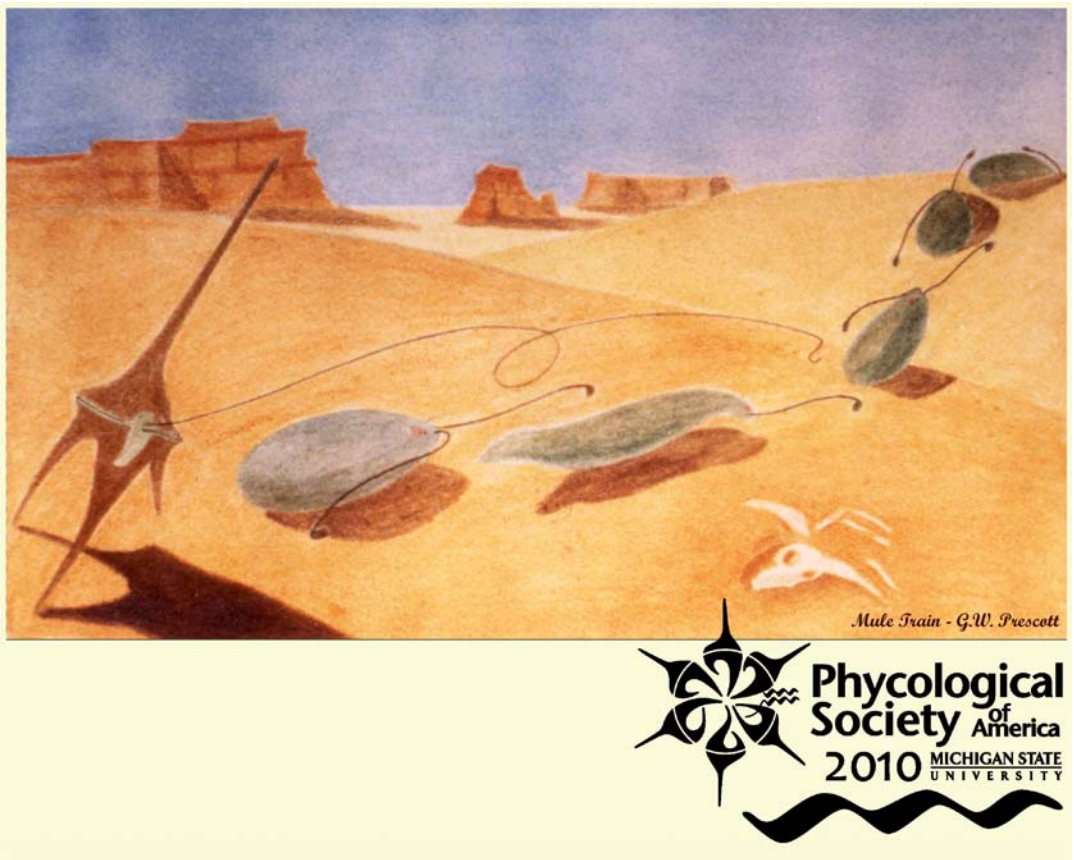
Annual Meeting of the Phycological Society of America

July 10-13, 2010

Michigan State University East Lansing, Michigan



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

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Eric Linton, *Central Michigan University*

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*ex-officio member
**ex-officio and non-voting member

History of Michigan State University

(From Wikipedia)

“Laboratory Row of the Michigan Agricultural College” ca. 1912

The history of **Michigan State University** (MSU) dates back to 1855, when the Michigan Legislature established the Agricultural College of the State of Michigan, with three buildings, five faculty members and 63 male students. As the first agricultural college in the United States, the school served as a prototype for future Land Grant institutions under the Morrill Act enacted during Abraham Lincoln's presidential administration. The school's first class graduated in 1861 right after the onset of the American Civil War. That same year, the Michigan Legislature approved a plan to allow the school to adopt a four-year curriculum and grant degrees comparable to those of the University of Michigan.

In 1870, the College became co-educational and expanded its curriculum beyond agriculture into a broad array of coursework commencing with home economics for women students. The school admitted its first African American student in 1899. Not long before this, in 1885, the College had begun offering degrees in engineering and other applied sciences to students. The 26th U.S. President, Theodore Roosevelt, addressed the school at the 1907 commencement, an event coinciding with the 50th anniversary of the school's opening. During this period, the school established "Farmers' Institutes" as a means of reaching out to the state's agricultural community and informing the membership of developments in agricultural science; the program gradually became the MSU Extension Services.

After World War II, the college gained admission to the Big Ten Conference, joining the rival University of Michigan, and grew to become one of the largest educational institutions in the United States with 44,937 currently enrolled. In its centennial year of 1955, the state officially made the school a university and the current name was adopted in 1964 after Michigan voters adopted a new constitution. Today, Michigan State University emphasizes biotechnology research and residential college learning as a modern paradigm for America's Land Grant institutions.

The university has undergone several name changes throughout its history, reflecting the evolution of the university and its mission:

1855 Agricultural College of the State of Michigan
1861 State Agricultural College
1909 Michigan Agricultural College
1925 Michigan State College of Agriculture and Applied Science
1955 Michigan State University of Agriculture and Applied Science
1964 Michigan State University

Gerald W. Prescott
Professor of Botany
Michigan State University 1946-1968
Phycologist and Artist

GERALD W. PRESCOTT [Sept. 25, 1899-July 7, 1988] received his B.A. (1923) at Univ. of Oregon, M.A. and Ph.D. in Botany at Univ. Iowa. After his Associate Professor services at Willamette Univ. (1928-29) and Albion Coll., Michigan (1929-46), Gerry served as Professor of Botany at Michigan State College/University (1946-68) and Professor Emeritus at Yellow Bay, Flathead Lake, University of Montana (1968-79). Gerry produced 22 graduate students and published >100 research papers and books mostly on systematics and ecology of freshwater New World algae. He led the founding of The Phycological Society of the Americas (1946) which gathered 158 members (1947) of which about 50 were bonafide phycologists. Gerry served as Secretary-Treasurer (1946-52), Vice-President (1952-53), and President (1954-55). Receiving awards, such as an Honorary Doctorate from the University of Montana, and having the honor of presenting the first Phycological Society of America's G.W. Prescott Award (1968), Gerry remained active at the Society's Annual Meetings throughout his life.

Please stop by the PSA headquarters room (Heritage Room) and visit the G.W. Prescott Display

We would like to express our gratitude for the generous financial support provided by:

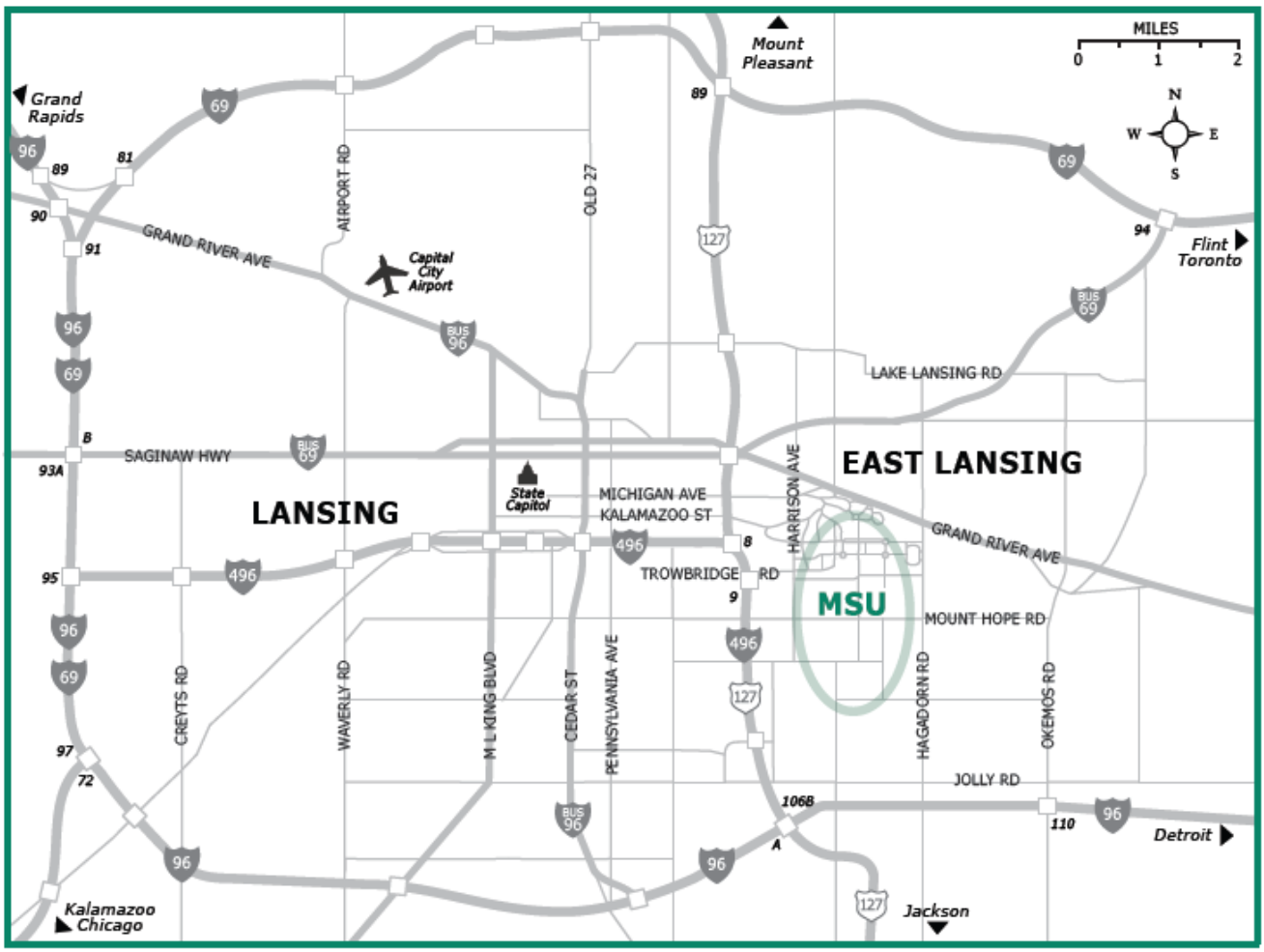
The Office of the Vice President for Research and Graduate Studies, Michigan State University

The George E. Leroi -College of Natural Science Strategic Vision Endowment, Michigan State University

The Department of Plant Biology, Michigan State University

LANSING AREA

MICHIGAN STATE UNIVERSITY



DRIVING DIRECTIONS TO MICHIGAN STATE UNIVERSITY

From Traverse City or Points North via I-75
Proceed south on I-75 to US-127 near Grayling. Proceed south on US-127 to East Lansing. Take the Trowbridge Road exit. Follow Trowbridge Road east to Michigan State University.

From Detroit or Points East via I-96
Proceed west on I-96 to northbound US-127; follow US-127 north to East Lansing. Take the Trowbridge Road exit. Follow Trowbridge Road east to Michigan State University.

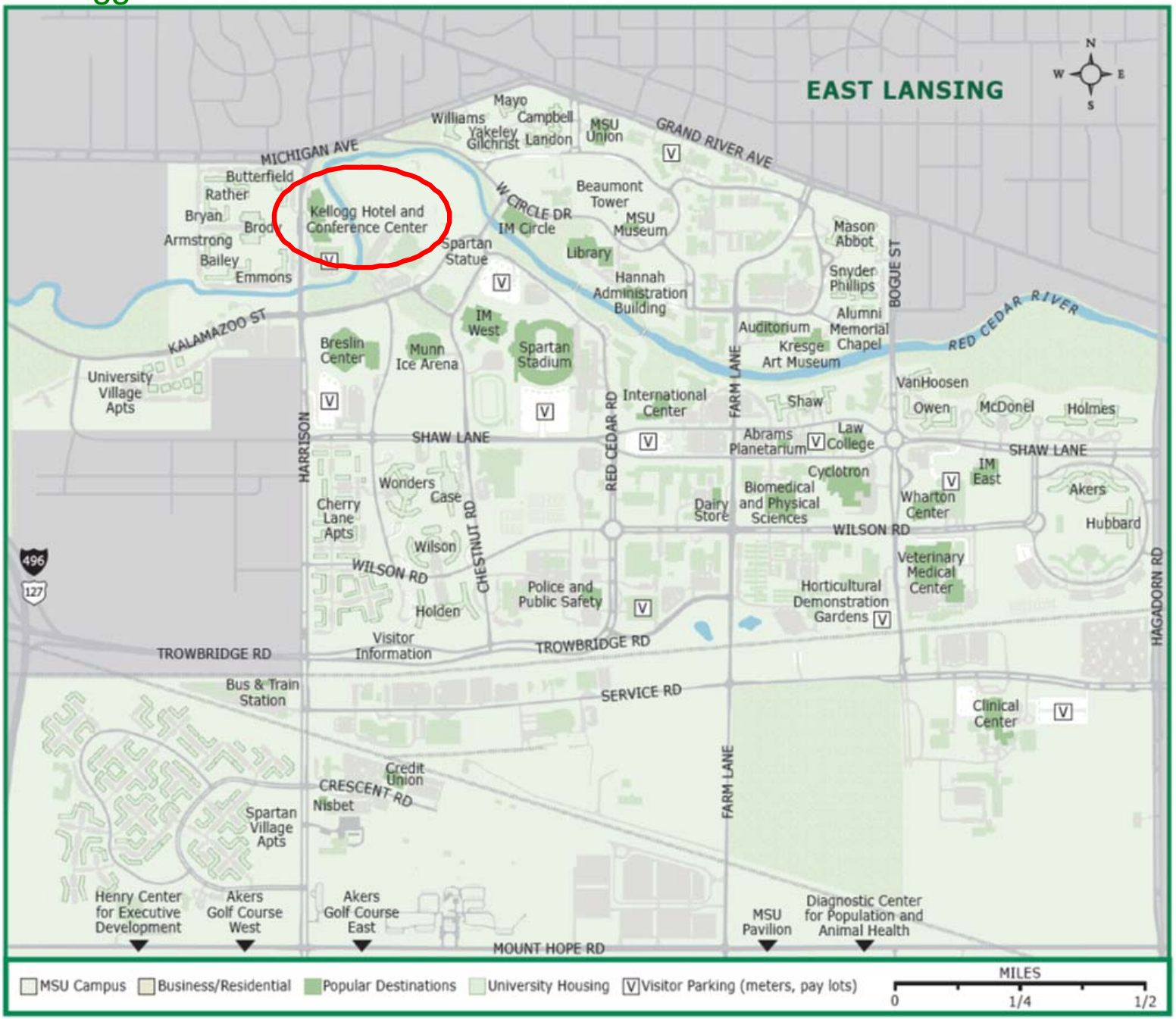
From Grand Rapids or Points West via I-96
Proceed east on I-96 to eastbound I-69. Proceed east on I-69 to southbound US-127. Take US-127 south to East Lansing. Take the Trowbridge Road exit. Follow Trowbridge Road east to Michigan State University.

From Flint or Points East via I-69
Proceed southwest on I-69 to southbound US-127. Take US-127 south to East Lansing. Take the Trowbridge Road exit. Follow Trowbridge Road east to Michigan State University.

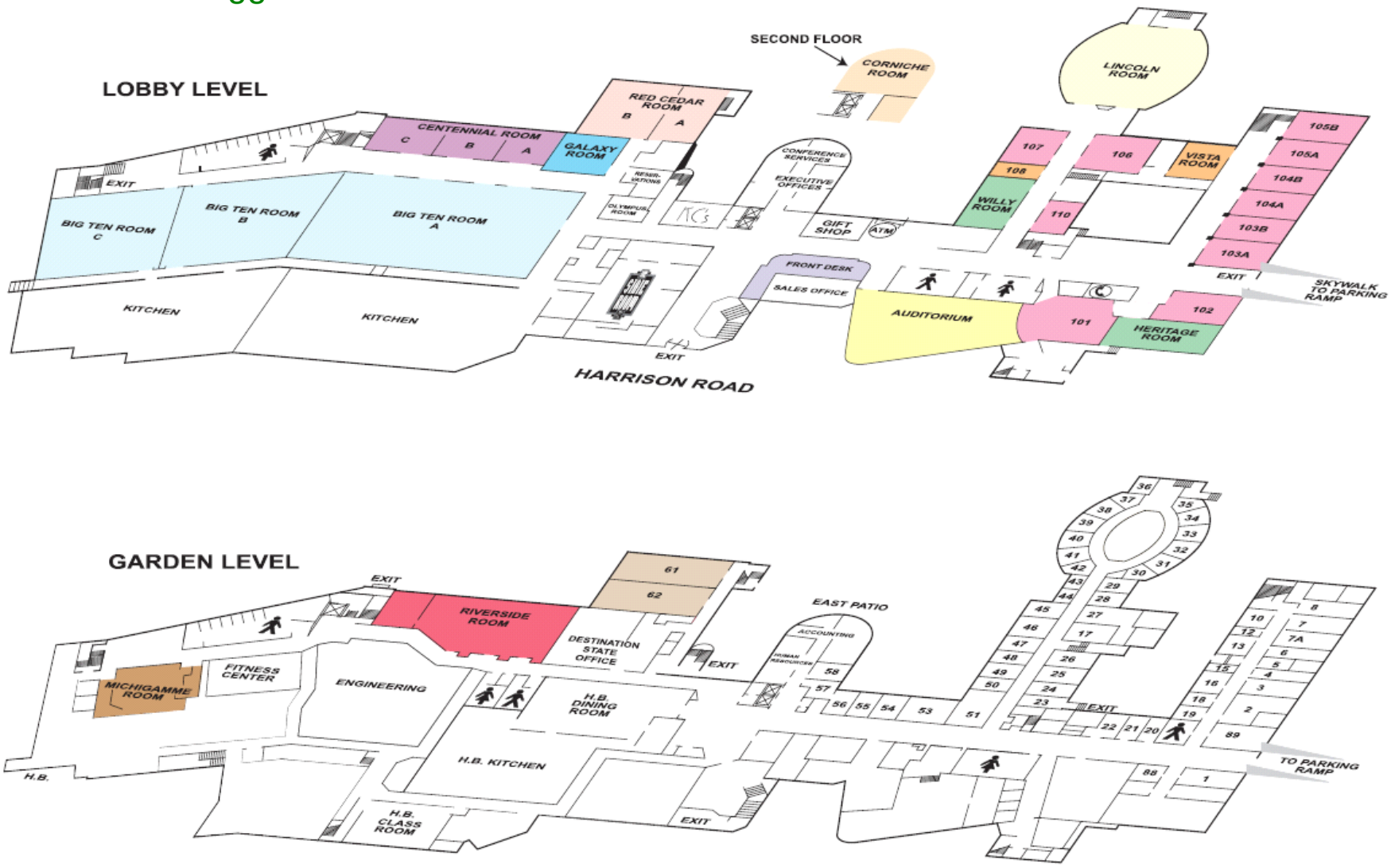
From Kalamazoo or Points South via I-69
Proceed east on I-94 to northbound I-69. Take I-69 north to Lansing. Take I-496 east to the Trowbridge Road exit. Follow Trowbridge Road east to Michigan State University.

From Jackson or Points South via US-127
Proceed north on US-127 to East Lansing. Take the Trowbridge Road exit and continue east to Michigan State University.

Kellogg Hotel & Conference Center and Northern MSU



Kellogg Hotel & Conference Center Floor Plan



	Central Lobby	Auditorium	Lincoln Room	Big Ten Room B	Big Ten Room C
Sunday, 11 July	Continental Breakfast (07:00-08:00)				(Poster Set-Up Available)
		PSA Special Session: Algae and the Tree of Life (08:00-10:15)			
	Mid-Morning Beverages (10:15-10:45)				(Poster Set-Up Available)
		Bold Award Competition (10:45-12:45)			Posters Open
	Lunch (12:45-14:15)	Lunch (12:45-14:15)	Lunch (12:45-14:15)	Lunch (12:45-14:15)	Lunch (12:45-14:15)
		Phylogenetics & Taxonomy-I (14:15-15:35)	Physiology & Biochemistry-I (14:15-15:35)		Posters Open
	Afternoon Break (15:35-16:05)				Posters Open
		Phylogenetics & Taxonomy-II (16:05-17:25)	Ecology & Population Biol-I (16:05-17:45)		Posters Open
				PSA Auction (20:00-22:00)	Posters Open

	Central Lobby	Auditorium	Lincoln Room	Big Ten Room B	Big Ten Room C
Monday, 12 July	**Continental Breakfast (07:00-08:00)**				**Posters Open**
		PSA Special Session: Charophycean Green Algae (Streptophytes) and the Origin of Land Plants (0800-10:10)			**Posters Open**
	Mid-Morning Beverages (10:10-10:40)				**Posters Open**
		Phylogenetics & Taxonomy-III (10:40-12:00)	**Physiology & Biochemistry-II (10:40-12:00)**		**Posters Open**
	Lunch (12:00-13:30)	**Lunch (12:00-13:30)**	**Lunch (12:00-13:30)**	**Lunch (12:00-13:30)**	**Lunch (12:00-13:30)**
		Phylogenetics & Taxonomy-IV (13:30-14:50)	**Phyco Speed-Dating (13:30-14:50)**		**Posters Open**
	Afternoon Break (14:50-15:20)				**Posters Open**
		Ecology & Population Biol-II (15:20-17:00)	**Cellular & Molecular Biol (15:20-17:00)**		**Posters Open**
			PSA Annual Business Meeting (17:30-18:30)		**Posters Open**
					Poster Session (19:00-21:00)

	Central Lobby	Auditorium	Lincoln Room	Big Ten Room B	Big Ten Room C
Tuesday, 13 July	**Continental Breakfast (07:00-08:00)**				**Posters Open**
		PSA Special Session: Lipids and Lipidomics in Algae (08:00-10:10)			**Posters Open**
	Mid-Morning Beverages (10:10-10:40)				**(Poster Removal)**
		Phylogenetics & Taxonomy-V (10:40-12:00)			
	Lunch (12:00-13:30)	**Lunch (12:00-13:30)**	**Lunch (12:00-13:30)**	**Lunch (12:00-13:30)**	**(Poster Removal)**
		Phylogenetics & Taxonomy-VI (13:30-15:10)	**Biotechnology (13:30-15:30)**		
	Afternoon Break (15:30-16:00)				**(Poster Removal)**
				PSA Banquet & Awards Ceremony (18:00-21:00)	

SCHEDULE OF EVENTS

FRIDAY, 9 JULY

PSA Board of Trustees Meeting – Vista Room, 12:00 – 18:00

SATURDAY, 10 JULY

PSA Executive Committee Meeting – Vista Room, 08:30 – 17:30

PSA Opening Social and Mixer

Big Ten Room B, 19:00-22:00 PM

Come and enjoy a selection of hot and cold hors d'oeuvres, an open bar, and conversation from all of those phycologists you've been hoping to catch up with.

SUNDAY, 11 JULY

07:00-08:00 **CONTINENTAL BREAKFAST -- Central Lobby**

Auditorium, Sunday Morning:

Plenary Session – Algae and the Tree of Life

Moderator: Rick McCourt, Academmy of Natural Sciences, USA

08:00 **Opening Remarks**

08:10 **THE HETEROKONT ALGAL TREE OF LIFE**
Andersen, R A., *Univ. Washington-Friday Harbor, USA*
Ashworth, M. P., *Univ. Texas-Austin, USA*
Boo, S. M., Chungnam *Univ., Republic Of Korea*
Cattolico, R. A., *Univ. Washington-Seattle, USA*
Draisma, S. G., *Kobe Univ., Japan*
Julius, M. L., *St. Cloud State Univ., USA*
Kawai, H., *Kobe Univ., Japan*
Jacobs, M., Univ. *Washington-Seattle, USA*
Jansen, R. K., *Univ. Texas-Austin, USA*
Nakov, T., *Univ. Texas-Austin, USA*
Rocap, G., *Univ. Washington-Seattle, Seattle, Washington USA*
Ruck, E., *Univ. Texas-Austin, Austin, Texas USA*
Theriot, E. C., *Univ. Texas-Austin, Austin, Texas USA*
Yang, E.C., *Bigelow Lab. Ocean Sci., West Boothbay Harbor, Maine USA*
Yoon, H. S., *Bigelow Lab. Ocean Sci., West Boothbay Harbor, Maine USA*
Zhengqiu, C., *Univ. Texas-Austin, Austin Texas USA*

08:35 **ASSEMBLING THE EUGLENOZOAN TREE OF LIFE**
Farmer, M.A., *Univ. of Georgia, Athens, USA*

09:00 **ASSEMBLING THE DINOFLAGELLATE TREE OF LIFE**
Delwiche, C F., *University of Maryland, USA*

09:25 **REDTOL: PHYLOGENETIC AND GENOMIC APPROACHES TO RECONSTRUCTING THE RED ALGAL (RHODOPHYTA) TREE OF LIFE.**
Yoon, H S., *Bigelow Laboratory for Ocean Sciences, USA*
Bhattacharya, D., *Rutgers University, USA*
Boo, S. M., *Chungnam National University, Republic Of Korea*
Fredericq, S., *University of Louisiana at Lafayette, USA*
Hommersand, M., *University of North Carolina at Chapel Hill, USA*
Lopez-Bautista, J., *University of Alabama, USA*
Saunders, G. W., *University of New Brunswick, Canada*
Vis, M. L., *Ohio University, USA*

09:50 **BROADLY SAMPLED MULTIGENE ANALYSES YIELD A WELL-RESOLVED EUKARYOTIC TREE OF LIFE.**
Katz, L.A., *Smith College, Northampton MA, USA*

10:15-10:45 **COFFEE BREAK -- Central Lobby**

Auditorium, Sunday Morning:

10:45 **INTRODUCING THE PSA "PHYCOPEDIA": WHAT IS IT AND HOW CAN I PARTICIPATE?**
Vis, M.L. *Ohio University*

Bold Award Competition

Moderator: Jeff Leblond, Middle Tennessee State University

11:00 **INCREASING POLYUNSATURATED FATTY ACID PRODUCTION IN THE HOST, SACCHAROMYCES CEREVISIAE, BY ENTERING THE REALM OF LIPID DESATURATION IN TETRAHYMENA THERMOPHILA**
Dahmen, J L., *Washington State University, USA*
Olsen, B., *Washington State University, USA*
Wallis, J., *Washington State University, USA*
Browse, J., *Washington State University, USA*

11:15 **BIODIVERSITY AND SYSTEMATICS OF SUBAERIAL ALGAE IN THE NEOTROPICS AND HAWAII**
Lam, D W., *University of Alabama, USA*
Rindi, F., *National University of Ireland, Galway, Ireland*
Lopez-Bautista, J. M., *University of Alabama, USA*

11:30 **MOLECULAR ASSESSMENT OF THE PARAPHYLETIC GENUS DICTYOSPHAERIUM (TREBOUXIOPHYCEAE)**
Bock, C, *Leibniz-Institute of Freshwater Ecology and Inland Fisheries, Germany*
Pröschold, T., *Department of Limnology, Univ. of Vienna, Austria*
Krienitz, L., *Leibniz-Institute of Freshwater Ecology and Inland Fisheries, Germany*

11:45 **EVOLUTION TOWARDS DEPENDENCY IN A FREE-LIVING ORGANISM**
Morris, J J., *University of Tennessee, USA*
Szul, M. J., *University of Tennessee, USA*
Johnson, Z. I., *Duke University Marine Lab, USA*
Keller, M., *Oak Ridge National Laboratory, USA*
Zinser, E. R., *University of Tennessee, USA*

12:00 **FOUR CHLOROPLAST GENE ARRANGEMENTS IN A CLOSELY RELATED GROUP OF TREBOUXIOPHYCEAE (CHLOROPHYTA)**
Letsch, M R., *University of Connecticut, USA*
Lewis, L. A., *University of Connecticut, USA*

12:15 **DIVERSE BRYOPHYTE-CYANOBACTERIAL ASSOCIATIONS AND ENVIRONMENTAL CONTROLS IN A WISCONSIN BOREAL FOREST**
Ederer, S L., *University of Wisconsin, Department of Botany, USA*
Graham, L. E., *Department of Botany, Univerity of Wisconsin, USA*

12:30 **SIGNIFICANCE OF LAND PLANT CELL WALL POLYMERS IN THE CHAROPHYCEAN GREEN ALGAE**
Kiemle, S N., *Michigan Technological University, USA*
Gretz, M. R., *Michigan Technological University, USA*

12:45 – 14:15 **LUNCH BREAK**

Auditorium; Sunday Afternoon:

Phylogenetics & Taxonomy-I

Moderator: Amy Carlile, University of Hawaii at Manoa, USA

14:15 **PHYLOGENY OF GELIDIUM (GELIDIALES, RHODOPHYTA) FROM KOREA INCLUDING A CANDIDATE OF A NEW SPECIES BASED ON MORPHOLOGY AND THREE GENE ANALYSIS**
Kim, K M., *Chungnam National University, Republic Of Kore*a
Park, J. K., *Chungnam National University, Republic Of Korea*
Hwang, I. K., *Seaweed Research Institute, Republic Of Korea*
Boo, S. M., *Chungnam National University, Republic Of Korea*

14:35 **NEW INSIGHTS INTO THE SYSTEMATICS OF THE RED ALGAL FAMILY PEYSSONNELIACEAE (PEYSSONNELIALES)**
Fredericq, S, *Department of Biology, University of Louisiana at Lafayette, USA*
Krayesky, D., *Department of Biology, Slippery Rock University, USA*
Schmidt, W., *Dept. of Biology, Univ. of Louisiana at Lafayette, Portugal*
Gabriel, D., *Departamento de Biologia, Universidade dos Açores, Portugal*
Norris, J. N., *Dept. of Biology, National Museum Natural History, Smithsonian Institution, USA*

14:55 **GIGARTINA ALVEATA FROM NEW ZEALAND: AMONG THE OLDEST AND NEWEST MARINE RED ALGAE IN THE SOUTHERN HEMISPHERE**
Hommersand, M H., *University of North Carolina, USA*
Leister, G. L., *University of North Carolina, USA*
Nelson, W. A., *National Institute of Water and Atmosphere Research (NIWA), New Zealand*

15:15 **MOLECULAR SYSTEMATICS OF THE FRESHWATER RED ALGAL GENUS, KUMANOA (BATRACHOSPERMALES, RHODOPHYTA)**
Vis, M L., *Ohio University, USA*
Necchi Jr, O., *São Paulo State University, Brazil*
Chiasson, W. B., *Ohio University, USA*
Entwisle, T. J., *Botanic Gardens Trust, Australia*

15:35 – 16:05 **COFFEE BREAK -- Central Lobby**

Auditorium; Sunday Afternoon:

Phylogenetics & Taxonomy-II

Moderator: Heroen Verbruggen, Ghent University, Belgium

16:05 **THE RED ALGAL GENUS *CHAMPIA* IN THE GULF OF MEXICO AND THE CARIBBEAN**
Schmidt, W, *Department of Biology, University of Louisiana at Lafayette, USA*
Fredericq, S., *Department of Biology, University of Louisiana at Lafayette, USA*
Wysor, B., *Department of Biology and Marine Biology, Roger Williams University, USA*
Norris, J. N., *Department of Biology, National Museum Natural History, Smithsonian Institution, USA*

16:25 **MOLECULAR DATA RESOLVES DISPUTE IN THE GELIDIALES (RHODOPHYTA)**
Maggs, C A., *Queen's University Belfast, United Kingdom*
Mineur, F., *Queen's University Belfast, United Kingdom*
Lim, P. E., *University of Malaya, Malaysia*
Sohrabipour, J., *University of Malaya, Malaysia*
Phange, S. M., *University of Malaya, Malaysia*

16:45 **PHYLOGENETIC AFFINITIES OF 'CHANTRANSIA' STAGES IN MEMBERS OF BATRACHOSPERMALES AND THOREALES (RHODOPHYTA)**
Necchi, O, *UNESP, Brazi*l
Oliveira, M. C., *USP, Brazil*

17:05 **SOLEXA AMPLIFICATION AND SEQUENCING OF RRNA GENES FROM THE CHLOROPLAST AND THE CYTOPLASM OF EUGLENA VELATA AND DETERMINATION OF ITS PHYLOGENETIC POSITION**
Kwiatowski, J, *University of Warsaw, Poland*
Karnkowska-Ishikawa, A., *University of Warsaw, Poland*
Dunin-Horkawicz , S., Max *Planck Institute for Developmental Biology, Germany*
Ayala, F. J., *University of California, USA*

Lincoln; Sunday Afternoon:

Physiology & Biochemistry-I

Moderator: Hilary McManus, University of Connecticut, USA

14:15 **KLEPTOPLASTIDY AND ALGAL DIET SPECIFICITY OF KOREAN SACOGLOSSAN MOLLUSKS**
Kim, G H., *Kongju National University, Dept. of Biology, Republic Of Korea*
Han, J. W., *Kongju National University, Dept.of Biology, Republic Of Korea*
Klochkova, T. A., *Kongju National University, Dept. of Biology, Republic Of Korea*
Kim, K. Y., *Chonnam National University, Dept. of Oceanography, Republic Of Korea*
Kim, J. H., *Chonnam National University, Dept. of Oceanography, Republic Of Korea*

14:35 **EFFECTS OF PROROCENTRUM MINIMUM ON JUVENILE BAY SCALLOPS ARE DEPENDENT UPON ALGAL PHYSIOLOGICAL STATUS**
Li, Y, *NOAA Fisheries, USA*
Sunila, I., *State of Connecticut, USA*
Wikfors, G., *NOAA Fisheries, USA*

14:55 **BIOCHEMICAL ANALYSIS OF LOW-TEMPERATURE ACCUMULATED SECONDARY METABOLITE AND ITS ENZYMES FROM A FRESHWATER GREEN ALGA, SPIROGYRA VARIANS**
Han, J W., *Department of Biology, Kongju National University, Republic Of Korea*
Kim, G. H., *Department of Biology, Kongju National University, Republic Of Korea*

15:15 **TRANSCRIPT PROFILING ACROSS VERTICAL ENVIRONMENTAL GRADIENTS IN THE GIANT KELP, *MACROCYSTIS PYRIFERA***
Konotchick, T, *Scripps Inst. of Oceanography, USA*
Dupont, C. L., J. *Craig Venter Institute, USA*
Badger, J. H., J. *Craig Venter Institute, USA*
Allen, A. E., J. *Craig Venter Institute, USA*

15:35 – 16:05 **COFFEE BREAK -- Central Lobby**

Lincoln; Sunday Afternoon:

Ecology & Population Biology-I

Moderator: Philip Bucolo, University of Alabama at Birmingham, USA

16:05 **VIDEO ANALYSIS OF ULVOID ALGAL AND ZOSTERA IN GREATER PUGET SOUND**
Nelson, T A., *Seattle Pacific University, USA*
Olson, J., *Seattle Pacific University, USA*
Imhoff, L., *Seattle Pacific University, USA*
Bowen, A., *Seattle Pacific University, USA*
Melton, M., *Seattle Pacific University, USA*

16:25 **SANCTUARY IN MACROALGAE: CHANGES IN AMPHIPOD DENSITIES AMONG MACROALGAL HABITATS IN DAY VERSUS NIGHT COLLECTIONS ALONG THE WESTERN ANTARCTIC PENINSULA**
Aumack, C F., *Univeristy of Alabama at Birmingham, USA*
Amsler, C. D., *Univeristy of Alabama at Birmingham, USA*
McClintock, J. B., *University of Alabama at Birmingham, USA*
Baker, B. J., *University of South Florida, USA*

16:45 **HIGH-FREQUENCY WATER QUALITY MONITORING IN THE CENTRAL INDIAN RIVER LAGOON, FLORIDA.**
Hanisak, M D., *Harbor Branch Oceanographic Institute at Florida Atlantic University, USA*
Davis, K. S., *Harbor Branch Oceanographic Institute at Florida Atlantic University, USA*

17:05 **RESERVOIRS VERSUS NATURAL LAKES IN PHYTOPLANKTON COMMUNITY ECOLOGY**
Bowles, B D., *Missouri State University, USA*

17:25 **ALGAL COMPOSITION AND DYNAMICS IN MESOPHOTIC CORAL REEFS, SOUTHWEST PUERTO RICO**
Ballantine, D L., *Dept. Marine Sciences, Univ. Puerto Rico, USA*
Ruiz, H., *Dept. Marine Sciences, Univ. Puerto Rico, USA*
Aponte, N. E., *Dept. Marine Sciences, Univ. Puerto Rico, USA*

Big Ten Room B, Sunday Evening – 20:00 – 22:00:

Phycological Society of America Annual Auction

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

MONDAY, 12 JULY

07:00-08:00 **CONTINENTAL BREAKFAST -- Central Lobby**

Auditorium; Monday Morning:

Plenary Session - Charophycean Green Algae (Streptophytes) and the Origin Of Land Plants

Moderator: Mike Gretz, Michigan Technological University, USA

08:00 **Opening Remarks**

08:10 **STREPTOPHYTE ALGAE AND THE EVOLUTION OF EMBRYOPHYTES**
Becker, B, *University of Cologne, Germany*

09:10 **PHYLOGENOMIC RECONSTRUCTION OF THE CHAROPHYTES: A MULTILOCUS APPROACH TO RESOLVING THE PHYLOGENY OF PLANTS' CLOSEST RELATIVES**
Timme, R E., *University of Maryland, USA*
Delwiche, C. F., *University of Maryland, USA*

09:40 **WHAT DO THE CELL WALL POLYMERS OF ALGAE TELL US ABOUT THE ORIGIN OF LAND PLANTS?**
Gretz, M R., *Michigan Technological University, USA*

10:10 – 10:40 **COFFEE BREAK -- Central Lobby**

Auditorium Monday Morning:

Phylogenetics & Taxonomy-III

Moderator: Daryl Lam, University of Alabama, USA

10:40 **RECONCILING MORPHOLOGICAL AND PHYLOGENETIC SPECIES CONCEPTS IN DESMIDS (DESMIDIALES, CHAROPHYTA).**
Hall, J D., The New York Botanical Garden, USA
Karol, K. G., The New York Botanical Garden, USA

11:00 **A SYSTEMATIC INVESTIGATION OF NITELLEAE (CHARALES, CHAROPHYTA) AND IMPLICATIONS FOR CONVENTIONAL TAXONOMY.**
Karol, K G., *The New York Botanical Garden, USA*
Casanova, M. T., *Royal Botanic Gardens, Australia*
Hall, J. D., *The New York Botanical Garden, USA*
Peréz, W., *The New York Botanical Garden, USA*
Proctor, V. W., *Texas Tech University, USA*
McCourt, R. D., *Academy of Natural Sciences, USA*

11:20 **A SYSTEMATIC INVESTIGATION OF THE *NITELLA FLEXILIS* (CHARALES, CHAROPHYTA) SPECIES COMPLEX.**
Meyer, H M., *Sarah Lawrence College, USA*
Karol, K. G., *The New York Botanical Garden, USA*

11:40 **PHYLOGENY OF THE CHAREAE (CHAROPHYTA) BASED ON ANALYSIS OF TWO PLASTID GENES (ATPB, RBCL) AND IMPLICATIONS FOR CONVENTIONAL TAXONOMY**
McCourt, R M., *Academmy of Natural Sciences, USA*
Casanova, M. T., *Royal Botanic Gardens, Australia*
Peréz, W., *New York Botanical Garden, USA*
Proctor, V. W., *Texas Tech University, USA*
Karol, K. G., *New York Botanical Garden, USA*

12:00 – 13:30 **LUNCH BREAK**

12:00 – 13:30 **Journal of Phycology Editorial Board Luncheon – State Room, Kellogg Hotel**

Lincoln; Monday Morning:

Physiology & Biochemistry-II

Moderator: Wayne Litaker, NOAA-COS, USA

10:40 **ALKALINE PHOSPHATASE ACTIVITY AND USE OF ALTERNATIVE PHOSPHORUS SOURCES BY PHYTOPLANKTON IN P-LIMITED FRESHWATER ECOSYSTEMS**
Young, E B., *University of Wisconsin-Milwaukee, USA*
Lowes, C. I., *University of Wisconsin-Milwaukee, USA*
Hanson, A. M., *University of Wisconsin-Milwaukee, USA*
Tucker, R., Purdue University, Indiana, USA
Onorevole, K., *University of Wisconsin-Milwaukee, USA*

11:00 **THE ALGAL HYPERMEDIUM CONCEPT -- HOW TO NAVIGATE THROUGH MULTIVARIATE ION-SPACE WITHOUT GETTING LOST**
Evens, T J., *USDA-ARS, US Horticultural Research Laboratory, USA*
Niedz, R.P. *USDA-ARS, US Horticultural Research Laboratory, USA*

11:20 **ALLOCATION TO CHEMICAL DEFENSES IN RESPONSE TO NUTRIENT MANIPULATIONS IN THE ULVOID GREEN ALGAE ULVA LACTUCA AND ULVARIA OBSCURA**
Van Alstyne, K L., *Western Washington University, USA*
Gifford, S. A., *Western Washington University, USA*
Gehman, A. M., *Western Washington University, USA*
Nicely, A., *Western Washington University, USA*
Chomiczewski, L. A., *Western Washington University, USA*

11:40 **METABOLIC RELOCATIONS IN DIATOMS**
Kroth, P G., *University of Konstanz, Germany*
Rio Bartulos, C., *University of Konstanz, Germany*
Ast, M., Technical *University of Kaiserslautern, Germany*
Haferkamp, I., *Technical University of Kaiserslautern, Germany*
Gruber, A., *University of Konstanz, German*

12:00 – 13:30 **LUNCH BREAK**

12:00 - 13:30 **Journal Of Phycology Editorial Board Luncheon -- State Room, Kellogg Hotel**

Room 106, Monday Afternoon:

Phyco Speed Dating! 13:30 – 14:50

Moderator: Rick McCourt, Academy of Natural Sciences, USA

Presenters can communicate short, concise, and brilliant ideas, hypotheses, half-baked theories, and cool images in 3 minutes or less! Powerpoint accepted but not required. Hand waving encouraged. This is your chance to change the paradigm. No editing, no pressure, no pain, all gain! Just sign up with Rick McCourt at rmccourt@gmail.com and show up.

Auditorium; Monday Afternoon:

Phylogenetics & Taxonomy - IV

Moderator: Naomi Philips, Arcadia University, USA

13:30 **ALGAE: HOW NUMBERLESSE THEIR NATION**
Guiry, M D., *AlgaeBase, National University of Ireland*
Guiry, G. M., *AlgaeBase, National University of Ireland*

13:50 **GEOGRAPHIC AND ECOLOGICAL ASPECTS OF SPECIATION IN MARINE MACROALGAE**
Verbruggen, H, *Ghent University, Belgium*
Tyberghein, L., *Ghent University, Belgium*

14:10 **A BIODIVERSITY SURVEY OF SUBAERIAL ALGAE FROM AN AFRICAN TROPICAL RAINFOREST**
Allali, H A., *The University of Alabama, USA*
Lopez-Bautista, J. M., *The University of Alabama, USA*

14:30 **GAMBIERDISCUS TAXONOMY AND GLOBAL DISTRIBUTION**
Litaker, R W., *NOS/NOAA, USA*

14:50 – 15:20 **COFFEE BREAK -- Central Lobby**

Auditorium; Monday Afternoon:

Ecology & Population Biology-II

Moderator: Beth Bowles, Missouri State University, USA

15:20 **COASTAL EUTROPHICATION, LAND USE CHANGES AND CERATIUM FURCA BLOOMS IN PAGO PAGO HARBOR, AMERICAN SAMOA – OR – WHY IS SOCCER BAD FOR THE ENVIRONMENT**
Morton, S L., *NOAA/NOS, USA*
Vargo, D., *American Samoa Community College, American Samoa*

15:40 **CHEMOKINETIC RESPONSES OF MOTILE PROPAGULES OF ANTARCTIC EPIPHYTE *ELACHISTA ANTARCTICA* IN THE PRESENCE OF HYDROPHILIC EXTRACTS OF COMMON RHODOPHYTES**
Bucolo, P, *University of Alabama at Birmingham, USA*
Amsler, C. D., *University of Alabama at Birmingham, USA*
McClintock, J. B., *University of Alabama at Birmingham, USA*
Baker, B. J., *University of South Florida, USA*

16:00 **LOSS OF DIATOM BIODIVERSITY IN FRESHWATERS OF THE UNITED STATES**
Stevenson, R J., *Michigan State University, USA*
Zalack, J. T., *Michigan State University, USA*

16:20 **CHEMICAL MEDIATION OF PREDATOR-PREY AND MUTUALISTIC INTERACTIONS BETWEEN ANTARCTIC MACROALGAE AND INVERTEBRATES**
Amsler, C D., *University of Alabama at Birmingham, USA*
Aumack, C. F., *University of Alabama at Birmingham, USA*
Zamzow, J. P., *University of Alabama at Birmingham, USA*
Amsler, M. O., *University of Alabama at Birmingham, USA*
McClintock, J. B., *University of Alabama at Birmingham, USA*
Baker, B. J., *University of South Florida, USA*

16:40 **FACILITATION OF TWO MORPHOLOGICALLY SIMILAR BLOOM-FORMING ULVA SPECIES BY A CO-OCCURRING SNAIL**
Guidone, M, *University of Rhode Island, USA*
Thornber, C. S., *University of Rhode Island, USA*

14:50 – 15:20 **COFFEE BREAK -- Central Lobby**

Lincoln; Monday Afternoon:

Cellular & Molecular Biology

Moderator: Erica Young, University of Wisconsin-Milwaukee, USA

15:20 **INVASION OF PROTEIN CODING GENES BY GREEN ALGAL RIBOSOMAL GROUP I INTRONS**
McManus, H A., *University of Connecticut, USA*
Lewis, L. A., *University of Connecticut, USA*
Fucíková, K., *University of Connecticut, USA*
Haugen, P., *University of Tromso, Norway*

15:40 **THE ACTIN CYTOSKELETON FROM SYMBIODINIUM CELLS**
Arzápalo-Castañeda, G I., *Unidad Académica de Sistemas Arrecifales, Instituto de Ciencias del Mar y Limnología, UNAM, Mexico*
Villanueva, M. A., *Unidad Académica de Sistemas Arrecifales, Instituto de Ciencias del Mar y Limnología, UNAM, Mexico*

16:00 **THE PHYSIOLOGICAL AND BIOCHEMICAL RESPONSE OF *GRACILARIA* UNDER PB^{2+} STRESS**
Du, H., *Florida Institute of Technology, USA*
Yan, H. B. *University of Shantou,Shantou, China*
Du, H, *University of Shantou, China*

16:20 **BIOCHEMICAL FEATURES AND SUBCELLULAR LOCALIZATION OF A 28 KDA MEMBRANE PROTEIN FROM SYMBIODINIUM.**
Castilo-Medina, R E., *Unidad Académica de Sistemas Arrecifales, Instituto de Ciencias del Mar y Limnología, UNAM, Mexico*
Thomé-Ortiz, P., *Unidad Académica de Sistemas Arrecifales, Instituto de Ciencias del Mar y Limnología, UNAM, Mexico*
Villanueva, M. A., *Unidad Académica de Sistemas Arrecifales, Instituto de Ciencias del Mar y Limnología, UNAM, Mexico*

16:40 **CONTROL OF RHIZOID FORMATION IN *VALONIA***
Elvira, P V., *Kochi University, Japan*
Okuda, K., *Kochi University, Japan*

Lincoln; Monday Evening 17:30-18:30:

PSA Annual Business Meeting

Presiding: Paul Hayes, PSA President

Big Ten Room C; Monday Evening 19:00 – 21:00

Poster Session

Hot and cold hors d'oeuvres and a cash bar

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

Presenting authors of ODD numbered posters are requested to stand with their posters at least between 19:00 and 20:00.
Presenting authors of EVEN numbered posters are requested to stand with their posters at least between 20:00 and 21:00.

P1 CELL GROWTH RATE AFFECTS LUTEIN CONTENT IN DARK GROWN CHLORELLA PYRENOIDOSA
Jiang, Y, *Dept Biology and Kwong Living Trust Food Safety & Analysis Lab, Hong Kong Baptist Univ, Hong Kong POC*
Wu, Z. Y., *Dept Biology and Kwong Living Trust Food Safety & Analysis Lab, Hong Kong Baptist Univ.*
Li, T., *Dept Biology and Kwong Living Trust Food Safety & Analysis Lab, Hong Kong Baptist Univ, Hong Kong POC*
Chen, F., *School of Biological Sciences, Univ of Hong Kong, Hong Kong POC*

P2 FRESHWATER DIATOMS AS A SOURCE OF LIPIDS FOR BIOFUELS
Graham, L K., *University of Wisconsin, USA*
Graham, J. M., *University of Wisconsin, USA*
Zulkifly, S., *University of Wisconsin, USA*
Pfleger, B., *University of Wisconsin USA*
Hoover, S., *University of Wisconsin, USA*

P3 ALGAL SPECIES DIVERSITY IN TWO EXPERIMENTAL ALGAL PRODUCTION SYSTEMS IN SOUTHEASTERN PENNSYLVANIA
Laughinghouse, H D., *Natl. Museum of Natural Hist., Smithsonian Inst. & Univ. of Maryland, USA*
Kangas, P. C., *Environmental Science and Technology Dept., Univ. of Maryland, USA*
Adey, W. H., *Dept. of Botany, Natl. Museum of Natural Hist., Smithsonian Inst., USA*

P4 SEQUENCING AND ANALYSIS OF THE MITOCHONDRIAL GENOME OF *GRACILARIA TENUISTIPITATA* (GRACILARIALES, RHODOPHYTA)
Takahashi, M M., *Dept of Botany, Inst of Biosciences, University of Sao Paulo, Brazil*
Oliveira, M. C., *Dept of Botany, Inst of Biosciences, University of Sao Paulo, Brazil*

P5 THE ROLE OF WOUND-RESPONSIVE GENES FROM A MARINE RED ALGA, GRIFFITHSIA MONILIS

Han, J H., *Department of Biology , Kongju National University, Republic Of Korea*
Kim, G. H., *Department of Biology, Kongju National University, Republic Of Korea*

P6 PURIFICATION OF FETUIN BINDING LECTIN FROM THE MARINE BROWN ALGA, SCYTOSIPHON LOMENTARIA

Yang, H Y., *Department of Biology, Kongju National University, Republic Of Korea*
Kim, G. H., *Department of Biology, Kongju National University, Republic Of Korea*

P7 MOLECULAR CLONING AND CHARACTERIZATION OF WINGED BEAN LECTIN (WBL)-LIKE GENE FROM FRESHWATER GREEN ALGA, SPIROGYRA VARIANS

Moon, K H., *Kongju Uni., Republic Of Korea*
Han, J. W., *Kongju Uni., Republic Of Korea*
Kim, G. H., *Kongju Uni., Republic Of Korea*

P8 POLYCLONAL ANTIBODIES TO DIMETHYLSULFONIOPROPIONATE (DMSP): INITIAL CHARACTERIZATION AND SPECIFICITY TESTING

Moon, J, *Seattle Pacific University, USA*
Nguyen, M. A., *Seattle Pacific University, USA*
Nelson, T. A., *Seattle Pacific University, USA*
Ridgway, R. L., *Seattle Pacific University, USA*

P9 ISOLATION AND CHARACTERIZATION OF SEX-SPECIFIC ACONITASE-LIKE GENE FROM SCYTOSIPHON LOMENTARIA

Kim, R W., *Department of Biology, Kongju National University, Republic Of Korea*
Han, J. W., *Department of Biology, Kongju National University, Republic Of Korea*
Kim, G. H., *Department of Biology, Kongju National University, Republic Of Korea*

P10 ASSEMBLING THE CHLOROPLAST GENOMES OF EUGLENOIDS

Wiegert, K E., *Michigan State University, USA*
Bennett, M. S., *Michigan State University, USA*
Triemer, R. E., *Michigan State University, USA*

P11 PURIFICATION AND CHARACTERIZAGTION OF A SEX-SPECIFIC LECTIN FROM AGLAOTHAMNION CALLOPHYLLIDICOLA (RHODOPHYTA)

Shim, E Y., *Department of Biology, Kongju National University, Republic Of Korea*
Kim, G. H., *Department of Biology, Kongju National University, Republic Of Korea*

P12 IDENTIFICATION OF THE HIGH TEMPERATURE RESPONSIVE GENES FROM PORPHYRA SERIATA ESTS AND ENHANCEMENT OF HEAT TOLERANCE BY EXPRESSING OF PORPHYRA HTR2 GENE

Kim, E C., *Chonnam National University, Republic Of Korea*
Park, H. S., *Chonnam National University, Republic Of Korea*
Jung, Y. J., *Chonnam National University, Republic Of Korea*
Park, H. S., *Korea Research Institute of Bioscience and Biotechnology, Republic Of Korea*
Jeong, W. J., *Korea Research Institute of Bioscience and Biotechnology, Republic Of Korea*
Hwang, M. S., *Seaweed Research Institute, NFRDI, Republic Of Korea*
Park, E. J., *Seaweed Research Institute, NFRDI, Republic Of Korea*
Gong, Y. G., *Seaweed Research Institute, NFRDI, Republic Of Korea*
Choi, D. W., *Chonnam National University, Republic Of Korea*

P13 SEX-SPECIFIC EXPRESSION OF TRANSPOSABLE ELEMENTS IN AGLAOTHAMNION CALLOPHYLLIDICOLA (RHODOPHYTA)
Shim, J B., *Department of Biology, Kongju National University, Republic Of Korea*
Kim, G. H., *Department of Biology, Kongju National University, Republic Of Korea*

P14 APOPTOTIC AND ANTI-INFLAMMATORY EFFECT OF METHANOLIC EXTRACT FROM FRESHWATER GREEN ALGA, SPIROGYRA VARIANS, ON CHONDROCYTES AND CANCER CELLS
Kwak, M S., *Department of Biology, Kongju National University, Republic Of Korea*
Yu, S. M., *Department of Biology, Kongju National University, Republic Of Korea*
Kim, S. J., *Department of Biology, Kongju National University, Republic Of Korea*
Kim, G. H., *Department of Biology, Kongju National University, Republic Of Korea*

P15 GENETIC DIVERSITY OF INVASIVE GRACILARIA VERMICULOPHYLLA (GRACILARIALES, RHODOPHYTA) BASED ON MITOCHONDRIAL COX1 SEQUENCE.
Kim, K, *Chungnam National University, Republic Of Korea*
Weinberger, W., *IFM-GEOMAR, Germany*
Boo, B., *Chungnam National University, Republic Of Korea*

P16 A SEASONAL STUDY OF CHANGES IN PHYTOPLANKTON AND NUTRIENTS IN THE CALUMET RIVER, ILLINOIS.
Bertucci, A, *Chicago State University, USA*
Potluri, V., *Chicago State University, USA*
Dennis, N., *Chicago State University, USA*

P17 ENVIRONMENTAL FACTORS CONTROLLING THE PHYTOPLANKTON COMMUNITY STRUCTURE IN FRESH WATER BODIES OF MISSISSIPPI
Anzola, N R., *The University of Southern Mississippi, USA*
Pessoney, G. F., *The University of Southern Mississippi, USA*

P18 CALOTHRIX – A REVIEW OF FRESH WATER SPECIES FOUND IN THE USA AND PRELIMINARY DISTRIBUTION DATA FROM THE RECENT NATIONAL RIVERS AND STREAMS ASSESSMENT (NRSA).
Rinkel, B E., *Patrick Center for Environmental Research, Academy of Natural Sciences, USA*
Manoylov, K. M., *Georgia College and State Univ., Dept of Biological and Environmental Sciences, USA*

P19 THE EFFECT OF ENDOPHYTE INFECTION ON GROWTH AND SURVIVORSHIP OF ANTARCTIC MACROALGAE (RHODOPHYCEAE).
Schoenrock, K M., *University of Alabama, Birmingham, USA*
Amsler, C. D., *University of Alabama, Birmingham, USA*
McClintock, J. B., *University of Alabama, Birmingham, USA*
Baker, B. J., *University of South Florida, USA*

P20 REPORT OF A NEW INVASIVE ALGA IN THE ATLANTIC UNITED STATES: *'HETEROSIPHONIA' JAPONICA* YENDO IN RHODE ISLAND
Schneider, C W., Trinity College, USA

P21 ABUNDANCE AND DISTRIBUTION SURVEYS OF MACROALGAL BLOOMS IN NEW ENGLAND SALT MARSHES

Newton, C, *University of Rhode Island, USA*
Thornber, C., *University of Rhode Island, USA*

P22 REACTIVE OXYGEN SPECIES AS A POTENTIAL MACROALGAL DEFENSE ALONG THE WESTERN ANTARCTIC PENINSULA

McDowell, R E., *University of Alabama at Birmingham, USA*
Amsler, C. D., *University of Alabama, Birmingham, USA*
McClintock, J. B., *University of Alabama, Birmingham, USA*
Baker, B. J., *University of South Florida, USA*

P23 USING MACROALGAE TO TRACK ENVIRONMENTAL CHANGES IN THE GREAT BAY ESTUARINE SYSTEM

Nettleton, J C., *University of New Hampshire, USA*
Neefus, C. D., *University of New Hampshire, USA*
Mathieson, A. C., *University of New Hampshire, USA*

P24 A SURVEY OF PHYTOPLANKTON DIVERSITY AND ENVIRONMENTAL ATTRIBUTES ACROSS AN OLIGOHALINE, SUBTROPICAL ESTUARY UTILIZING PIGMENT ANALYSES AND PSBA DNA SEQUENCES

Wee, J L., *Loyola University - New Orleans, USA*
Lakeman, M. B., *University of Washington, USA*
Millie, D. F., *University of South Florida and Florida Fish and Wildlife Conservation Commission, USA*
Evens, T. J., *USDA-ARS, Horticultural Research Laboratory, USA*
Cattolico, R. A., *University of Washington, USA*

P25 COMPARATIVE ANALYSIS AND FUNCTIONAL ANNOTATION OF EXPRESSED SEQUENCE TAGS (ESTS) FROM COLD AND NON-ACCLIMATED FRESHWATER GREEN ALGA, SPIROGYRA VARIANS

Han, J W., *Department of Biology, Konju National University, Republic Of Korea*
Kim, G. H., *Department of Biology, Konju National University, Republic Of Korea*

P26 NUTRIENT CONTRIBUTIONS FROM *DREISSENA* TO THE BENTHIC CYANOBACTERIUM *LYNGBYA WOLLEI*.

Armenio, P M., *University of Toledo Lake Erie Center, USA*
Mayer, C. M., *University of Toledo Lake Erie Center, USA*

P27 EFFECTS OF IRON DEFICIENCY ON THE PHOTOSYNTHETIC APPARATUS AND ANTIOXIDANT DEFENSE SYSTEM OF DUNALIELLA TERTIOLECTA

Traggis, H M., *University of New Hampshire, USA*
Jahnke, L. S., *University of New Hampshire, USA*

P28 STEROL BIOSYNTHESIS IN THE MARINE DINOFLAGELLATE, KARENIA BREVIS

Roche, S A., *Middle Tennessee State Univ, USA*
Porter, N. M., *Middle Tennessee State Univ. USA*
Leblond, J. L., *Middle Tennessee State Univ, USA*

P29 WHAT IS THE ULTIMATE EFFECT ON SPOROPHYTE FORMATION AFTER LONG-TERM CULTIVATION OF GAMETOPHYTES FROM TWELVE SPECIES OF LAMINARIALES?

Muraoka, D, *Tohoku National Fisheries Research Institute, Fisheries Res. Agency, Japan*
Sakami, T., *Tohoku National Fisheries Research Institute, Fisheries Res. Agency, Japan*
Okumura, Y., *Tohoku National Fisheries Research Institute, Fisheries Res. Agency, Japan*

P30 WESTERN LAKE ERIE MICROCYSTIS IS PHOSPHORUS LIMITED EVEN UNDER LOW NITROGEN AVAILABILITY

Chaffin, J D., *University of Toledo, USA*
Bridgeman, T. B., *University of Toledo, USA*
Heckathorn, S. A., *University of Toledo, USA*
Mishra, S., *University of Toledo, USA*

P31 OPTIMAL CONDITIONS OF IRRADIANCE AND TEMPERATURE FOR TRIGLYCERIDE-ASSOCIATED FATTY ACID PRODUCTION IN THE GREEN ALGA, *CHLAMYDOMONAS REINHARDTII*

Gray, E L., *Middle Tennessee State University*
Leblond, J. D., *Middle Tennessee State University, USA*

P32 PHYLOGENY AND BIOGEOGRAPHY OF THE GENUS AGARUM (PHAEOPHYCEAE) BASED ON SEQUENCES OF THREE GENES

Boo, G H., *Chungnam National University, Republic Of Korea*
Lindstrom, S., *University of British Columbia, Canada*
Klochkova, N., *Kamchatka Institute of Ecol. and Nature Management, Russian Federation*
Yotsukura, N., *Hokkaido University, Japan*
Yang, E. C., *Bigelow Laboratory for Ocean Sciences, USA*
Kim, H. G., *Kangnung-Wonju National University, Republic Of Korea*
Waaland, J. R., *University of Washington, USA*
Cho, G. Y., *National institute of Biological Resources, Republic Of Korea*
Boo, S. M., *Chungnam National University, Republic Of Korea*

P33 SYSTEMATICS OF THE GENUS MONOMORPHINA (EUGLENACEAE)

Kim, J I., *Chungnam National University, Republic Of Korea*
Shin, W., *Chungnam National University, Republic Of Korea*

P34 PHYLOGENY OF AUSTRALASIAN ENDEMIC TAXA IN THE BATRACHOSPERMALES (RHODOPHYTA) USING THE RBCL AND LSU GENES.

Johnston, E T., *Ohio University, USA*
Stewart, S. A., *Ohio University, USA*
Entwisle, T. J., *Royal Botanic Gardens, Australia*
Vis, M. L., *Ohio University, USA*

P35 PHYLOGENY OF THE GENUS MALLOMONAS (SYNUROPHYCEAE) BASED UPON ULTRASTRUCTURE AND MOLECULAR DATA

Jo, B Y., *Chungnam National University, Republic Of Korea*
Shin, W. G., *Chungnam National University, Republic Of Korea*
Andersen, R. A., *Friday Harbor Laboratory, Univ. of Washington, USA*
Kim, H. S., *Kyungpook National University, Republic Of Korea*
Kim, J. H., *Kyungpook National University, Republic Of Korea*

P36 EXPLORING GELIDIALES (RHODOPHYTA) DIVERSITY ON SAO PAULO STATE (BRAZIL) WITH MOLECULAR MARKERS.
Milstein, D, *University of Sao Paulo, Brazil*
Iha, C., *University of Sao Paulo, Brazil*
Guimarães, S. M., *Institute of Botany, Brazil*
Oliveira, M. C., *University of Sao Paulo, Brazil*

P37 REVIEWING THE GENUS CYCLIDIOPSIS: IS THE CURRENT TAXONOMY VALID?
Bennett, M S., *Michigan State University, USA*
Triemer, R. E., *Michigan State University, USA*

P38 DIVERSITY OF DIATOM NITRATE TRANSPORTER GENES FROM ISOLATED SINGLE-CELLS AND MIXED SAMPLES FOR THE ESTABLISHMENT OF MRNA QUANTIFICATION IN THE EAST CHINA SEA
Kang, L, *Institute of Marine Biology, Taiwan Ocean University, Taiwan ROC*
Wang, H., *Institute of Marine Biology, Taiwan Ocean University, Taiwan ROC*
Chang, J., *Institute of Marine Biology, Taiwan Ocean University, Taiwan ROC*

P39 A UNIQUE NEW SPECIES OF *CALOGLOSSA* (DELESSERIACEAE, RHODOPHYTA) FROM PEDRO MIGUEL LOCKS, MIRAFLORES LAKE, PANAMA, CENTRAL AMERICA
Krayesky, D M., *Slippery Rock University, USA*
Norris, J. N., *Smithsonian Institution, USA*
West, J. A., *University of Melbourne, Australia*
Wysor, B., *Roger Williams University, USA*
Fredericq, S., *University of Louisiana at Lafayette, USA*

P40 CELL DIVISION IN THE CHAROPHYCEAN GREEN ALGA *ENTRANSIA FIMBRIATA*
Rockwell, T R., *Illinois State University, USA*
Vitale, A. M., *Illinois State University, USA*
Cook, M. E., *Illinois State University, USA*

P41 THE SPECIES EUGLENA DESES (EUGLENACEAE) REVISITED: NEW MORPHOLOGICAL AND MOLECULAR DATA
Karnkowska-Ishikawa, A, *University of Warsaw, Poland*
Milanowski, R., *University of Warsaw, Poland*
Zakryś, B., *University of Warsaw, Poland*

P42 NEW INSIGHTS INTO THE TAXONOMIC POSITION OF THE ENDEMIC BROWN ALGAL GENUS *CLADOPHYLLUM* FROM THE CARIBBEAN COAST OF COLOMBIA WITHIN THE SARGASSACEAE
Camacho, O, *Department of Biology, University of Louisiana at Lafayette, USA*
Mattio, L., *Institut de Recherche pour le Développement, New Caledonia*
Diaz-Pulido, G., *Griffith School of Environment, Griffith University, Australia*
Draisma, S. G., *Institute of Ocean & Earth Sciences, University of Malaya, Malaysia*

P43 PHYLOGENY OF FRESHWATER EUSTIGMATOPHYCEAE
Fawley, K P., *University of Arkansas at Monticello, USA*
Fawley, M. W., *University of Arkansas at Monticello, USA*
Eliáš, M., *Charles University in Prague, Czech Republic*
Nemjová , K., Charles *University in Prague, Czech Republic*
Probst, N., *University of Arkansas at Monticello, USA*

P44 A SYSTEMATIC REVISION OF TOLYPELLA A. BR. (CHARALES, CHAROPHYTA): PRELIMINARY INVESTIGATIONS.
Perez, W, *City University of New York, USA*
Karol, K. G., *The New York Botanical Garden,Lewis B. and Dorothy Cullman Program for Molecular Systematics Studies, USA*

P45 NEW INSIGHTS INTO THE SYSTEMATICS OF BLADE-LIKE MARINE RED ALGAE FROM THE GULF OF MEXICO
Arakaki, N C., *University of Louisiana at Lafayette, USA*
Fredericq, S., *University of Louisiana at Lafayette, USA*

P46 EUGLENOID PHYLOGENETICS BASED ON THE EVALUATION OF PROTEIN AND RIBOSOMAL CODING GENES
Watza, D G., *MSU Department of Plant Biology, USA*
Kim, J., *Chungnam National University, Republic of Korea*
Bennett, M., *MSU Department of Plant Biology, USA*
Lowery, C., *MSU Department of Plant Biology, USA*
Wiegert, K., *MSU Department of Plant Biology, USA*
Triemer, R., *MSU Department of Plant Biology, USA*

P47 THE HAWAIIAN FRESHWATER ALGAL DATABASE
Sherwood, A R., *University of Hawaii, USA*
Carlile, A. L., *University of Hawaii, USA*
Neumann, J. M., *University of Hawaii, USA*
Wang, N., *University of Hawaii, USA*
Presting, G. G., *University of Hawaii, USA*

P48 TWO RARE ZYGNEMA SPECIES (ZYGNEMATOPHYCEAE) FROM CALIFORNIA STREAMS
Stancheva, R, *California State University San Marcos, USA*
Sheath, R., *California State University San Marcos, USA*
Hall, J., *The New York Botanical Garden, USA*

P49 THE GENUS CERAMIUM ROTH IN CABO SAN ROMÁN, FALCÓN STATE WITH EMPHASIS ON SPECIES BEARING PSEUDOPERIAXIAL CELLS
García-Soto, G C., *Universidad del Zulia , Venezuela*
Sanchez, A. M., *Universidad del Zulia , Venezuela*

Tuesday, 13 JULY

07:00-08:00 **CONTINENTAL BREAKFAST -- Central Lobby**

Auditorium; Tuesday Morning:

Plenary Session – Lipids and Lipidomics in Algae

Moderator: Jeff Leblond, Middle Tennessee State University

08:00 Opening Remarks

08:05 **Joyce Yang, US Dept. of Energy – DOE and Algal Biofuels**

08:10 **ALGAE: DIVERSE LIPIDS WITH MANY USES**
Harwood, J.L., *School of Bioscience, Cardiff University, UK*

09:10 **LIPIDOMIC: LIPID TARGETED ALGAL TOXINS**
Place, A R., *UMCES/IMET, USA*

09:40 **LIPIDOMICS: RECENT APPLICATIONS TO THE STUDY OF DINOFLAGELLATE CHLOROPLAST LIPIDS**
Leblond, J D., *Dept. of Biology, Middle Tennessee State University, USA*

10:10 – 10:40 **COFFEE BREAK -- Central Lobby**

Auditorium; Tuesday Morning:

Phylogenetics & Taxonomy - V

Moderator: John Hall, The New York Botanical Garden, USA

10:40 **ULTRASTRUCTURE AND MOLECULAR EVIDENCE REVEAL ARAPHID PENNATE ANCESTRY FOR A ROUND, UNDESCRIBED TROPICAL DIATOM**
Ashworth, M P., *University of Texas at Austin, USA*
Ruck, E. C., *University of Texas at Austin, USA*
Romanovicz, D. K., *University of Texas at Austin, USA*
Lobban, C. S., *University of Guam, USA*
Theriot, E. C., *University of Texas at Austin, USA*

11:00 **PHYLOGENY OF THE DIATOMS BASED ON CHLOROPLAST GENES**
Theriot, E C., *University of Texas at Austin, USA*
Ruck, E. C., *University of Texas at Austin, USA*
Ashworth, M., *University of Texas at Austin, USA*
Nakov, T., *University of Texas at Austin, USA*
Jansen, R. K., *University of Texas at Austin, USA*
Brady, M., *University of Texas at Austin, USA*

11:20 **PHYLOGENETIC ANALYSES OF GLUTAMINE SYNTHETASE III PROVIDES EVIDENCE OF A RECENT HORIZONTAL GENE TRANSFER FROM DIATOMS TO THE PRASINOPHYTES**
Robertson, D L., *Clark University, USA*
Ghoshroy, S., *Clark University, USA*

11:40 **SIZING THE HERTEROKONT: PHAEOPHYCEAN GENOME**
Phillips, N, *Arcadia University, USA*
Kapraun, D., *Univ. of N. Carolina, USA*
Garreta, A. G., *Univ. de Barcelona, Spain*
Siguan, A. R., *Univ. de Barcelona, Spain*
Rull, J. L., *Univ. de Barcelona, Spain*
Soler, N. S., *Univ. de Barcelona, Spain*
Braun, E., *University of Florida, USA*
Lewis, R., *Wheaton College, USA*
Kawai, H., *Kobe University Research Center for Inland Seas, Japan*

12:00 – 13:30 **LUNCH**

Auditorium; Tuesday Afternoon:

Phylogenetics & Taxonomy - VI
Moderator: Ken Karol, The New York Botanical Garden, USA

13:30 **THE TANGLED TAXONOMIC HISTORY OF DICTYOCOCCUS, BRACTEACOCCUS AND PSEUDOMURIELLA (CHLOROPHYCEAE) AND THE IR DISTINCTION BASED ON A PHYLOGENETIC PERSPECTIVE**
Fucikova, K, *University of Connecticut, USA*
Rada, J. C., *University of Connecticut, USA*
Lewis, L. A., *University of Connecticut, USA*

13:50 **THE TROPICAL FRESHWATER GREEN ALGA *CLONIOPHORA SPICATA* IS A MEMBER OF ULVALES (ULVOPHYCEAE), NOT CHAETOPHORALES (CHLOROPHYCEAE)**
Carlile, A L., *University of Hawaii at Manoa, USA*
O'Kelly, C. J., *Friday Harbor Laboratories, USA*
Sherwood, A. R., *University of Hawaii at Manoa, USA*

14:10 **SPECIES CHARACTERIZATION IN DESMODESMUS (CHLOROPHYCEAE) USING NUCLEAR ITS AND PLASTID RBCL SEQUENCE DATA COMBINED WITH MORPHOLOGICAL ANALYSES.**
Fawley, M W., *University of Arkansas at Monticello, USA*
Fawley, K. P., *University of Arkansas at Monticello, USA*
Hegewald, E., *Institute of Chemistry and Dynamics of the Geosphere 3, Germany*

14:30 **CRYPTIC SPECIES DIVERSITY IN THE SHELL- AND REEF-BORING GREEN ALGAL GENUS PHAEOPHILA**
O'Kelly, C J., *Friday Harbor Laboratories, University of Washington, USA*

Lincoln; Tuesday Afternoon:

Biotechnology

Moderator: Marco Villanueva, Unidad Académica de Sistemas Arrecifales, Instituto de Ciencias del Mar y Limnología, UNAM, Mexico,

13:30 **AN OVERVIEW OF ALGAL BIOFUELS RESEARCH AND DEVELOPMENT EFFORTS AT THE DOE BIOMASS PROGRAM**
Yang, J C., *U.S. Department of Energy, Office of Energy Efficiency and Renewable Energy, Biomass Program, USA*
Pate, R. C., *US Dept. of Energy, Office of Energy Efficiency and Renewable Energy, Biomass Program, USA*
Morello, J. E., *US Dept. of Energy, Office of Energy Efficiency and Renewable Energy, Biomass Program, USA*
Fishman, D. B., *US Dept. of Energy, Office of Energy Efficiency and Renewable Energy, Biomass Program, USA*
Sarisky-Reed, V. A., *US Dept. of Energy, Office of Energy Efficiency and Renewable Energy, Biomass Program, USA*

13:50 **ACCELERATING RESEARCH AND DEVELOPMENT FOR ALGAL BIOFUELS THROUGH A COLLABORATIVE APPROACH**
Bhaduri, B, Oak Ridge National Laboratory
Rose, A., *Oak Ridge National Laboratory, USA*
Myers, A., *Oak Ridge National Laboratory, USA*
Goss Eng, A., *US Department of Energy, USA*

14:10 **TESTING A PRODUCT CLAIM WITH AN INTEGRATIVE APPROACH: ENGAGEMENT BY ALGAL BIOLOGISTS**
Brawley, S H., *University of Maine, USA*
Bradford, E. A., *University of Maine, USA*
Brown, S. W., *University of Maine, USA*
Carley, J. D., *University of Maine, USA*
Clark, A. R., *University of Maine, USA*
Marceau, N. F., *University of Maine, USA*
Philbrook, I. C., *University of Maine, USA*
Picard, M. R., *University of Maine, USA*
Webb, E. M., *University of Maine, USA*
Gettings, R., *Uniiversity of Maine, USA*
Snow, N., *University of Maine, USA*
May, R., *University of Maine, USA*
Caldwell, S., *University of Maine, USA*
McDaniel, H., *University of Maine, USA*
Bishop, C., *University of Maine, USA*
Erhart, S., *University of Maine, USA*

14:30 **CULTURE OF G. LEMANEIFORMIS 981 AND INDUSTRIAL CULTIVATION IN CHINA**
Zhang, X, *Ocean University of China, China, xczhang8@163.com; Fei, X., Institute of Oceanography, China*

14:50 **TYPE II PHOTOBIOREACTOR HYBRID SYSTEM WITH DISSOLVED CO2 MEMBRANE DISTRIBUTION TECHNOLOGY, MODULE INCLUDES ALGAL LIPID OIL EXTRACTION PROCESS.**
Tsoupeis, D D., *Culturing Solutions, USA*

15:10 **BIOMASS AND OIL PRODUCTIVITY OF A *SCENEDESMUS RUBESCENS* LIKE MICROALGA, A PROMISING CANDIDATE FOR BIODIESEL PRODUCTION**
Lin, Q., *Florida Institute of Technology, Melbourne, FL, USA*
Lin, J., *Florida Institute of Technology, Melbourne, FL, USA*
Tan, Y., *Florida Institute of Technology, Melbourne, FL, U*

Big Ten Room B; Tuesday Evening:

18:00-21:00 – PSA Banquet and Awards Ceremony

ABSTRACTS

ABSTRACTS NUMBERS ARE VERY CLOSE TO ABSTRACT PRESENTATION ORDER.

SEE AUTHOR INDEX STARTING ON PAGE 81 TO FIND SPECIFIC ABSTRACTS.

1.

THE HETEROKONT ALGAL TREE OF LIFE

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Zhengqiu, C., Univ. Texas-Austin, Austin Texas USA

The heterokont algae include large groups such as the diatoms and brown seaweeds as well as the chrysophytes, xanthophytes and about a dozen other classes. These algae are related to nonphotosynthetic stramenopiles such as the oomycetes, thraustochytrids and bicosoecids. Despite a long history dating from Linnaeus, the phylogenetic relationships among the heterokont algae still remain unresolved. Our group has addressed the problem using multi-gene phylogenetic analyses and chloroplast genome comparisons, and only the multigene analyses will be discussed in this talk. Our analyses recovered relationships found previously, and we have found support that expands those relationships. For example, the PX clade (Phaeophyceae/Xanthophyceae) includes the Schizocladiophyceae, Phaeothamniophyceae, Arearenophyceae, Chrysomerophyceae and Raphidophyceae. We also recover a large clade that includes the Chrysophyceae/Synurophyceae/Synchromophyceae/Eustigmatophyceae and perhaps the Pinguiophyceae. The relationships between the Bacillariophyceae/Bolidophyceae and Dictyochophyceae/Pelagophyceae are recovered, and there is weak evidence that these four classes form a larger clade. We continue to add new genes to our analyses, and we expect to add more resolution to the large clade of heterokont algae in the coming months.

2.

ASSEMBLING THE EUGLENOZOAN TREE OF LIFE

Farmer, M.A., Univ. of Georgia, Athens, USA, farmer@cb.uga.edu

The protistan clade Euglenozoa consists of a group of broadly diverse flagellates, exemplifying great evolutionary, ecological, medical and economic significance. Previous phylogenetic studies of these organisms have focused on a few gene sequences from a very limited number of taxa, producing conflicting results for evolutionary relationships. This project will clarify these

relationships at several different levels. The Euglenozoa may also represent a critical phase in the evolution of the eukaryotic cell. By some accounts they are among the most ancient group of mitochondrion bearing organisms. This project seeks to clarify the relationships among subgroups of Euglenozoa (Euglenida, Diplonemida, and Kinetoplastida), and the origins of many important and unusual biological processes exhibited by these organisms. The objectives of the project are: 1) deep sequencing of normalized cDNA libraries from 30-40 strategically selected species of Euglenozoa using 454 GS FLX technologies; 2) parallel phylogenetic analysis of as large orthologous gene panels from these organisms; 3) PCRamplification/ analysis of ~50 genes in 200-250 Euglenozoan spp.

3.
ASSEMBLING THE DINOFLAGELLATE TREE OF LIFE

Delwiche, C F., University of Maryland, USA, delwiche@umd.edu;

Dinoflagellates are environmentally important in aquatic environments ranging from the open ocean to lakes, ponds, and puddles. They display a wide range of trophic strategies including phototrophy, heterotrophy, and mixotrophy, and consequently play highly diverse environmental roles. Phylogenetic study of dinoflagellates has been similarly scattered and diverse, probably in part because they have historically been treated in more than one taxonomic tradition, and in part because they can be very difficult to study. To move toward a comprehensive phylogeny of dinoflagellates we have assembled a team with experience with both photosynthetic and non-photosynthetic species, and are applying multiple approaches to phylogeny. We have used both targeted PCR and environmental molecular sampling to explore the different views of diversity these approaches provide, and complement these studies with structural studies at the the light- and electron- microscopic levels, morphological and molecular studies of cysts. The goal is a phylogeny of at least 100 species of dinoflagellates that makes use of multiple genes and spans the full taxonomic, trophic, and habitat diversity found within the group.

4.
REDTOL: PHYLOGENETIC AND GENOMIC APPROACHES TO RECONSTRUCTING THE RED ALGAL (RHODOPHYTA) TREE OF LIFE.

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Red algae (Rhodophyta) are important aquatic primary producers that are one of the most anciently diverged eukaryotic phyla. The red algal plastid is widespread in the Tree of Life (ToL) among chromalveolates. In spite of its obvious importance, the Rhodophyta is under-studied. To fill this gap in eukaryote phylogeny, we assembled a research team of eight red algal taxonomy and genomics experts to address fundamental questions of red algal evolution and their place in the ToL. To accomplish the aims of RedToL, we will: 1) reconstruct a robust phylogeny of 471 red algal species using a concatenated dataset of 2 nuclear, 4 plastid, and 2 mitochondrial encoded gene markers, 2) sequence plastid genomes and generate transcriptome or genome databases for 16 key taxa that represent the phylogenetic (e.g., class- and order-level) breadth of red algae, and 3)

make freely available red algal multi-gene and genome data via release to GenBank and a project-specific web site. Here we will introduce the aims and strategies of RedToL with highlights of research results from Year-1 as well as outreach efforts.

5.
BROADLY SAMPLED MULTIGENE ANALYSES YIELD A WELL-RESOLVED EUKARYOTIC TREE OF LIFE.

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We have been using taxon-rich analyses to assess the eukaryotic tree of life, including the recently proposed high-level 'supergroups'. Phylogenomic studies support many of supergroups but the paucity of major eukaryotic lineages (19 or fewer of the ~75 lineages) included in such studies reduces power to evaluate hypotheses and may exaggerate systematic error. We show that emphasizing broad taxonomic sampling (we include up to 451 taxa representing 72 major lineages in our most recent analyses) combined with a moderate number of genes yield a well-resolved eukaryotic tree of life (Parfrey et al., in press, Syst. Biol). We find remarkable consistency across analyses with varying numbers of taxa (88-451) and levels of missing data (17-69%), supporting the accuracy of the resulting topologies. Further, a stable topology emerges without the removal of rapidly evolving genes or taxa, a practice common to phylogenomic analyses. Several major groups are both stable and strongly supported in these analyses (e.g. SAR, Rhizaria, Excavata), while the proposed supergroup 'Chromalveolata' is rejected. Further, the extensive instability in the position of many photosynthetic lineages suggests the presence of systematic biases such as endosymbiotic gene transfer from symbiont (nucleus or plastid) to host. Our analyses demonstrate that stable topologies of ancient evolutionary relationships can be achieved with broad taxonomic sampling and a moderate number of genes.

6.
INCREASING POLYUNSATURATED FATTY ACID PRODUCTION IN THE HOST, SACCHAROMYCES CEREVISIAE, BY ENTERING THE REALM OF LIPID DESATURATION IN TETRAHYMENA THERMOPHILA

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Olsen, B., Washington State University, USA
Wallis, J., Washington State University, USA
Browse, J., Washington State University, USA

Model organisms including yeast are often used in biotechnology to produce novel or unusual fatty acids. Delta 6 desaturases are vital in the production of these nutritional polyunsaturated lipids such as linolenic acid (18:3). The delta 6 desaturase from the ciliated protist, Tetrahymena thermophila (TtDes6) was characterized by expression in yeast. When yeast cells were fed 18:2(9,12), 4% is desaturated into 18:3(6, 9, 12). However, when coexpressed with the cytochrome b5 protein from Arabidopsis, desaturation increased to 40%. We have recently identified three putative cytochrome b5s in T. thermophila (TtCB5-A,B,and C). Two of the T. thermophila cytochrome b5s (TtCB5-A and TtCB5-B) when coexpressed with TtDes6 also shows an increase in desaturation to 40% and 25% respectively. The increases in desaturation observed with the addition of cytochrome b5s from Arabidopsis and T. thermophila illustrates the importance of the interaction between cytochrome b5s and desaturases in the synthesis of polyunsaturated fatty acids. Current studies are focused on the understanding of the protein-protein interactions between cytochrome b5s from T. thermophila and S. cerevisiae and the T. thermophila delta 6 desaturase. Elucidation of these interactions will aid in identifying factors required to produce an abundance of polyunsaturated fatty acids in heterologous systems.

7.
BIODIVERSITY AND SYSTEMATICS OF SUBAERIAL ALGAE IN THE NEOTROPICS AND HAWAII

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Terrestrial algae from the rainforests of Panama and Suriname as well as the beaches of Oahu were collected for biodiversity and systematic investigations. Biodiversity assessments were based on environmental DNA sequences. Systematic biology techniques include morphological observations via light and electron microscopy as well as multigene molecular phylogenies inferred via Bayesian inference, maximum likelihood, and parsimony methods. Environmental sequence results suggest that the Surinamese rainforest Raleighvallen is comprised of various chlorophytan, cyanobacterial, and diatom taxa. Molecular phylogenetic analyses of the chlorophytan order Trentepohliales collected from Panama strongly suggest that the genera *Printzina* and *Trentepohlia* do not form separate monophyletic lineages. These results indicate that the morphological characteristics currently used to distinguish these two genera need to be reassessed. The green alga *Spongiochrysis hawaiiensis* is a common epiphyte of *Casuarina* trees on Waimanalo state park on the island of Oahu. Molecular phylogenetic analyses as well as electron microscopy observations of this alga strongly suggest that it belongs to the order Cladophorales. Collectively, these results suggest that subaerial algae are both morphologically cryptic and exhibit a vast array of biodiversity.

8.
MOLECULAR ASSESSMENT OF THE PARAPHYLETIC GENUS DICTYOSPHAERIUM (TREBOUXIOPHYCEAE)

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The colonial genus Dictyosphaerium is characterized by Chlorella-like cells, mucous stalks connecting the individual cells and a surrounding mucilaginous envelope. Species were conventionally delineated by morphological criteria like absence vs. presence of pyrenoids, spherical vs. oval cells, cell and colony size, arrangements of the connecting stalks and habitat preferences. Molecular analyses based on combined SSU and ITS rRNA data showed that the type species D. ehrenbergianum forms a new lineage within the Parachlorella clade, assigning the genus to the Chlorellaceae (Trebouxiophyceae). Several independent lineages within the Chlorella and Parachlorella clades of the Chlorellaceae revealed the polyphyletic origin of the morphotype. Furthermore, taxa without pyrenoids cluster outside the Trebouxiophyceae, forming a lineage together with Mychonastes within the Chlorophyceae. By comparing morphological versus phylogenetic results, we were able to reveal several cryptic species within the different lineages. The spherical morphotype evolved independently in different clades, forming new molecular defined species because of a limited number of morphological characters that hampers suitable discrimination of individual taxa. Further studies need to be carried out, looking for morphological and ultrastructural differences between the individual lineages.

9.

EVOLUTION TOWARDS DEPENDENCY FOR A FREE-LIVING ORGANISM: HETEROTROPHIC "HELPERS" INCREASE RESISTANCE OF *PROCHLOROCOCCUS* TO ECOLOGICALLY RELEVANT CONCENTRATIONS OF HYDROGEN PEROXIDE

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The unicellular cyanobacterium Prochlorococcus is the most abundant phytoplankter in the harsh environment of the open ocean. However, axenic cultures of this organism have proven difficult to acquire and maintain. In this work, we demonstrate that axenic cultures of Prochlorococcus experience significant growth impairment when exposed to hydrogen peroxide (HOOH) at concentrations found in natural seawater, whereas co-cultures of Prochlorococcus and "helper" bacteria tolerate HOOH dosages up to two orders of magnitude higher. This relationship occurs at ecologically relevant concentrations of HOOH, Prochlorococcus, and heterotrophic bacteria. The specific cellular targets of HOOH damage are also discussed. We consider the hypothesis that this HOOH sensitivity and concomitant dependency on sympatric "helpers" is a product of the reductive evolution Prochlorococcus has undergone and is analogous to the evolved dependencies common in symbionts and parasites.

10.

FOUR CHLOROPLAST GENE ARRANGEMENTS IN A CLOSELY RELATED GROUP OF TREBOUXIOPHYCEAE (CHLOROPHYTA)

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Currently, twenty-four chloroplast genomes are published for green algae (Chlorophyta), representing species from diverse evolutionary histories. Each published green algae chloroplast genome has a unique gene arrangement. In contrast, many of the 131 published embryophyte chloroplast genomes share gene order motifs. In this study we compared the gene arrangement of a small segment of the chloroplast genome among nine closely related trebouxiophyte species, including several species of *Elliptochloris* and their close relatives *Hemichloris* and *Coccomyxa*. Sequence analysis was used to determine the identity and position of the two coding regions adjacent to the 3' end of the rbcL. In this region we detected four arrangements that are distinct from those of the four trebouxiophyte genera with published chloroplast genomes. Among the isolates of *Elliptochloris* that were sampled, three different gene arrangements were detected. All three isolates of *Hemichloris* shared one of the gene arrangements with *Elliptochloris*. Two *Coccomyxa* isolates had a fourth unique gene order. The extent of gene order rearrangement found among these closely related green algae is in stark contrast with the conserved gene order seen in embryophyte genera.

11.
DIVERSE BRYOPHYTE-CYANOBACTERIAL ASSOCIATIONS AND ENVIRONMENTAL CONTROLS IN A WISCONSIN BOREAL FOREST

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Cyanobacterial associations with bryophytes (mosses, liverworts, and hornworts) are of global importance in the nitrogen cycle, yet are little-studied in many ecosystems. In this study, approximately 500 randomly-selected bryophyte samples from a boreal forest in Wisconsin were screened for cyanobacteria using epifluorescence microscopy. Potential environmental controls such as bryophyte substrate, percent bryophyte cover, and season were also characterized. A diverse array of cyanobacterial morphotypes (various unicells, filaments, mucilaginous colonies) were detected. The percentage of samples containing cyanobacteria varied from approximately 20% to 50% across the four seasons. For all seasons, 50-60% of all samples with cyanobacteria contained heterocysts, suggesting potential nitrogen fixation. Logistic regression was used to explore potential control factors. The wet fall season had a significant positive influence (p-value 0.00432) on the likelihood of detecting cyanobacteria. Among bryophyte substrates, rock also had a significant positive influence (p-value 1.51 x 10-15), whereas conifer litter had a significant negative influence (p-value 7.45 X 10-9). These results are explored in light of current models of bryophyte-cyanobacterial symbioses, which emphasize the role of low nitrogen availability in initiating symbiosis.

12.
SIGNIFICANCE OF LAND PLANT CELL WALL POLYMERS IN THE CHAROPHYCEAN GREEN ALGAE

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Charophycean green algae (CGA) are thought to be progenitors of land plants. The presence of homologus polymers in the CGA has implications in our understanding of the function of the cell wall. We identified a variety of polymers previously only found in land plants in the CGA (cross-linking glycans, homogalacturonan, various β-glucans, and arabinogalactan protein [AGP]) using a combination of monoclonal antibody screening, analytical methods, and enzyme susceptibility analysis coupled with oligosaccharide characterization. The structure of mixed-linkage glucan (MLG) from *Cosmarium turpini* and *Chara corallina* was similar to that previously reported for land plants, although *Chlorokybus atmophyticus* and *Klebsormidium flaccidum* MLG appears to have a unique linear organization. The pectin homogalacturonan has a widespread occurrence in the CGA, with a particularly beautiful display in the cell walls of *Penium margaritaceum*. We also found β-(1,3)-glucans in six CGA species and AGP-like polymers were identified in three species. More insight into cell wall composition in the CGA will lead to a better understanding of the evolution of land plant cell wall and unique cell wall characteristics that enable life in aquatic habitats.

13.

PHYLOGENY OF GELIDIUM (GELIDIALES, RHODOPHYTA) FROM KOREA INCLUDING A CANDIDATE OF A NEW SPECIES BASED ON MORPHOLOGY AND THREE GENE ANALYSIS

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Gelidium J.V. Lamouroux is an economically and ecologically important red algal genus including about 118 species worldwide. A total of 17 species are reported in Korea. We collected G. crinale, G. divaricatum, G. elegans, G. vagum, an unidentified species and studied phylogenetic relationships of the species using rbcL, psaA, and cox1 genes. Topology of rbcL data is consistent with previously published tree. Korean species were divided into three groups, of which G. divaricatum was positioned outside of the genus. In all analyses of rbcL, psaA, and cox1 sequences, we found a distinctly independent clade that is different from published species of the genus. Thalli were collected in Geojedo and Wando on the south coast of Korea. The unidentified species is distinguished by cartilageneous thalli having creeping and erect main axes, acute apices with dome-shaped apical cells, rhizoidal filaments concentrated in the medullary layer, round bilocular cystocarps with up to six determinate branchlets, and spatulate tetrasporangial stichidia with cruciate tetrasporangia. It is often in association with Caulacanthus ustulatus and Chondracanthus intermedius in the intertidal zone at wave-exposed sites and is mature with cystocarps or tetrasporangia in summer.

14.

NEW INSIGHTS INTO THE SYSTEMATICS OF THE RED ALGAL FAMILY PEYSSONNELIACEAE (PEYSSONNELIALES)

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Norris, J. N., Dept. of Biology, National Museum Natural History, Smithsonian Institution, USA

Of the genera currently recognized in the family Peyssonneliaceae, a worldwide group of non-calcified or calcified, crust-forming red algae that are of great ecological significance, Peyssonnelia Decaisne is widely viewed to contain the largest number of species; however, comparative morphology, chloroplast-encoded rbcL and nuclear LSU rDNA sequence data suggest that species of Peyssonnelia sensu stricto do not occur in the Gulf of Mexico, and that previously reported Peyssonnelia species reported for the region actually belong to other genera of the Peyssonneliales. Other crustose taxa in the Gulf of Mexico that superficially resemble members of Peyssonneliaceae belong instead in the Rhizophyllidaceae of the Dumontiaceae-complex.

15.

GIGARTINA ALVEATA FROM NEW ZEALAND: AMONG THE OLDEST AND NEWEST MARINE RED ALGAE IN THE SOUTHERN HEMISPHERE

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The red alga *Gigartina alveata* (Turner) J. Agardh was collected by Joseph Banks in New Zealand in 1769 during Captain Cook's first voyage. The thallus is multiaxial, narrow, linear, channeled and repeatedly dichotomously branched with the apices often curled. Molecular systematics place this species in basal position in the Gigrtinaceae. Cystocarpic plants greatly outnumber male or tetrasporangial individuals. Spermatangia are borne in clusters of 4-5 in pits surrounded by exerted cortical filaments. Procarps are typical for Gigartinaceae. After presumed fertilization, the cortical cells above the auxiliary cell form rosettes of small-celled filaments and the medullary cells undergo intercalary transverse divisions to produce modified cells that also bear rosettes of small-celled filaments. Gonimoblast filaments ramify through the medulla and the carposporangial chains appear to arise from the modified medullary cells. Surface cortical cells form a multiaxial meristem that surrounds the developing gonimoblasts to produce an envelope with an ostiole, and a typical pericarp formed from secondary filaments is absent. Tetrasporangia are transformed solely from inner cortical cells. The unique features of this species infer that it belongs in a new genus.

16.

MOLECULAR SYSTEMATICS OF THE FRESHWATER RED ALGAL GENUS, KUMANOA (BATRACHOSPERMALES, RHODOPHYTA)

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The genus *Kumanoa* contains species formerly in *Batrachospermum* sections *Contorta* and *Hybrida*. Although a well-supported clade, the relationship among species lacks statistical support using rbcL data alone. Therefore, the current research was undertaken adding more taxa and sequence data from the universal plastid amplicon and cox1 barcoding region. Over half the taxa recognized in the genus were investigated and, when possible, multiple specimens analyzed. The three-marker data set provided high resolution (most nodes >0.95 posterior probability and >80% MP bootstrap support). The data suggest that sections within the genus based on the subsections proposed by Kumano are not advised, as they are not monophyletic. From these data, two new species are proposed and one variety is raised to species level. The entity previously known as *K. ambigua* from Australia is described as a new species and the name maintained for specimens from North and South America. The species, *K. mahlacense* only known from the south Pacific is reported from Texas and New Mexico in North America. Likewise, a specimen from Ohio was identified as *K. faroense* only collected from Guam.

17.

KLEPTOPLASTIDY AND ALGAL DIET SPECIFICITY OF KOREAN SACOGLOSSAN MOLLUSKS

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During feeding on algal cytoplasm, the sea slugs incorporate chloroplasts in their digestive cells through phagocytosis, and some species were reported to keep the chloroplasts photosynthetically active for several months. We collected 6 sacoglossans feeding on siphonous and siphonocladous green algae (Elysia ornata, E. atroviridis, E. nigrocapitata, Ercolania boodleae, Placida dendritica, Stiliger sp.) and 1 sacoglossan (Stiliger berghi) feeding on ceramiaceaen algae, and performed feeding experiments. Species of the genus Elysia were capable of photosynthesis and could tolerate prolonged periods of starvation from several weeks to over 4 months. The effective quantum yield was measured using diving PAM over time course in relation with irradiation level. P. dendritica, E. boodleae, Stiliger sp., and S. berghi were not “solar powered” and needed constant food consumption; the effective quantum yield was almost zero in the animals fed just 1 hour prior to measurements. The diet was restricted to a particular algal group, but some species could change from its primary diet to other algal food after prolonged starvation.

18.

EFFECTS OF PROROCENTRUM MINIMUM ON JUVENILE BAY SCALLOPS ARE DEPENDENT UPON ALGAL PHYSIOLOGICAL STATUS

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We evaluated the bioactive effects of Prorocentrum minimum upon bay scallops. P. minimum was grown under semi-continuous or batch culture modes to yield exponential or stationary populations. Scallops were exposed to these two different P. minimum cultures or to non-toxic Rhodomonas sp. as a control. Physiological and histological responses of the scallops differed significantly after exposure to either exponential or stationary growth phase P. minimum, demonstrating more-severe, adverse bioactive effects of the stationary-phase culture than the exponential. Mortality of 15% in scallops exposed for 24-hour to stationary-phase P. minimum culture was observed; no mortality was observed with exponential phase P minimum culture. These findings help explain the variable toxicity of P. minimum to scallops and other bivalves reported in the literature.

19.

BIOCHEMICAL ANALYSIS OF LOW-TEMPERATURE ACCUMULATED SECONDARY METABOLITE AND ITS ENZYMES FROM A FRESHWATER GREEN ALGA, SPIROGYRA VARIANS

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Simultaneous comparisons of radical scavenging activity and total phenolic contents from cold and warm temperature cultured Spirogyra varians were analyzed using DPPH and Folin Ciocalteu assay. When Spirogyra varians was cultured at low temperature (4) the antioxidant activity and total phenolic contents in methanolic extracts increases over time course. HPLC analysis of the extract showed four new compounds produced during cold acclimation process. The radical scavenging activities of the isolated compounds were 100% to 150% in comparison with ascorbic acid. Purification of the compounds was performed and the possible structures were predicted using H-NMR. The compounds were similar to gallic acid or flavonoid derivate which is involved in shikimate pathway. The activity of antioxidant enzymes (Catalase and Superoxide dismutase) was observed either unchanged or reduced during incubation at low temperature suggesting Spirogyra varians overcome cold stress using above compounds rather than antioxidant enzymes. A shikimate pathway related gene involved in the cold acclimation process of Spirogyra varians was isolated. Protein and mRNA of shikimate pathway related gene was rapidly increased during cold acclimation process (5 times than non acclimated plants).

20.

TRANSCRIPT PROFILING ACROSS VERTICAL ENVIRONMENTAL GRADIENTS IN THE GIANT KELP, *MACROCYSTIS PYRIFERA*

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The Giant Kelp, *Macrocystis pyrifera*, bridges biologically-relevant gradients in light, temperature, and nutrients. To examine the transcriptional diversity across these gradients, four depth-stratified and seasonally-separated cDNA libraries were sequenced using 454 pyrosequencing technology, assembled and annotated. While the majority of contigs (60.5% of 10561) were common between all four samples, the number of reads to each contig varied between the libraries. Transcriptional differences were validated using qPCR for several contigs assigned to photosystem and carbon metabolism annotations, supporting a model of material exchange with net movement of carbon sugars from surface to depth and vice versa for amino acids.

21.

THE RED ALGAL GENUS *CHAMPIA* IN THE GULF OF MEXICO AND THE CARIBBEAN

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Desvaux (1809) is a hollow thallus member of the Rhodymeniales and is well characterized based on a long history of developmental and morphological studies conducted on *Champia parvula* (C. Agardh) Harvey, and on the type *Champia lumbricalis* (L.) Desvaux from South Africa. This study investigates *Champia* samples from the Gulf of Mexico and the Caribbean Sea and other pertinent worldwide samples using both morphological and chloroplast-encoded *rbc*L sequence data. The results will help to clarify two taxonomically problematic members of the genus, *Champia parvula var. prostrata* L. G. Williams, and *C. compressa* Harvey, and include a comparison of the newly described monoecious Champia, *C. puertoricensis* Lozada-Troche & D.L.Ballantine, with another monoecious specimen from the Caribbean *Champia monoica*.

22.

MOLECULAR DATA RESOLVES DISPUTE IN THE GELIDIALES (RHODOPHYTA)

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In 1987 Maggs and Guiry described Gelidiella calcicola, a diminutive creeping member of the Gelidiales apparently confined to maerl beds (loose-lying coralline algae) in Europe. It was assigned to Gelidiella on the basis of lateral stichidia forming tetrasporangia in long chevron-like rows and the absence from the medulla of internal rhizines, considered characteristic of all genera of the Gelidiales except Gelidiella. Anomalous features of G. calcicola, including the formation of internal rhizines at the peg-like holdfasts, led the authors to suggest that the families Gelidiellaceae Fan and Gelidiaceae Kützing should be merged. However, this was not accepted by other workers and the Gelidiellaceae acquired a second genus, Parviphycus Santelices, and Pterocladiella Santelices & Hommersand was placed in the Gelidiaceae after its separation from Pterocladia (Pterocladiaceae) for its triangular unilocular cystocarps and peg-like holdfasts. During comparatives studies on Gelidiales of Europe and South-East Asia, the systematic position of G. calcicola was re-examined using rbcL sequences. G. calcicola is a member of a large Pterocladiella clade including a new species from Indonesia, and should be transferred to this predominantly Pacific genus.

23.

PHYLOGENETIC AFFINITIES OF 'CHANTRANSIA' STAGES IN MEMBERS OF BATRACHOSPERMALES AND THOREALES (RHODOPHYTA)

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Phylogenetic relationships among 17 populations of 'Chantransia' stage were determined from sequences of the plastid-encoded RUBISCO large subunit (rbcL) and the nuclear small subunit ribosomal DNA (SSU rDNA) genes. All sequences of macrospora 'Chantransia' belonged to B. macrosporum based on both molecular markers. In contrast, nine species are now unequivocally associated with pygmaea 'Chantransia', including seven species of Batrachopermales and two of Thoreales. Therefore, the presence of macrospora 'Chantransia' is a reliable evidence that it belongs to B. macrosporum, whereas pygmaea 'Chantransia' can not be associated with any particular species. We found incongruences in the phylogenetic affinities of the 'Chantransia' stages comparing the rbcL and SSU analyses: Thoreales positioned within Batrachospermales, indicating that the latter is more appropriate to infer phylogenies at higher levels. But affinities of 'Chantransia' stages to particular taxa were congruent for 76.5% of the samples, which were associated with the same or closely related species for both markers. Higher sequence divergences have been found in the 'Chantransia' stages in comparison to the gametophytes, suggesting that they might serve as a repository for genetic variation.

24.

SOLEXA AMPLIFICATION AND SEQUENCING OF RRNA GENES FROM THE CHLOROPLAST AND THE CYTOPLASM OF EUGLENA VELATA AND DETERMINATION OF ITS PHYLOGENETIC POSITION

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Using Solexa/Illumina sequencing method and assembling by Edena and Velvet programs we have obtained entire sequences of chloroplast LSU and SSU rDNA and about 95% of cytoplasmic SSU and 85% of LSU genes in Euglena velata. The sequences of these four genes were used to determine the phylogenetic position of E. velata. E. velata forms a clade with E. proxima at the base of the Euglena clade. This determination makes all recognized and molecularly sampled Euglenales, including Euglena, monophyletic.

25.
VIDEO ANALYSIS OF ULVOID ALGAL AND ZOSTERA IN GREATER PUGET SOUND

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Ulvoid algal blooms have been increasing world-wide and are known to cause loss of eelgrass meadows and deleterious human health effects. The history and spatial distribution of these blooms is not well-known in Washington State, although the State has taken action on occasion to remove problematic blooms in response to citizen complaints. Using underwater video compiled by the Washington State Department of Natural Resources Submerged Vegetation Monitoring Program, we determined ulvoid algal cover at 209 different sites over a 4 year period (2004-2007). The highest ulvoid cover and the greatest impact on eelgrass occurred in Central Puget Sound. Anecdotes to the effect that 2006 was a particularly "green" year were confirmed for Central Puget Sound, but not all regions responded similarly or equally from one year to the next. Analysis of depth distributions suggest that ulvoid algae and seagrasses (*Zostera* spp.) occur at similar depths, with site to site differences affecting whether ulvoids accumulate higher, lower, or at the same tidal elevation as eelgrass. Averaged across all regions and sites, however, ulvoid algal median distribution is slightly higher than that of *Zostera*.

26.
SANCTUARY IN MACROALGAE: CHANGES IN AMPHIPOD DENSITIES AMONG MACROALGAL HABITATS IN DAY VERSUS NIGHT COLLECTIONS ALONG THE WESTERN ANTARCTIC PENINSULA

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Observations in the Western Antarctic indicate that there is a strong inverse relationship between mesograzer abundance and algal feeding preference. Huang et al. (2007) demonstrated that unpalatable algae are occupied by significantly more amphipods than more palatable algae species. This may be a function of algal morphology, but it may have more to do with predator avoidance since these measurements were all conducted on macroalgae collected during the day while many amphipod species are reported to be nocturnal. Three species of macroalgae (Iridaea cordata, Palmaria decipiens, and Desmarestia menziesii) were collected two hours before darkness and separate individuals were collected from the same area again at night. Mesoherbivores were removed, identified to the lowest taxonomic level possible, and counted. Results were recorded in numbers per species per gram wet weight host algae. Initial results indicate significant amphipod density increases on palatable macroalage at night while increased densities on defended macroalage during daylight collections. Several species specific nocturnal behaviors were also found to be significant. These results suggest that amphipods are using chemically defended macroalgae to escape visual predators during the day while venturing out to graze in the safety of darkness.

27.

HIGH-FREQUENCY WATER QUALITY MONITORING IN THE CENTRAL INDIAN RIVER LAGOON, FLORIDA.

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Water quality in the Indian River Lagoon (IRL) has changed significantly over the past eight decades due to watershed alteration and land drainage patterns. High-frequency water quality monitoring, along a perceived water quality and seagrass gradient, has been underway since May 2005 in the IRL between northern Vero Beach and Fort Pierce. Temperature, salinity, dissolved oxygen, pH, turbidity, and chlorophyll a are being continuously monitored with datasonde multiprobes; color, suspended solids, nutrients, and light attenuation coefficients (K) are measured weekly. Overall, from north to south, salinity increases, while turbidity, color, suspended solids, and chlorophyll a (all attenuators of light) decrease, as do nutrients and K. The magnitude of most of these patterns varies considerably from year to year due to interannual variability in precipitation and freshwater discharge into the lagoon. Results to date demonstrate the tremendous climate-related interannual variability in water quality in the IRL and can be used in models of expected positive improvements in estuarine health following the reduction of freshwater inputs, which are recognized as the most significant human impacts on this estuary.

28.

RESERVOIRS VERSUS NATURAL LAKES IN PHYTOPLANKTON COMMUNITY ECOLOGY

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Reservoirs are artificial systems that contain assemblages of colonizing, or introduced, species that have no evolutionary history within the systems. While the lacustrine zone of reservoirs broadly mimics natural lakes there are important differences, such as higher light extinction, more frequent disturbance, and greater influence of the watershed. As a result, reservoir communities are thought to be less diverse than natural lakes and comprised of tolerant, widespread species. My goal was to evaluate richness and community characteristics of phytoplankton across lakes and reservoirs. I compared phytoplankton collected from the upper epilimnion of 300 systems in the northern US. Richness was similar in reservoirs relative to lakes of comparable size in northern latitudes. In addition, most genera that were widespread in lakes (occurred in at least 50% of lakes) also were widespread in reservoirs. The abundance of two heterotrophic groups, dinoflagellates and euglenophytes, was similar as well. General phytoplankton community attributes in the upper epilimnion of reservoirs appear to be closer to those of lakes than previously thought, although further examination of functional groups and dominant species is warranted.

29.

ALGAL COMPOSITION AND DYNAMICS IN MESOPHOTIC CORAL REEFS, SOUTHWEST PUERTO RICO

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Algae in mesophotic (defined arbitrarily as 40-100 m) coral reef habitats in southwest Puerto Rico were sampled utilizing mixed gas rebreather diving. Permanent transects were established at two sites and two depths per site (50 and 70 m). Sampling was conducted quarterly and utilized digital photographs. Thirty-four, quarter meter squared quadrats were quantified per site per depth. Algae are shown to be species rich with over 130 species identified based on limited collection. Algae dominate other live benthic cover at both 50 and 70 m depths with total algal cover being variable; however, exceeding 70% at 50 m and approaching 50% at 70 m. Much of the algal cover is dominated by crustose coralline algae as well as a number of Peyssonnelia species. The flora at 50 m would appear to be a transition from a shallower shelf edge flora to a distinct deep-water flora (70 m). A number of benthic algal species, including 7 Peyssonnelia species, collected at these depths both in the Bahamas and in Puerto Rico are restricted to deep-water habitats.

30.

STREPTOPHYTE ALGAE AND THE EVOLUTION OF EMBRYOPHYTES

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Land plants (embryophytes) evolved from streptophyte green algae, a small group of freshwater algae ranging from scaly, unicellular flagellates (Mesostigma) to complex, filamentous thalli with branching, cell differentiation and apical growth (Charales). The Charales (stoneworts) are often considered to be sister to land plants, suggesting progressive evolution towards cellular complexity within streptophyte green algae. Many cellular (e.g. phragmoplast, plasmodesmata, hexameric cellulose synthase, structure of flagellated cells, oogamous sexual reproduction with zygote retention) and physiological characters (e.g. type of photorespiration, phytochrome system) originated within streptophyte algae.

Projects to study genome evolution within streptophytes including protein families and polyadenylation signals have been initiated. We and others have started EST-sequencing of streptophyte algae and I will present an overview and recent results from these projects, including phylogeny of streptophyte algae based on a phylogenomic approach, evolution of polyandenylation signals in the Viridiplantae and the origin of sucrose metabolism in land plants.

31.

PHYLOGENOMIC RECONSTRUCTION OF THE CHAROPHYTES: A MULTILOCUS APPROACH TO RESOLVING THE PHYLOGENY OF PLANTS' CLOSEST RELATIVES

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The ancestry of all living land plants, or Embryophytes, can be traced back to a single colonization event from a charophycean green alga. In other words, the tremendous diversity we see in land plants today—from mosses to redwoods to orchids—all descended from a single common ancestor

that colonized land between 470-430 million years ago. Regardless of the branching order, there are six orders of charophycean green algae that, when embryophytes are included, comprise the Streptophyta s.l.: Mesostigmatales, Chlorokybales, Klebsormidiales, Zygnematales, Coleochaetales, Charales. There have been several studies focused on reconstructing the phylogeny of organisms involved in this important colonization event leaving the field in a somewhat contentious debate identifying exactly which lineage gave rise to land plants. To further muddle the story, most published phylogenies for the group have low bootstrap support for key nodes of interest. Using orthologs identified from eight charophyte Expressed Sequence Tag (EST) libraries in addition to whole genomes of two Chlorophytes (Chlamydamonas and Ostreococcus) and four land plants (Physcomitrella, Populus, Oryza, and Arabidopsis), we reveal exciting new data on the relationships among plants' closest relatives.

32.

WHAT DO THE CELL WALL POLYMERS OF ALGAE TELL US ABOUT THE ORIGIN OF LAND PLANTS?

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There has been a recent flurry of activity concerning the cell wall (CW) of the charophycean green algae (CGA) (streptophytes) and the relationship of the algal CW to that of land plants. Researchers have discovered true pectins in several CGA. These are not analogs, but homogalacturonan and other pectins chemically equivalent to those of land plants. Some of the CGA make mixed-linkage glucan, a distinct hemicellulosic polysaccharide found previously only in grasses and *Equisetum*. Arabinogalactan-protein appears to be a common component of CGA CWs, as it is in land plants. Interesting relationships between algal and land plant cellulose have been revealed by analysis of the structure/synthetic mechanism. Chemical fractionation of CGA walls revealed that polymers partition in the same way as in land plants, providing evidence of CW organization typical of land plants. The recent report of true lignin in red algae provides further evidence of CW commonalities. It appears that many of the key CW-biochemical properties (and associated morphogenetic events) found in modern land plants arose in their ancestors before emergence onto land approximately 470 million years ago.

33.

RECONCILING MORPHOLOGICAL AND PHYLOGENETIC SPECIES CONCEPTS IN DESMIDS (DESMIDIALES, CHAROPHYTA).

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Desmid taxonomy is based primarily on the morphological species concept. Most often characteristics of the cell wall are used for species identification. Variation in cell wall characteristics has resulted in the description of thousands of species and subspecific taxa. We tested the phylogenetic relationships among morphologically identified taxa in the genera *Desmidium*, *Gonatozygon*, *Micrasterias* and *Teilingia*. Our results suggest that in some genera taxa have been over-described while in others cryptic species diversity exists. These results and their implications for desmid identification and taxonomy will be discussed.

34.

A SYSTEMATIC INVESTIGATION OF NITELLEAE (CHARALES, CHAROPHYTA) AND IMPLICATIONS FOR CONVENTIONAL TAXONOMY.

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The extant Charales contain two tribes with six genera: the tribe Chareae (*Chara*, *Lamprothamnium*, *Lychnothamnus*, and *Nitellopsis*; and the tribe Nitelleae (*Tolypella* and *Nitella*). A number of morphological characters have been used to identify generic and subgeneric taxa within Nitelleae: branchlet branching patterns, dactyl (cells terminating branchlets) number and shape, and oospore morphology. The most recent and comprehensive treatment (Wood 1965) radically altered the classification of the Characeae by assigning more than 400 species to intra-specific ranks (i.e., variety or forma) or as synonyms of approximately 80 broadly defined species. We used two chloroplast genes (*rbc*L and *atp*B) from approximately 400 individuals belonging to Nitelleae to test whether (a) morphological characters used in taxonomy are synapomorphies for infrageneric subgenera and sections; and (b) whether the molecular data identified distinct clades corresponding to the conventional, narrower species concept, or to the more broadly defined species of Wood. The molecular data suggest that (a) most infrageneric taxa within *Nitella* are paraphyletic, and (b) numerous varieties and forma of Wood should be recognized as species, and several new species have been identified.

35.

A SYSTEMATIC INVESTIGATION OF THE *NITELLA FLEXILIS* (CHARALES, CHAROPHYTA) SPECIES COMPLEX.

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Wood and Imahori (1965) published *A Revision of the Characeae*, a global monograph of the fresh water algal family Characeae. In this monograph, a broad morphological species concept was used to reduce more than 400 species to approximately 80 loosely defined species, each with various subspecies, varieties, and forms. Currently, we are using molecular phylogenetic methods in combination with vegetative morphology and oospore membrane architecture to test and revise this classification. For this study, we present findings for *Nitella flexilis* (L.) Ag., which includes more than thirteen previously recognized species either as subspecific taxa or synonyms. Using chloroplast sequence data (*rbc*L and *atp*B) at least 12 distinct clades separate from *N. flexilis sensu stricto* have been identified. Gross morphological characters and oospore membrane architecture are generally consistent with these findings. Taken together, the taxa examined here appear to warrant species status separate from, but closely related to, *N. flexilis*.

36.

PHYLOGENY OF THE CHAREAE (CHAROPHYTA) BASED ON ANALYSIS OF TWO PLASTID GENES (ATPB, RBCL) AND IMPLICATIONS FOR CONVENTIONAL TAXONOMY

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The extant Charales, known commonly as stoneworts or brittleworts, are close relatives of land plants, possess an extensive fossil record, and are distributed worldwide. The extant Charales contains one family, with six genera in two tribes: the tribe Chareae (Chara, Lamprothamnium, Lychnothamnus, and Nitellopsis; and the tribe Nitelleae (Tolypella and Nitella). A number of morphological characters have been used to define subgenera, sections, and subsections within Chara: cortication (cells jacketing the internodal cells), rows of stipulodes (single celled projections at nodes), and spine cells on the surface of cortical cells. The most recent and comprehensive treatment (Wood 1965) radically altered the taxonomy and classification of the Characeae by assigning more than 400 species to intra-specific ranks (i.e., variety or forma) or as synonyms of approximately 80 broadly defined species. We used two chloroplast genes (rbcL and atpB) in a phylogenetic analysis to show (a) most infrageneric taxa of the species level are paraphyletic and incorrectly defined on the basis plesiomorphies, and (b) varieties and forma of Wood should be viewed as species. Implications for classification will be discussed.

37.

ALKALINE PHOSPHATASE ACTIVITY AND USE OF ALTERNATIVE PHOSPHORUS SOURCES BY PHYTOPLANKTON IN P-LIMITED FRESHWATER ECOSYSTEMS

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Phosphorus frequently limits growth of freshwater algae; the most readily available P form is phosphate (Pi) but is in vanishingly low concentrations during the growth season. Algae can use dissolved organic P as monophosphate esters via extracellular alkaline phosphatase activity (APA). Some cyanobacteria can also use phosphonates, previously considered unavailable for phytoplankton. The phosphonate herbicide glyphosate is widely used in freshwater catchments. This study aimed to examine use of organic P sources by freshwater algae and how algal APA is regulated in response to P supply. Growth and APA were examined in algal cultures and natural phytoplankton assemblages from Lake Michigan. APA in algae was only partially suppressed by high Pi exposure over several days, suggesting constitutive APA expression. In some species, APA was inefficiently regulated, with excess Pi released into growth medium. Monophosphate esters and glyphosate both stimulated growth of P-limited natural phytoplankton. We conclude that Lake Michigan phytoplankton are well adapted to use of organic P sources from internal Lake cycling and terrestrial runoff, and that constitutive APA may be adaptive for algae in chronically P-limited freshwater ecosystems.

38.

THE ALGAL HYPERMEDIUM CONCEPT -- HOW TO NAVIGATE THROUGH MULTIVARIATE ION-SPACE WITHOUT GETTING LOST

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Each unique algal medium is primarily defined by the particular types and concentrations of nutrients/ions specified in its recipe: Bold's Basal Medium (BBM) is different than BG-11 is different than Chu #10. There have been hundreds of media formulations published over the last century. These recipes cover an extremely broad range of ion mixtures, from seawater to freshwater to highly acidic to highly basic. However, we submit that there exists exactly one aqueous medium, the "Hypermedium". This medium is defined as an n-dimensional hypervolume where each dimension is a finite vector of an individual ion of interest, e.g. sodium, chloride, nitrate, etc., at concentration ranges from zero to the limits of solubility. Thus, the Hypermedium encompasses all possible ion combinations, all possible regions of algal growth, and perhaps most importantly, all possible media formulations. Any given medium, such as BBM or Lake Baikal, can be considered as merely a set of coordinates within the Hypermedium. This concept allows us to place all of the unique media developed to date within the same hyperspatial orientation, allows for intercomparisons between studies utilizing different media, and most importantly, it frees us from the limitations inherent to single medium formulations.

39.

ALLOCATION TO CHEMICAL DEFENSES IN RESPONSE TO NUTRIENT MANIPULATIONS IN THE ULVOID GREEN ALGAE ULVA LACTUCA AND ULVARIA OBSCURA

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Ulva lactuca and Ulvaria obscura are common constituents of green tide blooms in the southern Salish Sea. Both species produce dimethylsulfoniopropionate (DMSP), a feeding deterrent. Only Ulvaria produces dopamine, a nitrogen-containing compound with both antiherbivore and allelopathic properties. To determine the effects of nutrients on growth and chemical defense concentrations over 14 days, we conducted three experiments in which we grew Ulva and Ulvaria in artificial seawater with different amounts of nitrogen and phosphorus and different nitrogen types. Algae generally had high concentrations of tissue nitrogen (4-5% DM) at the beginning of the experiment. Tissue nitrogen concentrations decreased and C:N increased over 2 weeks in the low (0 and 10 uM N) treatments, but remained constant in the high (40 and 160 uM N) treatments. DMSP concentrations varied over time in all treatments but were lower in the 0 uM N treatments. Dopamine concentrations were also lower in the algae grown in lower nitrogen media. Manipulations of phosphorus (0-40 uM P) and nitrogen type (10 uM ammonia, nitrate and urea) did not affect algal growth or DMSP and dopamine concentrations.

40.

METABOLIC RELOCATIONS IN DIATOMS

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Diatoms are interesting organisms for several reasons, including their ecological relevance, their silicified cell walls and their peculiar evolution by secondary endocytobiosis. Especially the latter process resulted in differences with respect to physiology and cell biology of these algae when compared to green algae and land plants: (i) In diatoms very few enzymes of the Calvin cycle are redox regulated by small proteins termed thioredoxins that function as a “light switch” for CO2 fixation by reducing target enzymes. (ii) Essential pathways like the oxidative pentose phosphate together with nucleotide synthesis pathways have been removed from the diatom plastids. (iii) As a consequence, plastidic translocators for nucleotides and carbohydrates were established. (iv) Enzymes of the second half of glycolysis can be found in the cytosol, in the plastids and in the mitochondria. (v) We do have first indications that enzymes might be located in the periplastidic space of diatoms, including an NADP-dependent thioredoxin reductase and a phosphogluconate dehydrogenase. (vi) Diatoms also show a very unusual distribution of carboxylating and decarboxylating enzymes.

41.

ALGAE: HOW NUMBERLESSE THEIR NATION

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O What an endlesse worke haue I in hand,
To count the seas abundant progeny,
Whose fruitfull seede farre passeth those in land,
And also those which wonne in th'azure sky!
For much more eath to tell the starres on hy,
Albe they endlesse seeme in estimation,
Then to recount the Seas posterity:
So fertile be the flouds in generation,
So huge their numbers, and so numberlesse their nation.

- Edmund Spenser, The Faerie Queene, 1596

42.
GEOGRAPHIC AND ECOLOGICAL ASPECTS OF SPECIATION IN MARINE MACROALGAE

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We present two case studies of recent speciation in Indian Ocean macroalgae: the *Halimeda discoidea* and *Codium duthieae* species complexes. These species complexes consist of two and three cryptic species, respectively, and each of the sibling species is geographically disjunct from the others. Speciation events are dated with relaxed molecular clock techniques. Species distribution models are used to examine divergence of the macroecological niche of the sibling species and track their potential distribution through the Pleistocene glacial cycles, informing us about potential population connectivity in recent times. Using the molecular clock and distribution models as a guide, we speculate about the processes at the basis of the speciation events under study.

43.
A BIODIVERSITY SURVEY OF SUBAERIAL ALGAE FROM AN AFRICAN TROPICAL RAINFOREST

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Although economically and ecologically important, subaerial algae from African tropical rainforests have been largely understudied compared to their marine and freshwater counterparts. Since rainforests have been shown to be centers of subaerial algal biodiversity in South America, India, and Australia, it is reasonable to expect that they also host a higher diversity in tropical Africa. Algae living in these habitats, on surface above the soil, are constantly exposed to extreme environmental conditions. These algae are found on a wide variety of substrates, including rocks, road signs, walls, metal, bark, leaves of trees and even animals. Subaerial algae from African tropical rainforests included different algal lineages. Our work during the last two years has been centered in Gabon, a West African country with a large system of national parks. New findings and novel records of trentepohlialean taxa as well as other microchlorophytes are reported. A phylodiversity survey is in effect utilizing cloning techniques to generate environmental DNA algal phylosignatures. These approaches will provide with a better understanding of the biodiversity from these poorly known algal habitats.

44.
GAMBIERDISCUS TAXONOMY AND GLOBAL DISTRIBUTION

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Dinoflagellate species in the genus Gambierdiscus produce toxins which bioaccumulate in fish causing ciguatera fish poisoning (CFP). Globally, CFP is the leading cause of non-bacterial seafood poisoning. Preliminary evidence suggests a >100 fold difference in the toxicity among Gambierdiscus species. This suggests that species composition is a major determinant of CFP and that assessing CFP risks will require accurate species identification. Species identification using light microscopy, however, is difficult despite Gambierdiscus cells being relatively large. An overview of Gambierdiscus morphology will be presented to illustrate the challenges associated with species identification. In most cases, unambiguous identification requires additional

molecular confirmation. Molecular confirmation is possible because of the close concordance between the distinct genetic clusters found in rDNA phylogenies and the currently described species. To date, phylogenetic analyses of rDNA sequences from geographically dispersed isolates indicate the existence of at least 12 different Gambierdiscus species, ten of which have been formally described based on morphological criteria. Our data indicate five of these species are endemic to the Atlantic, five to the tropical Pacific, and that two species are globally distributed.

45.

COASTAL EUTROPHICATION, LAND USE CHANGES AND CERATIUM FURCA BLOOMS IN PAGO PAGO HARBOR, AMERICAN SAMOA – OR – WHY IS SOCCER BAD FOR THE ENVIRONMENT

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The bloom forming dinoflagellate, Ceratium furca, has been linked with coastal eutrophication worldwide. During the summer of 2007, an unusual 6 month long bloom of C. furca was observed in Pago Pago Harbor, American Somoa in May and dissipated in November 2007. In the Feburary-March 2009, a similar C. furca bloom was observed. Maximum cell counts were observed on 20 September 2007 at 9,300 cells/ml. Changes in land use practices may have been the primary driver of these blooms. Over- fertilization of athletic fields is hypothesized to have a direct link to the increase in nutrients found in the Pago Pago Harbor and may have been the trigger for the initialization of these blooms. For the construction of the athletic fields, coral sand was imported. Along with the sand, an invasive species of fire ant (Solenopsis geminate) was also imported. During 2008, these fields were not used due to an infestation of these colonial ants. Once controlled, the fields were open again in 2009 and fertilizers were applied in January, a month before the bloom was observed.

46.

CHEMOKINETIC RESPONSES OF MOTILE PROPAGULES OF ANTARCTIC EPIPHYTE *ELACHISTA ANTARCTICA* IN THE PRESENCE OF HYDROPHILIC EXTRACTS OF COMMON RHODOPHYTES

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The majority of subtidal macroalgae surrounding Anvers Island, Antarctica are in some way defended against predation, many using chemical defenses. Previous studies have reported chemical extracts from defended macrophytes deter grazers, but there has been no report of their effect on biofouling or swimming behavior of motile biofouling propagules. Although filamentous endophytes are present in macrophytes from this area, macroalgal thalli are devoid of emergent filamentous epiphytes. However, filamentous epiphyte *Elachista antarctica* is found growing exclusively out of the palatable rhodophyte, *Palmaria decipiens*. We hypothesize that motile propagules from this epiphyte cannot tolerate extracts of chemically defended macroalgae and will be chemokinetically attracted to *P. decipiens* but repelled by defended rhodophytes. To test this hypothesis we recorded changes in direction of travel of *E. antarctica* spores in presence of hydrophilic extracts from common rhodophytes presented in capillary tubes in filtered sea water. Controls were run without extracts for each trial. Although no significant differences from controls were found from extracts of host *P. decipiens*, extracts from other rhodophytes significantly impacted direction of travel of *E. antarctica* spores.

47.

LOSS OF DIATOM BIODIVERSITY IN FRESHWATERS OF THE UNITED STATES

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The Environmental Protection Agency of the United States has been conducting regional and national assessments of streams, lakes, and wetlands with characterizations of diatom assemblages, land use, and water quality. This provides an opportunity to measure effects of human activities on diatom biodiversity in freshwaters of the United States. Moderate increases in human disturbance and nutrient concentrations have a positive effect on apparent richness of taxa in habitats. This has been attributed to a combination of two factors: 1) the relaxation of constraints on species occurrence in habitats, and 2) high evenness of species growth rates. Threats to species diversity are indicated by: decreases in the proportion of low nutrient native taxa, decreases in apparent richness of taxa in high disturbance conditions, and homogenization of biodiversity (low beta-diversity) with increasing levels of human disturbance. In addition, taxa that were once widespread have greatly reduced distributions, and regional expansion of high nutrient, invasive taxa is common. Documenting extinction of taxa is complicated by many factors, but widespread and substantial alteration of diatom biodiversity in streams, lakes, and wetlands is great.

48.

CHEMICAL MEDIATION OF PREDATOR-PREY AND MUTUALISTIC INTERACTIONS BETWEEN ANTARCTIC MACROALGAE AND INVERTEBRATES

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Macroalgae dominate hard bottom areas along the western Antarctic Peninsula to depths of 40 m or more. Most of the macroalgae are chemically defended from a variety of macro- and mesograzers but harbor very high densities of amphipod mesograzers. These amphipods do not consume most of the macroalgal species, but benefit the macroalgae by keeping them relatively clean of epiphytic microalgae and filamentous macroalgae. They do, however, appear to have selected for a relatively high incidence of filamentous endophytes in the larger macroalgae. The amphipods benefit from living on the large, chemically-defended macroalgae because they gain refuge from fish which are their primary predators. Hence this represents a mutualistic relationship between the macroalgae and amphipods that is mediated, at least in part, by the macroalgal chemical defenses.

49.

FACILITATION OF TWO MORPHOLOGICALLY SIMILAR BLOOM-FORMING ULVA SPECIES BY A CO-OCCURRING SNAIL

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In Narragansett Bay, Rhode Island, macroalgal blooms are an annual occurrence. These blooms are mainly composed of two morphologically similar blade-forming Ulva species: U. rigida and U. compressa. Pilot studies investigating the impact of mud snail (Ilyanassa obsoleta) grazing on

Ulva blades indicated that mud snail presence increases Ulva blade growth. To determine whether the growth of U. rigida and U. compressa are facilitated by the same mechanism(s), we investigated: 1) I. obsoleta fecal nutrient input and 2) I. obsoleta grazing of microalgal films. We found that: 1) snail nutrient addition did not enhance U. rigida growth but did enhance U. compressa growth and 2) removal of the microalgal films via mechanical means resulted in significant increased growth for U. rigida, but not U. compressa. This indicates that, while the growth of both species is facilitated by I. obsoleta presence, the facilitative mechanism differs for each species.

50.

INVASION OF PROTEIN CODING GENES BY GREEN ALGAL RIBOSOMAL GROUP I INTRONS

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Group I introns can invade ribosomal and protein-coding genes due to their association with functional homing endonuclease genes (HEGs). The evolution of group I introns is not fully understood, though recent studies have shed light on their distribution across the tree of life and how they have spread into new hosts and genic sites. Recent phylogenetic surveys of chlorophyceaen green algae (order Sphaeropleales) revealed 23 out of 204 included isolates contained at least one group I intron in the plastid-encoded rbcL gene. The introns belong to two different intron lineages, group IA3 intron-HEG (GIY-YIG family) inserted after nucleotide position 462 in the rbcL gene, and group IA2 inserted after position 699. The distribution of the introns was mapped on an exon phylogeny and patterns were recovered that are consistent with both horizontal and vertical inheritance. A separate phylogenetic analysis of a broad sampling of group I introns indicates that the rbcL introns were each independently derived from ribosomal RNA introns.

51.

THE ACTIN CYTOSKELETON FROM SYMBIODINIUM CELLS

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We applied a freeze-fracture/fixation and solvent extraction technique to *Symbiodinium* cells, in order to reduce the high intrinsic autofluorescence and, at the same time, make the cells available to fluorescently-labeled phalloidin and antibodies to actin. The cells showed the actin microfilaments associated with thick tubule-like structures with a regular pattern of tubules and empty areas just underneath the cell membrane. Finer filaments derived from these thick structures seemed to make a fine web surrounding the cell. Anti-actin antibodies showed a similar pattern but appeared to stain diffuse areas within the empty areas previously undetected by phalloidin. Latrunculin treatment disorganized the regular pattern and showed a diffuse staining resulting from depolymerization of the actin cytoskeleton. These results indicate that the actin cytoskeleton in *Symbiodinium* cells is highly structured and susceptible to actin-depolymerizing agents. This is the first report on how the actin microfilament network in these cells is organized. (This work was supported by grant IN200409 from DGAPA-UNAM.)

52.

THE PHYSIOLOGICAL AND BIOCHEMICAL RESPONSE OF *GRACILARIA* UNDER PB^{2+} STRESS

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Pb^{2+} is one of the major abiotic stressors limiting algal growth and productivity in many parts of the world. The physiological and biochemical response of *Gracilaria* under different concentrations of Pb^{2+} was studied. The growth, soluble protein and phycoerythrin decreased significantly under 5 mg/L Pb^{2+}. The activity of Superoxide dismutase, Peroxidase and Glutathione S-transferase increased in low concentrations of Pb^{2+} ($\leq$2.5 mg/L), and then decreased linearly with increasing Pb^{2+} concentration. The results of two-dimensional gel electrophoresis (2-DE) coupled with mass spectrometry found a group of novel proteins including sugar transport ATP-binding protein, ABC transporter, DNA mismatch repair protein MutL under 0.5-5 mg/L Pb2+. These proteins are involved in several cellular processes, including metabolism and energy production, DNA repair, gene expression and detoxification. Some of the protein express increased under 0.5-2 mg/L Pb^{2+} and decreased under 5 mg/L Pb^{2+} which indicated that the Pb^{2+} tolerance value of *Gracilaria* is about 5 mg/L.

53.

BIOCHEMICAL FEATURES AND SUBCELLULAR LOCALIZATION OF A 28 KDA MEMBRANE PROTEIN FROM SYMBIODINIUM.

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A 28 kDa protein from *Symbiodinium* previously shown to be present in several species and to associate with membrane fractions, was also shown to be associated with microsomal particles. Serial extraction of these microsomes with high salt and detergent removed some, and then all of the protein, respectively. TX-114 phase-partition assays made the protein migrate to the hydrophilic phase indicating that it is not highly hydrophobic. The protein had the same molecular weight under reducing or non-reducing conditions by SDS-PAGE and western blot analysis indicating that it does not form oligomers bound by disulfide bonds. Subcellular localization by fluorescence microscopy using immunoaffinity purified antibodies showed that the protein was associated with tubular structures of an endomembrane system that was present throughout the cell. This localization is very interesting but the sequence that the antibody binds to, is a short 8-peptide and is present in many proteins including ABC type transporters and plant desiccation-related proteins; therefore, we are in the process of purifying and obtaining enough protein for internal sequencing to unequivocally identify this endomembrane protein from *Symbiodinium*.
(This work was supported by grant IN200409 from DGAPA-UNAM, from which R.E. Castillo-Medina also received a B.S. thesis scholarship.)

54.
CONTROL OF RHIZOID FORMATION IN *VALONIA*

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Rhizoids were artificially induced by the contact or the approach of substrata towards *Valonia macrophysa* Kützing, *V. fastigiata* Harvey ex J. Agardh and *V. aegagropila* C. Agardh cell surfaces. Local induction of rhizoid formation did not always require direct contact with substrata; occurring when two living cells were placed apart but closer than 0.5 mm. Induction of rhizoid formation required continuous contactless exposure to a substratum for at least 48-60 h. In these cases, amorphous materials were secreted from the outer surfaces of cells and accumulated in the space between two adjacent cells but when washed out, the number of rhizoids induced decreased remarkably. The amorphous materials were bound with fluorescein-conjugated lectins that recognized glucose, galactose, N-acetyl-glucoseamine and N-acetyl-galactoseamine residues. Once rhizoid formation was induced, protoplasmic mass containing chloroplasts and nuclei aggregated locally, coinciding with the disassembly of perinuclear microtubules. This was followed by re-arrangement of cortical microtubules from parallel to radial. The aggregation of protoplasm was then split from the cell by a septum and began to elongate towards a substratum, differentiating into a rhizoid.

P1.
CELL GROWTH RATE AFFECTS LUTEIN CONTENT IN DARK GROWN CHLORELLA PYRENOIDOSA

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Chlorella has the long history to be consumed as food supplement and is a promising alternative resource of lutein. Lutein is one of the primary photosynthetic pigments and naturally occurs in Chlorella cultivated under light. Its content increases continuously with the elongation of the cultivation in batch culture under light condition, whereas declined gradually under dark conditions. In this study, the influence of cell growth rate on lutein production in dark-grown C. pyrenoidosa was investigated by means of continuous cultivation operated under different dilution rates. It was found that the contents of lutein, β-carotene, chlorophyll b and a, as well as protein in C. pyrenoidosa decreased significantly with an increase in dilution rate. The contents of lutein was highly related to protein based on correlation analysis (correlation coefficient>0.999). A mathematic model was developed to describe the relationship between lutein formation and cell growth of C. pyrenoidosa. It was suggested that maintaining relatively low cell growth rate would be useful in obtaining higher lutein content in either batch, fed-batch or continuous culture and the production of lutein was closely related to the accumulation of protein in C. pyrenoidosa.(This research is supported by the GRF from Research Grant Council of Hong Kong SAR)

P2.

FRESHWATER DIATOMS AS A SOURCE OF LIPIDS FOR BIOFUELS

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Until recently biodiesel production has been derived from terrestrial plants such as soybean and canola, leading to competition between biodiesel production and agricultural production for source materials. Microalgae have the potential to synthesize 30x more oil per hectare than terrestrial plants without competing for agricultural land, but at present microalgae used for biodiesel have been limited to a few species of greens and cyanobacteria. We examined four species (*Cyclotella, Aulacoseira, Fragilaria, Synedra*) of common freshwater diatoms (Bacillariophyceae) for growth and lipid content in defined medium (sD11) and optimized the medium for silicon content. *Cyclotella* and *Aulacoseira* produced the highest levels of total lipids, 60 and 43ug total lipids/ml respectively. Both diatoms are rich in fatty acids designated C14, C16, C16:1, C16:2,7,10, and C22:5n3. Of the diatoms examined, *Cyclotella* reached the highest population density (>2.5 x 10^6 cells/ml) in stationary phase when many of the cells appeared to be filled entirely with oil. With a high growth rate (0.036/hr), high population density and lipid content, and rapid settling rate, *Cyclotella* appears to be a promising candidate for biodiesel production.

P3.

ALGAL SPECIES DIVERSITY IN TWO EXPERIMENTAL ALGAL PRODUCTION SYSTEMS IN SOUTHEASTERN PENNSYLVANIA

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Algal diversity in two experimental algal turf scrubber raceway systems was inventoried during 2008-2009. In the algal turf scrubber, algae grow attached to screens in shallow troughs where flowing water passes, thus uptaking nutrients in their growth and are harvested on a weekly basis to remove the nutrients, providing water quality benefits. These systems were each 1 foot wide and 300 feet long with a 1-2% slope. Water flow to the systems came from the Muddy Run Hydroelectric Facility, located on the Susquehanna River in southeastern Pennsylvania. The presence/absence of algal species was recorded seasonally. A total of 280 species were inventoried in the systems: 195 species in the aluminum raceway and 196 species in the wood raceway. The majority of species in the experimental raceways were diatoms (44% of the total diversity) followed by green algae (38% of the total diversity) and Cyanobacteria (14% of the total diversity). The most frequent species were Melosira varians Agardh, Ulnaria ulna (Nitzsch) Compere, Spirogyra sp. and Phormidium sp. Possible explanations for the relatively high diversity of species in these raceways are discussed.

P4.

SEQUENCING AND ANALYSIS OF THE MITOCHONDRIAL GENOME OF *GRACILARIA TENUISTIPITATA* (GRACILARIALES, RHODOPHYTA)

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We have sequenced and analyzed the mitochondrial genome of Gracilaria tenuistipitata var. liui Zhang et Xia, a red macroalgae that has been used as model organism in physiological, biochemical and molecular studies, including the sequencing of the whole chloroplast genome. Total DNA was PCR amplified and sequenced using primer walking. The whole mitochondrial circular genome sequence (25.565 nucleotides, 27% C+G content) presented 50 genes organized in two groups on each strand, in two opposite directions, including seven NADH dehydrogenase complex subunits (nad1-6, nad4L), three succinate dehydrogenase complex subunits (sdh2-4), the apocytochrome b gene (cob), three cytochrome c oxidase subunits (cox1-3), three ATP synthase complex subunits (atp6, atp8-9), five ribosomal proteins (rps3, rps11-12, rpl16, rpl20), three ribosomal RNA genes (rrn5, rnl, rns) and 22 tRNAs. One group II intron was found in the tRNAHis. The mitochondrial genome of G. tenuistipitata is compact, with short intergenic regions and uses a modified genetic code. The gene content and its order in the mitochondrial genome of G. tenuistipitata are extremely similar to the Chondrus crispus mt genome, presenting nucleotide identity above 70%.

P5.

THE ROLE OF WOUND-RESPONSIVE GENES FROM A MARINE RED ALGA, GRIFFITHSIA MONILIS

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The wound healing process in Griffithsia monilis occurred by a somatic cell fusion between the two cells that were formed from the neighboring cells of the wounded part. FITC-ConA, labeled tips of the growing repair cells. Their somatic cell fusion was inhibited by 0.05 M a-methyl-D-mannose. Proteomic studies showed the presence of a glycosyl transferase specifically expressed during wound response. The apical and the basal part of the filaments were separated at the wounded cell in 24 h after wounding, and mRNA was extracted for differentially expressed gene (DEG) analysis. Wound-responsive gene profiles were analyzed using annealing control primer (ACP)-based PCR. Sixty ACP-primers yielded total of 120 bands and 18 of them were wound responsive; 6 apical-part specific, 6 basal-part specific and 6 appeared both part of wounded plants. Full cDNA sequence was obtained from two wound responsive genes. The first one was an apical-part specific gene and named as GWR1. The second one was a basal part specific gene and named as GWR2. GWR1 showed high sequence similarity with trehalase. GWR2 showed high similarity with mannosyl-glycerate synthase (89%).

P6.

PURIFICATION OF FETUIN BINDING LECTIN FROM THE MARINE BROWN ALGA, SCYTOSIPHON LOMENTARIA

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Two fetuin-binding lectins were purified from the marine brown alga, Scytosiphon lomentaria, by affinity chromatography. The lectins agglutinated sheep erythrocytes. The hemagglutinating activity was not inhibited by monosaccharides and disaccharides but glycoproteins, especially fetuin (min. concentration 625 μg/ml) and asialo fetuin (15.6 μg/ml) blocked hemagglutination. The molecular weights of the lectins were 45 kDa (SLA-1, Scytosiphon lomentaria agglutinin-1) and 22 kDa (SLA-2). Activities of separated SLA-1 and SLA-2 were 38,819 HU/mg and 7,152 HU/mg, respectively. N-terminal sequence data showed that these lectins were noble. We compared and analyzed information on 5 types of lectin-like proteins obtained from S. lomentaria EST library and features of separated lectins.

P7.

MOLECULAR CLONING AND CHARACTERIZATION OF WINGED BEAN LECTIN (WBL)-LIKE GENE FROM FRESHWATER GREEN ALGA, SPIROGYRA VARIANS

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During conjugation in Spirogyra spp., the filaments can recognize each other through lectin-carbohydrate interaction system. In this study, we analyzed lectin labeling pattern of several Spirogyra species using FITC-lectin labeling method and cloned possible lectin- like gene from Spirogyra varians. Papilla of S. varians was strongly labeled with RCA, but not other lectins. Otherwise, Spirogyra sp. (JHK-2006-1) was strongly labeled with RCA as well as ConA, but weakly labeled with PNA and SBA. Winged bean lectin-like gene, which is specific to N-acetylD-galactosamine and galactose, was isolated and cloned from cDNA library of S. varians. The protein consisted of 277 amino acids and had similarity with Winged Bean Lectin (56%). WBL-like gene in S. varians was up-regulated (5 times than normal condition) by treatment of stresses, e.g. light and temperature, which also lead to sexual reproduction. The variation of WBL-like gene among 4 related species was analyzed. It has high similarity with few modifications of amino acids.

P8.

POLYCLONAL ANTIBODIES TO DIMETHYLSULFONIOPROPIONATE (DMSP): INITIAL CHARACTERIZATION AND SPECIFICITY TESTING

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Dimethylsulfoniopropionate (DMSP) serves as an anti-herbivore defense molecule in ulvoid macroalgae via its metabolic products dimethylsulfide and acrylic acid. With the goal of localizing

DMSP in ulvoid tissues, we generated a rabbit polyclonal antiserum against DMSP as a hapten conjugated to bovine serum albumin (BSA) via a carbodiimide-type linker. We report our initial characterization of this DMSP-BSA antiserum by indirect competitive enzyme-linked immunosorbant assay (ELISA). Using a 1:100,000 dilution of the antiserum, an IC50 of ~7µg/mL was calculated with a dynamic range of ~0.1µg/mL to 0.1mg/mL. We also used competitive ELISA to test antiserum specificity using competitor molecules and their BSA conjugates in three categories: DMSP metabolites, analogues, and synthesis intermediates. These tests revealed minimal binding of the antiserum to the competitor molecules, their BSA-conjugate forms, or DMSP alone. These results suggest that the main epitope recognized by the antiserum is DMSP in its conjugate form; that is, linked to lysine residues of BSA or other proteins. Thus, the DMSP-BSA antiserum may prove useful in localizing conjugated DMSP in ulvoid tissue and perhaps quantifying DMSP in broader applications.

P9.

ISOLATION AND CHARACTERIZATION OF SEX-SPECIFIC ACONITASE-LIKE GENE FROM SCYTOSIPHON LOMENTARIA

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Sex-related genes in a brown alga, Scytosiphon lomentaria, were screened comparing the transcripts in two EST libraries of male and female gametes. Ten ESTs showing high reads in each database were chosen and the sex-specificity was examined using real-time PCR. An aconitase-like gene which was highly expressed in male gametes (500 times than female) was isolated. Blast search showed that this gene had high similarity (63%) with aconitase family protein of Trichodesmium erythraeum. Northern blot analysis showed this gene was rarely expressed in the female gametes as well as the asexual zoospores. Full cDNA sequence (2,460 bp, reduced 554 amino acids in ORF) was cloned using lambda Zap-cDNA library of male gametes. Predicted molecular weight of the protein and isoelectric point were about 60 kDa and pI 8.5, respectively. Possible involvement of this aconitase-like gene in maternal inheritance of mitochondria in Scytosiphon lomentaria is discussed.

P10.

ASSEMBLING THE CHLOROPLAST GENOMES OF EUGLENOIDS

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The Euglena gracilis chloroplast genome was first sequenced in 1993 by Hallick et al. but no other chloroplast genomes have been sequenced for photosynthetic euglenoids. Thus, sequencing of additional euglenoid chloroplast genomes has been initiated with Eutreptia viridis, Colacium vesiculosum and Discoplastis spathirhyncha. DNA extraction, purification, 454 sequencing, and assembly of the chloroplast genome has provided preliminary data with respect to gene order, conservation, and sequence similarity. Numerous methods have been employed to achieve this including phenol/chloroform extractions, CsCl gradients to extract cpDNA from whole genomic

DNA, as well as DNA extraction kits, and Multiple Displacement Amplification (MDA). As a result, contigs upwards of 65Kb have been achieved in E. viridis showing evidence of vast gene rearrangements. In addition, comparisons between taxa confirm the presence of numerous key chloroplast genes suggesting a high level of gene conservation within the euglenoid lineage. Further comparisons with the plastid genome of the colorless Euglena longa and close green algal taxa may provide insight into chloroplast evolution within the Euglenophyta and help deduce a putative green algal chloroplast donor.

P11.

PURIFICATION AND CHARACTERIZAGTION OF A SEX-SPECIFIC LECTIN FROM AGLAOTHAMNION CALLOPHYLLIDICOLA (RHODOPHYTA)

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The spermatial binding to trichogynes of a red alga, Aglaothamnion callophyllidicola is mediated by a lectin-carbohydrate complementary system. Previous cytochemical study implied the presence of a female specific lectin(s) in this species. We isolated a noble lectin, ACL (Aglaothamnion callophyllidicola lectin) from the female plants by the affinity chromatography using fetuin column. Inhibition experiments showed that ACL was involved in the gamete recognition of this species. The haemagglutinating activity of ACL was inhibited by specific glycoproteins (fetuin and asialofetuin), but not by monosaccharides or disaccharides. N-terminal amino acid sequence of the lectin was analyzed and degenerated primers were designed. A full-length cDNA encoding the lectin was obtained using the rapid amplification of cDNA ends-PCR method. The cDNA was 930 bp in length and coded for a protein of 151 amino acids with a deduced molecular mass of Mr 14 kDa.

P12.

IDENTIFICATION OF THE HIGH TEMPERATURE RESPONSIVE GENES FROM PORPHYRA SERIATA ESTS AND ENHANCEMENT OF HEAT TOLERANCE BY EXPRESSING OF PORPHYRA HTR2 GENE

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Temperature is one of the major environmental factors effects on the distribution, growth rate and life cycle of the intertidal organism including red algae. To identify genes involved in the high temperature tolerance of Porphyra, we generate total 3,979 ESTs from two cDNA libraries constructed from gametophyte thalli of P. seriata under normal growth condition and high temperature condition. Comparison of the ESTs from two cDNA libraries allows identifying the HTR (high temperature response) genes, which are induced or up-regulated by high temperature

treatment. Among HTRs, HTR2 encode a novel small polypeptide consisting of 144 amino acids and up-regulated by high temperature. Transformed Chlamydomonas expressing Porphyra HTR2 gene show higher survival and growth rate than those of the wild-type after high temperature treatment. These results indicate that HTR2 may play a role in tolerance of high temperature stress conditions and this Porphyra ESTs data set will provide important information for the genes to study molecular basis of high temperature tolerance in marine algae as well as Porphyra.

P13.

SEX-SPECIFIC EXPRESSION OF TRANSPOSABLE ELEMENTS IN AGLAOTHAMNION CALLOPHYLLIDICOLA (RHODOPHYTA)

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Sex-specific genes were screened comparing the transcrypts in two EST libraries of male and female gametophytes of a red alga Aglaothamnion callophyllidicola. Two transposable elements (TE), a female specific transposon and a male specific retrotransposon, were isolated. Sex specific expression of the genes was confirmed by real-time PCR as well as northern blotting. Full cDNA sequence (1187 bp) of female specific transposon was obtained using RACE-PCR. BLAST search showed that the gene was an algal homologue of Tc3 transposable elements. TEs are genetic parasites that can make duplicate copies of themselves and insert into new chromosomal locations. Then, how can the TEs remain sex-specific in Aglaothamnion callophyllidicola? The role of sexual reproduction in spreading of TEs was examined by crossing experiment.

P14.

APOPTOTIC AND ANTI-INFLAMMATORY EFFECT OF METHANOLIC EXTRACT FROM FRESHWATER GREEN ALGA, SPIROGYRA VARIANS, ON CHONDROCYTES AND CANCER CELLS

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Apoptosis, anti-inflammatory and dedifferentiation effects of methanolic extracts from a total of 13 species of algae (10 green, 2 red and 1 brown) collected from arctic region and Korea were screened. Among screened algae, two species, Spirogyra varians and Spirogyra distenta, showed strong effect for dedifferentiation, apoptosis and anti-inflammatory property in chondrocytes (primary cultured) and human cancer cells (A549 and MDAMB231-p53 null). Death rate of screened cell line dropped to 50% by treatment of low concentration of methanolic extracts (5 μg/mL). The expression of type II collagen that senses induction of dedifferentiation was strongly inhibited, on the other hand, Extracts (5 μg/mL) from Spirogyra promoted up-regulation of COX-2 and p53 protein in rabbit chondrocytes. A549 and MDAMB231 cells also showed similar effect. Treatment of extract induced increment of COX-2 against A549 cells, while treatment against MDAMB231 cells induced increment of COX-2 and p53 genes.

P15.

GENETIC DIVERSITY OF INVASIVE GRACILARIA VERMICULOPHYLLA (GRACILARIALES, RHODOPHYTA) BASED ON MITOCHONDRIAL COX1 SEQUENCE.

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The red algae Gracilaria vermiculophylla introduced from Northeast Asia to Europe and North America. Sequence variation at the mitochondrial coxI gene was investigated from 312 individuals of G. vermiculophylla collected in 37 native and 32 introduced locations in order to assay its genetic diversity and identify the putative source of invasive populations. A total of 19 haplotypes were found: 17 in Northeast Asia and 3 in Europe and eastern and western North America, with only 1 shared among all regions. The shared haplotype was present in all introduced populations and in approximately 99% of individuals in the introduced areas. This haplotype was also found at three native locations in East Korea, West Japan, and Far-East Russia. Both haplotype and nucleotide diversities were extremely low in invaded areas compared to native areas. Our study suggests that the East Sea/Sea of Japan is a likely donor region of the invasive populations of G. vermiculophylla in the East and West Atlantic and the East Pacific.

P16.

A SEASONAL STUDY OF CHANGES IN PHYTOPLANKTON AND NUTRIENTS IN THE CALUMET RIVER, ILLINOIS.

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The Calumet River, which is connected to Lake Michigan, played an important role in industrial growth in North East Illinois and North West Indiana. This led to discharges from several industries located on the banks. The current work has been undertaken to study the biodiversity of phytoplankton and their relationships with nutrient and physical parameters. Monthly water samples were collected from May to October 2009 at four locations on the river. Algal species were identified at each site. Water pH, temperature, dissolved oxygen, turbidity; conductivity, nitrate, ammonium and phosphate were measured along with macro-nutrients, and micro-nutrients. A total of fifty-six phytoplankton species were identified during the study, with Chlorophyta being most diverse group while Dinophyta and Euglenophyta the least diverse groups. Significant positive correlations were observed for the overall May and August samples between algal diversity and nitrate, ammonium, and phosphorus. There was also a significant positive correlation between Fe and total number of algal species at one of the four sites. The present study concludes that N, P and Fe are the limiting factors for algal populations.

P17.

ENVIRONMENTAL FACTORS CONTROLLING THE PHYTOPLANKTON COMMUNITY STRUCTURE IN FRESH WATER BODIES OF MISSISSIPPI

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Investigations were done in six major taxa groups: Cyanobacteria, Chlorophyta, Bacillariophyta, Euglenophyta, Pyrrophyta, and Rhodophyta and four aquatic habitats of Mississippi to determine the abundance and richness of the algal community and to identify relevant environmental drivers of algal assemblage composition. Twelve algae data sets from previous studies on large streams and rivers, lakes and reservoirs, fish production ponds, and a long-term data set on small order streams were analyzed. Chlorophyta was dominant in lakes and reservoirs and the most diverse taxa in the phytoplankton of small order streams and large streams and rivers, whereas Cyanobacteria were the dominant taxa in fish production ponds. Other taxa were minor components of the phytoplankton. Nutrient input and temperature had the greatest influence on controlling phytoplankton abundance in production ponds. Multivariate analyses were done by using canonical correspondence analysis to determine the environmental factors controlling the structure of the algal community in the various habitats. Temperature, dissolved oxygen, pH, and alkalinity were the best predictors of algal community structure in small order streams whereas temperature, dissolved oxygen, pH, and conductivity were the key environmental factors affecting phytoplankton structure in lakes and reservoirs.

P18.

CALOTHRIX – A REVIEW OF FRESH WATER SPECIES FOUND IN THE USA AND PRELIMINARY DISTRIBUTION DATA FROM THE RECENT NATIONAL RIVERS AND STREAMS ASSESSMENT (NRSA).

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Species belonging to the genus Calothrix are blue-green, filamentous algae with a basal heterocyst found in both salt and fresh water. Tilden described 39 species, with 36 having distributions in the US, Greenland and the West Indies. Two later taxonomic keys by Prescott and Cocke list 9 and 12 fresh water species respectively with Cocke also listing 6 marine species. The National Rivers and Streams Assessment, undertaken by the EPA, encompassed over 2000 fresh water sample sites spread over 48 States. The study was developed to provide data to assess the current condition of U.S water resources. This review utilizes both a literature review and data obtained from the NRSA project. Species of Calothrix were found in the freshwater algal flora for 75 % of the included States. Nine species were identified, 7 of which are previously described. Calothrix fusca, C. braunii and C. epiphytica show the widest distributions in the preliminary findings. The highest species diversity was shown in Oregon samples (6 species) and California, Idaho, Montana, North Dakota and New Mexico (4 species). Preliminary findings indicate that species of Calothrix are generally distributed across the U.S.A in rivers and streams. The diversity identified was not as great as indicated by Cocke. The reduced diversity was thought due to two factors. Difficulties encountered identifying to a species level and method of sample assessment which did not look specifically at species diversity.

P19.

THE EFFECT OF ENDOPHYTE INFECTION ON GROWTH AND SURVIVORSHIP OF ANTARCTIC MACROALGAE (RHODOPHYCEAE).

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Filamentous algal endophytes are common in many species of chemically defended macroalgae along the Western Antarctic Peninsula. Effects of endophytism in these hosts are unknown, but may be detrimental to host due to competition for light and nutrients or pathogenic effects. To test the effect on host growth and survivorship, individuals representing three degrees of endophyte infection from three species of red macroalgae (Rhodophyceae) were out-planted and monitored for growth. The experiment occurred at the end of the Austral summer and lasted approximately 6 to 9 weeks until population senescence was imminent. Growth rate was measured by weight change of individuals every three weeks. Any fragmentation of individuals during the experiment was accounted for using surface area measurements. Loss of whole individuals due to habitat action was greatest among individuals with high levels of endophytes and similarly these individuals appeared to begin senescing early. Further inquiry into effects on reproduction and ecology of these algae are warranted.

P20.

REPORT OF A NEW INVASIVE ALGA IN THE ATLANTIC UNITED STATES: *'HETEROSIPHONIA' JAPONICA* YENDO IN RHODE ISLAND

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Recent collections of tetrasporangiate *'Heterosiphonia' japonica* from Watch Hill to Point Judith, Rhode Island, represent the first report of this non-native alga in the western Atlantic. Native to the Pacific Ocean, this species was unintentionally introduced into European waters by 1984 and has subsequently invaded the eastern Atlantic Ocean widely from France to Norway and south into the Mediterranean Sea. Thus far, all western Atlantic collections of this species are confined to the outer coast of Rhode Island, and at present, not found in Narragansett Bay or in Long Island Sound along the Connecticut coast. Molecular and morphological studies confirm the identity of this newly introduced invasive species.

P21.

ABUNDANCE AND DISTRIBUTION SURVEYS OF MACROALGAL BLOOMS IN NEW ENGLAND SALT MARSHES

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Observations of macroalgae growing or deposited among the stems of lower marsh plants have been made throughout the United States, particularly along the northeast and southwest coasts; however, no reports have been made regarding the abundance or species composition of these macroalgal blooms. Without this critical information, the extent to which these senescing blooms may impact salt marshes is unknown. Therefore, the purpose of this study was to document the abundance and species composition of macroalgae in a New England salt marsh, as well as to

determine areas within the marsh that are most likely to be impacted. Monthly surveys were conducted throughout Narragansett Bay, R.I. between May 2009 and May 2010. The percent cover of all macroalgae, Spartina alterniflora, exposed roots and dead S. alterniflora was recorded using 0.25 m2 quadrats placed at 1 m intervals along three 10 m transects. The biomass of each macroalgal species was also recorded. Macroalgae were most commonly found along the lower edge of the regularly flooded S. alterniflora zone, however, the dominant species of macroalgae present within each marsh varied among sites.

P22.

REACTIVE OXYGEN SPECIES AS A POTENTIAL MACROALGAL DEFENSE ALONG THE WESTERN ANTARCTIC PENINSULA

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Algal-dominated communities along the Western Antarctic Peninsula (WAP) are unique in the extent of both mesograzers and filamentous algal endophytes. WAP macrophytes exhibit a range of susceptibility to herbivory and colonization by endophtytes in nature. About half of all species studied produce secondary metabolites that deter grazing, so antifeedants and likely endophyte-specific natural products contribute to WAP macroalgal defense. However, some macrophytes lack chemical antifeedants but remain unpalatable to grazers and overall this unpalatability is predicted neither by physical toughness nor by nutritional content. The production of reactive oxygen species (ROS) as a chemical defense has never been investigated in polar waters and could play a significant role in WAP communities. This poster presents the dynamics of WAP macroalgal ROS release both constitutively and upon wounding, a state inherent to endophyte colonization and herbivory. Sympatric amphipods respond to micromolar concentrations of hydrogen peroxide, a common ROS, with a reduction in feeding rate, indicating that ROS release could potentially affect grazing. Future work will focus on quantifying ROS release and determining whether WAP ROS deter grazers and/or endophyte spores.

P23.

USING MACROALGAE TO TRACK ENVIRONMENTAL CHANGES IN THE GREAT BAY ESTUARINE SYSTEM

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Monitoring macroalgae populations is an effective means of detecting long term water quality changes in estuarine systems. To investigate the environmental status of New Hampshire's Great Bay National Estuarine Research Reserve, this study assessed the abundance/distribution of macrophytes, particularly Gracilaria and Ulva species, relative to eutrophication patterns; compared historical (1970s-1990s) and current algal biomass/cover at several sites; compared Ulva and Gracilaria tissue N/P content to ambient levels. Ulva and Gracilaria biomass/cover have increased significantly at several sites. Cover by Ulva species, at seasonal maxima, was over 90 times the value recorded in the 1970s at Lubberland Creek, and exceeded 50% at all sites in the upper estuary. Gracilaria cover was greater than 25% at Depot Road in the upper estuary, whereas the historical measure was 1%. Sequencing of ITS2, rbcL and CO1 revealed the presence of previously undetected Ulva and Gracilaria species, including Gracilaria vermiculophylla (Ohmi)

Papenfuss, an invasive species of Asian origin. G. vermiculophylla has exceeded G. tikvahiae as the dominant Gracilaria species in Great Bay. Historical voucher specimen screening suggests G. vermiculophylla was introduced as recently as 2003.

P24.

A SURVEY OF PHYTOPLANKTON DIVERSITY AND ENVIRONMENTAL ATTRIBUTES ACROSS AN OLIGOHALINE, SUBTROPICAL ESTUARY UTILIZING PIGMENT ANALYSES AND PSBA DNA SEQUENCES

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The Lake Pontchartrain basin estuary is a shallow, lagoonal system with typical salinities ranging from 0-8 ppt. Eight sites were sampled across the estuary during October 14-20 (21-24°C) and December 12-17, 2003 (10-12°C) and analyzed for physical/chemical parameters and overall phytoplankton composition as derived from suites of diagnostic photopigments. DNA sequences of cloned psbA PCR products were used to assess nanophytoplankton biodiversity (<10 μm) in four samples. Salinity varied east to west, but was less pronounced in the December samples. Ratios of N:P were lowest in Lake Maurepas in both seasons, but varied across central and eastern Lake Pontchartrain in December. Diatoms, cyanobacteria and chlorophytes contributed similarly to total chlorophyll, except in December when diatoms contributed about three times greater in central Lake Pontchartrain than cyanobacteria and chlorophytes combined. DNA sequences from each unique RFLP pattern were compared to the Genbank database; 57 sequences were identified. Of these 59.7% were viral, 15.8% cyanobacterial, 10.5% diatom and 8.8% chlorophyte. Five sequences provided database matches common to all four samples: one diatom, a cyanobacterium and three phages. No geographic distribution pattern was observed.

P25.

COMPARATIVE ANALYSIS AND FUNCTIONAL ANNOTATION OF EXPRESSED SEQUENCE TAGS (ESTS) FROM COLD AND NON-ACCLIMATED FRESHWATER GREEN ALGA, *SPIROGYRA VARIANS*

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Spirogyra varians (Hass.) Kuetzing is freshwater green alga that could survive wide range of temperature (0°C-25°C). Expressed Sequence Tags (ESTs) from warm (20°C) and cold (4°C) cultivated *S. varians* were compared simultaneously to isolate cold regulated genes. A total of 5,450 ESTs from warm and cold libraries were obtained. The results of assembly and clustering of ESTs were consisted of 2,693 unique sequences with 832 contigs (63%) and 1,861 singleton (37%). About 77% of genes could be assigned as known and putative functions using BLAST database (e-value: below e-10). The expression patterns of two libraries were similar. Total 216 genes were up-regulated and 201 genes were down-regulated under low-temperature. The analysis of gene ontology (GO) generally showed similar pattern between two libraries with exception of a

division of gene category. Most of cold regulated genes which were increased to 2 or 3 times than warm condition were belonging to stress response, polysaccharide bio-synthesis and antioxidant enzyme. On the other hand, phosphorylation and TCA cycle involved genes were down-regulated at low-temperature.

P26.

NUTRIENT CONTRIBUTIONS FROM *DREISSENA* TO THE BENTHIC CYANOBACTERIUM *LYNGBYA WOLLEI*.

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The cyanobacterium *Lyngbya wollei* has recently become abundant on the bottom of Lake Erie. Blooms of *Lyngbya* are considered harmful because it eventually floats to the surface and can form meter deep masses along the shoreline. *Dreissena* spp. (zebra and quagga mussels), which has been known to increase light to the benthos, may also contribute a limiting nutrient to benthic algae, thereby facilitating blooms. Manipulative experiments showed that *Lyngbya* had higher phycocyanin in tanks with live dreissenid mussels than tanks without live mussels. *Lyngbya* also had a higher amount of carbon, nitrogen, phosphorus, potassium, and sulfur in the tanks with live *Dreissena*. Conversely, *Lyngbya* had a lower amount of calcium in the tanks with live mussels. These results suggest that *Dreissena* are giving several nutrients to *Lyngbya* which is making it photosynthetically healthier. *Dreissena* can provide nutrient resources to benthic algae; therefore *Dreissena* can be a factor that promotes benthic algal growth and productivity, aiding in blooms.

P27.

EFFECTS OF IRON DEFICIENCY ON THE PHOTOSYNTHETIC APPARATUS AND ANTIOXIDANT DEFENSE SYSTEM OF DUNALIELLA TERTIOLECTA

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Iron deficiency stress effects on the photosynthetic apparatus and antioxidant defense system are investigated in the Chlorophyte alga, Dunaliella tertiolecta. D. tertiolecta was cultured under low (100 nM) and high (500 nM) iron concentrations. PSII efficiency exhibits a 14% reduction, chlorophylls are reduced by nearly 50%, and carotenoid:chlorophyll ratios increase in iron deficient cultures accompanied by a 40% reduction in photosynthesis.

P28.

STEROL BIOSYNTHESIS IN THE MARINE DINOFLAGELLATE, KARENIA BREVIS

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The objective of this study is to elucidate important biochemical steps in the biosynthesis of brevesterol and gymnodinosterol, the primary sterols produced by *Karenia brevis*, by determining structures of selected intermediates that accumulate during exposure to particular fungicides known to inhibit sterol biosynthesis. The fungicides utilized included econazole, an inhibitor of cytochrome P-450-dependent 14-alpha-demethylation, and fenpropidine, an inhibitor of delta14-reductase and delta 8(9)-7(8) isomerase.

Our data suggest a combination of fungal- and plant-like pathways are present in *K. brevis*. Exposure of *K. brevis* to econazole produced a $C_{29:2}$ intermediate that resembles lanosterol, and exposure to fenpropidine produced two tri-unsaturated intermediates $C_{28:3}$,and $C_{29:3}$, with one having the same side-chain as ergosterol, a key fungal sterol. Characterization of these intermediates will be presented. Also discussed

will be the discovery of stigmasterol, a common plant sterol, in *K. brevis*, independent of fungicide treatment. As stigmasterol is a major component of haptophytes, it is possible that production of stigmasterol in *K. brevis* is the result of sterol biosynthesis genes that have been incorporated from its haptophyte endosymbiont.

P29.

WHAT IS THE ULTIMATE EFFECT ON SPOROPHYTE FORMATION AFTER LONG-TERM CULTIVATION OF GAMETOPHYTES FROM TWELVE SPECIES OF LAMINARIALES?

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The capability of long-term cultured strains (gametophytes) of several species of Laminariales to produce viable sporophytes was assessed. 41 stock culture strains of 3 annual species (*Undaria pinnatifida* etc.) and 27 strains of 9 perennial species (*Ecklonia cava* etc.) were used for the experiment. Male and female gametophytes that generated from the same adult sporophyte were mixed in the same culture vessel. After 45 days cultivation, the maturation capability was determined as whether juvenile sporophytes were generated or not. In 49 strains (72.1% of the total) the generation of juvenile sporophytes was confirmed. Generation of juvenile sporophytes were observed in most of the short-term (within 5 years) cultured strains. On the other hand, several strains that had been long-term (over 20 years) cultured did not generate juvenile sporophytes. The decrease of the maturation capability caused by long-term cultivation was observed especially in the perennial species. In annual species, many strains generated juvenile sporophytes even though cultured over a long-term. These results indicate that the maturation ability of cultured gametophytes is related to the period of cultivation and to the species.

P30.

WESTERN LAKE ERIE MICROCYSTIS IS PHOSPHORUS LIMITED EVEN UNDER LOW NITROGEN AVAILABILITY

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Low total nitrogen to total phosphorus ratios (TN:TP) often signify N-limitation. Blooms of *Microcystis*, a non-N-fixer, have been common in western Lake Erie the past decade. TN:TP is very low (< 15, by moles) by the end of the summer in Lake Erie because nitrate loading declines throughout summer. During 2008, we measured TN:TP from 6 sites on 9 dates and *Microcystis* intracellular carbon (C), N and P on 4 dates during the bloom. TN:TP declined from 78.8 to 14.8 throughout the summer. Intracellularly, C:N was < 8.3 for 95% of samples, indicating no N deficiency, and C:P was > 129 for 70% of samples, indicating a moderate P deficiency. Thus, P limits *Microcystis* in Lake Erie even during low TN:TP. The ammonium-N level was stable during the summer and likely provided the N source for *Microcystis*. The lack of nitrate-N may favor *Microcystis* because *Microcystis* is a superior competitor for ammonium-N when nitrate-N is depleted, leaving other algae N-limited. Future research will address the role of N species in the competitive outcome of Lake Erie phytoplankton under low TN:TP.

P31.

OPTIMAL CONDITIONS OF IRRADIANCE AND TEMPERATURE FOR TRIGLYCERIDE-ASSOCIATED FATTY ACID PRODUCTION IN THE GREEN ALGA,*CHLAMYDOMONAS REINHARDTII*

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The unicellular, photosynthetic, green alga *Chlamydomonas reinhardtii* is a model organism for lipid research because it is one of very few algae that have extensive genomic and physiological data existing. This study examined the effects of variations in temperature and irradiance on the production of triglyceride-associated fatty acids in *C. reinhardtii*. The experimental design matrix used encompassed culture growth at five different irradiances (50, 287, 525, 762, and 1,000 micromoles photons m^{-2} s^{-1}) and five different temperatures (8, 15, 23, 30, and 38 C) to generate a set of twenty-three samples with an additional sample grown at 20 C and 525 micromoles photons m^{-2} s^{-1} (the cultures at a temperature of 8 C and light intensities of 762 and 1,000 micromoles photons m^{-2} s^{-1} did not grow due to an inability to tolerate intense irradiance at this low temperature). There were four C_{16} fatty acids and four C_{18} fatty acids found consistently throughout all twenty-four samples. Using color models, the optimum light and temperature conditions were determined for the production of each of the eight fatty acids in *C. reinhardtii*.

P32.

PHYLOGENY AND BIOGEOGRAPHY OF THE GENUS AGARUM (PHAEOPHYCEAE) BASED ON SEQUENCES OF THREE GENES

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Agarum is a perennial kelp genus that has an ocean-wide distribution from the north Pacific Ocean to the northwest Atlantic Ocean region. In order to address questions regarding the phylogenetic relationships and current distribution patterns of the genus, we analyzed nuclear ITS2, plastid Rubisco spacer, and mitochondrial cox3 regions from 108 samples of the genus including Thalassiophyllum and Costaria. All analyses of three genes consistently produced a monophyletic clade of Agarum including Thalassiophyllum. The clade consisted of two well-resolved subclades: one for A. fimbriatum and A. oharaense, and the other for A. clathratum, A. turneri, A. yakishiriense, and Thalassiophyllum clathrus. In all trees, A. clathratum showed a wide distribution from the east coast of north America via Alaska to northwest Pacific, whereas remaining species of the genus were limited to certain ranges. The low degree of substitutions between A. clathratum and A. yakishiriense suggests their recent divergence from a common ancestor.

P33.

SYSTEMATICS OF THE GENUS MONOMORPHINA (EUGLENACEAE)

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To clarify systematics of the genus Monomorphina, we analyzed 24 taxa based on morphological and molecular data. The analyzed morphological data was cell shape, flatness, size, and ratio of tail to cell. However, the morphological characters of M. pyrum complex showed no significant species-specific pattern. Bayesian and maximum likelihood (ML) analyses based on combined dataset of nuclear SSU and LSU and plastid SSU and LSU rDNA. M. aenigmatica was branched first on the tree. M. pseudopyrum was located at the middle of the tree and formed sister clade with a new taxon from Michigan. M. pyrum complex strains divided into four clades (M. pyrum, M. pseudonorstedii, M. inconspicuus, and M. rudicula) and had their own molecular signatures. The species of Monomorphina has genetic diversity with inter-specific sequence similarity of 90.8%-98.0% and intra-specific similarity of 97.6% - 99.9%. Our results suggest that a new species M. michiganensis differ from M. pseudopyrum based on specific molecular signature, and M. aenigmatica , M. inconspicuus, M. pseudonorstedii, M. pseudopyrum, M. pyrum, and M. rudicula should be emend their diagnoses and establish epitype.

P34.

PHYLOGENY OF AUSTRALASIAN ENDEMIC TAXA IN THE BATRACHOSPERMALES (RHODOPHYTA) USING THE RBCL AND LSU GENES.

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In previous research using the rbcL gene alone, the majority of Australasian endemics have grouped together, but with little support for the relationships among taxa. More collections from Australia, New Zealand, and New Caledonia provided data for taxa not previously sequenced and new sequences for widespread taxa. Data from the first half of the LSU (~1350bp; nuclear) and the rbcL (1282bp; chloroplast) genes were used in phylogenetic analyses. Unfortunately, the larger data set did not provide additional support, especially to the nodes of interest. Nevertheless, new insights were gained. For example, the section *Setacea* is paraphyletic with the addition of *B. diatyches* to the analyses. New specimens of *B. theaquum* showed this taxon to be paraphyletic. The three taxa, *B. bourrellyi*, *B. campyloclonum* and *B. pseudogelatinosum*, are in three closely related clades and are in need of further morphological circumscription. Although most taxa in the group are Australasian endemics, two taxa from South America (*B. puiggarianum* and *Petrohua bernabei*) and one cosmopolitan species (*B. atrum*) are present leading to interesting biogeographic questions for future exploration.

P35.

PHYLOGENY OF THE GENUS MALLOMONAS (SYNUROPHYCEAE) BASED UPON ULTRASTRUCTURE AND MOLECULAR DATA

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To understand taxonomy and molecular phylogeny of the genus Mallomonas, we examined the ultrastructure of silica scales using FE-SEM and we analyzed molecular data from the uclear SSU and LSU rDNA and the plastid rbcL sequences. Our analyses showed that the genus Mallomonas is comprised of five clades separated by substantial genetic distances and morphological features. Taxa within clades shared common morphological characteristics: C1 - scales lacked a V-rib on the shield; C2 - scales lacked a dome but had a shield, flange and V-rib; C3 - scales had an indiscernible dome or V-rib; C4 - scales had a well-developed V-rib and there was a dome on collar scales; C5 - scales had both a well-developed V-rib and a dome. The molecular phylogenetic relationships and the scale phenotypic characteristics were generally consistent within the sections of genus. However, our molecular results suggested that M. heterospina should be transferred to the section Planae. In addition, M. bronchartiana, previously classified in the section Planae, was not related to other members of that section. Taxa classified in Section Striatae had similar scale characteristics, but the Section was a not monophyletic group in the molecular analyses. In our molecular studies, M. lelymene was intermixed within the section Striatae species. Our molecular and ultrastructural data suggests that a taxonomic revision of the Section Striatae is appropriate.

P36.

EXPLORING GELIDIALES (RHODOPHYTA) DIVERSITY ON SAO PAULO STATE (BRAZIL) WITH MOLECULAR MARKERS.

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As part of an ongoing DNA barcode project on Sao Paulo State (Brazil), this work aims to characterize the Gelidiales flora. Known to be a well represented group in this region, this is the first time that molecular markers are being employed for the identification of Gelidiales from Brazil. Three molecular markers (COI, UPA and rbcL) were sequenced for 25 specimens, which were analyzed in clustering trees. Results obtained were consistent for the three markers and indicate the occurrence of four different genera and a total of ten species: Gelidiella (N=3, one species), Gelidium (N=10, four species), Parviphycus (N=1, one species) and Pterocladiella (N=11, four species). The last floristic survey of this order on Sao Paulo Coast was done on 1985 and only six species in two genera were recognized. By the completion of this work, a new perspective of the Gelidiales on Sao Paulo Coast will be pictured.

P37.

REVIEWING THE GENUS CYCLIDIOPSIS: IS THE CURRENT TAXONOMY VALID?

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The genus Cyclidiopsis was erected in 1917 by Korschikow and includes colorless, elongated, free-swimming, osmotrophic cells with an eyespot. The type species, C. acus, is similar to the photosynthetic euglenoid Lepocinclis acus, differing only in its apical canal opening and lack of pigment.

In this study, we have applied recent advances in sequencing techniques that were initially adopted for clinical applications and forensic analysis. The technique, called Multiple Displacement Amplification (MDA), allows for the sequencing of genetic material from only a few cells.

A Multiple Displacement Amplification was performed on 2 Cyclidiopsis acus cells isolated from field samples. The MDA amplified DNA was then processed by PCR and sequenced for the SSU and LSU rDNA genes. These sequences were used to generate a phylogenetic tree that placed Cyclidiopsis acus firmly in the Lepocinclis clade, suggesting that this taxon should be considered a species of Lepocinclis. Taking into account that C. acus is the type species for Cyclidiopsis, this finding also suggests that the genus itself may no longer be valid, and that it should be absorbed into the genus Lepocinclis.

P38.

DIVERSITY OF DIATOM NITRATE TRANSPORTER GENES FROM ISOLATED SINGLE-CELLS AND MIXED SAMPLES FOR THE ESTABLISHMENT OF MRNA QUANTIFICATION IN THE EAST CHINA SEA

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Transcript abundance of nitrate transporter genes, Nrt2, has been proposed as a potential marker for nitrogen deficiency in marine diatoms. To correctly design primers for the quantification of diatom Nrt2 mRNA in the East China Sea (ECS), we utilized both bulk sequencing and single-cell PCR to expand the sequence database of this region. Using single-cell PCR, 9 new sequences of diatom Nrt2 belonging to 5 genera whose Nrt2 sequences have never been reported before were obtained. On the other hand, a total of 291 sequences homologous to Nrt2 were retrieved in bulk sequencing, and these sequences were clustered into 12 major groups according to phylogenetic analysis. Based on sequence alignments, 11 pairs of group-specific primers were designed, and 3 of these primer pairs showed high specificity to target species. In ECS samples, Nrt2 transcript levels were readily detected using Q-RT-PCR with a preamplification of aRNA production. Our results indicated that an investigation of sequence diversity followed by careful primer design and evaluation forms a good algorithm for the quantification of gene expression in ecologically important phytoplankton.

P39.

A UNIQUE NEW SPECIES OF *CALOGLOSSA* (DELESSERIACEAE, RHODOPHYTA) FROM PEDRO MIGUEL LOCKS, MIRAFLORES LAKE, PANAMA, CENTRAL AMERICA

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Although the red alga Caloglossa (Harvey) G. Martens has long been investigated taxonomically, the species diversity of the genus is not yet fully understood. Comparative chloroplast-encoded rbcL and nuclear 26S LSU rDNA sequence analyses, combined with morphological observations, reveal a new species for Central America. This new species, collected from the intertidal in the Panama Canal, Panama, is characterized by thalli of lanceolate blades arranged in tufts, with adventitious branching, and strong constrictions at the thallus nodes; The proposed new species forms a monophyletic group with other species whose only mode of secondary branching is also adventitious. The taxonomic importance of rhizoid morphology, degree of constriction at the thallus nodes, secondary branching pattern, blade morphology, blade width, number of cell rows cut off from the first axial cell of the main axis, and presence of an adaxial cell row derived from the first axial cell from lateral axis is illustrated and discussed.

P40.

CELL DIVISION IN THE CHAROPHYCEAN GREEN ALGA *ENTRANSIA FIMBRIATA*

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Differential interference contrast light microscopy and transmission electron microscopy were used to study cell division in *Entransia fimbriata*, a member of the Klebsormidiales. Cells contained a single large vacuole and a single large parietal chloroplast, each of which extended the length of the cell. The nucleus resided next to the chloroplast at the midpoint. The first indication of cell division was cleavage of the chloroplast, which divided completely or almost completely prior to mitosis. Initiation of a septum occurred after chloroplast division and before or during prophase, but the septum did not continue to develop until later. The late prophase nucleus was diamond shaped, and the nucleolus was present until just before metaphase. Though the telophase nuclei initially formed near the division plane, they had moved to opposite ends of the cell and were no longer aligned with each other during cytokinesis. Septum formation was centripetal. *Entransia*, like *Chlorokybus*, exhibits chloroplast division and septum initiation before prophase. These processes are reported to occur later in *Klebsormidium*. Cell division in *Entransia* is consistent with that in other early divergent charophycean algae.

P41.

THE SPECIES EUGLENA DESES (EUGLENACEAE) REVISITED: NEW MORPHOLOGICAL AND MOLECULAR DATA

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Morphological variability of Euglena deses has occupied researchers since long ago resulting in abundant literature on numerous descriptions of taxa with morphology similar to that of E. deses. Nevertheless, the relationships between taxa and their distinguishing criteria still remain unclear.

We have studied morphological diversity of 13 strains from "Euglena deses group" and performed Bayesian and Maximum Likelihood analyses based on SSU rDNA to resolve phylogenetic relationships.

Our research supports previous observations regarding the high morphological diversity among E. deses with respect to the size and shape of the cells, the morphology of the chloroplasts and large paramylon grains; at the same time showing that these characteristics have no diagnostic significance. Based on our results and literature studies, we recognize only three species in the "Euglena deses group": E. adhaerens, E. deses and E. satelles. While E. adhaerens and E. satelles are closely related to each other, E. deses constitutes a distinct clade, and is highly characteristic morphologically, exhibiting papillae and having the canal opening located in the lateral position.

P42.

NEW INSIGHTS INTO THE TAXONOMIC POSITION OF THE ENDEMIC BROWN ALGAL GENUS *CLADOPHYLLUM* FROM THE CARIBBEAN COAST OF COLOMBIA WITHIN THE SARGASSACEAE

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The widespread tropical to temperate genus *Sargassum* C. Agardh is one of the morphologically most complex genera of brown algae. This genus is traditionally divided into subgenera, sections, subsections, series, and species groups based on highly polymorphic characters such as the shape of the axes, leaf-like phylloids, vesicles, and receptacles. However, recent DNA analyses have highlighted incongruities in the traditional classification criteria of the genus, prompting several new systematic revisions. In this study the generic concept of the monospecific and closely related genus *Cladophyllum* Bula-Meyer was assessed and inferred on the basis of five molecular markers in 59 taxa within the Sargassaceae: nuclear ITS-2, part of the chloroplast-encoded RuBisCO operon and 23S, and mitochondrial cox3 and mtsp. Our results indicate that *Cladophyllum* does not represent a monophyletic clade but instead may represent a new section in the genus *Sargassum*. *Cladophyllum schnetteri* Bula-Meyer was originally described based exclusively on morphological characteristics. This species has a very restricted extant distribution and has only been reported from and observed growing on a small rocky shore in the Caribbean coast of Colombia.

P43.

PHYLOGENY OF FRESHWATER EUSTIGMATOPHYCEAE

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Freshwater Eustigmatophyceae are a group of microalgae that have generally been considered rare and of low diversity, with only a few genera and species. Although much of the recent work in Eustigmatophyceae taxonomy has focused on the genus *Nannochloropsis*, this study does not include characterization of *Nannochloropsis* isolates. We examined twenty-four freshwater Eustigmatophyceae isolates from Itasca State Park, Minnesota (Microbial Observatory), and Lake Chicot, Arkansas using DNA sequence analysis of the plastid rbcL gene. We also generated rbcL sequences for all of the named Eustigmatophyceae from the Culture Collection of Algae at the University of Texas at Austin (UTEX), and some additional taxa held in other culture collections. The results of our phylogenetic analyses indicate the presence of two major lineages within the Eustigmatophyceae and suggest that this class may comprise four or more orders. A companion data set of 18S rDNA sequences is in preparation. Results of preliminary analyses of 18S sequence are congruent with the results of rbcL sequence analysis. This group of isolates comprises more genera than have previously been described among the Eustigmatophyceae.

P44.

A SYSTEMATIC REVISION OF *TOLYPELLA A*. BR. (CHARALES, CHAROPHYTA): PRELIMINARY INVESTIGATIONS.

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Characeae contains 2 tribes with 6 genera: tribe Chareae, which includes *Chara*, *Lamprothamnium*, *Lychnothamnus* and *Nitellopsis*; and tribe Nitelleae, which includes *Tolypella* and *Nitella*. Characeae exhibits a broad range of morphological diversity and in the most recent taxonomic treatment (Wood & Imahori, 1965) over 400 species were reduced to 81, including 16 *Tolypella* species subsumed under 2 species (*T. nidifica* and *T. intricata*) representing sections Tolypella and Rothia. It was further suggested that *Tolypella* may be a derived species of *Nitella*. There are no comprehensive molecular phylogenetic studies of *Tolypella* that address the relationships within the genus or to the rest of Characeae. In a preliminary investigation into species diversity in the genus, chloroplast DNA sequence data for *rbcL* and *atpB* and nuclear DNA sequence data for enolase were assembled for field collected and herbarium specimens. Phylogenetic analyses of plastid sequence data support monophyly of *Tolypella* and the sections within but a relationship to the rest of Characeae was unspecified. Nuclear sequence data for two species supports monophyly of the genus and suggests a utility for enolase in phylogenetic studies.

P45.

NEW INSIGHTS INTO THE SYSTEMATICS OF BLADE-LIKE MARINE RED ALGAE FROM THE GULF OF MEXICO

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The Gulf of Mexico hard banks harbor a remarkably diverse benthic red algal flora, with many foliose taxa attached to unconsolidated rubble and algal nodules (rhodoliths) at depths ranging from 45-90 m. The vegetative and reproductive morphology of previously unreported foliose taxa occurring throughout the NW, SW, SE, and NE Gulf region is newly documented with light microscopy observations. *rbc*L-based phylogenetic trees indicate that four species of *Halymenia* and three species of *Cryptonemia* are of uncertain taxonomic status, and that two undescribed species do not group with any of the known foliose genera in the Halymeniaceae. *Kallymenia* in the Kallymeniaceae comprises many perforated species, including a small taxon that needs further analysis. A foliose member of the Solieriaceae shows a close phylogenetic relationship to *Sarcodiotheca* and *Anatheca* but is morphologically and molecularly distinct from the other blade-like taxa in the family. In general, the foliose taxa within a family are scattered among non-blade-like members in *rbc*L-based phylogenetic trees.

P46.

EUGLENOID PHYLOGENETICS BASED ON THE EVALUATION OF PROTEIN AND RIBOSOMAL CODING GENES

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Molecular phylogenies have been instrumental in determining relationships among the major genera of photosynthetic euglenoids. The majority of these analyses have relied on the use of nuclear or chloroplast ribosomal genes. Two nuclear genes, psbO and HSP90, were added to the data set to assess the impact of these protein coding genes on these phylogenetic relationships. The psbO gene, a nuclear encoded plastid targeted gene involved in oxygen evolution, and HSP90, a nuclear encoded heat shock gene coding for a molecular chaperone, were sequenced in a total of 52 euglenoid taxa representing Colacium, Cryptoglena, Discoplastis, Euglena, Lepocinclis, Monomorphina, Phacus, and Trachelomonas. HSP90 and psbO datasets were analyzed individually and in combination with the nuclear SSU and LSU ribosomal genes and the chloroplast SSU ribosomal gene. Results confirm that the combined dataset of protein and ribosomal sequences resulted in phylogenetic trees that were congruent with previous analyses based on ribosomal genes only. Furthermore, results suggest that the ribosomal genes as well as the protein coding genes all share phylogenetic utility, and combined, yield a more robust phylogeny.

P47.

THE HAWAIIAN FRESHWATER ALGAL DATABASE

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The Hawaiian Freshwater Algal Biodiversity Survey (2009-2012) is a collaborative effort to characterize the non-marine algae of the Hawaiian archipelago, and is expected to yield thousands of samples by project completion. Multiple forms of data are collected, including collection site and collector details, taxonomic designation, specimen photographs and/or micrographs, and DNA sequences, all of which are organized for easy access and comparison. The Hawaiian Freshwater Algal Database (HfwADB) was designed to organize these data and enable their presentation on the internet, and was constructed using MySQL and PHP. HfwADB is modeled after the Hawaiian Algal Database (HADB), with the principal difference being the ability to accommodate the identification of multiple taxa from species-rich environmental samples. Data are organized according to a two-tier accession number, with the first five digits corresponding to the environmental sample ("environmental accession") and the last five digits to the specific taxon identified from that site ("isolate accession"). Here we present the structure of HfwADB, summarize current content, demonstrate search capabilities, and illustrate how it can be used to access and organize biodiversity data.

P48.

TWO RARE ZYGNEMA SPECIES (ZYGNEMATOPHYCEAE) FROM CALIFORNIA STREAMS

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This study was carried out on more than 500 stream samples collected from California watersheds in the summer and fall of 2008 to 2010 as part of water quality analyses sponsored by the California Water Board. Two rare Zygnema species were observed. Zygnema argillarii Kadlubowska was characterized by golden colored zygospores positioned in a gametangium, while an unidentified Zygnema possessed blue to dark brown zygospores situated in the conjugation tubes, and also constantly forming aplanospores. In both species, the zygospores were separated from gametangia by a prominent additional cellulose wall, characteristic of Zygogonium. The chemical composition of the sporangia wall was examined for cellulose and pectic substances by using a number of histochemical techniques. Molecular analyses were attempted to ascertain relatedness of the two taxa to each other and other members of Zygnema and Zygogonium.

P49.

THE GENUS CERAMIUM ROTH IN CABO SAN ROMÁN, FALCÓN STATE WITH EMPHASIS ON SPECIES BEARING PSEUDOPERIAXIAL CELLS

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The main diagnostic features used to determine the species in the red algal Genus Ceramium Roth (Ceramiae, Ceramiaceae, Ceramiales) are the branching pattern, cortication pattern and tetrasporangial arrangement. On the Venezuelan coast, there are 14 records of Ceramium species, of which only four taxa produce pseudoperiaxial cells, i.e. C. clarionense, C. tenerrimum, C. brevizonatum var. caraibicum and C. uruguayense. In this preliminary study we report on three Ceramium species that bear pseudoperiaxial cells, a useful taxonomic feature to distinguish among the species in the Genus. In addition, two species bear multiple hyaline hairs produced by the cortical cells. These specimens are considered at the moment to represent new records for the Venezuelan coast.

55.

ALGAE: DIVERSE LIPIDS WITH MANY USES

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Algae contain many diverse types of lipids and fatty acids. Although certain types of algae (e.g. brown, red etc.) tend to have increased amounts of the more unusual constituents, it is almost impossible to make precise generalisations. Glycosylglycerides are usually significantly more abundant than phosphoglycerides while different types of ether lipids are a third type of membrane constituent. Trialglycerol is the usual, although by no means the only, storage compound. A whole battery of different fatty acids ranging from medium chains to very long chain polyunsaturated compounds are found in different species. These aspects will be summarised. In the presentation, I will also describe biosynthetic pathways for algal fatty acid synthesis, features of the enzymes concerned and how these can be manipulated. Algae are also sources of enzymes with special properties. Recent interest in the biotechnological use of algae will be described including their use in agriculture, pharmaceuticals, cosmetics and, especially, as sources of polyunsaturated fatty acids and biofuel.

56.

LIPIDOMIC: LIPID TARGETED ALGAL TOXINS

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Algae, especially the dinoflagellates, make some of the most complex and toxic natural compounds described. Since the 1930s, the haptophyte Prymnesium parvum has been known to cause toxic algae blooms with catastrophic fish-kills in various regions of the world. Prymnesin, a polycyclic ether with polyhydroxy and polyenyne side chains, has been implicated as the causative agent. The mode of action appears to be the formation of membrane pores requiring desmethyl sterols like cholesterol or ergosterol to be present in the membranes. Recently, a new class of linear polyhydroxyl-polyaliphatic toxins called karlotoxins have been isolated from the dinoflagellate Karlodinium veneficum. These molecules show many of the same properties of prymnesin with the formation of a non-specific membrane pores with membranes containing desmethyl sterols. Leblond and Chapman (2002) found that the sterol profile of K. veneficum is dominated by (24S)-4alpha-methyl-5alpha-ergosta-8(14),22-dien-3beta-ol (gymnodinosterol) which does not form stable membrane pores and hence is impervious to effects of its toxins. We discuss the structural similarities of these two toxins and others like amphidinol as it relates to lipid binding.

57.
LIPIDOMICS: RECENT APPLICATIONS TO THE STUDY OF DINOFLAGELLATE CHLOROPLAST LIPIDS

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Because of their importance as primary producers in marine and freshwater systems, dinoflagellates have had a long history of lipid characterization studies. Traditionally, fatty acid-containing lipids, such as mono- and digalactosyldiacylglycerol (MGDG and DGDG, respectively) that comprise the majority of the chloroplast membrane, are analyzed via gas chromatography/mass spectrometry after the fatty acids are cleaved from the glycerol backbone. This leads to a loss of important structural information (i.e. which fatty acids are connected to which lipid and in which regiochemical positions) that prevents identification of the intact forms of these lipids. The advent of improved analytical technology, such as electrospray mass spectrometry, has revolutionized the study of intact forms of MGDG and DGDG in the rapidly emerging field of lipidomics. This presentation will cover recent applications of lipidomic techniques to the study of MGDG and DGDG in dinoflagellates. Included will be a discussion of the MGDG and DGDG composition of dinoflagellates of different plastid ancestries, and the influence of temperature on MGDG and DGDG composition in the example peridinin-containing dinoflagellate genus, *Pyrocystis*.

58.
ULTRASTRUCTURE AND MOLECULAR EVIDENCE REVEAL ARAPHID PENNATE ANCESTRY FOR A ROUND, UNDESCRIBED TROPICAL DIATOM

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Recent sampling of diatoms in Guam has revealed a wealth of undescribed diversity. One of these undescribed taxa, tentatively referred to as “starry centric,” is a round diatom with elongate chloroplasts that radiate from an internal cup-like structure in the center of the valve. This cup-like structure is similar to structures found in the araphid pennate diatom genera *Cyclophora* and *Hustedtiella*, and in fact a 3-gene molecular phylogenetic analysis suggested a close relationship between “starry centric,” *Cyclophora* and *Hustedtiella*. Further investigations into the ultrastructure of these diatoms (determined by TEM) showed that the cup-like structure shared by all three taxa is also similar in that the pyrenoids appear to be localized within the structure. While this is hardly the first radially-symmetrical diatom suggested to be derived from an araphid pennate lineage, it might be the most distinct synapomorphy (in this case, the cup-like structure in the valve and the localization of pyrenoids within) uniting such morphologically dissimilar diatoms.

59.

PHYLOGENY OF THE DIATOMS BASED ON CHLOROPLAST GENES

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We have sequenced SSU rDNA and four chloroplast genes from about 140 diatoms specifically selected to provide coverage of all major morphological and structural groups. The chloroplast genes seem to have a low signal to noise ratio. Any one chloroplast gene recovers unusual trees (e.g., radial centrics may be recovered in the middle of araphid diatoms). However, addition of genes results in trees that increasingly seem to converge on traditional classifications and results from analysis of the SSU gene. We use these trees to formally test a recent reclassification of the diatoms as well as several major traditionally derived (using morphological, stratigraphic and ecological data in non-canonical ways) phylogenies.

60.

PHYLOGENETIC ANALYSES OF GLUTAMINE SYNTHETASE III PROVIDES EVIDENCE OF A RECENT HORIZONTAL GENE TRANSFER FROM DIATOMS TO THE PRASINOPHYTES

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The glutamine synthetase (GS) superfamily is comprised of three families (GSI, GSII, and GSIII) that are broadly distributed among prokaryotic and eukaryotic organisms. Multiple GS isoenzymes are observed in most photosynthetic eukaryotes and function in the cytosol and chloroplasts, and in some instances, in mitochondria. Genomic sequencing of marine Prasinophytae (Micromonas and Ostreococcus) revealed an unusual distribution of the GS gene families within these genera and this study explores the evolutionary history of the prasinophyte GS isoenzymes. GSII genes were identified in Micromonas spp. but not in Ostreococcus spp. In addition, Micromonas spp. and Ostreococcus spp. genomes encode a GSIII-type enzyme. GSIII genes have also been identified in some chromalveolate lineages, Dictyostelium discoideum, and Entamoebea histolytica. The prasinophyte GSIII sequences formed a well-supported clade that branched within the chromalveolate GSIIIs and was sister to the diatom GSIIIs. GSIII is not present in other red or green algal lineages and thus we propose that the GSIII of Micromonas and Ostreococcus arose by a recent horizontal gene transfer from the diatoms or an ancestral chromalveolate.

61.
SIZING THE HERTEROKONT: PHAEOPHYCEAN GENOME

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Heterokonts comprise one the largest and most heterogeneous groups of protists with species numbering into the millions. Most of these species are unicellular with only the Phaeophyceae successfully shifting to complex multicellularity. Heterokonts are ecologically critical, being the base of many food chains in aquatic environments with an estimated carbon fixation contribution of ~50% of the world's primary production. Heterokonts are part of the supergroup Chromalveolata, which acquired chloroplasts when their ancestor engulfed a red alga and co-opted their plastids. Despite the diversity of the heterokonts and their fascinating evolutionary history, only a small number of heterokont genomes are sequenced. One of the first steps in initiating genome projects and lineage selection is to size the genome. Thus, to examine heterokont genome evolution and the shift to multicellularity in the Phaeophyceae we initiated a genome sizing project. Using the DNA localizing florochrome DAPI and the RBC (chicken erythrocyte) standard we estimated the 2C values with static microspectrophotometery across the heterokonts emphasizing the brown algae. Results of this project and its implications on genome projects will be discussed.

62.
THE TANGLED TAXONOMIC HISTORY OF DICTYOCOCCUS, BRACTEACOCCUS AND PSEUDOMURIELLA (CHLOROPHYCEAE) AND THE IR DISTINCTION BASED ON A PHYLOGENETIC PERSPECTIVE

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Phylogenetically diverse algae, especially unicellular forms from similar habitats, can have nearly indistinguishable morphology when viewed with light microscopy. Consequently, the light microscopic-based historical taxonomy of many green coccoids is a tangled mess because over time systematists have taxonomically emphasized different traits. We present an example of molecular data helping resolve phylogenetic relationships of coccoids and augmenting the interpretation of morphology. Using phylogenetic analyses of rbcL and 18S rDNA sequences, we clarify the relationship of *Bracteacoccus*, *Dictyococcus* and *Pseudomuriella*. We show that *Bracteacoccus engadinensis* and *Dictyococcus schumacherensis* are closely related to *Pseudomuriella aurantiaca*, rather than to the rest of examined *Bracteacoccus* and *Dictyococcus* representatives, respectively. In both cases, the new placement agrees with the species' ecology and vegetative morphology. We therefore propose *Pseudomuriella schumacherensis* and *P. engadinensis*, and emend the description of the former with an altered interpretation of chloroplast features. Our photomicroscopic observations suggest that *Bracteacoccus* and *Pseudomuriella*, although genetically distinct, are morphologically cryptic genera. Chloroplast morphology, observed using light microscopy, clearly separates *Dictyococcus* from the other two genera.

63.

THE TROPICAL FRESHWATER GREEN ALGA *CLONIOPHORA SPICATA* IS A MEMBER OF ULVALES (ULVOPHYCEAE), NOT CHAETOPHORALES (CHLOROPHYCEAE)

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The green algal genus *Cloniophora* was originally designated by Tiffany (1936) to include two species, *C. willei* (the generitype) and *C. capitellata*. *Cloniophora* has frequently been placed in synonymy with *Stigeoclonium* or *Draparnaldia* due to their similar morphology, and all three genera have traditionally been placed in the Chaetophorales. After extensive field collections in freshwater habitats in the six main Hawaiian Islands, we have found only one species of *Cloniophora*, *C. spicata*, which is a reduction from the 3-4 that were previously reported based on morphological variations. DNA sequence data from the nucleus (SSU) and chloroplast (tufA, UPA) show that all Hawaiian collections, plus a specimen from the SAG culture collection (originating from Portugal) are identical, and do not have close affinities to the Chaetophorales. Phylogenetic inference reveals that this taxon is ulvoid, it does not belong to any currently described family, and instead represents a newly recognized lineage in the Ulvales. Further study of type specimens will reveal if the entire genus *Cloniophora* should be reassigned.

64.

SPECIES CHARACTERIZATION IN DESMODESMUS (CHLOROPHYCEAE) USING NUCLEAR ITS AND PLASTID RBCL SEQUENCE DATA COMBINED WITH MORPHOLOGICAL ANALYSES.

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We examined 29 strains from the *Desmodesmus serratus* lineage by analysis of sequences of partial rbcL genes and the complete nuclear ITS1, 5.8S, ITS2 ribosomal RNA region. Twelve additional strains were examined by ITS sequence data only. The ITS2 was the most variable region, followed by rbcL and then ITS1. Separate phylogenetic analyses of the ITS regions and rbcL produced congruent topologies and the phylogenetic signal of these loci were similar. Morphological analysis of monophyletic lineages within the *D. serratus* group, analysis of compensatory base changes in the ITS2 region, and recombination analysis supported the designation of five new species. We propose the new species, *D. pseudoserratus*, *D. serratoides, D. perdix, D. santosii, and D. itascaensis*. A similar analysis of strains assigned to *D. denticulatus* revealed less diversity and supported the retention of the two taxa, *D. denticulatus* var. *denticulatus* and *D. denticulatus* var. *linearis*. Our results demonstrate that the use of combined ITS1, ITS2, and rbcL sequence data is more powerful for characterizing *Desmodesmus* species than ITS2 alone.

65.

CRYPTIC SPECIES DIVERSITY IN THE SHELL- AND REEF-BORING GREEN ALGAL GENUS PHAEOPHILA

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Ulvophyte green algae presently assigned to Phaeophila dendroides (Crouan & Crouan) Batters are common in calcareous substrates (shells, coral rock) in tropical, temperate, and boreal waters, and play a significant role in reef degradation in the tropics. Thirteen strains of Phaeophila, isolated from reef rock and algae collected off O`ahu (Hawaiian Islands), segregated into three groups based on 18s rRNA gene sequences. One of these groups was identical to a Phaeophila strain isolated from the Mediterranean coast of France, while the other two were novel. The algae from one of the novel groups had morphological features similar to those of Phaeophila divaricata Huber, a species described from the Mediterranean coast of France. The findings bring the total number of sequence-based operational taxonomic units (OTUs; putative species) in "P. dendroides" to five, and suggest that the OTUs from Hawaiian waters may represent pantropically-distributed species. A series of collections from topotype localities is needed to reconcile the sequence-based OTUs with the several names of species that, until now, had been considered synonymous with "P. dendroides".

66.

AN OVERVIEW OF ALGAL BIOFUELS RESEARCH AND DEVELOPMENT EFFORTS AT THE DOE BIOMASS PROGRAM

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The U.S. Department of Energy’s Biomass Program has focused on research, development and demonstration (RD&D) of cellulosic ethanol since it was consolidated as a single office in 2002. The American Recovery and Reinvestment Act of 2009 has enabled the Biomass Program to expand our scope to include other advanced biofuels such as renewable gasoline, diesel and jet fuel. Algae can supply additional biomass beyond lignocellulosic feedstocks, and some strains can produce precursor molecules that can be further processed into advanced biofuels and bio-based products. The Program’s initiative on algal biofuels began with a roadmapping effort to identify both challenges and opportunities. The Roadmap was intended to document the state of technology development and to highlight areas where innovations are needed to achieve commercialization. In recent months, the Biomass Program announced the release of the Roadmap as well as the selection of 4 unique collaborative algal biofuel research consortia that are addressing the challenge areas identified in the Roadmap, including algal strains development, cultivation methods, harvesting, conversion, sustainability, and techno-economic analyses.

67.
ACCELERATING RESEARCH AND DEVELOPMENT FOR ALGAL BIOFUELS THROUGH A COLLABORATIVE APPROACH

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A successful algae-based biofuel industry requires understanding and managing the complex interdependencies across the bioenergy supply chain. Consequently, an integrated decision support environment must be developed where comprehensive data, models, and analytical tools can be shared by stakeholders to understand, design, and develop efficient local and regional practices for the bioenergy infrastructure to ensure bioenergy reliability. The Bioenergy Knowledge Discovery Framework (Bioenergy KDF) is a standards-based dynamic and scalable architecture that integrates bioenergy infrastructure data, models, and tools developed by government, academic, and private sectors. For example, the KDF currently stores large volumes of feedstock production data on woody and herbaceous biomass from particular regions. We believe that the KDF will be amenable to help integrate algae datasets, and allow for informed management decisions in the future. This presentation will discuss and demonstrate the current functionalities of the Bioenergy KDF and the opportunity for the phycology research community to participate and contribute to this initiative.

68.
TESTING A PRODUCT CLAIM WITH AN INTEGRATIVE APPROACH: ENGAGEMENT BY ALGAL BIOLOGISTS

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Dulse (Palmaria palmata) is a major product of Maine Coast Sea Vegetables (MCSV), which sells dried dulse as a whole leaf health snack (e.g., apple-smoked dulse) and as milled ingredients used in seasonings, chips, etc. MCSV became aware of a potentially competitive product and needed to know whether this product was dulse, as was claimed. We used anatomy (vegetative and reproductive) and molecular markers (rbcL, p23S rDNA) to study native Maine dulse and the potential competitor. This research determined that the potential competitor did not belong to the

Palmariales but fits a member of the Gigartinales. This work required students to collect and study samples, extract DNAs, run PCRs, edit sequences, conduct BLAST searches and present an integrated oral report to MCSV. In reviewing this successful service learning application of biotechnology, we urge the Phycological Society of America and phycologists to engage in outreach at local, national, and international levels in areas such as mitigation of invasive species, evaluation of algal biofuels, application of integrated polytrophic aquaculture, promotion of algal products, conservation of biodiversity, and evaluation of ecosystem productivity.

69.

CULTURE OF *G. LEMANEIFORMIS* 981 AND INDUSTRIAL CULTIVATION IN CHINA

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In China, cultivation of seaweeds at the end of the last century was not able to satisfy the demand for agar. *Gracilaria lemaneiformis*, owing to its high growth rate, and high agar quality and content, had long been considered a qualified candidate for supplying the agar industry, but in its original habitat of the Shandong Peninsula seacoast, growth could not be maintained during the hottest and coldest months. To realize industrial cultivation of *G. lemaneiformis*, we tried transferring the plant from the Yellow Sea to the South China Sea, where the species can maintain continuous growth from December to May, and even to June. Also, we sought genetic improvement of the wild type. After repeated efforts for 5 years, *G. lemaneiformis* 981, a highly branched tetrasporophytic variety, was obtained in 1998. Growth characteristics and agar content of the new type will be described. Over the last decade, cultivation of the new variety has spread rapidly with current production of 150,000 t. Cultivation of *G. lemaneiformis* also removes large amounts of inorganic nitrogen and phosphate, mitigating eutrophication of inshore sea water.

70.

TYPE II PHOTOBIOREACTOR HYBRID SYSTEM WITH DISSOLVED CO_2 MEMBRANE DISTRIBUTION TECHNOLOGY, MODULE INCLUDES ALGAL LIPID OIL EXTRACTION PROCESS.

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The Type II Hybrid consists of a combination of a proprietorially designed tubular photobioreactor, as an algae inoculator, and a closed looped covered pond as an algae production unit. Utilizing advantages of both solutions, this design will increase algae productivity by accelerating the growth rate after harvesting the portion of algae biomass used for oil extraction. The hybrid concept of the systems combined allows this module to be successful in various climate zones, including the northern regions. As an option, in the cases that modules are located in an area with substantial unused off-peak (night time) electric power, the artificial lighting by LED devices will be developed. Module will comprise a proprietary non-energy consuming anti-fouling system. Enhanced CO2 distribution with membrane technology allows for the complete dilution of CO2 and other essential nutrients like Nitrogen and Sulfur. This membrane has been proven to increase growth rates up to 4x. A lipid extraction system as a final part of the module uses ultrasonic cavitation treatment and a non-energy consuming oil/biomass separation technique. The automatic computerized system for controlling algae growth and technological process parameters are also implemented.

71.

BIOMASS AND OIL PRODUCTIVITY OF A *SCENEDESMUS RUBESCENS* LIKE MICROALGA, A PROMISING CANDIDATE FOR BIODIESEL PRODUCTION

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A *Scenedesmus rubescens* like microalga shows great potential as a biofuel feedstock. This investigation examined the effects of nitrogen source and concentration on the ash free dry biomass (AFDB), oil accumulation and fatty acid methyl esters (FAME) productivity of the alga cultivated in indoor photo-bioreactors and outdoor raceway ponds. In the 17 days indoor photo-bioreactors cultivation, the algae fed with the mixture of urea-N and NaNO3-N had the highest AFDB productivity of 0.539±0.040 g/L/d. The algae fed with (NH4)2CO3-N had the FAME productivity of 0.133 g/L/d and its content of FAME reached 42.94±2.05%. The content of C18 series (as % of total FAME) was high in all the treatments of nitrogen sources. The 20-day outdoor raceway cultivation showed that the mean FAME productivity of the algae cultivated in the ammonia concentration of 1.0-1.5 mg/L were the highest (0.556±0.112g/m2/d). Also, the sum of C16 and C18 series accounted for most of the FAME whose content could be increased through the nitrogen starvation.

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