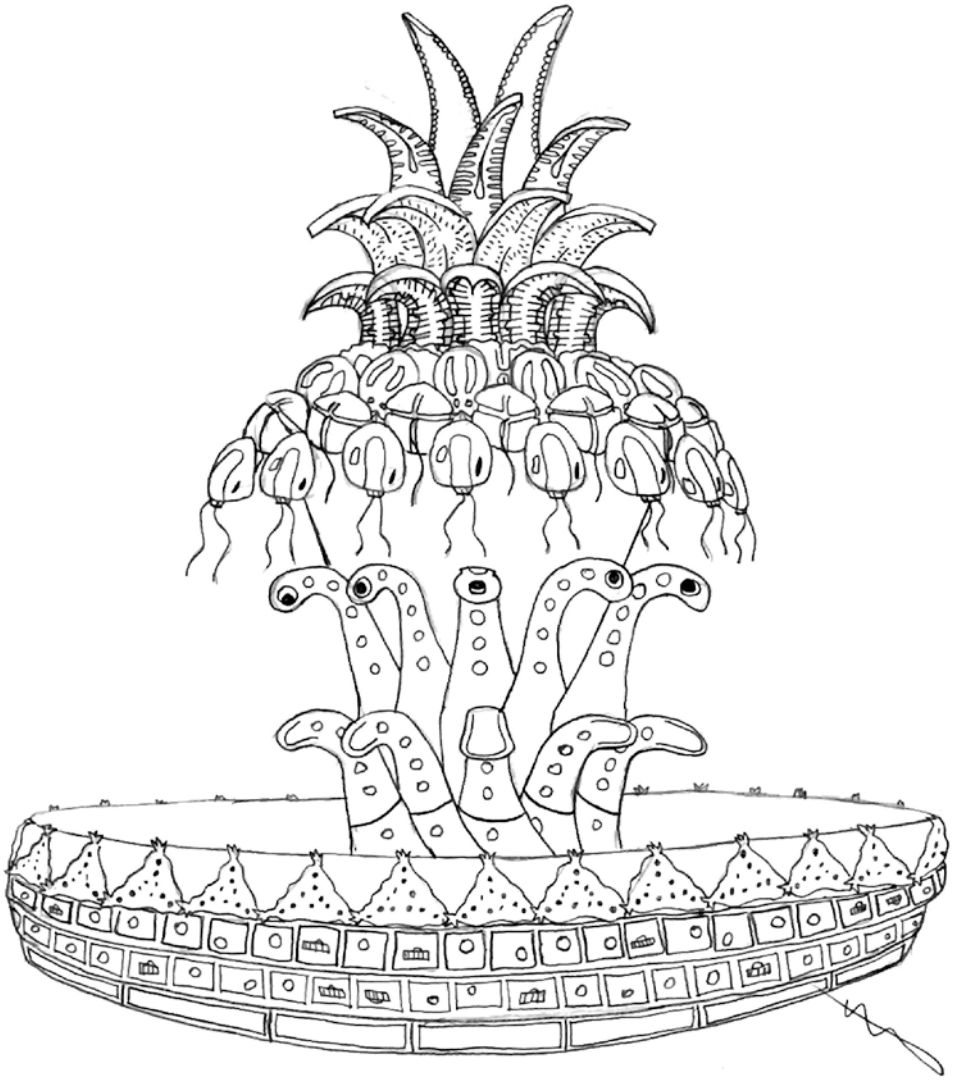
Annual Meeting of the Phycological Society of America

June 20-23, 2012



Frances Marion Hotel
Charleston, SC

Welcome to Charleston SC!

Our annual meeting offers a vibrant and exciting scientific program of oral and poster presentations while promoting the advancement of Phycology and fostering phycological research opportunities. The broad range of scientific interests of our members will be reflected in the variety of activities organized from workshops, fieldtrips and discussions. Our PSA 2012 program director Dale Casamatta in conjunction with local organizers, Jack DiTullio and Frances van Dolah, have prepared a fantastic program including pre and post meeting activities as well as a delightful banquet at the wonderful South Carolina Aquarium!

Please do not hesitate to ask questions, we will be available at the Registration Desk and the PSA Headquarter, or just contact any of the PSA officers.

Enjoy the beauty and southern hospitality at Charleston and wishing you a productive and pleasant meeting!

Juan Lopez-Bautista
PSA President

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. PSA awards include the **Bold Award** for the 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*, The **PSA Award of Excellence** (given to an eminent phycologist to recognize career excellence) 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, **Hoshaw Travel Awards** for travel to the annual meeting and **Grants-In-Aid** for supporting research. To join PSA, contact the membership director or visit the website: www.psaalgae.org

LOCAL ORGANIZERS FOR THE 2012 PSA ANNUAL MEETING:

Frances van Dolah, NOAA Center for Coastal Environmental Health and Bimolecular Research

Jack DiTullio, College of Charleston, Grice Marine Laboratory

PROGRAM DIRECTOR FOR 2012:

Dale Casamatta, University of North Florida

2012 Organizing Committee

Dale Casamatta
Jonathan Zehr
Juan M. Lopez-Bautista
Alexandra Worden
Mike Guiry
Linda Graham
Jack DiTullio
Frances van Dolah
Dennis Hanisak
Julie Koester
Stephanie Verhulst

Please visit the conference headquarters at for registration, assistance, awesome merchandise and up-to-date conference information.

PSA OFFICERS AND EXECUTIVE COMMITTEE

President
Juan M. Lopez-Bautista, *University of Alabama*

Past President
Susan H. Brawley, *University of Maine*

Vice President/President Elect
Linda Graham, *University of Wisconsin*

Secretary
Alison R. Sherwood, *University of Hawai`i at Manoa*

Treasurer
Charles F. Delwiche, *University of Maryland at College Park*

Program Director
Dale A. Casamatta, *University of North Florida*

Membership Director
Deborah L. Robertson, *Clark University*

Chair, Board of Trustees
Richard M. McCourt, *Academy of Natural Sciences*

Fund Manager of the Endowment
Tim Nelson, *Seattle Pacific University*

Managing Editor, *Journal of Phycology*
Michael H. Graham, *Moss Landing Marine Laboratories*

Communications Director
Louise A. Lewis, *University of Connecticut*

Student Member Representative
Matthew Bennett, *Michigan State University*

PSA BOARD OF TRUSTEES

Chair, Board of Trustees
Richard McCourt, *Academy of Natural Sciences*

Fund Manager, PSA Endowment
Tim Nelson, *Seattle Pacific University*

Member, selected by the EC Member
Morgan Vis, Ohio University
Paul Zimba, USDA
Jeanine Olsen, University of Groningen

President, *ex officio*, non- voting
Susan Brawley, *University of Maine*

Vice-president/President-elect, *ex officio*, non-voting
Juan Lopez-Bautista, *University of Alabama*

Treasurer, *ex officio*
Chuck Delwiche, *University of Maryland at College Park*

Meetings Notes and Such

- Bruce Parker, PSA Archivist, shall present a special display: EARLY AMERICAN PHYCOLOGISTS AND THEIR INDISPENSABLE TOOL---THE LIGHT MICROSCOPE. The display includes several 19th Century American phycologists, brief biographies, and pictures of the microscopes they used. This will be on display for the duration of the meeting.

- Looking for a scenic route to the SC Aquarium for the banquet? While it lies within walking range, there is also the free DASH trolly (http://www.discovercharleston.com/maps/images/DASHAquarium.pdf). We will also have some brochures and such in the registration room. There is a route that runs ~every 10-20 minutes until 10:54 pm, with a stop at the corner of Calhoun and Meeting or Calhoun and St. Phillip, each one block from the FM hotel.

- The mark of a great scientific society is the ability to eat your study organisms (except for the American Society of Pediatrics, perhaps). Thus, if you are in the mood for some sea-weed goodness, we would like to draw your attention to an excellent local restaurant with some wonderful algal constituents:

The Grocery

Evoking memories of the small-town grocery, executive chef and owner Kevin Johnson has created a gathering place of warmth and familiarity, with a menu based on seasonal ingredients available from local and regional farmers and fishermen he knows and has worked with for many years. The Grocery's kitchen is stocked with house-made charcuterie and fresh, local fish and seafood, and the restaurant accommodates an in-house canning program to preserve fresh vegetables for the menu. An extensive cocktail and wine list are available as is craft beer on tap, and a wood-burning oven heightens the cordial atmosphere in the former furniture warehouse.

Meeting acknowledgements

The number of people who have contributed to the meeting is legion, and I would be remiss if I failed to mention a mere fraction of the people whose excellent assistance allowed the meeting to truly form:

Frances Van Dolah, Local organizer and general go-to person extraordinaire

Jessica Muhlin, Workshop coordination and implementation

Paul Gabrielson, Bold Award Enthusiast

Robin Kodner, Genomics Workshop guru

Reid Wiseman, Field trip excursion maestro

The excellent staff at the FM, especially Brittany Woods O'Shaughnessy

Nicole Bishop for the great logo

All of the excellent members of the PSA Program Committee

Stephanie Verhulst and Holly Stocks (the best lab ever) for their help in putting the program book together

Last, but certainly not least, we express our gratitude of the hard work of our symposia organizers: Juan Lopez-Bautista, Debashish Bhattacharya, Kalina Manoylov, Curtis Suttle, Frances Van Dolah and Greg Doucette

Schedule of Events

Monday, June 18

PSA Board of Trustees (5:00-8:00 pm) **Laurens Room**

Tuesday, June 19

PSA Executive Committee (10:00-6:00 pm) **Laurens Room**

Marine algal fieldtrip

Arrival and registration (registration desk open after noon) **Drayton Room**

Workshop: Genomic techniques (9:00 am-5:00 pm) **Calhoun Room**

Opening Social and Evening Mixer (6:00-9:00 pm) **Colonial Ballroom**

Wednesday, June 20

Morning Symposium (8:00-12:10) **Carolina Room**

Afternoon Sessions (1:15-4:15) **Carolina Room** (Bold Talks)

Phycol Philm Phest (4:45-5:30) **Carolina Room**

RedToL Workshop/Symposium (6:00-8:15) **Carolina A Room**

NSF/Career Panel Discussion (6:00-8:00) **Carolina Room B**

Student Social (hosted by Matt Bennett, 8:30-???) **FM Lobby**

Thursday, June 21

Morning Symposium (8:15-11:45) **Carolina Room**

Journal of Phycology Editorial Lunch (11:45-1:45) **Middleton Room**

Afternoon Sessions (1:00-5:00)
Biodiversity I (1:00-2:30) **Carolina Room A**
Biodiversity II (3:00-5:00) **Carolina Room A**
Phylogenetics & Taxonomy I (1:00-2:30) **Carolina Room B**
Phylogenetics & Taxonomy II (3:00-4:30) **Carolina Room B**

Poster Session (6:00-8:00) **Colonial Ballroom**

Auction (8:00-9:30) **Colonial Ballroom**

Friday, June 22

Morning Symposium (8:15-11:45) **Carolina Room**

Afternoon Sessions (1:00-4:00)
Cell and Molecular Biology (1:00-2:15) **Carolina Room A**
Biotechnology (2:45-4:00) **Carolina Room A**
Phylogenetics & Taxonomy III (1:00-2:30) **Carolina Room B**
Parasitology (3:00-4:00) **Carolina Room B**

PSA Business Meeting (4:30-5:30) **Carolina Room A**

Banquet (7:00-10:30) **South Carolina Aquarium**

Saturday, June 23

Morning Symposium (8:00-12:00) **Carolina Room**

Afternoon Sessions (1:00-3:00)
Coastal/HABs (1:00-3:15) **Carolina Room**
Ecology: Experimental (3:45-5:15) **Carolina Room**

	Breaks	Carolina Room A/B	Carolina Room B
Wednesday, June 20	**Continental Breakfast (07:00-08:00)**		
		Opening Remarks and Symposium: *Red Algal Phylogenomics* (8:00-10:10)	
	Mid-Morning Beverages (10:10-10:40)		
		Symposium continued (10:05-12:10)	
	Lunch (12:10-1:15)	**Lunch (12:20-1:15)**	
		Bold Talks I (1:15-2:45)	
	Mid-Afternoon Beverages (2:45-3:15)		
		Bold Talks II (3:15-4:15)	
		Phyco Philm Phest (4:45-5:30)	
		REDToL Symposium (6:00-8:00)	**NSF/Career Panel Discussion (6:00-8:00)**

-The PSA President's Graduate Student Social shall meet in the Lobby of the FM and leave for uncharted waters at 8:15.

	Breaks	Carolina Room A/B	Carolina Room B
Thursday, June 21	**Continental Breakfast (07:00-08:00)**		
		Symposium: *Bioassessment of freshwater ecosystems in the 21st century* (8:15-9:45)	
	Mid-Morning Beverages (9:45-10:15)		
		Symposium continued (10:15-11:45)	
	Lunch (11:45-1:00)	**Lunch (11:45-1:00)**	**Lunch (11:45-1:00)**
		Ecology: Biodiversity I (1:00-2:30)	**Phylogenetics & Taxonomy I (1:00-2:30)**
	Mid-Afternoon Beverages (2:30-3:00)		
		Ecology: Biodiversity II (3:00-5:00)	**Phylogenetics & Taxonomy II (3:00-5:00)**
		Poster Session (6:00-8:00)	
		Auction (8:00-9:30)	

- *The Journal of Phycology Editorial Lunch shall be from 11:45-1:45 in the Rutledge Room*

	Breaks	Carolina Room A/B	Carolina Room B
Friday, June 22	**Continental Breakfast (07:00-08:00)**		
		Symposium: *Algal/viral Interactions* (8:15-9:45)	
	Mid-Morning Beverages (9:45-10:15)		
		Symposium continued (10:15-11:45)	
	Lunch (11:45-1:00)	**Lunch (11:45-1:00)**	**Lunch (11:45-1:00)**
		Cell Biology (1:00-2:30)	**Phylogenetics & Taxonomy III (1:00-2:30)**
	Mid-Afternoon Beverages (2:30-3:00)		
		Biotechnology (3:00-4:15)	**Parasitology (3:00-4:15)**
		PSA Business Meeting (4:30-5:30)	
	PSA Banquet (7-10)		

- Please note that the lovely PSA banquet shall be held from 7-10 p.m. at the South Carolina Aquarium.

	Breaks	Carolina Room A/B
	Continental Breakfast (07:00-08:00)	
Saturday, June 23		**Symposium: *Molecular insights into the Ecology and Physiology of Harmful Algal Blooms* (8:00-10:00)**
	Mid-Morning Beverages (10:00-10:30)	
		Symposium continued (10:30-12:00)
	Lunch (12:00-1:00)	**Lunch (12:00-1:00)**
		Coastal/HABs (1:00-3:00)
	Mid-Afternoon Break (3:00-3:30)	
		Ecology: Experimental (3:30-5:15)

Wednesday, June 20

07:00-08:00 Continental Breakfast

***Plenary Session*- Red Algal Phylogenomics** (Chairs: Juan Lopez-Bautista, *University of Alabama,* and Debashish Bhattacharya, *Rutgers*)

8:00 Opening Remarks (Juan Lopez-Bautista, PSA President)

8:10 THE RED ALGAL TREE OF LIFE (H.S. Yoon, Bigelow Laboratory for Ocean Sciences)

8:45 THE *PORPHYRA* GENOME (John Stiller, East Carolina University)

9:20 THE *CHONDRUS CRISPUS* GENOME AND THE DEVELOPMENT OF A FLORIDEOPHYTE MODEL (Jonas Collen, Station Biologique de Roscoff, C. Boyen, Station Biologique, Roscoff, France, B. Porcel, Genoscope, Evry, France, & P. Wincker, Genoscope, Evry, France)

9:55-10:30 COFFEE BREAK

10:30 RECENT ADVANCES IN THE *CALLIARTHRON* GENOME: CLIMATE RESPONSES AND CELL WALL EVOLUTION (Cheong Xin Chan, University of Queensland and Patrick T. Martone, University of British Columbia)

11:05 THE *PORPHYRIDIUM* GENOME (Debashish Bhattacharya, Rutgers & Dana Price, Rutgers)

11:40 A TASTE OF ALGAL GENOMES FROM THE JOINT GENOME INSTITUTE (Alan Kuo, Eukaryotic Genomics Program, DOE Joint Genome Institute)

11:55 PHYLOGENETIC ANALYSIS OF METAGENOMES AND METATRANSCRIOPTOMES: NEW METHODS FOR MEASURING COMMUNITY DIVERSITY (Robin Kodner, UW Center for Environmental Genomics)

12:10-1:15 LUNCH BREAK

***Bold Award Competition I* Carolina Room**
Moderator: Paul Gabrielson, University of North Carolina

1:15 SPECIES DELIMITATION IN THE *CAULERPA RACEMOSA/PELTATA* COMPLEX (CHLOROPHYTA, CAULERPACEAE)
Belton, G. S., University of Adelaide, Australia, gareth.belton@adelaide.edu.au
Prud'Homme van Reine, W. H., Leiden University, Netherlands
Huisman, J. M., Murdoch University and the Western Australian Herbarium, Australia
Sauvage, T., University of Louisiana, USA
Draisma, S. G., University of Malaya, Malaysia

Gurgel, C. F., University of Adelaide, the State Herbarium of South Australia and SARDI Aquatic Sciences, Australia

1:30 WHAT DO CHLOROPLAST GENOMICS TELL US ABOUT EUGLENOID PHYLOGENIES?
Bennett, M. S., Michigan State University, USA, benne124@msu.edu
Wiegert, K. E., Michigan State University, USA, wiegertk@msu.edu
Watza, D. G., Michigan State University, USA, watzadon@msu.edu
Triemer, R. E., Michigan State University, USA, triemer@msu.edu

1:45 A TAXONOMIC REVISION OF AUSTRALIAN *SARGASSUM*, WITH A NEW PERSPECTIVE ON THE SUBGENERIC CLASSIFICATION OF THE GENUS
Dixon, R., Murdoch University, Australia, rains.rmd@gmail.com
Huisman, J. M., Murdoch University and WA Herbarium, Australia
Gurgel, C. F., University of Adelaide, State Herbarium of SA and SARDI Aquatic Sciences, Australia

2:00 THE CASPASE REACTOME OF *KARENIA BREVIS* DURING ROS-DRIVEN CELL DEATH
Johnson, J. G., Medical University of South Carolina, USA, jill.johnson821@gmail.com
Van Dolah, F. M., NOAA Center for Coastal Environmental Health and Biomolecular Research, USA, fran.vandolah@noaa.gov

2:15 THE SYSTEMATICS AND BIOGEOGRAPHY OF THE THOREALES, A FRESHWATER RED ALGAL ORDER
Johnston, E. T., Ohio University, USA, ej363707@ohio.edu
Buhari, N., Hasanuddin University, Indonesia, li_buhari@yahoo.com
Djawad, I., Hasanuddin University, Indonesia, iqbaldj@yahoo.com
Vis, M. L., Ohio University, USA, vis-chia@ohio.edu

2:30 MULTIPLE CLIMATE STRESSORS NEGATIVELY IMPACT INTERTIDAL KELP ZOOSPORE MOTILITY
Jorve, J. P., University of British Columbia, Canada, jorve@zoology.ubc.ca
Harley, C. D., University of British Columbia, Canada, harley@zoology.ubc.ca
Martone, P. T., University of British Columbia, Canada, patrick.martone@botany.ubc.ca
Zimmer, R. K., University of California, Los Angeles, USA, z@biology.ucla.edu
Himes, J. E., University of California, Los Angeles, USA, juliehimes@gmail.com

2:45- 3:15 AFTERNOON COFFEE BREAK

Bold Award Competition II **Carolina Room**
Moderator: Paul Gabrielson, University of North Carolina

3:15 TWO TRACK CONTROL OF PHOTOMOVEMENT IN *SPIROGYRA*: PHYTOCHROME AND PHOTOTROPIN USE DIFFERENT MACHINERY FOR THE CONTROL OF MOVEMENT
Lee, J. W., Department of Biology, Kongju National University, Republic Of Korea, ljw86@kongju.ac.kr
Han, J. W., Department of Biology, Kongju National University, Republic Of Korea, fop9440@kongju.ac.kr
Kim, G. H., Department of Biology, Kongju National University, Republic Of Korea, ghkim@kongju.ac.kr

3:30 NEXT GENERATION TRANSCRIPTOMICS ELUCIDATES BROWN ALGAL SEXUAL REPRODUCTION GENES

Lipinska, A., Ghent University, Belgium, agnieszka.lipinska@ugent.be
Van Damme, E. J., Ghent University, Belgium
De Clerck, O., Ghent University, Belgium

3:45 MOLECULAR AND MORPHOLOGICAL INVESTIGATION OF SPECIES DIVERSITY IN *BATRACHOSPERMUM* SECTION *HELMINTHOIDEA* (BATRACHOSPERMALES, RHODOPHYTA)
Salomaki, E. D., Ohio University, USA, es289510@ohio.edu
Kwandrans, J., Institute of Nature Conservation, Poland
Eloranta, P., Finland
Kostkeviciene, J., Vilnius University, Lithuania
Vis, M. L., Ohio University, USA

4:00 COMPLETE PLASTID AND MITOCHONDRIAL GENOMES OF THE FRESHWATER BROWN ALGA *PLEUROCLADIA LACUSTRIS* A. BRAUN
Wang, X., Fordham University, USA, wang@fordham.edu
Wehr, J. D., Fordham University, USA, wehr@fordham.edu
Karol, K. G., The New York Botanical Garden, USA, kkarol@nybg.org

4:15 HORIZONTAL GENE TRANSFER IS A SIGNIFICANT DRIVER OF GENE INNOVATION IN DINOFLAGELLATES
Wisecaver, J. H., University of Arizona, USA, hughesj@email.arizona.edu
Hackett, J. D., University of Arizona, USA, hackettj@email.arizona.edu

Wednesday Evening

Phyco Philm Phest (4:45-5:30) **Carolina Room**

REDTol Symposium (6:00-8:00) **Carolina Room A**

NSF/Career Panel Discussion (6:00-8:00) **Carolina Room B**

PSA President's Student Reception (8:15-???) **Lobby of the Frances Marion**

Thursday, June 21

07:00-08:15 Continental Breakfast

Plenary Session- Bioassessment of Freshwater Ecosystems in the 21st Century **(**Session Chair: Kalina Manoylov)

8:15 SPECIES MATTER! UNDERSTANDING THE ROLES AND DISTINCTIONS OF ALGAL SPECIES IS CRITICAL IN UNDERSTANDING STREAM ECOSYSTEMS (Rex Lowe, Bowling Green University)

9:00 BIOASSESSMENT WITH ALGAE: GOALS, THEORY, METHODS, AND BENEFITS (Jan Stevenson, Michigan State University)

9:45-10:15 COFFEE BREAK

10:15 BIOSSESSMENT OF AQUATIC BIODIVERSITY WITH COARSE AND FINE LEVELS OF DIATOM TAXONOMY (Kalina Manoylov, Georgia College and State University)

11:00 CHALLENGES IN BIOASSESSMENT OF ACID MINE DRAINAGE (Morgan Vis, Ohio University)

11:45-1:00 LUNCH BREAK

Ecology: Biodiversity I **Carolina Room**
Moderator: Rick McCourt, Academy of Natural Sciences of Drexel University

1:00 O FATHER, WHERE ART THOU? PATERNITY ANALYSES IN A NATURAL POPULATION OF THE RED SEAWEED *CHONDRUS CRISPUS*
Krueger-Hadfield, S. A., Marine Biological Association of the UK, United Kingdom, stakru@mba.ac.uk
Roze, D., Station Biologique de Roscoff, France, roze@sb-roscoff.fr
Mauger, S., Station Biologique de Roscoff, France, mauger@sb-roscoff.fr
Destombe, C., Station Biologique de Roscoff, France, destombe@sb-roscoff.fr
Valero, M., Station Biologique de Roscoff, France, valero@sb-roscoff.fr

1:15 ALGAL DIVERSITY OF THE BURICA PENINSULA, PACIFIC PANAMA
Wysor, B., Roger Williams University, USA, bwysor@rwu.edu
Freshwater, D. W., Center for Marine Science, USA, freshwaterw@uncw.edu
Leon, N., University of Panama, Panama
Fernandez-Garcia, C., Universidad de Costa Rica, Costa Rica
Gabrielson, P. W., UNC-Chapel Hill, USA
Charbonneau, V., Roger Williams University, USA
Green, C., Roger Williams University, USA
Idol, J., UNC-Wilmington, USA
Parham, S., Center for Marine Science, USA

1:30 DIVERSITY AND EVOLUTION OF ENDOSYMBIOTIC BACTERIA IN THE SIPHONOUS GREEN ALGA *BRYOPSIS* (BRYOPSIDALES, CHLOROPHYTA)
Leliaert, F., Ghent University, Belgium, frederik.leliaert@gmail.com
Hollants, J., Ghent University, Belgium
Verbruggen, H., Ghent University, Belgium
Willems, A., Ghent University, Belgium
De Clerck, O., Ghent University, Belgium

1:45 DISPERSAL ASSEMBLY OF BENTHIC MICROALGAL COMMUNITIES: EFFECTS OF TIDAL RESUSPENSION
Plante, C. J., College of Charleston, USA, plantec@cofc.edu
Fleer, V., Northwest Missouri St. Univ., USA
Jones, M. L., College of Charleston, USA

2:00 THE EPIPHYTIC MICROBIOTA OF THE GLOBALLY WIDESPREAD MACROALGA *CLADOPHORA* (CHLOROPHYTA, CLADOPHORALES)
Zulkifly, S. B., University Putra Malaysia, Malaysia, shahrizim@gmail.com
Hanshew, A., University of Wisconsin-Madison, USA, hanshew@wisc.edu

Young, E. B., University of Wisconsin-Milwaukee, USA, ebyoung@uwm.edu
Lee, P., University of Wisconsin-Milwaukee, USA, ebyoung@uwm.edu
Graham, M. E., University of Wisconsin-Madison, USA, mgraham3@wisc.edu
Graham, M. E., Hologic, Inc., USA, lankage@yahoo.com
Piotrowski, M. J., University of Wisconsin-Madison, USA, mpiotrowski@wisc.edu
Graham, L. E., University of Wisconsin-Madison, USA, lkgraham@wisc.edu

2:15 PARMALES, AN INSIGHT INTO DIATOM ANCESTRY?
Kuwata, A., Tohoku National Fisheries Research Institute (FRA), Japan, akuwata@affrc.go.jp
Ichinomooiya, M., Prefectual Univ. of Kumamoto, Japan, ichinomiya@pu-kumamoto.ac.jp
Yoshikawa, S., Prefectural Univ. of Fukui, Japan, syoshika@fpu.ac.jp
Ohki, K., Prefectural Univ. of Fukui, Japan, kaoriohki@fpu.ac.jp
Kamiya, M., Prefectural Univ. of Fukui, Japan, mkamiya@fpu.ac.jp
Takaichi, S., Nippon Medical School, Japan, takaichi@nms.ac.jp
Kawachi, M., National Institute for Environmental Studies, Japan, kawach9i@nies.go.jp
Saitoh, K., National Research Institute of Fisheries Science (FRA), Japan, ksaitoh@affrc.go.jp
Sato, N., Univ.of Tokyo, Japan, naokisat@bio.c.u-tokyo.ac.jp
Sawada, K., Hokkaido Univ., Japan, sawadak@mail.sci.hokudai.ac.jp

Ecology: Biodiversity II **Carolina Room**
Moderator: Tim Nelson, Seattle Pacific University

3:00 EUGLENAPHYCIN TOXIN IS PRODUCED BY AT LEAST 18 EUGLENOPHYCEAE, INCLUDING 7 STRAINS OF *EUGLENA SANGUINEA*
Zimba, P.V., Texas A&M University Corpus Christi, Corpus Christi, TX, USA
Rafalski, A., Texas A&M University Corpus Christi, Corpus Christi, TX, USA
Savage, M., Texas A&M University Corpus Christi, Corpus Christi, TX, USA
Ordner, P., Texas A&M University Corpus Christi, Corpus Christi, TX, USA
Triemer, R., Michigan State University, East Lansing, MI, USA

3:15 TRACKING CHANGES IN THE GREAT LAKES – NEW DIATOM-BASED TOOLS FOR RETROSPECTIVE ANALYSES
Reavie, E. D., University of Minnesota Duluth, USA, ereavie@nrri.umn.edu
Allinger, L. E., University of Minnesota Duluth, USA, lallinge@nrri.umn.edu
Kireta, A. R., University of Minnesota Duluth, USA, akireta@nrri.umn.edu
Chraïbi, V., University of Minnesota Duluth, USA, vlshaw86@hotmail.com

3:30 A COMPARISON OF UPA AND 16S: PERFORMANCE EVALUATION FOR PHYLOGENETIC RECONSTRUCTION AND DNA BARCODING OF CYANOBACTERIA
Sherwood, A. R., Dept. of Botany, University of Hawaii, USA, asherwoo@hawaii.edu
Carlile, A. L., Dept. of Botany, University of Hawaii, USA
Vaccarino, M., Dept. of Biology, John Carroll University, USA
Johansen, J., Dept. of Biology, John Carroll University, USA

3:45 THE INDIAN RIVER LAGOON OBSERVATORY (IRLO): BIODIVERSITY AND ECOSYSTEM FUNCTION OF AN ESTUARY IN TRANSITION: PHYCOLOGY PROJECTS.
Hanisak, M.D. Harbor Branch Oceanographic Institute at Florida Atlantic University, Fort Pierce, Florida, USA

4:00 ECOLOGY OF ANNUAL POPULATIONS OF GIANT KELP IN SOUTHERN CHILE
Buschmann, A. H., Universidad de Los Lagos, Puerto Montt, Chile, abuschma@ulagos.cl
Hernandez-Gonzalez, M. C., Universidad de Los Lagos, Puerto Montt, Chile, mhernand@ulagos.cl
Varela, D. A., Universidad de Los Lagos, Puerto Montt, Chile, dvarela@ulagos.cl
Pereda, S. V., Universidad de Los Lagos, Puerto Montt, Chile, spereda@ulagos.cl
Rodríguez-Maulén, J. F., Universidad de Los Lagos, Chile, juan.maulen@ulagos.cl
Henríquez, L. A., University of Tasmania, Luis.HenriquezAntipa@utas.edu.au
López, A. P., Universidad de Los Lagos, Chile, alejandralopez@ulagos.cl
Maldonado, M. A., Universidad de Los Lagos, Chile, miguelmaldonadoa@gmail.com
Graham, M. H., Moss Landing Marine Laboratories, USA, mgraham@mlml.calstate.edu

4:15 EPIPHYTIC BIODIVERSITY REFLECTING SEASONAL FLUCTUATIONS AND NUTRIENT MANIPULATIONS FROM *SPARTINA ALTERNIFLORA* WITHIN THE GTMNERR
Verhulst, S.A., Department of Biological Sciences, University of North Florida, Jacksonville, FL
Stocks, H.S., Department of Biological Sciences, University of North Florida, Jacksonville, FL
Casamatta, D.A., Department of Biological Sciences, University of North Florida, Jacksonville, FL

4:30 CHARACTERIZATION OF OFFSHORE RHODOLITH BEDS IN THE NW GULF OF MEXICO: TRIALS AND TRIBULATIONS SINCE THE BP DEEPWATER HORIZON OIL SPILL DISASTER
Fredericq, S., University of Louisiana at Lafayette, USA, slf9209@louisiana.edu
Schmidt, W. E., University of Louisiana at Lafayette, USA, weschmidt01@yahoo.com
Gabriel, D., Universidade dos Açores, Portugal, danielalgabriel@gmail.com
Sauvage, T., University of Louisiana at Lafayette, USA, tom.sauv@gamila.com
Norris, J. N., Smithsonian Institution, USA, NORRISJ@si.edu
Krayesky, D., Slippery Rock University, USA, david.krayesky@sru.edu

4:45 NEW INSIGHTS IN THE DIVERSITY OF DELESSERIACEAE (CERAMIALES) FROM OFFSHORE LOUISIANA AND CARIBBEAN PANAMA
Richards, J., University of Louisiana at Lafayette, USA, jlr0420@louisiana.edu
Fredericq, S., University of Louisiana at Lafayette, USA, slf9209@louisiana.edu

Phylogenetics and Taxonomy I
Moderator: Naomi Phillips, Arcadia University

1:00 STUDIES ON THE PRASIOLALES (TREBOUXIOPHYCEAE, CHLOROPHYTA) FROM THE SOUTHERN HEMISPHERE REVEAL MAJOR TAXONOMIC AND BIOGEOGRAPHIC SURPRISES
Moniz, M. J., National University of Ireland, Galway, Ireland, monica.j.moniz@gmail.com
Rindi, F., Università Politecnica delle Marche, Italy, f.rindi@univpm.it
Guiry, M. D., National University of Ireland, Galway, Ireland, michael.guiry@nuigalway.ie

1:15 NEW PERSPECTIVES ON THE DEVELOPMENTAL MORPHOLOGY, MOLECULAR SYSTEMATICS AND BIOGEOGRAPHY OF THE SARCODIACEAE (RHODOPHYTA)
Rodriguez-Prieto, C., University of Girona, Faculty of Sciences, Campus de Montiliva Spain, conxi.rodriguez@udg.edu
Lin, S. M., Institute of Marine Biology, National Taiwan Ocean University, Taiwan ROC, linsm@ntou.edu.tw
Hommersand, M. H., Department of Biology, University of North Carolina, USA, hommersand@bio.unc.edu

1:30 TRENTEPOHLIALES (ULVOPHYCEAE, CHLOROPHYTA) FROM COASTAL SOUTH CAROLINA
Green, M. S., Department of Biology, Tennessee Technological University USA, mark.green@hgtc.edu
Ball, B., Department of Biology, Duke University, USA, Bernie.Ball@Duke.edu
Lutzoni, F., Department of Biology, Duke University, USA, flutzoni@duke.edu
Zi-Min, H., Department of Biological Sciences, The University of Alabama, USA, hzimin@as.ua.edu
López-Bautista, J. M., Biological Sciences, The University of Alabama, USA, jlopez@ua.edu

1:45 GENETIC STRUCTURE AND PHYLOGEOGRAPHY OF *PTEROCLADIELLA CAPILLACEA* (GELIDIACEAE, RHODOPHYTA) BASED ON PLASTID RBCL AND MITOCHONDRIAL COX1 AND COB
Boo, G. H., Chungnam National University, Daejeon, Republic Of Korea, gahunboo@gmail.com
Jang, H. J., Chungnam National University, Republic Of Korea
Freshwater, D. W., Center for Marine Science, USA
Fujii, M. T., Institute of Botany, Brazil
Nelson, W. A., National Institute of Water and Atmospheric Research, New Zealand
Lee, K. M., Chungnam National University, Republic Of Korea
Boo, S. M., Chungnam National University, Republic Of Korea, smboo@cnu.ac.kr

2:00 ASSESSMENT OF CRYPTIC *RHODYMENIA* SPP. (RHODYMENIACEAE, RHODOPHYTA) IN BRITISH COLUMBIA, CANADA: AN INTEGRATIVE TAXONOMIC APPROACH
Filloramo, G. V., Centere for Environmental & Molecular Algal Research, Dept. of Biology, University of New Brunswick, Canada, gina.filloramo@gmail.com
Saunders, G. W., Centere for Environmental & Molecular Algal Research, Dept. of Biology, University of New Brunswick, Canada, gws@unb.ca

2:15 MOLECULAR DIVERSITY OF MAËRL-FORMING CORALLINES (CORALLINALES, RHODOPHYTA)
Hernandez-Kantun, J. J., National University of Ireland, Galway, Ireland, j.hernandez2@nuigalway.ie
Rindi, F., Università Politecnica delle Marche, Italy, f.rindi@univpm.it
Riosmena-Rodriguez, R., Universidad Autonoma de Baja California Sur, Mexico, riosmena@uabcs.mx
Maggs, C. A., Queen's University, United Kingdom, c.maggs@qub.ac.uk
Hall-Spencer, J. M., University of Plymouth, United Kingdom, jason.hall-spencer@plymouth.ac.uk
Peña, V., Museum National d'Histoire Naturelle, France, vpena@udc.es

Phylogenetics and Taxonomy II
Moderator: Daryl Lam, Ohio University

3:00 CRYPTIC DIVERSITY WITHIN THE AUSTRALIAN HALYMENIACEAE (HALYMENIALES, RHODOPHYTA)
Kraft, L. G., University of New Brunswick, Canada, lesleigh.kraft@unb.ca
Saunders, G. W., University of New Brunswick, Canada, gws@unb.ca

3:15 A COMPARISON OF THE CHLOROPLAST GENOME AMONG *EUGLENA HIEMALIS*, *EUGLENA GRACILIS* AND *EUGLENA LONGA* (EUGLENOPHYTA)
Wang, J., Central Michigan University, USA, wang3j@cmich.edu
Linton, E. W., Central Michigan University, USA, eric.linton@cmich.edu

3:30 NEW ADVANCES OF THE GREEN ALGAL TREE OF LIFE (GRATOL): CHLOROPLAST-ENCODED RBCL MARKER FROM THE ORDER CLADOPHORALES

Hu, Z. M., University of Alabama, USA, hzimin@bama.ua.edu
Lopez-Bautista, J., the University of Alabama, USA

3:45 MARINE PRASIOLALES FROM NEW ZEALAND AND THE NEW ZEALAND SUBANTARCTIC
Sutherland, J. E., University of Auckland New Zealand, j.sutherland@auckland.ac.nz
Nelson, W. A., National Institute for Water & Atmospheric Research, New Zealand, Wendy.Nelson@niwa.cri.nz
Heesch, S., Irish Seaweed Research Group, Ryan Institute, Ireland, Svenja.Heesch@gmx.de

4:00 DIVERSITY OF THE GENUS *HYPNEA* (GIGARTINALES, RHODOPHYTA) ON THE SOUTHEASTERN COAST OF BRAZIL
Guimaraes, N. R., University of Sao Paulo Brazil, nati_guimaraes@yahoo.com.br
Oliveira, M. C., University of Sao Paulo, Brazil, mcdolive@usp.br
Oliveira, E. C., University of Sao Paulo, Brazil, euricodo@usp.br
Yokoya, N. S., Instituto de Botânica, Brazil, nyokoya@hotmail.com

4:15 ESTIMATING DIVERGENCE TIMES OF THE RED ALGAL FAMILY PEYSSONNELIACEAE (PEYSSONNELIALES, RHODOPHYTA) WITH A MOLECULAR CLOCK
Schmidt, W. E., University of Louisiana at Lafayette, USA, weschmidt01@yahoo.com
Sauvage, T., University of Louisiana at Lafayette, USA, tomsauv@gmail.com
Gabriel, D., Universidade dos Açores, Portugal, Danielalgabriel@gmail.com
Krayesky, D., Slippery Rock University, USA, david.krayesky@sru.edu
Fredericq, S., University of Louisiana at Lafayette, USA, slf9209@louisiana.edu

Thursday Evening

PSA Poster Session (odd numbered posters) (6:00-7:00) **Carolina Room**

PSA Poster Session (even numbered posters) (7:00-8:00) **Carolina Room**

PSA Auction (8:00-9:30) **Carolina Room**

Please note that Posters are listed as Abstracts in the lovely Program Guide.

Friday, June 22

07:00-08:00 Continental Breakfast

Plenary Session- Algal/viral Interactions **Carolina Room (**Session Chair: Curtis Suttle, University of British Columbia)

8:15 VIRUSES IN THE DRIVER'S SEAT OF PHYTOPLANKTON MORTICIANS (Corina Brussaard, Royal Netherlands Institute of Oceanography)

9:00 HIGH ESTIMATES OF DIVERSITY IN ALGAL VIRUSES SUGGEST AN

IMPORTANT ROLE IN PHYTOPLANKTON MORTALITY (Curtis Suttle, University of British Columbia)

9:45-10:15 MORNING BREAK COFFEE BREAK

10:15 CYANOPHAGES – UBIQUITOUS MEMBERS OF FRESHWATER AND MARINE SYSTEMS (Steven Wilhelm, University of Tennessee, Knoxville)

11:00 COCCOLITHOVIRUSES: LIFE AND DEATH AFTER GENOME SEQUENCING (Willie Wilson, Bigelow Institute for Ocean Sciences)

11:45-1:00 LUNCH BREAK

Cell Biology **Carolina Room**
Moderator: Deborah Robertson, Clark University

1:00 LIPID METABOLISM AND TRAFFICKING IN TWO RED ALGAE SPECIES FROM THE GENUS *PORPHYRA*
Zaeuner, S., Michigan State, University, BMB Department, USA, zaeuner@uni-bonn.de
Benning, C., Michigan State University, BMB Department, USA, benning@msu.edu

1:15 PHOTOSYNTHETIC EFFICIENCY AND REGULATION OF EARLY LIGHT INDUCIBLE PROTEIN (ELIP) BY THE INFLUX OF CO2 IN *SPIROGYRA VARIANS*
Han, J. W., Department of Biology, Kongju National University, Republic Of Korea, fop9440@kongju.ac.kr
Kim, G. H., Department of Biology, Kongju National University, Republic Of Korea, ghkim@kongju.ac.kr

1:30 EXPLORATION OF THE ROLE OF 3' UTRS IN REGULATING MRNA STABILITY IN THE MARINE DIATOM *THALASSIOSIRA PSEUDONANA*
Scott, D. W., Clark University, USA, dscott@clarku.edu
Robertson, D. L., Clark University, USA, debrobertson@clarku.edu

1:45 BIOSYNTHETIC LABELING OF DINOFLAGELLATE RNA FOR THE MEASUREMENT OF RNA SYNTHESIS AND DECAY RATES USING DNA MICROARRAYS AND QPCR
Morey, J. S., Marine Biotoxins Program, NOAA Center for Coastal Environment Health and Biomolecular Research, USA, jeanine.morey@noaa.gov
Van Dolah, F. M., Marine Biotoxins Program, NOAA Center for Coastal Environmental Health and Biomolecular Research, USA, fran.vandolah@noaa.gov

2:00 SRNAS OF *CYANOPHORA PARADOXA* AND *CHLAMYDOMONAS REINHARDTII*, A SYSTEM GENOMICS APPROACH TO UNDERSTAND ALGAL EVOLUTION
Gross, J., Rutgers University, USA, jeferson.gross@googlemail.com
Wajid, S., Rutgers University, USA, swajid@eden.rutgers.edu
Price, D., Rutgers University, USA, dana.price@gmail.com
Chan, C. X., The University of Queensland, Australia, chancx@gmail.com
Bhattacharya, D., Rutgers University, USA, Bhattacharya@AESOP.Rutgers.edu

2:15 HIGH SEQUENCE VARIABILITY AND DIVERSE SUBCELLULAR LOCALIZATIONS, AND ECOLOGICAL IMPLICATIONS OF ALKALINE PHOSPHATASE IN DINOFLAGELLATES AND OTHER ALGAE
Lin, X., Xiamen University, China, xinlin@xmu.edu.cn
Zhang, H., University of Connecticut, USA, huan.zhang@uconn.edu
Cui, Y., Xiamen University, China, coffee16th@126.com
Lin, S., Xiamen University, China, senjie.lin@xmu.edu.cn

Biotechnology **Carolina Room**
Moderator: Asher Wishkerman, IRTA-SCR, Spain

3:00 INFLUENCE OF CHLORINE ION CONCENTRATIONS AND DIFFERENT MEDIA FOR *RHODOMONAS SALINA* GROWTH AND LIPID CHARACTERIZATION
Wishkerman, A., IRTA-SCR, Spain, Asher.Wishkerman@irta.cat
Estevez, A., IRTA-SCR, Spain
Mimendia, A., IRTA-SCR, Spain
Ibáñez, C., IRTA-SCR, Spain
Trobajo, R., IRTA-SCR, Spain

3:15 OPTIMIZING USE OF WASTEWATER AS A GROWTH MEDIUM FOR MICROALGAL BIOFUEL FEEDSTOCK
Novoveska, L., Oklahoma State University, USA, lucie.novoveska@okstate.edu
Liefer, J. D., Dauphin Island Sea Lab, USA
MacIntyre, H. L., Dalhousie University, Canada

3:30 STABILIZING CONTINUOUS MICROALGAL POLYCULTURES
Novoveska, L., Oklahoma State University, USA, lucie.novoveska@okstate.edu
Henley, W. J., Oklahoma State University, USA
Wulfers, T. A., Oklahoma State University, USA, twulfer@ostatemail.okstate.edu

3:45 NUTRIENT BIOEXTRACTION BY *SACCHARINA LATISSIMA* AND *GRACILARIA TIKVAHIAE* IN LONG ISLAND SOUND AND THE BRONX RIVER ESTUARY
Kim, J. K., Department of Marine Sciences, University of Connecticut, USA, jakejuly@hotmail.com
Yarish, C., Department of Ecology & Evolutionary Biology, University of Connecticut, USA, charles.yarish@uconn.edu

4:00 IDENTIFICATION OF *PORPHYRA* SPECIES IN MAINE COAST SEA VEGETABLES' "LAVER" USING MOLECULAR TECHNIQUES
York, G. E., University of Maine, Orono, Maine, USA
Arnold , D. S., University of Maine, Orono, Maine, USA
Brehm, L. J., University of Maine, Orono, Maine, USA
DeMerchant, J. R., University of Maine, Orono, Maine, USA
Jensen, A. J., University of Maine, Orono, Maine, USA
Lyczkowski, E.R., University of Maine, Orono, Maine, USA
Ouellette, A. R., University of Maine, Orono, Maine, USA
Rankin, J. A., University of Maine, Orono, Maine, USA
Phillips, J. C., University of Maine, Orono, Maine, USA
Brawley, S. H., University of Maine, Orono, Maine, USA
Erhart, S., Maine Coast Sea Vegetables, Inc., Franklin, Maine, USA

Phylogenetics & Taxonomy III
Moderator: Alison Sherwood, University of Hawaii

1:00 MOLECULAR PHYLOGENY OF THE NEMALIOPHYCIDAE (FLORIDEOPHYCEAE, RHODOPHYTA)
Lam, D. W., Ohio University USA, lam@ohio.edu
Vis, M. L., Ohio University, USA, vis-chia@ohio.edu
Saunders, G. W., University of New Brunswick, Canada, gws@unb.ca

1:15 USING NEXT GENERATION SEQUENCING TO EXAMINE PATTERNS OF ALGAL BIODIVERSITY IN A HAWAIIAN STREAM
Carlile, A. L., University of New Haven, USA, acarlile@newhaven.edu
Sherwood, A. R., University of Hawaii, USA, asherwoo@hawaii.edu

1:30 TESTING THE GENERIC LIMITS OF THE BIDDULPHIACEAE (BACILLARIOPHYCEAE): REVISITING ROSS & SIMS (1971) WITH MOLECULAR DATA
Ashworth, M. P., University of Texas at Austin, USA, mashworth@utexas.edu
Nakov, T., University of Texas at Austin, USA
Theriot, E. C., University of Texas at Austin, USA

1:45 A SEVEN GENE ESTIMATE OF THE DIATOM PHYLOGENY AND INFERENCES ABOUT THE UR-DIATOM
Theriot, E. C., University of Texas at Austin, USA, etheriot@austin.utexas.edu
Ashworth, M. A., University of Texas at Austin, USA, mashworth@mail.utexas.edu
Nakov, T., University of Texas at Austin, USA, teofiln@gmail.com
Brady, M., University of Texas at Austin, USA, mariska.brady@gmail.com
Yu, A., University of Texas at Austin, USA, annaymj_2010@mail.utexas.edu

2:00 ANCIENT GENE PARALOGY MAY MISLEAD INFERENCE OF PLASTID TREE OF LIFE
Qiu, H., Bigelow Laboratory for Ocean Sciences, USA, hqiu@bigelow.org
Yang, E. C., Bigelow Laboratory for Ocean Sciences, USA, ecyang@bigelow.org
Bhattacharya, D., Rutgers University, USA, BHATTACHARYA@aesop.rutgers.edu
Yoon, H. S., Sungkyunkwan University, Republic Of Korea, hsyoon2011@skku.edu

2:15 DETERMINING THE POSITION OF THE TREUBARINIA AND OTHER INCERTAE SEDIS TAXA IN THE CHLOROPHYCEAN TREE OF LIFE
Fucikova, K., University of Connecticut, USA, karolina.fucikova@gmail.com
Lewis, L. A., University of Connecticut, USA, louise.lewis@uconn.edu
Lewis, P. O., University of Connecticut, USA, paul.lewis@uconn.edu

Parasitology
Moderator:

3:00 SECRETION KILLERS: THE ORIGIN AND EVOLUTION OF PATHOGENICITY FACTORS IN THE OOMYCETE 'SECRETOME'
Misner, I., Univ. Rhode Island, USA, ianmisner@my.uri.edu
Leonard, G., Natural History Museum, United Kingdom, g.leonard@nhm.ac.uk

Bapteste, E., Université Pierre et Marie Curie, France, .bapteste@snv.jussieu.fr
Lopez, P., Université Pierre et Marie Curie, France, philippe.lopez@snv.jussieu.fr
Richards, T., Natural History Museum, United Kingdom, T.A.Richards@exeter.ac.uk
Lane, C., University of Rhode Island, USA, clane@mail.uri.edu

3:15 RED ALGAL PARASITE CONTRIBUTIONS TO HETEROKARYON ORGANELLAR PROTEOMES
Blouin, N. A., University of Rhode Island, USA, nblouin@mail.uri.edu
Lane, C. E., University of Rhode Island, USA, clane@mail.uri.edu

3:30 META-GENOMIC ANALYSIS OF A NONAXENIC CULTURE OF *BOTRYOCOCCUS PROTUBERANS* REVEALED A PROBABLE PARASITE *VERRUCOMICROBIUM SPINOSUM*
Sun, D., Genome Institute of Singapore, Singapore, sundy@gis.a-star.edu.sg
Datta, P., Genome Institute of Singapore, Singapore
Poon, S.Y., Genome Institute of Singapore, Singapore
Fang, L., Genome Institute of Singapore, Singapore
Liu, J., Genome Institute of Singapore, Singapore, liujh@gis.a-star.edu.sg

3:45 OUTBREAK OF AN ALGAL VIRUS DISEASE IN *PORPHYRA* FARMS IN KOREA
Kim, G.H., Department of Biology, Kongju National University, Republic Of Korea, ghkim@kongju.ac.kr

4:00 AN INVESTIGATION OF ENDOPHYTE IMPACTS ON MACROPHYTE HOST PHYSIOLOGY ALONG THE WESTERN ANTARCTIC PENINSULA
Schoenrock, K.M., University of Alabama at Birmingham, USA, ksrock@uab.edu
Amsler, C.D., University of Alabama at Birmingham, USA, amsler@uab.edu
Baker, B.J., University of South Florida, USA, bjbaker@usf.edu
McClintock, J.B., University of Alabama at Birmingham, USA, mcclinto@uab.edu

Friday Evening

PSA Business Meeting (4:30-5:30) **Carolina Room**

PSA Banquet **(South Carolina Aquarium)**

Saturday, June 23

07:00-08:00 Continental Breakfast

***Plenary Session*- Molecular Insights into the Ecology and Physiology of Harmful Algal Blooms**
(Chairs: Frances van Dolah, NOAA Center for Coastal Environmental Health and Bimolecular Research and Greg Doucette NOAA Center for Coastal Environmental Health and Bimolecular Research)

8:00 UNDERSTANDING THE NICHE OF HARMFUL ALGAE THROUGH THE LENS OF ECO-GENOMICS, -TRANSCRIPTOMICS, AND –PROTEOMICS (Chris Gobler, Stony Brook University)

8:40 GENOMIC INSIGHTS INTO THE PHYSIOLOGY OF THE DOMOIC ACID PRODUCING DIATOM *PSEUDO-NITZSCHIA MULTISERIES* (Micaela Parker, University of Washington)

9:20 UNRAVELING THE MYSTERY OF BREVETOXIN BIOSYNTHESIS IN THE FLORIDA RED TIDE DINOFLAGELLATE, *KARENIA BREVIS* (Frances Van Dolah, NOAA Center for Coastal Environmental Health and Bimolecular Research)

10:00-10:30 MIDMORNING BREAK

10:30 TRANSCRIPTOME ANALYSIS REVEALS NUCLEAR ENCODED PROTEINS FOR THE MAINTENANCE OF STOLEN PLASTIDS IN THE OKADAIC ACID PRODUCER, *DINOPHYSIS ACUMINATA* (Jeremiah Hackett, University of Arizona)

11:10 CHARACTERIZING HAB DYNAMICS AND TOXICITY VIA COORDINATED AUV-BASED SAMPLING AND IN SITU DEPLOYMENT OF MOLECULAR TOOLS (Greg Doucette, NOAA Center for Coastal Environmental Health and Bimolecular Research)

12:00-1:00 LUNCH BREAK

Coastal Issues/HABs
Moderator: Fran van Dolah, NOAA Center for Coastal Environmental Health and Bimolecular Research

1:00 THE ROLE OF SPHINGOLIPIDS IN VIRUS-INDUCED CELL LYSIS IN *EMILIANIA HUXLEYI*
Zaeuner, S., University of Hamburg, Germany, zaeuner@uni-bonn.de
Michaelson, L. V., Rothamsted Research, United Kingdom
Markham, J. E., University of Nebraska, USA
Allen, M. A., Plymouth Marine Laboratory, United Kingdom

1:15 AKINETE DEVELOPMENT IN THE HARMFUL CYANOBACTERIUM *APHANIZOMENON OVALISPORUM*
Sukenik, A., IOLR, Israel, assaf@ocean.org.il
Kaplan-Levy, R. N., IOLR, Israel, ruth@ocean.org.il
Mark Welch, J., MBL, USA, jmarkwelch@mbl.edu
Post, A. F., MBL, USA, apost@mbl.edu

1:30 TAXONOMIC REVISIONS OF MARINE CYANOBACTERIA TO FACILITATE NATURAL PRODUCTS DISCOVERIES AND HARMFUL ALGAE BLOOM MONITORING
Engene, N., Smithsonian Institution, USA, engenen@si.edu
Rottacker, E. C., National Center for Microscopy and Imaging Research, University of California San Diego, USA, erottack@ucsd.edu
Kaštovský, J., Faculty of Science, University of South Bohemia, Czech Republic, hanys@prf.jcu.cz
Komárek, J., Faculty of Science, University of South Bohemia, Czech Republic, komarek@butbn.cas.cz
Ellisman, M. H., National Center for Microscopy and Imaging Research, University of California San Diego, USA, mark.ellisman@gmail.com
Gerwick, W. H., Center for Marine Biotechnology and Biomedicine, Scripps Institution of Oceanography, USA, wgerwick@ucsd.edu
Paul, V., Smithsonian Institution, USA, Paul@si.edu

1:45 DEVELOPMENT OF SEMI-QUANTITATIVE PCR ASSAYS DETECTING AND ENUMERATING POTENTIALLY TOXIC CARIBBEAN *GAMBIERDISCUS* SPECIES
Vandersea, Mark W., NOS/NOAA, Center for Coastal Fisheries and Habitat Research, Beaufort, North Carolina USA, mark.w.vandersea@noaa.gov

Kibler, S.R., NOS/NOAA, Center for Coastal Fisheries and Habitat Research, Beaufort, North Carolina USA, steve.kibler@noaa.gov
Holland, W.C., NOS/NOAA, Center for Coastal Fisheries and Habitat Research, Beaufort, North Carolina USA, chris.holland@noaa.gov
Tester, P.A., NOS/NOAA, Center for Coastal Fisheries and Habitat Research Beaufort, North Carolina USA, pat.tester@noaa.gov
Schultz, T.F., Marine Conservation Molecular Facility, Duke University Marine Laboratory, Beaufort, North Carolina USA, tom.schultz@duke.edu
Faust, M.A., United States National Herbarium, National Museum of Natural History, Smithsonian Institution, Suitland, Maryland USA, faustm@si.edu
Homes, M.J., Water Quality and Aquatic Ecosystem Health, Queensland Department of Environment & Resource Man., Brisbane, Queensland Australia, michael.holmes@derm.qld.gov.au
Chinain, M., Laboratoire Des Micro-Algues Toxiques, Institut Louis Malardé, Tahiti, Papeete French Polynesia, MChinain@ilm.pf
Litaker, R.W., NOS/NOAA, Center for Coastal Fisheries and Habitat Research, Beaufort, North Carolina USA, Wayne.litaker@noaa.gov

2:00 CELL CYCLE, SAXITOXIN, AND PROTON PUMP RHODOPSIN: INSIGHTS FROM GENE EXPRESSION PROFILING FOR AN *ALEXANDRIUM FUNDYENSE* CULTURE AND A NATURAL BLOOM
Zhuang, Y., University of Connecticut, USA, yunyun.zhuang@uconn.edu
Zhang, H., University of Connecticut, USA, huan.zhang@uconn.edu
Hannick, L., J. Craig Venter Institute, USA, lhannick@jcvi.org
Lin, S., University of Connecticut, USA, senjie.lin@uconn.edu

2:15 BREVETOXIN PRODUCTION BY THE DINOFLAGELLATE *KARENIA BREVIS*: DO BACTERIA PLAY A ROLE?
Mikulski, C. M., Marine Biotoxins Program, NOAA Center for Coastal Environmental Health and Biomolecular Research, USA, tina.mikulski@noaa.gov
Monroe, E. A., Marine Biotoxins Program, NOAA Center for Coastal Environmental Health and Biomolecular Research, USA
Morey, J. S., Marine Biotoxins Program, NOAA Center for Coastal Environmental Health and Biomolecular Research, USA
Wang, Z., Marine Biotoxins Program, NOAA Center for Coastal Environmental Health and Biomolecular Research, USA
Roth, P. B., Marine Biotoxins Program, NOAA Center for Coastal Environmental Health and Biomolecular Research, USA
Twiner, M. J., Marine Biotoxins Program, NOAA Center for Coastal Environmental Health and Biomolecular Research, USA
Van Dolah, F. M., Marine Biotoxins Program, NOAA Center for Coastal Environmental Health and Biomolecular Research, USA
Doucette, G. J., Marine Biotoxins Program, NOAA Center for Coastal Environmental Health and Biomolecular Research, USA

2:30 DISTRIBUTION AND SEASONAL FLUCTUATION OF DIVERSE RIBOTYPE OF *COCHLODINIUM POLYKRIKOIDES* IN SOUTHERN KOREA COASTAL WATERS
Park, B. S., Hanyang University, Republic Of Korea, parkbs@hanyang.ac.kr
Kim, J., Hanyang University, Republic Of Korea, ikart00@nate.com
Kim, J., Hanyang University, Republic Of Korea, neozin83@naver.com

Wang, P., Hanyang University, Republic Of Korea, wpbdavid@163.com
Li, Z., Hanyang University, Republic Of Korea, lovecxx@naver.com
Han, M., Hanyang University, Republic Of Korea, hanms@hanyang.ac.kr

2:45 OVERWINTERING STRATEGY OF THE MIXOTROPHIC MARINE CILIATE *MESODINIIUM RUBRUM*
Park, J., Saemangeum Marine Environment Research Center, Kunsan National University, Republic Of Korea, cyanopark@hanmail.net
Kim, H., Department of Marine Biotechnology, Kunsan National University, Republic Of Korea, mudskip@kunsan.ac.kr
Jang, B., Department of Oceanography, Kunsan National University, Republic Of Korea, maria1728@kunsan.ac.kr
Yih, W., Department of Oceanography, Kunsan National University, Republic Of Korea, ywonho@kunsan.ac.kr

3:00 NITROGEN FIXATION AND MICROCYSTIN PRODUCTION BY CYANOBACTERIA IN EUTROPHIC LAKES
Monchamp, M., Department of Biological Sciences, University of Montreal, Canada, marie-eve.monchamp@umontreal.ca;
Maranger, R., Department of Biological Sciences, University of Montreal, Canada
Pick, F. R., Center for Advanced Research in Environmental Genomics, University of Ottawa, Canada, frances.pick@uottawa.ca;
Villemur, R., Institut National de la Recherche Scientifique Armand-Frappier, Canada
Beisner, B. E., Department of Biological Sciences, University of Quebec at Montreal, Canada

Ecology: Experimental
Moderator:

3:45 THE STIMULATION OF OXIDATIVE STRESS IN TEMPERATURE-STRESSED, IRON-DEPLETED CULTURES OF *SYMBIODINIUM* (FRUDENTHAL) MAINTAINED UNDER CONTINUOUS GROWTH
Laurent, J. K., University of Western Ontario, Canada, kiglic@uwo.ca
Trick, C. G., University of Western Ontario, Canada, cyano@uwo.ca

4:00 IMPACTS OF COMPETITION AND HERBIVORY ON THE GROWHT OF TWO BLOOM-FORMING *ULVA* SPECIES IN NARRAGANSETT BAY, RI
Guidone, M., University of Rhode Island, USA, mguidone@my.uri.edu
Rinehart, S., University of Rhode Island, USA
Thornber, C., University of Rhode Island, USA

4:15 EVOLUTION OF DEPENDENCY IN *PROCHLOROCOCCUS*: AN EMPIRICAL TEST USING AN *E. COLI* MODEL
Morris, J. J., Michigan State University, USA, jmorris@msu.edu
Zinser, E. R., University of Tennessee, USA, ezinser@utk.edu
Lenski, R. E., Michigan State University, USA, lenski@msu.edu

4:30 COMPARATIVE RATES OF PHOTOACCLIMATION IN HAWAIIAN ENDEMIC AND INVASIVE SPECIES OF *GRACILARIA* (RHODOPHYTA)
Hamel, K., University of Hawai'I, USA, khamel@hawaii.edu
Smith, C. M., University of Hawai'I, USA, celia@hawaii.edu

4:45 DISTURBANCE MEDIATED RESOURCE ALLOCATION: PHYSIOLOGIC RESPONSES TO BIOMASS LOSS IN *MACROCYSTIS PYRIFERA*
Fox, M. D., Moss Landing Marine Labs, USA, mfox@mlml.calstate.edu

5:00 TEASING APART TEMPERATURE AND NUTRIENT EFFECTS ON *MACROCYSTIS PYRIFERA* RECRUITMENT FROM BRITISH COLUMBIA TO SOUTHERN CHILE
Muth, A. F., Moss Landing Marine Labs, USA, amuth@mlml.calstate.edu
Graham, M. H., Moss Landing Marine Labs, USA, mgraham@mlml.calstate.edu

Saturday Evening

Bonus free night!

Abstracts

Please note that abstracts are presently thusly:

Invited Symposia speakers: S1-S18
Bold Award participants: T1-T12
Contributed talks: T13-T80
Poster presentations: P1-P48

Symposia Talks

S1. PROGRESS REPORT OF REDTOL: THE RED ALGAL TREE OF LIFE

Yoon, H. S., Sungkyunkwan University, Republic Of Korea, hsyoon2011@skku.edu
Bhattacharya, D., Rutgers University, USA, bhattacharya@aesop.rutgers.edu
Boo, S. M., Chungnam National University, Republic Of Korea, smboo@cnu.ac.kr
Fredericq, S., University of Louisiana at Lafayette, USA, slf9209@louisiana.edu
Hommersand, M., University of North Carolina, USA, hommersand@bio.unc.edu
Vis, M., Ohio University, USA, vis-chia@ohio.edu
Lopez-Bautista, J., University of Alabama, USA, jlopez@ua.edu
Saunders, G., University of New Brunswick, Canada, gws@unb.ca

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 photosynthetic 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 in red algal evolution and their place in the ToL. Since 2009, the RedToL team has made significant progress in: 1) generating a multi-gene phylogeny using eight gene markers from 500 red algal species, and 2) generating genome and transcriptome data from 16 key taxa that represent the phylogenetic (e.g., class- and order-level) breadth of red algae. Here we will introduce the aims and strategies of RedToL with highlights of recent research results.

S2. GENOME-WIDE TRANSCRIPTOMICS OF *PORPHYRA*

Stiller, J. W., East Carolina University, USA, stillerj@ecu.edu

This presentation provides an overview of collaborative analyses carried out by researchers from the *Porphyra* Genome Project through the Joint Genomics Institute, and the National Science Foundation sponsored *Porphyra*/Algal Genomics Research Collaboration Network, on a large expressed sequence tag (EST) data set from two closely related species of *Porphyra* (Bangiales, Rhodophyta). Approximately 4.7 million EST reads were assembled into 36,276 and 68,506 contigs for *Porphyra umbilicalis* and *P. purpurea*, respectively. About 20% of these contigs are inferred to encode proteins of known function, and these have been the subject of comprehensive investigations of various protein families and metabolic pathways. Comparative bioinformatics indicate that 482 contigs encode membrane transporters, most of which can be assigned to one of 57 distinct transporter families. These and other sequences suggest a complex history, including evidence for vertical descent, endosymbiotic gene transfer and associations that are not easily explained by current phylogenetic models. Paralogs of major developmental (MADS-box and Homeodomain) gene families are present, and several exhibit differential expression between the *Porphyra* blade (gametophyte) and conchocelis (sporophyte); however, there is no evidence that these or other key developmental families have expanded substantially in the transition from unicellular to multicellular forms in red algae. Most expected genes for histones and ribosomal proteins also were identified and, as with developmental regulators, some show evidence for differential regulation between

the life history stages. These and other major findings will be presented. Overall, the EST data provide novel insights into *Porphyra* and red algal biology, and point to exciting new directions for further experimental research.

S3. RECENT ADVANCES IN THE *CALLIARTHRON* GENOME: CLIMATE RESPONSES AND CELL WALL EVOLUTION

Chan, C.X., The University of Queensland, Institute for Molecular Bioscience, and ARC Centre of Excellence in Bioinformatics, Brisbane, Australia
Martone, P.T., Department of Botany, University of British Columbia, Vancouver, Canada

Corallines are a distinct group of calcifying red algae that are important ecological components of marine communities around the world, inducing settlement and providing habitat for invertebrates and other organisms. According to the fossil record, corallines have been abundant on Earth and perhaps ecologically central for millions of years. The recent discovery of secondary cell walls enriched with cellulose and lignin in *Calliarthron* has prompted a genomic search for clues about the deep evolution of cell wall biosynthesis. Moreover, coralline species (and associated communities) are particularly vulnerable to anthropogenic climate change, as temperature and pH changes complicate coralline growth and calcification. Studies of genes regulating heat shock proteins and calcification may shed light on corallines anticipated response. Here we present our progress in genome sequencing of *Calliarthron tuberculosum*, utilizing 454 pyrosequencing and Illumina sequencing-by-synthesis technologies. Initial combined assembly from these raw data generated sequence contigs spanning 487Mbp (N50 = 594), after which putative bacterial contaminants, sequencing errors were carefully removed. The filtered 172,667 genome contigs (N50 = 2299) cover 210Mbp. Using *Arabidopsis thaliana* as a training model and a stringent screening threshold, a total of 87,864 coding sequences (each corresponding protein with length ≥100 amino acids) were predicted, but the exact number of genes remains to be verified using full-length cDNAs. This project is on-going, but genes of interest discovered so far include those involved in biosynthesis of lignin (and secondary cell walls), membrane transports and abiotic stresses. With the availability of genome data from other mesophilic, multicellular red algae, the *Calliarthron* genome represents an excellent addition in the studies of evolutionary genomics and ecophysiology, particularly with respect to environmental adaptations of red algae to climate change and cell wall evolution.

S4. THE *CHONDRUS CRISPUS* GENOME AND THE DEVELOPMENT OF A FLORIDEOPHYTE MODEL.

Collén, J., Station Biologique, Roscoff, France,
Boyen, C., Station Biologique, Roscoff, France
Porcel, B., Genoscope, Evry, France,
Wincker, P., Genoscope, Evry, France.

The florideophyte red algae are an ecologically and economically important group of seaweeds. Despite their importance relatively little is known about their biology. One of the main reasons for this lack of knowledge is the lack of a recognized model species. We have therefore decided to promote *Chondrus crispus*, Irish moss, a common seaweed found on rocky shores on both sides of the Northern Atlantic Ocean, as a model species. One important part of this approach is the sequencing and analysis of its genome. The genome project is a collaboration between an international consortium and the sequencing agency Genoscope. The analysis of the 105 Mbp genome has demonstrated 9,606 protein coding genes, the majority (88%) without introns. The genome structure is characterised by gene-rich regions surrounded by regions dominated by transposable elements.
The further development of *Chondrus*as a model organism includes i.e. the construction of a large transcriptomic database, studies on population genetics, crossing and culture experiments, the construction of expression libraries, the development of probes for exploring cell wall components, and studies on photosynthesis.

S5. SEQUENCING AND ANALYSIS OF THE *PORPHYRIDIUM CRUENTUM* GENOME

Bhattacharya, D., Rutgers University, USA, bhattacharya@aesop.rutgers.edu
Price, D. C., Rutgers University, USA, dana.price@gmail.com
Yoon, H. S., Bigelow Laboratory for Ocean Sciences, USA, hsyoon@bigelow.org
Rajah, V. D., Rutgers University, USA, divino@]rci.Rutgers.edu
Zaeuner, S., University of Bonn, Germany, zaeuner@uni-bonn.de

We sequenced to completion the nuclear genome of the mesophilic red alga *Porphyridium cruentum* (Gray) Nägeli CCMP 1328. This species offers the opportunity to understand the evolution of a unicellular bangiophyte that has not undergone severe genome reduction as in their early diverging sisters, the Cyanidiales. The data comprise 4,770 contigs for a total genome size of 19.53 Mbp at 60x average coverage with a N50=20,301 bp. These genome data were combined with mRNAseq data to predict 8,355 proteins for downstream analysis. These data were used as a teaching tool by assigning 6 graduate students in an NSF-IGERT biofuels class different metabolic pathways or functions to study using a custom BLAST and annotation web site. Areas explored were the evidence for sex (meiosis and recombination) in *Porphyridium*, the evolution of light-harvesting component proteins, lipid metabolism, starch biosynthesis, support for Plantae monophyly, and the composition and origin(s) of the predicted plastid proteome. In this talk, we will discuss how the analyses of *Porphyridium* inform us about the evolution of this important missing link in the world of algal genomes.

S6. SPECIES MATTER! UNDERSTANDING THE ROLES AND DISTINCTIONS OF ALGAL SPECIES IS CRITICAL IN UNDERSTANDING STREAM ECOSYSTEMS.

Lowe, R. L., Bowling Green State University, USA, lowe@bgsu.edu

Microbial algal communities are composed of hundreds of different species with unique morphologies, physiologies, resource needs and tolerances. The structure and function of the micro-algal assemblage is regulated by a complex suite of biotic and abiotic variables that include physical disturbance, nutrients, grazers, toxic substances, solar radiation and many others. To gain a clearer understanding of environmental factors important in structuring algal communities it is important to measure variables at appropriate spatial and temporal scales and to better understand the autecology or niche of important species within the assemblage. In aquatic ecosystems like the Eel River (northern California) where dissolved organic nitrogen is scarce interactions between disturbance, grazers and key algal species result in widely divergent food web pathways. Understanding algal species' niches leads to a clearer prediction of ecosystem function in the Eel River.

S7. BIOASSESSMENT WITH ALGAE: GOALS, THEORY, METHODS, AND BENEFITS

Stevenson, R.J., Department of Zoology, Michigan State University, East Lansing, MI 48824

Biological assessment provides characterizations of ecosystem goods and services as well as human alterations of ecosystems needed to manage problems. As the base of food webs, algae support fisheries, but can also impair drinking water and recreational uses by producing toxins, reducing water clarity, fouling beaches, and increasing exposure to pathogenic bacteria. Assessments of algae involve platforms ranging from laboratory to satellite imagery, but most extensively the sampling and microscopic analyses for 1000's of streams, lakes, wetlands, and coastal zones around the world. Assessments of algae provide the most sensitive and precise ecological indicators of all groups of biota, e.g. the species composition of algae in a habitat and knowledge of species environmental preferences provide more precise and accurate characterizations of pollutants than one time water sampling. Although algae have been used extensively to characterize changes in pH and nutrients in ecological systems, only recently have biodiversity assessments been emphasized. In addition to characterizing ecological condition for management of aquatic resources, assessments provide invaluable descriptions of relationships between algae and their environment, biodiversity and species traits, and evolution of algae.

S8. BIOASSESSMENT OF AQUATIC BIODIVERSITY WITH COARSE AND FINE LEVELS OF DIATOM TAXONOMY

Manoylov, K. M., Georgia College and State University, USA, kalina.manoylov@gcsu.edu

Benthic diatoms are well suited for use as biological indicators for assessment of environmental conditions. The State of Georgia is divided into 5 Ecoregions: Appalachian Plateau, Valley & Ridge, Blue Ridge, Piedmont and Coastal areas. Indicators developed within an area will be different among regions and cannot infer aquatic quality from another area. 155 samples from wadeable streams were enumerated. A detailed analysis of living diatoms within each sample was performed. Routine taxonomy was performed with LM, and taxa identification was finalized with SEM images of common taxa. Three levels of analyses for diatom species composition were employed: live 300 diatoms identified to species, the traditional 600 count on permanent slides with acceptable *sensu lato* concepts and finest level taxonomy with *sensu stricto* differentiations if attainable. Indicators for the State of Georgia were linked to community indices. Based on diatom species composition sites were designated as good, fair and bad. Diatom-based weighted average models were used to infer nutrient concentrations for each approach. Finest level taxonomic identification outperformed traditional *sensu lato* based taxonomic assessment for some site designations.

S9. CHALLENGES IN BIOASSESSMENT OF ACID MINE DRAINAGE

Vis, M.L., Ohio University, USA, vis-chia@ohio.edu

Acid mine drainage (AMD) is dominant in coal mining areas such as Ohio, which has affected ~1,300 stream miles. AMD is produced when the mineral pyrite is exposed to air and water, resulting in sulfuric acid, drastically lowering pH. When AMD mixes with neutral waters, dissolved metals, especially ferric hydroxide, precipitate and coat the benthos with fine sediment. My laboratory has been studying the effects of AMD on periphyton communities in order to use them as biomonitors. We have primarily focused on community structure, examining how AMD affects diversity metrics. We have developed an index of biotic integrity specific to AMD, which compliments macroinvertebrates and fish biomonitoring, as well as making our results more amenable for management applications. Along with structural measures, we are investigating functional measures of stream health, which include periphyton biofilm enzyme activities. We have used these tools to evaluate current remediation projects using alkaline doser technology. Our research has shown structure and function of periphyton communities can be used to assess both the impact of AMD and success of remediation efforts.

S10. VIRUSES IN THE DRIVER'S SEAT OF PHYTOPLANKTON MORTALITY

Brussaard, C. Biological Oceanography, NIOZ-Royal Netherlands Institute for Sea Research, Texel, The Netherlands, corina.brussaard@nioz.nl

Quantification of rates, patterns and mechanisms that control uptake of CO_2 by phytoplankton and the fate of the resultant organic carbon is an important central theme in oceanographic research. Phytoplankton make up the base of most marine pelagic food webs, providing more than 99% of the organic matter available to higher trophic levels. Phytoplankton grazing and viral infection-induced mortality are productivity controlling processes but influence the cycling of energy and biogeochemically relevant elements each very differently, directly affecting the production/respiration ratio of the ocean and the efficiency of the biological pump. Viruses have been shown to infect a large variety of phytoplankton, thereby removing algal prey from the traditional food chain. Here I will present the current state of the art on viral lysis of phytoplankton (from field, mesocosm studies and laboratory experiments), illustrate their significance as phytoplankton loss factor and discuss the ecological implications of viruses as drivers of phytoplankton mortality.

S13. COCCOLITHOVIRUSES: LIFE AND DEATH AFTER GENOME SEQUENCING

Wilson, W., Bigelow Laboratory for Ocean Sciences, East Boothbay, Maine, wwilson@bigelow.org

The virus genus Coccolithovirus (Cocco: derived from Greek *kokkis*, meaning berry or grain referring to their shape and Lith: from Greek *Lithos*, meaning stone) is a group of large, double stranded DNA viruses that infect the globally important marine coccolithophorid *Emiliania huxleyi*. The first observation of virus-like particles in *E. huxleyi* was reported back in 1974 though they are now known to be one of the causative agents of *E. huxleyi* bloom demise. We sequenced the 407,339 bp genome of one coccolithovirus and revealed that only 14% of the predicted genes confer any significant database homology. Here we will present data that shows how we use virus genomic information to help determine the ecological function of coccolithoviruses, helped by an overview of a mesocosm experiment carried out in June 2008. I will also present some methodological advances in analysis of single viruses and single infected cells sorted by flow cytometry. It is a real hotch potch of data but hopefully it will start to tell us something about this intriguing virus.

S14. UNDERSTANDING THE NICHE OF HARMFUL ALGAE THROUGH THE LENS OF ECO-GENOMICS, TRANSCRIPTOMICS, AND PROTEOMICS.

Gobler, C.J., School of Marine and Atmospheric Sciences, Southampton, NY, USA
Berry, D.L., Stony Brook University, School of Marine and Atmospheric Sciences, Southampton, NY, USA
Dyhrman, S.T. Woods Hole Oceanographic Institution, Biology Department, Woods Hole, MA
Wurch, L., Woods Hole Oceanographic Institution, Biology Department, Woods Hole, MA,
Wilhelm, S.W., The University of Tennessee, Department of Microbiology, Knoxville, TN 37996, USA.

The sequencing and annotation of the genome of *Aureococcus anophagefferens* has presented the opportunity to understand the niche of this harmful alga through the lens of eco-genomics, transcriptomics, and proteomics. We have specifically examined gene sets in *A. anophagefferens* that may facilitate its dominance within the environmental conditions present during blooms and have compared these genes to those of six competing phytoplankton species identified during brown tides via metaproteomics. *A. anophagefferens* possesses an expansion in genes involved in light harvesting, organic carbon and nitrogen utilization, and encoding selenium- and metal-requiring enzymes. This suggests that anthropogenic activities that have elevated levels of turbidity, organic matter, and metals have consequently opened a niche that ideally suits the unique genetic capacity of *A. anophagefferens* and thus have facilitated its proliferation. To test this hypothesis, subsequent transcriptomic and protemic studies have been performed on field and laboratory populations. The availability of a reference genome has permitted the unambiguous mapping of gene and protein targets and has provided a heightened understanding of the role of genes involved in nutrient acquisition and processing in bloom proliferation.

S.15 GENOMIC INSIGHTS INTO THE PHYSIOLOGY OF THE DOMOIC ACID PRODUCING DIATOM PSEUDO-NITZSCHIA MULTISERIES

Parker, M. S., University of Washington, School of Oceanography, USA, micaela@uw.edu
Schruth, D. M., University of Washington, School of Oceanography, USA, dschruth@uw.edu
Armbrust, E. V., University of Washington, School of Oceanography, USA, armbrust@uw.edu

The cosmopolitan diatom genus *Pseudo-nitzschia* thrives in coastal environments and can produce the potent neurotoxin domoic acid (DA). Previous studies have demonstrated variability in DA production among species and strains of *Pseudo-nitzschia* with environmental triggers further modulating cellular DA levels. To uncover the molecular basis for toxin production, the whole genome of *Pseudo-nitzschia multiseries* CLN-47 was sequenced by the Joint Genome Institute. The 219Mb draft genome is largely composed of repeat sequences (75%) that are either transposable elements or unclassified, and includes ~19,000 predicted genes. Putative phage-like integrases were detected and may represent footprints of

previous viral infections. To assess whether differential gene expression correlates with DA production, whole transcriptomes of *P. multiseries* were sequenced from cultures harvested under conditions yielding varying amounts of DA per cell: exponential phase (nitrate or urea as N source), iron-limitation, silicate-starvation and phosphate-starvation. Signaling and defense-related genes are strongly represented, highlighting the ability of *Pseudo-nitzschia* to sense and respond to suboptimal conditions. Comparisons across treatments reveal candidate genes putatively involved in DA synthesis or regulation, with transcription patterns correlated to observed DA levels.

S16. UNRAVELING THE MYSTERY OF BREVETOXIN BIOSYNTHESIS IN THE FLORIDA RED TIDE DINOFLAGELLATE, *KARENIA BREVIS*

Van Dolah, F. M., NOAA Center for Coastal Environmental Health and Biomolecular Research, USA, fran.vandolah@noaa.gov

Karenia brevis is a prolific producer of polyketides, including potent brevetoxin neurotoxins that comprise 2-4% of cellular carbon. Understanding brevetoxin biosynthesis may elucidate the purpose for this significant metabolic investment. *K. brevis* has unusual TypeI polyketide synthases that appear to be conserved among dinoflagellates. PKSs, like fatty acid synthases (FASs), build carbon backbones through the sequential condensation of carboxylic acid subunits. Unlike FASs, PKSs produce unsaturated carbon chains. Several lines of evidence suggest that *K. brevis* PKSs may function in a role other than or in addition to brevetoxin biosynthesis: (1) PKS proteins are localized to the chloroplast, but brevetoxin is not; (2) 3H-acetate labeling demonstrates that fatty acid synthesis occurs in the chloroplast; however, the labeled products include unsaturated fatty acids; (3) PKS transcripts show expression patterns consistent with primary, not secondary metabolism; (4) no unique FAS transcripts are identified among ~65,000 *K. brevis* ESTs. We propose that *K. brevis* PKSs may have both FAS and PKS activity. Precursors to brevetoxin may be synthesized in the chloroplast, but exported to other cellular compartment(s) for cyclization into mature toxin molecules.

S18. CHARACTERIZING HAB DYNAMICS AND TOXICITY VIA *IN SITU* DEPLOYMENT OF MOLECULAR TOOLS AND COORDINATED AUV-BASED SAMPLING.

Doucette, G.J., Marine Biotoxins Program, NOAA/National Ocean Service, Charleston, SC, USA
Mikulski, C.M., Marine Biotoxins Program, NOAA/National Ocean Service, Charleston, SC, USA
Wang, Z., Marine Biotoxins Program, NOAA/National Ocean Service, Charleston, SC, USA
Harvey, J.B., MBARI, Moss Landing, CA, USA
Ryan, J.P., MBARI, Moss Landing, CA, USA
Zhang, Y., MBARI, Moss Landing, CA, USA
Marin III, R., MBARI, Moss Landing, CA, USA
Scholin, C.A., MBARI, Moss Landing, CA, USA

The molecular tools available for characterizing harmful algal bloom (HAB) growth and toxicity continue to expand, but their application is largely restricted to the laboratory and the time required for analyses can limit their usefulness. New generations of an autonomous, robotic molecular detection system (Environmental Sample Processor; ESP), coupled with observations from satellites, ships, drifters, and autonomous underwater vehicles (AUVs), now permit description of HABs in the context of ecosystem variability from regional to molecular scales. Domoic acid (DA) producing diatoms of the genus Pseudo-nitzschia were the focus of field experiments conducted in southern and central California, during which their abundance, toxicity, and associated zooplankton were monitored. In situ, near-real time molecular analyses of planktonic communities and DA by moored ESPs, recently augmented with bloom tracking/sampling by AUVs using autonomous feature recognition, revealed variation in Pseudo-nitzchia abundance, toxicity, and DA trophic transfer potential, in concert with changes in oceanographic conditions. The next generation ESP will integrate in situ molecular analyses with AUV-based intelligent

sampling to enable Lagrangian tracking and near-real time analyses of a bloom population's genomic and biochemical signatures.

Bold Talks

T1. SPECIES DELIMITATION IN THE *CAULERPA RACEMOSA/PELTATA* COMPLEX (CHLOROPHYTA, CAULERPACEAE)

Belton, G. S., University of Adelaide, Australia, gareth.belton@adelaide.edu.au
Prud'Homme van Reine, W. H., Leiden University, Netherlands
Huisman, J. M., Murdoch University and the Western Australian Herbarium, Australia
Sauvage, T., University of Louisiana, USA
Draisma, S. G., University of Malaya, Malaysia
Gurgel, C. F., University of Adelaide, the State Herbarium of South Australia and SARDI Aquatic Sciences, Australia

The rampant morphological plasticity displayed by many species of *Caulerpa* has resulted in numerous infraspecific taxa and synonymies. This is most evident in the *C. racemosa/peltata* complex, which currently has more than 30 described varieties and forms. Although recent molecular studies have indicated that many of these infraspecific taxa deserve recognition at the species level, no major taxonomic revisions have been made. The present study investigated molecular and morphological variation within and between taxa currently assigned to the complex, with emphasis on the Indo-pacific region. Molecular variation was assessed by analyses of partial *tuf*A, *rbc*L and *rps*3-*rpl*16 gene sequences. Our results revealed that the *C. racemosa/peltata* complex represents at least 10 distinct genetic species, with morphology alone unable to delimit many of these species. *Caulerpa peltata* and *C. racemosa* vars. *laetevirens* and *turbinata* were found to represent environmentally induced forms of a single, earlier-described species, and thus *C. chemnitzia*, currently regarded as a synonym of *C. racemosa* var. *turbinata*, is reinstated. *Caulerpa cylindracea*, *C. lamourouxii*, *C. macrodisca*, C. *nummularia* and *C. oligophylla* are also reinstated and three new species proposed.

T2. WHAT DO CHLOROPLAST GENOMICS TELL US ABOUT EUGLENOID PHYLOGENIES?

Bennett, M. S., Michigan State University, USA, benne124@msu.edu
Wiegert, K. E., Michigan State University, USA, wiegertk@msu.edu
Watza, D. G., Michigan State University, USA, watzadon@msu.edu
Triemer, R. E., Michigan State University, USA, triemer@msu.edu

Current understanding of photosynthetic euglenoid phylogenetics is largely based on 18S, 28S, 16S and 23S rRNA genes. Recent works sequencing the chloroplast genomes of photosynthetic euglenoids have enabled the phylogenetic analysis to be expanded and include a large number of chloroplast-encoded genes. A dataset including 8 photosynthetic euglenoid taxa and 11 representative green algal taxa was created and analyzed for over 60 genes using both ML and Bayesian analyses. The resulting tree topologies were consistent with previous studies of both chloroplast-encoded and nuclear-encoded rRNA genes, placing the Eutreptiales at the base of the euglenoid lineage followed by the divergence of Discoplastis prior to *Euglena*, *Colacium*, and *Strombomonas*. However, the new phylogenetic trees demonstrated greater support within the euglenoids than has previously been seen. Additionally, the basal position of *Pyramimonas* relative to the photosynthetic euglenoid taxa strongly supports this taxon as an extant representative of the euglenoid green algal chloroplast donor and implies that acquisition of the chloroplast was the result of a single endosymbiotic event.

T3. A TAXONOMIC REVISION OF AUSTRALIAN *SARGASSUM*, WITH A NEW PERSPECTIVE ON THE SUBGENERIC CLASSIFICATION OF THE GENUS

Dixon, R., Murdoch University, Australia, rains.rmd@gmail.com
Huisman, J. M., Murdoch University and WA Herbarium, Australia
Gurgel, C. F., University of Adelaide, State Herbarium of SA and SARDI Aquatic Sciences, Australia

There are currently over 100 *Sargassum* species in Australia representing three of the four subgenera. A recent study of the Sargassaceae transferred the most widely distributed species of subgenus *Phyllotricha*, *S. decurrens*, to the reinstated genus *Sargassopsis*. Using a combination of morphological and molecular sequence data, the present study examined subgenus *Phyllotricha*, alongside other species of *Sargassum*, and the closely related genera *Sargassopsis*, *Sirophysalis* and *Carpophyllum*. Our results suggest that the genus *Sargassum* and subgenus *Phyllotricha* are polyphyletic with four species, *S. decipiens*, *S. varians*, *S. verruculosum* and the *Phyllotricha* generitype, *S. sonderi*, clustering as a monophyletic group sister to *Carpophyllum*. As such, the genus *Phyllotricha* is resurrected. The remaining species of subgenus *Phyllotricha sensu lato* were transferred to Sargassopsis and *Sargassum peronii* is synonymised with *Sargassopsis decurrens*. Species from subgenus *Arthrophycus* were found to be monophyletic and distinct from other Australian subgenera but showed low levels of genetic diversity among species. Subgenus *Sargassum* remains the most diverse and widespread of the subgenera, however, recent species additions and a growing number of synonyms indicate that much taxonomic work remains.

T4. THE CASPASE REACTOME OF *KARENIA BREVIS* DURING ROS-DRIVEN CELL DEATH

Johnson, J. G., Medical University of South Carolina, USA, jill.johnson821@gmail.com
Van Dolah, F. M., NOAA Center for Coastal Environmental Health and Biomolecular Research, USA, fran.vandolah@noaa.gov

Although many phytoplankton demonstrate morphological characteristics typical of programmed cell death, the proteases involved in potentiating death signals for cell suicide remain unresolved. Metacaspases, caspase-like homologs present in phytoplankton, are often proposed to be responsible. Quantification of caspase 3-like activity, using both the fluorogenic substrate DEVD and live cell imaging using the CellEvent Caspase 3/7 marker, identified significant induction in caspase activity during oxidative stress-induced death in *Karenia brevis*. Bioinformatic mining of a *K. brevis* EST library for caspase-like enzymes suggests that subtilisins and/or vacuolar processing enzymes (VPEs), not metacaspases, may be responsible for the caspase 3-like activity observed. In concordance, caspase 3-like protein abundance was induced during ROS-driven cell death as demonstrated by western blotting, while metacaspase 1 (KbMC1) significantly decreased. Furthermore, MALDI-TOF analysis of a candidate substrate revealed an increase in cleavage of its caspase 3-specific DEVD recognition motif by ROS-activated cell extracts. Together these results indicate metacaspases do not mediate dinoflagellate PCD. Computational prediction of downstream substrates for caspase 3-like activity identified a wide range of biological processes likely involved in the execution of death in dinoflagellates.

T5. THE SYSTEMATICS AND BIOGEOGRAPHY OF THE THOREALES, A FRESHWATER RED ALGAL ORDER

Johnston, E. T., Ohio University, USA, ej363707@ohio.edu
Buhari, N., Hasanuddin University, Indonesia, li_buhari@yahoo.com
Djawad, I., Hasanuddin University, Indonesia, iqbaldj@yahoo.com
Vis, M. L., Ohio University, USA, vis-chia@ohio.edu

The order Thoreales is composed of freshwater macroalgae with a worldwide distribution and contains only two genera, *Nemalionopsis* with two species, and *Thorea* with four to 11 species recognized by various authors. The controversy surrounding the number of species in *Thorea* stems from a lack of

discrete morphological characters to define taxa and little molecular data generated to date. The primary goal of this research was to determine the number of phylogenetic species within the order and assess major biogeographical trends. Specimens were collected in Europe, temperate and sub-tropical North America, the Caribbean, South America, Eastern Asia and South Pacific Islands. Sequence data were generated for the rbcL (chloroplast) gene, the LSU (nuclear) gene, and the COI-barcoding region (mitochondrial). Bayesian Inference and Maximum Likelihood analyses were conducted and indicated two major lineages within *Thorea*, one tropical and one from the temperate regions of both hemispheres. Additionally, the greatest species diversity appears to be concentrated in Eastern Asia, and South Pacific islands. Due to genetic divergence and paraphyly within the Thoreales, previous synonymous species are resurrected and new species are proposed.

T6. MULTIPLE CLIMATE STRESSORS NEGATIVELY IMPACT INTERTIDAL KELP ZOOSPORE MOTILITY

Jorve, J. P., University of British Columbia, Canada, jorve@zoology.ubc.ca
Harley, C. D., University of British Columbia, Canada, harley@zoology.ubc.ca
Martone, P. T., University of British Columbia, Canada, patrick.martone@botany.ubc.ca
Zimmer, R. K., University of California, Los Angeles, USA, z@biology.ucla.edu
Himes, J. E., University of California, Los Angeles, USA, juliehimes@gmail.com

Kelps play an integral role in structuring nearshore, temperate coastal communities. Understanding how climate change stressors will impact these habitat-forming species' population dynamics is integral in predicting how community structure will change in the coming century. This experiment targeted the response of the vulnerable, unattached microscopic life history stage to multiple climate factors, using an intertidal species (*Egregia menziesii*) found along the Pacific coast of North America. Specifically, we looked at how kelp zoospore motility (speed, rate of change of direction, net distance traveled) and settlement behavior varied with warming, ocean acidification, and increased ultraviolet radiation (UV). Results indicated that as zoospores increased in age, swimming speed decreased in response to increased CO2 and temperature. Since sessile organisms reproduce in the low intertidal during 1) limited emersion periods or 2) when immersed facing turbulent water and crashing waves, the speed and manner in which they find suitable substrate to settle could determine population persistence if negative effects ripple through subsequent life history stages.

T7. TWO TRACK CONTROL OF PHOTOMOVEMENT IN *SPIROGYRA*: PHYTOCHROME AND PHOTOTROPIN USE DIFFERENT MACHINERY FOR THE CONTROL OF MOVEMENT

Lee, J. W., Department of Biology, Kongju National University, Republic Of Korea, ljw86@kongju.ac.kr
Han, J. W., Department of Biology, Kongju National University, Republic Of Korea, fop9440@kongju.ac.kr
Kim, G. H., Department of Biology, Kongju National University, Republic Of Korea, ghkim@kongju.ac.kr

The filamentous green algae *Spirogyra* spp. shows a different pattern of movement in response to red and blue light. In blue light the filament shows typical positive phototropism. In red light, however, the filaments bend or twisted irregularly. The red light movement can be reversed by short exposure (<30s) to far-red light suggesting the involvement of phytochrome. The blue light responsive movement was stronger than the red light responsive movement. When the blue and red light were given together the filament shows positive phototropism just like the blue light responsive movement. Inhibition experiment on photoreceptors also showed different result in red and blue light. When the filaments were treated with phototropin inhibitor, K-252a, all photomovement stopped immediately. However, phytochrome inhibitor gabaculine could block only the red light responsive movement. The movement in response to red and blue light was controlled by different machinery. The red light responsive movement was inhibited by the

treatment of the microtubule inhibitor, Oryzalin (10 µM). The actin inhibitor, cytochalasin D did not show any inhibitory effect up to the concentration of 50 µM. The blue light responsive movement, however, stopped only when the filaments were treated together with cytochalasin D as well as Oryzalin. The phototropin and phytochrome genes were cloned in *Spirogyra varians*. Both photoreceptor genes showed high homology with land plants. The expression level of photoreceptor genes was not affected by the prolonged exposure of filaments to blue and red light. To study signaling pathway of the photoreceptors, seven different GTPase were cloned and the expression level of each GTPase under red and blue light was compared. The results suggested that the blue light and red light responsive movement are controlled through different signaling pathways.

T8. NEXT GENERATION TRANSCRIPTOMICS ELUCIDATES BROWN ALGAL SEXUAL REPRODUCTION GENES

Lipinska, A., Ghent University, Belgium, agnieszka.lipinska@ugent.be
Van Damme, E. J., Ghent University, Belgium
De Clerck, O., Ghent University, Belgium

Brown algae have served extensively as model organisms for algal life cycle studies and sexual reproduction. Yet, little is known about the molecular basis of sex determination, gamete attraction and fertilization. To provide a better understanding of the molecular mechanisms underlying physiological differentiation, gamete recognition and fusion, we sequenced the transcriptome of male and female *Ectocarpus siliculosus* gametes using AB SOLiD Next Generation Sequencing technology. Despite being morphologically identical, digital expression analysis identified approx. 4700 differentially expressed genes between male and female gametes. Functional analysis was performed based on Gene Ontology (GO) and KEGG categories and provided valuable insight into complex transcriptome adjustment to diverse functions fulfilled by male and female gametes. Several new genes and pathways with a putative function in the recognition and attraction process were identified. We evaluated the SOLiD RNA-seq results by qPCR across different life stages in *Ectocarpus*, providing foundations for more detailed research on the fertilization mechanisms and the evolution of gamete recognition genes in brown algae.

T9. MOLECULAR AND MORPHOLOGICAL INVESTIGATION OF SPECIES DIVERSITY IN *BATRACHOSPERMUM* SECTION *HELMINTHOIDEA* (BATRACHOSPERMALES, RHODOPHYTA)

Salomaki, E. D., Ohio University, Athens, OH, USA, es289510@ohio.edu
Kwandrans, J., Institute of Nature Conservation, Poland
Eloranta, P., Finland
Kostkeviciene, J., Vilnius University, Lithuania
Vis, M. L., Ohio University, Athens, OH, USA

Previous research has provided strong support for *Batrachospermum* section *Helminthoidea* as a clade. However, relationships among taxa within the clade were not clearly distinguished. Additionally, there were only a few specimens representing taxa that have been reported from a broad geographic range including more than one continent. This research was undertaken to provide data on 57 specimens collected at locations throughout North America, Europe, and New Zealand, representing all known taxa in this clade. Sequence data has been generated for the chloroplast *rbc*L gene, the nuclear ITS (1 & 2) region, and the mitochondrial *cox*1 barcode region. These data showed that within the current circumscription of *B. boryanum* alone, there are 5 separate clades/taxa, with several having distinct geographical ranges. The morphology of specimens from each clade has been evaluated for discrete characters to differentiate taxa. In order to associate historical species epithets with the clades, the morphology of syntypes, isotypes, and lectotypes have been examined and DNA has been sequenced from these specimens, when possible. Descriptions of four species will be revised and three new species will be proposed.

T10. COMPLETE PLASTID AND MITOCHONDRIAL GENOMES OF THE FRESHWATER BROWN ALGA *PLEUROCLADIA LACUSTRIS* A. BRAUN

Wang, X., Fordham University, USA, wang@fordham.edu
Wehr, J. D., Fordham University, USA, wehr@fordham.edu
Karol, K. G., The New York Botanical Garden, USA, kkarol@nybg.org

Of an estimated 2000 brown algal species, less than 1% occur in freshwater environments. Historically, *Pleurocladia lacustris* has been classified with either Ectocarpaceae or Chordariaceae. This study aims to better understand the organellar genome evolution and the phylogenetic position of this species. Physical maps of organllar genomes are presented here, which represent the third brown algae for which both organellar genomes have been completely sequenced. The mitochondrial genome is 37.8 kb, has a GC content of 32.9%, and includes genes for three rRNAs, 26 tRNAs and 34 protein-coding genes. The plastid genome is 138.8 kb, has a GC content of 29.8%, and includes genes for three rRNAs, 30 tRNAs, and 136 known protein-coding genes. Phylogenetic trees among Phaeophyceae were constructed and supported the contention that *P. lacustris* is a member of the Ectocarpaceae. Comparison of the structure, gene content and order of both organellar genomes with previously published genomes suggested gene order is more conserved among brown algal mitochondrial genomes than plastid genomes. Sequence similarities among brown algal species identified candidate loci for future biogeographic level questions.

T11. HORIZONTAL GENE TRANSFER IS A SIGNIFICANT DRIVER OF GENE INNOVATION IN DINOFLAGELLATES

Wisecaver, J. H., University of Arizona, USA, hughesj@email.arizona.edu
Hackett, J. D., University of Arizona, USA, hackettj@email.arizona.edu

The dinoflagellates are an evolutionarily and ecologically important group of microbial eukaryotes. Previous work suggests that horizontal gene transfer (HGT) has had a significant impact on dinoflagellate biology and genome evolution. We sequenced the transcriptome of the dinoflagellate *Alexandrium tamarense* CCMP 1598 to investigate how HGT has contributed to gene innovation in this organism. Rarefaction curve analysis suggests that the vast majority of *A. tamarense*'s transcriptome is represented in our assembly. We compared this comprehensive dinoflagellate unigene set to those of sixteen fully sequenced, related eukaryotes. Ancestral gene content reconstruction of KEGG orthologs shows that *A. tamarense* has the largest number of genes gained relative to all other organisms in the analysis. Phylogenomics suggests that HGT from bacteria is a significant driver of this gene influx as is gene transfer from other eukaryotes either through HGT or endosymbiosis. *A. tamarense* also shows interesting cases of gene loss, and some of these missing genes have been functionally replaced by bacterial homologs. The transcriptome of *A. tamarense* lends support to a growing body of evidence that dinoflagellate genomes are extraordinarily impacted by HGT.

Contributed Talks

T13. O FATHER, WHERE ART THOU? PATERNITY ANALYSES IN A NATURAL POPULATION OF THE RED SEAWEED *CHONDRUS CRISPUS*

Krueger-Hadfield, S. A., Marine Biological Association of the UK, United Kingdom, stakru@mba.ac.uk
Roze, D., Station Biologique de Roscoff, France, roze@sb-roscoff.fr
Mauger, S., Station Biologique de Roscoff, France, mauger@sb-roscoff.fr
Destombe, C., Station Biologique de Roscoff, France, destombe@sb-roscoff.fr
Valero, M., Station Biologique de Roscoff, France, valero@sb-roscoff.fr

Chondrus crispus follows an isomorphic haploid–diploid life history in which male gametophytes release non-motile spermatia and fertilization is followed by zygotic amplification. The objective of this study was to understand the impacts of haploid-diploidy, male gamete dispersal and the intertidal shorescape on the genetic structure of *C. crispus*. Individual fronds were sampled every 25 cm in two 5mx5m grids located high and low on the shore. Fronds (N=472) and cystocarps (N=565, excised from 29 female gametophytes) were genotyped using polymorphic microsatellite loci. The maternal allele at each locus can be determined from the haploid female thallus. The remaining allele is the paternal contribution. Large levels of inbreeding detected using indirect methods were supported by the paternity analyses. Larger kinship coefficients were detected between males siring cystocarps on the same female than between males in the entire population. However, only 1 of 424 sires was sampled in the populations suggesting fertilization distances of less than 25 cm. More detailed sampling of genets is necessary to resolve the high levels of inbreeding associated with low levels of genetic differentiation.

T14. ALGAL DIVERSITY OF THE BURICA PENINSULA, PACIFIC PANAMA

Wysor, B., Roger Williams University, USA, bwysor@rwu.edu
Freshwater, D. W., Center for Marine Science, USA, freshwaterw@uncw.edu
Leon, N., University of Panama, Panama
Fernandez-Garcia, C., Universidad de Costa Rica, Costa Rica
Gabrielson, P. W., UNC-Chapel Hill, USA
Charbonneau, V., Roger Williams University, USA
Green, C., Roger Williams University, USA
Idol, J., UNC-Wilmington, USA
Parham, S., Center for Marine Science, USA

The marine flora of Panama harbors a rich diversity of green, red and brown algae and, despite chronic understudy, it is reported as the second most diverse marine flora along the Pacific Central American coast with 174 macroalgal species. Extensive new collections and molecular assisted identification (MAI) by an international team of researchers are revealing an even greater diversity for this region. Here, we introduce the marine flora of the remote Burica Peninsula, which is characterized by an extensive and interesting intertidal environment composed of firm, sedimentary benthos known as mudrock, on which abundant algal communities thrive, even during extended periods of exposure. Our collection of nearly 200 specimens from January 2011 represents the first marine floristic inventory of this region. DNA sequence data for a variety of loci (*rbc*L; UPA; COI barcode) have been generated for MAI and guiding morphological assessments. This work has revealed new species and extended known ranges, including previously unrealized transisthmian distributions.

T15. DIVERSITY AND EVOLUTION OF ENDOSYMBIOTIC BACTERIA IN THE SIPHONOUS GREEN ALGA *BRYOPSIS* (BRYOPSIDALES, CHLOROPHYTA)

Leliaert, F., Ghent University, Belgium, frederik.leliaert@gmail.com
Hollants, J., Ghent University, Belgium
Verbruggen, H., Ghent University, Belgium
Willems, A., Ghent University, Belgium
De Clerck, O., Ghent University, Belgium

Many algae maintain close associations with bacteria that are linked with various metabolic functions and influence the shape and life cycle of the host. Siphonous green algae frequently contain bacteria within their giant cells, which form interesting biotic environments for bacterial communities. We examined the diversity and evolution of endosymbiotic bacteria in the genus *Bryopsis*. Using algal cultures and molecular methods (fluorescence in situ hybridization, denaturing gradient gel electrophoresis and 16S rRNA gene clone libraries), we show that *Bryopsis* species harbor well-defined and rather stable bacterial communities composed of *Labrenzia*, *Mycoplasma*, *Rickettsia*, Rhizobiaceae, Phyllobacteriaceae,

Bacteroidetes and Flavobacteriaceae. These mixed communities of generalists and specialists are differently influenced by host phylogenetic relationships, geographic and environmental factors. The presence of Flavobacteriaceae is strictly determined by host phylogeny, indicating an obligate symbiotic association and vertical transmission of these bacteria. Comparative phylogenetic analyses of symbiont and host indicate a complex pattern of coevolution that is obscured by factors such as host-switching and incomplete sorting of symbionts within host lineages.

T16. DISPERSAL ASSEMBLY OF BENTHIC MICROALGAL COMMUNITIES: EFFECTS OF TIDAL RESUSPENSION

Plante, C. J., College of Charleston, USA, plantec@cofc.edu
Fleer, V., Northwest Missouri St. Univ., USA
Jones, M. L., College of Charleston, USA

Benthic microalgae (BMA) provide vital food resources for heterotrophs and stabilize sediments with their exopolymeric secretions. Our objectives were to assess the effects of sediment resuspension on microalgal community structure. We tested whether taxa-abundance distributions could be predicted using neutral community models (NCMs) and also specific hypotheses about passive migration: 1) As migration to sediment patches increases, variation in individual population sizes will decline, and 2) As migration increases, species diversity will increase. Three intertidal sites, differing in resuspension regime, were sampled throughout the tidal cycle. Dyed sediment plugs were used to measure erosion/accretion, and BMA biomass (chl *a*) was tracked. DGGE was utilized to investigate diatom community structure. Observed taxa-abundances fit those predicted from NCMs reasonably well (R2 of 0.68-0.88). In general, predictions about relationships between migration and species richness, diversity, and individual population variability were supported for local community dynamics. BMA at low tide (lowest migration) exhibited reduced diversity as compared to high tide times, whereas variability for individual taxa was higher. In between-site metacommunity comparisons, low- and high-resuspension sites exhibited distinct community composition but similar diversity.

T17. THE EPIPHYTIC MICROBIOTA OF THE GLOBALLY WIDESPREAD MACROALGA *CLADOPHORA* (CHLOROPHYTA, CLADOPHORALES)

Zulkifly, S. B., University Putra Malaysia, Malaysia, shahrizim@gmail.com
Hanshew, A., University of Wisconsin-Madison, USA, hanshew@wisc.edu
Young, E. B., University of Wisconsin-Milwaukee, USA, ebyoung@uwm.edu
Lee, P., University of Wisconsin-Milwaukee, USA, ebyoung@uwm.edu
Graham, M. E., University of Wisconsin-Madison, USA, mgraham3@wisc.edu
Graham, M. E., Hologic, Inc., USA, lankage@yahoo.com
Piotrowski, M. J., University of Wisconsin-Madison, USA, mpiotrowski@wisc.edu
Graham, L. E., University of Wisconsin-Madison, USA, lkgraham@wisc.edu

The herbivore- and pathogen-resistant, filamentous green algal genus *Cladophora* Kütz. occurs along rocky marine and freshwater shorelines worldwide, commonly dominating periphyton communities, and produces nuisance growths of societal concern under eutrophic conditions. We evaluated the microbiota of actively growing *C. glomerata* from hypereutrophic Lake Mendota, Dane, Co., WI, collected monthly during the 2011 growing season, by correlative SEM and fluorescence microscopy and Roche 454 pyrosequencing. Microscopy revealed several distinctive prokaryotic morphotypes. 11,670 16S rRNA gene amplicons (200-600 bp long) were evaluated using RDP classifier to identify epiphytic bacterial genera at the 80% level or species at the 96-97% level. We found evidence for about 100 distinct bacterial genera or species within 9 bacterial phyla representing diverse functional characteristics. We inferred that the normal epiphytic bacterial flora of Lake Mendota *C. glomerata* includes oxygenic and anoxygenic autotrophs, organisms that engage in diverse mineral redox reactions, many types of organic degraders including several cellulose-degraders, and predators. Some of the bacterial epiphytes are known to display

metabolic functions (vitamin B12 production, nitrogen fixation, or methanotrophy) that imply mutualistic interactions with the *Cladophora* host.

T18. PARMALES, AN INSIGHT INTO DIATOM ANCESTRY?

Kuwata, A., Tohoku National Fisheries Research Institute (FRA), Japan, akuwata@affrc.go.jp
Ichinomooiya, M., Prefectual Univ. of Kumamoto, Japan, ichinomiya@pu-kumamoto.ac.jp
Yoshikawa, S., Prefectural Univ. of Fukui, Japan, syoshika@fpu.ac.jp
Ohki, K., Prefectural Univ. of Fukui, Japan, kaoriohki@fpu.ac.jp
Kamiya, M., Prefectural Univ. of Fukui, Japan, mkamiya@fpu.ac.jp
Takaichi, S., Nippon Medical School, Japan, takaichi@nms.ac.jp
Kawachi, M., National Institute for Environmental Studies, Japan, kawach9i@nies.go.jp
Saitoh, K., National Research Insitute of Fisheries Science (FRA), Japan, ksaitoh@affrc.go.jp
Sato, N., Univ.of Tokyo, Japan, naokisat@bio.c.u-tokyo.ac.jp
Sawada, K., Hokkaido Univ., Japan, sawadak@mail.sci.hokudai.ac.jp

A small siliceous marine phytoplankton, *Parmales* (Heterokonta), was isolated for the first time with the aid of a fluorescent silicon trace, PDMPO from the coastal Oyashio region of Japan. Molecular phylogenetic analysis showed that *Parmales* is within the bolidophycean clade of naked flagellates and a sister group of silicified diatoms, the most successful microalgal group in modern oceans. This evolutionary relationship was supported by ultrastructure and pigment composition. Our results suggest a possible life cycle, similar to centric diatoms, that switches between a parmalean silicified, non-flagellated stage and a bolidophycean-type, naked flagellate stage. Further study of *Parmales* may help understand the origin of silica synthesis and the early evolution of diatoms. We present our ongoing study of the evolutionary close relationship between *Parmales*, Bolidophycea and diatoms using ecological, physiological, genomic and biogeochemical approaches.

T20. TRACKING CHANGES IN THE GREAT LAKES – NEW DIATOM-BASED TOOLS FOR RETROSPECTIVE ANALYSES

Reavie, E. D., University of Minnesota Duluth, USA, ereavie@nrri.umn.edu
Allinger, L. E., University of Minnesota Duluth, USA, lallinge@nrri.umn.edu
Kireta, A. R., University of Minnesota Duluth, USA, akireta@nrri.umn.edu
Chraïbi, V., University of Minnesota Duluth, USA, vlshaw86@hotmail.com

Monitoring data from the Great Lakes have revealed dramatic food web changes within the last decade. The diatoms are powerful indicators of environmental change, and retrospective data are needed to distinguish natural from human trends, and to reveal the causes and magnitudes of environmental insults that inform management matters regarding climate change, pollution and invasive species. Pelagic algae have been calibrated to water quality conditions and are shown to reflect water quality and human stressors. While these algal indicators will serve to track conditions via ongoing monitoring, they are especially suited to paleolimnology. Sediment cores contain diatom archives that can be used to reveal long-term impacts of natural drivers and anthropogenic stressors. Hence, historical diatom data from the lakes have been compiled into a chronological database of assemblages. A new multivariate tool integrating monitoring and paleoecological collections has been developed to put modern assemblages in a long-term context. It is anticipated that algal indicators and paleoecological applications will serve to address the myriad environmental issues that require long-term data in order to make critical remedial decisions.

T21. A COMPARISON OF UPA AND 16S: PERFORMANCE EVALUATION FOR PHYLOGENETIC RECONSTRUCTION AND DNA BARCODING OF CYANOBACTERIA

Sherwood, A. R., Botany, University of Hawaii, USA, asherwoo@hawaii.edu
Carlile, A. L., Botany, University of Hawaii, USA

Vaccarino, M., Botany, University of Hawaii, USA
Johansen, J., Botany, University of Hawaii, USA

During our biodiversity survey of Hawaiian freshwater algae we obtained UPA and 16S sequences for a number of non-marine cyanobacteria (emphasis on Nostocales and Pseudanabaenales), and constructed alignments for these markers of 52 Hawaiian accessions and 32 from GenBank. Given the ease with which UPA can be amplified and sequenced, we investigated whether this marker could delimit cyanobacterial species as effectively as 16S, and evaluated the phylogenetic performance of the markers based on both individual and concatenated alignments. Analyses of the individual markers produced similar, but not identical tree topologies, with some unexpected relationships appearing in both trees. Concatenated analyses displayed increased nodal support and also yielded a tree that more accurately reflected current understanding of cyanobacterial phylogeny. Within-species divergences were lower for UPA (generally zero) than for 16S (p-distances 0-0.005). UPA and 16S assigned sequences to the same cluster in most, but not all cases. Thus, if 16S divergence is used to define cyanobacterial species (in spite of known issues) then UPA will not always function as an effective DNA barcode for this group.

T22. THE INDIAN RIVER LAGOON OBSERVATORY (IRLO): BIODIVERSITY AND ECOSYSTEM FUNCTION OF AN ESTUARY IN TRANSITION: PHYCOLOGY PROJECTS.
Hanisak, M.D. Harbor Branch Oceanographic Institute at Florida Atlantic University, Fort Pierce, Florida, USA.

The Indian River Lagoon (IRL) is a unique, highly diverse, shallow-water estuary of national significance stretching along 40% of Florida's east coast. The IRL's economic value to Florida is more than $3.7 billion per year. Urbanization, excessive freshwater releases, degradation of water quality, contaminant loading, loss of habitat, decline of fisheries, and emerging diseases in marine mammals are increasingly important issues in the IRL, as they are throughout the world's estuaries and coastal waters. The Indian River Lagoon Observatory (IRLO) is a long-term, multidisciplinary and ecosystem-based program, designed to address emerging issues of environmental health in the IRL system by achieving a better understanding of the biodiversity and ecological functions of the lagoon and how they are impacted by the surrounding human population. IRLO's goal is to acquire and disseminate new data and knowledge on components of the IRL critical to its ecological function and its sustainable management. Some of the IRLO research questions of interest to phycologists include: (1) How does temporal and spatial variability of water quality affect biodiversity and ecological function in the IRL? (2) Do chronic and/or acute exposures to cyanobacterial metabolites lead to ecosystem degradation and impact human/marine mammal health? (3) How do environmental changes affect critical seagrass habitats? (4) How are macroalgal blooms in the IRL related to anthropogenic nutrient sources? (5) What is the macroalgal community of Florida's northernmost coral reef? IRLO's researchers are actively working with federal and state agencies responsible for the IRL's management to integrate IRLO research with existing and future agency programs and seek collaborations with other researchers who are interested in these and other important research questions.

T23. NUTRIENT BIOEXTRACTION BY *SACCHARINA LATISSIMA* AND *GRACILARIA TIKVAHIAE* IN LONG ISLAND SOUND AND THE BRONX RIVER ESTUARY
Kim, J. K., Department of Marine Sciences, University of Connecticut, USA, jakejuly@hotmail.com
Yarish, C., Department of Ecology & Evolutionary Biology, University of Connecticut, USA, charles.yarish@uconn.edu

The objective of this study is to design, demonstrate, and promote the bioextraction of inorganic nutrients from urban coastal waters using native seaweeds (*Gracilaria tikvahiae* & *Saccharina latissima*). *Gracilaria* was cultivated and harvested at two near-shore research sites in Long Island Sound (LIS; Fairfield, CT) and the Bronx River estuary (BRE; Bronx, NY) during the summer and fall, 2011. The

growth rates and nitrogen (N) removal at the BRE site in August were as high as 11.8% and 343 g N ha-1 d-1, respectively. During the same period, the growth rates and N removal at the LIS site were as high as 6.0% d-1 and 50 g N ha-1 d-1, respectively. These results suggest that N was being rapidly assimilated and used to fuel the growth of new *Gracilaria* tissue grown at the BRE site. *Saccharina* is currently being farmed at the LIS during the winter of 2012. After outplanting juvenile kelp (<1mm) in December, the aquacultured sugar kelp grew as much as 2.5m in length after 4 months with a tissue nitrogen content as high as 5%.

T24. EPIPHYTIC BIODIVERSITY REFLECTING SEASONAL FLUCTUATIONS AND NUTRIENT MANIPULATIONS FROM *SPARTINA ALTERNIFLORA* WITHIN THE GTMNERR

Verhulst, S.A., Department of Biological Sciences, University of North Florida

Stocks, H.S., Department of Biological Sciences, University of North Florida
Casamatta, D.A., Department of Biological Sciences, University of North Florida

Saltmarsh estuaries are known to have high levels of primary productivity associated with vascular plants, epiphytes, plankton, and benthic algae. As anthropogenic impacts continue to escalate, nutrient additions may affect algal communities in coastal habitats. In order to assess the impacts of eutrophication on saltmarsh epiphytic algal biodiversity, clay pots containing four separate nutrient treatments (0.5M nitrogen, 0.5M phosphorus, 0.5M N+P, and control) were placed at the base of *S. alterniflora* stands in a coastal estuary located within the Guana Tolomato Matanzas National Estuarine Research Reserve in Ponte Vedra Beach, Florida. Cell counts, biovolume estimates, chlorophyll *a*, and ash-free dry mass were assessed on a monthly basis. Samples collected from April through October, 2011 were primarily composed of cyanobacteria and diatoms in terms of cell counts and total biovolume. The majority of cyanobacteria identified belonged to the form genus *"Leptolyngbya"*, a polyphyletic genus traditionally found in freshwater habitats. Four unique morphovars were most commonly identified, none of which fit into any currently circumscribed taxa. The dominance of these putatively new taxa decreased after July, at which time *Microcoleus* spp. became increasingly abundant. In the end, the epiphytic biodiversity may be a useful tool in assessing changes in water quality and provide insights into previously undescribed biodiversity.

T25. CHARACTERIZATION OF OFFSHORE RHODOLITH BEDS IN THE NW GULF OF MEXICO: TRIALS AND TRIBULATIONS SINCE THE BP DEEPWATER HORIZON OIL SPILL DISASTER

Fredericq, S., University of Louisiana at Lafayette, USA, slf9209@louisiana.edu
Schmidt, W. E., University of Louisiana at Lafayette, USA, weschmidt01@yahoo.com
Gabriel, D., Universidade dos Açores, Portugal, danielalgabriel@gmail.com
Sauvage, T., University of Louisiana at Lafayette, USA, tom.sauv@gamila.com
Norris, J. N., Smithsonian Institution, USA, NORRISJ@si.edu
Krayesky, D., Slippery Rock University, USA, david.krayesky@sru.edu

Rhodoliths are free-living marine algal nodules composed mostly of crustose corallines precipitating calcium carbonate. In the NW Gulf of Mexico rhodoliths and unconsolidated rubble are associated with unique offshore deep bank habitats, the salt domes or diapirs, and they are dominated by crust-forming Peyssonneliaceae and Rhizophyllidaceae (Rhodophyta) at depths of 45-80 m. So far for the region we have characterized 34 rhodolith species of the former and 6 spp. of the latter. These rubble habitats are prominent features harboring the highest known seaweed diversity in the NW Gulf prior to the April 2010 BP oil spill. Results from post-spill expeditions indicate that seaweed diversity in all dredged sites was severely depressed or altogether absent relative to pre-spill sampling. "Bare" or partly algal-denuded unconsolidated rubble brought back from post-spill cruises as "live rocks" have been maintained in 20-

gallon tanks and gradually became covered by a suite of red, green and brown seaweed germlings that to this day continue to grow to adult size revealing biodiversity repressed in the NW Gulf at the time of the post-spill sampling. Many of these species currently growing and reproducing in our tanks had not been observed in the field during our pre-spill samplings. Testing for algal spore presence in the seawater used to partly fill the tanks based on a PCR approach tested negative, providing evidence that the intrinsic source of the propagules is the "bare" rubble retrieved. The rate of algal succession is being documented by digital photography and their taxonomic identity is confirmed by ongoing molecular barcoding and morphological evidence. The implications of these exciting results indicating that undetected algal propagules, spores and endolithic filaments collected along with the "bare" rocky substrata have been triggered to germinate, grow, and reproduce under laboratory conditions that exclude herbivores, are far-reaching.

T26. NEW INSIGHTS IN THE DIVERSITY OF DELESSERIACEAE (CERAMIALES) FROM OFFSHORE LOUISIANA AND CARIBBEAN PANAMA

Richards, J., University of Louisiana at Lafayette, USA, jlr0420@louisiana.edu
Fredericq, S., University of Louisiana at Lafayette, USA, slf9209@louisiana.edu

The Delesseriaceae (Ceramiales, Rhodophyta) is a family of marine red algae consisting of almost 100 genera and over 400 species. It was established by Kylin in 1924 and originally included 11 groups of taxa within two subfamilies, the Delesserioideae and Nitophylloideae. Lin et al. (2001) amended the family to recognize three subfamilies, the Delesserioideae, Nitophylloideae, and Phycodryoideae. Although species diversity is well documented and described from many parts of the world, phylogenetic relationships remain unresolved. Morphological analysis and comparative gene sequencing (rbcL, LSU, COX, and UPA) conducted on specimens dredged from 45-90 meters depth offshore Louisiana in the northwestern Gulf of Mexico and collected by SCUBA diving in Caribbean Panama apparently reveal new species within the three subfamilies, *Grinnellia* sp. (Delesserioideae), *Augophyllum* sp. and *Nitophyllum* sp. (Nitophylloideae), and *Anisocladella* sp. and *Haraldiophyllum* sp. (Phycodryoideae).

T27. STUDIES ON THE PRASIOLALES (TREBOUXIOPHYCEAE, CHLOROPHYTA) FROM THE SOUTHERN HEMISPHERE REVEAL MAJOR TAXONOMIC AND BIOGEOGRAPHIC SURPRISES

Moniz, M. J., National University of Ireland, Galway, Ireland, monica.j.moniz@gmail.com
Rindi, F., Università Politecnica delle Marche, Italy, f.rindi@univpm.it
Guiry, M. D., National University of Ireland, Galway, Ireland, michael.guiry@nuigalway.ie

Molecular data produced in the last decades have shed light on the genetic diversity and biogeography of the order Prasiolales in the northern hemisphere, but limited information was so far available for the southern hemisphere. We studied collections of Prasiolales from Tasmania and Antarctica using culture observations and molecular data (rbcL and psaB sequences). The taxonomy of marine Prasiolales from Tasmania is reassessed: the presence of *Rosenvingiella constricta* (for specimens previously identified as *R. polyrhiza*) and *Prasiola borealis* (previously identified as *P. crispa*) is demonstrated, and the new species *R. tasmanica* is described. These results show an unexpected genetic similarity between the Prasiolales of Tasmania and those of Pacific North America, two regions that have never been in geographic proximity. *Prasiola crispa* from Antarctica, the most common terrestrial alga in this continent, represents a complex of three different cryptic species, identified as *P. crispa*, *P. antarctica* and *P. glacialis sp. nov*. The diversity and biogeography of the Prasiolales are fascinating topics still holding major surprises, and little-explored regions of the southern hemisphere may still host unknown taxa.

T28. NEW PERSPECTIVES ON THE DEVELOPMENTAL MORPHOLOGY, MOLECULAR SYSTEMATICS AND BIOGEOGRAPHY OF THE SARCODIACEAE (RHODOPHYTA)

Rodriguez-Prieto, C., University of Girona, Faculty of Sciences, Campus de Montiliva Spain, conxi.rodriguez@udg.edu
Lin, S. M., Institute of Marine Biology, National Taiwan Ocean University, Taiwan ROC, linsm@ntou.edu.tw
Hommersand, M. H., Department of Biology, University of North Carolina, USA, hommersand@bio.unc.edu

Kylin (1956, Die Gattungen der Rhodophyceen) placed three genera in his family Sarcodiaceae that are still recognized: *Chondrymenia* Zanardini 1861, *Trematocarpus* Kützing 1843 and *Sarcodia* J. Agardh 1852. We found that the carpogonial branch first develops inwardly and the gonimoblasts are thrust outwardly within an elaborate placenta in *Chondrymenia*, a genus that is unrelated to the Sarcodiaceae. In contrast, carpogonial branches and gonimoblasts develop outwardly in *Trematocarpus* and *Sarcodia*, and the gonimoblast filaments fuse and link laterally to produce a gonimoblast reticulum that forms carposporangia in distal chains and connects basally to the gametophyte to form a placenta. At present, *Chondrymeni*a is endemic to the Adriatic and Mediterranean Sea, but may have a worldwide distribution in warm waters. *Trematocarpus* appears to have originated on the Pacific side of Gondwanaland and is presently found in cold to cool temperate waters, mainly in the Southern Hemisphere. *Sarcodia* seems to have originated in tropical waters in the Indo-West Pacific Ocean and is distributed throughout the Indian Ocean and adjacent regions to the north and south. The systematic and biogeographical conclusions presented here will be supported by morphological evidence using haematoxylin stained material and molecular data drawn from rbcL sequence analyses.

T29. TRENTEPOHLIALES (ULVOPHYCEAE, CHLOROPHYTA) FROM COASTAL SOUTH CAROLINA

Green, M. S., Department of Biology, Tennessee Technological University USA, mark.green@hgtc.edu
Ball, B., Department of Biology, Duke University, USA, Bernie.Ball@Duke.edu
Lutzoni, F., Department of Biology, Duke University, USA, flutzoni@duke.edu
Zi-Min, H., Department of Biological Sciences, The University of Alabama, USA, hzimin@as.ua.edu
López-Bautista, J. M., Biological Sciences, The University of Alabama, USA, jlopez@ua.edu

The Trentepohliales is an order of algae that occurs in subaerial form and in symbiosis with lichen-fungi commonly found in warm humid climates. Most ecological research has occurred outside the continental United States with emphasis on free-living subaerial epiphytes. This research project investigated the diversity and ecology of subaerial and lichenized Trentepohliales from coastal forests of South Carolina. Species identifications are based on microscopic observations, cultures and molecular sequencing of the chloroplast-encoded large subunit of ribulose-1,5-bisphoshate/oxygenase (rbcL) genes. Several different species of free-living Trentepohlia, Printzina, Phycopeltis and Cephaleuros were documented. Phycobiont diversity was explored for Pyrenula, Trypethelium, Graphis, Phaeographis, Graphina, Opegrapha, Strigula and Cryptothecia. The use of rbcL primers to amplify genetic sequences of the plastid gene has continued to aid in the phylogenetic analysis of this algal group. Only recently have researchers begun to move toward revealing the rich phylogeny of this elusive group. In agreement with previous research, the results of this study indicated that taxonomic schemes produced from morphological characters previously used for classification are not congruent with phylogenetic trees inferred from gene sequence information.

T30. GENETIC STRUCTURE AND PHYLOGEOGRAPHY OF *PTEROCLADIELLA CAPILLACEA* (GELIDIACEAE, RHODOPHYTA) BASED ON PLASTID RBCL AND MITOCHONDRIAL COX1 AND COB

Boo, G. H., Chungnam National University, Daejeon, Republic Of Korea, gahunboo@gmail.com
Jang, H. J., Chungnam National University, Republic Of Korea
Freshwater, D. W., Center for Marine Science, USA

Fujii, M. T., Institute of Botany, Brazil
Nelson, W. A., National Institute of Water and Atmospheric Research, New Zealand
Lee, K. M., Chungnam National University, Republic Of Korea
Boo, S. M., Chungnam National University, Republic Of Korea, smboo@cnu.ac.kr

Pterocladiella capillacea, one of the sources for agar production in East Asia, is suitable for studying phylogeography of marine organisms since it commonly occurs in temperate to tropical waters around the planet. In order to understand its current distribution pattern, more than 340 specimens from Korea, Japan, Brazil, France, Italy, Mexico, New Zealand, Spain, and USA were analyzed using three molecular markers: plastid rbcL for identifying the species, and mitochondrial cox1 and cob for phylogeography. The rbcL analysis resolved all *P. capillacea* samples within a single monophyletic clade. Analyses of mitochondrial cox1 and cob sequence data revealed six subclades within *P. capillacea*: group I from Korea and Japan; II from USA (California) and Mexico; III from New Zealand and Korea; IV from France, Italy and Spain; V from Brazil, and VI from USA (Hawai'i). Forty seven cox1 haplotypes were detected among the samples. Haplotype and nucleotide diversities were compared between clades. Despite geographical structure of most populations, the finding of clade III suggests a genetic connectivity *P. capillacea* between Korea and New Zealand.

T31. ASSESSMENT OF CRYPTIC *RHODYMENIA* SPP. (RHODYMENIACEAE, RHODOPHYTA) IN BRITISH COLUMBIA, CANADA: AN INTEGRATIVE TAXONOMIC APPROACH

Filloramo, G. V., Centere for Envrionmental & Molecular Algal Research, Dept. of Biology, University of New Brunswick, Canada, gina.filloramo@gmail.com
Saunders, G. W., Centere for Environmental & Molecular Algal Research, Dept. of Biology, University of New Brunswick, Canada, gws@unb.ca

Combined with morphological assessments, DNA barcoding has revolutionized our ability to delimit red algal species. A recent survey in British Columbia, Canada used the DNA barcode to reveal new and previously overlooked species within the genus Rhodymenia . Although two species of Rhodymenia were recognized in British Columbia (*R. pacifica* and *R. californica*), our molecular data resolved four distinct species groups. Analysis of vegetative and reproductive features confirmed the presence of *R. pacifica* and *R. californica*. Some samples field identified as *R. pacifica*, resolved as a separate genetic species and were determined to be *R. rhizoides*, which consequently resurrected this species. Additionally, some samples field identified as *R. californica* were found to be genetically distinct. To accommodate these samples we investigated synonyms of *R. californica* as well as *Rhodymenia* species from the west coast of North America, Japan and Russia. Among those species we could not find a good match to our collections and we thus propose *R. bamfieldiensis* sp. nov. for this group. In recognizing these four species we have doubled the number of species for this genus in British Columbia.

T32. MOLECULAR DIVERSITY OF MAËRL-FORMING CORALLINES (CORALLINALES, RHODOPHYTA)

Hernandez-Kantun, J. J., National University of Ireland, Galway, Ireland, j.hernandez2@nuigalway.ie
Rindi, F., Università Politecnica delle Marche, Italy, f.rindi@univpm.it
Riosmena-Rodriguez, R., Universidad Autonoma de Baja California Sur, Mexico, riosmena@uabcs.mx
Maggs, C. A., Queen's University, United Kingdom, c.maggs@qub.ac.uk
Hall-Spencer, J. M., University of Plymouth, United Kingdom, jason.hall-spencer@plymouth.ac.uk
Peña, V., Museum National d'Histoire Naturelle, France, vpena@udc.es

Maërl-forming corallines are calcareous red algae with unattached thallus. Despite their ecological and economic importance, to date there are few molecular data concerning these algae, and the present knowledge of their taxonomy and biogeography is mostly based on morphological information. The

molecular diversity of maërl-forming species was investigated using SSU, *psb*A, *rbc*L, *cox*1, *cox*2-3 and ITS sequences. The phylogenies recovered showed that these organisms belong to several separate clades, in which they co-occur with crustose corallines of the genera *Lithophyllum*, *Hydrolithon*, *Phymatolithon*, *Lithothamnion* and *Mesophyllum*; four maërl-forming species of *Neogoniolithon* form a monophyletic group. A large number of cryptic species was observed in *Lithophyllum* for Europe (in the morphospecies *Lithophyllum incrustans* and *L. dentatum*) and Gulf of California (*L. margaritae*). Some species that were previously believed to exist only as encrusting forms (*Lithophyllum incrustans* and *Phymatolithon purpureum*) are shown to occur also as maërl. Our results suggest that the diversity of maerl-forming species has been considerably underestimated and additional studies are required to clarify the evolutionary history and phylogeography of this group.

T33. CRYPTIC DIVERSITY WITHIN THE AUSTRALIAN HALYMENIACEAE (HALYMENIALES, RHODOPHYTA)

Kraft, L. G., University of New Brunswick, Canada, lesleigh.kraft@unb.ca
Saunders, G. W., University of New Brunswick, Canada, gws@unb.ca

The Halymeniaceae is a family of red algae that are unique in their possession of auxiliary cell ampullae. Globally the family encompasses roughly 270 species; in Australia, with its extremely rich algal flora, records exist for 13 genera and 27 species – 22 with Australian type localities. Like almost all red algae, members of the Halymeniaceae have simple morphologies and are subject to high degrees of morphological plasticity and convergent evolution. In addition, Australia has long suffered from a Eurocentric bias with regards to marine macroalgal identification. As a result, traditional taxonomic approaches can be ineffective at resolving relationships among taxa and species richness can be under appreciated, with both novel and cryptic species overlooked. The DNA barcode (mitochondrial COI-5P) has demonstrated utility at identifying species diversity among red algae. Preliminary screening of Australian Halymeniaceae with COI-5P sequence data has revealed a two-fold increase in species richness compared to current morphological lists. These species are now being subjected to detailed alpha taxonomic and molecular phylogenetic studies. These combined approaches will identify novel/cryptic/overlooked Halymeniaceae in Australia, describe them in all of their anatomical detail, and include them in a wider halymeniacean classification.

T34. A COMPARISON OF THE CHLOROPLAST GENOME AMONG *EUGLENA HIEMALIS*, *EUGLENA GRACILIS* AND *EUGLENA LONGA* (EUGLENOPHYTA)

Wang, J., Central Michigan University, USA, wang3j@cmich.edu
Linton, E. W., Central Michigan University, USA, eric.linton@cmich.edu

Currently, there are three published euglenoid chloroplast genomes: those of Euglena gracilis, Eutreptia viridis, and the colorless *Euglena (Astasia) longa*, which has secondarily lost the ability to photosynthesize. These studies have shown that there is a great diversity in the size of euglenoid chloroplast genomes and in the arrangement of gene clusters. In an effort to address genomic variability within the single genus *Euglena*, we have sequenced the chloroplast genome of the photosynthetic *Euglena hiemalis* and compared this to the *E. gracilis* chloroplast genome in order to explore intrageneric chloroplast evolution. Our results show that the chloroplast genome of *E. hiemalis* closely resembles that of *E. gracilis*, with only minor differences. The chloroplast genome of *E. hiemalis* has two gene clusters that are reversed in strand orientation with one also being reversed in gene order, with nearly identical number and arrangement of introns. It is clear from the chloroplast genome sequence that *E. hiemalis* and *E. gracilis* are very closely related, and that the majority of chloroplast evolution probably occurred before the divergence of the genus *Euglena*.

T35. NEW ADVANCES OF THE GREEN ALGAL TREE OF LIFE (GRATOL): CHLOROPLAST-ENCODED RBCL MARKER FROM THE ORDER CLADOPHORALES

Hu, Z. M., University of Alabama, USA, hzimin@bama.ua.edu
Lopez-Bautista, J., the University of Alabama, USA

GrAToL is a collaborative project using multi-genomic sequences to explore the speciation processes and evolutionary relationships of the major green algal groups. Among the various gene markers screened for phylogenetic reconstruction, the chloroplast rbcL marker is a widely used and extensively tested candidate marker for green algae. However, there are a very few number of rbcL sequences available for the order Cladophorales, in part probably due to the presence of introns, which restricts the understanding of the molecular phylogeny and diversification in Ulvophyceae. Here, we developed several methods based on general or nested PCR and obtained for the first time rbcL sequences of a variety of representatives from the order Cladophorales. Specifically the nested-PCR scheme has been showing promising amplification for several members in the Ulvophyceae (37 out of 40 taxa). Phylogenetic analyses (MP, ML and BI) using the newly obtained rbcL sequences consistently recovered the Ulvophyceae as monophyletic, and most ulvophycean orders can be grouped into two phylo-clades, the TBCD clade (Trentepohliales, Bryopsidales, Cladophorales and Dasycladales) and the UU clade (Ulotrichales and Ulvales).

T36. MARINE PRASIOLALES FROM NEW ZEALAND AND THE NEW ZEALAND SUBANTARCTIC

Sutherland, J. E., University of Auckland New Zealand, j.sutherland@auckland.ac.nz
Nelson, W. A., National Institute for Water & Atmospheric Research, New Zealand, Wendy.Nelson@niwa.cri.nz
Heesch, S., Irish Seaweed Research Group, Ryan Institute, Ireland, Svenja.Heesch@gmx.de

Green algae from the order Prasiolales (Trebouxiophyceae, Chlorophyta) are found worldwide in marine, freshwater and terrestrial habitats. Marine taxa are typically found in the high intertidal zone, often associated with guano deposits, and terrestrial taxa are found in habitats such as on bark, soil and urban walls (as well as growing on sloths!). Recently three papers have published descriptions of new taxa from New Zealand, Tasmania and Antarctica. Here we integrate data from these three studies and additional sequences of New Zealand material to summarise information regarding *Prasiola* and *Rosenvingiella*, the two species of Prasiolales present in New Zealand and the New Zealand subantarctic region. Our studies, limited to habitats close to the sea (eulittoral to supralittoral), show the presence of at least four species of *Prasiola*, and two species of *Rosenvingiella*, one of which is apparently also present in Tasmania.

T38. DIVERSITY OF THE GENUS *HYPNEA* (GIGARTINALES, RHODOPHYTA) ON THE SOUTHEASTERN COAST OF BRAZIL

Guimaraes, N. R., University of Sao Paulo Brazil, nati_guimaraes@yahoo.com.br
Oliveira, M. C., University of Sao Paulo, Brazil, mcdolive@usp.br
Oliveira, E. C., University of Sao Paulo, Brazil, euricodo@usp.br
Yokoya, N. S., Instituto de Botânica, Brazil, nyokoya@hotmail.com

The genus *Hypnea* Lamouroux (1813) has a wide geographical distribution on the tropical and subtropical coasts around the world. However, the relatively simple morphology, often influenced by the conditions of its habitat, complicates taxonomy. In this study, the DNA barcode *cox*1 was sequenced for 55 samples from the southeastern coast of Brazil, indicating the occurrence of six different taxonomic entities. Additionally, the UPA and *rbc*L markers were sequenced for representatives of each of those groups confirming the existence of six different taxa. These taxonomic entities were named as follows: *H. cervicornis*; *H. flexicaulis*, cited for the first time to the Atlantic Ocean; *H. musciformis*; *H. spinella*; *Hypnea* sp. 1 and *Hypnea* sp. 2. *Hypnea cervicornis*, often considered as a later synonym of *H. spinella*, should be considered as a distinct species based on morphology and divergence of the three molecular

markers used. *Hypnea nigrescens*, quoted earlier for the State of São Paulo, is a morphological variation of H. musciformis. Our data also indicate the existence of a *H. musciformis* species complex.

T39. ESTIMATING DIVERGENCE TIMES OF THE RED ALGAL FAMILY PEYSSONNELIACEAE (PEYSSONNELIALES, RHODOPHYTA) WITH A MOLECULAR CLOCK

Schmidt, W. E., University of Louisiana at Lafayette, USA, weschmidt01@yahoo.com
Sauvage, T., University of Louisiana at Lafayette, USA, tomsauv@gmail.com
Gabriel, D., Universidade dos Açores, Portugal, Danielalgabriel@gmail.com
Krayesky, D., Slippery Rock University, USA, david.krayesky@sru.edu
Fredericq, S., University of Louisiana at Lafayette, USA, slf9209@louisiana.edu

Members of the crust-forming red algal family Peyssonneliaceae are widely distributed in marine waters around the world. Our exceptional database of chloroplast-encoding rbcL sequences (and augmented by UPA, TufA, cox1, and LSU sequences) of Peysonneliaceae species worldwide, including taxa from both sides of the Isthmus of Panama and the Suez Canal, will enable us to generate a time-calibrated phylogeny of the family and establish a time frame of generic and species diversification. Of particular interest is testing the hypothesis of potential Lessepsian introductions through the Suez Canal on the basis of newly collected samples from the Red Sea and the Mediterranean Sea. We will also assess the evolution of trans-isthmian species pairs associated with the closure of the Tropical American Seaway. Divergence rates will be estimated using a maximum likelihood (RAxML + r8s) and a Bayesian (BEAST) approach, and published fossil calibrations.

T40. LIPID METABOLISM AND TRAFFICKING IN TWO RED ALGAE SPECIES FROM THE GENUS *PORPHYRA*

Zaeuner, S., Michigan State, University, BMB Department, USA, zaeuner@uni-bonn.de
Benning, C., Michigan State University, BMB Department, USA, benning@msu.edu

The genomes and transcriptomes of *Porphyra* species are currently being sequenced by the Porphyra NSF RCN. Here we reconstruct the putative lipid biosynthesis pathway. De novo fatty acid synthesis involves two enzyme complexes: Acetyl-CoA carboxylase and fatty acid synthase. Surprisingly, the acetyl-CoA carboxylase subunits are encoded in the plastid genome of Porphyra. Another interesting finding was the lack of a candidate gene for the acyl-ACP-thiolase, which seems necessary to release fatty acids for export from the plastid. Membrane lipids in Porphyra are predominantly composed of long chain polyunsaturated fatty acids. Since red algae lack a plastid desaturation pathway these fatty acids have to be ER derived, suggesting an important role for ER to chloroplast lipid trafficking. Orthologs were identified for the ABC-type transport complex from Arabidopsis composed of TGD1, 2, and 3. Interestingly, TGD1 and 2 were found in the plastid genome, while the gene for TGD3 was nuclear encoded. The positional distribution of fatty acids in red algae differs from other organisms. This may be due to a direct acyl-group exchange between ER and plastid lipids.

T41. PHOTOSYNTHETIC EFFICIENCY AND REGULATION OF EARLY LIGHT INDUCIBLE PROTEIN (ELIP) BY THE INFLUX OF CO2 IN *SPIROGYRA VARIANS*

Han, J. W., Department of Biology, Kongju National University, Republic Of Korea, fop9440@kongju.ac.kr
Kim, G. H., Department of Biology, Kongju National University, Republic Of Korea, ghkim@kongju.ac.kr

Spirogyra varians (Hass.) Kuetzing is a freshwater green alga that can survive at low-temperature (4°C). A cold-stress responsive protein was isolated from *S. varians* by comparing the protein profiles of the plants grown at two different temperatures, 4°C and 20°C. The isolated protein (SVCR1) showed

similarity to Early Light Inducible Proteins (ELIPs) of higher plants. The expression of SVCR1 responded much more sensitively to the cold stress. At the temperature over 10°C, SVCR1 was rarely expressed until the light intensity reached 1,200 µmol photon m-2s-1. At low-temperature (4°C), however, it was highly up-regulated even in the dark condition. The influx of 5% CO2 to the algal culture media suppressed the expression of SVCR1. The transcripts of SVCR1 began to disappear as soon as CO2 gas was introduced to plants grown in the cold condition (4°C). Effective quantum yield and maximum quantum yield were affected by SVCR1 expression level. Photosynthetic efficiency was rapidly decreased from 0.75 (20°C) to 0.4 (4°C) as soon as SVCR1 was expressed. On the other hand, CO2 influx recovered photosynthetic efficiency and also the expression of SVCR1 decreased.

T42. EXPLORATION OF THE ROLE OF 3' UTRS IN REGULATING MRNA STABILITY IN THE MARINE DIATOM *THALASSIOSIRA PSEUDONANA*

Scott, D. W., Clark University, USA, dscott@clarku.edu
Robertson, D. L., Clark University, USA, debrobertson@clarku.edu

Nitrate reductase (NR) catalyzes the reduction of nitrate to ammonium, and is considered the rate-limiting step nitrate assimilation. In marine diatoms, NR expression is highly regulated. Previous studies of *Thalassiosira pseudonana* have shown that *nia* mRNA, which encodes NR, accumulates in the absence of nitrogen, is translated in the presence of nitrate, and is degraded in the presence of ammonium. Furthermore, in the presence of ammonium and actinomycinD, *nia* transcripts were lower than in cells receiving actinomycinD alone. In contrast, there was no significant difference in the abundance of actin mRNA in the two treatments, suggesting *nia* mRNAs are targeted for degradation in the presence of ammonium. Regulatory sequences that influence mRNA stability are often observed in 3'UTRs of mRNA and thus, we tested the hypothesis that sequences in the 3'UTR of *T. pseudonana nia* mRNA are important in regulating mRNA stability in response to nitrogen availability. pTpNR and the pTpFCP/NAT plasmids were obtained from N. Poulsen(Dresden University). In pTpNR, the reporter gene, *egfp*, is flanked by ca. 1kb of DNA upstream of the *nia* start codon and 0.5kb of DNA downstream stop codon (*nia-egfp-nia*). We replaced the 3'*nia* sequence with 0.5kb of DNA downstream of the actin stop codon (*nia-egfp-actin*). Plasmids were co-transformed with the pTpFCP/NAT, which confers antibiotic resistance. Transformed clones were grown in f/2-supplemented seawater to mid-log phase before the addition of ammonium. If sequences in the *nia* 3'UTR regulate mRNA stability in response to ammonium, we predict that *egfp* mRNA abundance in *nia-egfp-nia* transformed cells will decrease in response to ammonium while *egfp* mRNA levels in *nia-egfp-actin* transformed cells will not. *efgp* transcript levels are currently being quantified and results from these experiments will be presented.

T43. BIOSYNTHETIC LABELING OF DINOFLAGELLATE RNA FOR THE MEASUREMENT OF RNA SYNTHESIS AND DECAY RATES USING DNA MICROARRAYS AND QPCR

Morey, J. S., Marine Biotoxins Program, NOAA Center for Coastal Environment Health and Biomolecular Research, USA, jeanine.morey@noaa.gov
Van Dolah, F. M., Marine Biotoxins Program, NOAA Center for Coastal Environmental Health and Biomolecular Research, USA, fran.vandolah@noaa.gov

Dinoflagellates possess many unique molecular traits supporting the hypothesis that genes are regulated post-transcriptionally. Nonetheless, microarrays reported rapid increases in a subset of transcripts following N or P addition to nutrient starved *Karenia brevis* (Morey et al 2011). It is unknown if these increases are due to de novo transcription or differential message stability. To address this, we have optimized methods to fractionate pre-existing and newly transcribed RNA in *K. brevis* for analysis of synthesis and decay rates by microarray and qPCR. Log-phase cultures were incubated with 0.2 mM 4-thiouracil or 4-thiouridine for 1 to 20 h and total RNA isolated. Following thiol-specific biotinylation and streptavidin-HRP detection on northern or slot blots, we determined that *K. brevis* is capable of incorporating 4-thiouracil, but not 4-thiouridine, in as little as 1h. Newly synthesized RNA was

efficiently isolated using streptavidin magnetic beads. Analysis of this fraction by microarray will help resolve the extent of transcriptional regulation in *K. brevis*. The ability of *K. brevis* to incorporate 4-thiouracil indicates the presence of uracil phosphoribosyl transferase, not identified in EST data available to date.

T44. SRNAS OF *CYANOPHORA PARADOXA* AND *CHLAMYDOMONAS REINHARDTII*, A SYSTEM GENOMICS APPROACH TO UNDERSTAND ALGAL EVOLUTION

Gross, J., Rutgers University, USA, jeferson.gross@googlemail.com
Wajid, S., Rutgers University, USA, swajid@eden.rutgers.edu
Price, D., Rutgers University, USA, dana.price@gmail.com
Chan, C. X., The University of Queensland, Australia, chancx@gmail.com
Bhattacharya, D., Rutgers University, USA, Bhattacharya@AESOP.Rutgers.edu

Small RNAs (sRNA) have emerged in the past years as key regulators of many aspects of the molecular biology of the cell, including the control of mRNAs stability, rates of protein synthesis, DNA methylation, and even histone modifications. We developed a genomic platform based on the Illumina sequencing technology and high throughput computational analysis to study the interplay between sRNA pools, mRNA turnover, and their impact on genome/epigenome evolution of algae. Through our approach we describe for the first time the presence of a complex sRNA system in the glaucophyte alga *Cyanophora paradoxa*. Tools established for this alga are now being applied to monitor the long term evolution of *Chlamydomonas* populations propagating in our lab for over one year under continuous light condition and presence of 200mM salt. Preliminary results are revealing the network of gene expression in *Chlamydomonas* in response to detrimental salt stress.

T45. HIGH SEQUENCE VARIABILITY AND DIVERSE SUBCELLULAR LOCALIZATIONS, AND ECOLOGICAL IMPLICATIONS OF ALKALINE PHOSPHATASE IN DINOFLAGELLATES AND OTHER ALGAE

Lin, X., Xiamen University, China, xinlin@xmu.edu.cn
Zhang, H., University of Connecticut, USA, huan.zhang@uconn.edu
Cui, Y., Xiamen University, China, coffee16th@126.com
Lin, S., Xiamen University, China, senjie.lin@xmu.edu.cn

We isolated a full-length AP cDNA from "*Alexandrium catenella*", and compared them with homologs from the more basal *Amphidinium carterae* and the later-diverging *Karenia brevis* as well as other eukaryotic algae. New data and literature showed that AP is common in dinoflagellates and most other eukaryotic algae. AP sequence is highly variable in dinoflagellates and other eukaryotic algae. APs in dinoflagellates and most other eukaryotic algae seem to belong to the phoA type. Phylogenetic analyses based on AP amino acid sequences indicated that the "red-type" eukaryotic lineages formed a monophyletic group, suggesting a common origin of their APs. Computational models were adopted to predict the subcellular localizations of AP in the three dinoflagellates and other eukaryotic phytoplankton. Results showed different subcellular localizations of APs in different dinoflagellates and other lineages. Within the three dinoflagellates, the predicted subcellular localizations are consistent to the varied localizations of the AP activity detected by enzymatic label fluorescence. Although ultimate verification requires more rigorous investigation, this study provides an initial insight about the potential ecological significance of AP sequence divergence through differential subcellular localization.

T46. INFLUENCE OF CHLORINE ION CONCENTRATIONS AND DIFFERENT MEDIA FOR *RHODOMONAS SALINA* GROWTH AND LIPID CHARACTERIZATION

Wishkerman, A., IRTA-SCR, Spain, Asher.Wishkerman@irta.cat
Estevez, A., IRTA-SCR, Spain
Mimendia, A., IRTA-SCR, Spain

Ibáñez, C., IRTA-SCR, Spain
Trobajo, R., IRTA-SCR, Spain

Microalgal species have potential for use in aquaculture, biodiesel production, pharmaceuticals and animal feed. For biodiesel production, high biomass, lipid productivity and the ability to tolerate and grow in extreme environments are desirable characteristics. In this study, growth and lipid characterization of *R. salina* after cultivation in three media (ESAW, Walne's and F/2), and different chlorine concentrations (11-40 g/L) in ESAW medium, were studied during a 7 day growth period. Although no changes were found in *R. salina* cellular growth using the three media, increased growth (30%) was shown with low chlorine ESAW medium (11 g/L), and minimal growth occurred at the highest chlorine concentration. Using the three media, the cultures of *R. salina* contained an average of 45% triacylglycerol (TAG), but at the highest chlorine concentration TAG was higher by approximately 37%. No differences were found between the neutral and polar lipid concentrations of the different treatments. The results suggested that cells of *R. salina* were sensitive to higher concentrations of chlorine, even though they produced higher TAG levels.

T47. OPTIMIZING USE OF WASTEWATER AS A GROWTH MEDIUM FOR MICROALGAL BIOFUEL FEEDSTOCK

Novoveska, L., Oklahoma State University, USA, lucie.novoveska@okstate.edu
Liefer, J. D., Dauphin Island Sea Lab, USA
MacIntyre, H. L., Dalhousie University, Canada

Microalgae are a feedstock that has high productivity, high lipid content, and lower land and water requirements than terrestrial crops. Wastewater could be an inexpensive and readily available growth medium, reducing operating expenditure at commercial scale. Equally, microalgae could be an efficient tertiary wastewater treatment by sequestering nutrients. Treated sewage wastewater effluent was tested as a culture medium in 20-liter outdoor cultures, using a natural assemblage as an inoculum. Experiments were conducted in summer in Alabama, USA, and temperatures in the cultures were 21-32°C. Cultures were carbon-limited in the absence of a DIC supplement. Carbon-sufficiency was achieved by aeration: addition of a further 4 mM sodium bicarbonate had no effect on growth rate, DIN and DIP uptake rates, and biomass yield. Similarly, addition of f/2 trace metals and vitamins had no effect on rates and yields. Microalgae were able to remove up to 99% of the dissolved nutrients in less than eight days in batch culture. This period could be shortened greatly if denser cultures were maintained in semi-continuous culture.

T48. STABILIZING CONTINUOUS MICROALGAL POLYCULTURES

Novoveska, L., Oklahoma State University, USA, lucie.novoveska@okstate.edu
Henley, W. J., Oklahoma State University, USA
Wulfers, T. A., Oklahoma State University, USA, twulfer@ostatemail.okstate.edu

Microalgae are a promising source of renewable biofuels because they are highly productive, require minimal freshwater input, utilize land unsuitable for many plants, and do not compete with food sources. Whereas microalgal monocultures are difficult to maintain, higher species diversity may increase productivity and stabilize the community. Our goal is to explore the physiological behavior and potential for stabilization of mixtures of different microalgae under variable environmental conditions. We monitored growth rates of three monocultures (cyanobacterium Aphanothece spp. CCMP 2529, diatom *Phaeodactylum tricornutum* CCMP 1327, and locally isolated chlorophyte *Dunaliella* spp.) under four salinity regimes (10 to 150 ppt) and three nutrient conditions (nitrogen and phosphorus: depleted, limited and replete) and their combinations. The growth rates varied significantly based on the culture condition both within and between species. Overall, Aphanothece spp. was abundant at low salinities while *Dunaliella* spp. was able to tolerate high salinities and reduced nutrients. Based on the monocultures

results, we attempted to manipulate the culture conditions in the turbidostat to regulate the biomass and species balance in mixed species cultures.

T49. ECOLOGY OF ANNUAL POPULATIONS OF GIANT KELP IN SOUTHERN CHILE

Buschmann, A. H., Universidad de Los Lagos, Puerto Montt, Chile, abuschma@ulagos.cl
Hernandez-Gonzalez, M. C., Universidad de Los Lagos, Puerto Montt, Chile, mhernand@ulagos.cl
Varela, D. A., Universidad de Los Lagos, Puerto Montt, Chile, dvarela@ulagos.cl
Pereda, S. V., Universidad de Los Lagos, Puerto Montt, Chile, spereda@ulagos.cl
Rodríguez-Maulén, J. F., Universidad de Los Lagos, Chile, juan.maulen@ulagos.cl
Henríquez, L. A., University of Tasmania, , Luis.HenriquezAntipa@utas.edu.au
López, A. P., Universidad de Los Lagos, Chile, alejandralopez@ulagos.cl
Maldonado, M. A., Universidad de Los Lagos, Chile, miguelmaldonadoa@gmail.com
Graham, M. H., Moss Landing Marine Laboratories, USA, mgraham@mlml.calstate.edu

Annual populations of giant kelp Macrocystis pyrifera in southern Chile recruit on filter feeders (Crepipatella fecunda and *Aulacomya ater*). Adult individuals undergo senescence due to changes in abiotic factors during summer and autumn, producing 100% mortality. Field experiments shows that high temperatures (> 10 oC) and nitrogen availability (< 1 µMol) determine mortality of adult plants. On the other hand, microscopic stages of these kelp populations have to survive 3 to 4 month under a strong grazing pressure. Grazing by macrograzers can reduce up to 50% of recruitment success of these kelp populations, but interestingly, filter feeders control the abundance of green algal turfs allowing the kelp microscopic stages to survive and recruit. *Macrocystis* seems to have a neutral effect on the filter feeders on which they colonize. Financial Support: FONDECYT 1080144 and 1100845.

T50. IDENTIFICATION OF *PORPHYRA* SPECIES IN MAINE COAST SEA VEGETABLES' "LAVER" USING MOLECULAR TECHNIQUES

York, G. E., University of Maine, Orono, Maine, USA
Arnold , D. S., University of Maine, Orono, Maine, USA
Brehm, L. J., University of Maine, Orono, Maine, USA
DeMerchant, J. R., University of Maine, Orono, Maine, USA
Jensen, A. J., University of Maine, Orono, Maine, USA
Lyczkowski, E.R., University of Maine, Orono, Maine, USA
Ouellette, A. R., University of Maine, Orono, Maine, USA
Rankin, J. A., University of Maine, Orono, Maine, USA
Phillips, J. C., University of Maine, Orono, Maine, USA
Brawley, S. H., Univ. of Maine, Orono, Maine, USA
Erhart, S., Maine Coast Sea Vegetables, Inc., Franklin, Maine, USA

Porphyra spp. are commercially valuable red algae in the northwestern Atlantic. Maine Coast Sea Vegetables (MCSV, Franklin, ME) collects, processes, and sells *Porphyra* as "Laver" for human consumption. This study sought to ascertain which *Porphyra* species compose MCSV's "Laver". Replicate samples from three bags of MCSV "Laver" were disrupted by grinding tissue in liquid nitrogen, and DNA was extracted using a Qiagen kit. PCR amplification of the *rbc*L gene was performed, and a restriction digest was done using *Hae*III and *Hind*III, as described by Teasdale et al. (2002). The fragments were run on an agarose gel, and analysis revealed two distinct species: *Porphyra umbilicalis* (most common) and *Boreophyllum birdiae* (formerly *Porphyra birdiae*). Some restriction digest-based identifications were confirmed by BLAST against the GenBank database. Samples identified as *B. birdiae* also had reproductive tissue reflective of the species. *Porphyra umbilicalis* and *B. birdiae* are morphologically similar and grow in the same zone, so it is not surprising that they are harvested together. This study provided useful information to MCSV regarding their "Laver".

T51. MOLECULAR PHYLOGENY OF THE NEMALIOPHYCIDAE (FLORIDEOPHYCEAE, RHODOPHYTA)

Lam, D. W., Ohio University USA, lam@ohio.edu
Vis, M. L., Ohio Unversity, USA, vis-chia@ohio.edu
Saunders, G. W., University of New Brunswick, Canada, gws@unb.ca

The red algal subclass Nemaliophycidae consists of the orders Acrochaetiales, Balbianiales, Balliales, Batrachospermales, Colaconematales, Nemaliales, Palmariales, Rhodachlyales, and Thoreales and includes both marine and freshwater algal species. Molecular phylogenetic analyses based on a multigene dataset were rooted with representative Ahnfeltiophycidae and Corallinophycidae taxa as outgroups. The Nemaliophycidae and the orders within it were inferred as monophyletic. The Acrochaetiales formed a strongly supported clade with the Palmariales. Genera in these two orders exhibit many similarities including: a lack of auxiliary cells, a common pit plug type, and cruciate tetrasporangia. Unfortunately, all other supraordinal relationships exhibited low support values on relatively short branches. The lack of resolution for deep level evolutionary relationships within this subclass could be attributed to a shortage of phylogenetically informative sites. Additionally, saturation in the selected molecular markers and multiple habitat range expansions (from marine to freshwater) with positive selection (convergence) may have altered the rate of molecular evolution in lineages across the tree and are possible explanations for a lack of supraordinal resolution.

T52. USING NEXT GENERATION SEQUENCING TO EXAMINE PATTERNS OF ALGAL BIODIVERSITY IN A HAWAIIAN STREAM

Carlile, A. L., University of New Haven, USA, acarlile@newhaven.edu
Sherwood, A. R., University of Hawaii, USA, asherwoo@hawaii.edu

A past study of benthic algal diversity in a Hawaiian stream used cloning methods to obtain UPA sequences from an environmental DNA sample, and while a variety of sequences were obtained, this method was unsuccessful in gaining complete coverage of the organisms present. In the current study, we used 454 pyrosequencing to sequence two markers (UPA and partial SSU) from samples obtained at five sites along Manoa Stream, Honolulu, HI. These sites spanned steep gradients of land use and rainfall from Manoa Falls to where the stream transitions to brackish water. While both markers yielded many non-algal sequences not targeted in this study, there was sufficient breadth in sequence coverage to produce a view of the biodiversity of algal species present in this stream, including new records for the island of Oahu. Environmental sequencing on this scale not only allows an insight into patterns of biodiversity, but also gives an appreciation of cryptic diversity not readily apparent on a macro scale.

T53. TESTING THE GENERIC LIMITS OF THE BIDDULPHIACEAE (BACILLARIOPHYCEAE): REVISITING ROSS & SIMS (1971) WITH MOLECULAR DATA

Ashworth, M. P., University of Texas at Austin, USA, mashworth@utexas.edu
Nakov, T., University of Texas at Austin, USA
Theriot, E. C., University of Texas at Austin, USA

The ocellate and pseudocellate diatoms in the Biddulphiaceae are distinctive and have a rich fossil history, making them common components of marine coring studies and good candidates for molecular dating work. Also, these diatoms are important to understanding the phylogeny of the diatoms as a whole, since the distinction between the araphid pennate and multipolar centric diatoms has become blurred by the increased use of molecular markers. However, the convoluted taxonomic history of these groups has the potential to disrupt both types of studies, as many taxa still have multiple generic designations that are commonly used in the literature. In 1971, Ross and Sims used scanning electron microscopy to examine valve characters of several ocellate and pseudocellate diatoms and came up with a scheme of morphological characters that could define these genera. In this study, we used molecular characters

(nuclear-encoded SSU rRNA and plastid-encoded rbcL and psbC) to test if Ross and Sims' morphological characters are synapomorphic with respect to the diatom molecular phylogeny. While some morphological characters do indeed appear to be synapomorphic, others do not.

T54. A SEVEN GENE ESTIMATE OF THE DIATOM PHYLOGENY AND INFERENCES ABOUT THE UR-DIATOM

Theriot, E. C., University of Texas at Austin, USA, etheriot@austin.utexas.edu
Ashworth, M. A., University of Texas at Austin, USA, mashworth@mail.utexas.edu
Nakov, T., University of Texas at Austin, USA, teofiln@gmail.com
Brady, M., University of Texas at Austin, USA, mariska.brady@gmail.com
Yu, A., University of Texas at Austin, USA, annaymj_2010@mail.utexas.edu

We have sequenced nuclear SSU and 6 chloroplast genes for over 200 diatoms, yielding an aligned dataset of about 10,000 nucleotides. Here we report on our preliminary analyses of this dataset, and give an overview of the diatom phylogeny. We specifically test the placement of several diatoms of interest, including species used as models in genomic studies (*C. nana* and *P. tricornutum*), and diatoms whose placement in the diatom phylogeny has been particularly problematic (e.g., *Striatella*). We find increasing support that the so-called radial centrics are not monophyletic, but rather are a grade. We discuss the implications of this tree for the diatom classification. We argue that previous inferences about the Ur-diatom as a small, perhaps siliceous flagellate, have been misinformed by implicit assumptions that the outgroup represented the ancestral morphology. Inferences from the diatom phylogeny, however, yields a very different view, suggesting that the Ur-diatom may have been highly elongate and perhaps filamentous.

T55. ANCIENT GENE PARALOGY MAY MISLEAD INFERENCE OF PLASTID TREE OF LIFE

Qiu, H., Bigelow Laboratory for Ocean Sciences, USA, hqiu@bigelow.org
Yang, E. C., Bigelow Laboratory for Ocean Sciences, USA, ecyang@bigelow.org
Bhattacharya, D., Rutgers University, USA, BHATTACHARYA@aesop.rutgers.edu
Yoon, H. S., Sungkyunkwan University, Republic Of Korea, hsyoon2011@skku.edu

Due to its ancient origin, the highly reduced plastid genomes of Plantae provide limited insights into the initial stages of endosymbiont genome reduction. The photosynthetic amoeba *Paulinella* provides a more useful model to study this process because its cyanobacterium-derived plastid originated ~60 MYA and the genome still contains about ~800 genes. We investigated features associated with genome reduction due to primary endosymbiosis in *Paulinella* plastids and revealed gene inactivation, concerted evolution, and contraction of gene families that impact highly conserved single-copy phylogenetic markers in the plastid such as psbA, psbC, and psbD. Our data suggest that these photosystem II genes may provide misleading phylogenetic signal because each of the constituent Plantae lineages has likely undergone a different, independent series of events that led to their reduction to a single copy. This issue might be most problematic for resolving basal Plantae relationships. Our work uncovers a key, previously unappreciated aspect of organelle genome reduction in Plantae and demonstrates "work in progress" models such as *Paulinella* to be critical to gain a fuller understanding of Plantae genome evolution.

T56. DETERMINING THE POSITION OF THE TREUBARINIA AND OTHER INCERTAE SEDIS TAXA IN THE CHLOROPHYCEAN TREE OF LIFE

Fucikova, K., University of Connecticut, USA, karolina.fucikova@gmail.com
Lewis, L. A., University of Connecticut, USA, louise.lewis@uconn.edu
Lewis, P. O., University of Connecticut, USA, paul.lewis@uconn.edu

Phylogenetic relationships within the class Chlorophyceae (Chlorophyta) have challenged phycologists for the past several decades, and certain elements of chlorophycean taxonomy have not yet been solidified despite modern taxonomic approaches, including ultrastructure and molecular sequence data analysis. The monophyly of most orders within Chlorophyceae has been established to some extent, and genus-level studies are increasing in number, working towards a complete chlorophycean tree of life. However, family-level taxonomy (i.e., grouping of genera within orders) requires further investigation. Additionally, several genera retain the "incertae sedis" status with no clear affiliation to a particular order within Chlorophyceae, although many were included in previous single- and even multi-gene phylogenetic studies. Notably, the clade informally called "Treubarinia" has been shown either as affiliated with the Sphaeropleales, or Volvocales, or to stand independent of all the established orders within Chlorophyceae. This group of genera is the target of the present study, along with other chlorophycean taxa of unknown phylogenetic affiliation, for a total of 12 incertae sedis genera. We analyzed a data set containing two nuclear ribosomal genes (18S and 28S) and three plastid-encoded protein coding genes (psaB, psbC, and rbcL) across 80 taxa to test hypotheses regarding the phylogenetic affiliations of these incertae sedis genera.

T57. SECRETION KILLERS: THE ORIGIN AND EVOLUTION OF PATHOGENICITY FACTORS IN THE OOMYCETE 'SECRETOME'

Misner, I., Univ. Rhode Island, USA, ianmisner@my.uri.edu
Leonard, G., Natural History Museum, United Kingdom, g.leonard@nhm.ac.uk
Bapteste, E., Université Pierre et Marie Curie, France, .bapteste@snv.jussieu.fr
Lopez, P., Université Pierre et Marie Curie, France, philippe.lopez@snv.jussieu.fr
Richards, T., Natural History Museum, United Kingdom, T.A.Richards@exeter.ac.uk
Lane, C., Univ. Rhode Island, USA, clane@mail.uri.edu

Saprobic organisms, such as oomycetes, fungi, bacteria and a variety of protists, rely on secreted proteins to obtain nutrients and breakdown complex macromolecules; these proteins are collectively termed the 'secretome'. Whereas free-living saprobes play a vital biological role in decomposition, it is the parasitic relatives of these organisms that have a greater direct economic and human health impact. Parasites also rely on the secretome for host attachment, cellular breakdown, and host defense avoidance. Little is known about how parasites have obtained these novel functions or how they evolved from proteins used by free-living relatives. To understand the evolutionary processes at work, we have sequenced the genomes and identified the secretomes from two oomycetes: the free-living Thraustotheca clavata and the facultative parasite Achlya hypogyna. Combining our data from these two Saprolegnian oomycetes with the available secretomes from parasitic Peronosporalen taxa, we have identified a core oomycete secretome. Additionally, we have identified unique gene family expansions, contractions, and horizontal gene transfer events that are key to the evolution of parasitism within this diverse group of organisms.

T58. RED ALGAL PARASITE CONTRIBUTIONS TO HETEROKARYON ORGANELLAR PROTEOMES

Blouin, N. A., University of Rhode Island, USA, nblouin@mail.uri.edu
Lane, C. E., University of Rhode Island, USA, clane@mail.uri.edu

Many virulent eukaryotic pathogens and parasites have are known or hypothesized to have evolved from a photosynthetic ancestor. It is not clear why or how photosynthetic organisms so readily become parasites. The genomes of many of these parasites have been sequenced, however, none have close free-living relatives from which fine-scale genetic comparisons can be made to elucidate the loss of photosynthesis, which is assumed to occur early in the evolutionary trajectory of parasite evolution. Parasites found throughout the florideophyte red algal lineage, however, provide a unique and powerful model to investigate the genetic origins of a parasitic lifestyle. This is because they share a recent common ancestor with an extant free-living red alga (adelphoparasitism). Cytological studies have shown

that the adelphoparasite *Gracilariophila oryzoides* contains a non-photosynthetic plastid (proplastid) that is derived from its host, *Gracilariopsis andersonii* while still maintaining its own mitochondria. The organellar genomes in green algal and apicomplexan parasites are highly conserved in their gene repertoire, suggesting that there are constraints to parasitic evolution in photosynthetic lineages. Aside from photosynthesis, plastids are also required for amino acid metabolism, fatty acid biosynthesis and pyrimidine biosynthesis in many organisms. These functions, however, require the targeting of proteins to the plastid from the nuclear genome where they are encoded. We identified candidate nuclear-encoded genes in this host-parasite pair through homology searches against known plastid proteomes and target signal prediction. We present ongoing bioinformatics research to determine which nuclear encoded, plastid-targeted genes remain in the parasite's genome and are transcriptionally active. Further, we investigate whether or not key ATP synthase genes (sdhC and atp8) not found in the parasite's mitochondrion genome have been transferred to its nucleus or lost entirely.

T59. META-GENOMIC ANALYSIS OF A NONAXENIC CULTURE OF *BOTRYOCOCCUS PROTUBERANS* REVEALED A PROBABLE PARASITE *VERRUCOMICROBIUM SPINOSUM*

Sun, D., Genome Institute of Singapore, Singapore, sundy@gis.a-star.edu.sg
Datta, P., Genome Institute of Singapore, Singapore
Poon, S.Y., Genome Institute of Singapore, Singapore
Fang, L., Genome Institute of Singapore, Singapore
Liu, J., Genome Institute of Singapore, Singapore, liujh@gis.a-star.edu.sg

We have acquired a nonaxenic culture of *Botryococcus protuberans* CCALA779 from the Culture Collection of Phototrophic Organisms at the Institute of Botany, Academy of Sciences of the Czech Republic (www.butbn.cas.cz/ccala). Contaminating bacteria became apparent after growing the culture in dark for a few days. Several attempts were made to purify the *B. protuberans* cells using the dilution method or picking-up method but were unsuccessful. To find out which bacterial spp. are present in the nonaxenic culture, genomic DNA from the nonaxenic culture was subjected to sequencing analysis using Solexa. Blast2GO analysis indicated that the majority of the sequences had a best hit to the genome of green microalgae such as *Chlamydomonas reinhardtii* (~24%), *Chlorella* sp. NC64A (~23%), and *Ostreococcus* RCC809 (~12%) and plant *Arabidopsis thaliana* (~7%). On the other hand, a quart of the sequences showed to have a best hit to the genomes of *Singulisphaera* DSM18658 (~12%) and *Verrucomicrobia* TAV1 (~12%). The presence of *V. spinosum* 16S rDNA but not *Singulisphaera* sp. was confirmed in the sequence analysis of the PCR-amplified 16S rDNA. *V. spinosum* contains wart-like prosthecae that may physically attach to the cell wall of *B. protuberans*, which explains why the *B. protuberans* could not be purified from the bacteria. We showed that the population size of *V. spinosum* in the nonaxenic *B. protuberans* culture in BB medium supplemented with additional 400mM NaCl was reduced by 16-fold when compared to that in BB medium without additional NaCl supplement. This is consistent with the notion that *Botryococcus* spp. are resistant to high salt and capable of growing in brackish water whereas *Verrucomicrobium* spp. are sensitive to high salt. Hence, we provide a method to grow *B. protuberans* with a reduced level of bacterial contamination. We propose that *V. spinosum* is a probable parasite of *B. protuberans*.

T60. OUTBREAK OF AN ALGAL VIRUS DISEASE IN *PORPHYRA* FARMS IN KOREA

Kim, G. H., Department of Biology, Kongju National University, Republic Of Korea, ghkim@kongju.ac.kr

As with land crops, algal cultivation beds are suffering from various diseases and parasitism, ranging from spectacular outbreaks in natural populations, down to significant losses in multibillion dollar crops such as *Porphyra* (nori). *Porphyra* culture is worth US$1.5 billion globally. Estimates for Japan and Korea show that on average, 10% of the annual production is lost, mostly due to fungal disease caused by the oomycete pathogens, *Olpidiopsis* spp. and *Pythium* spp. The recent development of intensive and

dense mariculture practices have made these diseases spread much faster and a crop of 100 ha can be destroyed within 2–3 weeks. During the winter 2011-2012, an outbreak of virus disease occurred and devastated many *Porphyra* farms of southern Jeollnamdo province where produce 70-80% of nori product in Korea. A noble DNA virus infecting *Porphyra* was isolated from the algal cultivation beds in this area. Viral replication occurred within the cytoplasm, and the latent period was 24 hours. This virus could infect several *Porphyra* species including *P. yezoensis*, *P. lucasii* as well as *P. tenera*. To our knowledge, this is the first report describing the biological properties of a virus infecting *Porphyra*. The results of ESTs analysis on infected *Porphyra* will be presented.

T61. AN INVESTIGATION OF ENDOPHYTE IMPACTS ON MACROPHYTE HOST PHYSIOLOGY ALONG THE WESTERN ANTARCTIC PENINSULA

Schoenrock, K. M., University of Alabama at Birmingham, USA, ksrock@uab.edu
Amsler, C. D., University of Alabama at Birmingham, USA, amsler@uab.edu
Baker, B. J., University of South Florida, USA, bjbaker@usf.edu
McClintock, J. B., University of Alabama at Birmingham, USA, mcclinto@uab.edu

Filamentous endophytic algae are commonly found within macrophyte hosts along the western Antarctic Peninsula. The impact of endophytes on their macrophyte hosts has been shown to vary between species. Previously, filamentous endophytes were shown to negatively impact host growth rates in two species of Antarctic algae. This study investigates the impact of endophytic algae on three aspects of host physiology: photosynthetic capacity, palatability and thallus toughness. These parameters were measured in a variety of common Antarctic macrophytes during field seasons from 2010 through 2012. Host species varied in their response to infection; however most were not negatively impacted by endophyte presence. The benign presence of these endophytic algae and host tolerance of a photosynthetic endosymbiont are indicative of a commensalism in many Antarctic species.

T62. THE ROLE OF SPHINGOLIPIDS IN VIRUS-INDUCED CELL LYSIS IN EMILIANIA HUXLEYI

Zaeuner, S., University of Hamburg, Germany, zaeuner@uni-bonn.de
Michaelson, L. V., Rothamsted Research, United Kingdom
Markham, J. E., University of Nebraska, USA
Allen, M. A., Plymouth Marine Laboratory, United Kingdom
Worthy, C. A., Plymouth Marine Laboratory, United Kingdom
Heinz, E., University of Hamburg, Germany
Warnecke, D., University of Hamburg, Germany
Napier, J. A., Rothamsted Research, United Kingdom

Emiliania huxleyi (Ehux) is an important marine calcifying alga whose blooms are easily visible from space. Recently, a novel virus group of the genus *Coccolithovirus* (*Emiliania huxleyi* Virus 86, EhV) was identified which specifically infects Ehux. Genome sequencing of different viral genomes (i.e. EhV strains 84, 86, 202 and 203) and the alga itself revealed the presence of sphingolipid synthesis-related genes in both organisms. Ehux synthesizes glucosylceramide. Its ceramide backbone shows some unexpected structural features such as a C9-methylbranch which is commonly found in fungi but not in plants. We expressed candidate sphingolipid genes from Ehux and EhV in appropriate deletion mutants of the yeast *Pichia pastoris*. The functionality of the C9-methyltransferase from Ehux and the Δ4-sphingolipid-desaturase from both organisms could be shown in vivo and in vitro. Since some sphingolipids species are known to have signaling functions, it is believed that virus-induced sphingolipids play a key role in preventing cell death before the newly synthesized virus-particles are ready to be released. This is also reflected by a change in sphingolipid composition of Ehux following infection with EhV.

T63. AKINETE DEVELOPMENT IN THE HARMFUL CYANOBACTERIUM *APHANIZOMENON OVALISPORUM*

Sukenik, A., IOLR, Israel, assaf@ocean.org.il
Kaplan-Levy, R. N., IOLR, Israel, ruth@ocean.org.il
Mark Welch, J., MBL, USA, jmarkwelch@mbl.edu
Post, A. F., MBL, USA, apost@mbl.edu

Akinetes are dormancy cells found among many toxic and/or nuisance, bloom-forming filamentous cyanobacteria. Akinete development is a process that involves morphological and biochemical modifications. We applied a single cell approach to quantify genome and ribosome content of akinetes and vegetative cells in *Aphanizomenon ovalisporum*. Vegetative cells were naturally polyploid and contained on average 8 genome copies per cell. However, the chromosomal content of akinetes increased up to 450 copies, with an average value of 119 genome copies per akinete, 15-fold higher that in vegetative cells. Using FISH hybridization with a probe targeting 16S rRNA and detection with confocal laser scanning microscopy we show that ribosomes accumulated in akinetes to a higher level than in vegetative cells. We further show that massive accumulation of nucleic acids in akinetes is supported by phosphate supply from inorganic polyphosphate bodies. The latter are abundant in vegetative cells, but suspiciously absent from akinetes. These results are interpreted in the context of cellular investments for gestation, as high nucleic acid contents would provide the basis for rapid resumption of metabolic activity and cell division upon germination

T64. TAXONOMIC REVISIONS OF MARINE CYANOBACTERIA TO FACILITATE NATURAL PRODUCTS DISCOVERIES AND HARMFUL ALGAE BLOOM MONITORING

Engene, N., Smithsonian Institution, USA, engenen@si.edu
Rottacker, E. C., National Center for Microscopy and Imaging Research, University of California San Diego, USA, erottack@ucsd.edu
Kaštovský, J., Faculty of Science, University of South Bohemia, Czech Republic, hanys@prf.jcu.cz
Komárek, J., Faculty of Science, University of South Bohemia, Czech Republic, komarek@butbn.cas.cz
Ellisman, M. H., National Center for Microscopy and Imaging Research, University of California San Diego, USA, mark.ellisman@gmail.com
Gerwick, W. H., Center for Marine Biotechnology and Biomedicine, Scripps Institution of Oceanography, USA, wgerwick@ucsd.edu
Paul, V., Smithsonian Institution, USA, Paul@si.edu

Marine cyanobacteria are notoriously known for their prolific biosynthetic capacities to produce structurally diverse secondary metabolites with biomedical application and the ability to form harmful algae blooms (HABs). According to the literature, the nearly 800 secondary metabolites isolated to date from marine cyanobacteria are taxonomically unequally distributed with only five genera being responsible for over 90% of these molecules. Our phylogenetic investigations of marine cyanobacterial strains responsible for over 100 bioactive secondary metabolites reveal novel biodiversity that previously was overlooked by traditional morphological-based taxonomic approaches. In our efforts to provide taxonomic clarity to better guide future natural products (NPs) drug discovery investigations and HABs monitoring, we are proposing revision of all these five NP-rich genera. As an example of these necessary taxonomic revisions, the new cyanobacterial genus *Moorea* will be discussed as well as our attempt to comply with both the Botanical and the Bacteriological codes. This hybrid classification approach involves phylogenetic, genomic, morphological, biochemical, ultrastructural, and ecological characterization of *Moorea gen. nov.*, a new group of tropical marine cyanobacteria rich in bioactive secondary metabolites

T65. DEVELOPMENT OF SEMI-QUANTITATIVE PCR ASSAYS DETECTING AND ENUMERATING POTENTIALLY TOXIC CARIBBEAN *GAMBIERDISCUS* SPECIES

Vandersea, Mark W., NOS/NOAA, Center for Coastal Fisheries and Habitat Research, Beaufort, North Carolina USA, mark.w.vandersea@noaa.gov
Kibler, S.R., NOS/NOAA, Center for Coastal Fisheries and Habitat Research, Beaufort, North Carolina USA, steve.kibler@noaa.gov
Holland, W.C., NOS/NOAA, Center for Coastal Fisheries and Habitat Research, Beaufort, North Carolina USA, chris.holland@noaa.gov
Tester, P.A., NOS/NOAA, Center for Coastal Fisheries and Habitat Research Beaufort, North Carolina USA, pat.tester@noaa.gov
Schultz, T.F., Marine Conservation Molecular Facility, Duke University Marine Laboratory, Beaufort, North Carolina USA, tom.schultz@duke.edu
Faust, M.A., United States National Herbarium, National Museum of Natural History, Smithsonian Institution, Suitland, Maryland USA, faustm@si.edu
Homes, M.J., Water Quality and Aquatic Ecosystem Health, Queensland Department of Environment & Resource Man., Brisbane, Queensland Australia, michael.holmes@derm.qld.gov.au
Chinain, M., Laboratoire Des Micro-Algues Toxiques, Institut Louis Malardé, Tahiti, Papeete French Polynesia, MChinain@ilm.pf
Litaker, R.W., NOS/NOAA, Center for Coastal Fisheries and Habitat Research, Beaufort, North Carolina USA, Wayne.litaker@noaa.gov

Ciguatera fish poisoning (CFP) is a serious health problem in tropical regions and is caused by the bioaccumulation of lipophilic toxins produced by dinoflagellates in the genus *Gambierdiscus*. *Gambierdiscus* species are morphologically similar and are difficult to distinguish from one another even when using scanning electron microscopy. Improved identification and detection methods that are sensitive and rapid are needed to identify toxic species and investigate potential distribution and abundance patterns in relation to incidences of CFP. This poster presents the first species-specific, semi-quantitative polymerase chain reaction (qPCR) assays that can be used to address these questions. These assays are specific for five *Gambierdiscus* species and one undescribed ribotype. The assays utilized a SYBR green format and targeted unique sequences found within the SSU, ITS, and the D1/D3 LSU ribosomal domains. Standard curves were constructed using known concentrations of cultured cells and tenfold serial dilutions of rDNA PCR amplicons containing the target sequence for each specific assay. Assay sensitivity and accuracy were tested using DNA extracts purified from known concentrations of multiple *Gambierdiscus* species. The qPCR assays were used to assess *Gambierdiscus* species diversity and abundance in samples collected from nearshore areas adjacent to Ft. Pierce and Jupiter, Florida USA. The results indicated that the practical limit of detection for each assay was 10 cells per sample. Most interestingly, the qPCR analysis revealed that as many as four species of *Gambierdiscus* were present in a single macrophyte sample.

T66. CELL CYCLE, SAXITOXIN, AND PROTON PUMP RHODOPSIN: INSIGHTS FROM GENE EXPRESSION PROFILING FOR AN *ALEXANDRIUM FUNDYENSE* CULTURE AND A NATURAL BLOOM

Zhuang, Y., University of Connecticut, USA, yunyun.zhuang@uconn.edu
Zhang, H., University of Connecticut, USA, huan.zhang@uconn.edu
Hannick, L., J. Craig Venter Institute, USA, lhannick@jcvi.org
Lin, S., University of Connecticut, USA, senjie.lin@uconn.edu

We used 454 pyrosequencing to investigate the global gene expression patterns over a 24h period in a cultured strain (CCMP1719) and a natural PSP bloom (in Long Island Sound) of "*Alexandrium fundyense*". We obtained more than 7.7 and 8.2 million spliced leader-based 5' expressed sequence tags from four time points (TPs) of the diel cycle. About 4.2% and 16.3% of the transcriptome were

differentially expressed in the four TPs in the cultures and the natural bloom, respectively. Cell cycle-related genes (e.g. proliferating cell nuclear antigen, cyclin-dependent kinases) were highly expressed, but expression dynamics was not dramatic, suggesting that regulation of these genes lie at posttranscriptional levels. Genes related to toxin production (e.g. saxitoxin A, S-adenosylmethionine synthetase, S-adenosylhomocysteine hydrolase) were expressed at different levels at the four TPs. Furthermore, proton-pump rhodopsin was highly expressed in both the cultures and the natural bloom, suggesting the potential of directly converting solar energy to ATP in this species to fuel cellular activities even when photosynthesis is compromised by environmental conditions.

T67. BREVETOXIN PRODUCTION BY THE DINOFLAGELLATE *KARENIA BREVIS*: DO BACTERIA PLAY A ROLE?

Mikulski, C. M., Marine Biotoxins Program, NOAA Center for Coastal Environmental Health and Biomolecular Research, USA, tina.mikulski@noaa.gov
Monroe, E. A., Marine Biotoxins Program, NOAA Center for Coastal Environmental Health and Biomolecular Research, USA
Morey, J. S., Marine Biotoxins Program, NOAA Center for Coastal Environmental Health and Biomolecular Research, USA
Wang, Z., Marine Biotoxins Program, NOAA Center for Coastal Environmental Health and Biomolecular Research, USA
Roth, P. B., Marine Biotoxins Program, NOAA Center for Coastal Environmental Health and Biomolecular Research, USA
Twiner, M. J., Marine Biotoxins Program, NOAA Center for Coastal Environmental Health and Biomolecular Research, USA
Van Dolah, F. M., Marine Biotoxins Program, NOAA Center for Coastal Environmental Health and Biomolecular Research, USA
Doucette, G. J., Marine Biotoxins Program, NOAA Center for Coastal Environmental Health and Biomolecular Research, USA

Karenia brevis is a toxic bloom-forming dinoflagellate that produces a suite of neurotoxins known as brevetoxins, which can cause human intoxication and harmful environmental effects. The role that co-occurring bacteria may play in the production of brevetoxins has long been debated. We measured the production of brevetoxin in triplicate bacteria-free and xenic cultures of *Karenia brevis* (C2) over parallel 21-day growth curves. There was no discernable difference in total intracellular brevetoxin concentrations between culture conditions, although some differences were evident among toxin congener profiles. Overall, the bacteria-free culture produced significantly more PbTx-1 and less PbTx-3. There was no significant increase in intracellular toxin quota during stationary phase when the bacterial load was the highest, lending further evidence to algal-derived toxin production. Microarray analyses of RNA from log-phase cultures showed that only 1% of 10,263 array features differed significantly between bacteria-free and xenic cultures. Moreover, transcripts represented by 14 probes for polyketide sythases, putative toxin biosynthesis genes, were present in both the xenic and bacteria-free cultures at similar expression levels, further discounting bacterial prodution of brevetoxin.

T68. DISTRIBUTION AND SEASONAL FLUCTUATION OF DIVERSE RIBOTYPE OF *COCHLODINIUM POLYKRIKOIDES* IN SOUTHERN KOREA COASTAL WATERS

Park, B. S., Hanyang Uiversity, Republic Of Korea, parkbs@hanyang.ac.kr
Kim, J., Hanyang University, Republic Of Korea, ikart00@nate.com
Kim, J., Hanyang University, Republic Of Korea, neozin83@naver.com
Wang, P., Hanyang University, Republic Of Korea, wpbdavid@163.com
Li, Z., Hanyang University, Republic Of Korea, lovecxx@naver.com
Han, M., Hanyang University, Republic Of Korea, hanms@hanyang.ac.kr

We developed a quantitative real-time PCR assay and analyzed field samples for distribution and seasonal fluctuation of three ribotypes of *C. polykrikoides* at Southern Korean coastal waters. Specific primers for three ribotypes of *C. polykrikoides* were designed to target the Large subunit ribosomal RNA region. The qRT-PCR assay analyzing Ct value and the log of copy number showed a significant linear relationship ($r2 \geq 0.99$). Using PCR assay with specific primers, Philippines and East Asian ribotype were detected, whereas American/Malaysian ribotype did not observe around Korean coastal waters. Philippines ribotype was distributed from early August to November and had the highest abundance at late August. East Asian ribotype was distributed from September to November and had the highest abundance at early November. In 2010, *C. polykrikoides* was detected from October to November. East Asian ribotype was detected from October to November and had the highest abundance in early November. Comparing results between 2009 and 2010, diverse ribotypes might be important role for maintaining *C. polykrikoides* bloom during long period.

T69. OVERWINTERING STRATEGY OF THE MIXOTROPHIC MARINE CILIATE *MESODINIIUM RUBRUM*

Park, J., Saemangeum Marine Environment Research Center, Kunsan National University, Republic Of Korea, cyanopark@hanmail.net
Kim, H., Department of Marine Biotechnology, Kunsan National University, Republic Of Korea, mudskip@kunsan.ac.kr
Jang, B., Department of Oceanography, Kunsan National University, Republic Of Korea, maria1728@kunsan.ac.kr
Yih, W., Department of Oceanography, Kunsan National University, Republic Of Korea, ywonho@kunsan.ac.kr

In 1832 Charles Dawin firstly recorded a remarkable red tide of *Mesodinium rubrum*, which has been then recurrently reported in various seas of the world including upwelling, coastal, and estuarine regions. Cyst formation or any other kind of dormancy in *M. rubrum*, however, were never observed or explored. However, the intermittent outbreaks of *M. rubrum*, sometimes with a few months to years of absence on Korean seas, may reflect on its previously unknown overwintering strategies. Here we performed a series of re-feeding experiments using 3-4 months starved *M. rubrum* and its prey cryptomonad. When spiked with 100 cells/mL cryptomonad M. rubrum population increased from 100 cells/mL to 1600 cells/mL in 7 days with mean daily growth of 0.56 divisions/day. When starved over 4.5 months, M. rubrum population did not show any growth. Such response of the long-starved *M. rubrum* to re-feeding may suggests that a very small seed population can overwinter without cryptomonad prey or cyst formation in temperate seas.

T70. NITROGEN FIXATION AND MICROCYSTIN PRODUCTION BY CYANOBACTERIA IN EUTROPHIC LAKES

Monchamp, M., Department of biological sciences, University of Montreal, Canada, marie-eve.monchamp@umontreal.ca
Maranger, R., Department of biological sciences, University of Montreal, Canada, r.maranger@umontreal.ca
Pick, F. R., Center for Advanced Research in Environmental Genomics, University of Ottawa, Canada, frances.pick@uottawa.ca
Villemur, R., Institut National de la Recherche Scientifique Armand-Frappier, Canada, richard.villemur@iaf.inrs.ca
Beisner, B. E., Department of biological sciences, University of Quebec at Montreal, Canada, beisner.beatrix@uqam.ca

Cyanobacteria can strongly influence aquatic ecosystems owing to their ability to fix atmospheric nitrogen and produce toxins such as microcystins. However, whether environmental factors simultaneously trigger and regulate N fixation as well as the presence and composition of microcystins in

lakes remains largely unknown. From May to October 2010, we followed changes in the cyanobacterial community structure, N fixation rates, and nutrient concentrations in three temperate lakes. We measured microcystin concentrations and composition, the presence of the *mcyE* gene (microcystins), and the *nifH* gene (N fixation) presence along with transcription of the latter. Both nitrate and light were negatively related to microcystin concentrations (R2=0.68). Microcystin congeners varied markedly between lakes with two of the most toxic forms (-LR and -LA) observed in the more hypereutrophic lake. The *nifH* gene was detected in all samples, but no *nifH* transcripts were detected even in samples with heterocysts and low concentrations of inorganic N. The lack of N-fixation was confirmed by 15N2 assimilation incubations. These results suggest that cyanobacteria either acquire their N through organic sources and/or ammonium was recycled rapidly.

T71. THE STIMULATION OF OXIDATIVE STRESS IN TEMPERATURE-STRESSED, IRON-DEPLETED CULTURES OF *SYMBIODINIUM* (FRUDENTHAL) MAINTAINED UNDER CONTINUOUS GROWTH

Laurent, J. K., University of Western Ontario, Canada, kiglic@uwo.ca
Trick, C. G., University of Western Ontario, Canada, cyano@uwo.ca

This study examined the effect of reduced iron availability on the stimulation of oxidative load within the symbiotic dinoflagellates of reef building corals, *Symbiodinium*, when exposed to elevated temperature and irradiance. Using a continuous culture grown facility, *Symbiodinium*, cultures were maintained at low continuous growth and a range of iron availabilities (11.7-0.0117 μM). Measurements of intracellular oxidative loads were determined using the fluorescent probes DHE, CMH2DCFDA, and DAF and flow cytometry after 6.5+/-0.5 hour incubation at an elevated temperature (30.5+0.5 °C). Cultures were then subjected to elevated temperature as above, followed by a shift to an elevated irradiance (790-820 μmolphotonm-2s-1) for 55 minutes and oxidative load measurements collected. Elevations in oxidative load under conditions of iron limitation were detected in *Symbiodinium* strain 2432 at elevated temperatures, but strain 831 required both elevated temperature and irradiance to elicit an iron-limited oxidative load response. The results of this study indicate that iron limitation has pronounced effects on the oxidative load of *Symbiodinium*, species when maintained under continuous growth, high temperature and irradiance, illustrating the potential for iron-limited enhancement of oxidative bleaching events.

T72. IMPACTS OF COMPETITION AND HERBIVORY ON THE GROWTH OF TWO BLOOM-FORMING ULVA SPECIES IN NARRAGANSETT BAY, RI

Guidone, M., University of Rhode Island, USA, mguidone@my.uri.edu
Rinehart, S., University of Rhode Island, USA
Thornber, C., University of Rhode Island, USA

In Narragansett Bay, RI, blooms composed of *U. compressa* and *U. rigida* are an annual occurrence. To determine whether competition occurs during blooms, we examined Ulva growth across a range of blade densities. Within mesocosms, we also examined the impact of light levels (sun/shade). In situ, we investigated the influence of herbivory; Ulva blades were placed in cages of two different mesh sizes that differentially excluded herbivores. We found that *U. compressa* was most impacted by interspecific competition in full sun, while intraspecific competition dominated in shade. In contrast, U. rigida experienced greater interspecific than intraspecific competition under all light levels. In the field, *U. compressa* showed decreased growth due to intraspecific competition in mud crab dominated large mesh cages; herbivory had a larger negative impact on growth in amphipod dominated small mesh cages. *U. rigida* experienced greater interspecific competition in the large, but not small, mesh cages. We conclude that *U. compressa* is a superior competitor to *U. rigida*. However, within Ulva blooms this competition is mediated by amphipods that preferentially consume *U. compressa*, allowing *U. rigida* to proliferate.

T73. EVOLUTION OF DEPENDENCY IN PROCHLOROCOCCUS: AN EMPIRICAL TEST USING AN *E. COLI* MODEL

Morris, J. J., Michigan State University, USA, jmorris@msu.edu
Zinser, E. R., University of Tennessee, USA, ezinser@utk.edu
Lenski, R. E., Michigan State University, USA, lenski@msu.edu

Prochlorococcus, Earth's most abundant photoautotroph, depends on hydrogen peroxide (HOOH) scavenging "helpers" to survive at the ocean's surface. This dependency is a product of reductive genome evolution. We proposed the Black Queen Hypothesis (BQH) to explain how natural selection could lead to mutualism between *Prochlorococcus* and helpers. Here, we empirically test the BQH using an experimental evolution approach with HOOH-sensitive (Hpx) mutants of *Escherichia coli*. These mutants are unable to grow in the presence of HOOH unless protected by catalase, which in the experimental regime is only available on a costly, high-copy number plasmid. When Hpx populations were started with 100% of cells carrying this plasmid and then serially propagated for 1000 generations, plasmid-free segregants appeared and rose to relatively high abundance. Consistent with the BQH, preliminary results suggest that the abundance of segregants was controlled by the cost of plasmid carriage and the per capita catalase activity of the plasmid-carrying cells. We also present simulations extending BQH dynamics to systems with multiple trophic levels, where relationships such as those observed between *Prochlorococcus* and its helpers can evolve.

T74. COMPARATIVE RATES OF PHOTOACCLIMATION IN HAWAIIAN ENDEMIC AND INVASIVE SPECIES OF *GRACILARIA* (RHODOPHYTA)

Hamel, K., University of Hawai'I, USA, khamel@hawaii.edu
Smith, C. M., University of Hawai'I, USA, celia@hawaii.edu

Invasive marine algae are a major threat to coral reef ecosystems in Hawai'i. Identifying characteristics of algae that facilitate their invasiveness can contribute to preventing future introductions and aid in the early identification of potential invaders. One characteristic that may be instrumental in invasiveness is an accelerated photoacclimation potential, which may increase the competitiveness of an organism. Prior studies found significant disparities between photoacclimation rates for invasive and native tropical rhodophytes, with invasive rhodophytes responding to changes in irradiance much more rapidly than their native counterparts. Here we compared two closely related species with similar distribution, habitat and morphology using in vivo spectrophotometry and PAM fluorometry. In this full factorial experiment, the invasive *Gracilaria salicornia* and the native *G. coronopifolia* were grown in outdoor culture, acclimated to one of two irradiance regimes and then reciprocally transplanted. Results indicate that *G. salicornia* has remarkable tolerance to irradiance extremes, retains accessory pigments in the face of degradative influences longer, and experiences rapid growth when transplanted from low to high PPFD environments; however, it does not photoacclimate faster than the native *G. coronopifolia*.

T75. DISTURBANCE MEDIATED RESOURCE ALLOCATION: PHYSIOLOGIC RESPONSES TO BIOMASS LOSS IN *MACROCYSTIS PYRIFERA*

Fox, M. D., Moss Landing Marine Labs, USA, mfox@mlml.calstate.edu

The exceptional morphologic and physiologic plasticity within giant kelp, *Macrocystis pyrifera*, has allowed it to become the most globally successful kelp species. Despite extensive knowledge of *Macrocystis* biology few studies have examined the physiological mechanisms for recovery from disturbance within this species. Climate models suggest an intensification of North Pacific winter storms and a concomitant increase in significant wave heights, both of which are sources of considerable biomass loss and mortality within *Macrocystis* populations in California. A biomass removal experiment was conducted to model the impacts of winter wave damage on *Macrocystis* in order to elucidate mechanisms for recovery. Tissue samples for carbon and nitrogen analysis were collected from 3 tissue types: mature

blades, juvenile blades, and holdfasts. Comparisons across experimental treatments and among tissue types were made to explore changes in resource allocation as a function of increasing biomass loss. Preliminary analyses suggest increased resource allocation to hapteral tissue may occur under conditions of extreme biomass loss. Such deviation from typical resource allocation patterns may provide evidence for a novel storage mechanism used to facilitate recovery from disturbance.

T76. TEASING APART TEMPERATURE AND NUTRIENT EFFECTS ON *MACROCYSTIS PYRIFERA* RECRUITMENT FROM BRITISH COLUMBIA TO SOUTHERN CHILE

Muth, A. F., Moss Landing Marine Labs, USA, amuth@mlml.calstate.edu
Graham, M. H., Moss Landing Marine Labs, USA, mgraham@mlml.calstate.edu

Nutrient concentrations are typically considered to be the primary factor regulating recruitment success of the giant kelp *Macrocystis pyrifer*a, even though high nutrients generally co-occur with cold temperatures throughout its range. Experiments were conducted on *M. pyrifera* cultured from British Columbia, central and southern California, and southern Chile to tease apart the effects of temperature and nutrients on recruitment success. Cultures were grown at two temperatures (12°C and 18°C) and three nitrate concentrations (1, 5, and 10 µmol) under saturating irradiances, and monitored weekly for sporophytes. Contrary to expectation, regardless of nitrate concentration, sporophytes were always present and more abundant at 12°C relative to 18°C. Furthermore, differences in recruitment success between temperatures increased in the colder regions (southern Chile, central California, and British Columbia) relative to southern California. Under temperature conditions where sporophytes were produced, recruitment success did vary with nitrate concentration, however sporophytes were present in all nitrate levels. These results suggest that nitrate concentrations are secondary to temperature in driving recruitment success in *M. pyrifera*, and that giant kelp populations are capable of acclimating to increasing temperature.

T77. EUGLENAPHYCIN TOXIN IS PRODUCED BY AT LEAST 18 EUGLENOPHYCEAE, INCLUDING 7 STRAINS OF *EUGLENA SANGUINEA*.

Zimba, P.V., Texas A&M University Corpus Christi, Corpus Christi, TX, USA
Rafalski, A., Texas A&M University Corpus Christi, Corpus Christi, TX, USA
Savage, M., Texas A&M University Corpus Christi, Corpus Christi, TX, USA
Ordner, P., Texas A&M University Corpus Christi, Corpus Christi, TX, USA
Triemer, R., Michigan State University, East Lansing, MI, USA

Euglenaphycin toxin previously was confirmed from one species (*Euglena sanguinea)* -this novel compound is allelopathic to other microalgae, and toxic to fish and mammalian cell lines. Seven unialgal strains of *Euglena sanguinea* Ehrenberg from four continents produced euglenophycin toxin. A total of 33 species of euglenoids were grown in batch cultures to mid-exponential phase and sampled for cell number, chlorophyll *a* content, and euglenophycin toxin accumulation. A total of 18 species of euglenoids were found to accumulate euglenophycin in addition to *E. sanguinea*.

T78. A TASTE OF ALGAL GENOMES FROM THE JOINT GENOME INSTITUTE.

Kuo, A. DOE Joint Genome Institute.
Grigoriev, I., DOE Joint Genome Institute.

Algae play profound roles in aquatic food chains and the carbon cycle, can impose health and economic costs through toxic blooms, provide models for the study of symbiosis, photosynthesis, and eukaryotic evolution, and are candidate sources for bio-fuels; all of these research areas are part of the mission of DOE's Joint Genome Institute (JGI). To date JGI has sequenced, assembled, annotated, and released to the public the genomes of 18 species and strains of algae, sampling almost all of the major clades of photosynthetic eukaryotes. With more algal genomes currently undergoing analysis, JGI continues its commitment to driving forward basic and applied algal science. Among these ongoing projects are the

pan-genome of the dominant coccolithophore *Emiliania huxleyi*, the interrelationships between the 4 genomes in the nucleomorph-containing *Bigelowiella natans* and *Guillardia theta*, and the search for symbiosis genes of lichens.

T79. PHYLOGENETIC ANALYSIS OF METAGENOMES AND METATRANSCRIOPTOMES: NEW METHODS FOR MEASURING COMMUNITY DIVERSITY.
Kodner, R., UW Center for Environmental Genomics

Defining the diversity of communities of microbes has remained a challenge, even in the age of molecular biology. Metagenomics and metatranscriptomics are new methods that have the potential to capture whole community diversity, structure, and function from a single sample. Despite their potential, these methods have a number of major analytical challenges. Two of the primary challenges are (1) efficient and accurate annotations of the short, shotgun environmental sequences and (2) comparisons of short read metagenomic and metatranscriptomic data sets, which have been limited to comparison based on taxonomic classification. To address these challenges, we use a pplacer, a phylogenetics package designed to analyze short environmental sequences that contains a suite of phylogenetic-based statistics for comparative metagenomics. Phylogenetic analysis provides an alternative to sequence similarity-based methods that classify reads into known taxonomic bins. In addition to the coarseness of such annotations, it is well known that individual genes may not follow the established taxonomic hierarchy, and sosuch taxonomic binning may obscure interesting differences between samples. In contrast, this phylogenetic approach provides evolutionary information for sequence reads, allows for classification of yet unidentified groups, and provides new statistics for comparing diversity across samples. Phylogenetic statistics for comparative metagenomics give new insights into community diversity and help focus in on taxonomic changes that drive the difference in communities between samples. This talk will give examples of the power of these methods from a eukaryote phytoplankton focused metagenomes from the coast of California and a eukaryotic metatranscriptome from an iron fertilization experiment from the North Pacific Ocean.

Posters

Please note that presenting authors are indicated by underline.

P1. BIOTRANSFORMATION OF SEWAGE SLUDGE BY MICROALGAE TOWARDS BIOFUEL PRODUCTION.
Mohammady, N. G., Alexandria University, Egypt, nagwa_phyco@yahoo.com
Lindell, S. R., Marine Biological Laboratory, USA
Reddy, C. M., Woods Hole Oceanographic Institute, USA
Carmichael, C. A., Woods Hole Oceanographic Institute, USA
Lau, C. L., The Chinese University of Hong Kong, China

A laboratory study was carried out to evaluate the influence of the waste (as an integral component of the basal growth media, 1: 9 V/V) on the amounts of algal lipids accumulated in three microalgae *Tetraselmis chuii*, *Chaetoceros muelleri* and *Isochrysis* sp. (clone c Iso). The gravimetric data showed an obvious increase of total lipids in the treated cultures 13.16, 1.65 and 1.8 times for *T. chuii*, *C. muelleri* and *Iso*. sp. respectively. On the other hand, the algal oil increased 16, 1.73 and 5 times in the same order, compared to the none treated cells. Fatty acid methyl esters of the examined strains are dominated by C14:0, C16:0, C16:1, C18:0, C18:1, C18:2, C18:3, C18:4 and C22:6. The influence of the waste on the fatty acid pool showed a significant variation in the amounts of both total lipids and oil fatty esters. In addition, some fractions have disappeared, while others have been newly synthesized in the treated cells. The results demonstrated that the application of sewage sludge could enhance the accumulation of algal lipid and improve the quality of biofuel produced.

P2. FIRST REPORTS OF *HALOPELTIS* (RHODOPHYTA, RHODYMENIACEAE) FROM THE NON-TROPICAL NORTHERN HEMISPHERE: PROCUMBENT SPECIES FROM BERMUDA, NORTH CAROLINA AND KOREA

Schneider, C. W., Trinity College, USA, cschneid@trincoll.edu
Freshwater, D. W., University of North Carolina Wilmington, USA, freshwaterw@uncw.edu
Saunders, G. W., University of New Brunswick, Canada, gws@unb.ca

Using genetic sequencing (COI-5P, LSU, *rbc*L) to elucidate their phylogenetic positions and then morphological markers to distinguish each from existing species, three procumbent species, including two novel taxa, from warm temperate Northern Hemisphere waters are added to the recently resurrected genus *Halopeltis* J. Agardh: *H. adnata* (Okamura) comb. nov. from Korea, *H. pellucida* sp. nov. from Bermuda and *H. willisii* sp. nov. from North Carolina, USA. Prior to these reports, the genus was confined to the Southern Hemisphere and tropical equatorial waters of the Northern Hemisphere although the latter records lack molecular confirmation. These three additional species join the six known species presently residing in *Halopeltis*.

P3. EFFECTS OF EUTROPHICATION AND TROPHIC STRUCTURE ALTERATION ON ESTUARINE PHYTOPLANKTON GROWTH AND COMMUNITY COMPOSITION

Cira, E., Dept. of Life Sciences, Texas A&M University-Corpus Christi, USA, ecira@tamucc.edu
Wetz, M., Dept. of Life Sciences, Texas A&M University-Corpus Christi, USA
Kimmel, D., Dept. of Biology, East Carolina University, USA
Paerl, H., Institute of Marine Sciences, University of North Carolina-Chapel Hill, USA

Because estuarine phytoplankton growth is controlled largely by nitrogen availability, the amount and form of nitrogen in estuaries has been implicated as a primary control upon eutrophication in these systems. However, recent studies have shown that in addition to nitrogen availability, trophic cascades and relaxation of grazing pressure may be critically important for phytoplankton bloom formation in estuaries. With a goal of better understanding how these bottom-up and top-down anthropogenic factors interact to control estuarine phytoplankton growth and community composition, we conducted experimental manipulations of nitrogen and grazing pressure on mesohaline phytoplankton communities from North Carolina's Neuse River Estuary. During each of three sampling events (June 2011, August 2011, March 2012), we controlled the quality (organic vs. inorganic) and quantity of nitrogen available to natural phytoplankton assemblages, in combination with reducing grazing pressure on these assemblages through zooplankton removal (filtration). Pigment analysis results suggest differential effects of treatments across phytoplankton groups, but overall, treatments with least grazing pressure and added nitrogen in the organic form showed highest sustained growth. Species-specific responses are currently being verified and expanded through cell enumeration.

P4. SEASONAL PHYTOPLANKTON COMPOSITION AND THE INFLUENCE OF FLOW IN LOWER CHESAPEAKE BAY 1985-2011.

Marshall, H. G., Old Dominion Univ., USA, hmarshal@odu.edu
Egerton, T. A., Old Dominion Univ., USA, tegerton@odu.edu

A major determiner of phytoplankton composition, distribution and abundance in Chesapeake Bay is the timing, degree and duration of flow through this ecosystem. This interaction, plus the influence of flow to other ecological variables results in different multi-year patterns of phytoplankton development. These interactions were analyzed within Chesapeake Bay using a long-term data set (1985-2011) of phytoplankton and water quality parameters. Annual flow rates were used to identify wet and dry years, and to test the effect of flow on water quality and phytoplankton parameters. Wet years had significantly higher concentrations of total nitrogen and chlorophyll, and significantly lower levels of salinity and water clarity than drier years. Diatoms and cryptomonads were more abundant in wet years, with

cyanobacteria densities higher during dry years. All years showed similar seasonal developmental patterns (e.g. diatoms dominant in late winter, early spring; flagellates throughout spring and summer; and cyanobacteria in summer). Future changes in weather patterns will likely affect both the total abundance as well as the makeup of the algal community in the Bay. Supported by the Virginia Department of Environmental Quality.

P5. THE EFFECTS OF LIGHT SLOP CRUDE OIL ON THE GROWTH OF THE DIATOM *SKELETONEMA COSTATUM*

Nguyen, N. K., Loyola University New Orleans, USA, wee@loyno.edu
Wee, J. L., Loyola University New Orleans, USA, wee@loyno.edu
Calzada, M. E., Loyola University New Orleans, USA, wee@loyno.edu

A strain of *S. costatum* was isolated from the Lake Pontchartrain basin estuary, LA and aged seawater from the site (salinity = 7.7 ppt) was used to make f/2 culture medium. Oil contamination was introduced to the culture media via emulsification (1:9, 24 hours, 200 rpm). Experimental treatments included uncontaminated f/2, oil-emulsified f/2 and oil-emulsified f/2 diluted with uncontaminated f/2 to produce culture media containing 25%, 50% and 75% of oil-emulsified f/2. In preliminary experiments hydrocarbon chain lengths decreased during the experiment. To observe growth of cultures, OD730 readings were recorded on alternate days for ten days. The slopes of the growth curves were compared among the different experimental treatments from day 4 to day 10. Uncontaminated f/2, 25% and 50% treatments showed similar growth curves; the 75% treatment exhibited inhibited growth before recovering at day 4, while no growth occurred in the undiluted, oil-emulsified f/2 treatment. The slopes for the uncontaminated f/2 culture media and 25% treatment were the same ($p < 0.001$), suggesting that oil contamination in the 50% treatment can inhibit growth.

P6. ACETOLYSIS AS A SCREEN FOR DEGRADATION-RESISTANT MODERN ALGAL STRUCTURES FOR PALEONTOLOGICAL COMPARISONS

Graham, L. E., University of Wisconsin-Madison, USA, lkgraham@wisc.edu
Lewis, L. A., University of Connecticut, USA, louise.lewis@uconn.edu
Wellman, C. H., University of Sheffield, United Kingdom, c.wellman@sheffield.ac.uk
Taylor, W. A., University of Wisconsin-Eau Claire, USA, taylorwa@uwec.edu
Cook, M. E., Illinois State University, USA, mecook1@ilstu.edu

The fossil remains of early eukaryotes often occur as degradation-resistant bits and pieces whose taxonomic affinities can be difficult to assign. Standard acetolysis–boiling organic samples in a mixture of acetic anhydride and concentrated sulfuric acid for at least half an hour–of modern bryophytes and fungi has revealed the occurrence of chemically resistant cells and tissues that can be compared with such microfossils. We investigated the acetolysis-resistance of: 1) modern cladophoraleans and xanthophyceans for which paleoanalogues 750 million years or more in age have been described, 2) communities of eukaryotic and prokaryotic algae cultured from sediments collected from water bodies located in modern extreme terrestrial environments that serve as models of early terrestrial habitats, and 3) filamentous cyanobacteria that produce specialized cells, some forms of which have been described from the fossil record. Collections of the xanthophycean *Vaucheria* and the chlorophycean *Oedogonium* were remarkably resistant to decay and acetolysis, consistent with previous observations made of structurally similar remains in the fossil record. A database of images representing such acetolysis remains is proposed to aid the interpretation of ancient microfossils.

P7. CHANGES IN ACTIN MICROFILAMENT REORGANIZATION AND OXYGEN EVOLUTION IN CULTURED *SYMBIODINIUM* AS A RESPONSE TO LIGHT AND LATRUNCULIN TREATMENT

Villanueva, M. A., Instituto de Ciencias del Mar y Limnología, Unidad Académica de Sistemas Arrecifales, UNAM, Mexico, marco@cmarl.unam.mx
Priouzeau, F., Univ. de Nice-Sophia Antipolis, UMR 7138SAE, Equipe , France, Fabrice.PRIOUZEAU@unice.fr
Barnay-Verdier, S., Univ. de Nice-Sophia Antipolis, UMR 7138SAE, Equipe , France, stephanie.barnay-verdier@upmc.fr
Furla, P., Univ. de Nice-Sophia Antipolis, UMR 7138SAE, Equipe , France, Paola.Furla@unice.fr

The actin cytoskeleton is a dynamic structure that provides an interactive platform for organelles and cellular components such as membranes, intermediate filaments and microtubules. It also serves as track for membranes and vesicles that move via myosin. The organization of the actin cytoskeleton in *Symbiodinium* and its multiple membrane interactions are so far unknown but they must include interactions with chloroplast membranes. Thus, we tested the oxygen evolution of these cells grown in culture under various light conditions in the presence of latrunculin, an actin microfilament disrupting agent. Upon latrunculin addition, the oxygen production decreased, compared to non-treated cells. However, this was not observed after long-term latrunculin treatment. Observation of the actin microfilament network with fluorescent phalloidin revealed changes in the network organization depending on the light conditions and confirmed its disorganization after latrunculin treatment. These data suggest that the cytoskeleton is important for the normal photosynthetic function but its disruption produces only an immediate and transient effect on oxygen production that can be reversed over time.
M.A. Villanueva was supported by a PASPA sabbatical fellowship from DGAPA-UNAM.

P8. FRESHWATER RHODOPHYTES OF SOUTH CAROLINA

Hollingsworth, E. K., South Carolina Department of Health and Environmental Control, USA, hollinek@dhec.sc.gov
Vis, M. L., Ohio University, USA, vis-chia@ohio.edu

In development of the benthic algal assessment program for the state of South Carolina, approximately 170 samples (primarily diatoms) were collected. During visits to these stations, rhodophytes were observed in numerous locations. South Carolina has five Level III Ecoregions, providing a wide variety of stream habitat. The freshwater reds seemed to be particularly abundant in the Southeastern Plains and Piedmont regions. *Batrachospermum macrosporum*, which appears to prefer blackwater, sandy bottom streams, was most often encountered. *Tuomeya americana* was also abundant, but occurred in more diverse habitats. *Batrachospermum boryanum* was observed in rocky, clearwater Piedmont streams. *Batrachospermum helminthosum* was collected in three ecoregions (Piedmont, Southeastern Plains and Middle Atlantic Coastal Plain) spanning a variety of stream types. The only non-batrachospermalean taxon, *Boldia erythrosiphon*, was collected in a single stream. Both *Tuomeya* and *Boldia* are restricted to eastern North America. In total, nine different taxa were found throughout the state in a wide variety of stream habitats.

P9. A PRELIMINARY CONCEPTUAL DESIGN OF AN ALGAL BIOMASS FACILITY ON AN INDUSTRIAL SITE

Henley, W. J., Oklahoma State Univ., USA, bill.henley@okstate.edu
Novoveská, L., Oklahoma State Univ., USA, lucie.novoveska@okstate.edu
Holland, S., Oklahoma State Univ., USA
Mukherjee, A., Oklahoma State Univ., USA
Noland, M., Oklahoma State Univ., USA
Porec, S., Oklahoma State Univ., USA
Wilson, T., Oklahoma State Univ., USA

Several growing global environmental issues have defied solution. Fossil fuel supplies, particularly petroleum, cannot indefinitely keep pace with growing demand, causing geopolitical and economic instability. Associated CO_2 emissions are a major contributor to climate change. Increased eutrophication causes harmful algal blooms and hypoxic dead zones. Regional fresh water supply is often inadequate to meet municipal and agricultural needs. Based on theoretical productivity and other advantages, algae are the most promising feedstock for biofuels. Production of vast quantities of algal biomass can simultaneously address all of the aforementioned environmental and economic problems if the facilities are co-located with sources of nutrient-rich wastewater and CO_2. We have identified an industrial site in Oklahoma that has large on-site or nearby sources of CO_2, N-rich process water and P-rich animal waste. We describe preliminary conceptual design and basic life cycle analyses using realistic algal productivities from the literature. Nutrient demand and potential CO_2 absorption rates are the primary foci, using a hybrid system of open raceways continuously fed by bioreactors.

P10. EFFECTS OF ELEVATED CO2 LEVELS ON ESTUARINE PHYTOPLANKTON GROWTH AND TAXONOMIC COMPOSITION

Marshall, K. M., Texas A&M, University, Corpus Christi, USA, krista.marshall@tamucc.edu
Wetz, M. S., Texas A&M, University, Corpus Christi, USA, michael.wetz@tamucc.edu

Atmospheric CO2 levels are rising at an unprecedented rate, yet relatively little is known about how this may affect aquatic primary producers. Current studies suggest that freshwater phytoplankton can be carbon-limited and their growth and photosynthesis stimulated by CO2 enrichment, while marine phytoplankton are generally not. Given that estuaries lie at the interface of these two systems, response of estuarine phytoplankton to CO2 enrichment may vary along a salinity gradient. This study investigates the response of estuarine phytoplankton assemblages to increased CO2 levels. Samples have been collected seasonally at four sites along a salinity and eutrophication gradient (oligohaline, mesohaline upstream and downstream of a wastewater treatment plant outflow, polyhaline) to elucidate the effect of CO2 enrichment on estuarine phytoplankton growth and taxonomic composition. Laboratory manipulations involve incubation at ambient (~390 ppm) and "high" (~750ppm) CO2 treatments. Results from experiments conducted in summer and fall show no stimulation of chlorophyll a at high CO2. Effects on phytoplankton biomass and community composition will be further verified through CHN analyses and cell counts.

P11. PALATABILITY OF LIVING AND DEAD DETACHED ANTARCTIC MACROALGAE TO CONSUMERS

Amsler, C. D., University of Alabama at Birmingham, USA, amsler@uab.edu
McClintock, J. B., University of Alabama at Birmingham, USA
Baker, B. J., University of South Florida, USA

Macroalgae form impressive undersea forests along the western Antarctic Peninsula and their carbon has been traced to numerous groups of shallow water consumers. However, the vast majority of the standing macroalgal biomass is represented by chemically defended algae which are not readily consumed by grazers, raising the question of how the carbon reaches the consumers. We examined how palatability to grazers of one of the most abundant brown algae, *Desmarestia anceps*, is impacted by detachment and death when transplanted within algal drift in nature. There were no significant changes in the palatability of detached, live algae over the 43 weeks of the experiment and amphipod feeding rates were never significantly different from zero. Other algae were killed by three weeks of exposure to anaerobic conditions. Amphipod consumption rates on dead macroalgae were significantly different from zero and from corresponding live material at each weekly sample for four weeks. Repeated measures ANOVA revealed a significant increase in consumption over this time period. Dead algae remaining after 43 weeks were insufficient for bioassays.

P12. GRATOL: ASSEMBLING THE GREEN ALGAL TREE OF LIFE

Hall, J. D., Academy of Natural Sciences of Drexel University, USA, hall@ansp.org
Karol, K. G., The New York Botanical Garden, USA, kkarol@nybg.org
Lewis, L. A., University of Connecticut, USA
Lewis, P. O., University of Connecticut, USA
Fucikova, K., University of Connecticut, USA
Hu, Z. M., University of Alabama, USA
Wysor, B., Roger Williams University, USA
Lopez-Bautista, J. M., University of Alabama, USA
Cooper, E., University of Maryland, USA
Delwiche, C. F., University of Maryland, USA

Green algae and land plants comprise one of the most structurally and taxonomically diverse groups of eukaryotes. There are more than 14,000 species of green algae and a few hundred thousand species of land plants. Green plants are important primary producers in terrestrial and aquatic ecosystems. They are also important sources of food and fuel throughout the world. Although green algae have been the subject of numerous morphological and molecular phylogenetic studies, many of the important relationships remain controversial: the sister taxon to land plants; placement of early-branching lineages; and relationships among three large green algal clades, Chlorophyceae, Trebouxiophyceae and Ulvophyceae. Assembling a robust phylogeny for the green plants is critically important to our understanding of algal evolution and the origin of land plants.

The Green Algal Tree of Life (GrAToL) project is a collaborative research effort involving six PIs at five different institutions. More than 25 postdocs, collaborators and students have contributed time and expertise to the GrAToL project. The overall goal of the project is to provide a molecular phylogenetic framework for the study of systematics and evolution in the green algae. Our sequencing efforts involve traditional targeted gene sequencing, as well as next generation sequencing of organellar genomes and transcriptomes of selected taxa. A public website has been developed (www.gratol.org) that provides information about the project, green algae and outreach efforts at schools and science festivals. We will present an update on the project's progress, the methods being used and some challenges facing us as we continue to assemble the Green Algal Tree of Life.

P13. PRESERVING ALGAE ON MICROSLIDES USING EUPARAL

Hall, J. D., Academy of Natural Sciences of Drexel University, USA, hall@ansp.org
McCourt, R. M., Academy of Natural Sciences of Drexel University, USA, mccourt@ansp.org

The preparation of permanent voucher specimens of microalgae is critically important as a means of documenting their morphological characteristics. Permanent vouchers of microalgae allow future researchers to examine previously studied materials. However, most preservation methods in general use are either only semi-permanent, with a much shorter proven shelf life than other types of vouchers (e.g., herbarium sheets), or result in serious distortion of the structural characteristics. Methods for making permanent slides of microalgae using Euparal were described many years ago, but the medium is not widely used by phycologists. By modifying existing protocols, we were able to prepare permanent voucher specimens of microalgae using Euparal that leave the cytoplasmic characteristics intact. We also explored different fixatives and dehydration schedules for the preparation of optimal permanent mounts. We found that glutaraldehyde was the best fixative for the preservation of fine structure. We also found a dehydration schedule using ethanol that caused little damage to subcellular structures.

P14. SYSTEMATICS OF THE POLYPHYLETIC GENUS *CYLINDROCYSTIS* (ZYGNEMATOPHYCEAE)

Adair, J. C., Drexel University, USA, jca55@drexel.edu

Hall, J. D., Academy of Natural Sciences of Drexel University, USA, hall@ansp.org
McCourt, R. M., Academy of Natural Sciences of Drexel University, USA

Cylindrocystis is a unicellular conjugating green alga (Zygnematophyceae) with bacilliform cells and two asteroid chloroplasts. Recent phylogenetic analyses suggest that the genus *Cylindrocystis* is not monophyletic; moreover one of the *Cylindrocystis* clades also includes *Zygnemopsis* and *Mesotaenium kramstai*. In previous work, too few strains were studied to create a comprehensive phylogeny of the genus *Cylindrocystis*. Previous morphological studies of *Cylindrocystis* focused on sexuality, spore morphology and vegetative characteristics. We tested the hypothesis that morphological characteristics are correlated with a two-gene phylogeny of *Cylindrocystis*. We began by preparing cultures of available strains and placing them under conditions that induce sexual reproduction. Light microscopy was used to examine the reproductive and vegetative characteristics. We attempted to sequence *rbc*L and *atp*B from all strains. We will use the resulting phylogeny to determine the relationships among the strains of *Cylindrocystis* and to infer the evolution of their vegetative and reproductive characteristics. Preliminary results from our investigation will be presented.

P15. EFFECTS OF LIGHT INTENSITY AND TEMPERATURE ON *ETTLIA OLEOABUNDANS*: BALANCING BIOMASS WITH LIPID YIELD AND QUALITY

Yang, Y., Worcester Polytechnic Institute, USA, yyang@wpi.edu
Mininberg, B., Worcester Polytechnic Institute, USA
Tarbet, A., Worcester Polytechnic Institute, USA
Weathers, P. J., Worcester Polytechnic Institute, USA, weathers@wpi.edu

The effect of temperature and light intensity on biomass and lipid production was investigated in *Ettlia oleoabundans*. The species grew at 10 °C reaching a biomass yield of > 2.0 g L-1 and FAMEs of 11.5 mg L-1. Highest biomass productivity was at the 15 and 25°C regardless of light intensity. Although growth was low at 35°C, lipid content was 10.37 mg L-1, with oleic acid dominating which is one of the desirable biodiesel precursors, but without nitrate depletion. In a two-phase temperature shift experiment at two nitrate levels, after 21 days at 15°C, cells were shifted to 35°C for 8 days. Although growth continued after shifting to the higher temperature, lipid productivity per cell was less than that in the 35°C culture, again without nitrate depletion. This study showed that this species grows well at low temperatures and light intensity, conditions that with further study may prove useful for production of oil from *E. oleoabundans*.

P16. HETEROGENEOUS DISTRIBUTION OF THE ICHTHYOTOXIC DINOFLAGELLATE *GAMBIERDISCUS* SPP. ON MACROALGAE IN THE COASTAL WATERS OF JEJU ISLAND, KOREA

Jang, B., Department of Oceanography, Kunsan National University, Republic Of Korea, maria1728@kunsan.ac.kr
Kim, H., Department of Marine Biotechnology, Kunsan National University, Republic Of Korea, mudskip@kunsan.ac.kr
Park, J., Saemangeum Marine Environmental Reseach Center Researcher, Kunsan National University, Republic Of Korea, cyanopark@hanmail.net
Yih, W., Department of Oceanography, Kunsan National University, Republic Of Korea, ywonho@kunsan.ac.kr

First report on the occurrence epiphytic dinoflagellate genera in Korea (Kim et al. 2011) was followed by Jeong et al. (2012) on *Coolia* species. Here we estimated the abundance of the *Gambierdiscus* spp. (GAMBI) from samples collected in Jeju coasts when water temperature was lowest during 2011. GAMBI exhibited quite heterogeneous distribution among stations and substrate macroalgal species. At Kang-jung mean abundance of GAMBI in February was 24±6 cells g-1 *wwt* (CGT) on 4 macroalgal

species while 14±2 CGT in April on 2 substrate algae. The maximum abundance at Kang-jung was 32 CGT on *Cladophora wrightiana* in February, 4734 on *Hydroclathrus clathratus* in April at Seong-san, 78 on *Colpomenia sinuosa* in April at Namwon, 9 on articulated coralline algae in April at Shin-do, 30 on *Undaria pinnatifida* in February at Aeh-wol, and 57 on *Grateloupia elata* in February at Joe-chun. GAMBI was not observed from samples collected at Shin-do in February or at Joe-chun in April while very abundant at Seong-san in both months. The abundant GAMBI at Seong-san might be favored by 'tolerable' water temperature.

P17. A RE-ASSESSMENT OF THE DIATOM COMMUNITIES IN THE NORTHEASTERN GULF OF MEXICO IN RESPONSE TO THE DEEPWATER HORIZON OIL SPILL

Adhikari, A., Valdosta State University, USA, aadhikari@valdosta.edu
Malik, H. I., Valdosta State University, USA, himalik@valdosta.edu
Nienow, J. A., Valdosta State University, USA, jnienow@valdosta.edu

We are currently re-assessing the status of the diatom communities in the Northwestern Gulf of Mexico in response to the recent Deepwater Horizon oil spill, with an emphasis on Choctawhatchee, Pensacola and Perdido Bays. Net plankton and sediment samples were collected from nine stations at bi-monthly intervals between September, 2010, and May, 2011. Cleaned samples were analyzed with respect to species composition and relative numbers. So far, we have documented the presence of more than 150 species belonging to at least 50 genera. The dominant taxa in terms of both numbers of species and relative abundance were the genera *Chaetoceros, Amphora, Cocconeis, Mastogloia, and Nitzschia*; the presence of the latter four genera in both net and sediment samples is consistent with the shallow nature of the sampling sites. No impact of the oil spill on community structure could be detected. A small number of abnormal valves were observed in the samples. However, because of their relatively low numbers (less than 0.1% of the total valves counted), their presence could not be directly attributed to the oil spill.

P18. GENETIC TRANSFORMATION AND MOLECULAR CHARACTERIZATION OF A LECTIN, BPL-3, FROM *BRYOPSIS PLUMOSA* USING *CHLAMYDOMONAS REINHARDTII* AS AN EXPRESSION SYSTEM

Jung, M. G., Department of Biology, Kongju National University, Republic Of Korea, jwhan@kongju.ac.kr
Han, J. W., Department of Biology, Kongju National University, Republic Of Korea, fop9440@kongju.ac.kr
Han, J., Department of Biology, Kongju National University, Republic Of Korea, jhhan@kongju.ac.kr
Kim, G. H., Department of Biology, Kongju National University, Republic Of Korea, ghKim@kongju.ac.kr

A novel lectin, BPL-3, was isolated and characterized from *Bryopsis plumosa*. The BPL-3 showed specificity to N-acetyl-D-galactosamine as well as N-acetyl-D-glucosamine. The full length sequence of the cDNA encoding this lectin was obtained using cDNA library and the sequence was analyzed. To examine carbohydrates binding domains, genetic transformants were obtained using *Chlamydomonas reinhardtii* as an expression organism. Codon optimized BPL-3 cDNA was synthesized and was inserted into pCr102 expression vector with *psa*D promoter and introduced to *Chlamydomonas* genome using glass bead method. A hygromycine resistance gene was used for the selection maker. Transformation efficiency was high (3012 colonies/108 cells) and about 90% of transformants had BPL-3 gene in their genome. The cells transcribed high-level of BPL-3 mRNA. To assess the genetic load of transformation to the general performance of *Chlamydomonas reinhardtii* cells the transformants were grown in bioreactors and their growth rate was compared with the original strain. The recombinant BPL-3 protein was purified using chromatography method and the structural characteristics were discussed.

P19. GENE EXPRESSION WITHOUT CELL MEMBRANE: COMPARATIVE ESTS ANALYSIS OF THE REGENERATING PROTOPLASTS OF *BRYOPSIS PLUMOSA*

Chah, K., Department of Biology, Kongju National University, Republic Of Korea, kyeonghwacha@naver.com
Han, J. W., Department of Biology, Kongju National University, Republic Of Korea, fop9440@kongju.ac.kr
Klochkova, T. A., Department of Biology, Kongju National University, Republic Of Korea, algae8504@hotmail.com
Kim, G. H., Department of Biology, Kongju National University, Republic Of Korea, ghkim@kongju.ac.kr

When multinucleate giant cells of the green alga *Bryopsis plumosa* are injured, the protoplasm is extruded from the cells and can generate spontaneously numerous new cells in seawater. The cell organelles aggregate rapidly in seawater and become covered with a gelatinous envelope within 15 min. A lipid-based cell membrane developed inside the gelatinous envelope about 12h after wounding. To study the gene expression during the regeneration of cell membrane, three large EST databases were constructed using pyrosequencing. The assembled data for 6h after protoplast regeneration included 12,527 contigs (36,589 singletons), 12h after protoplast regeneration - 9,691 contigs (33,565 singletons), and vegetative plants - 7,896 contigs (28,893 singletons). GO analysis showed several stage-specific gene groups which are involved in various cellular processes including antioxidative activity, signaling process and photosynthesis. Comparative analysis of ESTs databases using PESTAS software revealed groups of genes which were newly expressed during the regeneration of cell membrane. Interestingly, the genes involved in cellular lipid and polysaccharide catabolic process and glycerolipid biosynthetic process were expressed at 6h after protoplast regeneration. At 12h after protoplast regeneration, the genes involved in glycerolipid metabolic process and signaling pathways were specifically expressed. Microarray analysis was also carried out on the stage-specific genes during protoplast regeneration. Our results suggest that there are specific signal pathways which turn on and off at each stage of protoplast regeneration in *Bryopsis plumosa*.

P20. DEVELOPMENT OF A FUNGICIDE FOR RED ROT DISEASE AND CHYTRID BLIGHT OF *PORPHYRA* SPP.

Kim, M., Department of Biology, Kongju National University, Republic Of Korea, kmh0309@kongju.ac.kr
Shim, J., Department of Biology, Kongju National University, Republic Of Korea, matthew80@kongju.ac.kr
Shin, Y., Department of Biology, Kongju National University, Republic Of Korea, yunju0722@kongju.ac.kr
Klochkova, T. A., Department of Biology, Kongju National University, Republic Of Korea, algae8504@gmail.com
Kim, G., Department of Biology, Kongju National University, Republic Of Korea, ghkim@kongju.ac.kr

The red rot disease and chytrid blight caused by fungal pathogens, *Pythium porphyrae* and chytrids, respectively, are serious problems in *Porphyra* farms of East Asia. However, an effective treatment for these diseases has not yet been developed because two difficult premises should be fulfilled; to be practical fungicide for *Porphyra* farming 1) the chemicals should be okay to be dumped directly into open seawater 2) the treatment time and the amount of fungicide should be minimal. Immersing the cultivation nets in acidic (pH 2-3) solution is commonly used treatment for these diseases but it is not only ineffective but also unfriendly to the environment because serious amount of heavy metals dissolved in the acidic solution may be dumped to the seawater. To develop non-acidic fungicide various food preservatives were tested for the infectivity of *Pythium porphyrae* and *Olpidiopsis* spp. Among them two salts, Ca(C2H5COO)2 and Na2S2O5, were most effective in preventing infection of the fungi. When the

Porphyra blades were incubated in 10 mM solution of Ca(C2H5COO)2 and Na2S2O5 the fungal infection stopped completely. When the *Porphyra* blades were immersed to 0.1 M Ca(C2H5COO)2 for 30 sec prior to the inoculation of *Pythium porphyrae* the infection rate dropped to 5.86% of control in three days. The same treatment could also reduce the growth of fungal hyphae (14.3 % of control) on infected *Porphyra* blades. However, Ca(C2H5COO)2 showed no effect on survival and binding of the zoospores while 0.05 M of Na2S2O5 could kill 99% of zoospores. A combined treatment of Ca(C2H5COO)2 and Na2S2O5 is proposed as a new method to treat red rot disease and chytrid blight in the field.

P21. EXPRESSION OF THE PHOTOSYNTHESIS GENES IN THE HETEROTROPHIC DINOFLAGELLATE *PFIESTERIA PISCICIDA*

Kim, S. H., Department of Biology, Kongju National University, Republic Of Korea, rosyrouge_@kongju.ac.kr
Moon, K. H., Department of Biology, Kongju National University, Republic Of Korea, khmoon@kongju.ac.kr
Han, J. H., Department of Biology, Kongju National University, Republic Of Korea, jhhan@kongju.ac.kr
Han, J. W., Department of Biology, Kongju National University, Republic Of Korea, fop9440@kongju.ac.kr
Kim, G. H., Department of Biology, Kongju National University, Republic Of Korea, ghkim@kongju.ac.kr

Pfiesteria piscicida is a heterotrophic dinoflagellate and does not have plastids for photosynthesis. However, *P. piscicida* grows much faster when the preys were given under the high light condition. To examine possible kleptoplastidy and horizontal gene transfer, we analyzed a large-scale EST database obtained from 454 pyrosequencing. Although *P. piscicida* does not have any sub-cellular structure assignable as plastids most of the genes involved in Calvin cycle were expressed in mRNA level. Some genes of photosynthesis associated pathways including chorismate pathway and starch metabolism were also detected in the EST database. Phylogenetic analysis on chosen genes suggested that *P. piscicida* have experienced long-term endosymbiosis with several different species and that the acquisition and loss of plastid occurred at least two times. Photosynthesis efficiency was examined using water-PAM after feeding. The enhanced growth of *P. piscicida* does not seem to be the result of kleptoplastidy because the plastids lost photosynthetic ability as soon as they were ingested into *P. piscicida* cells. The ingestion rate of the preys was enhanced under high light condition. Therefore, *P. piscicida* show enhanced growth rate under high light condition not because of the kleptoplastidy but because of the enhanced hunting success.

P22. SYSTEMATICS AND PHYLOGENY OF THE GENUS *PHACUS* (PHACACEAE, EUGLENOPHYCEAE)

Kim, J. I., Chungnam National University, Republic Of Korea, jongim@cnu.ac.kr
Yoon, H. S., Sungkyunkwan University, Republic Of Korea, hwansu@gmail.com
Shin, W., Chungnam National University, Republic Of Korea, shinw@cnu.ac.kr

The photosynthetic euglenoids genus *Phacus* is commonly found in freshwater and characterized by rigid, flat cell shape and numerous small discoid chloroplasts without pyrenoids. Recent taxonomic studies showed unresolved phylogenetic relationships among these taxa. Because of simple morphology and limited available culture strains of *Phacus*, the taxonomic studies have been challenged. To understand species diversity and phylogenetic relationships within the genus *Phacus*, we investigated morphological characters using light microscopy and analyzed a combined nuclear SSU and LSU and plastid SSU and LSU rDNA sequence data from 111 strains. The molecular phylogeny reveals strongly supported nine subclades which is congruent with morphological characters. We propose a new systematic of the genus *Phacus* in this study.

P23. THE COMPLETE MITOCHONDRIAL GENOME OF *PYROPIA HAITANENSIS* CHANG ET ZHENG

Mao, Y. X., Ocean University of China, China, yxmao@ouc.edu.cn
Zhang, B. L., Ocean University of China, China
Kong, F. N., Ocean University of China, China
Wang, L., Ocean University of China, China

The complete mitochondrial genome (mitogenome) of a red alga, *Pyropia haitanensis* Chang et Zheng, a circular-mapping molecule, was determined to be 37,023 bp. The overall AT content of the mitogenome is 69.3%. It contains 54 genes, including 49 conserved genes, four intronic reading frame and an additional free-standing open reading frames. The *rnl* gene and *cox*1 gene are the only two interrupted genes in the mitogenome. All the protein coding genes and ORFs have typical ATG start codon, except for *cox*1 and *cox*2, which contain the unusual GTG and CTG as an initiator codon, respectively. Relative differences are found by comparing the mitogenome of *Py. haitanensis* with that of *Porphyra purpurea*, reenforcing the viewpoint that these two species belong to different genus

P24. ANALYSES OF THE MITOCHONDRIAL AND PLASTID GENOMES IN *TOLYPELLA* A. BRAUN (CHARACEAE, CHAROPHYCEAE)

Pérez, W., The New York Botanical Garden, USA, wperez@nybg.org
McCourt, R. M., Philadelphia Academy of Natural Sciences, USA, rmccourt@gmail.com
Karol, K. G., The New York Botanical Garden, USA, kkarol@nybg.org

Tolypella is one of six extant genera in Characeae, an evolutionarily important group of freshwater green algae with an uncertain phylogenetic relationship to land plants. Organellar genome analyses have recovered Characeae as sister to land plants or to a larger clade that includes other charophycean algae plus land plants. Thus far, mitochondrial and plastid genomes in Characeae have been sequenced for only one species, *Chara vulgaris*. The research presented here is an investigation into the organellar genomes of *Tolypella intricata* and *T. glomerata* that represent the two recognized sections (sections Acutifolia and Obtusifolia). In *T. intricata*, the mitochondrial genome is 78.0 kb and is 13% larger than that of *C. vulgaris* whereas the plastid genome is 164.7 kb and 10% smaller than that of *C. vulgaris*. Preliminary analyses of the mitochondrial and plastid genomes for *T. glomerata* suggest a similar pattern. A comparison of genome architecture as well as phylogenetic relationships based on genes from each organellar genome will be presented as part of a larger study to understand genome evolution and the phylogenetic position of Characeae.

P25. COMPARISONS OF OPEN-COASTAL AND ESTUARINE POPULATIONS OF *PORPHYRA UMBILICALIS* (RHODOPHYTA)

Eriksen, R. L., University of New Hampshire, USA, renee.eriksen@unh.edu
Klein, A. S., University of New Hampshire, USA, anita.klein@unh.edu

Local adaptation is one of the driving forces of evolution, but we are only beginning to understand which genes are responsible in non-model organisms. The genus *Porphyra* (Rhodophyta) contains many species with similar blade morphology, but has recently been split into multiple genera to reflect considerable genetic divergence. Evolutionary innovations in this group are thus not reflected in morphology, but may be expressed in physiological traits related to the environment. *Porphyra umbilicalis* is a stress-tolerant species that lives in the high inter-tidal region of the open-coast in the north Atlantic. An isolated population has also been identified in the Great Bay Estuary System in New Hampshire, USA, and previous research identified 0.1% divergence among these populations in the chloroplast gene *rbc*L. Individuals living in open-coastal or estuarine habitats experience differences in salinity, temperature, and nutrient levels, and local adaptation may enable these populations to persist. EST-SSR assays revealed two distinct haplotypes: the open-coastal population has both haplotypes, while the estuarine population

has only one of those haplotypes. We also consider differences among populations in physiological traits such chlorophyll fluorescence.

P26. A MOLECULAR CHARACTERIZATION OF *ULVA/ENTEROMORPHA* SPECIES IN NORTH CENTRAL GULF OF MEXICO

Melton, J. T., Department of Biological Sciences, The University of Alabama, USA, melto006@crimson.ua.edu
Lopez-Bautista, J. M., Department of Biological Sciences, The University of Alabama, USA, jlopez@bama.ua.edu

Ulva and *Enteromorpha* were once considered to be two separate genera of green algae, but there is reason to question this idea from molecular analyses. Species of *Enteromorpha* were considered monostromatic and tubular, while *Ulva* species are distromatic blades. Species of these green seaweeds are difficult to identify due to morphological plasticity from varying environmental conditions. Recent molecular analyses of these taxa have been reported in areas such as Europe, Australia, and the Pacific coast of the United States, but limited molecular data is available from the Gulf of Mexico. This research is focusing on the systematics of *Ulva*/*Enteromorpha* from the Gulf of Mexico using a multi-gene molecular approach of the plastid-encoded *rbc*L gene and the nuclear-encoded ITS rDNA. Our results are providing a better understanding of these species located within the North Central Gulf of Mexico.

P27. THE EFFECTS OF VARIABLE LIGHT CONDITIONS ON WATER COLUMN DISTRIBUTION AND LIPID SYNTHESIS IN THE PLANKTONIC DIATOM *THALASSIOSIRA WEISSFLOGII*

Smith, C. B., Georgia College and State University, USA, cody.smith@bobcats.gcsu.edu
Manoylov, K. M., Georgia College and State University, USA, kalina.manoylov@gcsu.edu

Diatoms use oil synthesis to accumulate storage products and to regulate buoyancy. This study examined the effects of varying light conditions on the water column distribution and density of the planktonic diatom *Thalassiosira weissflogii*. It was predicted that with a change in a light source, diatoms will change position in the water column and this change can infer oil synthesis and change in buoyancy. In two separate experiments, four genetically identical algal populations were placed under variable top, bottom, mixed or full light availability in triplicate. Tall and thin test tubes were originally used but capillary action prevented proper agitation. Therefore, larger and wider test tubes were used in the second experiment to allow mixing and to ensure active position change of the diatom cells. The results from both studies showed that the *Thalassiosira* settled to the bottom for all treatments and was not suspended in the water column. This is likely a result of cells adhering together in the water column or reproducing fast, becoming heavy and settling to the bottom of the test tube.

P28. HAPLOTYPES OF *BOSSIELLA DICHOTOMA* (CORALLINALES, RHODOPHYTA) ALONG THE WEST COAST OF NORTH AMERICA SHOW A DISTINCT GEOGRAPHIC PATTERN

King, K. A., University of North Carolina, Chapel Hill, U.S. Virgin Isles, kingka@live.unc.edu
Gabrielson, P. W., University of North Carolina, Chapel Hill, USA, drseaweed@hotmail.com

A haplotype analysis of *Bossiella dichotoma* along the west coast of North America was performed using two plastid encoded genes, *rbcL* and *psbA*. A 700 base pair (bp) portion of the *rbcL* gene had nearly twice the number of single nucleotide polymorphisms (SNPs) compared to the 850 bp of *psbA*. A TCS analysis that estimated geneologies from DNA sequence data revealed two major haplotypes, one north of Point Conception, California (CA) and the other south of this location, with Monterey Bay, CA being the only exception by having both haplotypes. All northern haplotypes from Purisima Point, Santa Barbara Co., CA to Crescent City, Del Norte Co., CA contained the same SNPs in both genes. South of Point

Conception *rbcL* and *psbA* SNPs distinguished several unique geographic populations, one in San Diego Co., CA and two in Baja California Norte, Mexico. A site north of Salsipuedes, Baja California Norte had two haplotypes, one of which exhibited a distinctive morphology. The two major *B. dichotoma* haplotypes support the longstanding recognition of Point Conception, CA as the boundary between the Oregonian and Californian biogeographic provinces.

P29. INCORPORATION OF MOLECULAR ANALYSIS IN ASSESSING ALGAL BIODIVERSITY IN THE SOUTHEASTERN UNITED STATES

France, Y. C., Georgia College and State University, USA, ellen.france@gcsu.edu
Geletu, A. Z., Georgia College and State University, USA, abeselom.geletu@bobcats.gcsu.edu
Dominy, J., Georgia College and State University, USA, joseph.dominy@bobcats.gcsu.edu
Manoylov, K., Georgia College and State University, USA, kalina.manoylov@gcsu.edu

Algae represent a large and diverse group of photosynthetic organisms, which serve as primary producer and key environmental indicators. Although traditional assessment of algal diversity relies mainly on morphology, some limitations exist. In this study, we present an approach of combined molecular and morphological assessment taken to assess algal diversity in the aquatic habitats from Savannah River to Lake Sinclair, Georgia. 18S rDNA sequences were amplified via PCR from a total genomic DNA extracted from sediments, and the cloned sequences were analyzed via BLAST for the highest percent identity. The list of taxa was then compared to the taxa identified via microscopy from the same samples. The analysis identified some dominant taxa to species, but the exact matches were less than 1 %. Interestingly sequencing results identified large number of unknown eukaryotic algal sequences, which may indicate the presence of new or cryptic species that may not have been distinguished via traditional morphology.

P30. DEVELOPING BIOINFORMATIC TOOLS TO STUDY ALGAL EPIGENOMES

Wajid, S., Rutgers University, USA, swajid@eden.rutgers.edu
Bhattacharya, D., Rutgers University, USA, Bhattacharya@AESOP.Rutgers.edu
Gross, J., Rutgers University, USA, jeferson.gross@googlemail.com

Comparative genomics, the analysis of and comparison of genomes across species is the primary focus of my undergraduate research. A bioinformatic toolset and workflow for the analysis and exploration of genomic DNA, mRNA-seq data, and small RNA that is currently established for *Cyanophora paradoxa* is being further developed with *Chlamydomonas reinhardtii*. These comparative methods utilize R, a powerful programming language for statistical computing and graphics and the integrated Bioconductor package, an open source project for genome data analysis in R. Contributions to Bioconductor libraries related to comparative genomics and are expected in at least one of the following areas: bioinformatic analysis with genomic and epigenomic sequencing, along with general genetic and molecular studies. Furthermore, the CLC Genomics Workbench will continue to be utilized as the backbone of baseline bioinformatics study, based on its ease of use and reliability. In this poster I will provide examples of the types of tools that are being used to study epigenomic data from *Cyanophora* and *Chlamydomonas* and the resulting output.

P31. STEROL COMPOSITION AND BIOSYNTHETIC GENES OF THE RECENTLY DISCOVERED PHOTOSYNTHETIC ALVEOLATE, *CHROMERA VELIA* (CHROMERIDA), A CLOSE RELATIVE OF *APICOMPLEXANS*

Khadka, M., Middle Tennessee State University, USA, mk3i@mtmail.mtsu.edu
Dodson, J., Middle Tennessee State University, USA, vjd2e@mtmail.mtsu.edu
Leblond, J. D., Middle Tennessee State University, USA

Chromera velia is a recently discovered, photosynthetic, marine alveolate closely related to apicomplexan parasites, and more distantly to perkinsids and dinoflagellates. Because apicomplexans and perkinsids are not known to synthesize sterols *de novo*, but rather obtain them from their host organisms, our objective was to examine the composition of the sterols of *C. velia* to assess whether or not there is any commonality with dinoflagellates as the closest taxonomic group capable of synthesizing sterols *de novo*. Furthermore, knowledge of the sterols of *C. velia* may provide insight into the sterol biosynthetic capabilities of apicomplexans prior to loss of sterol biosynthesis. We have found that *C. velia* possesses two primary sterols, 24-ethylcholesta-5,22E-dien-3β-ol, and 24-ethylcholest-5-en-3β-ol, not common to dinoflagellates, but rather commonly found in other classes of algae and plants. In addition, we have identified computationally three genes, *SMT1* (sterol-24C-methyltransferase), *FDFT1* (farnesyl diphosphate farnesyl transferase, squalene synthase), and *IDI1* (isopentenyl diphosphate Δ-isomerase), predicted to be involved in sterol biosynthesis by their similarity to analogous genes in other sterol-producing eukaryotes, including a number of algae.

P32. THE GENUS *CLADOPHORA* (CLADOPHORALES): AN ECOLOGICAL AND MOLECULAR ASSESSMENT FROM THE ZAPARA ISLAND (ZULIA, VENEZUELA)

Garcia-Soto, G. C., The University of Alabama, USA, gcgarcasoto@crimson.ua.edu
Lopez-Bautista, J. M., The University of Alabama, USA, jlopez@ua.edu
Hu, Z. M., The University of Alabama, USA, hzimin@bama.ua.edu

The Zapara pier (Zulia, Venezuela) represents a great locality to study the effect of environmental constraints on species composition and morphological plasticity. The physical and chemical differences between both sides of this structure allow testing for the conspecificity of the *Cladophora* (Cladophorales, Chlorophyta) species. During a field trip to Zapara Island (February to September 2010), specimens of *Cladophora* were collected on both sides of the pier. The relative abundance was calculated and chemical parameters were measured (salinity, pH, Nitrogen and Phosphorus). Results indicate that based on morphological studies four species are found in the area, *Cladophora vagabunda*, *C. montagneana*, *C. sericea*, and *C. dalmatica*. Samples are being characterized using molecular data of the chloroplast-encoded *rbc*L and the nuclear-encoded D1/D2 LSU rDNA obtained with protocols developed in our laboratory for Cladophorales. Morphological and molecular results are discussed to complement and resolve the complex systematic situation within the *Cladophora* conundrum.

P33. A POISONED RED ALGA - NO SNOW WHITE SLEEPING FAIRY TALE FOR ONE ANTARCTIC AMPHIPOD.

Amsler, M. O., University of Alabama Birmingham, USA, mamsler@uab.edu
Amsler, C. D., University of Alabama Birmingham, USA, amsler@uab.edu
Aumack, C. F., Lamont-Doherty Earth Observatory, USA, caumack@ldeo.columbia.edu
McClintock, J. B., University of Alabama Birmingham, USA, mcclinto@uab.edu
Baker, B. J., University of South Florida, USA, bjbaker@usf.edu

Shallow-water benthic communities along the western Antarctic Peninsula support dense forests of large, mostly chemically defended macroalgae and dense assemblages of macroalgal-associated amphipods. These are thought to exist together in a community-wide mutualism. The amphipods are of benefit to the macrophytes by consuming epiphytes and themselves benefit from the association since they are less likely to be consumed by omnivorous fish. The amphipod *Paradexamine fissicauda* is an exception as it is able to consume some but not all species of chemically defended red macroalgae including *Plocamium cartilagineum*, one of the most strongly deterrent algae in the community in bioassays with other species. When *P. fissicauda* was maintained for two months in aquaria with nothing but *P. cartilagineum* to consume, feeding rates on *P. cartilagineum* increased 20-fold relative to initial rates, suggesting that the amphipods are able to increase the production or efficiency of the physiological mechanisms by which they tolerate the alga's chemical defenses. Such amphipods are also significantly less palatable to

omnivorous fish than amphipods fed non-defended algae, suggesting they may sequester algal defensive metabolites for their own protection.

P34. MONO- AND DIGALACTOSYLDIACYLGLYCEROL COMPOSITION OF DIATOMS: A MODERN INTERPRETATION USING POSITIVE-ION ELECTROSPRAY/MASS SPECTROMETRY/MASS SPECTROMETRY

Dodson, V. J., Middle Tennessee State University, USA, vjd2e@mtmail.mtsu.edu
Leblond, J. D., Middle Tennessee State University, USA, jleblond@mtsu.edu

Diatoms are one of the largest groups of primary producers in the oceans, yet despite their environmental importance little is known about their chloroplast lipid biochemistry. Previously, Yan et al. (2011) found *Skeletonema* species to contain primarily C16/C16 and C20/C16 forms of mono- and digalactosyldiacylglycerol (MGDG and DGDG, respectively). We seek to relate their study to other diatoms, both in the Centrales and Pennates, with particular focus on the marennine-producing pennate diatom, *Haslea ostrearia*. To this end, the composition and positional distribution of fatty acids of MGDG and DGDG were examined using positive-ion electrospray/mass spectrometry (ESI/MS). Two centric diatoms, *Skeletonema costatum* and *Thalassiosira weissflogii*, and the pennate diatom, *Phaeodactylum tricornutum*, contained primarily C20/C16 (sn-1/sn-2) and C16/C16 forms of MGDG and DGDG. The pennate diatoms, *Haslea ostrearia* and *Navicula perminuta*, contained primarily C18/C16 or C18/C18 forms of MGDG and DGDG, lacking the C20/C16 forms seen in the others, and indicating a previously unrecognized fatty acid diversity in diatom MGDG and DGDG.

P35. ENHANCING LIPID PRODUCTION IN THE MARINE MICROALGA *DUNALIELLA* THROUGH ENVIRONMENTAL STRESSORS

Mixson, S. M., North Carolina State University, USA, smmixson@ncsu.edu
Burkholder, J. M., North Carolina State University, USA, joann_burkholder@ncsu.edu

We assessed 13 strains of *Dunaliella* within four species, using a modified technique with fluorescent Nile Red stain to rapidly screen cultures for neutral lipid content. Several strains with high growth and high lipid production were selected for further efforts to enhance lipid production using environmental stressors such as high salinity, low nitrogen, high pH, and continuous light. Thus far, high-salinity stress has yielded the maximum total fatty acid (FA) content (up to ~65% by dry weight) in comparison to controls (~30% total FAs by dry weight). Nitrogen and/or phosphorus limitation, bubbling with CO2, and continuous light (~23%, 10%, and ~33% total FAs by dry weight, respectively) did not enhance lipid production. Preliminary experiments indicate that increasing pH in exponentially growing cultures one day before harvest significantly enhances lipid production (~54% total FAs by dry weight). In addition to increasing total lipids, the elevated pH acts as a flocculating mechanism to facilitate harvesting. Future research can build upon this study to develop and refine technologies to use these lipids from *Dunaliella* as a sustainable source of biofuel.

P36. GENETIC SURVEY OF FRESHWATER RED ALGAE IN INDONESIA AND MALAYSIA

Keil, E. J., Ohio University, USA, ek404609@ohio.edu
Johnston, E. T., Ohio University, USA, ej363707@ohio.edu
Buhari, N., Hasanuddin University, Indonesia
Djawad, I., Hasanuddin University, Indonesia
Lim, P. E., University of Malaysia, Malaysia
Vis, M. L., Ohio University, USA, vis-chia@ohio.edu

Freshwater red algal specimens were collected from Indonesia (Java and Sulawesi) and Peninsular Malaysia. The *rbc*L marker was sequenced for all specimens, combined with sequences from GenBank and analyzed using Maximum Likelihood and Bayesian Inference. Collected specimens represent 12

species in four Rhodophycean orders: the Batrachospermales, Ceramiales, Compsopogonales, and Thoreales. This research provides important information on taxonomic status, evolutionary relationships, and geographic ranges of many freshwater red algal species. The range of *Kumanoa faroensis* and *Nemalionopsis tortuosa* are extended to Indonesia. Malaysian *Balliopsis pinnulata* was sister to Brazilian specimens of *Balliopsis*. *Sirodotia delicatula* did not form a monophyletic clade with South American *S. delicatula* specimens. The Malaysian specimens are most likely the true *S. delicatula* due to proximity to the type location, while the specimens from Brazil are likely an undescribed species. Malaysian specimens previously attributed to *Caloglossa ogasawaraensis* may represent an undescribed species. Additionally, the first tropical collection of *B. arcuatum* was made, and a new species of *Batrachospermum* within the section *Turofsa* may need to be described.

P327. LOW SALINITY TOLERANCE OF *PORPHYRA UMBILICALIS*.

Rankin, J. A., University of Maine, USA, Joseph.Rankin@umit.maine.edu
Manning, J. C., University of Maine, USA, Joshua.C.Manning@umit.maine.edu
Miranda, L. N., University of Maine, USA, Lilibeth.Miranda@umit.maine.edu
Brawley, S. H., University of Maine, USA, Brawley@maine.edu

The red alga *Porphyra umbilicalis* Kützing is an economically important sea vegetable found in the Northwestern Atlantic. Currently, *P. umbilicalis* is the focus of a genome-sequencing project, which has drawn attention to both stress tolerance mechanisms and bacterial associations. Low salinity (4 ppt) treatments against controls in normal seawater (32 ppt) have produced several results, all of which show the strong resilience of *P. umbilicalis* to low salinity. Among the results are the development of callus in some experiments, which produced atypical spores and new blades that matured. In another experiment, the basal areas of blades grown for two weeks in 4 ppt brackish water died but most of the blade surface regained normal color, and blades developed normally with good growth. We have begun analyses of possible bacterial associations that influence the type of recovery, including bacterial readdition experiments.

P38. PANALYSIS OF THE BACTERIAL COMMUNITY ASSOCIATED WITH THE RED MACROALGA *PORPHYRA UMBILICALIS*

Lilibeth, L. N., University of Maine, USA, lilibeth.miranda@maine.edu
Hutchison, K., University of Maine, USA, keithh@maine.edu
Grossman, A. R., Carnegie Institution for Science, USA, argrossman@gmail.com
Brawley, S. H., University of Maine, USA, brawley@maine.edu

Macroalgae harbor bacterial communities whose biodiversity remains largely uncharacterized. Here, we analyzed the bacterial population associated with *Porphyra umbilicalis* Kützing from Schoodic Point, ME using 16S rDNA analyses. Our goals were to examine the composition and seasonal trends of the bacterial community associated with *P. umbilicalis*, determine whether a core group of bacteria exists, and define the bias in the bacterial population on clonal blades of *P.um*.1 (*P. umbilicalis*, JGI genome material) that were initially established in the presence of antibiotics. In this study, *P. umbilicalis* blades (n=5, fall 2010; n=5, winter 2011; n=2, P.um.1) were analyzed by pyrosequencing over two variable regions of the 16S rDNA (V5-V7 and V8-V9). The bacterial taxa present belonged to seven phyla (Actinobacteria, Proteobacteria, Firmicutes, Bacteroidetes, Planctomycetes, Chloroflexi and TM7), with the diversity of bacteria higher on blades in fall 2010 compared to winter 2011. All field and laboratory blades had *Litorimonas, Granulosicoccus* and *Hellea* in their bacterial assemblage; *Haliscomenobacter, Lewinella* and TM7 genera *incertae sedis* were also always present in field blades. Some of these taxa likely provide essential morphogenetic and beneficial nutritive factors to *Porphyra umbilicalis*.

P39. ASSESSING THE PHYLOGENETIC UTILITY OF CHLOROPLAST GENES WITHIN THE HYDRODICTYACEAE (SPHAEROPLEALES, CHLOROPHYCEAE)

McManus, H. A., Le Moyne College, USA, mcmanuha@lemoyne.edu
Baltrusitis, D. M., Le Moyne College, USA, baltrudm@stu.lemoyne.edu
Bigelow, T. M., Le Moyne College, USA, bigelotm@stu.lemoyne.edu
Schaub, J. A., Le Moyne College, USA, schaubja@stu.lemoyne.edu

Molecular phylogenetic studies of the freshwater green algal family Hydrodictyaceae (Sphaeropleales, Chlorophyceae) have revealed hidden genetic diversity and resulted in taxonomic revisions. Historically consisting of four genera, the family now encompasses nine genera. Although progress has been made determining the generic and species relationships within the family utilizing the nuclear 26S rDNA and the chloroplast-encoded *rbc*L genes, further data are necessary to determine generic and species boundaries between cryptic isolates, particularly within two phylogenetic groups of *Pediastrum duplex* that are separated by the morphologically distinct genus, *Hydrodictyon.* Recent studies of the Chlorophyceae indicate the chloroplast-encoded elongation factor Tu (*tuf*A) and photosystem I P700 chlorophyll a apoprotein A1 (*psa*A) genes provide improved species resolution when combined with *rbc*L and/or nuclear gene data. In the present study, the phylogenetic utility of *psa*A and *tuf*A between species of *Pediastrum* is tested and compared with *rbc*L and 26S rDNA sequence data.

P40. *NORRISSIA SETCHELLII* (KYLIN) BALAKRISHNAN AND OTHER RELATED TAXA FROM THE PACIFIC COAST OF NORTH AMERICA: ARCHIVAL SPECIMENS AND DNA ANALYSIS

DePriest, M. S., The University of Alabama, USA, msdepriest@crimson.ua.edu
Wynne, M. J., University of Michigan, USA, mwynne@umich.edu
López-Bautista, J. M., The University of Alabama, USA, jlopez@ua.edu

Norrissia Balakrishnan (Halymeniaceae Rhodophyta), based on *N. setchellii* (Kylin) Balakrishnan, is a monotypic genus of macroscopic red algae known only from the Pacific coast of North America, occurring from central California to British Columbia. This range overlaps with that of another species in the family Halymeniaceae, *Grateloupia postelsii* Parkinson, with a habit that closely resembles that of *N. setchellii*. To address the relationships among these taxa, DNA was extracted from herbarium specimens identified as one of these species or their respective basionyms, including type material for *N. setchellii*. Phylogenetic analysis was executed using the chloroplast-encoded *rbc*L marker amplified by PCR.

P41. NEW RECORDS OF FLORIDEAN MACROALGAE FOR VENEZUELA AND THE CARIBBEAN SEA

Garcia-Soto, G. C., The University of Alabama, USA, gcgarcasoto@crimson.ua.edu
Lopez-Bautista, J. M., The University of Alabama, USA, Jlopez@ua.edu
DePriest, M. S., The University of Alabama, USA, msdepriest@bama.ua.edu

Since Taylor's intensive survey in 1960, the Venezuelan Caribbean has proven to support high macroalgal diversity, especially in red algae. More than 80% of the marine macroalgae of the tropical and subtropical western Atlantic rests in the Caribbean Sea. This fact makes the Venezuelan coast an important contributor to the overall species richness. We recently started a sampling program in a poorly studied area, the Gulf of Venezuela. In this study, we report for the first time *Ceramium filiculum* for the Caribbean Sea based on both morphological and molecular evidence. Also, partial *rbc*L sequences of an unidentified species of *Grateloupia* provide evidence that the name *Grateloupia filicina* as been incorrectly assigned to some specimens in the Venezuelan Caribbean. These and other data point out that this area may represent an unexpected source for new algal records for the Venezuelan Caribbean and the Caribbean Sea.

P42. ENVIRONMENTAL MOLECULAR DIVERSITY OF DINOFLAGELLATES ON THE GREAT BARRIER REEF

Hyman, J. A., University of Maryland, USA, hyman.jake@gmail.com
Concepcion, G. T., University of Maryland, USA, gconcepcion@gmail.com
Delwiche, C. F., University of Maryland, USA, delwiche@umd.edu

Environmental molecular methods, which apply the techniques of molecular biology to naturally occurring populations, have revolutionized microbial ecology. These methods also hold great promise for understanding diversity of algae and other protists, but have not been as widely adopted for the study of eukaryotes as they have been for bacteria and archaea. Taking advantage of an opportunity presented by an undergraduate field trip, we collected a series of five grab samples from onshore open waters close to Lizard Island on the Great Barrier Reef, Queensland, Australia. These 2.4-liter samples were filtered, preserved with Lugol's Solution, and dried with silica gel for transport. Total DNA was isolated from the filters, then the small subunit of ribosomal RNA was amplified with dinoflagellate-specific primers, cloned, and several hundred arbitrarily selected clones were sequenced by Sanger sequencing. Even after 300 clones had been sequenced, the majority of new reads were continuing to yield novel sequences, and a single 2.4-liter sample contained a diversity of Dinoflagellate sequences representing and spanning the full range of dinoflagellate diversity. These findings emphasize the vast protist diversity present in even a minuscule fraction of the Pacific Ocean, and suggest that a combination of methodologies will be important for understanding that diversity.

P43. TOLERANCE TO HYPO-OSMOTIC STRESS AND LOW TEMPERATURE DETERMINES THE SPREAD OF NON-INDIGENOUS *GRACILARIA VERMICULOPHYLLA*.

Kim, J.K., Department of Marine Sciences, Univ. of Connecticut, CT, 06901, U.S.A.
Kovtun, K., Department of Ecology & Evolutionary Biology, Univ. of Connecticut, CT, 06901, U.S.A.
Stainton, R., Department of Ecology & Evolutionary Biology, Univ. of Connecticut, CT, 06901, U.S.A.
Yarish, C. Department of Marine Sciences & Department of Ecology & Evolutionary Biology, Univ. of Connecticut, CT, 06901, U.S.A.

The non- indigenous *Gracilaria vermiculophylla* has been replacing the native species *G. tikvahiae*. It has become the dominant species throughout New England and Long Island Sound. This study is focused on determining the effects of a hypo-osmotic stress and temperature on the growth and survival each *Gracilaria* species. Approximately one centimeter long apical segments from each *Gracilaria* species were cultivated over three weeks at five different salinities, 5, 15, 20, 25, and 30psu and at five different temperatures, 5, 10, 15, 20 and 25ºC. Both salinity and temperature affected the growth of both *Gracilaria* species. The native *G. tikvahiae* did not grow, or even had negative growth rates, at suboptimal conditions (< 20psu and < 20ºC). However, the non-native *G. vermiculophylla* grew equally well in the salinity range of 15-30psu and at temperatures as low as 5ºC. This result suggests that tolerance to the environmental stresses of salinity and temperature are key determinants that are contributing to the spread of the invasive *Gracilaria* species in the embayments and estuaries of New England.

P44. USING PHYLOGENOMICS FOR NUCLEAR LOCI DISCOVERY IN HETEROKONT LINEAGES

Han, G., Arcadia University, USA, ghan@arcadia.edu
Andersen, L., Arcadia University, USA, landersen@arcadia.edu
Niko, L., Arcadia Aniversity, USA, lniko@arcadia.edu
Braun, A., University of Florida, USA, ebraun68@ufl.edu
Phillips, N., Arcadia University, USA, phillipsn@arcadia.edu

The Brown algae are one of the most species rich and ecologically important groups of primary producers in marine environments. Despite their biological importance and recent advances, the evolutionary history of the brown algae remains poorly resolved. One drawback to evolutionary studies in brown algae is the

lack of molecular markers, especially nuclear. To date there are about 10 KB of loci (mostly chloroplast and mitochondrial) for phylogenetic studies within brown algae. Power analyses estimate that ~ 20 Kb are needed to resolve the backbone of the brown algal tree. The goal of this project was to mine available genetic data for nuclear markers to use for phylogenetic studies within brown algae and related heterokonts. Two genetic databases were created, one with all available genetic data for brown algae and Schizocladia and the other with all available genetic data for brown algae and closely related Heterokonts. These two databases were searched for all loci shared among the groups. Resulting gene alignments and Maximum Likelihood trees were evaluated and candidate loci were selected for PCR evaluation using taxa from 7 brown algal orders. Resulting amplicons from positive loci were sequenced to further verify PCR products and evaluate primers. To date, ~100 loci have been screened with 14 positive loci developed. The last step in locus evaluation is to infer evolutionary relationships within brown algae using the locus. Thus far, two of the 14 loci have been evaluated and verified to infer the correct phylogenetic topology. Future work will focus on evaluating the other 12 loci along with screening additional of additional loci from the two databases.

P45. A TASTE OF ALGAL GENOMES FROM THE JOINT GENOME INSTITUTE.

Kuo, A. DOE Joint Genome Institute.
Grigoriev, I., DOE Joint Genome Institute.

Algae play profound roles in aquatic food chains and the carbon cycle, can impose health and economic costs through toxic blooms, provide models for the study of symbiosis, photosynthesis, and eukaryotic evolution, and are candidate sources for bio-fuels; all of these research areas are part of the mission of DOE's Joint Genome Institute (JGI). To date JGI has sequenced, assembled, annotated, and released to the public the genomes of 18 species and strains of algae, sampling almost all of the major clades of photosynthetic eukaryotes. With more algal genomes currently undergoing analysis, JGI continues its commitment to driving forward basic and applied algal science. Among these ongoing projects are the pan-genome of the dominant coccolithophore *Emiliania huxleyi*, the interrelationships between the 4 genomes in the nucleomorph-containing *Bigelowiella natans* and *Guillardia theta*, and the search for symbiosis genes of lichens.

P46. *LEPTOLYNGBYA FERRUGINOSA SP. NOV*., A NOVEL SIDEROPHORIC CYANOBACTERIUM ISOLATED FROM AN IRON-DEPOSITING HOT SPRING.

Stocks, H.S., Department of Biological Sciences, University of North Florida
Verhulst, S.A., Department of Biological Sciences, University of North Florida
Brown, I.I., Jacobs Engineering/NASA Johnson Space Center
Sarkisova, S., Jacobs Engineering/NASA Johnson Space Center
Casamatta, D.A., Department of Biological Sciences, University of North Florida

Cyanobacteria are amongst the most ancient and abundant photooxygenic prokaryotes, yet much of their basic biodiversity, especially from habitats considered to be "extreme", is unknown. Here, we describe a new taxon isolated from an iron-depositing hot spring located in the Great Yellowstone Area employing a polyphasic approach. Morphologically, filaments are typical for *Leptolyngbya sensu lato*, with cells measuring 2.5 µm long to 2.2 µm wide, motile filaments, and peripheral thylakoids. Sheaths were colorless, thick, persistent, and laminated. Nearly complete 16S rDNA gene sequence was compared to the 50 closest sequences as determined by a BLAST search. Maximum Parsimony and Likelihood trees were largely congruent, and placed this taxon into a weakly supported clade with other *Leptolyngbya* taxa, sister to one containing the "true" *Leptolyngbya* as represented by *L. boryanum*. Interestingly, the closest relatives were all from very different habitats to our isolate. The weak bootstrap support is likely a result of depauperate taxon sampling, which may be expected given the highly endemic nature of the isolate (e.g., requires ≥ 40 µM Fe and was viable to 65 ºC). The isolate also was positive for the *nifH*

gene, although the abilityto fix nitrogen has not been studied yet. Given the unique physiology, ecology, and 16S gene sequence data, we propose to recognize this as a new taxon.

P47. LATE PLEISTOCENE GLACIATION AND TECTONIC CONFIGURATIONS INFLUENCED THE BIOGEOGRAPHIC DISTRIBUTION OF *SARGASSUM HORNERI* (FUCACEAE) IN THE NORTHWESTERN PACIFIC

Li, J. J., Institute of Oceanology, Chinese Academy of Sciences, Qingdao, China;
Hu, Z.M., The University of Alabama, Tuscaloosa, AL, USA and Institute of Oceanology, Chinese Academy of Sciences, Qingdao, China;
Shinya, U., Faculty of Science, Niigata University, Japan;
Duan, D.L., Institute of Oceanology, Chinese Academy of Sciences, Qingdao, China;
Lopez-Bautista, J., The University of Alabama, Tuscaloosa, AL, USA.

Pleistocene glacial oscillations and associated tectonic processes are believed to have influenced historical abundances and gradients of organisms in the Asia Northwest Pacific (ANP) Ocean. However, accumulating evidence indicates that factors shaping tempo-spatial population dynamics and distribution patterns of marine taxa vary with biogeographical latitudes, pelagic behavior and oceanographic regimes. Factors affecting genetic connectivity on the littoral macroalga *Sargassum horneri* in the ANP region were analyzed using COX3 and *rbc*L data. Five distinct clades were recovered. A strong signature of biogeographical structure was revealed derived from clade distribution, as clade A is highly homogenized along Chinese marginal seas, whereas clades B-E are discontinuously scattered around the main Island of Japan. This differentiation may reflect a historical glacial isolation in the Northwestern Pacific, which is congruent with the estimates of clade divergence and demographic expansion during the late Quaternary low sea levels. This phylogeographic structure in S. horneri, initially shaped by a late Pleistocene isolation and physical biogeographic barriers, may be complicated by oceanographic regimes and relocating behavior such as oceanic drifting.

P48. *GELIDIUM COREANUM*, *G. JEJUENSIS*, *G. MINIMUM*, AND *G. PROSTRATUM*, FOUR NEW SPECIES OF *GELIDIUM* (GELIDIALES, RHODOPHYTA) FROM KOREA

Kim, K. M., Sungkyunkwan University, Republic Of Korea, 777km@hanmail.net
Hwang, I. K., National Fisheries Research and Development Institute, Republic Of Korea, ikhwang@nfrdi.go.kr
Yoon, H. S., Sungkyunkwan University, Republic Of Korea, hsyoon2011@skku.edu
Boo, S. M., Chungnam National University, Republic Of Korea, smboo@cnu.ac.kr

Gelidium J.V. *Lamouroux* is the largest genus of the order Gelidiales (Rhodophyta) with 123 species distributed globally in tropical, subtropical, temperate, and even some polar regions. *Gelidium* is economically important as food and is one of the most promising agar sources in East Asia. Recently, it has been used for industrial paper pulp production. Here we describe four novel *Gelidium* species from Korea*: G. coreanum sp. nov*. from the eastern and southern coasts, *G. jejuensis sp. nov*. and *G. minimum sp. nov*. from Jeju Island, and *G. prostratum sp. nov*. from the western coast. The species were identified by molecular phylogenies of plastid rbcL and mitochondrial cox1, which were combined with distinct morphological features. Three of these new species (*G. coreanum*, *G. jejuensis*, and *G. prostratum*) formed a monophyletic clade with *G. eucorneum*, *G. vagum*, *G. chilense*, and *G. japonicum*, while *G. minimum* showed a sister group relationship to *G. pristoides*, *G. foliaceum*, *G. microdontium*, and *G. vittatum*. Further detailed morphological observations and life cycle evaluations are necessary to recognize synapomorphic characteristics of all species in each clade.

Author Index- please note that numbers refer to Abstract number in the abstract listing above, not to the page number.

Erhart, S.	T50	Linton, E. W.	T34	Trobajo, R.	T46
Eriksen, R. L.	P25	Lipinska, A.	T8	Twiner, M. J.	T67
Estevez, A.	T46	Litaker, R. W.	T65	Vaccarino, M.	T21
Fang, L.	T59	Liu, J.	T59	Valero, M.	T13
Faust, M. A.	T65	Lopez, P.	T57	Van Damme, E. J.	T8
Fernandez-Garcia, C.	T14	Lopez-Bautista, J.	S1, T19, T29, T35, P12, P26, P32, P40, P41	Van Dolah, F. M.	S16, T4, T43, T67
Filloramo, G. V.	T31	Lowe, R. L.	S6	Vandersea, M. W.	T65
Fleer, V.	T16	Lutzoni, F.	T29	Varela, D. A.	T49
Fox, M. D.	T75	Lyczkowski, E. R.	T50	Verbruggen, H.	T15
France, Y. C.	P29	MacIntyre, H. L.	T47	Verhulst, S. A.	T24, P46
Fredericq, S.	S1, T25, T26, T39	Maggs, C. A.	T32	Villanueva, M. A.	P7
Freshwater, D. W.	T14, T30, P2	Maldonado, M. A.	T49	Villemur, R.	T70
Fucikova, K.	T56, P12	Malik, H.	P17	Vis, M. L.	S1, S9, T5, T9, T51, P8, P36
Fujii, M. T.	T30	Manning, J. C.	P37	Wajid, S.	T44, P30
Furla, P.	P7	Manoylov, K. M.	S8 P27, P29	Wang, J.	T34
Gabriel, D.	T25, T39	Mao, Y. X.	P23	Wang, L.	P23
Gabrielson, P. W.	T14, P28	Maranger, R.	T70	Wang, P.	T68
Garcia-Soto, G. C.	P32, P41	Marin III, R.	S19	Wang, X.	T10
Geletu, A. Z.	P29	Markham, J. E.	T62	Wang, Z.	S19, T67
Gerwick, W. H.	T64	Marshall, H. G.	P4	Warnecke, D.	T62
Graham, L. E.	T17 P6	Marshall, K. M.	P10	Watza, D. G.	T2
Graham, M. H.	T49, T76	Martone, P. T.	T6	Weathers, P.	P15
Graham, M.E.	T17	Mauger, S.	T13	Wee, J. L.	P5
Green, C.	T14	McClintock, J. B.	T61, P11, P33	Wehr, J. D.	T10
Green, M. S.	T29	McCourt, R.	P13, P14, P24	Welch, M. J.	T63
Gross, J.	T44, P30	McManus, H. A.	P39	Wellman C. H.	P6
Grossman, A. R.	P38	Melton, J. T.	P26	Wetz, M.	P3, P10
Guidone, M.	T72	Michaelson, L. V.	T62	Wiegert, K. E.	T2
Guimaraes, N. R.	T38	Mikulski, C. M.	S19, T67	Willems, A.	T15
Guiry, M. D.	T27	Mimendia,A.	T46	Wilson, T.	P9
Gurgel, C. F.	T1, T3	Mininberg, B.	P15	Wilson, W.	S13

Hackett, J. D.	T11	Miranda, L. N.	P37	Wisecaver, J. H.	T11
Hall, J. D.	P12, P13, P14	Misner, I.	T57	Wishkerman, A.	T46
Hall-Spencer, J. M.	T32	Mixson, S. M.	P35	Worthy, C. A.	T62
Hamel, K.	T74	Mohammady, N. G.	P1	Wulfers, T. A.	T48
Han, G.	P44	Monchamp, M.	T70	Wynne, M. J.	P40
Han, J. H.	P21	Moniz, M. J.	T27	Wysor, B.	T14, P12
Han, J. W.	T7, T41, P18, P19, P21	Monroe, E. A.	T67	Yang, E. C.	T55
Han, M.	T68	Moon, K. H.	P21	Yang, Y.	P15
Hanisak, M. D.	T22	Morey, J. S.	T43, T67	Yarish, C.	T23, P43
Hannick, L.	T66	Morris, J. J.	T73	Yih, W.	T69, P16
Hanshew, A.	T17	Mukherjee, A.	P9	Yokoya, N. S.	T38
Harley, C. D.	T6	Muth, A. F.	T76	Yoon, H .S.	S1, S5, T37, T55, P22
Harvery, J. B.	S19	Nakov, T.	T53, T54	York, G. E.	T50
Heesch, S.	T36	Napier, J. A.	T62	Yoshikawa, S.	T18
Heinz, E.	T62	Nelson, W. A.	T30, T36	Young, E. B.	T17
Henley, W. J.	T48, P9	Nguyen, N. K.	P5	Yu, A.	T54
Henríquez, L. A.	T49	Nienow, J. A.	P17	Zaeuner, S.	S5, T40, S62
Hernandez-Gonzalez, M.C.	T49	Niko, L.	P44	Zhang, B. L.	P23
Hernandez-Kantun, J. J.	T32	Noland, M.	P9	Zhang, H.	T45, T66
Himes, J. E.	T6	Norris, J. H.	T25	Zhang, Y.	S19
Holland, S.	P9	Novoveska, L.	T47, T48, P9	Zhuang, Y.	T66
Holland, W. C.	T65	Ohki, K.	T18	Zi-Min, H.	T29
Hollants, J.	T15	Oliveira, E. C.	T38	Zimmer, R. K.	T6
Hollingsworth, E. K.	P8	Oliveria, M. C.	T38	Zinser, E. R.	T73
Homes, M. J.	T65	Paerl, H.	P3	Zulkifly, S. B.	T17
Hommersand, M.	S1, T28	Parham, S.	T14		
Hu, Z. M.	T19, T35, P12, P32	Park, B. S.	T68		
Huisman, J. M.	T1, T3	Park, J.	T69, P16		
Hutchinson, K.	P38	Parker, M. S.	S15		
Hwang, I. K.	T37	Paul, V.	T64		
Hyman, J. A.	P42	Peña, V	T32		