing in the Journal of Phycology during the previous year), the Croasdale Fund (1987, assists student participation in algae courses at field stations), the Hoshaw Travel Fund (1993, facilitates student travel to the annual meeting), and the Journal of Phycology Fund (1996, supports the Journal of Phycology). In 25 years, the Endowment has grown to over \$800,000. This success has been made possible by our membership's vision and leadership, careful, conservative stewardship of resources, continuing contributions of dozens of members, including the Board of Trustees, PSA officers and members who have participated in committees that administer the Endowment-supported programs or who have made financial contributions. Twenty-five years after its inception, the PSA Endowment has fostered the development and perpetuation of programs now considered vital to the Society and has become a critical component of the Society's financial stability.

10. Jeremy D. Pickett-Heaps^{*}

Botany, Univ. of Melbourne, Melbourne, VIC, Australia

Diatoms: Life in Glass Houses.

This DVD (58 mins.) covers most aspects of diatom biology using video of living cells, interspersed with some TEM, SEM and confocal images. The DVD can be played through continuously but is also divided into the following Chapters: 1: Introduction; 2: Distribution and Ecology; 3: Glass Walls; 4: Centrics, Pennates; 5: Chloroplasts; 6: Vacuoles, Streaming; 7: Microtubule Center (Centrosome); 8: Golgi Bodies; 9: Motility; 10: Phototaxis; 11: Chloroplast Movement; 12: Adhesives, Holdfasts; 13: Chitin; 14: Mitosis & Cleavage; 15: Valve Morphogenesis; 16: Spine Morphogenesis; 17: Growth: Sliding Thecae; 18: Growth: Girdle Bands; 19 Sex in Centrics; 20: Sex in Pennates. Supporting the disc are extensive "Teacher's Notes" downloadable from the Cytographics Web site (cytographics.com). The disc or a VHS tape version can be ordered through this address.

11. Roy L. Lehman^{*}

Physical & Life Sciences, Texas A&M University-Corpus Christi, Corpus Christi, TX

Ecological Field Methods for Marine Benthic Macroalgal Assessment: A Comparison of Traditional and Modern Methods.

Modern ecological research is characterized by quantitative methods designed to produce statistically sound results. Subjective surveys, arbitrary comparisons, and other anecdotal procedures are of limited use but may produce some important information. Nondestructive and destructive samplings are often used in combination to acquire certain types of essential information. During coastal and coral reef macroalgal studies, the standard method using the photogrammetric technique has been successful in producing detailed and highly reproducible information. In fact, it is the one of the most widespread used techniques for both algal and coral monitoring. Common techniques will be described and discussed. In addition, advances in technology and methodology will be compared to the standard methods including the use of digital cameras, video assessment and computer software.

12. Dina F. Mandoli^{*}

Department of Biology & Center for Developmental Biology, University of Washington, Seattle, WA

The joys and pitfalls of accessing non-model systems in the genomic age: what happens when evolution, development, physiology, systematics and genomics fuse in the kitchen sink of science.

Science is at an exciting crossroads: genomics and molecular technologies now enable studies of gene expression in whole organisms or of a whole class of organisms at once. This in turn has afforded unprecedented access to organisms,

exploding the opportunities possible for studies of non-model systems and shattered the boundaries between disciplines in an unprecedented fashion. For example, we can now study organisms that are hard to grow or remain unknown to mankind except by a gene sequence or two. I will briefly explain what I mean by a non-model organism, tell you why I think they are important, outline the opportunities I see in studying them and then spend most of the seminar giving examples to support my contentions from three NSF funded projects in my lab. First, I will provide a brief overview of 2 multi-institutional genomics projects designed to a) sort out the phylogenomics of all green things; and b) provide BAC resources for 16 non-model taxa critical to understanding the transition from water to land over deep time. Second, I will go into more depth on RNA localization as it pertains to morphogenesis and development in the classic unicell, *Acetabularia acetabulum* (the organism that in the 1930's revealed the role of the nucleus and predicted the existence of mRNA for the first time). HANDOUTS on each topic and on bioethics will be provided.

13. Jeremy D. Pickett-Heaps*

Botany, Univ. of Melbourne, Melbourne, VIC, Australia

Remarkable Plants: The Oedogoniales (Green Algae).

This is the final version of a video soon to be available on DVD and VHS through Cytographics. (cytographics.com). The DVD will cover the life history of living cells of *Oedogonium*, *Oedocladium* and *Bulbochaete*, with video sequences interspersed with images from the TEM and SEM. While presented as a continuous narrative, the DVD will be divided into the following Chapters: 1. Morphology of the Three Genera; 2. Mitosis and Cell Growth; Evolution of the Branched Morphology; 3. Asexual Reproduction by Zoospores; 4. Macrandrous Sexual Reproduction; 5: Nannandrous Sexual Reproduction. In due course, extensive "Teacher's Notes" will be downloadable from the Cytographics Web site (cytographics.com) and the disc (or VHS tape version) will be available through this address.

14. Richard Triemer^{*1}; Woongghi Shin³; Eric W. Linton¹; Maria A. Nudelman¹; Stacy Brosnan²; Anna K. Monfils¹; Matthew S. Bennett¹

1. Michigan State University, East Lansing, MI; 2. Rutgers University, New Brunswick, NY; 3. Chungnam National University, Daejeon, South Korea

Systematics and Evolution of the Euglenophyta: a Phylogenetic Approach Based on Combined Analysis of SSU and LSU rDNA.

Previous molecular studies of photosynthetic euglenoids suggested that many morphologically distinct key genera, such as *Euglena*, *Phacus* and *Lepocinclis*, were paraphyletic (Nudelman et al. 2003, Brosnan et al. 2003). Recently, phylogenies based upon SSU rDNA were used to redefine these genera (Marin et al. 2003). The genus *Monomorpha* was re-introduced to resolve paraphyly in the genus *Phacus*, and *Strombomonas* was dissolved into *Trachelomonas*. Our study expands the sampling from earlier work on photosynthetic euglenoids and presents bayesian and ML analyses using a combined dataset of both SSU and LSU rDNA to resolve relationships and clarify generic boundaries. In our analysis, *Euglena* remained paraphyletic; the majority of the species formed a well-supported clade at the crown of the tree, while a few formed a separate distinct clade near the base of the tree. This analysis showed some support for the monophyly of *Colacium*, *Trachelomonas* and *Strombomonas*, all of which produce copious amounts of mucilage to form either loricas (*Trachelomonas* and *Strombomonas*) or mucilaginous stalks (*Colacium*). Our analysis supported retaining *Strombomonas* and *Trachelomonas* as separate genera. The genus *Monomorpha* was well supported and included species with few chloroplasts formerly included in the genus *Phacus*. However, in this analysis, *Monomorpha* formed the sister clade to the crown *Euglena* clade. In addition, the basal monophyly of *Lepocinclis* sensu Marin et Melkonian was well supported. In summary, increased taxon sampling, multiple genes and combined datasets increased support for internal nodes on the euglenoid phylogenetic tree and resolved relationships among the major clades in the photosynthetic euglenoid lineage.

15. Eric W. Linton^{*}; Richard E. Triemer

Plant Biology, Michigan State University, East Lansing, MI

Structure and Phylogenetic Usefulness of the Euglenoid Beta-Tubulin Gene.

Recent evidence has shown the usefulness of using multiple gene sequences for determining phylogenetic relationships. We are investigating the usefulness of beta-tubulin gene sequences in clarifying evolutionary relationships among the euglenoids. Currently, we have two sequence databases (SSU and LSU rDNA) with a large number of taxa. The combination of these two genes has resulted in a more resolved tree. Additional protein gene sequences should help resolution and support at different levels of the tree structure, i.e. internal nodes versus terminal clades. A preliminary tree, using all three genes shows evidence that beta-tubulin may be useful for resolving relationships within terminal clades. In addition, comparisons of introns/exons present in the euglenoid beta-tubulin gene from different genera have yielded some evolutionarily intriguing results. The published complete sequence of *Euglena gracilis* beta-tubulin gene is composed of 7

exons and 6 introns. We have partial sequence of the beta-tubulin gene covering exon 3 to exon 5, from multiple representatives of *Euglena*, *Lepocinclis*, *Monomorphina*, *Phacus*, *Strombomonas* and *Trachelomonas*. None of these taxa contain intron 4 and half lack intron 3. So far five different intron 3 states (absence and 4 distinct sequences) have been found. Exons (3, 4 and 5) are easily alignable with an uncorrected distance among taxa of 0 to >18%. Divergence among genera is frequently lower than within a genus, with taxa from *Euglena*, *Phacus* and *Trachelomonas* having 0.6% or less divergence. These taxa have identical intron 3 sequences with the small amount of variation occurring within the exons. How many indel events does this represent? Does this represent a case of lateral gene transfer, convergence or symplesiomorphy? Further investigation of these questions may help elucidate evolutionary relationships among euglenoids.

16. Dale A. Casamatta* ; Jeffrey R. Johansen

Dept. of Biology, John Carroll University, University Heights, OH

Are cyanobacteria endemic? A case study employing newly described *Leptolyngbya* sp. (Cyanobacteria) isolated from desert soils based on morphology and 16S rDNA sequence data.

The extent of cyanobacterial endemism has been the subject of much recent debate. In order to elucidate potential patterns in endemism, an approximately 1200 base pair region of the 16S rDNA gene was sequenced for sixteen desert strains putatively placed in the genus *Leptolyngbya* (Pseudanabaenaceae) in order to assess phylogenetic relationships. Sequence data was combined with previously published sequences and newly sequenced outgroup taxa from European habitats, and diacritical morphological characters such as thylakoid placement and type of cell division were used in the analyses. Phylogenetic trees constructed using parsimony, distance and maximum likelihood methods were similar in topology. Nine of the sixteen newly sequenced strains formed a well-supported, monophyletic clade sister to a clade containing aquatic *Leptolyngbya*, including the type *L. boryana*. Based on molecular and morphological characters, we propose that these strains represent four species new to science. The remaining three strains well within highly supported clusters containing aerial or planktonic members of aquatic *Leptolyngbya* from European locales. However, all other desert strains (which are also likely species new to science) fall outside of the highly supported *Leptolyngbya* sensu stricto clade. Thus, the desert Pseudanabaenaceae appear to be genetically diverse and highly endemic, even though morphologically they closely resemble the aquatic taxa. As such, we conclude that while some cyanobacteria may be endemic, others actually possess high levels of dispersal.

17. Jeffrey R. Johansen* ; Dale A. Casamatta; Shannon R. Gomez

Biology, John Carroll University, University Heights, OH

Two new cyanobacterial taxa from the Great Smoky Mountains National Park (USA).

The Great Smoky Mountain National Park (GSMNP) serves as a refuge for one of the largest, richest collections of plants, animals and cryptogamic taxa in the world. We have recently discovered two new cyanobacterial taxa from waterfall splash zones within the GSMNP system. Both belong to the clade of heterocyte-bearing cyanobacteria, but their higher level taxonomic status is uncertain. The first species is *Capsosira lowii* (Capsosiraceae) which differs from the previously monotypic taxon *Capsosira brebissonii* Kuetz. ex Born. et Flah. with regard to cell size, filament morphology and ecology. *C. brebissonii* is described as an aquatic or subaerophytic taxon, while our isolate is a phycobiont from the lichen *Hydrothyria venosa* J.L. Russell. The genus *Capsosira* is currently placed in the Capsosiraceae of the Stigonematales due to its ability to divide in two planes. However, molecular evidence gathered in this study based on 16S rRNA gene data indicates closest affinity with *Aulosira* and *Nostoc commune* Vaucher, both in the Nostocaceae, Nostocales. *Rexia erecta* was also isolated from concurrently collected epilithic, aerophytic sites. The hormogonia production, near absence of heterocytes, and division in two planes are all typical of the Stigonematales. However, *Rexia* fits none of the currently circumscribed families in that order and appears morphologically similar to members of the Scytonemataceae and Microchaetaceae. Molecular evidence (16S rRNA sequence data and 16S-23S internal transcribed spacer region) places *Rexia* in the Microchaetaceae. These taxa are both problematic because they indicate that cell division in two planes has likely arisen more than once in the Nostocales, and thus the Stigonematales as currently circumscribed is not a monophyletic group. Both taxa are named in honor of Rex Lowe on the occasion of his 60th birthday.

18. Renhui Li^{*1}; Wayne M. Carmichael²; Makoto M. Watanabe³; Steven W. Wilhelm¹

1. Department of Microbiology, University of Tennessee, Knoxville, TN; 2. Department of Biological Sciences, Wright State University, Dayton, OH; 3. National Institute for Environmental Studies, Tsukuba, Ibaraki 305, Japan

Water bloom forming *Raphidiopsis* (Cyanobacteria): Its taxonomy, phylogeny and toxins.

The planktonic cyanobacterial genus *Raphidiopsis* was established by Fritsch et Rich in 1929 with the type species denoted as *R. curvata*. *Raphidiopsis* species are characterized by solitary free-floating filaments with both or one end

attenuated and sharply pointed, and heterocysts and a mucilaginous sheath are absent through the entire life cycle, while akinetes are present. *Raphidiopsis* species are much less common in the natural environment compared to other planktonic cyanobacterial group such as *Microcystis*, *Anabaena* and *Planktothrix*. They are, therefore, referred to as rare planktonic cyanobacteria. According to morphological features, the genus *Raphidiopsis* have been respectively designated into the families of Nostocaceae, Oscillatoriaceae and Rivulariaceae by different researchers, based on emphasis on different diacritical criteria. Therefore, the systematic problem of the genus *Raphidiopsis* is still unsolved. Two strains of *Raphidiopsis* were isolated from a fishpond in Wuhan city, China and rendered axenic. The taxonomy of these 2 strains was examined by combining morphological, physiological, biochemical and genetic characteristics. In addition, the taxonomic position of the genus *Raphidiopsis* was evaluated by 16S rDNA sequences. According to morphological observations, these 2 isolates belong to *Raphidiopsis mediterranea* with straight trichomes and *R. curvata* with coiled ones respectively. These 2 strains also showed the differences in growth temperature range and DNA base composition, although they shared some common points in exhibiting no heterotrophic growth, the same salinity tolerance (up to 0.78%) and the same fatty acid type. The strain of *R. mediterranea* was not detected to contain any cyanotoxins, however, the strain of *R. curvata* contained deoxy-cylindrospermopsin and cylindrospermopsin, which is similar to *Cylindrospermopsis*. The phylogenetic tree based on 16S rRNA gene sequences showed both *Raphidiopsis* strains in the same cluster with *Cylindrospermopsis*, implying their taxonomic position belonging to Nostocaceae.

19. Guillermo Diaz-Pulido^{*1}; Laurence J. McCook²

1. Programa de Biología & Instituto de Investigaciones Tropicales INTROPIC, Universidad del Magdalena, Santa Marta, Magdalena, Colombia; 2. Great Barrier Reef Marine Park Authority, Townsville, QLD, Australia

Macroalgal recruitment on coral reefs: Dynamics and roles of ecological processes.

The recruitment of algae is a critical process during algal colonization and invasions, particularly in coral to algal phase shifts. Despite algae are widely assumed to colonize and kill corals, there is very little known about the recruitment dynamics of coral reef algae, or the effects of ecological processes on such dynamics. To address these issues, we combined descriptive and experimental data from the Great Barrier Reef (GBR), Australia, focusing on two dominant macroalgae: *Sargassum* and *Lobophora variegata*. Recruitment abundance varied across the GBR, between habitats, species, and through time. *Sargassum* propagules recruited throughout the year but peaked during summer/autumn at inshore reefs, whereas, at offshore reefs, recruitment was nil. Reef slopes had lower densities of *Sargassum* recruits than reef flats. Contrary to *Sargassum*, *L. variegata* recruited across the entire GBR, being more abundant at inshore reefs and slopes. Adult *Sargassum* populations were highly seasonal and were related to algal recruitment, suggesting an important role of adult phenology in recruitment dynamics. We tested: 1) the ability of algal propagules to settle and grow on healthy coral tissue, 2) the relative importance of nutrient supply to and herbivory on recruits, and 3) the effects of herbivory and habitat on algal recruitment. Healthy corals were able to prevent attachment or survival of recruits of these macroalgae and variation in recruitment appeared related to the amount of turf algae or crustose algae on the plates. Herbivory strongly reduced both density and growth of recruits for both taxa, whereas nutrient supply had minor effects on growth of *L. variegata* recruits and no detectable effects on *Sargassum* recruits. Herbivory varied between species, habitats, and locations. These results emphasize the critical roles of coral disturbances to coral - algal phase shifts, and the importance of herbivores to the protection of coral reefs against algal overgrowth.

20. Michael S. Stekoll^{*1,2}; Elizabeth L. Calvert²; Erin Meyer¹; Doug Rasher¹

1. Natural Sciences, University of Alaska Southeast, Juneau, AK; 2. Juneau Center School of Fisheries and Ocean Sciences, University of Alaska Fairbanks, Juneau, AK

***Nereocystis luetkeana* as recruitment habitat for fish and invertebrates in southeast Alaska.**

Canopy-forming kelp communities have been recognized as important habitat for both fish and invertebrates. In southeast Alaska the dominant canopy-forming kelp in the inside waters is *Nereocystis luetkeana*. Its role as essential habitat for fish and invertebrates, especially with respect to commercially important species, is largely conjecture supported with little experimental evidence. A manipulation experiment was conducted near Juneau, Alaska to test the hypothesis that juvenile fish and invertebrate abundances are greater at sites with canopy-forming kelp species. The manipulations involved removing the overlying kelp canopies of *N. luetkeana* from two of the four sites selected. Monitoring of each site was accomplished using three different techniques: visual transects using scuba, Standard Monitoring Units for Recruitment of Fish (SMURFs) and light traps. Sampling was conducted at each site at two depths, canopy (near surface) and bottom. Preliminary data show that the monitoring methods differ in the types and numbers of species enumerated. Visual transects yielded little useful information. SMURF and light trap data revealed that fish and invertebrate abundances were greater at the bottom of all sites. SMURF data showed a trend towards significantly more fish at the bottom of canopy kelp sites. In contrast, light traps captured more fish at the bottom of cleared sites. The mean

invertebrate counts for the bottom light traps were 100 times greater than for the surface light traps. The total fish biomass supported by each of the habitats from the SMURF collectors was significantly greater at canopy kelp sites. There was no significant effect of canopy or location when looking at the total fish biomass sampled by the light traps. These preliminary results suggest that the presence and relative abundance of macroalgae and canopy-forming kelp species are associated with spatial variation and species composition of fish and invertebrates in southeast Alaska.

21. VA Fairhead^{*1}; CD Amsler¹; JB McClintock¹; BJ Baker²

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

Lack of phlorotannin induction by UV radiation in two species of dominant Antarctic macroalgae.

Phlorotannins are polyphenolic compounds found exclusively in the Phaeophyceae. They play a strengthening role in cell walls and act as a storage compound. Several secondary roles have also been proposed, including protection from UV radiation, antibacterial activity and herbivore deterrence. Previous work has shown that UV-B radiation can increase phlorotannin production and that they absorb strongly in the UV-B spectrum. *Desmarestia anceps* and *D. menziesii* are two dominant macroalgal species along the Antarctic Peninsula. This study investigated induction of phlorotannin production in both species in response to increased UV radiation at Anvers Is, Antarctica (63°S 63°W). Induction of phlorotannins as protection against UV radiation could impact trophic dynamics, as they have been found to affect herbivore feeding preference. Five sets of 3 experimental units were placed at 4m depth. Each set contained 2 units with Plexiglas covers (one UV transparent and one UV opaque) and an uncovered control treatment. Individuals were collected from 15m and 4 tips were removed from each individual, one tip was used for initial phlorotannin concentration, and the other 3 were transferred to one of the 3 experimental conditions. After 47 days the tips were collected and phlorotannin concentration determined. The concentration increased consistently in all treatments, indicating some factor other than UV radiation was involved. The transplanted algae were exposed to higher overall PAR and this may have been responsible for the increased levels. The effect of the treatments on feeding preference of the herbivorous amphipod *Gondogeneia antarctica* was tested using fresh tissue in a choice feeding assay. No preference for any treatment was detected. Subsequent feeding assays found a preference for artificial foods containing ground dry tissue from the final samples over the initial samples, but for foods containing phlorotannin enriched extracts from the initial samples over the final samples. This indicates that while the tissue with higher phlorotannin concentrations was more palatable, some factor other than phlorotannin concentration was responsible (e.g. nutritional quality).

22. Alison R. Sherwood^{*}

Botany, University of Hawaii, Honolulu, HI

Stream macroalgae of the Hawaiian islands: a floristic analysis.

A total of 171 stream segments on the islands of Kauai, Oahu, Maui and Hawaii were sampled between January 2001 and November 2003 for macroalgae. A suite of physical and chemical measurements, including pH, temperature, specific conductance, current velocity and stream segment dimensions, was made for each site in order to examine associations among taxa and stream conditions. Stream conditions were more greatly influenced by the degree of disturbance than by the island on which they were located. A total of 163 macroalgal taxa were identified from the sites, with 36% of these comprising new taxonomic records for the state of Hawaii, and 3% representing undescribed taxa. The endemism in the non-marine algal flora (ca. 5.0%) was very low compared with other groups of organisms from the Hawaiian islands. At a broad taxonomic scale, the stream macroalgal floras of all four islands were dominated by Chlorophyta and Cyanobacteria, followed by Rhodophyta, Bacillariophyta and Tribophyta. Multivariate analyses were employed to visualize trends in stream macroalgae composition among the four islands. Both principal co-ordinates and cluster analyses suggested that although the floras of Kauai, Oahu and Maui were similarly broad in taxonomic composition, the flora of the big island of Hawaii contained fewer unique taxa and was thus distinct from the others. This may be due to the comparatively young age of the island.

23. Olivier De Clerck^{*1}; Suzanne Fredericq²; Brigitte Gavio²; Eric Coppejans¹

1. *Biology, Ghent University, Ghent, Belgium*; 2. *Department of Biology, University of Louisiana at Lafayette, Lafayette, LA*

Diversity in *Grateloupia filicina* (Halymeniales, Rhodophyta) with Special Emphasis on Cypitic Diversity in the Atlantic Ocean.

No less than 12 years ago *Grateloupia filicina* was thought to represent perhaps the best example of a cosmopolitan marine macroalga. With the onset of gene sequencing to resolve phylogenetic relationships, this picture began to change. The western Pacific representatives of so-called *G. filicina* were shown to be phylogenetically only distantly related to

specimens collected near the type locality, and hence described as a new species *G. asiatica*. In this study relationships between specimens from several localities worldwide, which from a morphological perspective are usually classified as *G. filicina*, are determined based on DNA sequence analysis of the *rbcL* gene (cpDNA) and partial LSU (rDNA). Although some degree of hidden diversity was expected, results are startling in that so far genuine *G. filicina* has only been found in the Mediterranean Sea. Specimens from all other areas, including European Atlantic shores prove to represent different species. Each temperate biogeographic region seems to be characterized by only a single species with a *G. filicina*-type morphology. Sympatric cryptic species, as recently encountered in *Plocamium* and *Bostrychia* seem to be absent in temperate regions. In tropical and subtropical regions, however, several species with a common morphology seem to co-exist.

24. Boo Y. Won* ; Tae O. Cho; Suzanne Fredericq

Biology, University of Louisiana, Lafayette, LA

***Centroceras clavulatum* (Ceramiaceae, Rhodophyta): a cosmopolitan red algal species?**

Centroceras clavulatum (C. Agardh) Montagne (1846), originally described from Callao, Peru, is currently known as a widely distributed species worldwide. Over 40+ vouchers referred to in the literature as *C. clavulatum* were investigated on the basis of chloroplast-encoded *rbcL* sequence analysis and comparative morphology. Eight well-supported clades were identified. *Centroceras clavulatum* encompasses at least seven additional species that are either new or may have been placed under its synonymy. The eight clades under study are distinct from *C. internitens* Gallagher & Humm, *C. secundum* Wynne and *C. minutum* Yamada, and include, respectively, representative specimens with the following distribution: (1) Peru, (2) California, Gulf of California, Korea, Japan, Pac. Panama, S. Australia, (3) E Florida & Caribbean Panama, (4) California, (5) W and E Florida, (6) SW South Africa, (7) Chile, and (8) E & W Florida, Texas, Caribbean Sea. Correct species names, including resurrected and new names, are being assigned to each of the clades under study.

25. Tae O. Cho* ; Boo Y. Won; Suzanne Fredericq

Biology, University of Louisiana, Lafayette, LA

***Antithamnion nipponicum* Yamada & Inagaki (Ceramiaceae, Rhodophyta) is a recent introduction along the coast of North Carolina and the correct name of the species known as *A. hubbsii* in Pacific North America and *A. pectinatum* in Western Europe.**

Female and male reproductive structures in material known as *Antithamnion hubbsii* Dawson from California are illustrated and described for the first time. On the basis of similarity in vegetative and reproductive features and in *rbcL* sequence, *A. hubbsii* is subsumed under *A. nipponicum* Yamada & Inagaki, a species described from Japan. This prostrate species is characterized vegetatively by whorl-branches arranged in distichous opposite pairs bearing adaxial and abaxial branchlets, with the distal-most branchlets restricted to the abaxial side of whorl-branches; basal cells of whorl-branches producing multicellular rhizoids with digitate holdfasts as well as indeterminate filaments; and gland cells originating adaxially alongside the lower branchlet cells. In the current literature *Antithamnion nipponicum* has been placed in synonymy with *A. pectinatum* (Montagne) Brauner in Athanasiadis & Tittley, a species described from Auckland (I.), New Zealand. *Antithamnion pectinatum* is here recognized as a distinct southern hemisphere species bearing abaxial and adaxial distal-most branchlets and lacking rhizoidal filaments and new axes formed in place of whorl-branches. The correct name for the invasive species known in western Europe as *A. pectinatum* is *A. nipponicum*. We extend the distribution of *A. nipponicum* to Atlantic North Carolina and Pacific California, USA. Historical reports suggest that this species, along with other non-native species, was recently introduced from Japan. We confirm the synonymy of *Antithamnionella glandulifera* (Kyllin) Wollaston with *A. spirographidis* (Schiffner) Wollaston, a species showing an eastern Pacific-eastern Atlantic distribution.

26. Max H. Hommersand*¹; D. W. Freshwater²

1. Department of Biology, University of North Carolina, Chapel Hill, NC; 2. Center for Marine Science, Univ. of North Carolina at Wilmington, Wilmington, NC

"A Seaweed Goes To War" --- Taxonomic Status Of The Agarophyte *Gracilaria "confervoides"* Harvested In North Carolina During WWII.

Most commercial agar came from Japan prior to the outbreak of World War II. With the advent of war domestic production was greatly expanded to meet an essential wartime need. The principal agar sources were *Gelidium robustum* on the Pacific Coast supplemented by *Gracilaria "confervoides"* from the Beaufort region in North Carolina where 75-100 tons of dried seaweed were harvested in 1943 yielding approximately 60,000 pounds of agar. Harvesting was organized by Harold Humm at Duke University and the North Carolina plant was cultured and its agar analyzed by C.K.

Tseng, then at the Scripps Institution of Oceanography at La Jolla, CA. Though once so abundant it clogged fishermen's nets in the sounds around Beaufort, the North Carolina plant is less common now. Long thought to be identical with the European *G. confervoides* (= *G. verrucosa*, = *G. gracilis*), the NC plant is distinct. Unlike *G. gracilis* from Europe, the branches are markedly constricted at their bases and young carposporophytes are profusely attached to the floor of the cystocarp by numerous tubular cells and only later by tubular cells that reach the outer pericarp. Sequence analyses of the *rbcL* gene place the North Carolina plant in Gracilaria at the base of the *gracilis*-clade, well separated from other recorded members of this group. Our plan is to describe it as a new species of *Gracilaria*.

27. Sarah E. Hamsher^{*1}; Dale A. Casamatta²; Lee M. Luckeydoo³; Norman R. Fausey³

1. Division of Water, City of Lancaster, Lancaster, OH; 2. Department of Biology, John Carroll University, University Heights, OH; 3. Agricultural Research Service, United States Dept of Agriculture, Columbus, OH

Metaphytic algal succession of a newly constructed wetland in northwestern Ohio.

Constructed wetlands are increasingly being utilized as a method of reducing nutrient enrichment to aquatic ecosystems due to anthropogenic effects. Algae are one of the primary components of a wetland community and may be responsible for the majority of carbon fixation and nutrient removal from these systems. As such, the algal community may have a profound role in ameliorating agricultural eutrophication in these systems. However, little is known how the algal community develops. The purpose of this research was to document the seasonal and annual metaphyton community over a four year period (2000-2003) in a recently constructed wetland used to ameliorate agricultural drainage in Defiance County. Metaphyton samples were collected between April and November each year. Water samples were collected for ammonia, nitrate, and orthophosphate analysis. Metaphyton were identified, enumerated, and biovolume was calculated to determine dominant biomass. Samples were combined by season and diatoms were processed, identified, and enumerated. In each year, diatoms and green algae comprised the majority of biomass. Further, biomass was highest in September in three of the four years. Biomass and the average number of taxa per sample increased throughout the course of the study. Cyanobacteria, common components of constructed wetlands, were never dominant. A comparison of biomass at the inflow and outflow of the wetland showed that biomass was not significantly different ($p > 0.01$). Water chemistry showed no patterns seasonally or annually. Overall, it appears that the algal community structure changed from bacillariophytes to chlorophytes while average number of taxa per sample increased.

28. Nestor R. Anzola^{*}; George F. Pessoney; Carmen L. Hernandez

Biological Sciences, University of Southern Mississippi, Hattiesburg, MS

The role of environmental factors on the dynamic of the phytoplankton in streams of South Mississippi.

Phytoplankton have been monitored and collected seasonally since 1993 in headwater creeks in Forrest, Perry, and George Counties, South Mississippi, in order to examine seasonal and annual fluctuations in genera composition and density. These creeks are fast flowing, shallow, sandy bottomed streams, originating in and draining from Camp Shelby, the largest National Guard and Reserve training facility in the continental USA. Interactions of water quality variables in determining density and richness of phytoplankton within the streams were analyzed. Pennate diatoms were the most abundant and frequent types of algae found in the streams. The Chlorophyta were more diverse than Chrysophyta, in terms of genera, but their presence was not as constant as the diatoms. The most frequent algae in the creeks were the diatoms *Eunotia*, *Navicula*, *Nitzschia*, and *Tabellaria*, and the green algae *Closterium* and *Mougeotia*. When other algae genera causing bloom conditions in freshwater systems were reported, they accounted for a low proportion of the total phytoplankton. The statistically significant environmental factors that produced shifts in algae numbers and composition over time were temperature and flow. This presentation summarizes the results of water quality and algae abundance in the last 10 years focusing in the interactions among environmental variables and the numbers of algae present in the streams.

29. Karen P. Fawley^{*}; Marvin Fawley

North Dakota State University, Fargo, ND

Diversity and ecology of freshwater *Nannochloropsis* (Eustigmatophyceae).

The genus *Nannochloropsis* is well known from the marine environment but has only recently been reported from fresh and brackish waters. A single species, *N. limnetica*, was documented from a lake in Germany, and a second unnamed species isolated from a river in the United States has been characterized by sequence analysis and light microscopy. All of the *Nannochloropsis* species that have been described, both marine and freshwater, are small spheres with essentially no distinguishing morphological characteristics and therefore must be characterized using molecular techniques. We have cultured numerous isolates of *Nannochloropsis* from a series of lakes on the James River in the Arrowwood National Wildlife Refuge, North Dakota, USA, and 3 isolates from ponds in Itasca State Park, Minnesota, USA. The diversity

among some of these isolates has been determined by analyses of 18S rDNA and *rbcL* sequences. Seven genetically distinct types of *Nannochloropsis* have been found, one of which possesses 18S rDNA and *rbcL* sequences identical to those of *N. limnetica* from Europe. The 6 new types vary in both 18S rDNA and *rbcL* sequences and some morphological characters that distinguish them from *N. limnetica*. All of *Nannochloropsis* isolates from Arrowwood were cultured only from samples taken during cold-water periods, whereas 2 of the Itasca isolates came from summer samples. These results suggest that *Nannochloropsis* species may be better adapted to cold water conditions, including temperatures near 0 C and ice cover, than they are to warm water. More importantly, the *rbcL* sequence and morphological diversity present among freshwater *Nannochloropsis* isolates is truly astonishing compared to diversity from marine systems. This material is based upon work supported by the National Science Foundation under Grant Nos. DBI-0070387, MCB-0084188 and ND WRRI.

30. Sophia I. Passy^{*1}; Pierre Legendre²

1. Department of Biology, University of Texas at Arlington, Arlington, TX; 2. Department of Biological Sciences, University of Montreal, Montreal, QC, Canada

Power law relationships among hierarchical taxonomic categories in algae reveal a new paradox of the plankton.

In this continental-scale study, we show that in major stream habitats, both benthic and planktonic, algal richness at hierarchical taxonomic categories (genus to phylum) is a power function of species richness. The scaling exponent of this function, which captures the diversification rate of higher taxa, i.e. the rate of increase of their richness with the increase of species richness, is significantly different across environments. This suggests that the role of environment is of paramount importance in structuring communities of primitive organisms such as algae. The ensuing finding that the diversification rate of higher taxa is greater in the seemingly homogeneous planktonic environment, when compared to benthic habitats encompassing an array of ecological niches, poses a new paradox of the plankton. Species richness frequency distributions and biovolume-species richness relationships are habitat-specific but follow a common general pattern, indicating that in the studied stream environments communities are driven toward maximum productivity.

31. Michael J. Ferguson^{*1}; Kyle Scotese¹; Eduardo Morales²; Jeffrey R. Johansen¹

1. Biology Department, John Carroll University, University Heights, OH; 2. Academy of Natural Sciences, Philadelphia, PA

Species diversity in *Fragilaria sensu lato* from selected sites in the Great Lakes.

The Great Lakes Environmental Indicators (GLEI) project has been designed to identify taxa useful in determining ecological integrity in the near shore waters of the Great Lakes ecosystem. Through the analysis of the diatom taxa of Lake Michigan and Lake Huron, a rich and abundant flora of the Fragilariaceae was observed at 8 different locations. Initial observations of these taxa with the light microscope provided limited distinguishing features necessary to separate species even at the generic level. An estimate of twenty-five different morpho species was determined in the light microscope. Analysis using the scanning electron microscope revealed a diverse group of cryptic species in seven different genera which have been slit out from *Fragilaria* in the past 15 years, including *Fragilaria*, *Staurosira*, *Staurosirella*, *Pseudostaurosira*, *Frankophilla*, *Martyana*, and *Punctastriata*. We consider some of our species to be new to science.

32. Luis E. Aguilar-Rosas^{*}; J. A. Zertuche-Gonzalez; R. Aguilar-Rosas; G. Avila-Serrano

Biología, Universidad Autónoma de Baja California, Ensenada, Baja California, Mexico

Erradication program of *Undaria pinnatifida* (Harvey) Suringar (Laminariales, Phaeophyta) in Mexico.

A program for eradication/control of a recently reported bed of *Undaria pinnatifida* off the coast of Baja California, Mexico, was initiated in January of 2004. A subtidal bed of approximately 500 m² was found at Todos Santos Island. Plants were present from 6 to 24 m depth. Higher densities were found around 6 m (50 plants/m²). A population of 1350 plants were removed. Plant sizes vary from 1 to 110 cm in length, most of them juveniles. Few plants were reproductive. Most plants were attached to small pebbles and shells. Evidence of herbivory by sea urchin and snails was observed. A monthly survey is being carried on to study bed recovery and distribution.

33. Luis E. Aguilar-Rosas^{*1}; Raul Aguilar-Rosas²; Ignacio Sanchez Rodriguez³; Judy Broom⁴; Wendy Nelson⁵

1. Instituto de Investigaciones Oceanológicas, Universidad Autónoma de Baja California, Ensenada, Baja California, Mexico; 2. Facultad de Ciencias Marinas, Universidad Autónoma de Baja California, Ensenada, Baja California, Mexico; 3. Centro Interdisciplinario de Ciencias Marinas, Instituto Politécnico Nacional, La Paz, Baja California Sur, Mexico; 4. Department of Biochemistry, University of Otago, Dunedin, New Zealand; 5. Museum of New Zealand Te Papa Tongarewa, Wellington, New Zealand

***Porphyra pendula* Dawson (Bangiaceae, Rhodophyta) in the Pacific coast of Mexico: Endemic species from the Gulf of California.**

The occurrence and seasonality of *Porphyra pendula* E.Y. Dawson (Bangiaceae, Rhodophyta) in its macroscopic phase, is reported for the Pacific coast of Mexico, based on sampling conducted during November 2002 to May 2003 and specimens deposited in national and foreign herbaria. We describe in detail the vegetative and reproductive structure of the thallus, as well as its habitat and geographic distribution of the species. The specimens of *P. pendula* from Isla Carmen, Los Planes and Calerita, represents newly reported populations for the Gulf of California. Based on data obtained from herbarium specimens and observation of population in Calerita, Baja California Sur, we conclude that *P. pendula* is a seasonal species in its macroscopic phase, occurring from January to March (winter to the beginning of spring).

34. Raul Aguilar-Rosas^{*1}; Luis E. Aguilar-Rosas²; Guillermo Avila-Serrano¹

1. *Facultad de Ciencias Marinas, Universidad Autonoma de Baja California, Ensenada, Baja California, Mexico*; 2. *Instituto de Investigaciones Oceanologicas, Universidad Autonoma de Baja California, Ensenada, Baja California, Mexico*

***Undaria pinnatifida* (Harvey) Suringar (Laminariales, Phaeophyta) in Mexico.**

Undaria pinnatifida a laminarian kelp (Phaeophyta) native to Japan, Korea and northern China, has been recently introduced to the coast of southern California (USA). We present the first record of this invasive species on the Pacific Mexican coast, and show the current southern limit along the Pacific coast of North America. *U. pinnatifida* was found on September 28th, 2003, growing attached to small rocks on a sandy bottom in the subtidal zone at 12-14 m depth at Todos Santos Islands, in Baja California, Mexico. This population consisted of 15 sporophytes, with an average length of 50 cm and with mature sporophylls. This new finding suggests that the colonization of the Pacific coast of North America by this invasive species is still occurring, and its distributional range is expanding.

35. Maria A. Faust^{*}

Department of Botany, Smithsonian Institution, Washington D.C., DC

The Dinoflagellates of Twin Cays, Belize: Biodiversity.

Floating detritus, a unique microcosm, acts as a reservoir of diverse microalgae and meiofauna in mangrove areas found in Twin Cays, Belize. The Lair, Boston Bay, Hidden Creek and Main Channel four locations within Twin Cays, were used as the study sites. Large suspended detrital aggregates are specialized environments where benthic photosynthetic and heterotrophic organisms thrive as suspended free-floating cells in the water column. On the water surface, patches of detritus, a combination of benthic organisms, dinoflagellates, diatoms, cyanobacteria and dinoflagellate cysts are enclosed in a matrix of fibers. Heterotrophic organisms are also numerous in floating detritus. Phagotrophic fauna, along with nematodes, ciliates, copepods and crustacean larvae, rely on small algal forms in detritus as their food source. Vertical distribution and species composition of microalgae and associated meiofauna in rising and sinking detritus aggregates are reported using water depth and time series studies. The biodiversity of dinoflagellates included a total of thirty eight species, fifteen potentially harmful species, and eight neritic species. Populations of benthic dinoflagellates in floating detritus were measured against total cell counts and found to represent 28-43 % in the Lair and 18-68 % in Boston Bay. The highest concentration of dinoflagellate species were identified as being: *Bysmatrum subsalsum*, *Prorocentrum caribbeanum*, *Prorocentrum elegans* and *Prorocentrum mexicanum*. All other dinoflagellates were one to two orders of magnitude lower in cell numbers. Dominant meiofauna organisms were nematodes and ciliates in detritus. Illegal dumping of domestic waste in the Lair caused dinoflagellates to disappear from floating detritus and their recovery is briefly described.

36. Todd Egerton^{*}; Harold G. Marshall

Department of Biological Sciences, Old Dominion University, Norfolk, VA

Feeding behavior and conditioning in three *Pfiesteria*-like dinoflagellates.

Pfiesteria piscicida (CCMP1834), *Pfiesteria shumwayae* (NC1048C), and a related unnamed cryptoperidinopsoid species (DEQ029) were all observed in culture to feed on the cryptomonad *Rhodomonas sp.* as well as fish tissue and fish red blood cells. The effect of feeding history on the feeding behavior of the dinoflagellates was tested using two food treatments. For three months, clonal cultures from all three species were maintained on a *Rhodomonas* diet, while others were fed fish tissue and red blood cells from Atlantic Menhaden and Atlantic Croaker. Following the three-month conditioning, the grazing rates of the dinoflagellates on *Rhodomonas* were measured over a six-hour period. *P. shumwayae* showed a significantly higher grazing rate per cell than the other two species, however there was no significant difference in the grazing rates between the two feeding histories. The growth rates of *P. piscicida* and the cryptoperidinopsoid were then calculated in a three-week study following the conditioning treatments. There was no

significant difference in growth rate for either species between the two feeding histories. This data suggests that while *Pfiesteria*-like dinoflagellates are capable of preying on a diverse diet, feeding behavior may not be influenced by prior feeding conditions. This research is one component of several projects supported by the Virginia Department of Health and the CDC.

37. Catherine E. Olsen* ; Jeffrey R. Johansen

Biology Department, John Carroll University, University Heights, OH

Comparison of algal growth on trees at various ozone levels (elevations) in Great Smoky Mountains National Park (USA).

Air pollution, ozone levels specifically, are a significant problem at Great Smoky Mountains National Park (GSMNP) (USA). Annual ozone levels in the park exceed levels in all cities in the United States except Los Angeles. A correlation has been established between elevation and ozone levels. In general, the higher the elevation, the higher the ozone level. Ozone has been shown to have induced visible injury on sassafras, yellow poplar, black cherry, and beech trees. Photosynthetic production has also been shown to be decreased in beach trees, apple leaves, and tobacco plants due to ozone exposure. In addition, algal growth has been significantly reduced or eliminated when treated with ozone in the water purification process. This study examined algal growth at different ozone levels. Bark samples were taken from five trees at four sampling locations within GSMNP. Samples were cultured and the number of algal colonies that grew on each plate was counted. Ozone levels were averaged from data collected by the National Park Service from April to September 2002. ANOVA analysis showed no significant difference ($p=.594$) in algal growth among sampling locations, but a significant difference ($p<.01$) among the individual trees sampled. Kruskal Wallis analysis showed that there was a significant difference ($p=.035$) in the number of algal colonies found from each sampling location. Cades Cove had the lowest levels of algal growth, which was unexpected since this was the sampling location with the lowest elevation and ozone level. Possible reasons for this finding is that there are increased levels of other pollutants at this location due to high automobile traffic. In general, if Cades Cove was removed from the analysis, there was a slight trend towards higher ozone levels producing lower algal growth. Further sampling is planned to evaluate the effects of other environmental factors and to reduce the effect of variability among individual trees.

38. Slawomir Cerbin* ; Todd Stem; Todd Egerton; Harold G. Marshall

Department of Biological Sciences, Old Dominion University, Norfolk, VA

Morphology and physiology of a novel *Pfiesteria*-like-dinoflagellate from a Chesapeake Bay estuary.

In May of 2001 an unknown heterotrophic dinoflagellate was found in a sediment sample collected from Sarah's Creek, VA as part of the Virginia *Pfiesteria* monitoring program. This sample was incubated, and clonal cultures of the dinoflagellate (ODU strain 01VDH034) were established. Initial observations of the morphology, life cycle in culture, and physiology of this strain suggested that the dinoflagellate may be included in the complex of *Pfiesteria*-like-organisms. These observations are supported by 18s ribosomal genetic data. In this study, a cell membrane stripping technique and SEM were employed to allow for the determination of the kofoidian plate tabulation (4', 2a, 6'', 6c?, 4s?, 5''', 0p, 2'''). This study also begins to examine the physiology and ecology of this organism by determining the salinity tolerance of the strain (3-40 psu). The results of this work suggest that based on morphology and physiology, as well as genetic data, this strain is a member of the *Pfiesteria* complex. This is one component of several ongoing projects supported by the Virginia Department of Health and the CDC.

39. Kim Rattan* ; Andrew M. Gordon; Paul K. Sibley

Environmental Biology, University of Guelph, Guelph, ON, Canada

The Effects Of Forest Harvesting Practices On Phytoplankton Community Structure In Boreal Lakes: Establishing A Reference Condition.

Boreal riparian forests influence phytoplankton communities by controlling nutrient availability, habitat diversity, light intensity, and water chemistry. Communities at the boundaries between terrestrial and aquatic ecosystems have been viewed as highly responsive to changes in landscape characteristics such as the removal of riparian vegetation. Induced landscape alterations such as harvesting may lead to excess fluxes of nutrients, metals, and organic matter export to lakes leading to changes in the yield and structure of phytoplankton populations. The aim of this study is to establish a reference condition for phytoplankton communities in boreal lakes as a basis for defining appropriate widths of buffers that will maximize both the preservation of in-lake ecological integrity and the allowable removal of timber. Water and phytoplankton samples were collected from 21 lakes in 2002 and 2003 at the Esker Lakes Research Project (ELRA), located 70 km north of Cochrane, ON and analyzed for chlorophyll *a* (Chl *a*), phytoplankton abundance, biomass (biovolume), and water quality parameters. In 2002, chl *a* concentrations ranged from 0.63 $\mu\text{g/L}$ to 25.12 $\mu\text{g/L}$. Total

abundance (cells/L) ranged from 75,745 to 319,543 and was dominated by the group Cyanophyceae. Total biovolume (μm^3) ranged from 18,530 to 106,532, with Chlorophyceae species being most prevalent. In 2003, chl *a* concentrations ranged from 1.10 $\mu\text{g/L}$ to 16.14 $\mu\text{g/L}$. Total abundance ranged from 58,778 to 222,934, with Cyanophyceae again being most prevalent. Total Biovolume ranged from 18,975 to 107,720, with Chlorophyceae and Dinophyceae being the most prevalent. Canonical Correspondence Analysis (CCA) revealed a trophic gradient ranging from dystrophic (boggy lakes) to clear that were characterized by three groups of taxa. These results will be used to establish a reference condition for phytoplankton in which the consequences of harvesting in upland areas on boreal lakes will be compared.

40. Cindy Fernandez*

CIMAR, University of Costa Rica, San Pedro, San José, Costa Rica

***Caulerpa sertularioides*, a green alga spreading aggressively over coral reef communities in Culebra Bay, North Pacific of Costa Rica.**

Caulerpa sertularioides is a tropical green alga which has aggressively spread in Culebra Bay, North Pacific of Costa Rica. During recent surveys this alga has increased its coverage in the last two years. *C. sertularioides* in this bay, occur mostly in shallow but also in subtidal habitats, continuously extending its range. It has now colonised many of the substrates in the shallow littoral, including rock, sand, dead and live corals. It develops principally at depths from 0 to 17 m. In some areas between 3-6 m, coverage can be 100% and very dense. The alga has spread rapidly, mean stolon elongation rate studied in situ was approximately 14 cm/month, with maximal growths of 30cm/month. This study evaluate the modifications caused by *C. sertularioides* spreading on the structure of the benthic community changing the reef system, by crowding out the algal flora, altering biodiversity of organisms, overgrowing colonies of *Pocillopora* spp. and *Psammocora stellata*, and favoring organisms such as nudibranchia (4 per 10 cm^2) and poliquetes (475 per 50 cm^2). The extent to which biotic interactions influence the spread of the alga is not well know, but some factor that possibly contribute to the spread of *C. sertularioides* in Costa Rica include, the low incidence of herbivory, due to the presence of toxic compounds, nutrient supplied by anthropogenic sources and the high incidence of clonal reproduction through fragmentation, that may be promoted by anchors from tourist or fishing boats.

41. Teresita R. Perez*

Dept. of Environmental Science, Ateneo de Manila University, Quezon City, Philippines

Taxonomy, Distribution and Temporal Changes in the Abundance of Phytoplankton in Taal Lake, Batangas, Philippines.

Proliferation of fish cages in Taal lake is a major problem including the high nutrient inputs from river systems. This study investigates the phytoplankton composition of the lake; its taxonomy, distribution and temporal changes. Physico chemical parameters of the water were also monitored for a period of one year. Significant increase in the $\text{NH}_4\text{-N}$ was observed from June and July while a significant increase in total phosphorous (P), soluble P and $\text{NO}_3\text{-N}$ were observed during the dry season from the monthly collections. Despite the significant increase in the nutrient hold of the lake, there was no significant correlation between the nutrients and chlorophyll content (chl *a*) of the lake from the three sampling sites. On the other hand, pH and temperature ($p < 0.001$) showed a positive correlation with chl *a* concentration. There was no significant difference in nutrients and other physico-chemical factors between the sampling depths in all stations. No significant increase in the monthly chl *a* collected but significant amount of chl *a* was observed from 2.5 m and 5 m depth. A total of 45 species of phytoplankton were identified in the lake during the sampling regime belonging to 22 genera of Division Chlorophyta; 10 genera of Division Chrysophyta; 2 genera for Pyrrophyta and 11 genera for Cyanophyta. Four genera of phytoplankton namely *Ceratium*, *Merismopedia*, *Aulacoseira* showed dominance during the sampling regime ($p < 0.001$) except during the month January which was dominated by centric diatoms. The high cell count coincided with high chl *a* concentration. These genera showed positive correlation with pH, temperature, $\text{NO}_3\text{-N}$ and $\text{NH}_4\text{-N}$. Taal lake is in the process of eutrophication as indicated by the presence of *Ceratium* species.

42. Michele T. Buccellato* ; jon C. cawley

Biology, Roanoke College, Salem, VA

A Preliminary Diatom Community Analysis of the Upper Roanoke River, Southwest Virginia.

In spring 2004 the researchers sampled for benthic diatoms along the headwaters and upper reach of the Roanoke River in Southwestern Virginia. The river headwater provides the drinking water supply for cities of Salem and Roanoke. The upper portion of the river then flows through both cities, and into Smith Mountain Lake. Diatoms from cobble surfaces at approximately 20 individual sites were counted and identified via optical microscopy, with analysis of total numbers of genera as percentages. Counts of 300 individuals were made, and cluster analysis was performed on the counts. Statistical analysis identified several discrete diatom communities across this portion of the river. These communities appear to

correspond to differences in land use, from primarily forested/agricultural to urban-associated (higher nutrient) riparian and basin use. An identified list of the diatoms present was compiled for each site, and the differences are reported, along with discussion of land-use. This project has direct implications on management strategies for the upper Roanoke River drainage, including currently proposed large-scale tree-plantings in the urban portions of the basin.

43. Harold G. Marshall^{*1}; Lubomira Burchardt²; Slawomir Cerbin¹

1. Department of Biological Sciences, Old Dominion University, Norfolk, VA; 2. Department of Hydrobiology, Adam Mickiewicz University, Poznan, Poland

Morphological characteristics and occurrence of the diatom *Aulacoseira herzogii* from a dystrophic lake in southeastern Virginia, U.S.A.

Aulacoseira herzogii (Lemm.) Simonsen is a rarely reported diatom that has been associated with tropical and sub-tropical habitats of standing water or slowly moving rivers (Lemmermann, 1910; Hustedt, 1952; Jewson et al., 1993). Marshall and Poore (1972) reported its presence in Lake Drummond, a dystrophic lake, in the Great Dismal Swamp National Refuge in the central Atlantic coastal plain of the United States. It is shallow (ca. 2m), with a surface area of ca. 7,705 ha, and an annual pH range of 3.2-6.8. Nutrient values over a 12 month period determined by Phillips (1990) included ranges for TN (1.06-2.68 mg/l), TP (0.04-0.13 mg/l), silica (1.83-4.36 mg/l), with mean a TN:TP ratio as 66:1, and a range of 30-138:1. This taxon has been observed over the past 3 decades in this lake where *Asterionella ralfsii* W. Smith was the dominant diatom throughout the year, with *A. herzogii* a common sub-dominant species (Burchardt and Marshall, 2003). *A. herzogii* is typically found as single cells, or as 2 cells in a short filament, with longer filaments less common. The cells have a distinct sulcus and collar, with a flat valve face. Adjoining cells are typically linked together by two (often 4) equal length spines that extend to a recessed groove on the adjoining cell (Hickel and Hakansson, 1991). SEM observations in 2002-2003 indicate cell diameters ranged from 4.2-7.2 microns (5.4 mean), with 30-40 areolae/10 microns, and average spine lengths of 11.3 microns. The frustule lengths averaged 26.4 microns. In our studies in Lake Drummond, no auxospores have been observed, as noted for this species in Lake Banani, Bangladesh by Jewson et al. (1993). Occasions of high concentrations of *A. herzogii* in Lake Drummond occurred throughout the year including winter months (ca. 5°C water). Seasonal abundance peaks varied in development, but attained concentrations of 10-4 to 10-6 cells/liter. These results support the concept of a broader geographic range for *A. herzogii* beyond tropical and sub-tropical regions, and its continued presence in a temperate, shallow dystrophic lake where low pH levels and high TN:TP ratios exist.

44. Victor C. Galvan^{*}; Steven N. Murray

Biological Science, California State University, Fullerton, Fullerton, CA

Effects of temperature on rates of photosynthesis and respiration in *Caulacanthus ustulatus* (Rhodophyta), a new addition to the California seaweed flora.

The recent appearance of the aquarium strain of *Caulerpa taxifolia* in southern California waters has been widely publicized. However, introductions of the Asian kelp *Undaria pinnatifida* and the intertidal red alga *Caulacanthus ustulatus* have received much less attention. *C. ustulatus* is widely distributed in warm temperate and tropical seas in both the eastern Atlantic and western Pacific. This alga was recently detected in Brittany, and molecular studies suggest that *C. ustulatus* was introduced to northern France from Asia. *C. ustulatus* was first found on southern California shores in 1999 and has quickly become the dominant component of mid-shore algal turfs at mainland sites near harbors and marinas. Prior to its appearance on southern California shores, *C. ustulatus* was known in the eastern Pacific only from Baja California Mexico, Washington, and British Columbia. Culture studies of Brittany specimens indicate that *C. ustulatus* can tolerate temperatures of 6 °C to 26 °C, with best growth occurring at 17 °C. We have initiated a series of ecophysiological, growth, and field studies on California populations of *C. ustulatus* in an attempt to improve understanding of the requirements for *C. ustulatus* to establish populations on California shores. Here we report the photosynthetic and respiration rates of *C. ustulatus* at 11, 14, 17, and 20 °C, a range of temperatures encountered in California waters. We compare our results with published growth responses for *C. ustulatus* from France and with photosynthetic data for algal species found growing with *C. ustulatus* in southern California intertidal algal turfs.

45. Sarah K. Henkel^{*}

Ecology, Evolution, and Marine Biology, University of California, Santa Barbara, Santa Barbara, CA

Latitudinal variation in *Egregia menziesii*: Investigations of morphology, physiological response and gene flow.

Morphological plasticity within a species is widespread among seaweeds although the functional or evolutionary significance of this variation is often unclear. Possible drivers of the plasticity include limited gene flow (which may lead to nascent speciation), biological interactions (such as herbivory), and environmental conditions (e.g. temperature or wave exposure). In this study I am investigating the variation of three morphological traits in a kelp species across a large scale

in order to experimentally examine possible mechanistic drivers of this variation, in particular physiological response to temperature and gene flow. *Egregia menziesii* (O. Laminariales) morphology varies considerably throughout its range and has been believed to correlate with geographic distribution (British Columbia to Mexico). To date, populations of *Egregia* throughout California have been surveyed and morphological characters were quantified and mapped. Some characters, such as rachis morphology, vary with latitude. Immunochemical assays have been developed to examine the physiological response of *Egregia* to temperature (in terms of heat shock protein production as a biochemical index of temperature tolerance) under natural and experimental conditions. The amount of heat shock proteins (Hsps) present in a cell depends on the thermal history of the organism; consequently, this trait tends to vary with latitude as well. Finally, genetic investigations are underway to ascertain if the variation in morphology has a genetic basis. The mapping of function and genetics onto the distribution of this species may lead to an understanding of the adaptive significance of morphological plasticity in *Egregia* and its performance in the intertidal. Supported by UC Natural Reserve System Mathias and Southern California Academy of Sciences grants to SKH.

46. Kim E. Whiteside* ; Steven N. Murray

Biological Science, California State University, Fullerton, Fullerton, CA

Spatial and temporal patterns of abundance in southern California populations of *Caulacanthus ustulatus* (Rhodophyta).

The recent appearance of the aquarium strain of *Caulerpa taxifolia* in southern California waters has been widely publicized. However, introductions of the Asian kelp *Undaria pinnatifida* and the intertidal red alga *Caulacanthus ustulatus* have received much less attention. *Caulacanthus ustulatus* is widely distributed in warm temperate and tropical seas in both the eastern Atlantic and western Pacific. Molecular studies suggest that *C. ustulatus* was introduced to northern France from Asia presumably with Japanese oyster spat. *C. ustulatus* is an apparently introduced species, first found on southern California shores in 1999 where it has quickly become an abundant component of mid-shore algal turfs at several mainland sites near harbors and marinas. Prior to its appearance in California, *C. ustulatus* was reported to occur in the eastern Pacific in Baja California, Mexico, Washington, and British Columbia. The goals of this study are to: 1) determine the rate of increase in the abundance of *C. ustulatus* since its appearance at selected southern California sites, and 2) investigate the patterns of habitat utilization of *C. ustulatus* at local and microhabitat scales. Estimates of *C. ustulatus* cover were obtained for three sites during 2003 and 2004 using line transects and point-contact methodologies. These data were compared with cover data taken at the same sites prior to 2000. Data depicting the vertical intertidal habitat occupied by *C. ustulatus* and its utilization of substratum slope, type, and relief were collected simultaneously with cover assessments. Our results show that in less than 5 years, *C. ustulatus* has become the dominant species in mid-shore algal turf communities once occupied by other small, red algal species. *C. ustulatus* is limited to mid and upper shore intertidal habitats and grows on a variety of substrata besides rock, including the surfaces of mussels (*Mytilus californianus*), barnacles (*Balanus glandula*), and macro-algae such as the turf-forming *Corallina pinnatifolia* and the rockweed *Silvetia compressa*.

47. Charles D. Amsler*¹; Katrin Iken^{1,4}; James B. McClintock¹; Margaret O. Amsler¹; Kevin J. Peters¹; Joanna M. Hubbard²; Bill J. Baker³

1. Department of Biology, University of Alabama at Birmingham, Birmingham, AL; 2. Anchorage School District, Anchorage, AK; 3. Department of Chemistry, University of South Florida, Tampa, FL; 4. Institute of Marine Science, University of Alaska, Fairbanks, Fairbanks, AK

A Comprehensive Evaluation of the Palatability and Chemical Defenses of Subtidal Macroalgae from the Antarctic Peninsula.

The palatability of 35 non-encrusting, subtidal species of antarctic macroalgae was determined in laboratory bioassays utilizing sympatric sea stars (*Odontaster validus*) and fish (*Notothenia coriiceps*), both of which are omnivores known to consume macroalgae in nature. This included all subtidal, non-encrusting macroalgal species that could be collected in sufficient quantities near Palmer Station, Antarctica (64° 46' S, 64° 03' W) and included all of the ecologically dominant, overstory brown macroalgae in the western Antarctic Peninsula region. Overall, 63% of the macroalgal species offered to sea stars and 83% of the macroalgal species offered to fish in thallus bioassays were significantly unpalatable. When organic extracts of unpalatable macroalgal species were incorporated into artificial foods, 76% of the species unpalatable as thallus to sea stars were also unpalatable to them as extract and 53% of the species unpalatable as thallus to fish were also unpalatable to them as extract. If either sea stars or fish rejected thallus of a macroalgal species, palatability of organic extracts of that species to herbivorous amphipods known to consume macroalgae (*Gondogeneia antarctica*) was determined. Sixty three percent of such algal species were unpalatable as extract to the amphipods. It was concluded that antarctic macroalgae are commonly unpalatable to sympatric consumers and that much of this unpalatability is the result

of chemical defenses. Thallus toughness and a variety of nutritional quality parameters were also examined and none appeared to be related to macroalgal palatability to the animals.

48. Kevin J. Peters^{*1}; Charles D. Amsler¹; Margaret O. Amsler¹; James B. McClintock¹; Robert B. Dunbar²; Bill J. Baker³
1. Department of Biology, University of Alabama at Birmingham, Birmingham, AL; 2. Department of Geological and Environmental Sciences, Stanford University, Stanford, CA; 3. Department of Chemistry, University of South Florida, Tampa, FL

A comparative analysis of the biochemical and elemental composition of macroalgae from the western Antarctic Peninsula.

The biochemical composition (protein, carbohydrate, lipid, ash, refractory material) of 41 antarctic macroalgal species from the western Antarctic Peninsula was analyzed both early (November and December 2001) and late (March and April 2000) in the growing season. 36 species were further analyzed for C:N ratios as well as total %N and %C. Biochemical composition and elemental analysis was performed using recognized methods on macroalgal thalli which had been freeze-dried and ground into a fine powder. Protein levels were greater than levels reported in non-antarctic areas. These high protein levels are presumed to be due to the nutrient rich waters which the macroalgae reside in along coastal Antarctica. There were no significant differences in biochemical composition between the two different times in the growing season for the macroalgae as a whole. C:N ratios were found to be low with respect to those published from non-antarctic areas and similar to those reported in other studies on or near the Antarctic Peninsula. 19 of the 36 species had C:N ratios below 10:1 which is half of the mean C:N ratio of 20:1 reported for other benthic marine plants. Total %N levels were found to be above critical nitrogen levels (1.5%) needed for maximum growth in all but 2 species analyzed. Correlations between biochemical composition and elemental content were also analyzed. There were no correlations found between the protein levels and nitrogen content when all the macroalgae were combined. This lack of significant correlation suggests that nitrogen levels do not limit protein synthesis in antarctic macroalgae.

49. Blake Schaeffer^{*}; Dan Kamykowski; Edward Milligan; Laurie McKay; Geoff Sinclair
Marine, Earth, & Atmospheric Sciences, North Carolina State University, Raleigh, NC

Back to phytoplankton 101: An evaluation of *Karenia brevis* strain differences.

Physiological research performed on several different strains of a single marine phytoplankton species provides useful information on the physiology of field populations. Though previous studies have shown that strains of the same species can vary in physiological responses when grown under the same conditions, laboratory characterization of the red tide dinoflagellate species *Karenia brevis*, nevertheless, has focused primarily on the Wilson clone isolated in 1953. Multiple laboratory experiments investigated the PAM-FL responses and lipid class concentrations of ten different *K. brevis* strains. All strains were grown in a 22°C incubator, at 100 $\mu\text{mol quanta m}^{-2} \text{s}^{-1}$ with 12 hours of light and 12 hours of dark for one week. Experiments were conducted on a radial photosynthetron, which allowed for controlled conditions of light and temperature. This photosynthetron has 12 black boxes extending as spokes around a 250 watt bulb; each black box houses 10 culture bottles (120 samples). During the strain comparison experiments, maximum light level was 2000 $\mu\text{mol quanta m}^{-2} \text{s}^{-1}$ and minimum light level was 50 $\mu\text{mol quanta m}^{-2} \text{s}^{-1}$. The incubation time was 8 hours, just after the onset of photoinhibition. Culture concentration and division rates have significant roles in the determination of physiological and biochemical parameters. Despite this, individual strains retained their own relative physiological and biochemical characteristics.

50. Melba D. Apoya^{*1}; Michael R. Gretz¹; Graham J. Underwood²

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

Motility and aggregation of the mudflat diatom *Cylindrotheca closterium* (Bacillariophyceae) under varying environmental conditions.

Cylindrotheca closterium (Ehrenberg) Reiman *et* Lewin is widely distributed in mudflat assemblages and can be used as model organism in understanding the role diatoms play in mudflat habitats. Nutrient concentration and salinity have been reported to affect extracellular polymeric substance (EPS) production in diatoms although effects on motility and aggregation are not yet fully elucidated. Variation was observed on the type of movements, size of aggregates formed and the carbohydrate chemistry of various EPS extracts of *C. closterium* grown in different media and salinities. Low salinity (20 ppt) induced gliding movements and formation of large aggregates. At 34 ppt, pirouetting movements predominated and aggregation occurred only in later growth phases. Cultures grown in high nutrient conditions had higher cell densities, produced more aggregates, cells exhibited reduced gliding motility and had less carbohydrate EPS per cell. Cell number was reduced in low nutrient media and large aggregates formed only during stationary phase. The majority of cells in low

nutrient media exhibited pirouetting and gliding movements with a greater amount of carbohydrate EPS per cell. Monosaccharide composition of various extracellular polymers was unique between cells grown in different media and salinity. This implies that nutrient and salinity fluctuations in mudflats could cause variation in diatoms movements, aggregation and chemical composition of EPS produced. The significance of these findings in biofilm formation and ecological implications in mudflat environments will be discussed.

51. Jeremy L. Dahmen^{*1}; Jeffrey Leblond¹; Rebecca L. Seipelt¹; Matthew J. Elrod-Erickson¹; Bruce Cahoon¹; Rodney Kincaid¹; Terence J. Evens²; Peter J. Chapman³

1. Department of Biology, Middle Tennessee State University, Murfreesboro, TN; 2. United States Horticultural Research Laboratory, Ft. Pierce, FL; 3. United States Environmental Protection Agency, Gulf Ecology Division, Gulf Breeze, FL

Lipid Composition of Chlorarachniophytes (Chlorarachniophyceae): Unusual Polar Lipids and the Role of the Nucleomorph in Sterol Biosynthesis.

An initial effort to characterize the fatty acid and sterol composition of the representative chlorarachniophytes, *Bigelowiella natans*, *Gymnochlora stellata*, *Lotharella amoebiformis*, and a *Lotharella* sp., has shown that their chloroplast glycolipid-associated fatty acids were found to be derived from the common algal/plant lipids, monogalactosyldiacylglycerol (MGDG) and digalactosyldiacylglycerol (DGDG). These fatty acids were found to be of limited composition, containing principally eicosapentaenoic acid [20:5(n-3)] and hexadecanoic acid (16:0). Unlike many eukaryotic algae, the cytoplasmic membrane lipid fraction was found to be dominated by a number of polar, quaternary ammonium-containing lipids that did not contain phosphorus. The fatty acid composition of these polar lipids was both distinct and more variable than the glycolipids, with the fatty acids, 16:0 and docosapentaenoic acid [22:5(n-3)], dominant along with a number of minor C18 and C20 fatty acids. Only two sterols made up the free sterol fraction in all organisms. These were identified as 24-ethylcholesta-5,22E-dien-3 β -ol (70-95%) and 24-methylcholesta-5,22E-dien-3 β -ol (5-30%), with undefined C-24 stereochemistry. Several genes encoding activities required for synthesis of these sterols were computationally identified in *B. natans*. One sterol biosynthesis gene within this metabolic pathway showed the greatest similarity, by far, to SMT1 of the green alga, *Chlamydomonas reinhardtii*. However, genes homologues to other species, mostly green plant species, were also found. Further, the method of identification suggested that the sequences have been transferred to a genetic compartment other than the likely original location, the nucleomorph nucleus.

52. T.J. Evens^{*}; Randall P. Niedz

USDA-ARS, Ft. Pierce, FL

ARS-MEDIA: A new software program for the analysis, design and optimization of algal culture media.

The success of algal culturing efforts is highly influenced by the nature of the culture medium used. In general, media formulas are complex mixtures of inorganic salts, vitamins, amino acids, undefined supplements, buffers and carbon sources, and with few exceptions, are modifications of recipes that were empirically derived. Media selection depends on the species of alga, the kind of culture and/or the cultural stage being undertaken. To choose or formulate an optimal media recipe it is necessary to evaluate and/or manipulate multiple ion concentrations and ratios. Also, in order to determine the importance of a single ion the user must also consider the complementary cation/anion of the parent salt. This can be a daunting task if one considers the number and variety of salts within any given recipe. Accordingly, we have developed a LabVIEW-based software package that allows users to: 1) select potential media recipes from a comprehensive database of published media recipes, 2) systematically compare multiple recipes, and 3) manipulate target recipe ion concentrations via a linear programming approach. The ARS-MEDIA program is public-domain and will be available as a stand-alone executable file after beta-testing.

53. Amber Johnson^{*}; Frances Wilkerson; Richard Dugdale

Romberg Tiburon Center, San Francisco State University, Tiburon, CA

The effect of temperature on diatom cell size, growth rates and biogenic silica content.

Diatoms are unicellular phytoplankton that are important players in the biological pump and may account for up to 40% of total oceanic primary production. They have an obligate requirement for silicon to construct their silicified cell wall or frustule. This frustule acts as natural ballast and the more heavily silicified the frustule (as measured as biogenic silica concentration) the more likely they are to sink, carrying organic carbon to the deep ocean. It has been observed that Antarctic diatoms contain more biogenic silica per cell than equatorial diatoms. This study describes how decreasing temperatures affect diatom growth rates, cell size and biogenic silica content in two diatom species, *Skeletonema costatum* and *Chaetoceros debilis*. As temperature was lowered from 17 deg C to 6 deg C, growth rates were reduced, cells were larger and contained more biogenic silica per cell and per cell surface. It may be that at lower growth rates (as shown by Claquin et al. 2002), an increase in the G2+M phase of the cell cycle allows an increase in silicification that

results in the larger, heavier cells. The potential effects of these results on how global warming might impact the biological pump and the role of diatoms as a carbon sink will be discussed.

54. Z. Y. Hu^{1,2}; Milton R. Sommerfeld^{*1}; Q. Hu²

1. School of Life Sciences, Arizona State University, Tempe, AZ; 2. Phycology, Institute of Hydrobiology, Wuhan, Hubei, China

Astaxanthin's role in protecting *Haematococcus pluvialis* against oxidative stress: new evidence from an astaxanthin-overproduction mutant.

Haematococcus pluvialis (Chlorophyceae) synthesizes and accumulates large amounts of the red pigment astaxanthin under oxidative stress conditions. Numerous comparative physiological studies using astaxanthin-rich and astaxanthin-poor cells have suggested that astaxanthin may function as an antioxidant to protect the cell against oxidative stress. However, previous experimental systems were problematic. While astaxanthin-rich cells came from mature cysts, astaxanthin-poor cells were either green vegetative flagellates/immature cysts, or astaxanthin-less cysts obtained by blocking of the astaxanthin biosynthesis using carotenoid inhibitor/s, which is known to exert negative effects on normal cellular metabolism. As such, the conclusions on the effectiveness of astaxanthin, based on comparison of the cells of different life cycle phases or different physiological conditions, were less than convincing. Using chemical mutagenesis, we have obtained an astaxanthin-overproduction mutant (named MT#2877) that contains ca. 10% less chlorophyll, and grows slower (ca. 10%), compared to the wild type (WT) under favorable culture conditions. Upon stress induction (i.e., high light, and excess amounts of sodium acetate and Fe²⁺), MT#2877 synthesizes astaxanthin earlier and accumulates ca. 100% more astaxanthin (3.5~4.0% of dry weight) than WT (1.5-2.0% of dry weight) by day 7. During this time period, over 40% of WT cells were bleached or dead, whereas the mortality rate of MT#2877 was less than 15%. Based on flow cytometry, oxygen evolution, and chlorophyll fluorescence induction measurements, we conclude that the greater tolerance of MT#2877 to oxidative stress than WT was due to the ability of the mutant to overproduce and accumulate astaxanthin.

55. Linda A. Franklin^{*}; Patrick J. Neale

Smithsonian Environmental Research Center, Edgewater, MD

Seasonal changes in the effects of ultraviolet radiation on carbon partitioning in phytoplankton.

UV radiation inhibits phytoplankton photosynthesis, but the effect on subsequent partitioning of fixed carbon into macromolecular pools (carbohydrates, lipids, and proteins) is not clear. Changes in allocation patterns may carry over to other trophic levels; thus information on partitioning is critical for modeling ecosystem dynamics under higher UVB scenarios. Using a polychromatic approach, we have been monitoring seasonal changes in biological weighting functions (BWFs) for UV effects on carbon allocation in natural populations of phytoplankton in the Rhode River estuary (Chesapeake Bay region). In late spring, when nitrogen levels are falling, UV sensitivity of allocation to lipids and carbohydrates is similar to the overall sensitivity of carbon fixation by photosynthesis, in that there is greater inhibition of carbon uptake at shorter wavelengths. Of all macromolecular pools, allocation to protein synthesis is the least sensitive to UVA, but is relatively more sensitive to UVB than allocation to other compounds. These results are similar to those found for laboratory cultures of *Thalassiosira pseudonana* and *Gymnodinium instriatum*, species common to this area. These results will be compared to those obtained in the summer, winter and early spring, at various nitrogen concentrations. We hypothesize that carbon allocation is altered to conserve synthesis of nitrogen-rich compounds under ecologically relevant UV conditions.

56. Dan Pelah^{*}; Ephraim Cohen

Ben-Gurion University, Beer-Sheva, Israel

Cellular responses of *Chlorella zofingiensis* to selenium application.

An investigation of the cellular response of the freshwater microalga *Chlorella zofingiensis* to exogenous selenium showed that *Chlorella* cells can tolerate sodium selenite up to concentrations of 100 mg l⁻¹. Cells grown in a selenium-supplemented medium accumulated boiling-stable proteins in a concentration-dependant manner. Western blot analysis revealed that three of these boiling-stable proteins cross-reacted with anti-dehydrin antibody. Selenium was also found to exert an effect on antioxidative enzymes: superoxide dismutase (Fe-SOD and Mn-SOD isoforms) accumulated in response to the stress imposed by 100 mg l⁻¹ sodium selenite, as did a newly discovered form of selenium-dependent glutathione peroxidase. Upon transfer of the cells to a selenium-free medium, the boiling-stable proteins, the superoxide dismutase isoforms and the selenium-dependent glutathione peroxidase were all down regulated. The accumulation of boiling-stable proteins and the increased activities of the antioxidant enzymes in selenium-treated *Chlorella* cells suggest that these compounds are probably involved in the mechanism(s) of selenium tolerance of this alga.

57. Maria V. Sanchez Puerta* ; Tsvetan R. Bachvaroff; Charles F. Delwiche
Cell Biology and Molecular Genetics, University of Maryland, College Park, MD

The chloroplast genome sequence of the haptophyte *Emiliana huxleyi*.

Despite their ecological and environmental importance, the haptophytes have not been thoroughly studied, especially from a molecular prospective. Chloroplast genomes from representatives of all major photosynthetic groups except haptophytes have been sequenced. The chromophyte algae, namely haptophytes, cryptophytes, heterokonts and dinoflagellates, are unique because of the presence of secondary plastids with chlorophyll c as the main photosynthetic pigment. The plastids of haptophytes also contain 19'hexanyloxyfucoxanthin and/or 19'butanoyloxyfucoxanthin as characteristic accessory pigments of the group. Here, we report the (nearly complete) sequence of the chloroplast genome of the coccolithophorid *Emiliana huxleyi* (Lohmann) Hay et Mohler 1967 (CCMP#373). This species belongs to the coccolithophorids, the main group in the Haptophyta, and is likely to be the most globally abundant haptophyte. Preliminary annotation of the genome using database searches identified more than 100 genes, with base composition 61% AT. The data were also compared to the chloroplast genomes of green and red algae, as well as those of other chromophytes. The sequence of the *E. huxleyi* plastid genome represents an important source of information that may help to elucidate the origin of the plastids in the chromophyte algae, and is needed to test the chromoalveolate hypothesis. In particular, it will be useful to understand the relationships among the plastids in the haptophytes and dinoflagellates, about which competing hypotheses currently exist.

58. Jessica A. Kaufman* ; Elma Gonzalez
Organismic Biology, Ecology, and Evolution, UCLA, Los Angeles, CA

Heat-Shock Proteins expression in the coccolithophore *Emiliana huxleyi* under nutrient-replete and phosphorus limited conditions.

The cellular response to heat stress, better known as heat shock, is characterized by induced synthesis of Heat-Shock Proteins (HSP). The HSPs are thought to be one of the most highly conserved genetic systems known. It is known that the alteration of *hsp* expression is not limited to heat stress, but is also induced by a variety of other stressors. This study is the first to investigate the expression of *hsps* in the coccolithophore *Emiliana huxleyi*. Our primary goal was to examine the expression of both *hsp 70* and *90* in *E. huxleyi* under both nutrient replete and phosphorus limited (i.e. stressful conditions). We have examined the time-course responses of four strains (CCMP 379, CCMP 1516, CCMP 2090, CCMP 1949) of *E. huxleyi* under stressful and non-stressful conditions. Expression of specific mRNA was monitored by means of both Northern blot and Real Time PCR. In comparison to nutrient replete conditions, *hsp* expression was induced in all strains under nutrient deplete conditions. However, the amount of expression varied across strains such that in the non-calcifying strain CCMP 379 both *hsp 70* and *90* attained the highest expression under stressful conditions and in comparison to all other calcifying strains examined. HSP 70 protein was examined in situ by means of immunofluorescence microscopy. Immunofluorescence observed was most intense in cells of the non-calcifying strain under nutrient deplete conditions as compared to intensities observed in either calcifying strains or, in all cases, cells subjected to nutrient replete conditions. We conclude that both *hsp 70* and *hsp 90* expressions are induced as a result of exposure to stress. This may suggest a potential use for *hsps* as biomarkers for *E. Huxleyi* under stress conditions.

59. Jean-Francois Pombert* ; Christian Otis; Claude Lemieux; Monique Turmel
Biochimie et Microbiologie, Universite Laval, Quebec, QC, Canada

Unique architecture of the chloroplast genome in the green alga *Pseudoclonium akinetum*.

The green plant phylum Streptophyta comprises all land plants and the green algae belonging to the Charophyceae, whereas the Chlorophyta comprises virtually all of the other green algae, i.e. the members of the Prasinophyceae, Ulvophyceae, Trebouxiophyceae and Chlorophyceae. We have undertaken the sequencing of complete chloroplast genomes from representatives of various green algal lineages in order to elucidate their branching order and to understand the evolution of chloroplast DNA (cpDNA). Five green algal cpDNA sequences are currently available in public databases, three of which have been determined by our laboratory. The cpDNAs of *Mesostigma viride* (136 genes) and of the charophyte *Chaetosphaeridium globosum* (125 genes) closely resemble most of their land plant counterparts in overall structure and gene organization. They harbor a quadripartite structure characterized by the presence of two copies of a rRNA-encoding inverted repeat (IR) sequence, a small-single copy region (SSC) and a large single-copy region (LSC). Each of these regions shows a highly conserved gene content. The cpDNA of the prasinophyte *Nephroselmis olivacea* (127 genes) has retained a high degree of ancestral characters. It displays the typical quadripartite structure and features no introns, whereas the cpDNA of the trebouxiophyte *Chlorella vulgaris* (112 genes) has lost the IR as well as several genes and gained three introns. The cpDNA of the chlorophyte alga *Chlamydomonas reinhardtii* (94 genes) has an IR;

however, the genes usually found in the SSC and LSC regions have been exchanged so that the sizes of these regions are similar. This genome carries seven introns, and features many fragmented, ancestral gene clusters. We have recently completed the 195,867-bp cpDNA sequence of the ulvophycean green alga *Pseudendoclonium akinetum* and will present its detailed analysis. This genome (105 genes) displays an atypical, quadripartite structure that differs from the structure observed in *Chlamydomonas* cpDNA, and its overall gene organization is most similar to that of *Chlorella* cpDNA. Of all the chlorophyte cpDNAs sequenced thus far, it is the most rich in introns (27 introns). (Supported by NSERC)

60. Jean-Charles de Cambiaire* ; Christian Otis; Claude Lemieux; Monique Turmel

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

The chloroplast genome sequence of the chlorophycean alga *Scenedesmus obliquus*: a comparative analysis with its *Chlamydomonas* homolog.

The Chlorophyceae comprises green algae with a clockwise (CW) or directly opposed (DO) arrangement of the flagellar apparatus. Phylogenetic analyses indicate that the CW and DO lineages diverged early during chlorophycean algal evolution. Included within the CW group are members of the genus *Chlamydomonas*. Physical and gene mapping studies of chloroplast DNA (cpDNA) from selected *Chlamydomonas* species revealed that this genome has an atypical, quadripartite structure that is characterized by two copies of a rRNA-encoding inverted repeat (IR) sequence separated from one another by two single-copy (SC) regions of almost identical size. In all IR-containing cpDNAs of land plants and at least three green algal cpDNAs, the IR sequences are separated by SC regions of greatly unequal size, and each of the three genomic regions is highly conserved in gene content. In *Chlamydomonas*, the gene content of the IR and each SC region appears to be relatively well conserved, but the way the genes are partitioned between these regions is entirely different from the pattern seen in other green plant cpDNAs. The recently completed sequence of *C. reinhardtii* cpDNA (203,826 bp) disclosed a highly reduced gene content compared to the cpDNAs of the chlorophyte green algae *Chlorella vulgaris* and *Nephroselmis olivacea*, the total or partial breakage of most of the ancestral gene clusters shared by the latter cpDNAs, and a large number of short repeated elements in intergenic regions. To gain insights into how and when the distinctive features of *Chlamydomonas* cpDNAs were acquired during the evolution of chlorophycean algae, we have determined the complete cpDNA sequence of *Scenedesmus obliquus*, an alga belonging to the DO lineage. This 161,452 bp sequence shares several similarities with its *C. reinhardtii* counterpart, including an atypical, quadripartite structure with SC regions of about equal size, but differs greatly in the partitioning pattern of its 96 genes. As in *C. reinhardtii* cpDNA, only a few remnants of ancestral gene clusters are found in *Scenedesmus* cpDNA; however, several derived clusters are common to these cpDNAs. (Supported by NSERC)

61. Misaki Takabayashi* ; Frances Wilkerson

Romberg Tiburon Center, San Francisco State University, Tiburon, CA

Studying Species Abundance and Gene Expression in Marine Diatoms using Real-Time PCR.

Diatoms are some of the most numerous primary producers in coastal upwelling regions. They dominate the biological pump, new production and carbon biogeochemical cycling. It is, however, difficult to identify their specific contributions to carbon and nitrogen assimilation, unless molecular genetic approaches are used. Emerging real-time PCR technology offers a quantitative means to determine abundance of cells by measuring copy numbers of particular gene in environmental genomic DNA or by measuring expression of a particular gene by measuring its mRNA. In order to understand the enhanced ability of marine diatoms to assimilate nitrogen, we have used real-time reverse transcription PCR to measure changes in glutamine synthetase (GS), one of the key enzymes that link carbon and nitrogen metabolisms, in a common diatom, *Skeletonema costatum*. Transcription of *glnII* (gene that encodes for the enzyme isoform GSII) increased 2-3.5 times above background by nitrate (NO₃⁻) uptake by the cells but not by ammonium (NH₄⁺) uptake. A background level of *glnII* mRNA was expressed at a steady level up to 15 days of N starvation before decreasing to below detection by 21 days. These results confirm that *glnII* transcription is induced to express GSII, which catalyzes assimilation of NH₄⁺ made available in the chloroplast where nitrite reductase reduces NO₃⁻-derived nitrite to NH₄⁺. Because of this specific role of GSII in diatoms assimilating NH₄⁺ derived from NO₃⁻ assimilation rather than NH₄⁺ taken up directly from the environment, quantification of *glnII* mRNA by real-time reverse transcription PCR promises to be a useful indication of new production by phytoplankton. We are also using Real-time PCR to identify and enumerate phytoplankton taxa in San Francisco Bay. Since Taqman real-time PCR can differentiate DNA sequences differing by a single base, we can have identification resolution down to the species level as long as their DNA sequences of the focus gene are known. We have been exploring the application of this technique with small subunit ribosomal RNA (SSU rRNA) gene sequences in quantifying phytoplankton species found in bloom and non-bloom water of San Francisco Bay.

62. Peter J. Rizzo^{*}; Rodney Morris; Kristy Tyler; Robyn Shields

Biology, Texas A&M University, College Station, TX

Observations on Binucleate Dinoflagellates Using Long Term Fluorescent Nuclear Staining|o.

We have examined several binucleate dinoflagellates using a recently developed procedure designed to enhance the visibility of nuclei stained with fluorescent dyes. Among the dinoflagellates examined were *Kryptoperidinium foliaceum* (CCMP 1326), *Kryptoperidinium foliaceum* (CS-37), *Peridinium foliaceum* (UTEX LB 1688), and *Gymnodinium foliaceum* (CCAP 1116/3). The uninucleate dinoflagellate *Gyrodinium dorsum* (UTEX LB 2334) was also examined for comparison. In all binucleate dinoflagellates examined, the dinokaryotic nuclei revealed individual chromosomes, and the endosymbiont nuclei revealed a highly lobed morphology with no visible chromosomes. Generally speaking, fluorescent microscopy of dinoflagellate nuclei is of poor resolution, since the nuclei are obscured by the presence of plastids, pigment granules, and thecal plates. Autofluorescence also interferes with clear visualization of the nuclei. In regard to permanent mounts, the usual slide mounts using buffered glycerol are temporary, and fade after a week or so. We have developed a process to permanently fix the dinoflagellate cells, followed by a removal of pigments. These cells were then fluorescent-stained to clearly visualize the nuclei. The cells were then prepared as permanent mounts using an ultraviolet light-catalyzed resin of high refractive index. This results in final clearing of the cells for high-resolution fluorescent microscopy, to produce permanent stained samples, which may be kept for at least four years with little loss of fluorescence. This procedure was also used to prepare fluorescent-stained permeable plastic embedded cells, which were thin sectioned at 0.5-2 nm, stained, and permanently mounted. This procedure is especially useful to ascertain the binucleate condition of dinoflagellate samples taken from the field. □

63. Paul V. Zimba^{*1}; Mark Weaver²; Michael J. Sullivan³; Dave Czarnecki⁴

1. Catfish Genetics Research unit, USDA/ARS/MSA, Stoneville, MS; 2. Southern Weed Research Unit, USDA/ARS, Stoneville, MS; 3. Biology, Mississippi St. University, Starkville, MS; 4. Biology, Ioras College, Dubuque, IA

Fatty Acid Analyses of 8 *Craticula cuspidata* clones.

Fatty acid profiles have been used to elucidate food webs, and to assess evolutionary adaptations within plant genera. We raised clonal isolates of *Craticula cuspidata* (originally isolated from eight locations in temperate North America) axenically and analyzed late exponentially growing cells for fatty acid composition. Cultures were grown at both 20 and 27C. Samples were concentrated on filters, and processed for fatty acid analyses using a gas chromatograph equipped with gas capillary and flame ionization detection. A reference library (MIDI) was used to facilitate identification. Percent contribution of saturated fatty acids was generally higher at 27C, whereas cultures grown at 20C had more unsaturated fatty acids. Palmitic acid, a saturated fatty acid, and 16-carbon unsaturated forms were the most abundant fatty acids present

64. Maria Rovilla J. Luhan^{*}; Jesus Rodriguez

Aquaculture Department, Southeast Asian Fisheries Development Center, Tigbauan, Iloilo, Philippines

Growth and agar quality of *Gracilaria heteroclada* Zhang et Xia grown in a filter tank of a finfish broodstock tank.

Gracilaria heteroclada Zhang et Xia was grown in filter tank of finfish broodstock tank to determine the growth, agar quality and uptake pattern of nitrogen and to observe the water quality in a recirculating water system with seaweed. Rapid uptake of nitrogen in *G. heteroclada* was observed within the first 24 h of culture. Filling up of the nitrogen pools in the cell may have continued until the 3th day of culture. This suggests that, upon intracellular saturation of nitrogen on the 3th day, the plants started to increase in weight, as nitrogen in the seaweed stabilized during the experiment. *Gracilaria heteroclada* stocked at 1.25 and 1.0 kg m⁻² achieved an SGR of 12.2 and 9.4 % day⁻¹ during 15 days of culture. The residual nitrogen in the filter tank with seaweed was reduced more by approximately 11.6 %.

65. Jennifer L. Wolny^{*1}; Karen A. Steidinger¹; Leanne J. Flewelling²; Jay Abbott²; R W. Richardson²; Jan H. Landsberg²

1. Florida Marine Research Institute, Florida Institute of Oceanography, St. Petersburg, FL; 2. Florida Marine Research Institute, Fish and Wildlife Conservation Commission, St. Petersburg, FL

Morphometric and Toxicity Data for *Pyrodinium bahamense* from Florida.

Historically, the varieties of *Pyrodinium bahamense* have been separated from each other based on cell morphology and the production of toxin. Saxitoxin producing *Pyrodinium bahamense* from the Pacific were of the *compressum* variety, while non-saxitoxin producing *Pyrodinium bahamense* from the Atlantic have been referred to as the *bahamense* variety. In Florida this dinoflagellate has been identified as *Pyrodinium bahamense* var. *bahamense* based on cell morphology and the lack of documentation of saxitoxin poisonings. The recent discovery of a saxitoxin producing population of *Pyrodinium bahamense* from the Indian River Lagoon in Florida has warranted further investigation into the morphological characteristics used to differentiate the two varieties of this species. Field material and cultured isolates

from the east and west coasts of Florida were used to examine saxitoxin production and several morphological features. Morphometric comparisons include the apical pore complex and sulcal structures, surface markings, thecal pore location and size, and chain formation in field and cultured material. Morphological and toxicity comparisons are being conducted on *Pyrodinium bahamense* from non-Florida locales.

66. Michael J. Wynne*

Ecology & Evolutionary Biology, University of Michigan, Ann Arbor, MI

An Historical Account of the Depiction of Marine Algae: a Preview.

This project, culminating in a book manuscript entitled Portraits of marine algae: an historical perspective, was undertaken to pay homage to the early workers who studied marine algae and depicted them with great attention to detail. The scope of this study covers from the 1760s to around 1900, selecting authors who include seaweeds in their treatments. The project includes 58 authors, 64 works (books or journal articles), and 86 plates and highlights authors who included seaweeds in their treatments. During this period covered, many voyages of exploration were bringing back collections of plants (including algae) and animals to the museums and universities of Europe, where they were studied and described. By default, it is mostly a Euro-centric exercise. Most of the authors (e.g., W. Hudson, J. V. Lamouroux, R. K. Greville, J. G. Agardh, W. H. Harvey, and G. Zanardini) are reasonably well known to the phycological community, but others (e.g., Velley, Bertolini, Delle Chiaje, and Corda) are less familiar. An effort was made to give a balanced representation of the three classes of macro-algae: the Chlorophyceae, the Phaeophyceae, and the Rhodophyceae. The layout of the presentation was to compile examples of the depiction of marine algae, to say something about the author, or authors, and to put their life and contributions in the context of their time. The following six early workers will be used to preview this project: S. G. Gmelin, F. X. Wulfen, C. A. Agardh, C. F. P. von Martius, C. Montagne, and J. D. Hooker.

67. John A. West^{*1}; Giuseppe C. Zuccarello²; Joe Scott³; Jeremy Pickett-Heaps¹

1. School of Botany, University of Melbourne, Parkville, VIC, Australia; 2. National Herbarium Netherlands, University of Leiden, Leiden, Netherlands; 3. Biology, College of William and Mary, Williamsburg, VA

Observations on *Purpureofilum apyrenoidigerum* gen. et sp. nov. from Australia and *Bangiopsis subsimplex* from India (Stylonematales, Bangiophyceae, Rhodophyta).

Purpureofilum apyrenoidigerum gen. et sp. nov. was obtained from a mangrove habitat in New South Wales, Australia. It had unbranched uniseriate to multiseriate filaments less than 1 mm tall with a unicellular base. Each cell had a single multi-lobed parietal chloroplast without a pyrenoid. During reproduction vegetative cells were discharged directly as monospores that remained motile for several hours after release. Spores with long tails moved more slowly (0.053 to $0.195 \mu\text{m s}^{-1}$) than spores without tails which moved faster (0.43 to $1.76 \mu\text{m s}^{-1}$). Phylogenetic analysis of sequences of the small subunit of the nuclear-encoded rRNA and plastid-encoded ribulose biphosphate carboxylase/oxygenase genes revealed that *Purpureofilum* is a member of the Stylonematales and is most closely related to the filamentous genus *Bangiopsis*. *Bangiopsis* differs from *Purpureofilum* by having longer (to 5 mm) multiseriate filaments, cells containing a stellate chloroplast, a conspicuous central pyrenoid, and monospores formed in packets. Monospores of *Bangiopsis* were also motile. TEM investigation of *Purpureofilum* and *Bangiopsis* revealed that the Golgi complexes are associated only with rough endoplasmic reticulum and the plastid contains a peripheral thylakoid; this combination of features is the same as in all other multinucleate members of the Stylonematales. The low molecular weight carbohydrates of *Purpureofilum* and *Bangiopsis* were digeneaside and sorbitol, which were present in most other members of the Stylonematales.

68. Fabio Rindi²; Alison R. Sherwood^{*1}; Michael D. Guiry²

1. Botany, University of Hawaii, Honolulu, HI; 2. Botany, Martin Ryan Institute, National University of Ireland, Galway, Ireland

Diversity and distribution of *Trentepohlia* and *Printzina* (Trentepohliales, Chlorophyta) in the Hawaiian islands.

Members of *Trentepohlia* and *Printzina* are widespread subaerial algae. Although not uncommon in temperate areas, these genera are generally most diverse and abundant in tropical regions. To date, the information available on the taxonomy and distribution of these algae in the Hawaiian Islands is very scant, with only three taxa having been recorded. Visual inspections, however, revealed that *Trentepohlia* and *Printzina* are very common in the region; we investigated the taxonomy of these genera by examination of field collections over a period of a year and a half and culture observations. Eight taxa were recorded: *Printzina bosseae* var. *samoensis* (Wille) comb. nov., *P. effusa* (Krempelhuber) Thompson & Wujek, *P. lagenifera* (Hildebrandt) Thompson & Wujek, *Trentepohlia abietina* (Flotow) Hansgirg, *T. abietina* var. *tenue* (Zeller) Cribb, *T. arborum* (C. Agardh) Hariot, *T. cf. flava* (W.J. Hooker & Arnott) Cribb and *T. umbrina* (Kützing) Bornet. Two previously reported taxa, *T. cucullata* var. *sandvicensis* Wille and *T. diffracta* var. *sandvicensis* Wille, were not rediscovered. In the Hawaiian islands, *Trentepohlia* and *Printzina* are primarily corticolous algae; *T. abietina* and *T.*

arborum are the most common species, forming bright orange patches on the bark of a variety of tree species.

69. Tae O. Cho^{*1}; Suzanne Fredericq¹; Kim Yates²

1. Biology, University of Louisiana, Lafayette, LA; 2. U.S Geological Survey, Petersburg, FL

Towards the production of a photographic guide of macroalgal seagrass epiphytes in Tampa Bay, Florida.

Blooms of macroalgae growing as epiphytes on *Thalassia testudinum* and *Syringodium filiforme* potentially have important economic and ecological consequences in Tampa Bay, one of the Gulf of Mexico's largest estuaries. To monitor the impact of environmental stress, precise characterization of epiphyte diversity is required for efficient management of affected resources. A main goal of this ongoing study is the determination of epiphytes as indicator species for both healthy and stressed seagrass bed environments, and the production of photographic guide illustrating the overall habit and diagnostic features of each seagrass epiphyte. Checklists, descriptions of species, distributional records, and illustrations of the taxa collected will be made available to marine biologists, resource managers, scientific and recreational divers, and will form the foundation for a much needed modern taxonomic database electronically accessible on the WWW.

70. Tae O. Cho¹; Boo Y. Won^{*1}; Fred Gurgel¹; Suzanne Fredericq¹; Kim Yates²

1. Biology, University of Louisiana, Lafayette, LA; 2. U.S. Geological Survey, St. Petersburg, FL

Comparative DNA sequence analyses and morphological evidence reveal a diverse marine red algal flora in Tampa Bay, Florida.

Common macroalgal species reported from Tampa Bay include the red algae *Centroceras clavulatum* (Ceramiaceae, Ceramiales) which grow epiphytically on *Thalassia testudinum* and *Syringodium filiforme*, and the drift alga *Gracilaria tikvahiae* (Gracilariaceae, Gracilariales). Morphological and DNA sequence analysis of these species reveal that *C. clavulatum* reported from Tampa Bay comprises two species distinct from the type specimen described from Peru, and that three distinct species go under the name *G. tikvahiae*: *G. tikvahiae*, *G. secunda* and *G. venezuelensis*, with the latter two taxa newly recorded for Tampa Bay. The phylogenetic and biogeographic relationships of the marine flora in Tampa Bay are more diverse and complex than is generally appreciated.

71. Brian Wysor^{*}; Charles J. O'Kelly; Wendy K. Bellows; Jeffrey F. Brown

Bigelow Laboratory for Ocean Sciences, West Boothbay Harbor, ME

Evidence for polyphyly of *Ulothrix* and *Monostroma*, and other novel relationships in the Ulotrichales (Ulvophyceae).

Among the classic discoveries of the comparative ultrastructure phase of green algal systematic biology research was that species with an unbranched uniseriate filamentous morphology (genus *Ulothrix* sensu lato) form a complex assemblage with representatives of three of the five classes then recognized (*Ulothrix*, Ulvophyceae; *Uronema*, Chlorophyceae; *Klebsormidium*, "Charophyceae," now Klebsormidiophyceae). Species assigned to *Ulothrix* (Ulvophyceae) are known to be ultrastructurally heterogeneous, but the assignment to a single genus has not been questioned. Molecular phylogenetic investigations, however, indicate that *Ulothrix* (Ulvophyceae) remains polyphyletic within algae now placed in the order Ulotrichales, and that ultrastructural features, especially pyrenoid ultrastructure, are partially correlated with molecular signatures. To date, it is known that marine species of *Ulothrix* characterized by an entire pyrenoid matrix (not traversed by thylakoid membranes or cytoplasmic channels) are closely related to species of *Urospora* and *Acrosiphonia*, while the predominantly freshwater species *U. zonata*, characterized by pyrenoids traversed by thylakoids, is most closely related to microfilamentous species now placed in the genera *Chamaetrichon*, *Pseudendoctonium* and *Trichosarcina*. A similar situation exists for the genus *Monostroma*. *Monostroma undulatum* (or *Protomonostroma undulatum*), with entire pyrenoids, is closely related to *Ulothrix* species with entire pyrenoids, and with them belongs in the *Acrosiphonia* clade of Ulotrichales. *Monostroma grevillei*, with pyrenoids traversed by thylakoids, is most closely related to species now placed in the genera *Collinsiella*, *Gomontia* and *Eugomontia*, none of which have *Monostroma*-like gametophyte morphology. Neither *M. grevillei* nor *M. undulatum* appears to be closely related to *M. oxyspermum* (*Gayralia oxysperma*) or to species of *Capsosiphon*, sometimes included within *Monostroma*.

72. Juan M. Lopez-Bautista^{*1}; Todd W. Tragemann¹; Sarah M. Noble¹; Diana Sturm²

1. Biological Sciences, The University of Alabama, Tuscaloosa, AL; 2. Mobile Bay National Estuary Program, Mobile, AL

A Preliminary Account Of The Seaweeds Of Alabama, North Central Gulf Of Mexico.

The benthic marine algae from the Gulf of Mexico have been of great interest to phycologists since 1800s; however, reports of algae from the Alabama coast in the North Central Gulf of Mexico are lacking. To provide a preliminary account of the seaweeds of Alabama, benthic marine algae are being collected along several diverse locations and

habitats: rocky substrates, jetties, piers, sandy areas, mud flats, and marshes as well as gas/oil rigs. Protocols for morphological analyses, photodocumentation, and archiving specimens, as well as gene sequencing (when necessary) are being developed at the UA laboratory. Taxa of the green, brown, red and blue-green algal groups are represented in the Alabamian flora, and the number of identified taxa is constantly increasing. This algal flora is known to occur in other parts of the Gulf of Mexico and has a biogeographic affinity with tropical and subtropical regions, in particular with the Caribbean. Data from this study is updated and made public through our website the PHYCOLAB (<http://bama.ua.edu/~jlopez/>). This research is supported with a grant to JMLB from the Mississippi-Alabama SEAGRANT.

73. John D. Hall^{*1}; Richard McCourt²; Charles Delwiche¹

1. Cell Biology and Molecular Genetics, University of Maryland, College Park, MD; 2. Botany Department, The Academy of Natural Sciences, Philadelphia, PA

Classification of the Gonatozygaceae and its relation to *Roya* spp.

The family Gonatozygaceae (Desmidiaceae) is key to understanding evolution of form and complex ultrastructure within the desmids. This family is currently recognized to include the genera *Gonatozygon* and *Genicularia*. Placement of these genera within the Zygnematophyceae has been contested for nearly one hundred years. Molecular studies indicate that the genera *Gonatozygon* and *Genicularia* are very closely related and that *Genicularia spirotaenia* may have evolved from an ancestor within *Gonatozygon*. Molecular data also suggest a relationship between the Gonatozygaceae *sensu* Mix and *Roya* spp. *Roya* is morphologically similar to *Gonatozygon* except that it is reported to lack pores completely, resulting in its current classification within the Zygnematales. Field isolates of organisms that are morphologically similar to *Gonatozygon* and *Roya* may indicate that the genera are poorly defined and that it is more difficult to confidently identify these species than indicated in the literature. Current molecular data suggest that the genera and family require revision.

74. Susan Carty^{*}

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Species groups in *Peridinium* I. The Umbonatum Group.

Peridinium was erected in 1830 by Ehrenberg for thecate dinoflagellates lacking an eyespot. Many species have been removed from *Peridinium* into their own genera. *Peridinium* still contains nine groups of species with morphological characteristics different than the type species, *Peridinium cinctum*. *Peridinium cinctum* is large, heavily thecate, lacks an apical pore, has three apical intercalary plates in an asymmetrical arrangement, five cingular plates, and five sulcal plates. The Umbonatum Group, which contains *P. umbonatum*, *P. africanum*, *P. belizensis*, *P. centenniale*, *P. deflandrei*, *P. goslaviense*, *P. inconspicuum*, *P. lubieniense*, *P. morzinense*, and *P. pusillum*, are small cells, lightly thecate, have apical pores, two apical intercalary plates in plastic positions, six cingular plates and five sulcal plates unlike those in *P. cinctum*. Several of the groups in *Peridinium* warrant their own genus.

75. Julie A. Buchheim^{*1}; Andrea Kirkwood²; William Henley²; Mark A. Buchheim¹

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

Broad Diversity of *Dunaliella* at the Salt Plains National Wildlife Refuge (OK, USA): Inferences from Nuclear-Encoded rDNA Data.

Recent studies of *Dunaliella* phylogeny (Gomez and Gonzales 2004) using data from the two transcribed spacer regions of the nuclear rDNA array revealed substantial diversity among geographically distinct isolates of the β -carotene producer, *D. salina*. These data were used to provide a comparative context for an assessment of *Dunaliella* diversity from the Microbial Observatory at the Salt Plains National Wildlife Refuge, OK USA (SPMO). All SPMO *Dunaliella* spp. were isolated from three sampling sites within a 65 km² salt flat that can vary in salinity from near 0% (following heavy rains) to supersaturation. Pairwise comparisons of uncorrected p values indicated a range of 0.000 to 0.100 distances (ITS-1 and ITS-2) among the geographically diverse *D. salina* isolates. In contrast, the SPMO isolates exhibited a distance coefficient range that exceeded 0.113. Pairwise comparisons of 18S (ca. 1700 bases) and 26S (ca. 2100 bases) rDNA data from SPMO isolates and from *Dunaliella* isolates obtained from national culture collections also indicated higher levels of diversity among SPMO isolates. Moreover, phylogenetic analysis of data from the 18S and 26S rDNA genes strongly supports the existence of exclusive SPMO clades of *Dunaliella*. These observations raise several questions for further investigation. Is *Dunaliella* diversity at SPMO an example of microbial endemism? What role does the environment play in driving and/or sustaining the diversity of *Dunaliella* at SPMO? Supported by NSF DEB 0129030, MCB 0132083 and MCB 0132097.

76. Mariah Veit¹; Julie A. Buchheim¹; Richard Portman¹; Karen Fawley²; Marvin Fawley²; Mark A. Buchheim^{*1}

1. *Biological Science, The University of Tulsa, Tulsa, OK*; 2. *Biological Sciences, North Dakota State University, Fargo, ND*

Diversity of Chlamydomonadalean Algae at Itasca State Park.

Given the assumption of an absence of geographic barriers and broad habitat tolerances, some have argued that species-level diversity among the freshwater microalgae is comparatively low. Much of this perception can be attributed to a morphological species concept that may be underestimating microalgal diversity. A project to begin addressing these problems was initiated in which morphological and molecular evidence were collected from chlamydomonads isolated from different freshwater sites at Itasca State Park (MN, USA). To date, more than 80 18S rDNA sequences from Itasca unknowns have been characterized. Ultrastructural investigations of comparative pyrenoid architecture from more than 40 of these Itasca isolates also have been completed using transmission electron microscopy. Results from this study revealed substantial molecular (70 new 18S rDNA phylotypes) and ultrastructural diversity among the Itasca isolates. This profound diversity in the highly conserved 18S rDNA gene is difficult to reconcile with expectations of low species diversity; an assumption based on the notion that the Itasca sites are **not** extreme, unique, or isolated. Questions for further examination include: (1) How much more diversity remains to be discovered at Itasca (the data presented here are based on four samplings from a single year) and (2) Do unique microalgal floras exist in other freshwater systems, is Itasca unusual in its extensive diversity, or are the myriad of chlamydomonad inhabitants of Itasca also to be found elsewhere? Supported by NSF DEB 0129030 & 0128952, MCB 0132083 & 0084188, EPS 0132289, DBI 0070387 & 0139653.

77. Morgan L. Vis^{*1}; Wayne B. Chiasson¹; Robert G. Sheath²

1. *Env. & Plant Biology, Ohio University, Athens, OH*; 2. *Office of the Provost, California State University San Marcos, San Marcos, CA*

Phylogenetic affinities of *Batrachospermum* specimens from French Guiana.

Eighteen *Batrachospermum* gametophytes and nine chantransia isolates from streams in French Guiana, were analyzed using RUBISCO large subunit (*rbcL*) gene sequence data to assess phylogenetic placement and evaluate intraspecific sequence variation. The gametophytes represented eight species as follows: *B. ambiguum* (2 specimens), *B. gracillimum*, *B. guyanense*, *B. intortum* and *B. nodiflorum* (2 specimens), from section *Contorta*, *B. macrosporum* (6 specimens) and *B. cayennense* (3 specimens), from section *Aristata* and *B. turfosum* (2 specimens) from section *Turfosa*. One of the chantransia isolates fit the morphological description of "chantransia pygmaea." The other eight isolates were within the circumscription of "chantransia macrospora." The phylogenetic analyses showed the species from section *Contorta* were in a well-supported clade with previously sequenced taxa of that section. Specimens of *B. macrosporum* and *B. cayennense* were sister to each other. *B. turfosum* is the only species presently sequenced from section *Turfosa* and these specimens formed a well-supported clade on a long branch. Three of the species, *B. ambiguum*, *B. cayennense* and *B. macrosporum*, showed little to no variation within species for the French Guiana specimens, but varied considerable from previously published sequence data from other continents. In contrast, the *B. turfosum* samples differ little from a North American specimen. Sequence data confirmed that the "chantransia pygmaea" isolate was *B. ambiguum* and the "macrospora" isolates were *B. macrosporum*. There appears to be sufficient evidence from this and other studies that field-collected chantransia with the "macrospora" morphology are *B. macrosporum*, but whether the "pygmaea" morphology always represents *B. ambiguum* needs further research. The *B. macrosporum* chantransia was in numerous streams in which no gametophytes of this taxon were collected, but gametophytes of other *Batrachospermum* species were present. There was sequence variation among the *B. macrosporum* chantransia isolates and between a chantransia and gametophyte from the same stream segment, possibly suggesting that the diploid chantransia may serve as a repository for genetic variation.

78. Maria A. Nudelman^{*}; Richard E. Triemer

Plant Biology, Michigan State University, East Lansing, MI

Phylogeny and Taxonomic Revision of the Loricates *Trachelomonas* and *Strombomonas* (Euglenophyta) based on SSU rDNA and ultrastructure.

Previous studies using molecular data have revealed that the loricates are monophyletic, but the relationship between the genera *Trachelomonas* and *Strombomonas* as independent lineages remained unsolved. Recently, Marin et al. (2003) transferred the genus *Strombomonas* back into *Trachelomonas* based on a study of fourteen sequences, only two of which were from *Strombomonas* species. In our study we compared SSU rDNA sequences from thirty strains of *Trachelomonas* and ten strains of *Strombomonas*. Maximum likelihood and Bayesian analyses recovered two strongly supported monophyletic groups supporting the retention of two independent genera. The clade containing taxa belonging to the genus *Colacium*, was sister to both loricate clades. This genus also produce mucilage that is retained on the surface of the cell to build a stalk and sheath, but does not form a lorica. Within the genus *Trachelomonas* the sequence divergence

among the species ranged from 2 to 29% while the intergeneric divergence between both loricate genera was less than 25%. Five strongly supported subclades were recovered within the *Trachelomonas*. These are natural groups based on sequence divergence and lorica morphology. However, some taxa that are very similar in morphology showed high sequence divergence, suggesting a convergence of developmental stages of different species. Morphological features such as ornamentation and shape of the lorica have been traditionally used in *Trachelomonas* classification and this study confirms its validity as key taxonomic criteria. Conversely, *Strombomonas* species exhibited a high degree of morphological diversity, with little sequence divergence (6 to 14%), indicating that some taxa might be morphotypes. In summary, our results demonstrate the influence of taxon sampling, reinforce the importance of conducting studies in culture to assess the range of plasticity of key morphological characters and strongly confirm that *Trachelomonas* and *Strombomonas* are two clearly distinct genera and should be retained as different entities.

79. WITHDRAWN

80. Richard M. McCourt^{*1}; Kathleen Sprouffske²; Daniel Mellott²; Chamira Ratnayaka²

1. Botany, Academy of Natural Sciences of Philadelphia, Philadelphia, PA; 2. Patrick Center for Environmental Research, Academy of Natural Sciences of Philadelphia, Philadelphia, PA

Online Algae Discussion and Identification.

Identifying algae can often be daunting and difficult, even for experts in particular groups. We have developed an experimental, informal, and collaborative online facility for image submission, display, grouping, and comment that can be used by students, researchers, and the public to help them identify algae. The purpose is to provide a resource for people with algal images who would like to post them on the web and get help with identification as well as provide a space for taxonomic documentation and naming discussions. Visitors can use a web browser to submit image files for posting to the web site. A minimal amount of data is also provided with the image, such as collection date, locality, and submitter. The user may have more data on the algae in the image, but to streamline the site and encourage use, these data are not required or requested. URLs given by the user may provide links to other data and websites. The image is posted along with the associated data, and a comment box allows site visitors to offer opinions on identity or other aspects of the alga in question. Users may browse the images and associated data using queries based on taxonomic terms or other data provided by the submitter. This poster provides an outline of the database design and examples of the website interface.

81. Mark W. Vandersea^{*1}; Mellisa A. West¹; Steven R. Kibler¹; Maria A. Faust²; R. W. Litaker¹; Patricia A. Tester¹

1. Center for Coastal Fisheries Habitat Research, NOS / NOAA, Beaufort, NC; 2. Department of Botany, National Museum of Natural History, Smithsonian Institution, Suitland, MD

Phylogenetic relationship of *Coolia tropicalis* and *Prorocentrum* species isolated from Belizean barrier reef and oceanic mangrove systems relative to other dinoflagellates.

The mangrove islands of the south central lagoon of the Belizean Barrier Reef contain a large diversity of tropical dinoflagellate species. Sediment samples and samples of floating detritus were collected from Carrie Bow Cay, South Water Cay and Twin Cays, Belize (May, 2003) as part of ongoing field surveys that explore the dinoflagellate ecology and natural nutrient enrichment that occurs within these isolated barrier reef cays. Clonal cultures of *Coolia tropicalis* and two *Prorocentrum* species were established from these samples. Genomic DNA was extracted from each isolate and PCR-amplified using ribosomal DNA specific primers. The resulting SSU, ITS1, 5.8S, ITS2 and 5' LSU sequences were aligned with a representative sample of related dinoflagellate species using the CLUSTAL-W program. A maximum likelihood phylogenetic analysis of the aligned sequences was performed using the MrBayes 3.0 program. The resulting phylogenetic tree indicated that *Coolia tropicalis* was most closely related to *Alexandrium* species, consistent with similarities in Kofoidian plate tabulation of these two genera. The phylogenetic analysis also showed that the *Prorocentrum* species grouped into two distinct clades, suggesting this genus is polyphyletic. Based on ribosomal DNA sequence data, the *Prorocentrum* isolates appeared to be unique and may represent new species. Further SEM analysis will confirm the phylogenetic status of these isolates.

82. Joni L. Johnson; Karen P. Fawley^{*}; Marvin W. Fawley

North Dakota State University, Fargo, ND

A comparison of ITS sequences and cell wall structure of *Scenedesmus* and *Desmodesmus*.

Delineating species of the green algae genera *Scenedesmus* and *Desmodesmus* is difficult due to the presence of phenotypic plasticity. Morphological characters identified with light microscopy, such as cell shape and size, and spine length, were previously used to define species. However, several studies have shown that these characters are not stable. Thirty-seven isolates of *Scenedesmus* and *Desmodesmus* from lakes and ponds in Itasca State Park, Minnesota, USA were characterized by light microscopy and sequence analysis of the ribosomal internal transcribed spacer region (ITS). The

sequence analysis revealed a high level of diversity. Several of these isolates were found to have little or no difference in morphology, but possessed differences in ITS sequences. Scanning electron microscopy (SEM) was used to compare the morphologies of closely related types. SEM has been shown to distinguish cell wall ultrastructural features not visible with light microscopy.

83. Julie Buchheim^{*1}; Andrea Kirkwood²; William Henley²; Mark Buchheim¹

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

Diversity of Microalgae and Cyanobacteria at the Salt Plains National Wildlife Refuge (OK, USA).

The Salt Plains Microbial Observatory (SPMO) is located at the 65 km² Salt Plains National Wildlife Refuge. The SPMO study site is a terrestrial, hypersaline microbial community that experiences wide-ranging environmental conditions. One focus of research at SPMO has been a study of the resident photosynthetic microorganisms that include Cyanobacteria, Bacillariophyta and Chlorophyta. Conventional culture techniques and a range of salinities were used to isolate and characterize SPMO strains. The majority of organisms isolated at 1% salinity were filamentous cyanobacteria, whereas 5% salinity favored pennate diatoms. The majority of organisms isolated at $\geq 10\%$ salinity were attributed to the genus *Dunaliella*. Phylogenetic analyses of ribosomal data (16S and 18S rDNA) revealed extensive diversity among SPMO isolates in each of the three major groups, Cyanobacteria, Bacillariophyta and Chlorophyta. Although data from the 16S rRNA gene (ca. 700 bp) indicated that SPMO Cyanobacteria form a taxonomically diverse assemblage, a plurality of isolates are allies of *Geitlerinema* sp. Analysis of 18S rDNA data (ca. 1700 bp) indicated that a majority of SPMO diatom isolates form three large clades that are part of a broader *Amphora* alliance. Finally, analysis of 18S rDNA data indicated a relative paucity of green algal genera (*Dunaliella*, *Asteromonas*, *Chlamydomonas* sp. and *Tetraselmis*) at SPMO, but reveal a richness of diversity among isolates of *Dunaliella*. The results to date have revealed limited diversity at higher taxonomic levels within the green algae and diatoms, but extensive variability within at least some genera and species. Supported by NSF DEB 0129030, MCB 0132083 and MCB 0132097.

84. Lubomir Kovacik^{*1}; Dale A. Casamatta²; Jeffrey R. Johansen²

1. *Department of Botany, Comenius University, Bratislava, Slovakia*; 2. *Department of Biology, John Carroll University, University Heights, OH*

A new and distinctive *Leptolyngbya* species from aerial habitats in the Czech Republic.

A new *Leptolyngbya* taxon was isolated from tree bark in Trebon, Czech Republic. It differs from all other *Leptolyngbya* currently described by the distinctive formation of heteropolar trichomes. The trichomes have a swollen, non-growing base which forms at both poles of the trichome, with growth and fragmentation in the center of the trichome to produce the heteropolar trichomes. Analysis of the gene sequence of the ribosomal SSU revealed high sequence similarity to a clade of *Leptolyngbya* containing the type species of the genus, *L. boryana*. Phylogenies were constructed using parsimony, distance, and maximum likelihood, and all analyses placed our new taxon in the aquatic members of *Leptolyngbya* containing peripheral thylakoids peripheral along outside walls and crosswalls.

85. Hilary A. McManus^{*}; Louise A. Lewis

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

Phenotypic plasticity, molecules and species boundaries in *Pediastrum* Meyen 1829.

A phylogeny constructed from a multiple gene phylogenetic analysis of members of the freshwater green algal family Hydrodictyaceae (Sphaeropleales, Chlorophyceae), including both culture collection and wild isolates, sets the stage to explore morphological and genetic variation within the family and test species boundaries in the genus *Pediastrum*. Phylogenetic results indicate *Pediastrum* is not monophyletic and *Sorastrum* and *Hydrodictyon* each form individual monophyletic clades nested within *Pediastrum*. Using the phylogeny as a framework to study the morphological variation, it is apparent that some strains of *Pediastrum* do not conform to the morphological classification scheme that is currently in use. Specifically, some geographically separated strains with similar phenotypes are genetically distinct, and some taxa with striking morphological differences form distinct clades. Experiments are underway that test for phenotypic plasticity. These tests offer insight to what characteristics may be stable and taxonomically informative, as well as the influence of particular environmental factors on morphology.

86. Charles J. O'Kelly^{*}; Brian Wysor; Wendy K. Bellows; Jeffrey F. Brown

Bigelow Laboratory for Ocean Sciences, West Boothbay Harbor, ME

Marine microfilamentous green algae: new lineages in the Ulotrichales/Ulvales complex (Ulvophyceae).

Microfilamentous green algae, once known as the "marine Chaetophoraceae," are common in marine habitats worldwide, but their taxonomic diversity and phylogenetic relationships have been poorly understood. Phylogenetic analyses of

nuclear- and chloroplast-encoded gene sequences, coupled with light and electron microscopic investigation of algae in culture and from field-collected samples, reveal six distinct lineages of microfilamentous green algae within Ulvophyceae. These are: Gomontiaceae (Ulotrichales), and Kornmanniaceae, Ulvellaceae, the *Bolbocoleon* lineage, the *Phaeophila* lineage, the *Ctenocladus/Acroblaste* lineage, and the *Ochlochaete/Ruthnielsenia* lineage (Ulvaes). The latter two lineages are newly discovered, and the circumscriptions of Gomontiaceae, Kornmanniaceae, and Ulvellaceae are significantly revised. Microfilamentous green algae contain the only species known in the Ulvophyceae, apart from the Trentepohliales, to have plugged perforate septa or plasmodesmata. Phylogenetic analyses indicate that such septa have evolved three times. *Smithsoniella* (perforate septa) and *Sporocladopsis* (plasmodesmata) are phylogenetically distinct genera of Ulvellaceae. *Ctenocladus* and *Acroblaste* also have perforate septa, which are distinct from those of *Smithsoniella*, but these genera form a distinct lineage, separate from the Ulvellaceae. Phylogenetic distances among most microfilamentous green algae are relatively small for the markers used. Exceptions are found among the species of Kornmanniaceae and in the *Phaeophila* lineage. The sharp distinction in ultrastructural, reproductive, and life history characters between species assigned to Ulotrichales and to Ulvaes is not reflected in the molecular phylogenies, many of which tend to place Ulvaes within Ulotrichales, with coccoidal Ulotrichales as stem taxa. Taxon sampling, and unequal rates of sequence evolution, may be contributing to this result.

87. J. C. Hodge^{*1}; Orlando Necchi²; Morgan L. Vis¹

1. *Env. & Plant Biology, Ohio University, Athens, OH*; 2. *Depto. Zoologia e Botanica, UNESP Campos de Sao Jose do Rio Preto, Sao Jose do Rio Preto, Brazil*

Phylogeography of *Batrachospermum macrosporum* (Batrachospermales, Rhodophyta) in North and South America.

Phylogeographic trends among populations of the freshwater red alga, *Batrachospermum macrosporum*, were investigated utilizing a mitochondrial DNA region. This DNA segment consisted of the intergenic spacer between the cytochrome oxidase subunit 2 and cytochrome oxidase subunit 3 genes with the flanking gene regions (cox2-3). Six stream segments throughout the range of this taxon in North and South America were sampled as followed: 3 in Mississippi, USA, 1 in North Carolina, USA, 1 in southeastern Brazil and 1 in French Guiana. Fifteen thalli per stream reach were analyzed except for French Guiana in which 8 individuals were studied. Among the 83 individuals sequenced eight haplotypes were detected. Populations Mississippi 1 and North Carolina each had three haplotypes and all other populations had only one haplotype. One haplotype was shared among the three Mississippi populations, but the other seven haplotypes were unique to a particular stream segment. All the North American haplotypes were closely related (1-5 bp), but the two South American populations differed substantially (31 bp). These relationships were also evident in the phylogenetic analyses. These results may be due to the close geographic proximity of the North American populations in comparison to the more geographically distant South American population.

88. Marvin W. Fawley^{*}; Karen P. Fawley

Biological Sciences, North Dakota State University, Fargo, ND

The challenge of green algal diversity.

Current concepts of the systematics of the Chlorophyta imply low diversity at all taxonomic levels. This perception is apparently derived from the idea that green algae are not as important and interesting as other groups of organisms. However, the green algae have long been considered diverse in such fundamental characteristics as photosynthetic pigments, life history, and cellular structure. We will present evidence that the diversity of the green algae should be reassessed. Analyses of (primarily) 18S rDNA sequences indicate that more molecular diversity exists among the green algae than land plants. The numerous cytological and life history differences among lineages of green algae in combination with molecular results suggest that a taxonomic system with new classes, orders, and families should be considered. Studies of more rapidly evolving gene regions, such as the ribosomal ITS region and the *rbcL* gene, indicate that we have also grossly underestimated green algal diversity at the genus and species levels. Specifically, for many groups of microscopic green algae, identification to species or even genus level by light microscopy is nearly (if not totally) impossible at the present time. Our results imply that a significant new effort must be expended if we are to gain an understanding of the actual diversity of the green algae and establish a natural classification system that reflects this diversity. Moreover, this effort is important for understanding the true species-level ecology of these organisms. This material is based upon work supported by the National Science Foundation under Grant Nos. DEB-0128952, DBI-0070387 and MCB-0084188

89. Louise A. Lewis^{*1}; Shin Watanabe²

1. *Ecology and Evolutionary Biology, University of Connecticut, Storrs, CT*; 2. *Laboratory of Biology, Department of*

Education, Toyama University, Toyama, Japan

An evaluation of the phylogenetic signal present in morphological data across chlorophycean green algae.

Molecular systematics has had a dramatic impact on our interpretation of the evolution of green algae and on our concepts of diversity. Although phylogenetic analyses of molecular sequence data have helped to uncover relationships among members of the Chlorophyceae, some of the groups that are expected based on morphological or ultrastructural information are poorly supported. For example, in many published molecular analyses the support for a monophyletic Sphaeropleales is often weak or absent. Is this apparent conflict real, perhaps representing cases of non-homology in morphological data, or does the conflict result from a lack of signal in the molecular data? In order to address this question, we present a data set consisting of published and new discrete morphological/ultrastructural characters and DNA sequence data from two genes for a total of 34 ingroup taxa. These data are analyzed individually and in combination under both parsimony and Bayesian frameworks. We contrast the resulting trees and support values for key "expected" nodes, and find that morphology does provide support for certain nodes that are poorly supported in the molecular analysis. In addition, these data are also used to reconstruct ancestral character states of some ultrastructural characters. Lastly, we discuss the role of diversity studies in helping to target new ultrastructural studies.

90. Mark A. Buchheim* ; Julie A. Buchheim

Biological Science, The University of Tulsa, Tulsa, OK

Chlamydomonadalean Diversity and Phylogeny.

Although the Mattox and Stewart (1984) scheme was grounded in a large volume of structural data that included numerous investigations of chlamydomonad flagellar architecture, it would have been difficult to predict, on the basis of their phylogenetic framework, the extent of variation that has been uncovered by molecular methods. Phylogenetic schemes, based largely on 18S rDNA evidence, have revealed multiple lineages with deep divergences that are equivalent (in terms of nucleotide distance values) to ordinal, class and division-level divergences among vascular plants. These hypotheses are now being tested using additional rDNA markers (26S, 5.8S and ITS) and chloroplast (*atpB* and *rbcL*) genes. The earliest molecular investigations clearly demonstrated non-monophyly of a myriad of taxa assigned to the genus *Chlamydomonas*. More recent investigations clearly demonstrated that *Haematococcus* and *Chlorococcum* are polyphyletic chlamydomonad genera as currently circumscribed. Similarly, molecular approaches have challenged the status of at least one well known species--numerous varieties of *Chlamydomonas moewusii* fail the test of monophyly using 18S and 26S rDNA data. While molecular studies of named isolates have confronted the traditional chlamydomonad taxonomy, diversity studies that have revealed substantial diversity among a broad spectrum of unnamed chlamydomonads also raise questions about the role of morphology, the nature of species, and the meaning of diversity. Supported by NSF DEB 9726588, DEB 0129030 and MCB 0132083.

91. Thomas Friedl* ; Dominik Hepperle

Experimental Phycology and SAG, University of Goettingen, Goettingen, Germany

What are Trebouxiophyceae?

About 20 years ago a group of no more than five genera was found to exhibit unique differences in cell division and that these correlate with major differences in the structure of the flagellar apparatus. Consequently, the group was assumed to represent a distinct line of evolution and was taxonomically treated as the class Pleurastrorphyceae by Mattox & Stewart. Later phylogenetic analyses of 18S rRNA genes provided an independent set of characters for testing phylogenetic hypotheses and supported the distinctness of the group which has been renamed into Trebouxiophyceae due to an expanded knowledge. Phylogenetic analyses show the class as one major lineage in the almost immediate radiation within the Chlorophyta. Although its monophyletic origin is not always resolved, there is consensus that it is a sister-group with the Chlorophyceae and rather distinct from the Ulvophyceae. Presently it is impossible to define the Trebouxiophyceae other than by rDNA phylogenies; only for a very small fraction of its members ultrastructural characters are available. Today, more than 250 rDNA sequences are available from green algae that represent the class. They cover quite a variety of different morphologies, but coccoid or pseudofilamentous forms from terrestrial or specifically subaerial habitats are dominant. Recent phylogenetic analyses revealed an unexpected diversity of desiccation-tolerant trebouxiophytes in green biofilms on man-made substrates where only very few morphotypes were visible. Most green lichen symbionts are within the class and exhibit multiple origins there. Other trebouxiophytes are members of the picoplankton, may even be colourless with a parasitic life style or form macroscopically large thalli on marine coasts. In rDNA phylogenies the class is divided into several lineages and clades whose monophyletic origins are well supported, but relationships among these are ambiguous. Morphologically quite different algae may be united in one clade demonstrating that vegetative morphology is useless in the prediction of phylogenetic relationships. Autosporic coccoid green algae (e.g. *Chlorella*) are dispersed over various lineages indicating many putative losses of flagellated stages within the class.

92. Frederick Zechman*

Department of Biology, California State University, Fresno, Fresno, CA

Phylogeny of the Ulvophyceae green algae: Morphological and molecular evolution of siphonous and hemisiphonous lineages.

The class Ulvophyceae is a diverse assemblage of predominantly marine green algae originally defined on the basis of ultrastructural characteristics of mitosis, cytokinesis and flagellar apparatus. Defining features include (but are not limited to) a persistent interzonal spindle, absence of phycoplast and phragmoplast microtubules and counter-clockwise orientation of the flagellar apparatus. Although this suite of traits represents a unique combination of characters, none of these individual features represent clear synapomorphies to support monophyly of the Ulvophyceae. Early molecular phylogenetic studies based on 18S ribosomal RNA sequences, indeed, did not support monophyly of the Ulvophyceae (e.g., Zechman et al. 1990). These studies, however, suffered from limited taxon and character sampling and weak or unresolved nodal support. Current investigations based on broader taxon sampling and additional nuclear and chloroplast gene sequences (18S rDNA, 26S rDNA, atpB and rbcL) are being conducted to resolve phylogenetic relationships among the Ulvophyceae. To date, particular attention has been directed toward resolving relationships among siphonous and hemisiphonous orders assigned to the Ulvophyceae. Preliminary results indicated that the orders Caulerpales, Dasycladales, Cladophorales and Trentepohliales form a monophyletic group that generally excludes the ulotrichalean and ulvalean ulvophytes. The siphonous orders Caulerpales and Dasycladales are derived sister taxa, and in turn sister to the hemisiphonous order Cladophorales. The Trentepohliales was inferred to be the most basal lineage of the siphonous and hemisiphonous ulvophyceae clade. Specific relationships among and within these orders will be discussed in the context of molecular and morphological character evolution. Supported in part by NSF grant DEB-0128977 to FWZ.

93. Charles J. O'Kelly*

Bigelow Laboratory for Ocean Sciences, West Boothbay Harbor, ME

The Ulvophyceae: history, novel diversity and phylogenetic issues, with special reference to the orders Ulotrichales and Ulvales.

Of all the class-level taxa included in Mattox and Stewart's 1984 green algal classification system, the Ulvophyceae (originally, "Ulvophyceae") is the most problematic. The class contains much of the morphological, reproductive and life history diversity in green algae, and contains most of the marine species. Three ultrastructural characters defined it: counterclockwise absolute orientation of flagellar apparatus components, the absence of a phycoplast at cytokinesis, and the absence of a metacentric mitotic spindle. However, the first character is regarded as ancestral for green algae, and the second is inaccurate or (in the case of siphonous species) not relevant. Ulvophyceae algae are distinct from other Chlorophyta in gene sequence trees, but four of the seven included orders (Trentepohliales, Cladophorales, Dasycladales, Caulerpales) are separated from each other and from other greens by long evolutionary distances. Analyses of these sequences have suggested that Ulvophyceae sensu Mattox and Stewart is not monophyletic. This problem of interpretation is made worse by inadequate taxon sampling especially among the microscopic representatives of Ulvophyceae. New research has attempted to address this challenge. Ultrastructural and molecular investigations of several previously-unstudied microscopic Ulvophyceae have revealed the existence of several new lineages. These investigations may be telling us that the class is in fact monophyletic, with certain of its members exhibiting accelerated sequence evolution but constrained morphological evolution, and vice versa.

94. Juan M. Lopez-Bautista^{*1}; Russell L. Chapman^{2,3}; Fabio Rindi⁴; Michael D. Guiry⁴

1. Biological Sciences, The University of Alabama, Tuscaloosa, AL; 2. Department of Biological Sciences, Louisiana State University, Baton Rouge, LA; 3. Department of Oceanography and Coastal Sciences, Louisiana State University, Baton Rouge, LA; 4. Department of Botany, Martin Ryan Institute, Galway, Ireland

Phylogeny Of The Trentepohliaceae (Chlorophyta; Ulvophyceae).

The order Trentepohliales contains only subareal taxa. The representatives of this group, which has only the single family Trentepohliaceae, are mainly tropical and subtropical with a few species found in temperate climates. Results of our current phylogenetic studies have positioned this group inside the class Ulvophyceae and resolved the Trentepohliaceae as a monophyletic clade. Results of our ongoing evaluation of the genera Trentepohlia, Phycopeltis, Cephaleuros, and Stromatochroom, using the nuclear-encoded 18 SSU rDNA and the chloroplast-encoded rbcL genetic markers, challenge the classical taxonomic treatment of the genera. Morphological characters such as life-history and the position of the sporangiate lateral are recognized as important phylogenetic markers. Filament association (free, coalescent, discoid type) is a morphological character scattered among the lineages. Although Cephaleuros is a well-supported monophyletic genus, its most common species, *C. virescens*, with a worldwide distribution, may encompass a number of cryptic taxa.

This research is being funded by a grant from The University of Alabama.

95. Monique Turmel^{*}; Patrick Charlebois; Jean-Charles de Cambiaire; Jules Gagnon; Christian Otis; Jean-Francois Pombert; Claude Lemieux

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A chloroplast genome sequencing program to unravel phylogenetic relationships among chlorophytes.

Green plants are divided into the phyla Streptophyta and Chlorophyta. The Streptophyta comprises all land plants and the green algae belonging to the class Charophyceae, whereas the Chlorophyta comprises virtually all of the other green algae, *i.e.* the members of the classes Prasinophyceae, Ulvophyceae, Trebouxiophyceae and Chlorophyceae. A subgroup of green algae belonging to the Prasinophyceae (a non-monophyletic class) is known to represent the earliest divergence of the Chlorophyta, but the branching order of more advanced prasinophytes, of the Ulvophyceae, Trebouxiophyceae and Chlorophyceae remains uncertain. Although nuclear small subunit ribosomal RNA gene sequences are available for well over 100 chlorophyte taxa spanning various lineages, the phylogenies inferred from these sequences have been unable to resolve interclass relationships as well as relationships among a number of clades belonging to the same class. In an attempt to resolve some of these phylogenetic problems and also to understand the evolution of chloroplast DNA within the Chlorophyta, we have undertaken a few years ago an organelle genome sequencing program that aims at determining the complete nucleotide sequences of chloroplast and mitochondrial DNAs from representatives of the various chlorophyte classes. To date, we have completed the chloroplast genome sequences of 10 chlorophytes, which brings to 12 the total number of sequenced chlorophyte chloroplast genomes. We will present our phylogenetic analyses of the concatenated protein sequences encoded by the 51 genes common to these chloroplast genomes along with our structural genome analyses. Our results have provided new insights into chlorophyte relationships; however, they have not allowed us to identify in an unambiguous manner the divergence order of the Ulvophyceae, Trebouxiophyceae, and Chlorophyceae. Although the chloroplast genome was found to be highly fluid in its overall structure, gene content, gene organization and intron composition, even within members of the same clade, distinctive architectural features were observed for each class. (Supported by NSERC)

96. Patricia A. Tester^{*1}; Steven R. Kibler¹; Mark W. Vandersea¹; R. W. Litaker¹; Maria A. Faust²

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High Phytoplankton Productivity in a Mangrove Embayment, Belize, Central America.

Belize is home to the largest barrier reef in the western hemisphere. The reef complex is bounded by the azure Caribbean Sea and encloses a wide (10-40 km) central lagoon characterized by patch reefs and small mangrove islands. Much to our surprise some of the mangrove islands with shallow embayments have rich phytoplankton communities. A unique combination of island morphology, wind sheltering and low tidal amplitude favors accumulation of material and limits flushing in these embayments. Typically, these sheltered mangrove embayments are less than 3 meters deep with a shallow sill, which limits exchange with surrounding waters. Our study focused on a shallow, productive mangrove embayment at Peter Douglas Cay off south central Belize. At Douglas Cay the chlorophyll a concentrations were 20 fold higher than in the surrounding oligotrophic lagoon. In a study to examine the productivity of this mangrove embayment, a YSI Sonde 660 was moored for periods up to seven days to record chlorophyll fluorescence, salinity, temperature, PAR and oxygen every five minutes. In addition wind speed and direction and rain fall were recorded at a nearby location (Carrie Bow Cay). During a period of low rain fall and high, consistent winds a very regular daily cycle of productivity, indicated by chlorophyll a and oxygen production, was noted. Daytime oxygen saturation varied between 20 and 40 percent and was maximal at or near noon. However, the highest oxygen values did not coincide with the mid day chlorophyll peak or even lag it by several hours. After sunset around 1900 hours the oxygen saturation increased sharply with a maximum of 50 to 75 percent saturation at midnight. Subsequent temperature measurements in the surface, mid and bottom water verified destratification, caused by cooling after sunset, resulted in a daily turnover that oxygenated the entire water column. Benthic, rather than water column, productivity was the source of the high night time oxygen levels.

97. Steven R. Kibler^{*1}; Ryszard J. Chrost²; Maria A. Faust³; Mark W. Vandersea¹; R. Wayne Litaker¹; Patricia A. Tester¹

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Dinoflagellates in a Naturally Eutrophied Mangrove Embayment in Belize.

Phytoplankton and bacterial biomass within a remote mangrove embayment at Peter Douglas Cay were compared with control sites in the oligotrophic central lagoon of Belize (Central America). Average bacterial biomass (4×10^9 cells L⁻¹)

and bacterial production ($7.4 \mu\text{g C L}^{-1} \text{h}^{-1}$) were an order of magnitude higher in the embayment than at a nearby site in the lagoon. Bacterial turnover was also much more rapid in the mangrove embayment ($\sim 12 \text{ h}$ vs. $\sim 49 \text{ h}$). Dissolved NH_4^+ ($1.1 \mu\text{mol L}^{-1}$) and chl *a* ($3.4 \mu\text{g L}^{-1}$) concentrations were 5- and 20-fold higher, respectively, in the mangrove embayment relative to the lagoon. Consistently high NH_4^+ concentrations suggested phytoplankton in the embayment were not N-limited. Elevated bacterial abundance and activity, combined with low morning and afternoon O_2 saturation ($\sim 20\%$) and a negative correlation between O_2 and NH_4^+ concentrations ($r = 0.63$), were consistent with rapid remineralization of organic matter and nutrients within the embayment at Peter Douglas Cay. Microscopy, coupled with CHEMTAX analysis of photosynthetic pigments, indicated the phytoplankton community within the mangrove embayment was largely comprised of dinoflagellates ($>50\%$), many of which were potentially toxic. Dominant dinoflagellates included *Bysmatrum subsalsum* and *Gonyaulax reticulatum* as well as *Peridinium*, *Protoperidinium*, *Gambierdiscus*, *Prorocentrum* and *Ostreopsis* spp. Examination of the phytoplankton at a nearby mangrove site (Twin Cays) suggested a similar community structure. In contrast, lagoonal waters were dominated by cyanobacteria (52-81%) with lesser numbers of diatoms (11-16%). In summary, sheltered mangrove embayments within the Belizean central lagoon exhibit elevated bacterial and phytoplankton biomass. Rapid remineralization of nutrients favors a phytoplankton community dominated by dinoflagellates.

98. Erla B. Ornlófsdóttir^{*}; Patricia A. Tester; R. W. Litaker
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***Heterocapsa triquetra* bloom dynamics in Newport River, NC, during a cold subtropical winter.**

The non-toxic dinoflagellate *Heterocapsa triquetra* forms persistent winter blooms in the Newport River, NC. The initiation and maintenance of the bloom is well documented but the mechanisms that induce bloom termination are not as well understood, except for times of bloom dissipation due to freshwater inflow. In winter 2004 the phytoplankton biomass and community structure was mapped during the bloom season of *H. triquetra*. The goal was to address the question of the relative importance of viruses on the bloom decline of *Heterocapsa*. Samples for biological and chemical analyses were collected twice a week (when possible) at eight stations along the salinity gradient in the estuary, at the same time physical parameters were defined. Preliminary results of an ongoing study of the factors contributing to bloom termination will be presented. The intensity of the 2004 winter bloom was 10 fold lower than in previous years and was maintained in the upper part of the estuary, compared to the commonly observed down estuary propagation of the bloom. The potential impacts of biological, chemical and physical factors on *H. triquetra* bloom dynamics in the colder than normal winter of 2004 will be discussed and compared with previous observations.

99. Sylvia Bonilla^{*1,4}; Connie Lovejoy²; Suzanne Roy³; Warwick F. Vincent¹

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Pico-eukaryotic dominance of the Arctic Ocean phytoplankton.

Size fractionated plankton samples from the Beaufort Sea in arctic Canada were collected over Sept-Oct 2002 as part of the Canadian Arctic Shelf Exchange Study (CASES). We found that phytoplankton in the less than 3 micron fraction represented a high proportion of Chl *a* (41 to 80% of total biomass) over the study region, which included samples from the Mackenzie River Delta to marine waters at the edge of the Arctic Ice Cap. This size fraction was further characterized by microscopy, HPLC pigment analysis and molecular techniques (denaturing gradient gel electrophoresis, DGGE, and 18S rDNA clone libraries). Pigments (including Chl *b*, Chl *c2*, fucoxanthin, violaxanthin, alloxanthin, diadinoxanthin and zeaxanthin); clone libraries; and microscopy observations all confirmed the presence of a diverse pico-eukaryotic plankton community. The small size fraction accounted for 43 to 97% of the Chl *b* of the whole community, suggesting dominance by Chlorophytes. The class marker pigments MgDVP, prasinoxanthin, lutein and micromonol confirmed the importance of prasinophytes. These results were also in agreement with the molecular data where *Micromonas* spp. (Prasinophyceae) accounted for nearly 10 % of the total 18S rDNA clones in our library and represented over half of the those clones that were from photosynthetic groups. Other photosynthetic pico-eukaryotes included both Cryptophytes and Chrysophytes. Our results indicate that photosynthetic pico-eukaryotes are important members of the Arctic phytoplankton community and suggest that these organisms are well adapted to exploit and compete in cold marine environments.

100. David F. Millie^{*1,6}; Gary R. Weckman²; James L. Pinckney³; Hans W. Paerl⁴; Brian J. Bendis⁵; Ryan J. Pigg⁶

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University, College Station, TX; 4. Institute of Marine Sciences, University of North Carolina-Chapel Hill, Morehead City, NC; 5. AMJ Equipment Corporation, Lakeland, FL; 6. Florida Marine Research Institute, Fish & Wildlife Conservation Commission, St. Petersburg, FL

Modeling of Ecological Indicators: Characterizing Estuarine Phytoplankton and Trophic State using Artificial Neural Networks.

Artificial Neural Networks (ANNs) are becoming an increasingly popular tool for statistical-based modeling of ecological data. Through repetitive processing of historical data, ANNs learn and reproduce correlated non-linear relationships between input data (e.g. environmental conditions) and corresponding output values (e.g. phytoplankton biomass/production). Trained networks then can be implemented for hindcasting or forecasting (output) parameters within historical or evolving data sets, respectively. Estuarine trophic state (as Net Ecosystem Metabolism, NEM; St. Johns River, FL) and phytoplankton biomass (as chlorophyll *a*; Neuse River Estuary, NC) were modeled individually using abiotic parameters within multi-year data sets. A high correspondence between modeled/measured NEM values existed for both numerical regression ($r = 0.84$) and phototrophic/heterotrophic classification (80-86%) approaches. The correspondence between modeled/measured chlorophyll *a* ($r = 0.67-0.77$) was greatest at low concentrations, most likely due to inadequate representation of concentrations greater than 20 mg m^{-3} during model development and/or data trends not being resolvable given the sampling resolution. ANNs modeling both chlorophyll *a* concentrations and NEM values outperformed traditional linear modeling, thereby identifying the non-linear patterns of phytoplankton biomass and trophic state in relation to dynamic estuarine parameters.

101. Peter A. Thompson^{*1}; Paul Armstrong^{2,1}; John Parslow¹; Michael Herzfeld¹; Karen Wild-Allen¹

1. Marine, CSIRO, Hobart, TAS, Australia; 2. School of Aquaculture, University of Tasmania, Launceston, TAS, Australia

Phytoplankton blooms and ecosystem management: one approach to bringing them together.

SE Tasmania is the center of a growing salmon aquaculture industry that is concentrated in the Huon Estuary. The Estuary experiences periodic blooms of several species of phytoplankton including the toxic dinoflagellate *Gymnodinium catenatum*. Our research on *G. catenatum* has involved laboratory based experiments to determine growth rates at 72 combinations of light and temperature and physiological responses to various nitrogen sources. Field based experiments have measured ¹⁵NH₄, ¹⁵NO₃ and ¹⁵urea uptake over a diurnal cycle at two depths and two sites during four seasons. The data provide part of the quantification for the biogeochemical model for the Estuary and are coupled with a high resolution three dimensional hydrodynamic model. Outputs from the model are being used by regulators as a tool to assess potential environmental responses to increased nitrogen loading and set limits on nitrogen inputs from aquaculture.

102. Thierry B. Chopin^{*1}; Susan Bastarache¹; Manav Sawhney¹; Ellen Belyea¹; Julie MacDougall²; Ian Stewart³; Patrick Fitzgerald⁴

1. Centre for Coastal Studies and Aquaculture, University of New Brunswick, Saint John, NB, Canada; 2. Canadian Food Inspection Agency, Blacks Harbour, NB, Canada; 3. Atlantic Silver Inc., St. George, NB, Canada; 4. Heritage Salmon Company Inc., Blacks Harbour, NB, Canada

Cultivation of *Laminaria saccharina* as the extractive inorganic component of an integrated multi-trophic aquaculture system (salmon-kelp-mussel).

The development of sustainable integrated aquaculture systems requires combining fed aquaculture (fish or shrimp) with extractive inorganic aquaculture (seaweed) and extractive organic aquaculture (shellfish). This is based on an age-old, common sense, farming practice: the by-products (wastes) from one resource user become inputs into another. With the support of AquaNet, the Network of Centers of Excellence in Aquaculture in Canada, we are developing such a system at an industrial pilot scale by co-cultivating salmon (*Salmo salar*), kelp (*Laminaria saccharina*) and blue mussel (*Mytilus edulis*) at aquaculture sites in the Bay of Fundy, Canada. The entire cycle of rearing *Laminaria saccharina* has been completed and improved (from 113 to 35 days), both in the laboratory and at the integrated sites. Photoperiod, nutrient enrichment, spore density, and timing of the production schedule are key parameters. The biomass production in proximity of salmon pens has been increased from 8.01 to 17.42 kg. m⁻¹ of rope. At a reference site, 1250 m away from salmon pens, the biomass production reached 11.96 kg. m⁻¹. Chemical therapeutants used in the treatment of diseases in cultured salmon have not been detected since the beginning of our work (May 2001) in any of the periodically sampled kelps grown adjacent to the salmon pens. Increased kelp production in proximity to that of salmon and the absence of transfer of therapeutants validate the concept of integrated aquaculture. Adopting polytrophic practices will be key to the aquaculture industry to develop environmentally and economically balanced systems and increase its social acceptability.

103. Paula Bernasconi¹; Tavi Cruz-Uribe²; Gregory Rorrer²; Neil Bruce³; Donald Cheney^{*1}

1. Northeastern University, Boston, MA; 2. Oregon State University, Corvallis, OR; 3. University of York, York, United

Kingdom

Development of a TNT-Detoxifying Strain of the Seaweed *Porphyra yezoensis* Through Genetic Engineering.

2,4,6-Trirotoluene (TNT) is one of the most recalcitrant and toxic of all military explosives. It occurs in coastal sites as a result of leakage from exploded and unexploded ordinance and runoff from firing ranges and munition dumps on land. Current methods for eliminating toxic compounds like TNT from contaminated waters and sediments involve dredging and disposal, and are extremely costly and potentially harmful to the environment. This project's goal is to develop a strain of seaweed capable of "phycoremediating" TNT in marine waters. Our model seaweed is a fast-growing, fast-reproducing strain of the red marine macroalga *Porphyra yezoensis*, which we genetically transform using a strain of *Agrobacterium tumefaciens* carrying the plasmid pNITRED3. This plasmid carries the bacterial nitroreductase gene, *nfsI*. Preliminary toxicity experiments determined that a TNT concentration of 5 mg/L could be used for isolating single lines of TNT-tolerant plants. Several lines have been produced which demonstrate a striking ability to take up, tolerate and detoxify TNT in seawater. One line, for example, can completely remove 10mg/L TNT from seawater in less than 3 days and still grow, whereas wild-type plants stop photosynthesizing and die. The presence of the *nfsI* transgene has been confirmed using PCR probes and has been shown to be both inheritable and stable (i.e. present through at least the T3 generation and inherited in the absence of selection). In addition, the products of TNT reduction by nitroreductase have been detected. This research is supported by a grant from the Office of Naval Research.

104. Charles Yarish^{*1}; G. Kraemer²; C. D. Neefus³; R Carmona^{1,4}; D. Snellgrove¹; P. He^{1,5}; X. R. Tang^{1,6}; R. Pereira^{1,7}; G. C. Nardi⁸

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The bioremediation opportunities of *Porphyra* spp. in an integrated land-based aquaculture system with finfish in coastal New England.

Many aquaculture industries generate a nutrient-rich waste stream that can lead to eutrophication of coastal waters. To address this environmental issue, the bioremediation potential of several native Northeast American species of *Porphyra* was assessed and compared to the well-known Asian species. *Porphyra* thalli were cultured over 4 weeks at 15°C at a stocking density of 0.4g FW L⁻¹. At three to four day intervals nutrient uptake, tissue N accumulation and phycobiliprotein concentration (PBP) were determined as functions of nitrogen (N) concentration (25-300 µM) and N source (nitrate vs. ammonium). Growth rates were measured weekly. Growth and tissue N reached maximal levels at inorganic N concentrations of 150-300 µM. Maximum growth rates ranged from 10-25% d⁻¹, although induction of archeospores reduced average growth rates in many cases. No evidence of ammonium toxicity (reductions in growth rate) was observed; in fact, similar values were found with both N sources. Ammonium generally yielded higher PBP and tissue N contents than nitrate. *Porphyra amplissima* presented the highest growth rate, followed by the Asian *P. yezoensis*. Under the experimental conditions, *Porphyra* spp. removed 70-100% of N within 3-4 days at N concentrations up to 150 µM, but was less efficient in removing inorganic phosphorus (35-91% removal). The highest tissue N and PBP concentrations were found at 150-300 µM of N, with N values close to 7% DW. Overall, *Porphyra* appears to be an excellent choice for bioremediation of moderately eutrophic effluents, with the added benefit that tissue may be harvested for sale.

105. Chad A. Larson^{*}; Sophia I. Passy

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Spectral fingerprinting as a novel approach to biofilm analysis and biomonitoring.

All algae are not created equal as evidenced by the unique chlorophylls and/or accessory pigments contained by different algal groups. The specific combination of fluorescing pigments in algae, give rise to specific emissions following excitation. This fact has made the pursuit of quantifying algal composition based upon the different spectral emissions an attractive goal. Usual techniques for separating different algal taxonomic groups by chlorophyll excitation are typically time-consuming ventures often involving laborious methodology. Furthermore, most methods require the extraction of the various chlorophylls which leads to the destruction of the algal cells. This eliminates the ability for in vivo fluorescence which might be desirable for applications concerned with the spatial arrangement or composition of periphyton through time. Here, we propose a novel method for analyzing periphytic biofilms for the purposes of stream ecology, using laser scanning confocal microscopy and spectral fingerprinting. Live biofilms on slides containing several major freshwater

algal taxa, including cyanobacteria, diatoms, and chlorophytes were examined with a confocal microscope with an emission fingerprinting device (Zeiss LSM 510 with a META detector) to acquire their characteristic spectral signature, following incremental excitation. Results from this technique were compared to results of traditional microscopy analyses. The simple fingerprinting technique outlined here will provide a quick and easy method of quantifying and analyzing the accumulation and changes in composition of the various taxonomic groups of stream periphyton without having to disturb or destruct the attached community.

106. S. Banerjee¹; N. Chakravorty¹; A. Mukherjee¹; Ruma Pal^{*1}; D. Nayak²; S. Lahiri²

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Studies On Algae-metal interaction based on Cytological, Biochemical and Radio- Tracer Techniques.

Toxicity of a number of metals and metalloid in relation to changes in morphology, cytology, Biochemistry of pro- and Eukaryotic algal cell systems and their reproductive behaviour have been studied. Synechococcus, Spirulina, Lyngbya and Phormidium from Prokaryotic group and *Rhizoclonium*, *Oedogonium* and a few Diatoms have been exposed to stable salts of Pb, Cr and As and a number of radionuclides. Morphological changes include colony and bundle formation, false branching and extracellular sheath formation in case of Cyanobacteria. EC 50 doses were determined for different algae against various metals, which varied depending upon the resistance of the algae against particular Diatoms like *Fragillaria* and *Nitzschia* were found to be resistant against Cd but sensitive to As. *Rhizoclonium* and *Synechococcus* were found to be very resistant to As. Spirulina was found resistant to Pb than Cr. Radio-Tracer techniques were employed for both prokaryotic and eukaryotic algal systems. Radio-nuclides including ¹⁹⁷Hg; ^{198,199,200,201}Tl; ^{199,200,201}Pb and ²⁰⁴Bi and ^{204,205}Po in its carrier free state were produced by irradiating a gold metal foil with medium energy ⁷Li and ¹²C beams successively in a 12 MV Pelletron. The preferential uptake of radionuclides of different genera were studied and *Lyngbya major* and *Rhizoclonium hieroglyphicum* were found as suitable agents for bio-separation of Thallium from Hg and Pb.

107. Huan Zhang^{*1}; Debashish Bhattacharya²; Senjie Lin¹

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Phylogeny of dinoflagellates based on mitochondrial cytochrome b and nuclear small subunit rDNA sequence comparisons.

The dinoflagellates comprise a major lineage of photosynthetic protists (algae) that are important as primary producers and include a number of highly toxic, "red tide"-causing taxa as well as micrograzers. Despite their evolutionary and economic importance, dinoflagellate phylogeny remains unclear. In this study, we analyzed mitochondrial cytochrome b (cob) and nuclear-encoded small subunit (SSU) rDNA to address several important questions about dinoflagellate evolution. Phylogenetic trees using cob were inferred with distance matrix, maximum parsimony, maximum likelihood, and quartet puzzling methods and Bayesian inference and included members of the six major dinoflagellate orders (18 species). These trees were generally congruent with each other and with those derived from SSU rDNA sequence comparisons, although the cob trees provided greater bootstrap and Bayesian support for key nodes. Our results show that 1) *Cryptocodinium cohnii* represents a basal divergence in the dinoflagellates that is distantly related to other Gonyaulacales; 2) *Pfiesteria* spp. and related organisms form a strongly supported monophyletic clade; 3) the zooxanthallae *Symbiodinium* spp. appear to be more basal in our trees than previously thought; and 4) the fucoxanthin-containing taxa comprise a well-supported, monophyletic lineage placed at a derived position within the peridinin-containing dinoflagellates, which is consistent with the hypothesis that the haptophyte-derived plastid in these taxa was acquired later than the peridinin-containing plastid through a tertiary endosymbiosis in their common ancestor. Our results clarify key aspects of dinoflagellate evolution and indicate that cob is a promising marker for inferring the phylogeny of these protists.

108. Wayne Litaker^{*}; Mark Vandersea; Melissa West; Steven Kibler; Patrica Tester

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Using ITS rRNA Sequences To Define Dinoflagellate Species.

Current species level relationships among thecate dinoflagellates are based on Kofoidian plate tabulations. Determining these plate tabulations requires highly specialized SEM techniques. Many species have delicate thecal plates and are difficult to properly prepare for SEM analysis. Time-consuming modifications of existing SEM procedures are frequently required to identify these species. These modifications can take months to years to complete. Starting in the mid 1990s, investigators began using ribosomal internal transcribed spacer region sequences (ITS1 and ITS2) to delineate putative

dinoflagellate species. ITS regions were selected because they are not under strong stabilizing selection and tend to diverge rapidly during speciation compared to the flanking SSU, 5.8S and LSU rRNAs. Using ITS sequences for species identification is technically attractive because once a culture is established, sequencing can be completed in one to two weeks. The resulting sequence can then be aligned with existing sequences to determine whether the isolate is likely to be a new species. However, the actual genetic divergence necessary to distinguish isolates as different species has never been explicitly quantified. To address this problem our study used ITS sequences from species belonging to 16 taxonomically well-defined dinoflagellate genera to estimate the minimal divergence necessary to define a new dinoflagellate species. The goal was to validate a genetic classification system using traditional Kofoidian taxonomy. In addition to determining between species divergences, intra genomic and within species divergences were also estimated whenever possible. Intra genomic and within species sequence variation arises from the fact that there are 100 to 200 copies of the ITS region per genome, not all of which are identical. For an ITS-based classification system to be valid, the intra genomic and intra specific variation has to be small compared to between species variation. The results of these analyses will be presented with hopes of starting a community wide debate that will lead to a consensus on how to correctly define dinoflagellate species using molecular sequence data.

109. WITHDRAWN

110. Naomi Phillips^{*1}; Renaud Burrowes³; Florence Rousseau³; Bruno de Reviers³; Gary W. Saunders²
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Insights into brown algal phylogenetics using chloroplast and nuclear genes.

Despite brown algae ecological importance and rich biodiversity, research is just beginning to examine objectively evolutionary relationships among brown algae and a consensus in terms of a natural classification system that reflects phylogeny remains elusive. Our collaborative efforts have generated a comprehensive molecular phylogeny of brown algae using two divergent gene systems (LSU rDNA and rbcL genes). This work was designed to extend recent analyses based on rbcL and partial LSU by greatly increasing ordinal representation and sequence data (nearly complete LSU rDNA) with the primary goal of testing current phylogenetic concepts and evaluating diagnostic features at the ordinal and familial levels with emphases on the fuclean lineages. Representative taxa were included for each phaeophyceae order and family in the analyses, totaling over 60 taxa across all 18 orders, as well as outgroups. To control for saturation effects data were analyzed at two levels; globally (including all lineages, Shizocladiaceae, Xanthophyceae and Phaeothamniophyceae as outgroups, with the 3rd codon of rbcL &/divergent domains of the LSU excluded) and locally (excluding Schizocladiophyceae, Xanthophyceae, Phaeothamniophyceae, Choristocarpaceae and Dictyotales, using complete rbcL and LSU). Global analyses supported Choristocarpus (Choristocarpaceae) as the most basal brown lineage followed by representatives of the Dictyotales, Syringodermatales and Sphacelariales. Global analyses also supported using Syringodermatales as the outgroup in local analyses. In the local analyses (genes analyzed separately or combined), brown algae formed two main lineages with the Sphacelariales in one clade and all remaining orders in the second clade. The associations in the all other browns clade support many traditional ordinal and familial relationships, but with a few surprises. For example, the Fucales and allies form a strongly supported divergent group with the crust Nemerodermata as the closest sister lineage.

111. T.J. Evens^{*}; Randall P. Niedz
USHRL, USDA-ARS, Ft. Pierce, FL

New approaches to the design of algal media formulations for nutrition studies: the anionic/cationic balance problem.

Designing culture media for macro-/micro-nutrient studies is a complicated problem. The vast majority of algal media has been empirically derived and is inherently difficult to manipulate in a controlled manner. In order to evaluate the importance of a single ion it is necessary to alter the concentration of the two ions, a cation and an anion, that make up the parent salt. If it is necessary to assess multiple ions then the problem increases in complexity in an exponential manner. These types of problems are easily solved by linear programming (LP), a technique of applied mathematics devised specifically for solving a wide range of practical, complex, resource allocation problems such as scheduling, mixing, blending, and routing. The anionic/cationic balance problem, how it is easily solved using LP techniques, and a public domain software program designed for nutrient formulation research will be discussed.

112. G. X. Liu^{2,1}; Z. Y. Hu²; M. Sommerfeld¹; Q. Hu^{*1}
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***Haematococcus* lipid bodies: isolation, composition and biogenesis.**

The green microalga *Haematococcus pluvialis* accumulates large amounts of cytosolic lipid bodies, accompanied by cyst formation under oxidative stress conditions. Because astaxanthin, the molecular antioxidant, is synthesized and accumulates exclusively in lipid bodies, it has been suggested that lipid bodies may play an important role in protecting the cell against stress. However, the biochemical properties and physiological function of lipid bodies is not well known in this organism and other related green algal species. In this study, we have isolated *Haematococcus* lipid bodies using a French press, followed by sucrose density gradient centrifugation. Purified lipid bodies contain ca. 80% lipids (presumably triacylglycerol), 7 to 17% proteins and ca. 6% astaxanthin of various esterified forms. Trace amounts of chlorophyll were also detected in purified lipid bodies. Treatment of lipid bodies with 2M NaCl, 5 M urea, or 0.05% (w/v) Triton X-100 confirmed that chlorophyll is a constituent of lipid bodies (at least in the early stages of lipid body formation), and not the result of thylakoid contamination from the isolation process. SDS-PAGE analysis revealed that lipid bodies contain numerous proteins and that protein composition is similar to that of the thylakoid membranes. Peptide mapping, N-terminal sequencing, and MALDI-TOF mass spectrometry confirmed that the major lipid body proteins are identical to those in the thylakoid, suggesting that lipid bodies might originate from the chloroplast, or that the chloroplast plays an important role in lipid body formation and development. Changes in the biochemical composition of lipid bodies during cell transformation will also be described.

113. Gwang H. Kim^{*1}; Tatiana A. Klotchkova¹; Min-Chul Yoon¹; Tim Spurk²; John A. West²

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Time-lapse videography on the photomovement in the filamentous green alga *Spirogyra* (Chlorophyta, Zygnemataceae).

A blue-light induced phototactic movement in the filamentous eukaryotic alga, *Spirogyra* was studied with time-lapse videography. When *Spirogyra* filaments were scattered in a water chamber under a unilateral light source, they rapidly aligned towards the light source in an hour and bound with neighboring filaments to form thicker parallel bundles of filaments. The anterior of the filaments curved towards the light source first and then the posterior began to curve towards the light, forming an open-hoop shape. The bundle of filaments then moved towards the light source by repeated rolling and stretching of filaments. When the moving bundle met other filaments they joined and formed a bigger open-hoop-shaped mat. The coordination of filaments was essential for the phototactic movement. No single filament could move towards the light. The average speed of movement was 10 to 15 mm s⁻¹. The movement could be induced by relatively low irradiance (photon flux density = 1 to 50 μmol photons m⁻²s⁻¹). The photomovement of *Spirogyra* spp. was observed under various light types including UV light. The *Spirogyra* filaments showed random pattern of movement under red or green light. But some species showed phototaxis to UV light. The phototaxis in *Spirogyra* spp. may have evolved to occupy open space faster than other algae in shallow water environments and to aid the success of this alga in these environments.

114. Oswaldo K. Okamoto^{*1}; John W. Hastings²

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Novel Dinoflagellate Clock-Related Genes Identified Through Microarray Analysis.

Bioluminescent dinoflagellate species are long being used as models to study circadian rhythms but the genetics and molecular nature of their clock is virtually unknown. In a genome-wide study of circadian gene expression, we constructed microarrays containing 3,500 cDNAs from the species *Pyrocystis lunula* Schutt and compared the abundance of transcripts at circadian times separated by 12 hours. About 3% of the unique genes screened were identified as circadian-controlled, more than 50% of which could be identified with diverse known genes. Most were preferentially expressed in either early subjective day or late subjective night. Light exposures at times expected to induce phase shifts in the rhythm revealed 30 differentially expressed genes, including some potentially participating in photic entrainment and others in pathways connecting a central oscillator to output rhythms. Those that appeared in both screens were considered as possible core clock genes but there were no similarities with such genes from other organisms. This is the first report of circadian regulation of transcript levels in a dinoflagellate. Since very few genes have been previously obtained from this unusual and diverse group, an ancillary but significant contribution of the present work is in making available cDNAs of about 2,800 unique dinoflagellate genes, along with ESTs of almost 500, about half of which have homologies with sequences in the databank. Our data indicate that the gene repertoire of dinoflagellates is also distinct, possessing many novel sequences for further functional and evolutionary studies.

115. Senjie Lin* ; Huan Zhang

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Mitochondrial cytochrome b mRNA editing in wide range of dinoflagellates and possible evolutionary association.

To begin tackling questions as to how mt gene mRNA editing arose and evolved in the phylum of dinoflagellata, extensive analysis based on broad sampling is required. In this study, six dinoflagellate species representing distinct ecotypes and taxonomic classes were analyzed to characterize RNA editing in mt cytochrome b (cob). Totally, 61 colinear edited sites were inferred, 11 of which were common in these six new species and 4 common in all the nine dinoflagellates examined so far. Overall, the edited sites accounted for 2.15-3.54% of the gene length with apparently early diverging groups, Crypthecodinium and Symbiodinium, having the fewest edited sites. The edited sites generally fell into four clusters and occurred predominantly at first and second positions of codons (93%), overwhelmingly involves A-to-G, U-to-C or C-to-U substitutions, with smaller number of G-to-C, G-to-A, all but six of which changes the identity of the specified amino acid. On the phylogenetic tree containing both cDNA and genomic DNA sequences, cDNA and its corresponding gene sequences clustered together in all cases except in *Pfiesteria* spp., in which genomic DNA sequences formed a cluster distinct from their cDNA cluster, suggesting caution in using mixed gene and cDNA sequences in constructing trees. Only one edited cDNA is detected for each of the nine species examined to date, except in *Alexandrium tamarense* in which multiple partially edited cDNAs were detected in addition to the fully edited cDNA. Intriguingly, comparison of location of edited sites and the post-edited amino acid residues in different taxa yielded distance matrices that mirrored the taxonomic affinity of the species. Cladistic analyses based on the distance matrices resulted in a cladogram with the same topology as the phylogenetic tree inferred from cob sequences. The results indicate that 1) most major lineages of dinoflagellates share similar type and distribution of cob mRNA editing; 2) similarity in number and location of edited sites and post-edited aa identity seem to be correlated with phylogenetic affinity of the taxa.

116. Curt Pueschel*¹; John West²

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Effects of ambient calcium concentration on calcium oxalate crystals in marine red algae.

A survey of 17 species of the Ceramiales grown in culture revealed calcium oxalate crystals in *Antithamnion antillanum*, *A. callocladum*, and *A. densum*. The needle-shaped crystals were present within the cytoplasm of cells of the indeterminate axes, but not in cells of the determinate lateral branches. No calcium oxalate crystals were present in *A. pectinatum*. The four species of *Antithamnion* and three additional members of the Ceramiales that do not normally form crystals were grown in natural seawater culture medium in which calcium concentration was elevated by addition of 5-20 mM calcium chloride. Elevated calcium supply did not induce the deposition of calcium oxalate crystals in species that did not previously exhibit them, and it did not change the cellular or subcellular location patterns in species that did have crystals. At high calcium concentrations, the species able to deposit calcium oxalate did not show consistently less inhibition of growth than the species unable to sequester calcium as an oxalate salt. Subsequently, the four species of *Antithamnion* were grown in artificial seawater with reduced calcium concentrations. All appeared healthy and grew well in 2.5-10 mM calcium chloride. In 2.5 mM calcium chloride, *A. antillanum* released tetraspores which grew into thalli having abundant calcium oxalate crystals. Even in 1.0 mM calcium chloride, *A. callocladum* and *A. densum* continued to grow and deposit calcium oxalate crystals. Death of all four species occurred within a few days if only 0.1 mM calcium chloride was provided. Calcium oxalate crystals were present in many cells of the dead thalli, indicating that the crystals did not provide a calcium reserve that could be readily mobilized. Complete darkness for ten weeks also did not stimulate mobilization of the crystals. The stability of calcium oxalate crystals over a broad range of calcium concentrations and light intensities suggests that these inclusions are constitutive features and thus could serve as taxonomic characters. However, the physiological stability of the crystals makes their function even more enigmatic.

117. Sarah Marie Noble* ; Juan M. Lopez-Bautista

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Preliminary investigations on the subaerial Trentepohliales (Ulvophyceae, Chlorophyta) in the Southeastern USA.

The Trentepohliales, being neither aquatic nor terrestrial but subaerial, are a unique and understudied group of green algae which are found through out the Southeastern USA and in many habitats of high humidity world-wide. Important aspects of their unique biology, current phylogenetic position and ecology combine to present rather interesting challenges to the researcher. This study aims toward an exhaustive monographic study of the representatives of the trentepohlian flora in the Southeastern USA. Samples of Trentepohliales are being collected, preserved and cultured from the Southeastern USA as a basis for a thorough morphological, cytological and molecular investigation to reveal the diversity and phylogenetic relationships of the taxa distributed in the Southeastern USA. Molecular primers for the *rbcl* gene specifically designed for the Trentepohliales, necessary because of the group's intimate association with other organisms including plants and

fungi, are also being applied.

118. Mark A. Buchheim; Bindhu Verghese*

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Evolution of the Chlorophyceae and Trebouxiophyceae: Inferences from Chloroplast Genes.

Phylogenetic reconstruction using nuclear ribosomal genes has proven useful for many chlorophycean lineages, but some nodes remain poorly-resolved. The phylogenetic relationships within the Chlorophyceae were studied using chloroplast gene sequences (*atpB* and *rbcL*) to address phylogenetic problems in several green algal lineages. Distance analysis revealed high levels of divergence (as compared to the 18S and 26S rDNA data) for a variety of chlorophycean taxon pairs. Phylogenetic analysis (independent and combined) reveals a novel, but weakly-supported, relationship between Oedogoniales and Chaetopeltidales. Both genes also supported the existence of a distinct *Cylindrocapsa* lineage inferred from rDNA data. Molecular evolutionary studies revealed that the nonsynonymous to synonymous (n/s) amino acid substitution ratio for the *atpB* gene was 0.132 and for the *rbcL* gene was 0.22; indicating purifying selection is at work in both. Estimates of the transition/transversion ratio also support the notion of purifying selection (R=0.604 for *atpB* gene and R=0.843 for *rbcL* gene). A comparison of three major clades within the Viridiplantae revealed significant differences in their n/s ratio. These observations indicate that the chloroplast gene will provide a powerful complement to current phylogenetic and molecular evolutionary assessments of the Chlorophyta. Supported by NSF DEB 0129030.

119. Charles F. Delwiche*

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Morphological Species in Coleochaete.

Embryophytes are thought to include of the scale of a million species while their close relatives the Charales and Coleochaetales account for a tiny fraction as many. The Charales have roughly 500 named species, and the Coleochaetales less than 25. We are examining the relationship between morphological and molecular diversity in the Coleochaetales. Some morphological species clearly consist of several nominally cryptic species. For example, in samples of the endophytic Coleochaete nitellarum, substantial sequence variation in the conserved genes *rbcL* and *atpB* suggests that there are several previously unrecognized species. Although this diversity was not previously recognized, morphological distinctions among the isolates of *C. nitellarum* can be identified. At the same time, those species with distinctive autapomorphies, such as the monoecious "*C. orbicularis*" show congruent sequence variation (i.e., form monophyletic groups or have indistinguishable sequences in molecular analysis). Consequently, morphological methods remain suitable for identification of Coleochaete species, although molecular methods may be more suitable for many applications.

120. Christopher Drummond⁴; John Hall²; Kenneth G. Karol³; Charles F. Delwiche²; Richard M. McCourt^{*1}

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Phylogeny of *Spirogyra* and *Sirogonium* based on *rbcL* sequence data.

DNA sequence data were obtained for the gene encoding the large subunit of RUBISCO (*rbcL*) from 38 species or strains of *Spirogyra* and *Sirogonium*, using as outgroups 10 genera in the Zygnematales and Desmidiaceae (*Closterium*, *Cosmarium*, *Cylindrocystis*, *Gonatozygon*, *Mesotaenium*, *Netrium*, *Penium*, *Zygnema*, *Zygnemopsis*, *Zygogonium*). Sequence data were analyzed using maximum parsimony (MP), maximum likelihood (ML) and Bayesian inference (BI), with bootstrap replication (MP, ML) and posterior probabilities (BI) as measures of support. MP, ML and BI analyses of the *rbcL* data strongly support a single clade containing both *Spirogyra* and *Sirogonium*. *Spirogyra maxima* is nested among species in the genus *Sirogonium*, which form a monophyletic group of taxa with loosely spiraled chloroplasts. ML and BI analyses place this *Sirogonium/S. maxima* clade sister to the remaining *Spirogyra*. Morphological differences among closely related strains of *Spirogyra*, including laboratory strains derived from clonal cultures (*S. communis*, *S. pratensis*), indicate that many characters (filament width, chloroplast number) used in the traditional taxonomy of this group are poor measures of species identity. Other characters, such as replicate end walls may be synapomorphies for clades within *Spirogyra*. Further work on the evolution of key vegetative and reproductive features (heterothallism vs. homothallism, isogamy vs. anisogamy, zygospore ultrastructure, lateral vs. scalariform conjugation) and gene sequence data from the nucleus and organelles will be required to resolve the question of whether *Spirogyra* and *Sirogonium* constitute separate genera.

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